



Animal &
Plant Health
Agency

Salmonella in animals and feed in Great Britain in 2025

September 2026



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Glossary

ABPR	Animal By-Products Regulations
AMR	Antimicrobial resistance
APHA	Animal and Plant Health Agency
BSAC	British Society for Antimicrobial Chemotherapy
CSBO	Control of <i>Salmonella</i> in Broiler Flocks Order
CSPO	Control of <i>Salmonella</i> in Poultry Order
CSTO	Control of <i>Salmonella</i> in Turkey Flocks Order
DT	Definitive Phage Type of <i>S. Typhimurium</i> as described by Anderson et al (1977)
EFSA	European Food Safety Authority
MDR	Multi-drug resistant (resistance to 4 or more of the antimicrobials in the panel tested)
NCP	National Control Programme
NOPT	Not phage typed
PHS	Public Health Scotland
PT	Phage type
RDNC	Reacts with the phages but does not conform to a recognised pattern of lysis

Rough	Rough strains of <i>Salmonella</i> that cannot be serotyped due to autoagglutination
SE	<i>Salmonella</i> Enteritidis
SRUC	Scotland's Rural College
ST	Sequence Type
STM	<i>Salmonella</i> Typhimurium
U	Undesignated. A recognised phage designation with a particular pattern of lysis which has not been included in the definitive typing scheme. For example, U302
UKHSA	UK Health Security Agency
UNTY	A culture which does not react with any of the phages in the typing scheme (phage typing ceased in December 2024 at APHA)
Untypable	A culture which did not produce a result by Whole genome sequencing or phenotypic testing.
Untypable strains	Some cultures may fail to express one or both sets of flagella antigens, and consequently cannot be named. In such cases the antigenic structure is reported or isolates are grouped as 'untypable strains'
VIDA	Veterinary Investigation Diagnosis Analysis

Introduction

This publication presents data on *Salmonella* reports from animals, feeding stuff and Animal By Products (ABP) in Great Britain (England, Wales and Scotland) collected and collated by the Animal and Plant Health Agency (APHA) during 2025 and also provides data from previous years for comparative purposes.

The data in the first 11 chapters cover reports of *Salmonella* in livestock, with separate chapters for the main species, reports of *Salmonella* in dogs, reports of *Salmonella* in wildlife and reports of *Salmonella* in animal feeding stuffs. The 13th chapter covers the antimicrobial susceptibility of *Salmonella* (England and Wales only). Annex 1 reports MLST sequence types for isolates included in each of the above chapters (excluding chapter 13).

Since 1993, the date of a *Salmonella* incident has been recorded as the date it was reported to an Officer of the Minister. Under the present system, any *Salmonella* reports that are confirmed or identified after the publication of the annual report will be incorporated into the revised tables that appear in the following year's publication. This may result in the number of incidents and isolations differing from that previously given for a particular year. The most recent version of the report should therefore always be used when comparing data from year to year.

Revisions in the way that data have been compiled and presented since 1993 mean that, with the exception of the tables on *Salmonella* in animal feeding stuffs, data in this report cannot be compared directly with information published prior to 1993. A more detailed comparison can be generated, if required, for any *Salmonella* serovar. Requests for such data should be made to the Department of Epidemiological Sciences, APHA Weybridge (email address: Foodbornezoonoses@apha.gov.uk), who will be happy to assist with requests.

Care should be taken when comparing data from one year to another as an increase or decrease in the number of isolations and incidents does not necessarily indicate a similar change in prevalence. This is because the total number of samples examined and their distribution are often not known.

Statutory aspects of *Salmonella* control in Great Britain

On 1 January 2021 EU legislation, including legislation on animal health, food safety and food controls, as it applied to the UK on 31 December 2020, became part of [UK domestic legislation](#) under the European Union (Withdrawal) Act 2018. All references to EU legislations below and throughout this report are references to those as assimilated in UK law.

On 1 March 1989 the Zoonoses Order 1975 was revoked and replaced by the Zoonoses Order 1989. The 1989 Order added horses, deer and pigeons to the range of species from which *Salmonella* isolations are subject to reporting. Under the 1989 Order, the responsibility for reporting the isolation of a *Salmonella* was placed on the laboratory carrying out the examination or, in the case of examinations elsewhere, the person carrying out the examination.

From the late 1980s, there have been statutory *Salmonella* control programmes for certain sectors of the poultry industry in the UK. These controls have been amended over the years. The requirement to test poultry for *Salmonella* on a regular basis under the Poultry Laying Flocks (Testing and Registration etc.) Order 1989 and the Poultry Breeding Flocks and Hatcheries (Registration and Testing) Order 1989 increased the number of examinations carried out from 1989 onwards. These 2 orders were revoked in 1993 with the implementation of the Poultry Breeding Flocks and Hatcheries Order (PBFHO) 1993, which brought *Salmonella* control measures in poultry into line with the European Union Directive 92/117/EEC with the result that the level of monitoring in some poultry sectors altered.

Zoonoses Directive (EC) No. 92/117 required Member States to monitor the trends and sources of various zoonotic agents in animals, feed, food and humans, analyse them and report the findings to the Commission. In addition, it required Member States to monitor breeding flocks of domestic fowl (*Gallus gallus*) for *Salmonella*. If *S. Enteritidis* or *S. Typhimurium* was confirmed to be present in a breeding flock then the flock was slaughtered. The monitoring of breeding flocks took place at hatcheries with follow up confirmation in the birds on the farm.

A review of Directive (EC) No. 92/117 was carried out in the late 1990s by the Scientific Committee on Veterinary Measures relating to Public Health, and in its Opinion, published in April 2000, it was considered that the measures in place at that time to control food-borne zoonotic infections were insufficient. The Committee went on to propose other risk management options. As a result, in 2003, Member States agreed that the monitoring of specified zoonotic agents should be expanded and harmonised, where beneficial, in a new Directive (EC) No. 2003/99 and that the risk management measures required to control zoonotic infections should be extended in a new Regulation (EC) No. 2160/2003.

The Zoonoses Regulation (EC) No. 2160/2003 came into force on 21 December 2003. The aim of this Regulation is to reduce the prevalence of certain zoonotic infections at the primary production level by establishing the level in the Community and setting a target for reduction. As a result, each Member State is required to produce a programme to achieve the target.

In order to implement Regulation (EC) No. 2160/2003, the Poultry Breeding Flocks and Hatcheries Order (PBFHO) 2007 replaced the PBFHO 1993 and set out the requirements for registration and sampling for a new *Salmonella* National Control Programme (NCP) for

chicken breeding flocks. According to the new Order, statutory testing of breeding flocks of domestic fowl during the rearing phase and during the period of production of eggs for hatching takes place on the breeding flock holding only, and an enhanced sampling (boot swabs or composite faeces) and detection method using Modified Semi-Solid Rappaport Vassiliadis culture medium (ISO 6579: Annex D, now incorporated into ISO6579-1/17 as the method required for primary production samples) is used. The modified sampling protocol specified by the PBFHO 2007 is not directly comparable with that required under the PBFHO 1993.

The PBFHO 2007 was in turn revoked and replaced by the Control of *Salmonella* in Poultry Order (CSPO) 2007 which came into force in January 2008 and included the requirements for the implementation of a NCP in commercial laying flocks, together with that already in place for breeding chicken flocks. In 2009, respective Control of *Salmonella* in Broiler Flocks Order 2009 came into force in England and in Wales, while in Scotland the CSPO 2007 was revoked and replaced by the Control of *Salmonella* in Poultry (Breeding, Laying and Broiler Flocks) (Scotland) Order 2009. This legislation implements the requirement for a *Salmonella* National Control Programme in the broiler chicken sector which since the United Kingdom's withdrawal from the EU has included individual national control plans and targets.

In January 2010, respective Control of *Salmonella* in Turkey Flocks Orders 2009 came into force in England and Scotland, and in February 2010 the Control of *Salmonella* in Turkey Flocks Order 2010 came into force in Wales. This legislation enforced Regulations (EC) No. 2160/2003 and (EC) No. 584/2008, (later replaced by Regulation 1190/2012 which has since been assimilated into UK legislation) and implements the requirement for *Salmonella* National Control Programmes in the turkey sector. The Order makes provision for the testing of turkey flocks for *Salmonella*. As with the NCP in chicken flocks, it also prohibits the use of antimicrobials to control non-clinical *Salmonella* and live *Salmonella* vaccines that cannot be distinguished from field strains.

The above changes in legislation and subsequent levels of monitoring for *Salmonella* in the Great Britain commercial chicken and turkey sectors need to be borne in mind when examining long-term data for poultry. It should also be noted that the poultry industry is currently the only food animal production sector that has structured bacteriological surveillance programmes for *Salmonella* in place. This routine monitoring may be expected to result in larger numbers of *Salmonella* isolates than the scanning surveillance of diagnostic submissions that applies to other farm livestock. Please refer to Chapter 6 (chickens) and Chapter 7 (turkeys) for further information.

The reporting of *Salmonella* in dogs became a statutory requirement in England from 22 February 2021 and in Scotland and Wales from 21 April 2021, through respective amendments to the Zoonoses Order in early 2021. Prior to this all *Salmonella* notifications (and isolates) in dogs were received on a voluntary basis. This has resulted in an increase

in the number of submissions to APHA/SRUC for *Salmonella* testing. Further details are given in Chapter 10 (dogs).

Definition of isolate, isolation and incident

For all species not covered by a National Control Programme (NCP), the tables and figures of this publication give precedence to the number of isolations rather than the number of incidents. This is because the number of isolations gives a more representative picture of the number of *Salmonella* isolates reported in livestock, however incidents are still useful for epidemiological purposes.

Chapters 6 and 7 (chickens and turkeys, respectively, both of which are covered by NCPs) focus on the number of flocks from which the various *Salmonella* serovars have been reported and show these data together with the number of isolations. Incidents are not reported in this publication for chickens and turkeys.

Since the implementation of the NCPs for chicken breeding, laying and broiler flocks in 2007, 2008 and 2009, respectively, the data on positive findings of *Salmonella* in laying, breeding and broiler chicken flocks have been reported as the number of positive flocks, as required by the legislation, as well as the number of positive isolations detected during the year. This is also the case in turkey flocks, for which the NCP was implemented in 2010. The number of reported isolations of *Salmonella* detected in chickens and turkeys does not equate directly to the overall number of positive flocks that are detected during the year. A flock is counted as positive only once, irrespective of the number of isolations occurring and the number of serovars identified.

As the tables and figures of Chapter 1 present combined data for cattle, chickens, ducks, pigs, sheep and turkeys, incident data are not shown in this chapter.

Chapter 12 (Feeds and ABP) and Chapter 13 (Antimicrobial susceptibility) show only the number of isolations and cultures, respectively.

Isolates, isolations and incidents are defined in the following way:

- An isolate is a single culture of a particular *Salmonella*, and results from a single sample.
- An isolation is defined as the report of the first isolate of a given *Salmonella* (defined by serovar and or phage type, if available) from the same group of animals on a given occasion. If 2 submissions from the same group of animals on different dates give the same serovar, this is reported as 2 isolations.
- An incident comprises the first isolation and all subsequent isolations of the same serovar, or serovar and phage type if available, combination of a particular *Salmonella*, from the same animal, the same group of animals or their environment on a single premises, within a defined time period (usually 30 days). Subsequent

isolations arising from an incident reported in the previous year are included under the year in which they were reported.

In contrast to *Salmonella* infections in humans which are often associated with clinical disease in an individual, many isolations of *Salmonella* from livestock are not associated with clinical disease or occur on farm premises where *Salmonella* has been isolated from a group of animals rather than an individual. Since 1993, reports of *Salmonella* from livestock have been separated into isolations and incidents. 'Isolations' comprise individual reports of *Salmonella* made from samples and reported to Officers of the Minister. 'Incidents' do not include repeat isolations of a serovar that may result from a number of samplings during the course of an investigation or monitoring activities on a particular premises.

The first such report of any particular serovar or serovar and phage type combination of *Salmonella* from a particular animal, group of animals or their environment will therefore be recorded as one incident and one isolation. Further reports of the same *Salmonella* from the same group during the incident investigation will be recorded as further isolations, but not as further incidents unless the isolation is from an epidemiologically distinct group of animals. Examples of this would include a distinct group of the same species on a separate part of the same premises. Reports of a different serovar or phage type of *Salmonella* from the same animals will be recorded as a new incident. Thus 2 reports of *S. Typhimurium*, one of DT104 and another of DT193, from the same group of animals would count as one incident and one isolation of *S. Typhimurium* DT104 and one incident and one isolation of *S. Typhimurium* DT193, while 2 reports of *S. Typhimurium* DT12 from the same group of animals on different occasions within a 30 day period would count as one incident but 2 isolations.

Since 2006, any poultry hatchery isolates for which there are no supply flock details available have been treated as isolations only as they cannot be traced back to a specific flock.

The concept of an 'incident' is inappropriate when referring to isolations from animal feeding stuffs, so data for these are only reported in terms of isolations of *Salmonella*.

All isolates that have been reported to APHA in England and Wales are required to be sent to an APHA Laboratory for examination and confirmation of *Salmonella*. Of those samples taken in Scotland, the majority of poultry samples are sent to APHA Weybridge and mammalian samples are sent to the SAC Consulting (part of SRUC) and confirmed by Public Health Scotland (PHS).

Data from research projects and surveys are excluded from the tables in the species chapters in this publication. The antimicrobial susceptibility chapter (Chapter 13) contains data from routine surveillance and other surveillance projects.

Serotyping and phage typing methods

From 1 January 2023 whole genome sequencing (WGS)-based typing replaced phenotypic serotyping as the primary method of characterisation of *Salmonella* isolates submitted to APHA. A small number of submissions based on expert rules continue to be additionally characterised by phenotypic serotyping methods in parallel to WGS-based typing. In 2025 the majority of *Salmonella* characterisation was by WGS with a small number additionally parallel tested by phenotypic methods. In early December 2024, APHA ceased to carry out phage typing of *Salmonella*. For details of the phage typing methods used until December 2024, [see previous years *Salmonella* in animals and feed in Great Britain reports](#).

Briefly, genomic DNA of all isolates was extracted with a KingFisher MagMAX™ CORE instrument and the MagMAX™ CORE Nucleic Acid Purification Kit (Thermo Fisher Scientific, UK) from overnight LB broth cultures of single colonies. Libraries were normalised and pooled before running on an Illumina NextSeq 500/550 instrument to generate 150 base pair paired-end reads. The WGS data of the sequenced isolates were analysed using the APHA in-house in-silico *Salmonella* typing pipeline to confirm the serovar. An additional output of the in-silico *Salmonella* typing pipeline is the sequence type (ST) for each of the analysed isolates. *Salmonella* STs are determined through multilocus sequence typing (MLST), a bioinformatics method that analyses DNA sequence variation at seven house-keeping genes (doi:10.1371/journal.ppat.1002776). Each ST is characterised by a unique combination of alleles (DNA sequence variants) detected in the seven house-keeping genes. The move to WGS-based typing will have negligible impact on the presentation of results in this report other than the differentiation of monophasic *S. Typhimurium* variants and reporting of monophasic variants *S. Idikan* (formerly *S. 13,23:i:-*). Work is ongoing to validate the in-silico *Salmonella* typing pipeline for differentiation of the monophasic *S. Typhimurium* structures 4,5,12:i:- and 4,12:i:-. In previous years 4,5,12:i:- and 4,12:i:- have been reported separately, these will now be reported together as monophasic *S. Typhimurium*. Data for *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- in years preceding 2023 have therefore also been combined as monophasic *S. Typhimurium*, to allow comparison between years in this report. In addition, pending re-validation of the in-silico *Salmonella* typing pipeline, monophasic and biphasic variants of *S. Idikan* and *S. Kedougou*, will be reported as “*S. Idikan* (including monophasic variants)” and “*S. Kedougou* (including monophasic variants)”. Historic data has also been reclassified in the 2024 and 2025 books to allow comparison. Please refer to previous years’ books for *S. 13,23:i:-* and *S. Idikan* incidents and isolations pre-2024.

Confirmation and phenotypic serotyping of *Salmonella* isolated from animals and feed is still carried out on some isolates using micro, tube and, or slide agglutination tests. These isolates are tested for the presence of somatic and flagella antigens by agglutination with specific *Salmonella* antisera. Where homologous antiserum and antigen react, clumps of bacteria form as visible agglutination. Serovars are derived by reference to the White-

Kauffmann-Le Minor Scheme. Additional biochemical tests are needed to confirm some serovars.

Whole genome sequencing of samples received from premises in England and Wales is carried out by APHA. Mammalian isolates, and some poultry isolates, from Scotland undergo WGS at PHS laboratories, while the majority of poultry samples from Scotland are sequenced by APHA.

Monophasic or aphasic group B *Salmonella* strains, which lack one or both sets of flagella antigens, can be confirmed as variants of *S. Typhimurium* by monophasic *S. Typhimurium* specific PCRs. PCR methods can also be used to confirm the absence of flagella genes (rather than poor expression of flagella proteins) and the presence of a particular genomic island that is characteristic of the monophasic *S. Typhimurium* DT193/120 variant strains that have emerged since 2006.

Methods used for screening *Salmonella* vaccine strains

Following the introduction of live vaccines for *Salmonella* Enteritidis and *Salmonella* Typhimurium in poultry, additional testing is required to distinguish field strains from vaccine strains, to differentiate infected from vaccinated animals (DIVA). An effective DIVA test for use at the NRL is a requirement for the use of live *Salmonella* vaccines in poultry under the NCPs. For the currently available poultry vaccines licensed for use in poultry in Great Britain this differentiation is achieved through phenotypic methods and by WGS.

Salmonella Enteritidis and relevant *S. Typhimurium* isolates are compared to the *Avipro Vac E* and *Vac T* vaccine strains, which carry antimicrobial resistance markers, using a panel of 4 relevant antimicrobials in a disc diffusion technique. Both *Avipro Vac E* and *Avipro Vac T* are sensitive to erythromycin and resistant to rifampicin to distinguish them from *Salmonella* field strains. To differentiate between the 2 *Avipro* vaccine strains, *Vac E* has additional high level resistance to streptomycin and *Vac T* has an additional resistance to nalidixic acid. *Avipro Duo* comprises a mixture of *Avipro Vac E* and *Vac T*.

Differentiation of *Avipro Vac E* and *Vac T* vaccine strains, is also a validated component of the WGS pipeline.

Cevac Salmovac (which used to be called *Gallivac SE* and then *Salmovac 440*) vaccine has no resistance markers but contains mutations causing auxotrophism for histidine and adenine. *Salmonella* Enteritidis isolates are compared to the vaccine strain by growth on minimal media with and without histidine and adenine.

Differentiation of the *Cevac Salmovac* vaccine strain, is also a validated component of the WGS pipeline.

Tests for *Vac E* and *Vac T* vaccine strains and *Cevac Salmovac* and *Ceva Salmoporc* vaccine tests are carried out at APHA Weybridge.

Vaccine strains are excluded from the text, tables and figures of this report.

Nomenclature

The nomenclature used throughout this publication follows that devised by Le Minor and Popoff which divides the bacterial genus *Salmonella* into 2 species: *Salmonella enterica* and *Salmonella bongori*. The species *Salmonella enterica* is further divided into 6 subspecies: *enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae* and *indica*.

The method of naming serovars of subspecies *enterica* largely differs from that used for the other 5 subspecies in that the familiar serovar names are assigned to serovars within subspecies *enterica* while members of the other subspecies are designated by antigenic formulae.

For example, following this method the serovar originally referred to as *Salmonella typhimurium* is now known as *Salmonella enterica* subspecies *enterica* serovar Typhimurium, which may be shortened to *Salmonella* Typhimurium and the naming of serovars of subspecies *diarizonae* is, for example, *Salmonella enterica* subspecies *diarizonae* serovar 61:k:1,5,7 (or *Salmonella* III 61:k:1,5,(7)). For further details of this nomenclature see Grimont and Weill (2007).

Historic changes to serovar names prior to the date range presented in the current report can be found in the quality statement at the end of this book.

Chapter 1: Overview of *Salmonella* in livestock, dogs, feeds and humans

This chapter provides information on *Salmonella* isolated from livestock and dogs from samples taken from all types of premises, including but not limited to farms, hatcheries, and veterinary practices. An overview of the number of isolations of *Salmonella* reported from farm animal species is given in Table 1.1 (poultry refers to reports from chickens, turkeys and ducks).

It is important to note that data for the different species are not directly comparable. Most *Salmonella* reports from cattle, sheep and pigs result from the investigation of clinically diseased animals whereas reports from chickens and turkeys are mostly from statutory surveillance. However, trends over time within species are largely comparable, especially for chickens and turkeys since the introduction of the *Salmonella* National Control Programmes (NCPs).

For comparison purposes, data have been reproduced here on the number of laboratory reports of human isolations of *Salmonella* reported to UK Health Security Agency (UKHSA) in England (Figure 1.1.1).

Figures 1.1.2 to 1.1.7 show the most common *Salmonella* serovars isolated from the relevant livestock species in Great Britain in 2025 alongside the most common serovars isolated from human cases of salmonellosis in England (Figure 1.1.1). Figures under headings 1.2 and 1.3 provide data for sequence types of *S. Typhimurium* (including monophasic variants) and *S. Enteritidis* in livestock. Apart from *S. Typhimurium* (including monophasic variants), *S. Enteritidis*, *S. Mbandaka* and *S. Newport*, other serovars commonly associated with human cases are generally reported relatively less frequently from British livestock and dogs. However, *S. Infantis* which was the fifth most frequently reported serovar in humans in 2025 was the fourth most commonly reported from dogs in 2025.

In 2025, a total of 10,406 isolations of *Salmonella* from humans in England were reported to UKHSA. This is a 0.2% increase compared to 2024, when 10,388 isolations of *Salmonella* from humans in England were reported to UKHSA. No link has been inferred between the rise in human *Salmonella* cases to animal cases. UKHSA monitor and investigate the rise in human cases of *Salmonella*. Comparable data from Scotland and Wales were not available for inclusion.

During 2020 and 2021 there was a reduction in submissions to APHA for non-statutory surveillance and a reduction in diagnostic submissions in many species as a consequence of the COVID-19 pandemic and associated lockdown measures. This should therefore be borne in mind when comparing, 2022, 2023, 2024 and 2025 data with these years and those prior to the pandemic.

Figures showing the relative frequency of the most common *Salmonella* serovars in each animal species during 2025 (Figures under heading 1.1) should be considered alongside absolute numbers of isolations (Table 1.1). This is because the relative proportions of each serovar may remain similar despite a change in number of isolations, in which case we assume that the change in number of isolations is likely to be constant across serovars. Similarly, if there is a change in the relative serovar frequencies, it is only by examining changes in absolute numbers that we can ascertain the size of any increase or decrease.

In 2025, the total number of *Salmonella* isolation reports from cattle, sheep, pigs and poultry increased by 10.2% compared with 2024 (3,354 isolations versus 3,043 isolations) and decreased by 7.6% compared with 2023 (3,630 isolations) (Table 1.1). Trends were also variable across serovars, for example, reports of *S. Dublin* increased by 39.1% in 2025 and reports of *S. Idikan* (including monophasic variants) increased by 32.9% in 2025 compared to 2024. However, reports of *S. Newport* decreased by 36.2% in 2025 compared to 2024 and reports of *S. Typhimurium* decreased by 27.6% in 2025 compared to 2024.

The most important factor which may bias the number of *Salmonella* reports from species not covered by NCPs (that is species other than commercial chickens and turkeys) is the submission rate. This report presents numerator data but the denominator, in most cases, is unknown and may change over time. However, we use the number of diagnostic submissions to APHA and Scotland's Rural College (SRUC) as a proxy to understand if the denominator may have significantly changed.

Most *Salmonella* reports from cattle, sheep and pigs result from the investigation of clinically diseased animals, and economic factors may exert a strong influence on diagnostic practices, such as whether a veterinary surgeon is consulted and whether samples are submitted for laboratory examination. The *Salmonella* data from these species is likely to be most influenced by changes in submission rate.

The number of diagnostic submissions to APHA and SRUC decreased by 6.2% in 2025 compared with 2024. An increase was seen for poultry, game birds and other birds with the greatest increase being in other birds (97.1%). The increase may be partly explained by a change to SRUC recording wild birds as other birds in 2025. The number of submissions decreased for cattle, sheep, pigs, goats and miscellaneous species, with the greatest decrease seen in goats (25.1%). As the majority of the isolations from species other than poultry relate to clinical investigations (although the *Salmonella* detected may not always be the primary cause of the clinical presentation), the current prevalence of subclinical infection in these species of livestock is not known. Most sample submissions from poultry are associated with statutory or voluntary surveillance activities. Although trends in *Salmonella* reports from species not covered by NCPs can be compared with diagnostic submission rates to APHA and SRUC, it should be remembered that not all submissions will have been examined for *Salmonella*. Private laboratories also report the isolation of *Salmonella* and the total number of submissions to these laboratories is unknown.

The reporting of *Salmonella* in dogs became a statutory requirement in England from 22 February 2021 and in Scotland and Wales from 21 April 2021. This has resulted in an increase in the number of submissions to APHA and SRUC for *Salmonella* testing. Isolations and incidents of *Salmonella* in dogs are now reported in this publication (Chapter 10).

There were 4,025 isolations of *Salmonella* in livestock and dogs in 2025 which represents an increase of 8.1% compared with 2024 (3,725 isolations). This comprised 3,857 isolations from species covered by the statutory reporting requirements of the Zoonoses Order 1989 and its amendments (2,407 isolations from chickens, 466 isolations from cattle, 416 isolations from dogs, 253 isolations from pigs, 113 isolations from ducks, 82 isolations from sheep, 71 isolations from horses, 33 isolations from turkeys, 12 isolations from pigeons, 3 isolations from pheasants, one isolation from deer, plus 168 isolations from non-statutory species (for example, cats and reptiles, which are not reported in detail in this publication).

Relative to 2024, in 2025 there were increased isolations from chickens (2,407 versus 1,961 isolations) and cattle (466 versus 366 isolations). In contrast, there were fewer isolations from turkeys (33 versus 108 isolations), ducks (113 versus 196 isolations) and pigs (253 versus 311 isolations). Isolations stayed relatively stable in sheep in 2025 (82 versus 101 isolations).

The surveillance data for 2025 show that 23.8% of the isolations of *Salmonella* reported to APHA resulted from samples relating to clinical disease in livestock. This is similar to during 2024, when 23.0% of isolations were from clinical disease investigations, and lower than 2023 when 33.2% of isolations were from clinical disease investigations. This contrasts with data for *Salmonella* in humans where reports predominately originate from cases of clinical disease.

The majority of the isolations reported from chicken and turkey flocks (93.1% and 93.9%, respectively) during 2025 were the result of statutory surveillance activities due to the NCPs that are in place for these sectors (further information on the NCPs is included in Chapter 6 and Chapter 7). This differs from years prior to the introduction of the NCPs when the majority of chicken and turkey isolations originated from voluntary surveillance. Voluntary *Salmonella* surveillance of healthy flocks is common practice in the duck industry. In 2025, 99.1% of the *Salmonella* isolations from ducks resulted from voluntary surveillance.

Reports of *S. Enteritidis* from cattle, sheep, pigs and poultry in 2025 were 23.1% higher than in 2024 (16 versus 13 isolations) and were 45.5% higher than in 2023 (11 isolations). As in previous years, the majority of *S. Enteritidis* isolations in 2025 were reported from chickens (15 of 16 isolations), and there was also one isolation from cattle. This is similar to 2024 when most isolations of *S. Enteritidis* came from chickens (12 of 13 isolations), with one isolation from cattle (Figure 1.4). In 2025, the most common *S. Enteritidis* sequence type (ST) isolated was ST11.

The total number of *S. Typhimurium* isolations from cattle, sheep, pigs and poultry fell by 27.6% in 2025 (184 isolations) relative to 2024 (254 isolations). There was an increase in the number of isolations of this serovar in 2 sectors relative to the previous year; isolations from sheep increased two-fold (12 versus 6 isolations) and isolations from ducks also

increased (one versus no isolations) (Figure 1.5). Isolations of *S. Typhimurium* in chickens decreased by 58.8 % in 2025 compared to 2024 (7 versus 17 isolations). Isolations of *S. Typhimurium* in pigs fell by 32.1% in 2025 relative to 2024 (106 versus 156 isolations). Isolations of *S. Typhimurium* in cattle decreased by 5.9% in 2025 compared to 2024 (58 versus 62 isolations). There were no isolations of *S. Typhimurium* from turkeys in 2025, compared to 13 isolations in 2024. The most common *S. Typhimurium* sequence type from isolations in cattle, sheep, pigs and poultry in 2025 was ST19, accounting for 71.4% of isolations.

Total isolations of monophasic *S. Typhimurium* from cattle, sheep, pigs and poultry decreased by 6.7% in 2025 compared to 2024 (70 versus 75 isolations, Figure 1.6). There was an increase in isolations of monophasic *S. Typhimurium* in chickens and cattle in 2025 compared to 2024 (4 versus one isolation and 5 versus 3 isolations, respectively). Isolations of monophasic *S. Typhimurium* fell in pigs in 2025 compared to 2024 (61 versus 70 isolations).

Highlights

Cattle

Isolations of *Salmonella* from cattle in 2025 were 27.3% higher than during 2024 (466 versus 366 isolations) and 6.9% higher than during 2023 (436 isolations).

As in previous years, *S. Dublin* remained the most common serovar identified in cattle (314 isolations, 67.4% of total cattle isolations). The number of isolations of *S. Dublin* increased by 46.0%, compared with 2024 and by 24.6%, compared with 2023.

There were 58 isolations of *S. Typhimurium* from cattle in 2025, which is a decrease of 6.5% compared with 2024. The relative number of *S. Typhimurium* isolations fell in 2025 and this serovar was the second most common serovar isolated from cattle (12.4% of total cattle isolations) and *S. Mbandaka* was the third most common serovar isolated (54 isolations, 11.6% of total cattle isolations). This is the same as during 2024 and 2023 and a change from 2022 and 2021 when *S. Mbandaka* was the second most common serovar isolated and *S. Typhimurium* was the third most common serovar isolated (Figure 2.2). All isolations of *S. Typhimurium* in cattle in 2025 were sequence type (ST) 19.

There were 5 isolations of monophasic *S. Typhimurium* (1.1% of total cattle isolations) during 2025 compared with 3 isolations during 2024, and 14 isolations during 2023. In 2025 all isolations of monophasic *S. Typhimurium* were ST34.

There was one isolation of *S. Enteritidis* from cattle during 2025, the same as in 2024 and 2023 which also had one isolation in each year. The isolation in 2025 was ST11.

Small ruminants

Isolations of *Salmonella* from sheep in 2025 were 18.8% lower than during 2024 (82 versus 101 isolations) and 16.3% lower than during 2023 (98 isolations) (Table 3.1).

Salmonella enterica subspecies *diarizonae* serovar 61:k:1,5,(7) remained the most common serovar isolated from sheep in 2025 (57 isolations, 69.5% of total sheep isolations).

Salmonella Typhimurium was the second most common serovar isolated from sheep in 2025 (12 isolations, 14.6% of total isolations), double the number of isolations than recorded in 2024 (6 isolations, 5.9% of total sheep isolations). All isolations of *S. Typhimurium* in sheep in 2025 were ST19.

Salmonella Montevideo was the third most common serovar isolated from sheep in 2025 (6 isolations, 7.3% of total isolations). For comparison, in 2024 *S. Montevideo* was the joint second (along with *S. Dublin*) most common serovar isolated, with 14 isolations (13.9% of

total isolations). *S. Dublin* was the fourth most common serovar isolated in 2025, with 5 isolations (6.1% of total isolations).

There were no isolations of *Salmonella* from goats in 2025 compared to 2 isolations in 2024 (*S. enterica* subspecies *diarizonae* 61:k:1,5,(7) and *S. Dublin*) and one isolation in 2023 (*S. enterica* subspecies *diarizonae* 61:k:1,5,(7)).

Pigs

There were 253 *Salmonella* isolations from pigs in 2025 which was 18.6% lower compared to 2024 (311 isolations) and similar to during 2023 (258 isolations) (Table 4.1).

Salmonella Typhimurium and monophasic *S. Typhimurium* were together responsible for 66.0% of all isolations from pigs in 2025 (167 isolations). This is lower than in both 2024 and 2023 when these serovars accounted for 72.7% and 77.5% of all isolations in pigs, respectively. As has been the case since 2020, the number of *S. Typhimurium* isolations exceeded isolations of monophasic *S. Typhimurium*.

The majority of *S. Typhimurium* isolations from pigs in 2025 were ST19 (102 isolations, 96.2% of total *S. Typhimurium* isolations in pigs) and there were single isolations of both ST34 and ST8336. Most monophasic *S. Typhimurium* isolations from pigs in 2025 were ST34 (60 isolations, 98.4% of total monophasic *S. Typhimurium* isolations) and there was a single isolation of ST19.

After *S. Typhimurium* and its monophasic variants, *S. Derby* was the next most common serovar isolated from pigs in 2025 (33 isolations, 13% of total isolations). This is similar to 2024 when there were also 33 isolations of *S. Derby* from pigs, and almost double than that seen in 2023 when there 17 isolations.

Deer, horses and rabbits

There was one isolation of *Salmonella* Coeln from deer during 2025, this is compared to 2 isolations during 2024 (one each of monophasic *S. Typhimurium* and *S. Typhimurium*), one isolation of *S. Typhimurium* during 2023 and no isolations in 2022 or 2021 (Table 5.1).

There were no isolations of *Salmonella* from rabbits during 2025, 2024 or 2023 and during 2022 there were 2 isolations (one isolation each of *S. Fluntern* and *S. Newport*). (Table 5.2).

There were 71 isolations of *Salmonella* from horses during 2025, 34.0% higher than during 2024 (53 isolations) and 29.1% higher than during 2023 (55 isolations) (Table 5.3).

Salmonella Typhimurium was the most common serovar isolated from horses in 2025 (30 isolations, 42.3% of total horse isolations). This is higher than the number of isolations in

2024 and 2023 (24 and 20, respectively). The most common sequence type of *S. Typhimurium* in 2025 was ST19 (27 isolations, 90.0% of *S. Typhimurium* isolations).

Salmonella Enteritidis was the second most common serovar reported from horses during 2025 (12 isolations, 16.9% of total horse isolations), which is an increase compared to 2024 (8 isolations) and a large increase compared to 2023 (1 isolation). In 2025, three sequence types were reported in *S. Enteritidis* isolations which were ST8943 (6 isolations), ST11 (5 isolations) and ST10467 (2 isolations). One isolation of *S. Enteritidis* yielded 2 sequence types (ST11 and ST10467) in 2025. This isolation is only counted once in the overall number of isolations, hence the sequence types total exceeds the isolations total.

There were 3 isolations of monophasic *S. Typhimurium* in horses in 2025, compared to one isolation in both 2024 and 2023. In 2025, two isolations of monophasic *S. Typhimurium* were ST34 and one was ST19.

Chickens

Including both NCP and non-statutory surveillance data, there were 2,407 isolations of *Salmonella* from chickens in 2025. This is an increase of 22.7% compared with 2024 (1,961 isolations) and a decrease of 8.6% compared with 2023 (2,633 isolations) (Table 6.1).

The most commonly reported serovars were:

- *S. Idikan* (including monophasic variants) (909 isolations, 37.8% of total chicken isolations)
- *S. Kedougou* (including monophasic variants) (423 isolations, 17.6% of total chicken isolations)
- *S. Montevideo* (341 isolations, 14.2% of total chicken isolations)
- *S. Mbandaka* (237 isolations, 9.8% of total chicken isolations)
- *S. Agona* (133 isolations, 5.5% of total chicken isolations)

There were 15 isolations of *S. Enteritidis* in 2025 compared with 12 isolations during 2024 and 9 isolations during 2023. The most commonly reported sequence type in 2025 was ST11 (10 isolations).

There were 7 isolations of *S. Typhimurium* in 2025 compared with 17 isolations in 2024 and 21 isolations in 2023. The most commonly reported sequence type in 2025 was ST19 (6 isolations). There were 4 isolations of monophasic *S. Typhimurium* in 2025, compared with one isolation in 2024 and 6 isolations in 2023. All 4 isolations reported in 2025 were ST34.

Information and data are given in Chapter 6 (Reports of *Salmonella* in Chickens) on the National Control Programmes (NCPs) for *Salmonella* in breeding flocks, laying hen flocks and broiler flocks. The estimated prevalence of regulated serovars in all 3 chicken sectors

were well below the national targets of 1% for breeders and broilers and 2% for layers, with Great Britain prevalences estimated at 0.18% for breeders, 0.43% for layers and less than 0.01% for broilers. Since 2021, each devolved nation in Great Britain has its own individual target of 1.0% (breeders and broilers) or 2.0% (layers) of regulated serovars rather than a combined Great Britain target. See individual species chapter for devolved administration prevalences for breeders and layers.

Turkeys

Including both NCP and non-statutory surveillance data, there were 33 isolations of *Salmonella* from turkeys in 2025. This is a 69.4% decrease compared to 2024 (108 isolations) and a 69.7% decrease compared to 2023 (109 isolations) (Table 7.1).

During 2025 the most common serovar isolated from turkeys was *S. Kedougou* (including monophasic variants) (10 isolations, 30.3% of total turkey isolations). The joint second most common serovars were *S. Agona* and *S. Goldcoast* (5 isolations of each, 15.2% of total turkey isolations) and the third most common was *S. Senftenberg* (4 isolations, 12.1% of total turkey isolations).

There were no isolations of *S. Typhimurium* during 2025, compared with 13 isolations during 2024 and 2 isolations during 2023. There were no isolations of monophasic *S. Typhimurium* during 2025, compared with no isolations during 2024 and 1 isolation during 2023.

Information and data are given in Chapter 7 (Reports of *Salmonella* in turkeys) on the National Control Programmes (NCP) for *Salmonella* in turkeys. The Great Britain prevalence of regulated serovars was 0.00% for turkey fatteners and 0.00% for turkey breeders. Since 2021, each devolved nation in Great Britain has its own individual target of 1.0% (breeders and fatteners) of regulated serovars rather than a combined Great Britain target. See individual species chapter for devolved administration prevalences.

Ducks and geese

There were 113 isolations of *Salmonella* from ducks in 2025. This is a 42.3% decrease compared to 2024 (196 isolations) and a 17.7% increase compared within 2023 (96 isolations) (Table 8.1). The upturn in isolations in 2024 was influenced by an increase in voluntary surveillance testing carried out by the duck industry which can vary from year to year.

The most common serovars isolated from ducks in 2025 were *S. Indiana* (78 isolations, 69.0% of total duck isolations), *S. Give* (11 isolations, 9.7% of total duck isolations), *S. Lexington* (8 isolations, 7.1% of total duck isolations) and *S. Newport* and *S. Kottbus* (7 isolations of each, 6.2% of total duck isolations each).

The number of isolations of *S. Hadar* from ducks have been declining in recent years from 17 isolations in 2022 which decreased during 2023 (6 isolations) and 2024 (2 isolations) to no isolations in 2025.

There was one isolation of *S. Typhimurium* from ducks in 2025. This is compared to no isolations during 2024, one isolation during 2023 and no isolations during 2022 and 2021 when for the first time *S. Typhimurium* was not recorded from ducks in Great Britain since 2001. The isolation of *S. Typhimurium* reported in 2025 was ST19. There were no isolations of *S. Enteritidis* from ducks in 2025 compared with no isolations during 2024 and one isolation during 2023.

There were no isolations of *Salmonella* from geese in 2025, compared to one isolation during 2024 (*S. Typhimurium*) and no isolations during 2023.

Other statutory birds (as specified in the Zoonoses Order)

There were 3 isolations of *Salmonella* from game birds in 2025, which is an increase from 2024 (no isolations) and similar to 2023 (4 isolations). Game birds include guinea fowl, partridges, pheasants and quail.

In 2025 there were 3 isolations of *Salmonella* from pheasants, compared to no isolations in 2024 and 2 isolations in 2023. The serovars isolated in 2025 from pheasants were *S. Senftenberg* (x2) and *S. Typhimurium* (ST19) (x1). In 2025 there were no isolations of *Salmonella* from partridges, compared to no isolations in 2024 and 2 isolations in 2023. There were no isolations of *Salmonella* in quail or guinea fowl in 2025, 2024 or 2023.

There were 12 *Salmonella* isolations from pigeons in 2025, which is lower than in 2024 and 2023 (22 and 18 isolations, respectively). Of the isolations in 2025, all 12 were *S. Typhimurium*. The sequence types *S. Typhimurium* isolated in 2025 were ST128 (x5), ST19 (x4) and ST8937 (x3).

Dogs

The reporting of *Salmonella* in dogs became statutory on 22 February 2021 in England and on 21 April 2021 in Scotland and Wales through an amendment of the Zoonoses Order.

There were 416 isolations of *Salmonella* from dogs in 2025, a decrease of 13.7% compared to 2024 (482 isolations) (Table 10.1). The majority of these isolations (99.3%) were from reports of clinical disease. The most common serovars reported were *S. Typhimurium* (61 isolations, 14.7% of total isolations from dogs), monophasic *S. Typhimurium* (32 isolations, 7.7% of isolations from dogs), *S. Dublin* and *S. Infantis* (29 isolations each, 7.0% of isolations from dogs each). *Salmonella Typhimurium* (including monophasic strains) and *S. Infantis* were in the top 5 human serovars in 2025.

The most common sequence types of *S. Typhimurium* from dogs during 2025 were ST19 (51 isolations) and ST313 (9 isolations). The majority of monophasic *S. Typhimurium* sequence types during 2025 were ST34 (30 isolations).

There were 15 isolations of *S. Enteritidis* from dogs during 2025. The most common sequence types were ST11 (7 isolations) and ST10467 (4 isolations).

Wildlife

There were 17 isolations of *Salmonella* from wildlife during 2025. Among wild mammals there were 7 isolations from hedgehogs (5 isolations of *S. Enteritidis* and 2 isolations of *S. Typhimurium*), 2 isolations of *S. Typhimurium* from badgers and one isolation of *S. Typhimurium* from otters (Table 11.1). In wild bird species there were 3 isolations of *S. Hessarek* from rooks, 2 isolations of *S. Typhimurium* from gulls and one isolation of *S. Hessarek* from jackdaws (Table 11.2). This is higher than in 2024 where there were 14 isolations and also higher than 2023 when there were 9 isolations of *Salmonella* from wildlife.

Feeding stuffs

There were 798 isolations of *Salmonella* from feeding stuffs during 2025, including 60 isolations from compound feeds (Tables 12.3 to 12.6) and 738 from feed ingredients or products associated with testing under Animal By-Products Regulations (ABPR) (Tables 12.8a and 12.8b). This is similar to 2024 (795 isolations) and a decrease of 11.0% compared with 2023 (897 isolations).

There were 137 isolations of regulated *Salmonella* serovars from animal feeding stuffs and related products during 2025. Regulated serovars are key serovars of public health importance targeted by the NCPs. This is 27.9% fewer than in 2024 (190 isolations) and 48.3% fewer than in 2023 (265 isolations). There were 56 isolations of *S. Infantis*, 46 isolations of *S. Typhimurium*, 17 isolations of monophasic *S. Typhimurium*, 11 isolations of *S. Enteritidis*, 5 isolations of *S. Hadar* and 2 isolations of *S. Virchow*.

There were 234 reports of *Salmonella* from raw meat pet food (Table 12.8b). This is lower than during 2024 (290 isolations) and 2023 (331 isolations). The most common serovars reported in raw pet food during 2025 were *S. Indiana* (26 isolations), *S. Typhimurium* (25 isolations) and *S. London* (16 isolations). Overall, there were 62 isolations of regulated serovars from raw meat pet food in 2025. This is a decrease of 34.7% compared with 2024 (95 isolations) and 37.4% lower than in 2023 (99 isolations).

The proportion domestic processed animal protein samples positive for *Salmonella* in 2025 was 3.4%, which is higher than in 2024 (1.7%).

No batches of imported processed animal protein were tested during 2025, which is the same as during 2024 and 2023.

Antimicrobial resistance

Of the 4,929 *Salmonella* isolates examined during 2025, 76.0% were susceptible to all 16 antimicrobial compounds tested against (Table 13.6). This is higher than in 2024, when 73.3% of isolates were susceptible to all 16 antimicrobials.

A total of 349 isolates of *S. Dublin* were examined in 2025, of which 94.3% were susceptible to all the antimicrobials tested against. This is higher than in 2024 when 91.5% were susceptible to all antimicrobials tested against.

A total of 443 isolates of *S. Typhimurium* were examined in 2025, of which 51.1% were susceptible to all the antimicrobials tested against which is lower than in 2024 and 2023 (54.3% and 55.0%, respectively).

A total of 161 isolates of monophasic *S. Typhimurium* were examined in 2025, of which 1.9% were susceptible to all the antimicrobials tested against. This is lower than in 2024 when 4.3% were susceptible to all antimicrobials tested against.

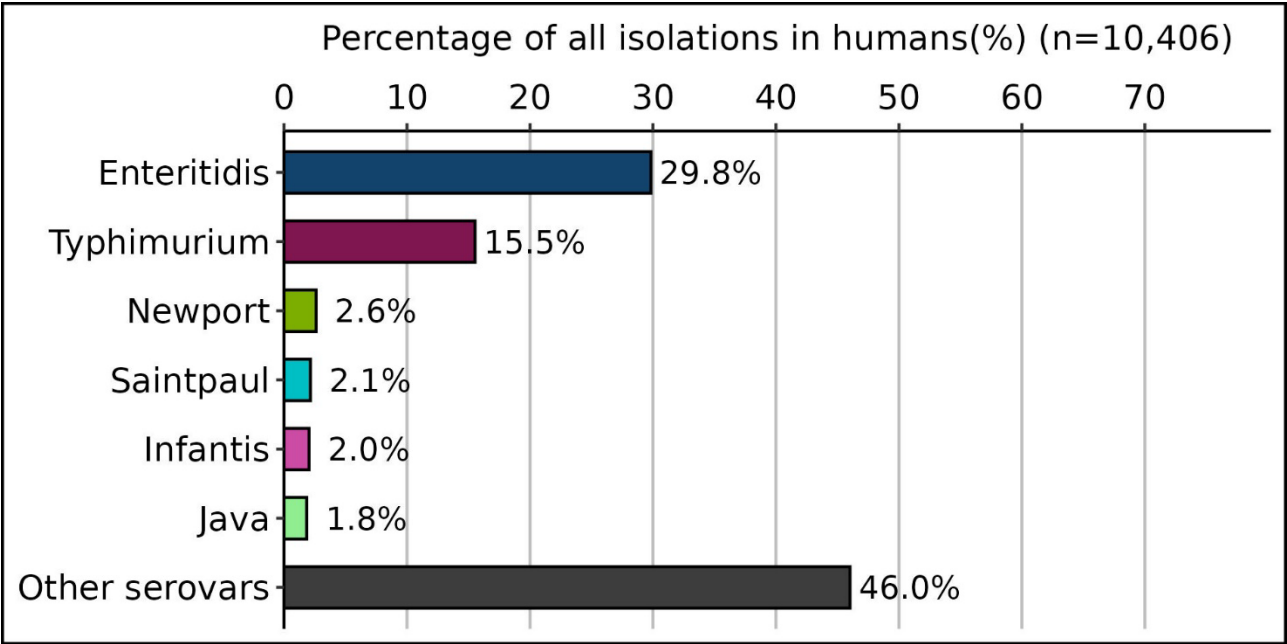
In total, 3,976 isolates of serovars other than *S. Dublin* or *S. Typhimurium* were tested in 2025 and 80.2% of these were sensitive to all the antimicrobials tested against. This is higher than in 2024 when 74.9% of isolates were fully sensitive.

Resistance to third generation cephalosporins and fluoroquinolones is considered of high importance, since these antimicrobials are used for the treatment of more serious cases of human salmonellosis. The percentage of *Salmonella* isolates that were resistant to ciprofloxacin in 2025 was 0.3%. Cefotaxime and ceftazidime resistance remained stable in 2025 at 0.2% (12 isolates) with 4 *Salmonella* isolates from both horses and turkeys.

Full details of the above highlights can be found in the individual chapters.

Figure 1.1: Isolations of the most common *Salmonella* serovars in livestock and humans in England (isolations in humans) and Great Britain (isolations in livestock) in 2025

Figure 1.1.1: Isolations in humans



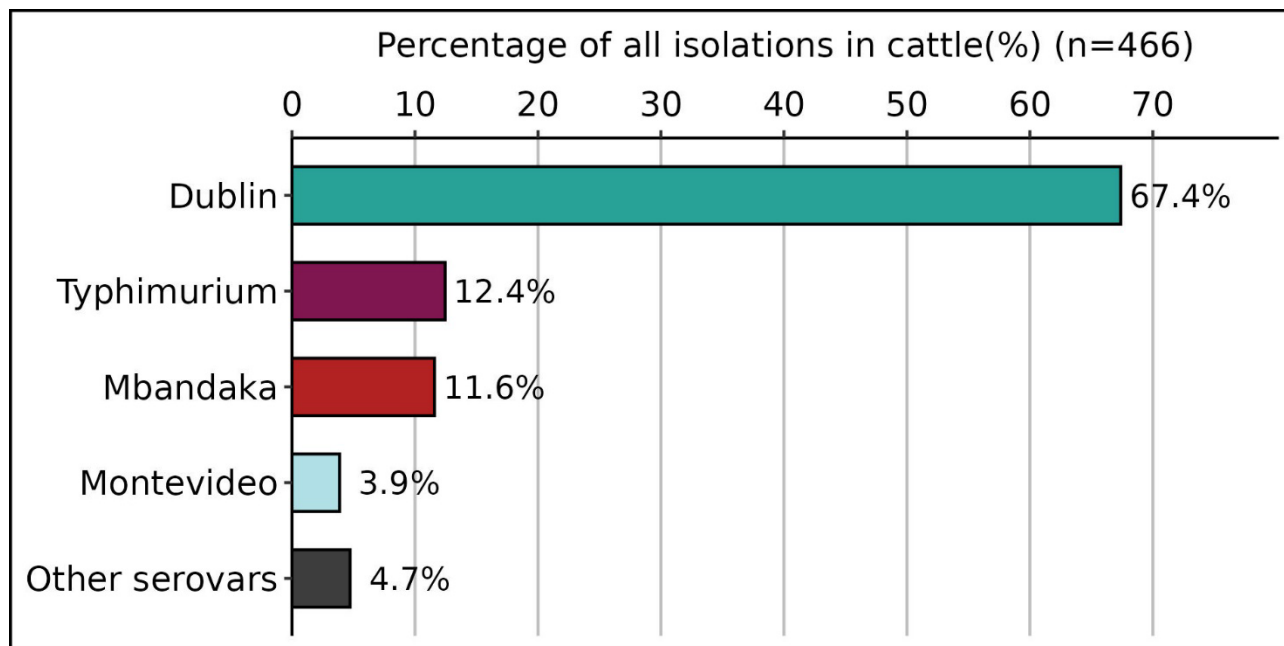
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in humans in England in 2025. The most commonly reported *Salmonella* serovar in humans in 2025 was *S. Enteritidis*, accounting for 29.8% of total isolations, followed by *S. Typhimurium* (15.5%), *S. Newport* (2.6%) and *S. Saintpaul* (2.1%).

The human data presented are included for contextual comparison only. These laboratory-confirmed human *Salmonella* isolations represent cases from a wide range of potential exposure sources, including food, environmental and travel-associated infections. The data should not be interpreted as indicating that reported human cases were linked to animal, feed or livestock findings presented elsewhere in this report unless such links have been identified through separate epidemiological investigations.

S. Typhimurium isolates in humans include monophasic strains.

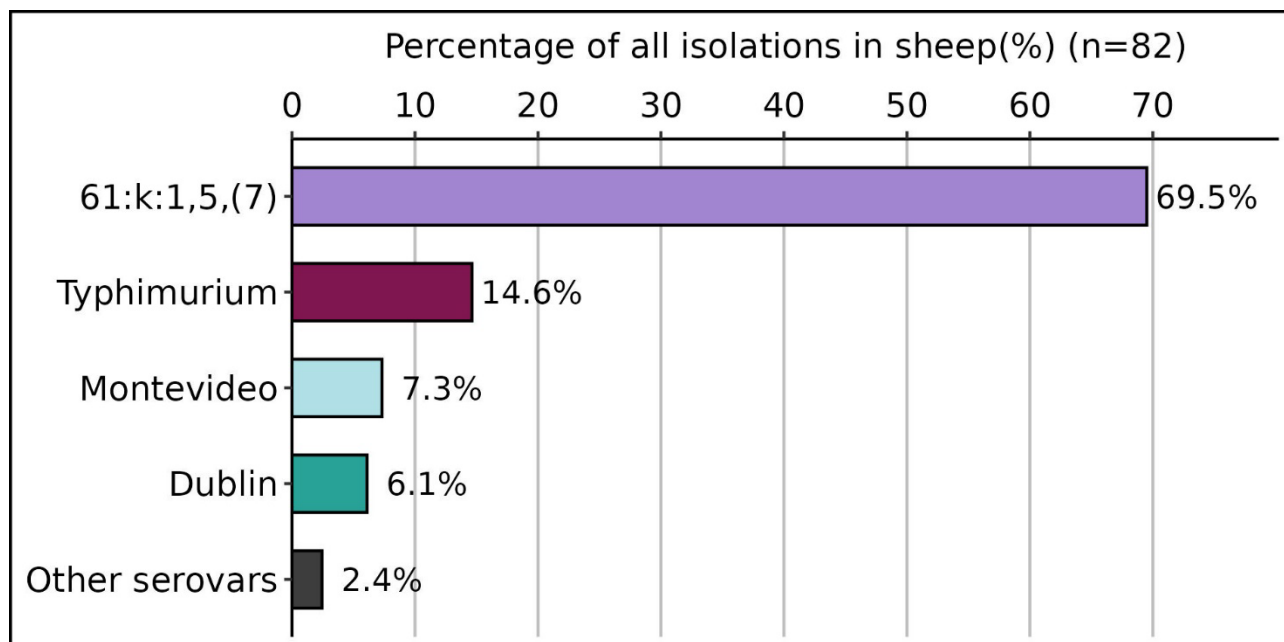
Data on human isolates in England was provided by UK Health Security Agency (UKHSA). The UKHSA Second-Generation System (SGSS) is a live laboratory reporting system therefore numbers are subject to change and may not be directly comparable with data reported in previous years.

Figure 1.1.2: Isolations in cattle



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in cattle in 2025. The most common serovar in cattle in 2025 was *S. Dublin* (67.4% of isolations), followed by *S. Typhimurium* (12.4% of isolations) and *S. Mbandaka* (11.6% of isolations) and *S. Montevideo* (3.9% of isolations).

Figure 1.1.3: Isolations in sheep

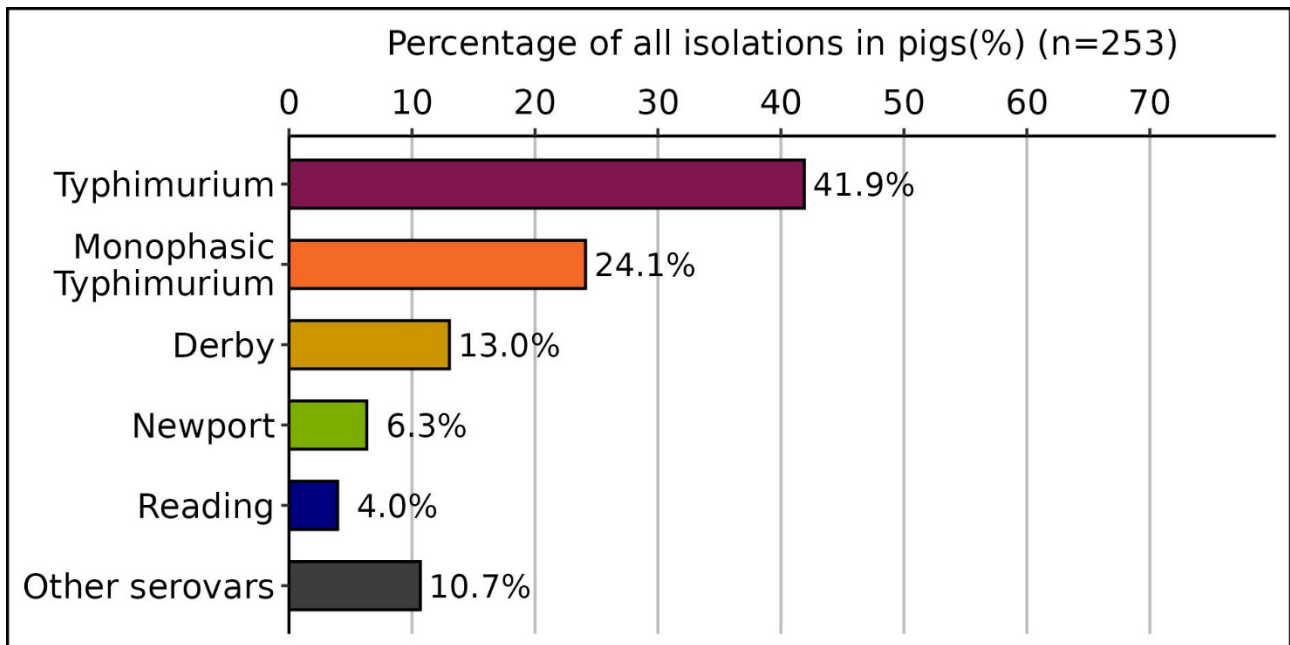


Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in sheep in 2025. The most common serovar in sheep in 2025 was *Salmonella*

61:k:1,5,(7) (69.5% of isolations), followed by *S. Typhimurium* (14.6% of isolations), *S. Montevideo* (7.3% of isolations) and *S. Dublin* (6.1% of isolations).

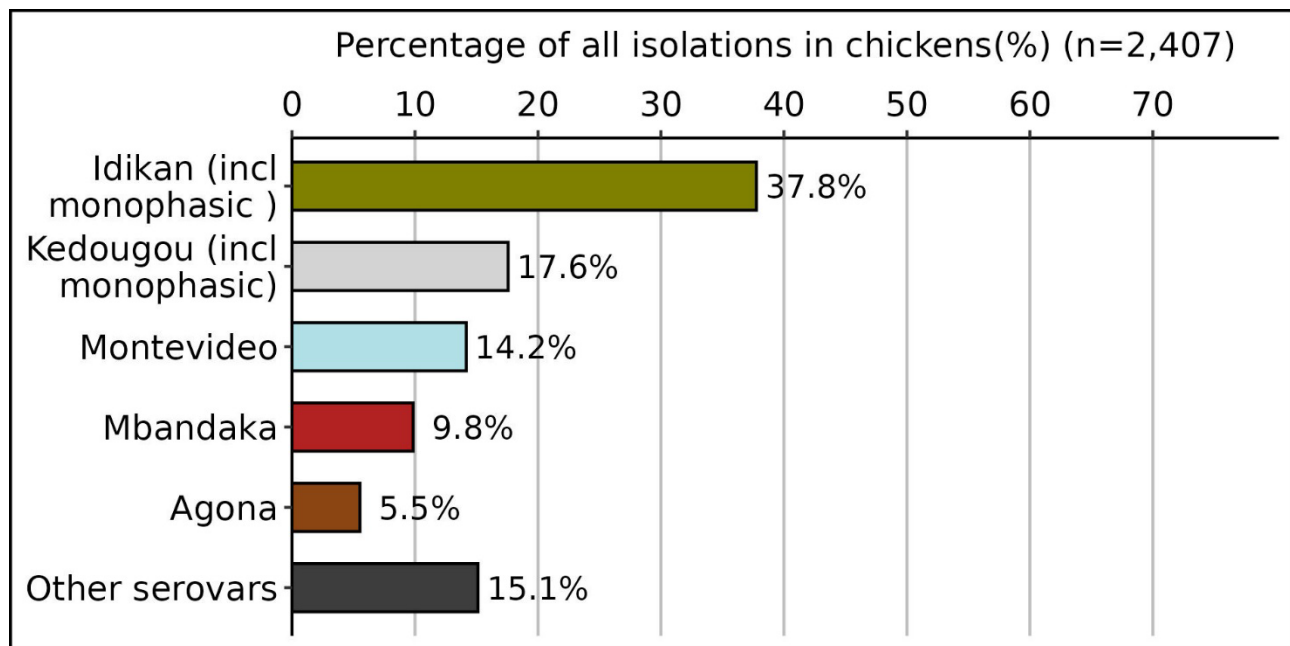
All isolations of 61:k:1,5,(7) are variants of *Salmonella enterica* subspecies *diarizonae*.

Figure 1.1.4: Isolations in pigs



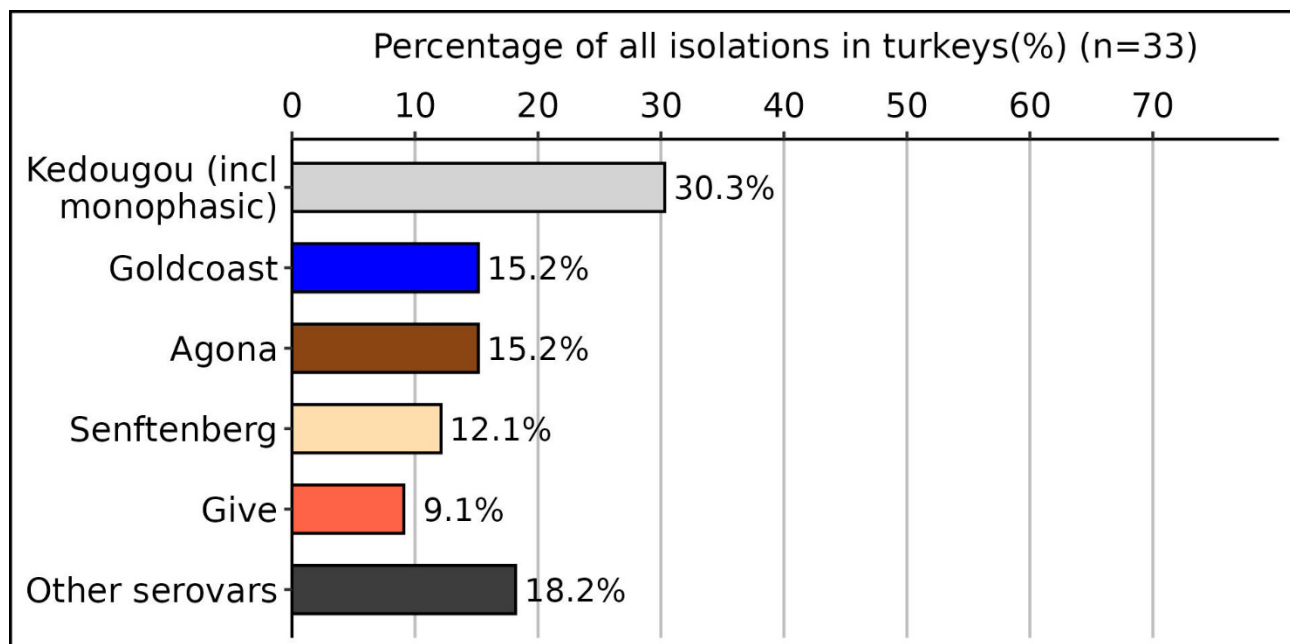
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in pigs in 2025. The most common serovar in pigs in 2025 was *S. Typhimurium* (41.9% of isolations), followed by monophasic *S. Typhimurium* (24.1% of isolations), *S. Derby* (13.0% of isolations) and *S. Newport* (6.3% of isolations).

Figure 1.1.5: Isolations in chickens (statutory and non-statutory testing)



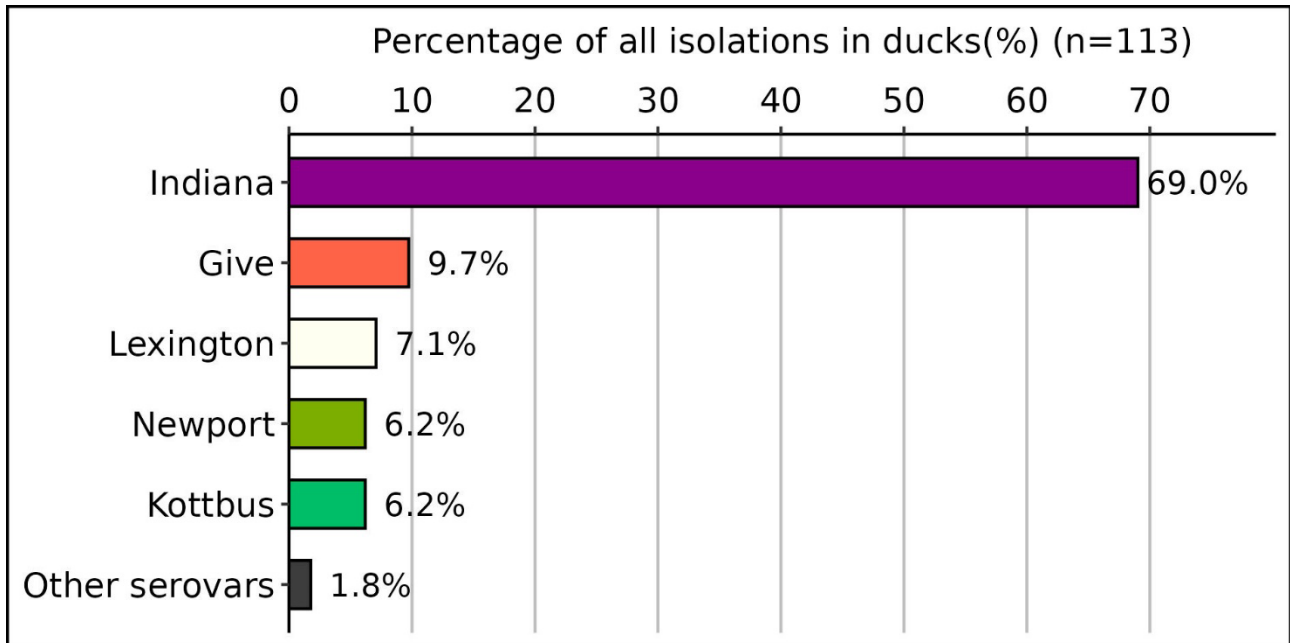
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in chickens in 2025. The most common serovar in chickens in 2025 was *S. Idikan* (including monophasic variants), accounting for 37.8% of total isolations, followed by *S. Kedougou* (including monophasic variants) (17.6%), *S. Montevideo* (14.2%) and *S. Mbandaka* (9.8%).

Figure 1.1.6: Isolations in turkeys (statutory and non-statutory testing)



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in turkeys in 2025. The most common serovar in turkeys in 2025 was S. Kedougou (including monophasic variants), accounting for accounting for 30.3% of total isolations, followed by S. Goldcoast and S. Agona (15.2% each), and S. Senftenberg (12.1%).

Figure 1.1.7: Isolations in ducks



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in ducks in 2025. The most common serovar in ducks in 2025 was S. Indiana, accounting for 69.0% of total isolations, followed by S. Give (9.7%), S. Lexington (7.1%), S. Newport (6.2%) and S. Kottbus (6.2%).

Table 1.1: *Salmonella* isolations in cattle, sheep, pigs and poultry on all premises in Great Britain

The following table shows *Salmonella* isolations in cattle, sheep, pigs and poultry on all premises in Great Britain from 2021 to 2025. Poultry includes chickens, turkeys and ducks.

The data includes statutory and non-statutory results.

<i>Salmonella</i> serovar	2021 isolations	2022 isolations	2023 isolations	2024 isolations	2025 isolations
Agama	5	3	3	2	12
Ago	0	0	0	1	0
Agona	42	139	208	156	139
Ajiobo	1	0	1	0	0
Altona	0	0	0	0	1
Amsterdam	0	0	1	0	0
Anatum	42	70	25	32	5
Bareilly	1	0	0	0	0
Bardo	10	5	0	0	0
Berta	0	2	1	1	0
Bovismorbificans	30	18	3	8	6
Braenderup	2	2	5	2	2
Brandenburg	0	1	0	0	0
Bredeney	1	0	0	1	0
Cerro	0	0	1	0	1
Chester	0	0	3	2	3
Chomedey	0	0	1	0	0
Coeln	1	4	7	3	0
Corvallis	0	3	0	1	0
Cubana	0	0	1	0	1
Derby	49	40	35	45	40
Dublin	321	274	258	230	320
Durham	0	0	1	0	0
Eboko	0	1	0	0	0
Enteritidis	11	25	11	13	16
Essen	1	0	0	0	0
Ferruch	2	0	0	0	0
Fresno	0	0	1	0	0
Gaminara	1	1	0	0	0
Give	6	3	14	5	24

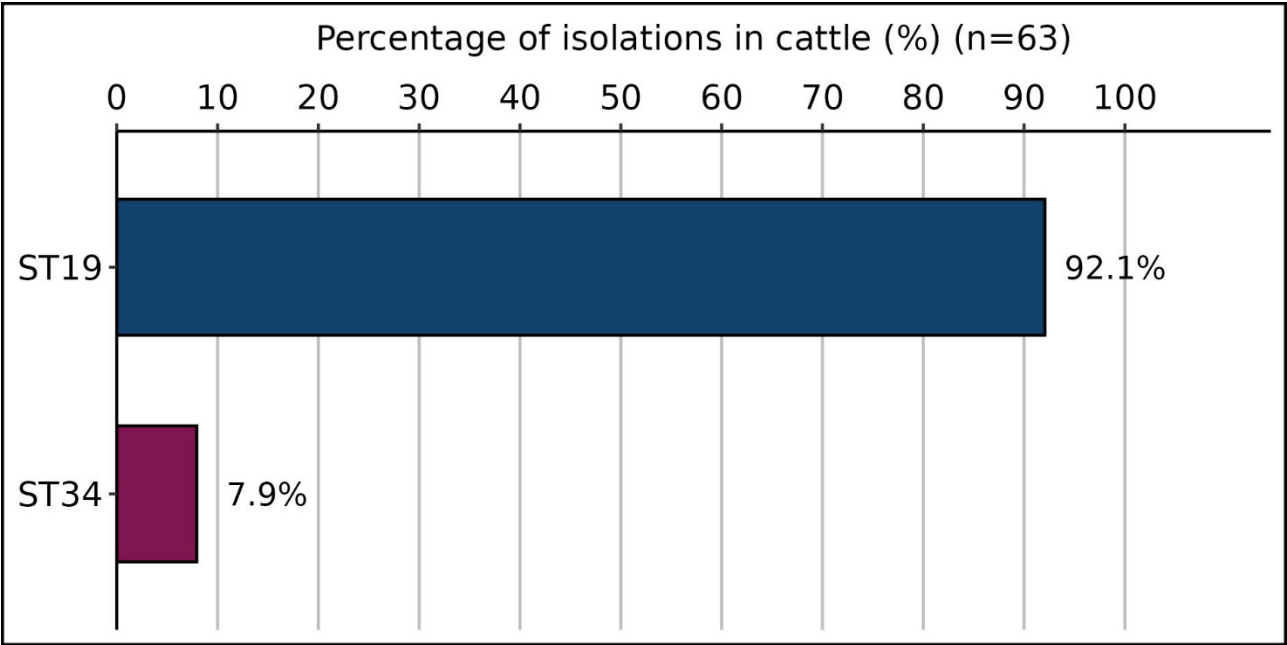
<i>Salmonella</i> serovar	2021 isolations	2022 isolations	2023 isolations	2024 isolations	2025 isolations
Give var. 15⁺	23	23	5	3	0
Goldcoast	1	0	0	0	5
Grumpensis	0	0	0	0	1
Hadar	1	17	6	2	0
Havana	2	6	0	1	0
Hessarek	0	0	0	1	0
Idikan (including monophasic variants)	288	390	686	684	909
Indiana	44	40	57	166	82
Infantis	42	98	64	20	27
Isangi	3	0	0	0	2
Javiana	0	0	0	2	0
Kedougou (including monophasic variants)	235	310	583	410	439
Kentucky	0	4	1	18	5
Kingston	1	3	2	2	3
Kottbus	15	7	15	16	13
Lexington	10	9	8	1	8
Liverpool	0	1	0	0	0
Livingstone	18	3	14	8	5
London	12	14	2	2	3
London var 15⁺	0	1	0	0	0
Mbandaka	369	754	351	213	291
Meleagridis	0	0	0	0	1
Menston	2	0	0	0	0
Minnesota	1	0	0	0	1
Molade	1	0	0	0	0
Monophasic Typhimurium	100	79	83	75	70
Montevideo	454	491	621	346	365
Muenchen	4	9	5	27	20
Muenster	0	0	3	0	0
Newport	62	33	25	69	44
Nottingham	7	4	0	1	0
Nima	0	0	0	0	1
Odozi	4	0	0	0	0
Ohio	55	50	37	44	83
Orion	12	3	3	3	4

<i>Salmonella</i> serovar	2021 isolations	2022 isolations	2023 isolations	2024 isolations	2025 isolations
Orion var. 15⁺	47	80	77	56	73
Oslo	3	0	4	4	4
Ouakam	0	0	0	0	1
Oxford	0	0	1	0	0
Panama	5	13	11	8	10
Paratyphi B var. Java	0	0	0	0	1
Poona	0	0	1	1	0
Reading	3	4	2	7	10
Richmond	0	0	0	0	1
Rissen	0	1	2	1	3
Schwarzengrund	0	0	2	0	2
Senftenberg	84	63	25	14	19
Stanley	0	1	0	0	0
Stanleyville	0	1	0	0	2
Stourbridge	3	1	0	0	0
Takoradi	0	1	0	0	0
Tennessee	0	1	0	0	2
Typhimurium	200	185	257	254	184
Uganda	0	0	0	0	4
Urbana	0	0	0	0	1
Virchow	0	0	0	0	3
Wangata	0	0	1	0	1
Yoruba	0	0	2	0	0
61:k:1,5,(7)	74	71	75	73	72
untypable strains	64	57	17	9	9
rough strains	33	32	2	0	0
Total	2,808	3,451	3,630	3,043	3,354

All serovars are *Salmonella* enterica subspecies enterica, with the exception of isolates of 61:k:1,5,(7), which are variants of *Salmonella* enterica subspecies diarizonae.

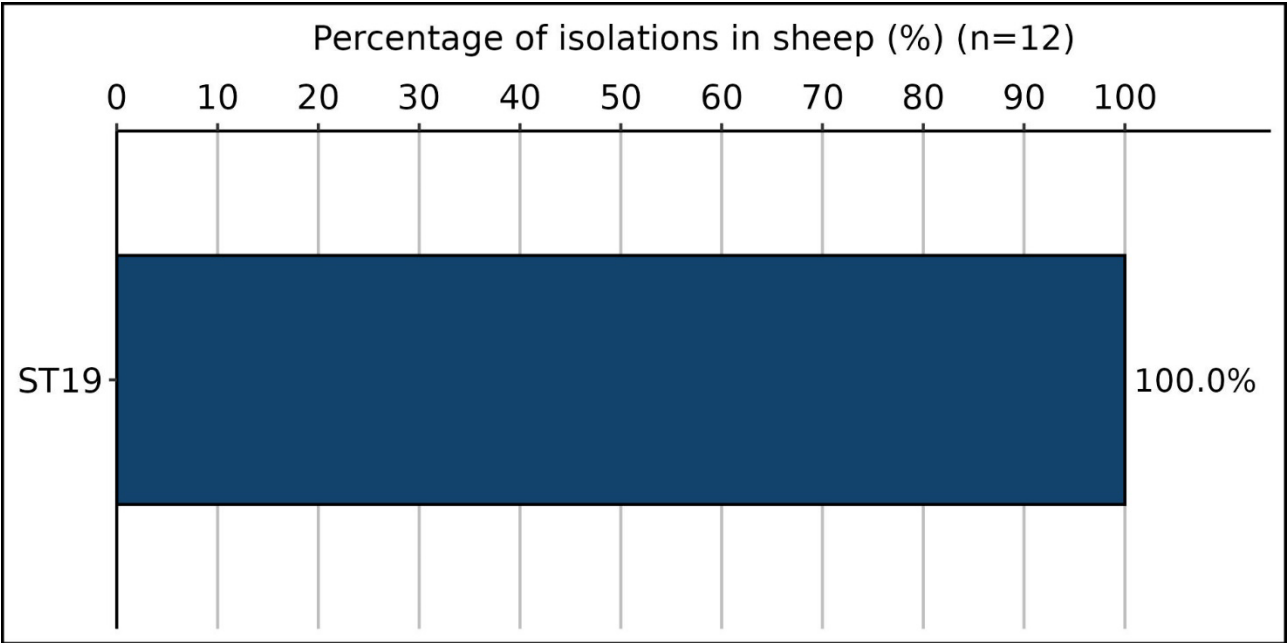
Figure 1.2: Isolations of *S. Typhimurium* sequence types (including monophasic strains) in livestock in 2025

Figure 1.2.1: Isolations in cattle



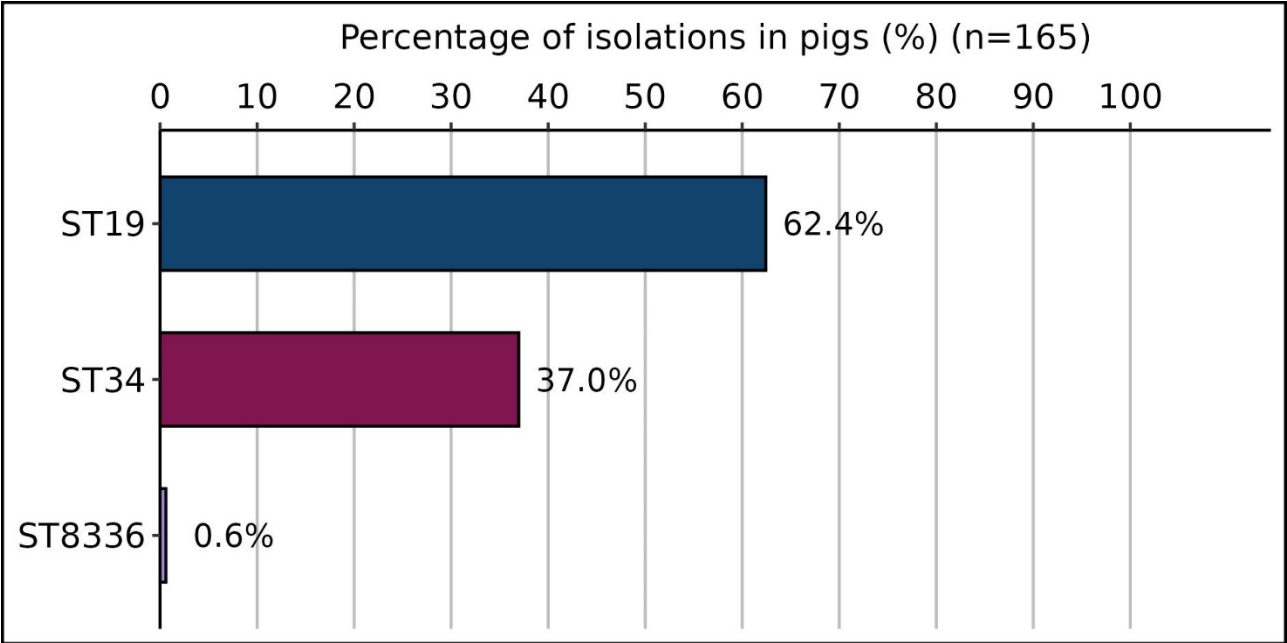
Horizontal bar graph showing the percentage of isolations of *Salmonella* Typhimurium (including monophasic strains) sequence types in cattle in 2025. The most common *S. Typhimurium* sequence type in cattle in 2025 was ST19 (92.1% of all cattle isolations) and the remaining 7.9% of sequence types were ST34.

Figure 1.2.2: Isolations in sheep



Horizontal bar graph showing the percentage of isolations of *Salmonella* Typhimurium (including monophasic strains) sequence types in sheep in 2025. All isolations of *S.* Typhimurium in sheep in 2025 were ST19.

Figure 1.2.3: Isolations in pigs

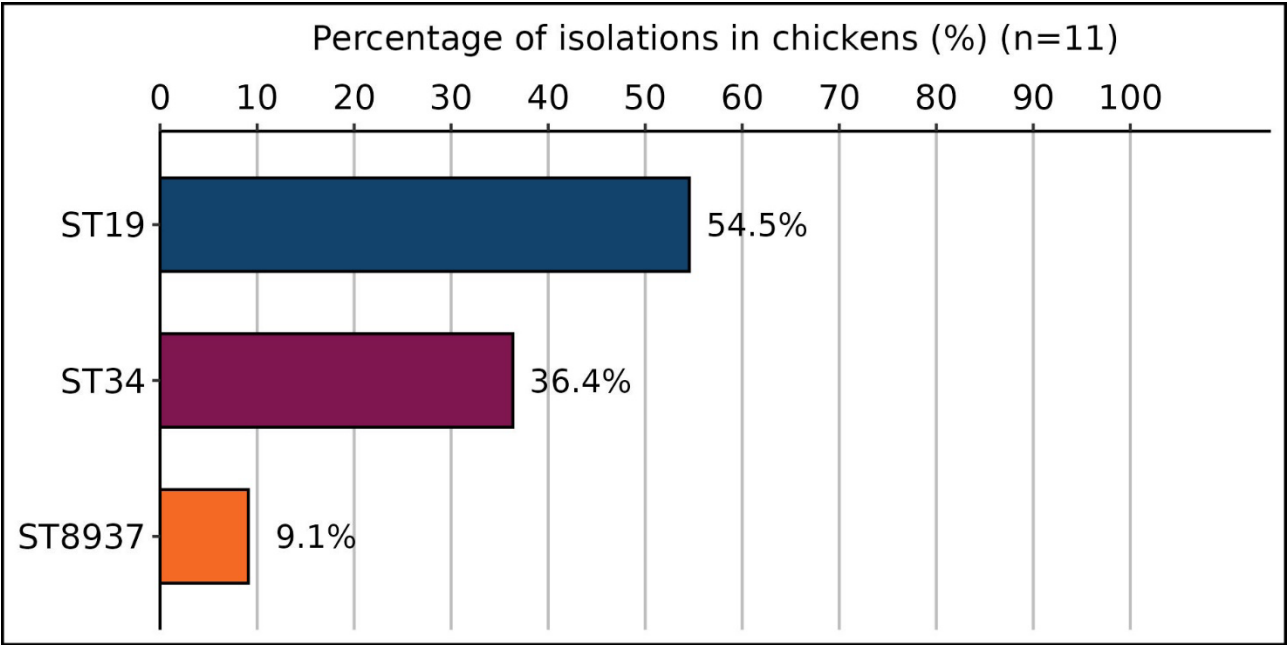


Horizontal bar graph showing the percentage of isolations of *Salmonella* Typhimurium (including monophasic strains) sequence types in pigs in 2025. The most common *S.*

Typhimurium sequence type in pigs in 2025 was ST19 (62.4% of all pig isolations), followed by ST34 (37.0%) and ST8336 (0.6%).

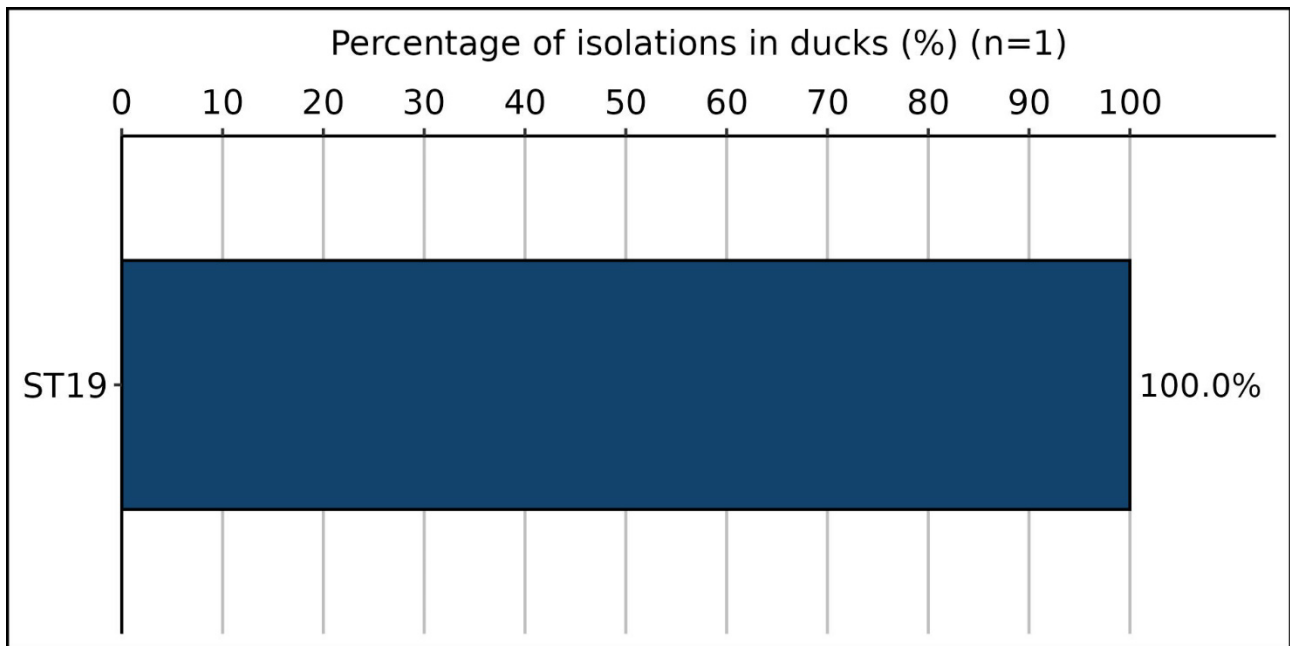
There were 2 isolations of *S. Typhimurium* in pigs in 2025 where sequence type data was not available. These are not included in this figure.

Figure 1.2.4: Isolations in chickens (statutory and non-statutory testing)



Horizontal bar graph showing the percentage of isolations of *Salmonella* Typhimurium (including monophasic strains) sequence types in chickens in 2025. The most common *S. Typhimurium* sequence type in chickens in 2025 was ST19 (54.5% of all chicken isolations), followed by ST34 (36.4%) and ST8937 (9.1%).

Figure 1.2.5: Isolations in ducks

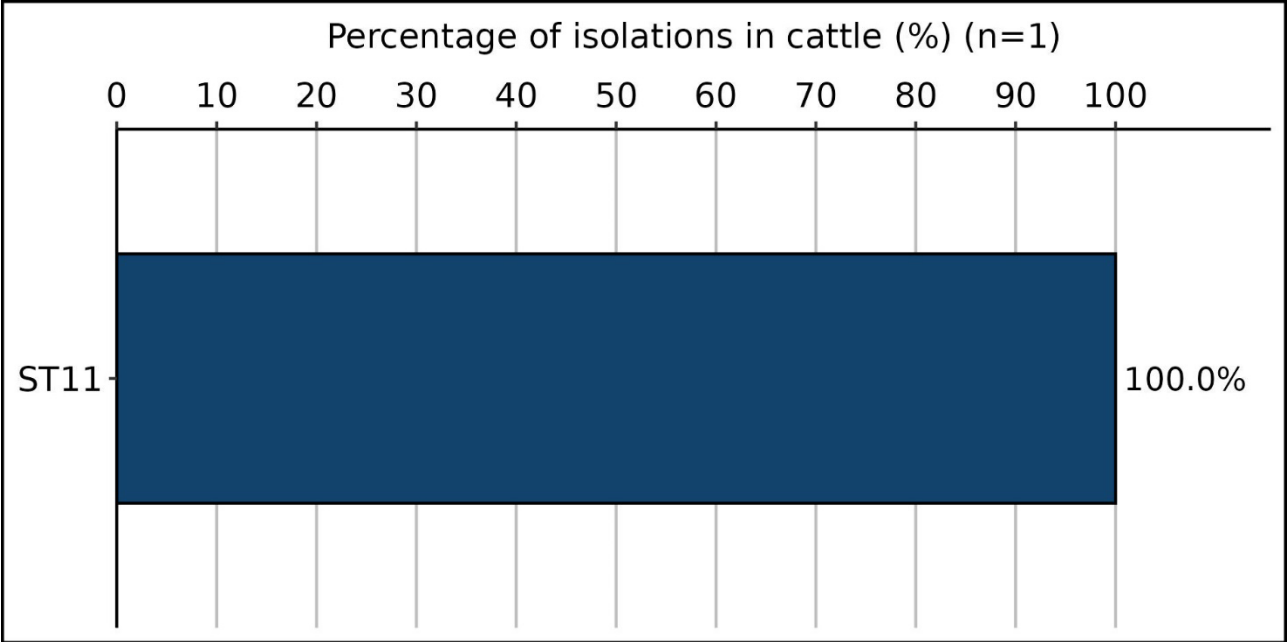


Horizontal bar graph showing the percentage of isolations of *Salmonella* Typhimurium (including monophasic strains) sequence types in ducks in 2025. All isolations of *S. Typhimurium* in ducks in 2025 were ST19.

There were no isolations of *S. Typhimurium* in turkeys in 2025.

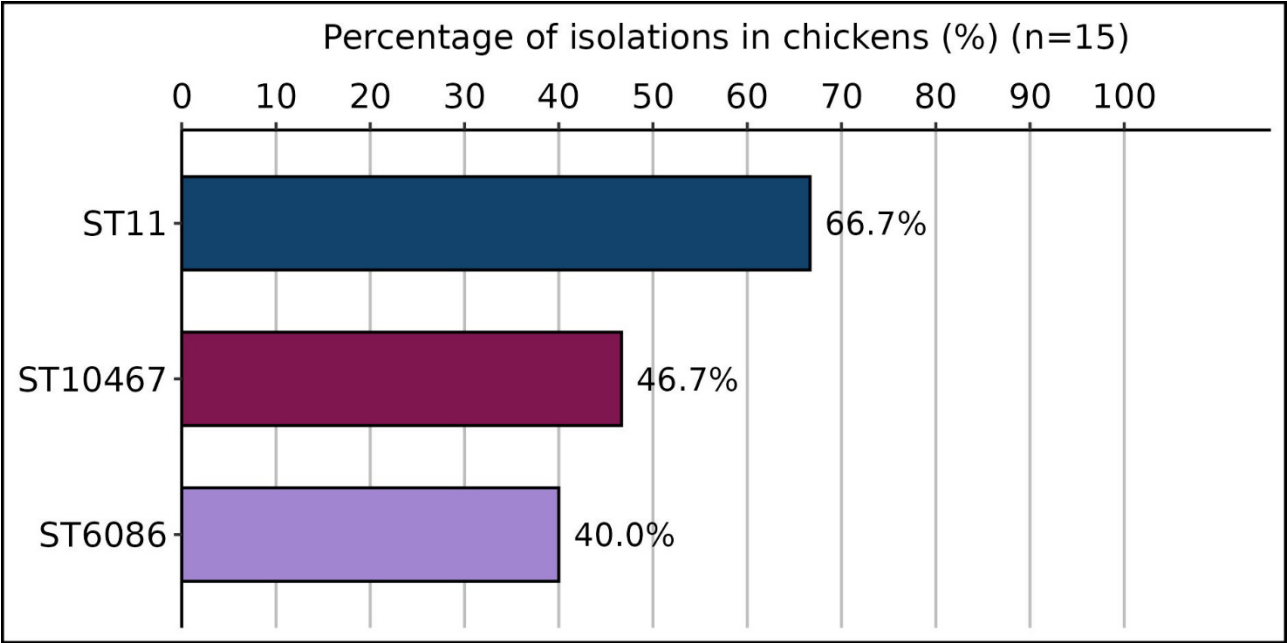
Figure 1.3: Isolations of *S. Enteritidis* sequence types in livestock in 2025

Figure 1.3.1 Isolations in cattle



Horizontal bar graph showing the percentage of isolations of *Salmonella* Enteritidis sequence types in cattle in 2025. All isolations of *S. Enteritidis* in cattle in 2025 were ST11.

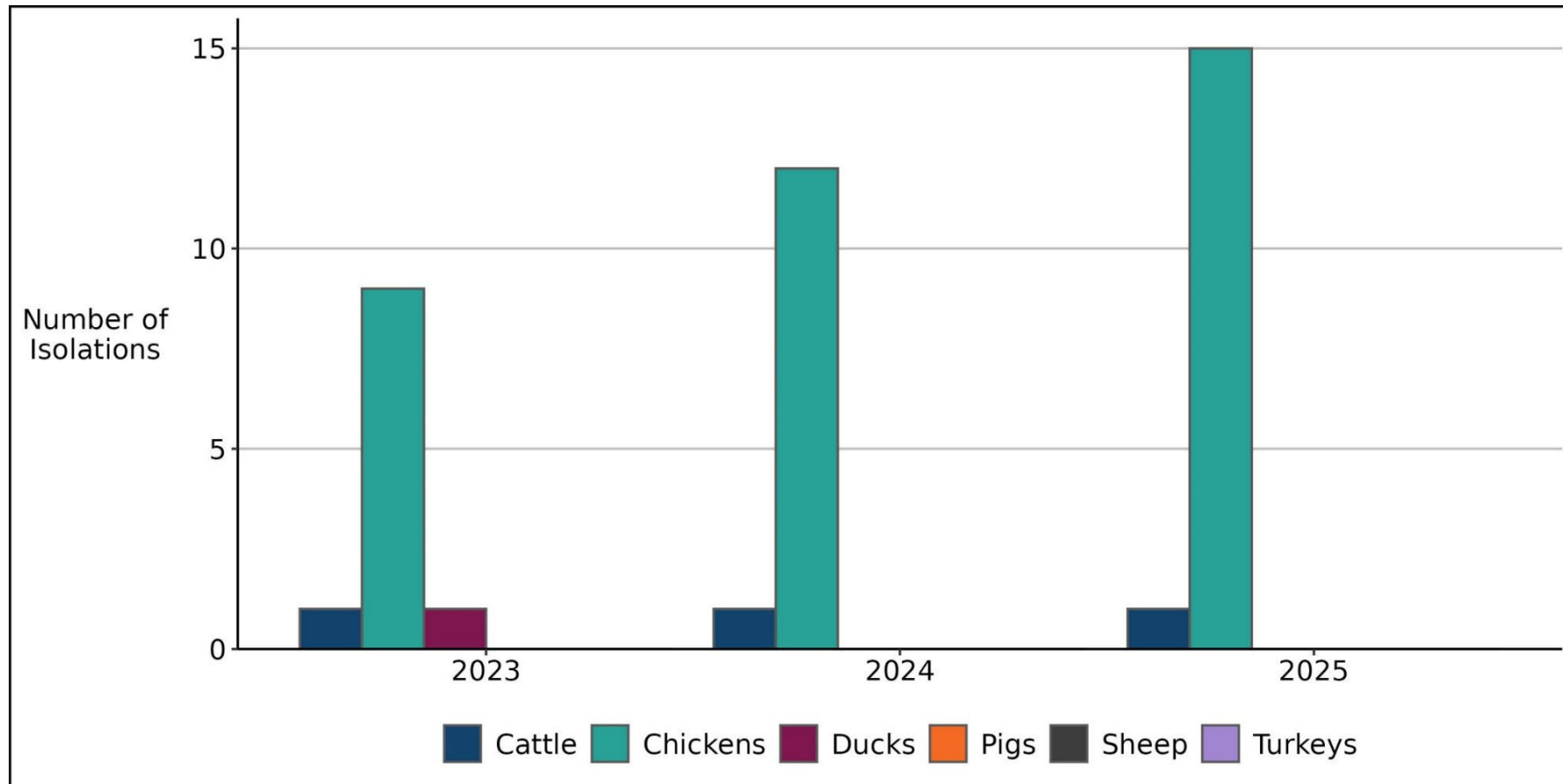
Figure 1.3.2 Isolations in chickens (statutory and non-statutory testing)



Horizontal bar graph showing the percentage of isolations of *Salmonella* Enteritidis sequence types in chickens in 2025. The most common *S. Enteritidis* sequence type in chickens in 2025 was ST11 (66.7% of all chicken isolations), followed by ST10467 (46.7%) and ST6086 (40.0%). In 2025 3 isolations of *S. Enteritidis* yielded 3 sequence types and 2 isolations yielded 2 sequence types. These are each counted only once in the total number of isolations, therefore summed percentages of all serovars exceeds 100%.

There were no isolations of *S. Enteritidis* in sheep, pigs, turkeys or ducks in 2025.

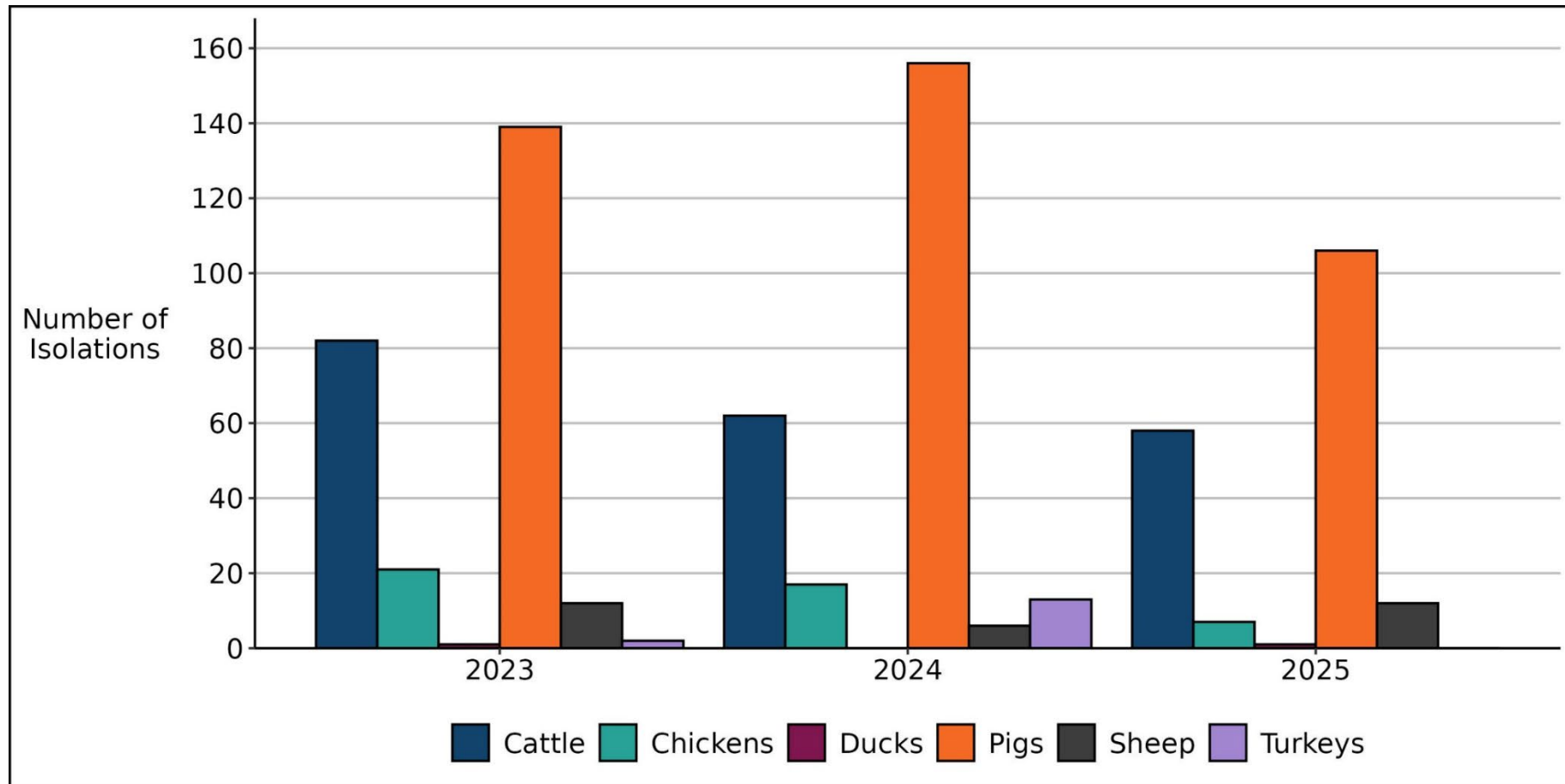
Figure 1.4: Isolations of *S. Enteritidis* in livestock in Great Britain 2023 to 2025



Vertical bar graph showing the number of isolations of *Salmonella* Enteritidis in cattle, chickens, ducks, pigs, sheep and turkeys in 2025. The figure shows *Salmonella* Enteritidis was most commonly isolated from chickens during 2025, and in fewer numbers from cattle. This compares to chickens also being the most commonly isolated species in 2024 and 2023. *S. Enteritidis* was isolated from ducks in 2023, though not in 2024 or 2025. *S. Enteritidis* was not isolated in pigs, sheep or turkeys in 2023, 2024 or 2025.

Data for chickens and turkeys include both statutory and non-statutory testing.

Figure 1.5: Isolations of *S. Typhimurium* in livestock in Great Britain 2023 to 2025

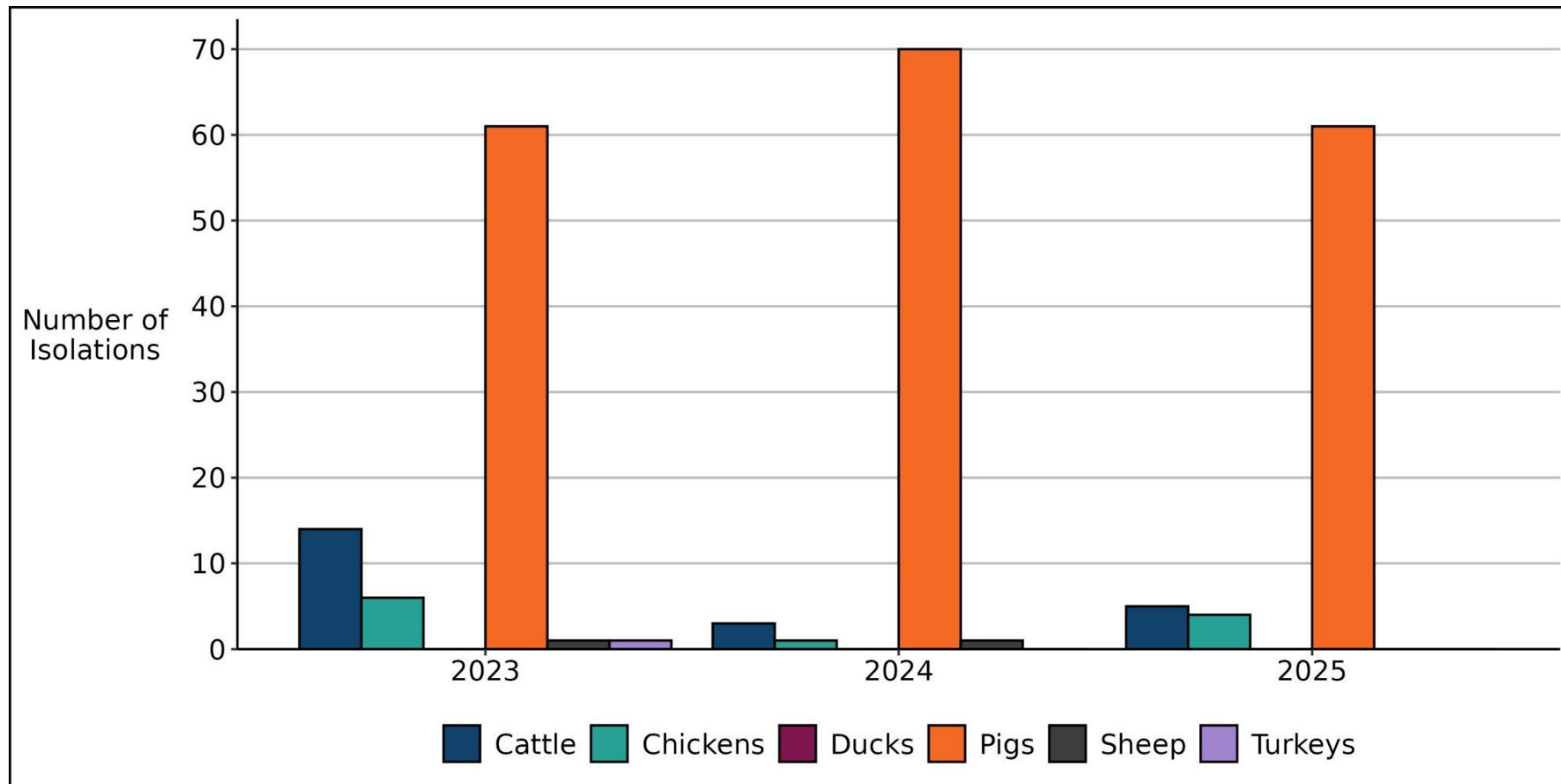


Vertical bar graph showing the number of isolations of *Salmonella Typhimurium* in cattle, chickens, ducks, pigs, sheep and turkeys in 2025. *Salmonella Typhimurium* was most commonly isolated from pigs amongst livestock species during 2025, and in lesser numbers

from cattle, chickens, ducks, sheep and turkeys. This compares to pigs also being the most commonly isolated species in 2024 and 2023. *S. Typhimurium* was also isolated from cattle, chickens, sheep and turkeys in 2024.

Data for chickens and turkeys include both statutory and non-statutory testing.

Figure 1.6: Isolations of monophasic *S. Typhimurium* in livestock in Great Britain 2023 to 2025



Vertical bar graph showing the number of isolations of monophasic *Salmonella* Typhimurium isolated in cattle, chickens, ducks, pigs, sheep and turkeys in 2025. Monophasic *S. Typhimurium* was most commonly isolated from pigs among livestock species during 2025,

and in lesser numbers from cattle and chickens. This compares to pigs also being the most commonly isolated species in 2024 and 2023. Monophasic *S. Typhimurium* was also isolated from cattle, chickens and sheep in 2024.

Data for chickens and turkeys include both statutory and non-statutory testing.

Chapter 2: Reports of *Salmonella* in cattle

The total number of cattle and calves in Great Britain decreased by 1.2% to 7.6 million, as recorded in the June 2025 agricultural survey. The number of commercial cattle holdings has also decreased by 2.5% to 50,797. Figure 2.1 shows the population data for all cattle (including calves) and the numbers of commercial cattle holdings in Great Britain, for the last 10 years.

During 2020 and 2021 there was a reduction in submissions for non-statutory surveillance and in diagnostic submissions in many species because of the Covid-19 pandemic and associated lockdown measures. This should therefore be borne in mind when comparing data including those years.

On the [Veterinary Investigation Diagnoses Analysis \(VIDA\) database](#) there were a total of 14,587 submissions recorded from cattle in 2025, which was a decrease of 11.8% compared to 2024 (16,530). Of these, 8,819 were diagnostic submissions, which compares with 9,062 diagnostic submissions in 2024. There is no active monitoring for *Salmonellae* in bovines, with nearly all isolations arising from diagnostic submissions (animals with clinical disease). These also include isolates from private laboratories.

Salmonella infection in cattle may be subclinical or be part of a clinical complex with other conditions influencing the clinical presentation. The majority of *Salmonella* isolates reported to APHA result from clinical investigations and diagnostic submissions in which *Salmonella* may be the causal pathogen or a secondary incidental finding. Surveillance data, including clinical signs, age and country information, associated with diagnoses of salmonellosis in cattle can be accessed through the [Cattle Dashboard | Tableau Public](#) link.

There were 466 *Salmonella* isolations from cattle in 2025, an increase of 27.3% from 2024 when there were 366 isolations (Table 2.1). There had been a general decreasing trend in isolations since 2021 when a total of 521 isolations were recorded. The three most common serovars were *S. Dublin*, *S. Typhimurium* and *S. Mbandaka*, which have been the most common serovars isolated from cattle every year since 2013 (Figure 2.2 and 2.3). In 2025 as in 2024, *S. Typhimurium* was the second most isolated serovar. The number of *S. Dublin* isolations, the commonest serovar in cattle, rose by 46.0% from 215 isolations in 2024 to 314 isolations in 2025. The proportion of *S. Dublin* isolations in relation to the total number of *Salmonella* isolations from cattle rose to 67.4% in 2025 compared to 58.7% in 2024. There was a reduction of 6.5% in isolations of *S. Typhimurium* in 2025, compared to 2024. Isolations of *S. Mbandaka* increased in 2025 by 20% compared to 2024.

Salmonella Dublin

The most common serovar isolated from cattle in Great Britain was *Salmonella* Dublin for the 26th successive year. There were 314 isolations, representing 67.4% of the total 466 *Salmonella* isolations from cattle and an increase of 46.0% for this serovar compared with 2024. The reason for this is likely to be multifactorial, with both on farm and between farm disease risks well known. Whilst there is a robust understanding of the disease, its control continues to present challenges. The issues of spread to naïve herds, concurrent disease, stress, cost of control measures including vaccine usage all have significant impacts. A comprehensive review of the control and risk factors associated with *S. Dublin* is provided in the article [Diagnosis and control of *Salmonella* Dublin in dairy herds](#) by Henderson and Mason from 2017.

As in previous years, the number of isolations peaked in the autumn (Figure 2.4). The seasonal peak seen with *S. Dublin* has always been attributed to a number of factors centred on the principle that housing increases faeco oral transmission rates. In addition, a number of stressful events typically take place such as weaning and calving of dairy heifers. Dietary changes represent a significant threat with introduction onto winter rations, though any dietary change without an effective transition period is a potential risk. Alimentary tract disease was the most common presentation in *S. Dublin*, with most incidents arising from cases reporting enteritis. This was recorded in all ages of animals, compared with isolations from abortions, a diagnosis restricted to adult cattle.

Salmonella Typhimurium and monophasic Salmonella Typhimurium

As stated, the second most common serovar isolated from cattle submissions in 2025 was *S. Typhimurium*. The number of isolations was similar to that in 2024 (58 versus 62 isolations), although was 29.3% lower compared to 2023 (82 isolations). The proportion of *Salmonella* Typhimurium in respect to total *Salmonella* isolations fell from 16.9% in 2024 to 12.4% in 2025. All isolations of *S. Typhimurium* in 2025 were sequence type (ST) 19 (Table 2.2) which has been the predominant sequence type reported in cattle in 2023-2025.

The number of isolations of monophasic *S. Typhimurium* increased from 3 in 2024 to 5 in 2025. All isolations in 2025 were ST34 (Table 2.3).

Salmonella Mbandaka

The third most common serovar in cattle was *S. Mbandaka* with 54 isolations representing 11.6% of the cattle isolations. This compared to 45 isolations in 2024 when it represented 12.3% of isolations.

Other serovars

The number of *Salmonella* Montevideo isolates, the fourth most common serovar in cattle decreased to 18 isolations in 2025 from 24 in 2024. Consistent with 2023 and 2024 there was one isolation of *S. Enteritidis* from cattle in 2025.

Reports of non-Great Britain origin

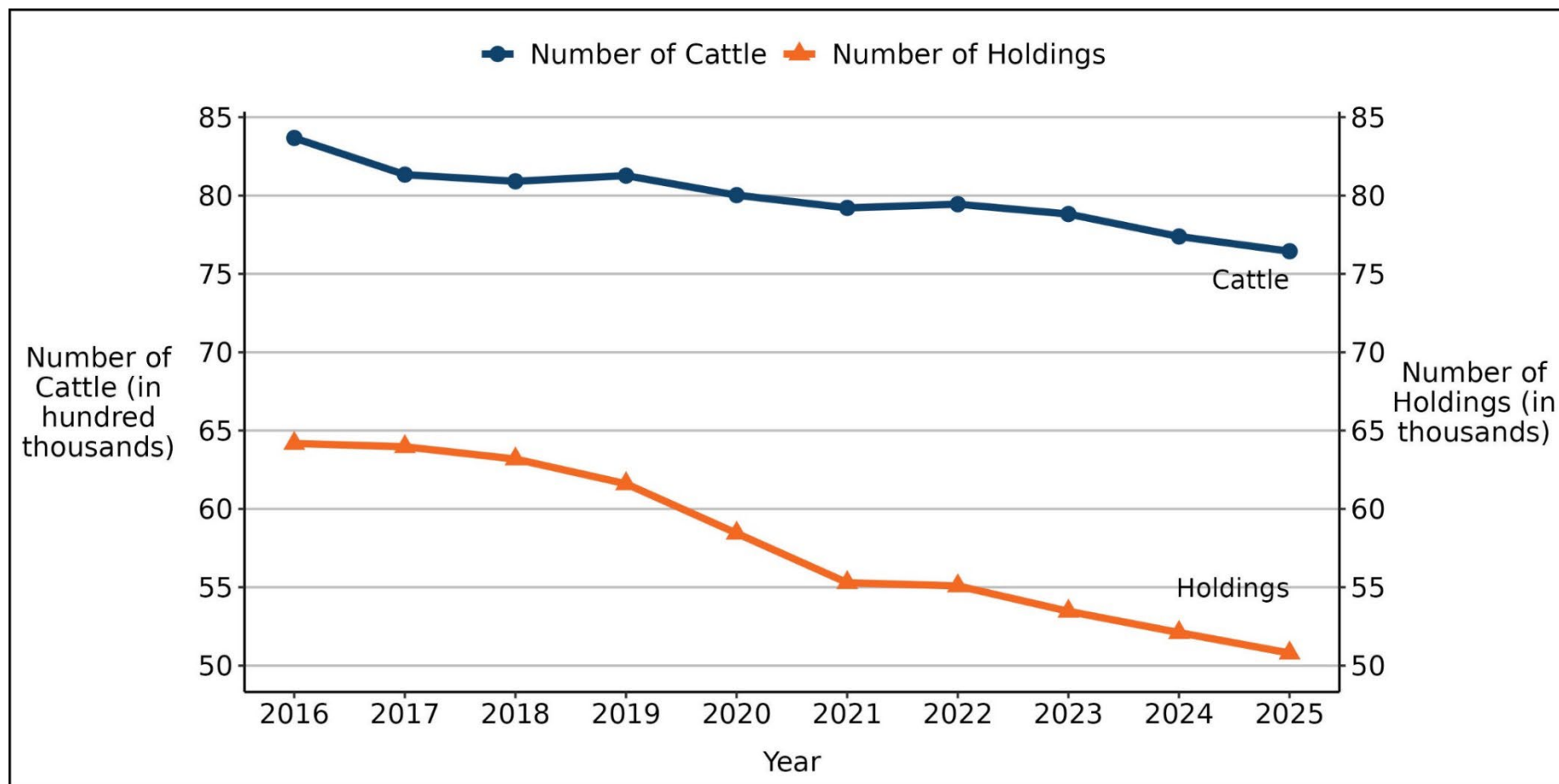
Two reports of *S. Dublin* in cattle imported from the Republic of Ireland were made following non statutory diagnoses. These reports are excluded from the tables and figures of this publication.

Antimicrobial susceptibility in cattle

A total of 456 isolates from cattle were tested against a panel of 16 antimicrobials in 2025. Fully susceptible isolates accounted for 93.6%, an increase from 2024 (89.6%). Only 5 isolates (1.1%) were MDR.

S. Dublin (14 isolates) and *S. Typhimurium* (11 isolates) were the most frequently resistant serovars. However, *S. Dublin* isolates were almost exclusively resistant to only one antimicrobial (one had 4 resistances and another had 5 resistances). The other MDR isolates comprised of 2 monophasic *S. Typhimurium* and one *S. Typhimurium*. Resistance patterns mainly included streptomycin (4.4%), tetracycline (3.5%), and sulphonamides (3.3%), all at low levels. One isolate showed resistance to amoxicillin/clavulanic acid – this was a *S. Mbandaka* isolate. None of the *Salmonella* isolates from cattle showed resistance to third-generation cephalosporins or fluoroquinolones, which are considered “highest priority critically important antibiotics” (HP-CIAs). Three isolates showed resistance to apramycin in 2025; none were detected in 2024. One isolate resistant to apramycin was detected in 2023.

Figure 2.1: Cattle population and numbers of commercial holdings with cattle in Great Britain 2016 to 2025



A line graph showing the cattle population and number of commercial holdings from 2016 to 2025. There was a steady decline in the number of cattle holdings since 2016 and while the number of cattle has also declined there was a small upturn in 2022 before declining again from 2023.

Scotland (animals and holdings) 2021 survey data used for 2022.

Number of holdings in 2020 is estimated.

Source: June 2025 Agricultural Survey. For the definition of a commercial holding in the agricultural survey, see the [survey methodology](#).

Table 2.1: Isolations and incidents of *Salmonella* in cattle on all premises in Great Britain 2021 to 2025

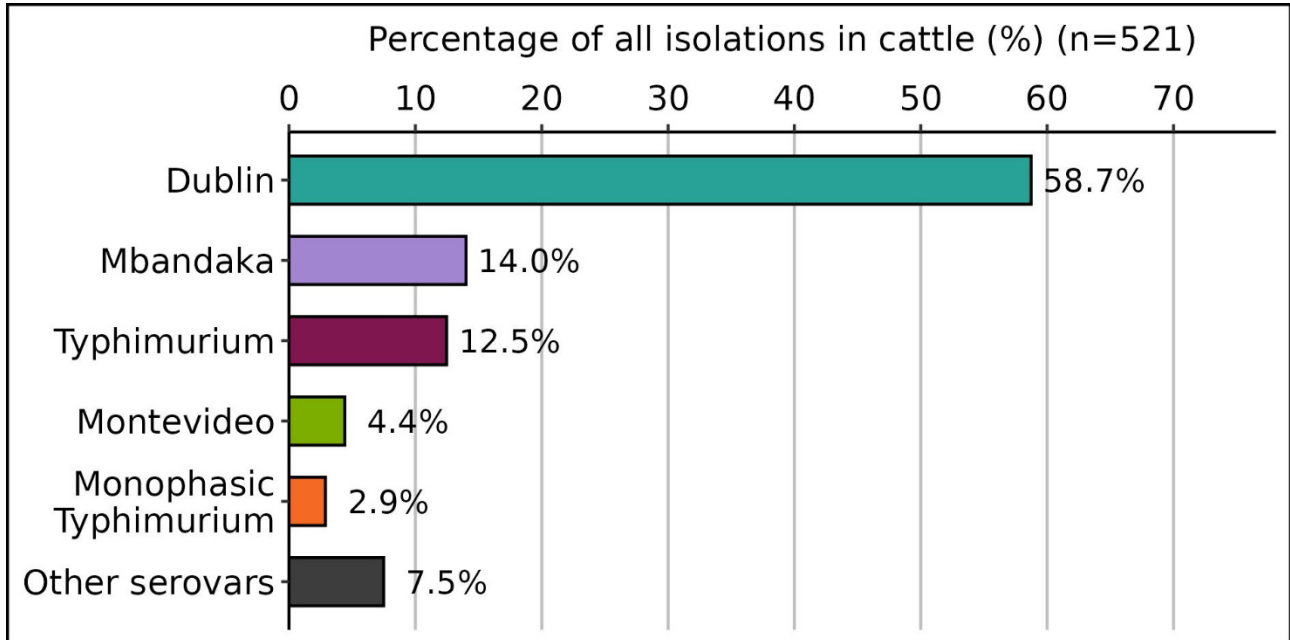
<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Agama	1	1	0	0	0	0	0	0	0	0
Agona	0	0	0	0	0	0	0	0	1	1
Anatum	5	4	1	1	1	1	1	1	0	0
Bovismorbificans	0	0	0	0	0	0	0	0	1	1
Bredeney	1	1	0	0	0	0	0	0	0	0
Chester	0	0	0	0	1	1	0	0	0	0
Coeln	1	1	0	0	3	2	2	1	0	0
Derby	0	0	0	0	1	1	0	0	1	1
Dublin	306	253	265	219	252	217	215	181	314	260
Enteritidis	1	1	0	0	1	1	1	1	1	1
Gaminara	1	1	1	1	0	0	0	0	0	0
Indiana	0	0	1	1	0	0	3	3	0	0
Infantis	0	0	0	0	1	1	0	0	0	0
Kingston	1	1	0	0	1	1	0	0	0	0
Kottbus	6	6	0	0	0	0	0	0	1	1
London	0	0	0	0	0	0	1	1	0	0
Mbandaka	73	64	59	54	46	42	45	40	54	48
Menston	2	2	0	0	0	0	0	0	0	0
Monophasic Typhimurium	15	14	3	3	14	12	3	3	5	4

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Montevideo	23	19	18	17	16	13	24	21	18	17
Muenster	0	0	0	0	1	1	0	0	0	0
Newport	2	2	0	0	3	3	3	3	4	4
Orion	0	0	0	0	0	0	1	1	0	0
Oslo	1	1	0	0	3	2	0	0	0	0
Panama	0	0	1	1	1	1	0	0	0	0
Stanleyville	0	0	0	0	0	0	0	0	1	1
Typhimurium	65	46	58	48	82	73	62	49	58	43
61:k:1,5,(7)	5	5	6	6	8	8	0	0	6	5
untypable strains	9	9	12	12	1	1	5	4	1	1
rough strains	3	3	5	5	0	0	0	0	0	0
Total	521	434	430	368	436	381	366	309	466	388

All serovars are subspecies *Salmonella enterica* subspecies *enterica*, with the exception of isolations of 61:k:1,5,(7), which are variants of *Salmonella enterica* subspecies *diarizonae*.

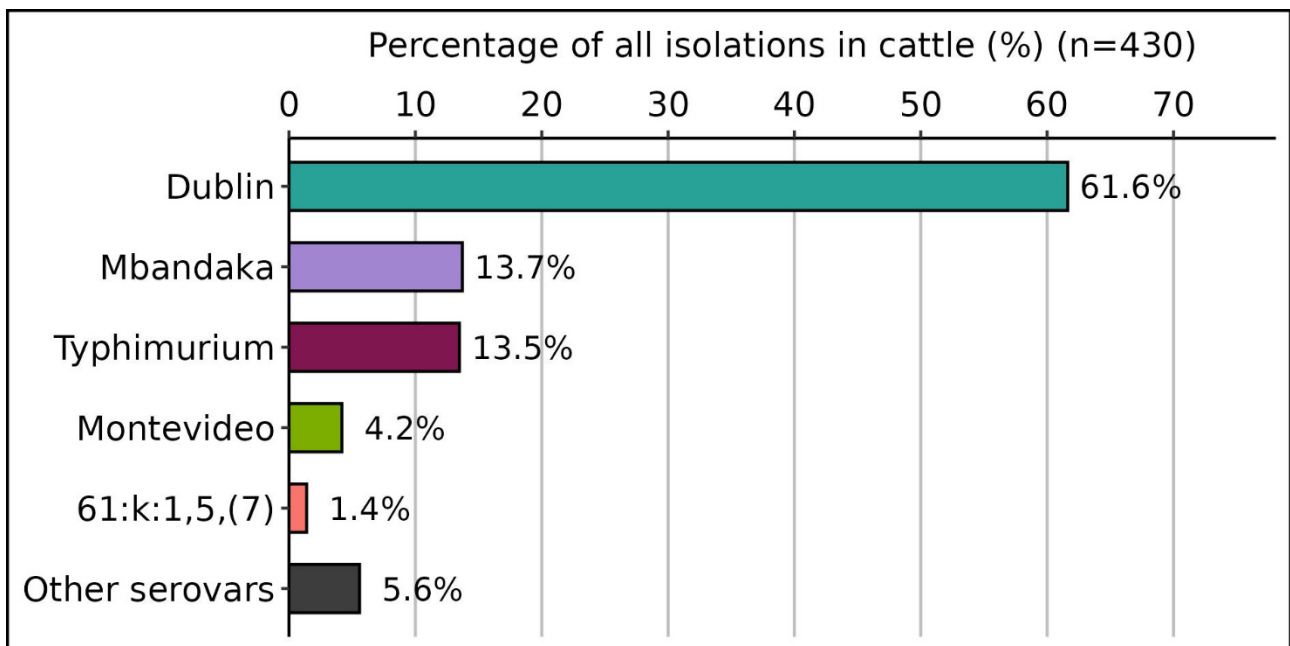
Figure 2.2: Isolations of the most common *Salmonella* serovars in cattle in Great Britain 2021 to 2025

Figure 2.2.1: Isolations in cattle in 2021



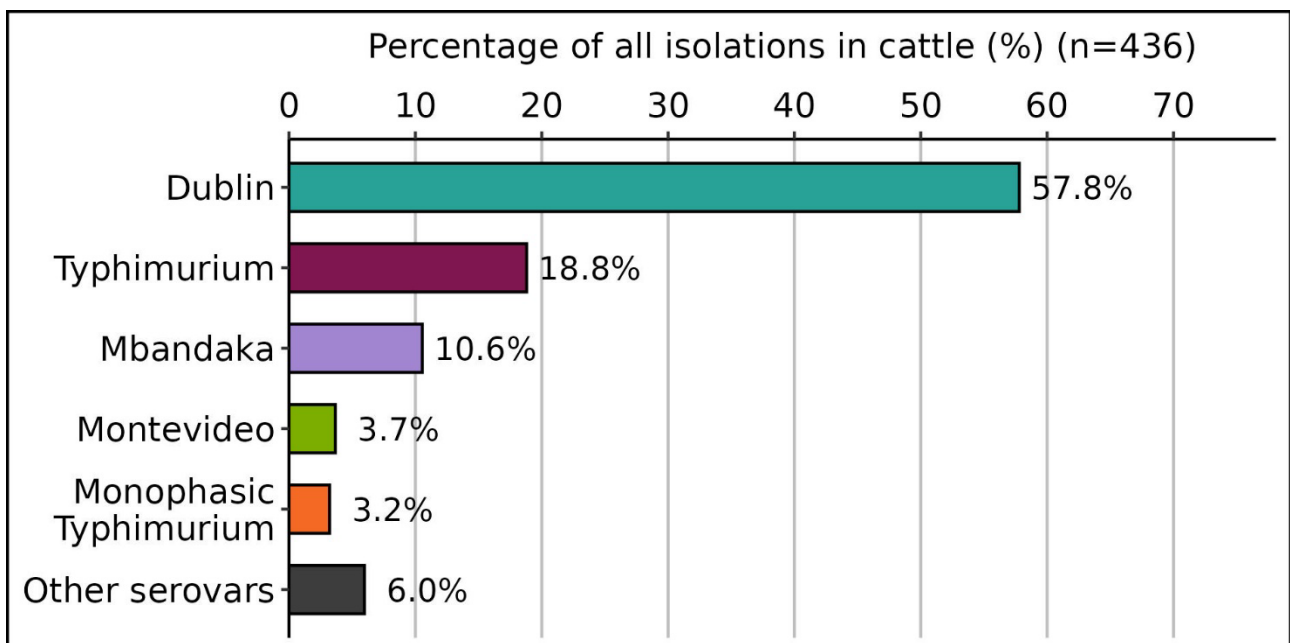
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in cattle in 2021. The most common serovar in cattle in 2021 was *S. Dublin* (58.7% of isolations), followed by *S. Mbandaka* (14.0% of isolations), *S. Typhimurium* (12.5% of isolations) and *S. Montevideo* (4.4% of isolations).

Figure 2.2.2: Isolations in cattle in 2022



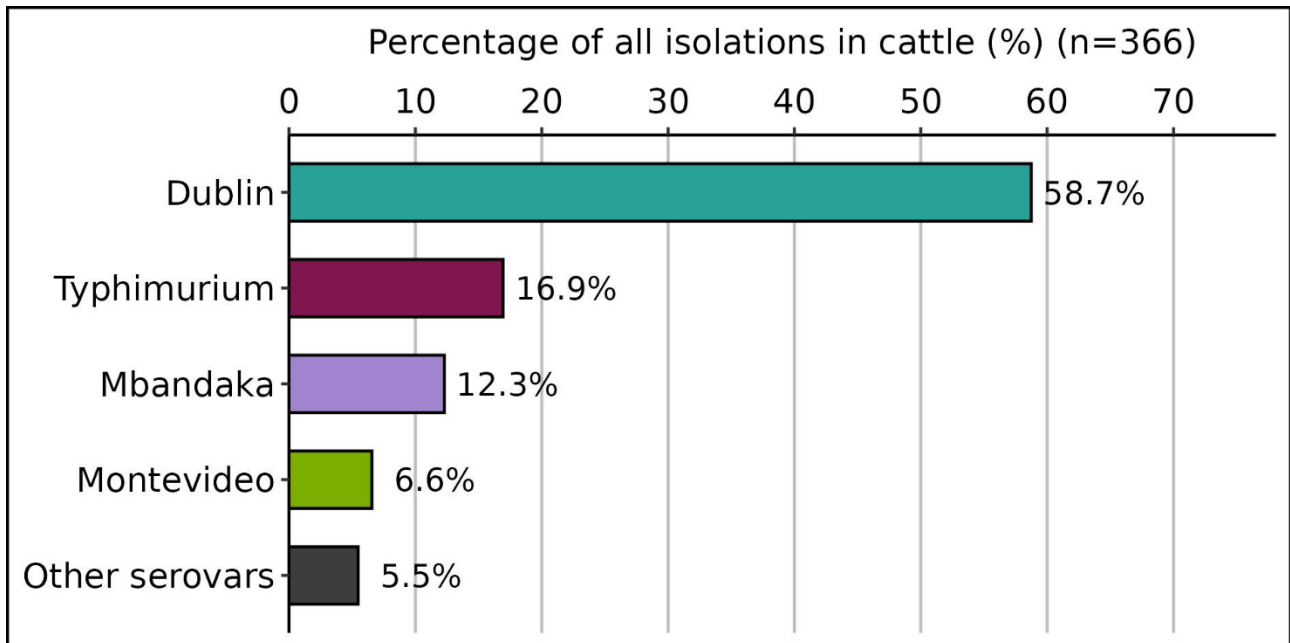
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in cattle in 2022. The most common serovar in cattle in 2022 was *S. Dublin* (61.6% of isolations), followed by *S. Mbandaka* (13.7% of isolations), *S. Typhimurium* (13.5% of isolations) and *S. Montevideo* (4.2% of isolations).

Figure 2.2.3: Isolations in cattle in 2023



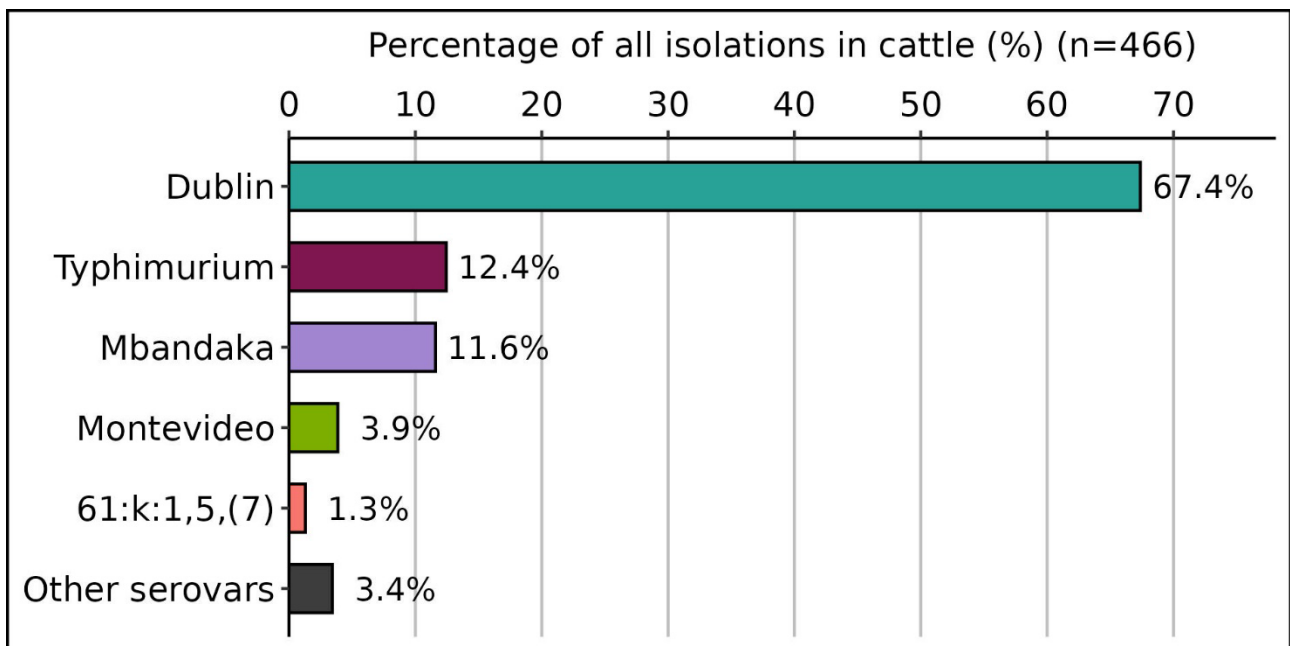
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in cattle in 2023. The most common serovar in cattle in 2023 was *S. Dublin* (57.8% of isolations), followed by *S. Typhimurium* (18.8% of isolations), *S. Mbandaka* (10.6% of isolations) and *S. Montevideo* (3.7% of isolations).

Figure 2.2.4: Isolations in cattle in 2024



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in cattle in 2024. The most common serovar in cattle in 2024 was *S. Dublin* (58.7% of isolations), followed by *S. Typhimurium* (16.9% of isolations) and *S. Mbandaka* (12.3% of isolations) and *S. Montevideo* (6.6% of isolations).

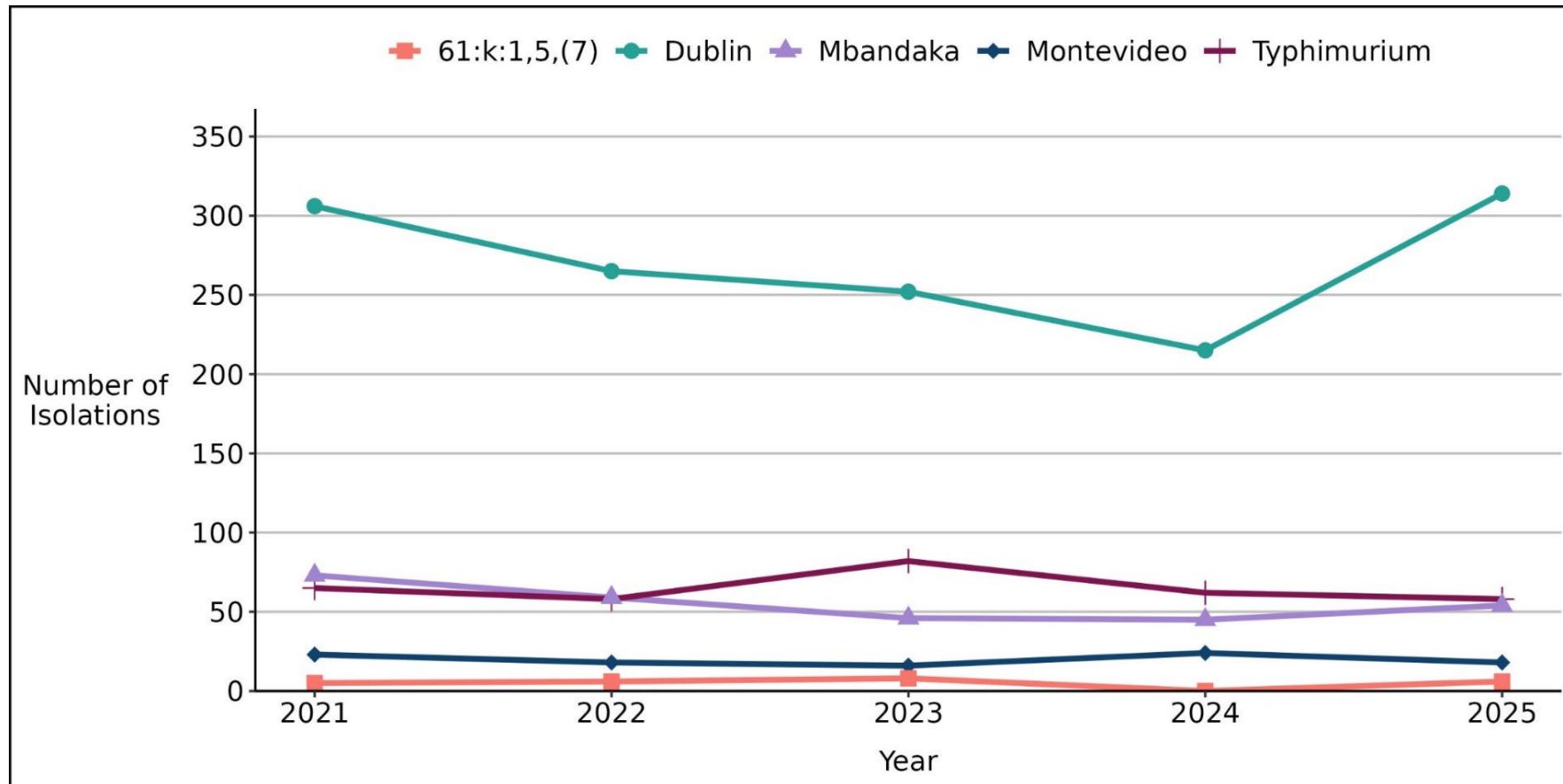
Figure 2.2.5: Isolations in cattle in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in cattle in 2025. The most common serovar in cattle in 2025 was *S. Dublin* (67.4% of isolations), followed by *S. Typhimurium* (12.4% of isolations) and *S. Mbandaka* (11.6% of isolations) and *S. Montevideo* (3.9% of isolations).

All isolations of 61:k:1,5,(7) are variants of *Salmonella enterica* subspecies *diarizonae*.

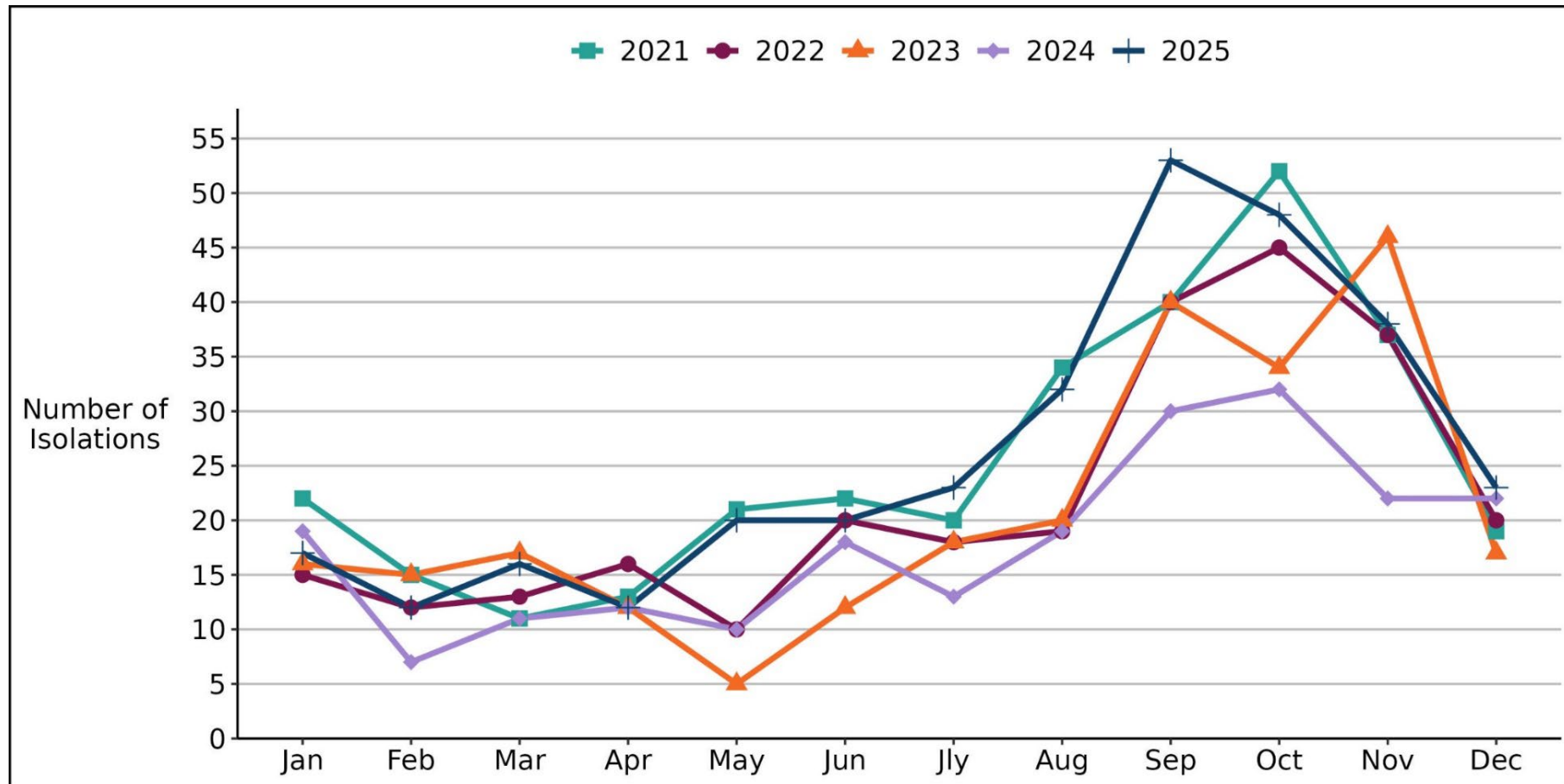
Figure 2.3: The 5 most common *Salmonella* serovars in cattle in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in cattle from 2021 to 2025. The figure shows the most common serovar in cattle for all years was *S. Dublin* with above 215 isolations in all years. There was a steady decline in isolations between 2021 and 2024 though in

2025 isolations increased to 314. The number of isolations of *S. Typhimurium*, *S. Mbandaka*, *S. Montevideo* and *Salmonella* 61:k:1,5,(7) have shown less fluctuation and were consistently less than 100.

Figure 2.4: Seasonality of *Salmonella* Dublin in cattle in Great Britain 2021 to 2025



A line graph showing the number of isolations of *Salmonella* Dublin each month in 2021 to 2025. It shows a marked seasonality in *S. Dublin* in all years peaking in September to November, dropping to lower levels in January to June.

Table 2.2: Sequence types of *S. Typhimurium* isolations in cattle in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	76	62	58
313	1	0	0
No ST data	5	0	0
Total	82	62	58

Table 2.3: Sequence types of monophasic *S. Typhimurium* isolations in cattle in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	2	0	0
34	12	3	5
Total	14	3	5

Table 2.4: Sequence types of *S. Enteritidis* isolations in cattle in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
11	0	1	1
6086	1	0	0
Total	1	1	1

Chapter 3: Reports of *Salmonella* in sheep and goats

Sheep

There was a decrease in total numbers of sheep in Great Britain in 2025, from 29.0 million animals in 2024 to 28.7 million animals in 2025, according to the June agricultural survey (Figure 3.1). In contrast, the numbers of commercial sheep holdings gradually increased from 2022 to 2024 and then plateaued in 2025, to just over 68,200.

During 2020 and 2021 there was a reduction in submissions for non-statutory surveillance and a reduction in diagnostic submissions in many species as a consequence of the Covid-19 pandemic and associated lockdown measures. This should therefore be borne in mind when comparing data from 2020 and 2021 with other years.

There were 5,623 diagnostic submissions recorded from sheep in Great Britain in 2025 compared to 6,040 diagnostic submissions in 2024, a decrease of 6.9%. This differs to the slight increase in submission numbers seen between 2023 and 2024. However there has been a general decreasing trend in submission numbers seen since 2016 (with the exception of 2021 when submissions increased compared to 2020).

Salmonella infection in sheep may be subclinical or be part of a clinical complex with other conditions influencing the clinical presentation. The majority of *Salmonella* isolates reported to APHA result from clinical investigations and diagnostic submissions in which *Salmonella* may be the causal pathogen or a secondary incidental finding. Surveillance data, including age category and geographical distribution, associated with diagnoses of salmonellosis in sheep can be accessed at [Sheep Dashboard | Tableau Public](#).

A total of 82 isolations of *Salmonella* were reported from sheep in 2025 compared to 101 isolations in 2024. This is the lowest number of isolations compared to the previous four years, with isolations ranging from 94 to 144 (Table 3.1).

Continuing the trend from 2008 onwards, *Salmonella enterica* subspecies *diarizonae* 61:k:1,5,(7), including its antigenic variants, was the most common *Salmonella* serovar isolated from sheep in 2025 (Figure 3.2.5). There were 57 isolations in 2025, within the annual range of 37 to 109 isolations seen since 2008. *Salmonella* Typhimurium (12 isolations), *S. Montevideo* (6 isolations), and *S. Dublin* (5 isolations) were the next most commonly isolated serovars. Although the number of isolations of these three serovars fluctuates year on year, they regularly appear within the top four most frequently isolated serovars from sheep. There were twice as many *Salmonella* Typhimurium isolations in 2025 compared to 2024, with isolation numbers within the typical range seen for this serovar over the preceding four years. Both *S. Montevideo* and *S. Dublin* isolations were

less than half the number of isolations compared to the preceding year, and isolation numbers were at the lower end of the typical range seen for each of these two serovars between 2021-2024.

Salmonella enterica subspecies diarizonae

Salmonella enterica subspecies *diarizonae* 61:k:1,5,(7) (and associated incompletely typable strains) is typically the most common *Salmonella* serovar isolated from sheep. In 2025 there were 57 isolations, accounting for 67.1% of the total isolations obtained from sheep samples (Figure 3.2.5). This is comparable to the percentage contribution of this serovar in 2024 (64.4%), 2023 (66.3%), and 2022 (69.1%) but higher than 2021 (47.9%). *S. enterica* subspecies *diarizonae* is considered a sheep adapted strain being regularly carried by healthy sheep and can be isolated from the reproductive, enteric, and occasionally the respiratory tract. It is considered to be of low pathogenic significance and isolation of the organism is generally considered an incidental finding. However, it can be associated with disease in individual sheep, often being detected in addition to other concurrent disease processes. In 2025, predominant clinical signs recorded included abortion, diarrhoea, and sudden death, with wasting and respiratory signs also reported.

Salmonella Typhimurium and monophasic Salmonella Typhimurium

Salmonella Typhimurium was the second most common serovar isolated from sheep in 2025, representing 14.6% of the total *Salmonella* isolations (Figure 3.2.5). Isolations were higher compared to 2024 (12 isolations versus 6 isolations) and were within the range seen for this serovar over the preceding four years (6-17 isolations). This year, the most common reason for submission was sudden death. Other clinical signs recorded were malaise and diarrhoea. There was one recorded case of abortion. Approximately half of the isolations were from adults, and the other half were from younger age categories, with neonatal, pre-weaned, and post-weaned lambs all represented.

Sequence typing was carried out on all 12 of the *S. Typhimurium* isolations from sheep in 2025; all 12 isolations were sequence type 19 (Table 3.3).

There were no isolations of monophasic *S. Typhimurium* in 2025, compared to a single isolation each year for the preceding two years.

Salmonella Montevideo

Salmonella Montevideo was the third most commonly isolated serovar from sheep in 2025 with a total of 6 isolations accounting for 7.3% of all isolations from sheep (Figure 3.2.5). Some strains of *S. Montevideo* are considered endemic within Great Britain's sheep

population. As in all previous years, abortion was the principal presenting clinical sign in submissions. This serovar can also be found in birds and poultry and as a contaminant of animal feed.

Salmonella Dublin

There were 5 isolations of *Salmonella* Dublin in sheep in 2025, representing 6.1% of the total sheep *Salmonella* isolations (Figure 3.2.5), making it the fourth most common serovar. This was a marked decrease compared to 2024 (14 isolations), which represented 13.9% of total sheep *Salmonella* isolations for that year (Figure 3.2.4). Isolation numbers were close to the lower end of the range seen for this serovar over the preceding four years (4-14 isolations). Although typically a cattle adapted strain, infection in sheep was predominately associated with sudden deaths and abortion in 2025.

Other serovars

There were single isolations of *S. Chester* and *S. Urbana* in 2025. *S. Chester* has never previously been reported in sheep in GB. Details of clinical signs were not available for this isolation. The main clinical sign for the *S. Urbana* isolation was abortion. This serovar was last reported from sheep in GB in 2017.

Antimicrobial susceptibility in sheep

A total 60 isolates from sheep were tested against a panel of 16 antimicrobials in 2025. The proportion of fully susceptible *Salmonella* isolates in sheep remained above 90.0% (91.7%), consistent with findings from previous years.

None of the isolates tested were classed as MDR. Only 4 isolates showed resistances: 2 to only neomycin (61:k:1,5,7), one *S. Montevideo* showing resistance to only tetracycline, and one *S. Typhimurium* showing resistance to tetracycline, streptomycin, and sulphonamides. None of the *Salmonella* isolates from sheep showed resistance to third-generation cephalosporins or fluoroquinolones, which are considered “highest priority critically important antibiotics” (HP-CIAs).

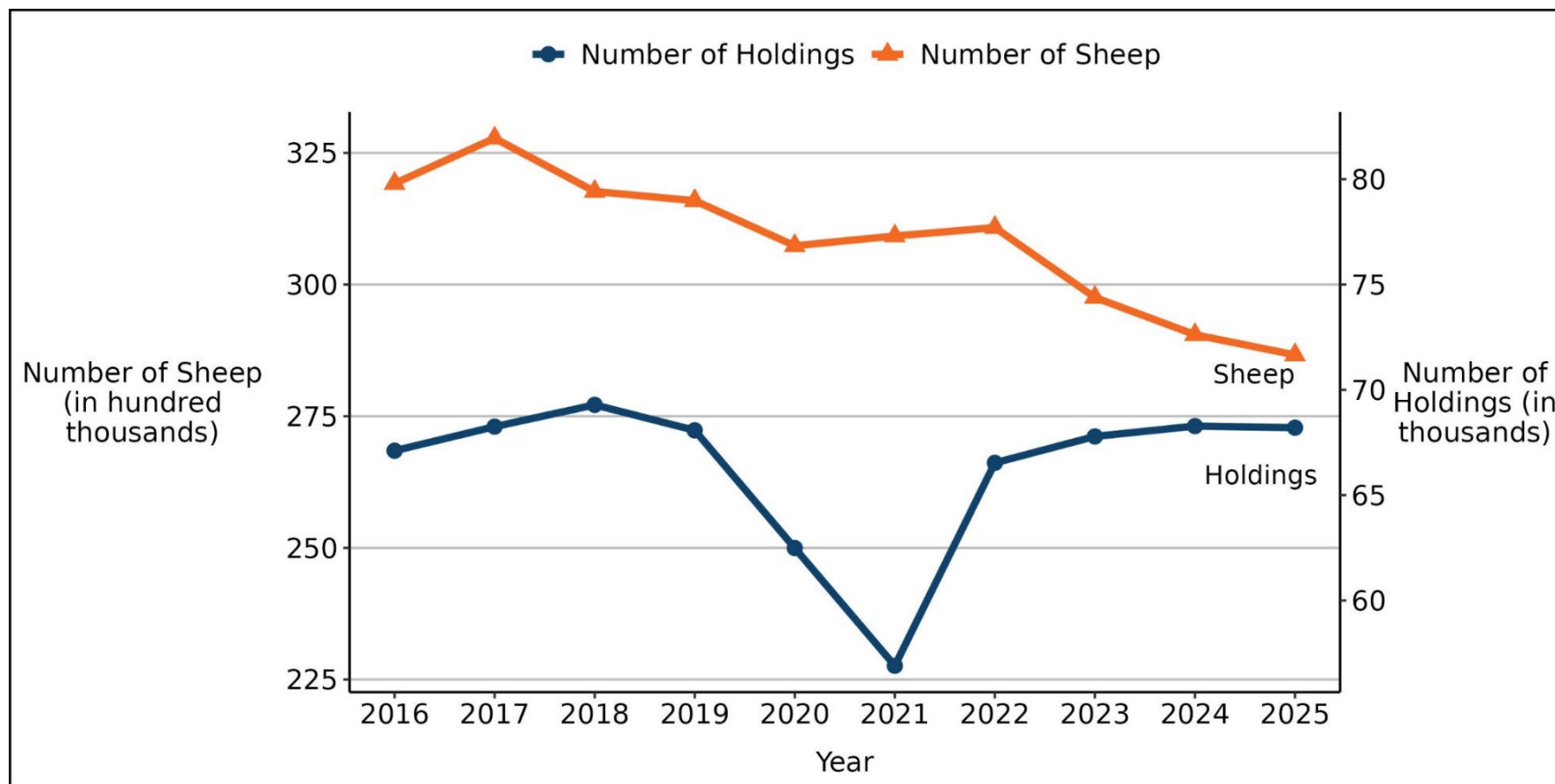
Goats

The Great Britain goat population fell slightly in 2025 to 104,781 compared to 106,716 in 2024 (June 2025 Agricultural Survey).

There were 378 diagnostic submissions recorded from goats in 2025 compared to 505 diagnostic submissions in 2024, a decrease of 25.1%. This differed from the increase of 13.7% in diagnostic submissions between 2023 and 2024.

Salmonellae are seldom isolated from goats, in most years single or no isolations are reported. There were no isolations of *Salmonella* in goats during 2025.

Figure 3.1: Sheep population and number of commercial holdings with sheep in Great Britain 2016 to 2025



A line graph showing the sheep population and number of commercial holdings from 2016 to 2025 in Great Britain. Sheep holding numbers were relatively constant until 2019 when they declined in 2020 and 2021, followed by an upturn until 2024 before a small

decrease to 68,206 holdings in 2025. The number of sheep in Great Britain increased peaking in 2017 with approximately 32,800,000 after which it declined until 2020 before increasing again to approximately 31,000,000 in 2022. Numbers in 2023, 2024 and 2025 declined to approximately 28,660,000 in 2025.

Scotland (animals and holdings) 2021 survey data used for 2022.

Source: June 2025 Agricultural Survey. For the definition of a commercial holding in the agricultural survey, see the [survey methodology](#).

Table 3.1: Isolations and incidents of *Salmonella* in sheep on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Agama	1	1	1	1	0	0	1	1	0	0
Ajiobo	1	1	0	0	0	0	0	0	0	0
Anatum	1	1	0	0	0	0	0	0	0	0
Chester	0	0	0	0	0	0	0	0	1	1
Derby	1	1	1	1	1	1	0	0	0	0
Dublin	14	12	5	4	4	4	14	13	5	5
Enteritidis	0	0	2	2	0	0	0	0	0	0
Indiana	1	1	0	0	0	0	0	0	0	0
Infantis	0	0	0	0	1	1	0	0	0	0
Kingston	0	0	1	1	0	0	0	0	0	0
Mbandaka	1	1	0	0	0	0	0	0	0	0
Monophasic Typhimurium	1	1	2	2	1	1	1	1	0	0
Montevideo	28	18	5	5	13	10	14	12	6	5
Ohio	0	0	1	1	1	1	0	0	0	0
Stourbridge	1	1	0	0	0	0	0	0	0	0
Typhimurium	17	13	8	8	12	11	6	6	12	10
Urbana	0	0	0	0	0	0	0	0	1	1
61:k:1,5,(7)	69	66	65	61	65	64	65	64	57	53
untypable strains	8	8	1	1	0	0	0	0	0	0

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
rough strains	0	0	2	2	0	0	0	0	0	0
Total	144	125	94	89	98	93	101	97	82	75

All serovars are subspecies *Salmonella enterica* subspecies *enterica*, with the exception of isolations of 61:k:1,5,(7), which are variants of *Salmonella enterica* subspecies *diarizonae*.

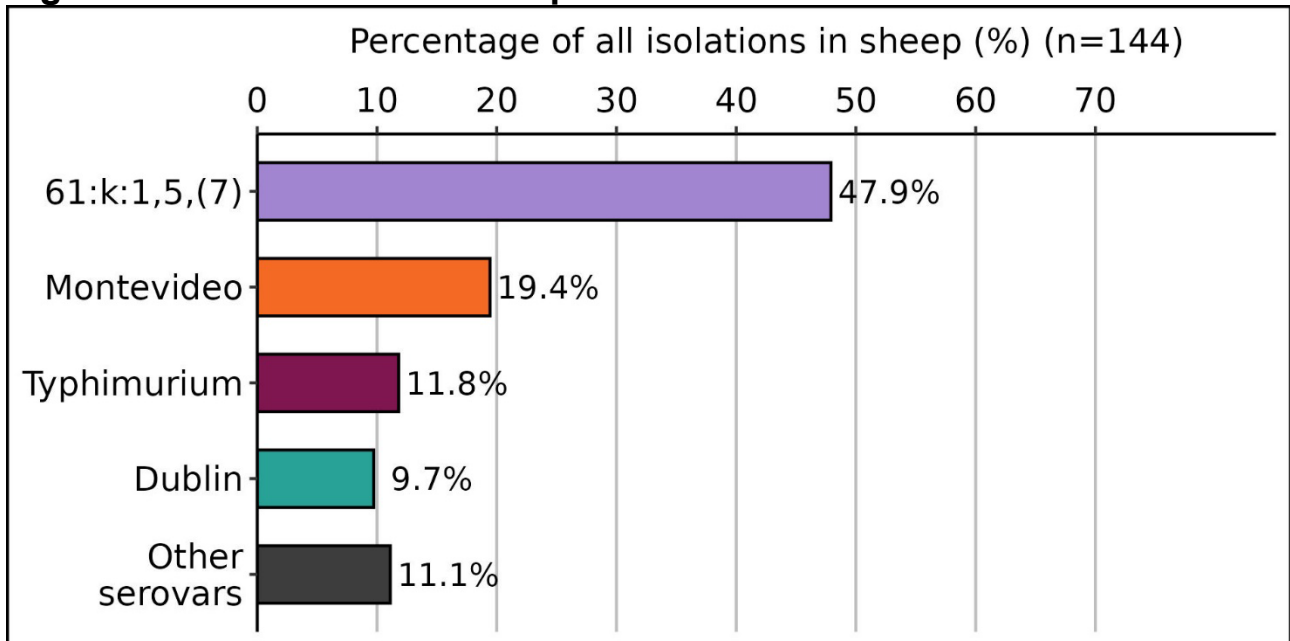
Table 3.2: Isolations and incidents of *Salmonella* in goats on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Dublin	1	1	0	0	0	0	1	1	0	0
61:k:1,5,(7)	1	1	2	2	1	1	1	1	0	0
Total	2	2	2	2	1	1	2	2	0	0

All serovars are subspecies *Salmonella enterica* subspecies *enterica*, with the exception of isolations of 61:k:1,5,(7), which are variants of *Salmonella enterica* subspecies *diarizonae*.

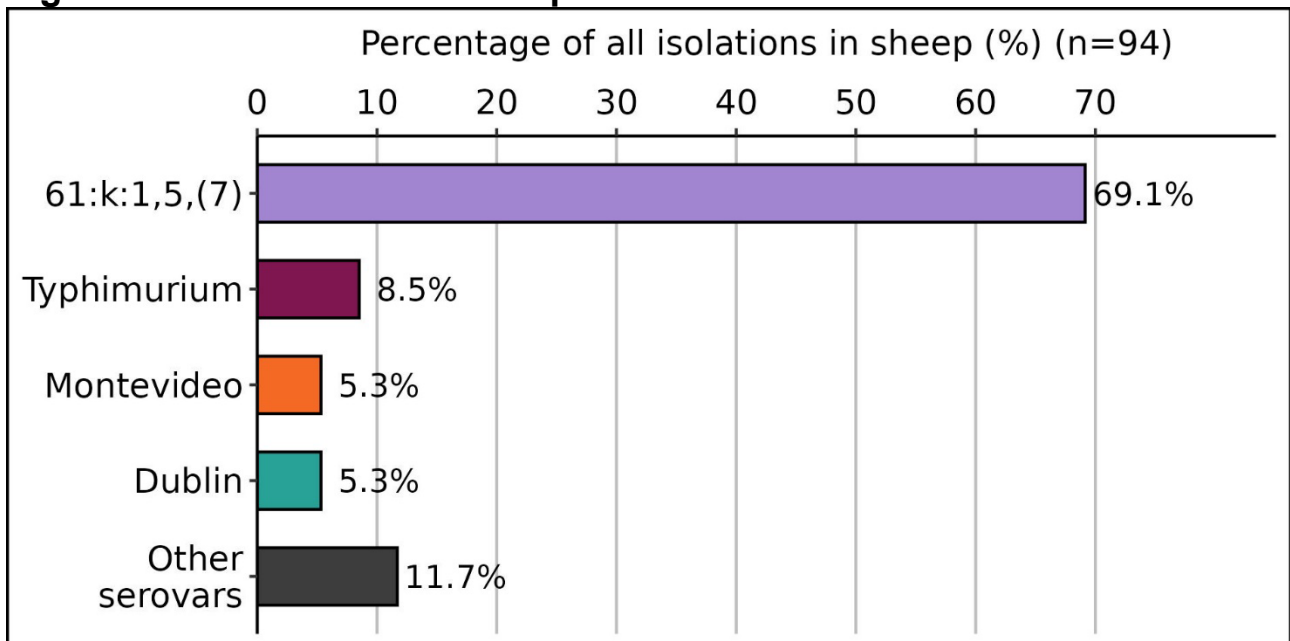
Figure 3.2: Isolations of the most common *Salmonella* serovars in sheep in Great Britain 2021 to 2025

Figure 3.2.1: Isolations in sheep in 2021



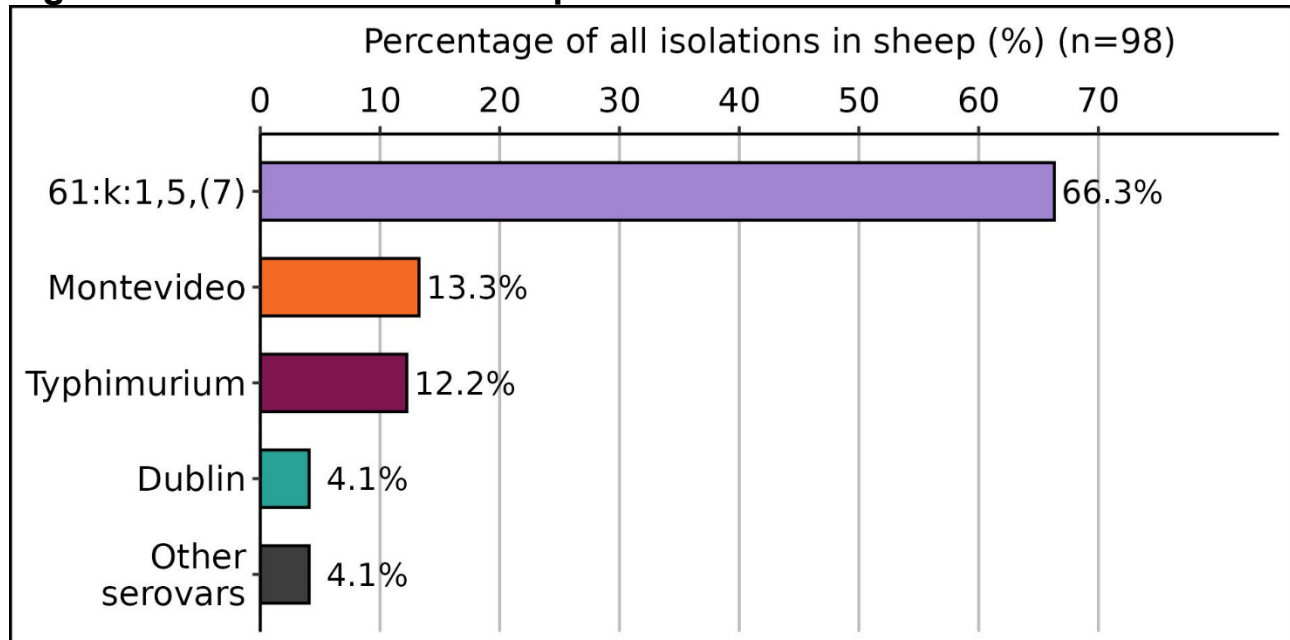
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in sheep in 2021. The most common serovar in sheep in 2021 was *Salmonella* 61:k:1,5,(7) (47.9% of isolations), followed by *S. Montevideo* (19.4% of isolations), *S. Typhimurium* (11.8% of isolations) and *S. Dublin* (9.7% of isolations).

Figure 3.2.2: Isolations in sheep in 2022



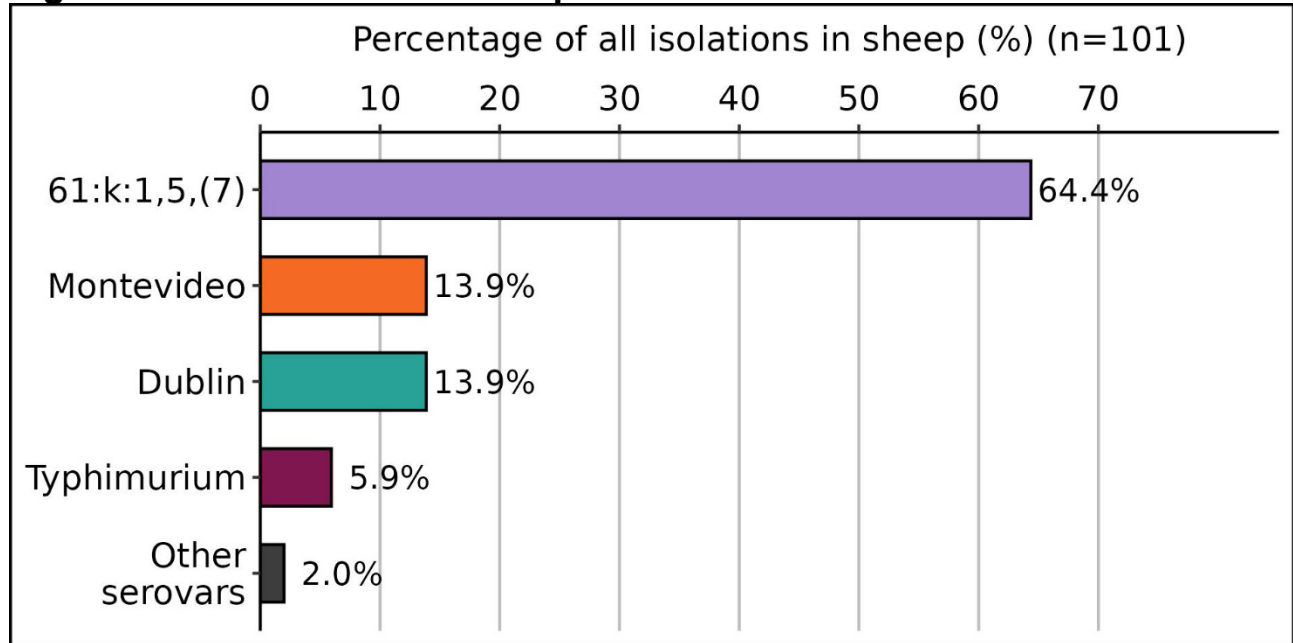
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in sheep in 2022. The most common serovar in sheep in 2022 was *Salmonella* 61:k:1,5,(7) (69.1% of isolations), followed by *S. Typhimurium* (8.5% of isolations), *S. Dublin* and *S. Montevideo* (5.3% of isolations each).

Figure 3.2.3: Isolations in sheep in 2023



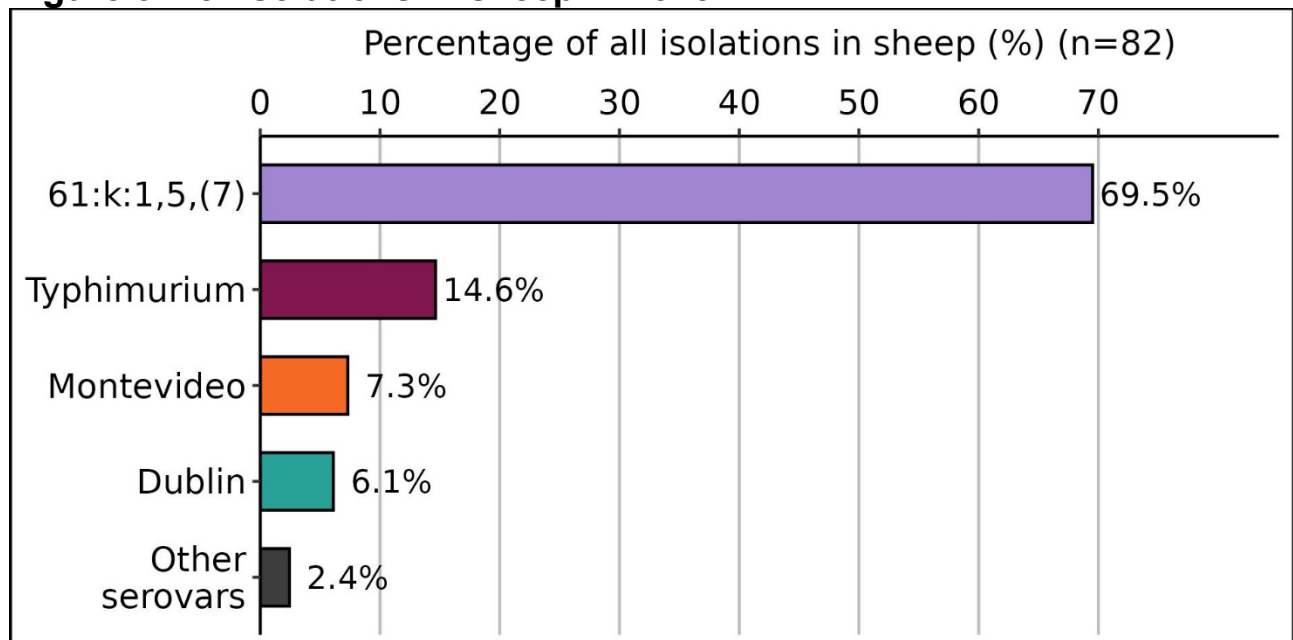
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in sheep in 2023. The most common serovar in sheep in 2023 was *Salmonella* 61:k:1,5,(7) (66.3% of isolations), followed by *S. Montevideo* (13.3% of isolations), *S. Typhimurium* (12.2% of isolations) and *S. Dublin* (4.1% of isolations).

Figure 3.2.4: Isolations in sheep in 2024



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in sheep in 2024. The most common serovar in sheep in 2024 was *Salmonella* 61:k:1,5,(7) (64.4% of isolations), followed by *S. Montevideo* and *S. Dublin* (13.9% of isolations each) and *S. Typhimurium* (5.9% of isolations).

Figure 3.2.5: Isolations in sheep in 2025

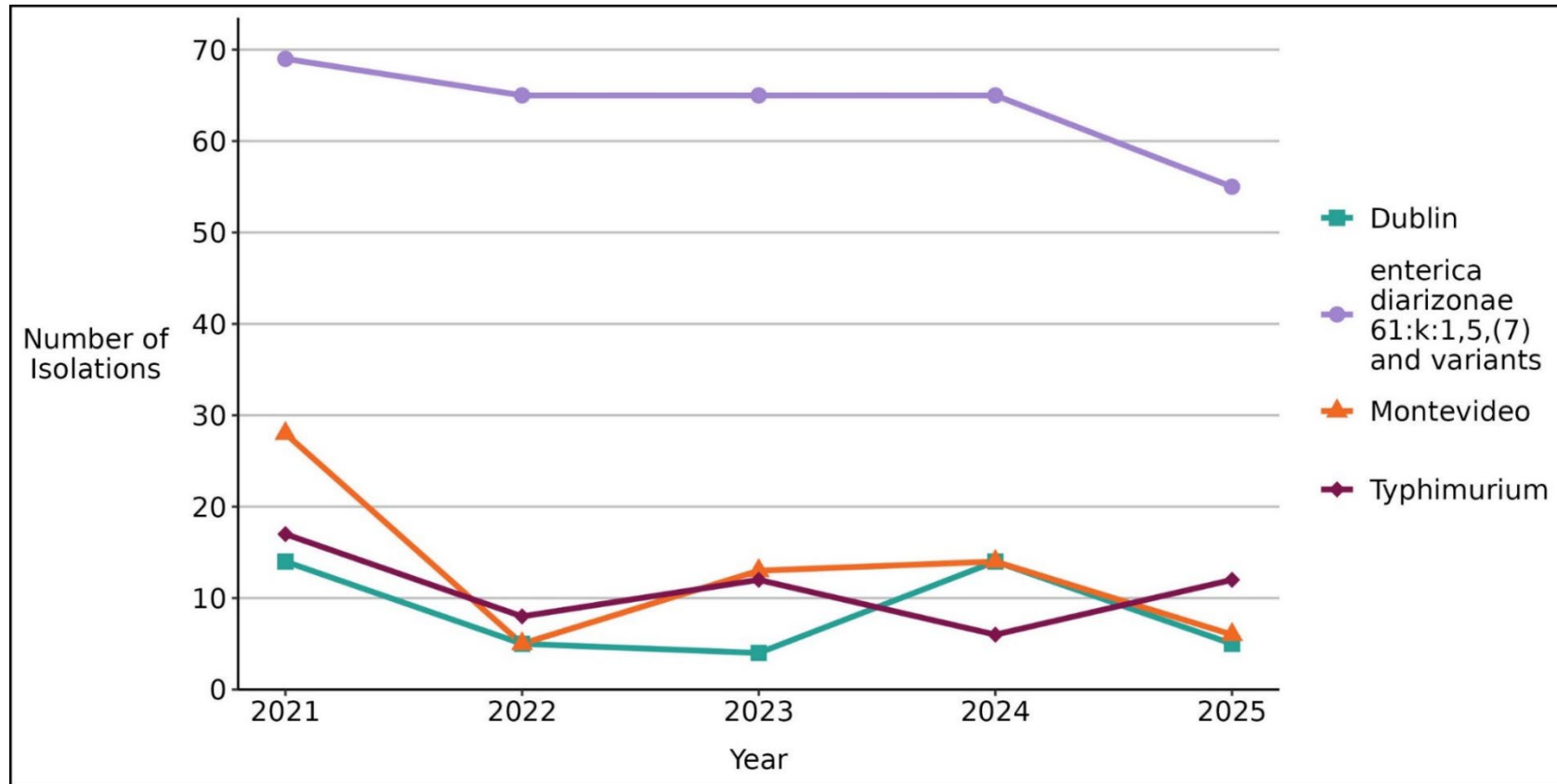


Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in sheep in 2025. The most common serovar in sheep in 2025 was *Salmonella*

61:k:1,5,(7) (69.5% of isolations), followed by *S. Typhimurium* (14.6% of isolations), *S. Montevideo* (7.3% of isolations) and *S. Dublin* (6.1% of isolations).

All isolations of 61:k:1,5,(7) are variants of *Salmonella enterica* subspecies *diarizonae*.

Figure 3.3 The 4 most common *Salmonella* serovars in sheep in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 4 most common serovars in sheep from 2021 to 2025. The figure shows the most common serovar in sheep for all years was *S. enterica diarizonae* 61:k:1,5,(7) and its variants with 57 isolations in 2025. *Salmonella* Typhimurium was the second most common serovar isolated in 2025 with 12 isolations, followed by *S. Montevideo* with 6 isolations and *S. Dublin* with 5 isolations.

All isolations of 61:k:1,5,(7) are variants of *Salmonella enterica* subspecies *diarizonae*.

Table 3.3: Sequence types of S. Typhimurium isolations in sheep in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	12	6	12
Total	12	6	12

Table 3.4: Sequence types of monophasic S. Typhimurium isolations in sheep in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
34	1	1	0
Total	1	1	0

Chapter 4: Reports of *Salmonella* in pigs

Compared with 2024, there was a slight decrease in the total Great Britain pig herd in 2025 to just under 4 million animals according to the 2025 agricultural survey (Figure 4.1). Overall, however, the total pig herd numbers were stable over 2024 and 2025, following a decrease of 10.7% in 2023. The number of commercial pig holdings in 2025 decreased to 9,374, compared to 9,530 in 2024.

There is currently no national scheme for monitoring *Salmonella* on pig farms in England and Wales since the withdrawal of meat juice enzyme-linked immunosorbent assay (ELISA) testing of slaughter pigs in 2012. Despite *Salmonella* infection in pigs being largely subclinical, the majority of *Salmonella* isolates reported to APHA result from clinical investigations and diagnostic submissions in which *Salmonella* may be the causal pathogen or a secondary incidental finding. Submissions to the GB scanning surveillance network where *Salmonella* is considered the cause of disease are recorded as diagnoses of salmonellosis in the [Veterinary Investigation Diagnoses Analysis \(VIDA\) database](#). Surveillance data, including clinical signs, pig age and county information, associated with diagnoses of salmonellosis in pigs can be accessed via the [GB disease surveillance dashboard](#).

There was a decrease (13.2%) in the total number of pig submissions (all types) from pig premises in GB to the GB scanning surveillance network (APHA, APHA's surveillance pathology partners and SRUC) during 2025 (3,584 submissions) compared to 2024 (4,089 submissions). Similarly, there was a decrease (9%) in diagnostic pig submissions during 2025 (1,845 submissions) compared to 2024 (2,024 submissions).

There were 253 isolations of *Salmonella* in pigs in 2025, across 240 incidents. The number of isolations is fewer than in recent years (258 in 2023 and 311 in 2024). The number of incidents of *Salmonella* as a proportion of the total pig submissions to the GB scanning surveillance network was 6.7%, compared to 7.1% in 2024. The number of diagnoses of salmonellosis does not equate with the number of *Salmonella* incidents derived from diagnostic scanning surveillance submissions because only a proportion of isolations are deemed to be clinically significant. The number of diagnoses of salmonellosis made through the GB scanning surveillance network in pigs was 139 in 2025, which was lower than in both 2024 (171) and 2023 (169).

The different serovars isolated are detailed in Table 4.1 and Figure 4.2. Fourteen different serovars were identified from pigs in 2025 which accounted for all isolations.

Salmonella Typhimurium and its monophasic variants

As in previous years, isolations of *S. Typhimurium* and its monophasic variants together accounted for the majority of isolations of *Salmonella* from pigs in 2025 (167 isolations, 66% of all isolations, Figures 4.2 and 4.3). This proportion was lower than in recent years (2021 to 2024 ranged from 70.5 to 77.5%). As has been the case since 2020, the number of *S. Typhimurium* isolations exceeded isolations of monophasic *S. Typhimurium* in 2025.

As in previous years, the most common serovar isolated from pigs in 2025 was *S. Typhimurium* (106 isolations 41.9% of all isolations). There was a decrease in isolations from 2024 and 2023 (156 and 139 isolations, respectively (Table 4.1)). Sequence type (ST) 19 was the most commonly isolated ST of *S. Typhimurium* in 2025, which decreased from 150 isolations in 2024 to 102 isolations in 2025. Other STs were ST24 (1 isolation) and ST8336 (1 isolation). No ST data were available for 2 *S. Typhimurium* isolates.

The next most common *Salmonella* serovar isolated from pigs in 2025 was monophasic *S. Typhimurium* (61 isolations, 24.1% of all isolations). Isolations of monophasic *S. Typhimurium* decreased by 12.9% in 2025 compared to 2024 (Figure 4.3). Of the monophasic *S. Typhimurium* isolations, 60 were ST34 and 1 was ST19.

Other serovars

There were 33 isolations of *S. Derby* from pigs in 2025, which was consistent with 2024 but an increase compared with the previous three years (15 to 17 isolations per year from 2021 to 2023, Table 4.1 and Figure 4.2). Other frequently isolated serovars from pigs in 2025 were *S. Newport* (16 isolations), *S. Reading* (10 isolations) and *S. Panama* (9 isolations).

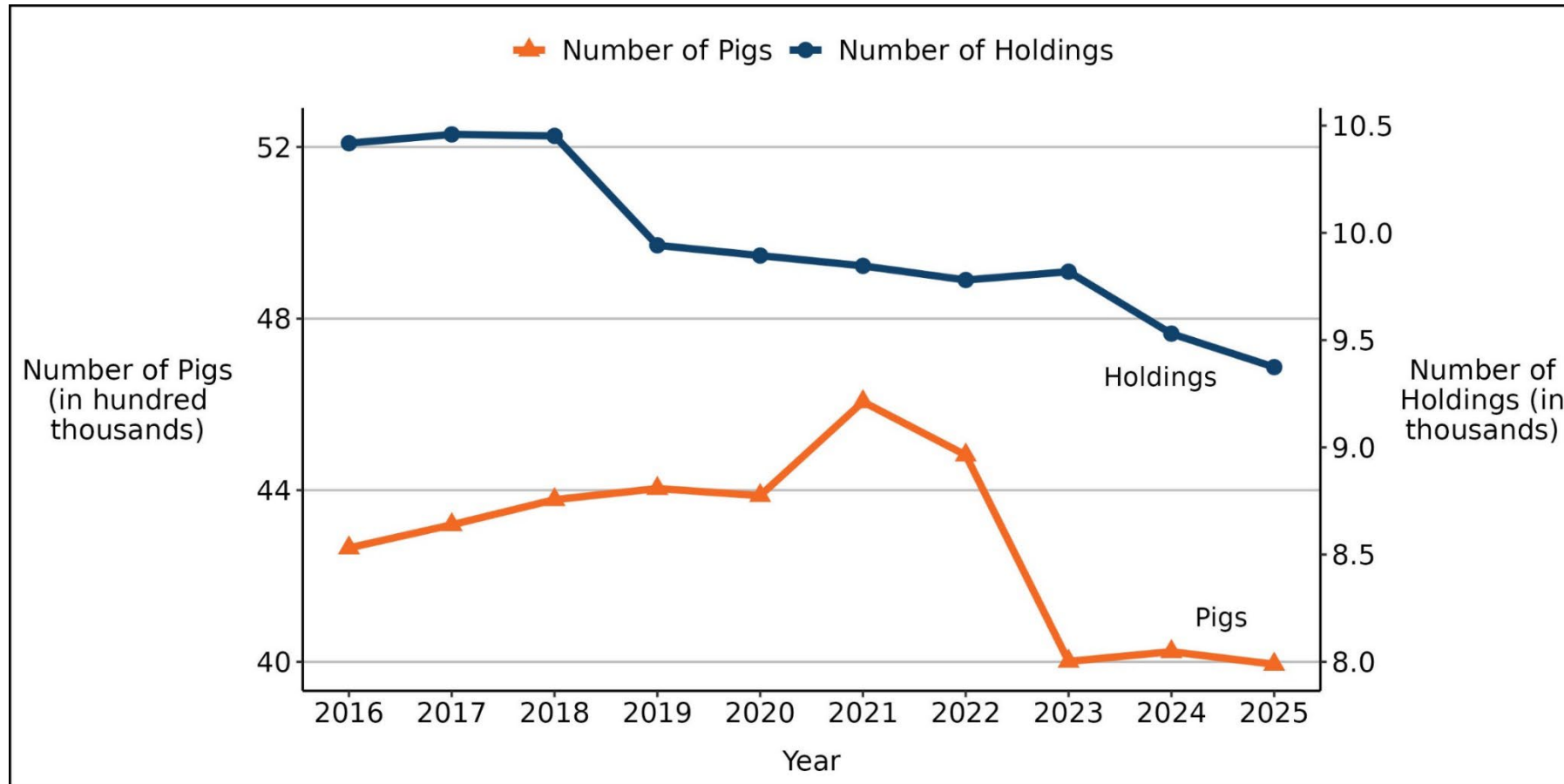
One serovar, *S. Braenderup*, was detected in 2025 from a pig sample for the first time in Great Britain from post-weaned pigs with mortality and diarrhoea. *S. Derby* was also detected from samples in the same submission, making the clinical significance of the *S. Braenderup* uncertain. *S. Braenderup* is most frequently isolated from dogs and chickens. There were no isolations of *S. Enteritidis* in 2025, which was last isolated on one occasion in pigs in 2019.

Antimicrobial susceptibility in pigs

A total of 328 *Salmonella* isolates from pigs were tested against a panel of 16 antimicrobials in 2025. In this species, antimicrobial resistance remained high, with 69.8% of isolates classified as MDR. The main serovars associated with resistance were *S. Typhimurium* (143 isolates) and monophasic *S. Typhimurium* (80 isolates).

There were 21.6% of *Salmonella* isolates from pigs which were fully susceptible. Resistance to ampicillin (70.1%) and sulphonamides (72.0%) remained widespread. Patterns with resistance to the sulphamethoxazole and trimethoprim combination (54.3%), tetracycline (57.6%), and chloramphenicol (53.4%) also showed consistently high levels. Amikacin resistance was observed in 2 *S. Typhimurium* isolates. All amikacin resistant isolates also displayed neomycin and gentamicin resistance. None of the isolates were resistant to third-generation cephalosporins or ciprofloxacin, which are considered HP-CIAs. Nalidixic acid resistance was observed in 2 *S. Derby* isolates.

Figure 4.1: Pig population and number of commercial holdings with pigs in Great Britain 2016 to 2025



A line graph showing the pig population and number of commercial holdings from 2016 to 2025 in Great Britain. There were a variable number of pig holdings until 2019 when numbers slowly start to decline until 2022 before increasing slightly, then declining again to 9,374

in 2025. The number of pigs in Great Britain increased until 2021 after which there was a decline in 2022 and 2023, with relatively stable numbers since and a population of 3,994,134 in 2025.

Scotland (animals and holdings) 2021 survey data used for 2022.

The number of holdings in 2020 is estimated.

Source: June 2025 Agricultural Survey. For the definition of a commercial holding in the agricultural survey, see the [survey methodology](#).

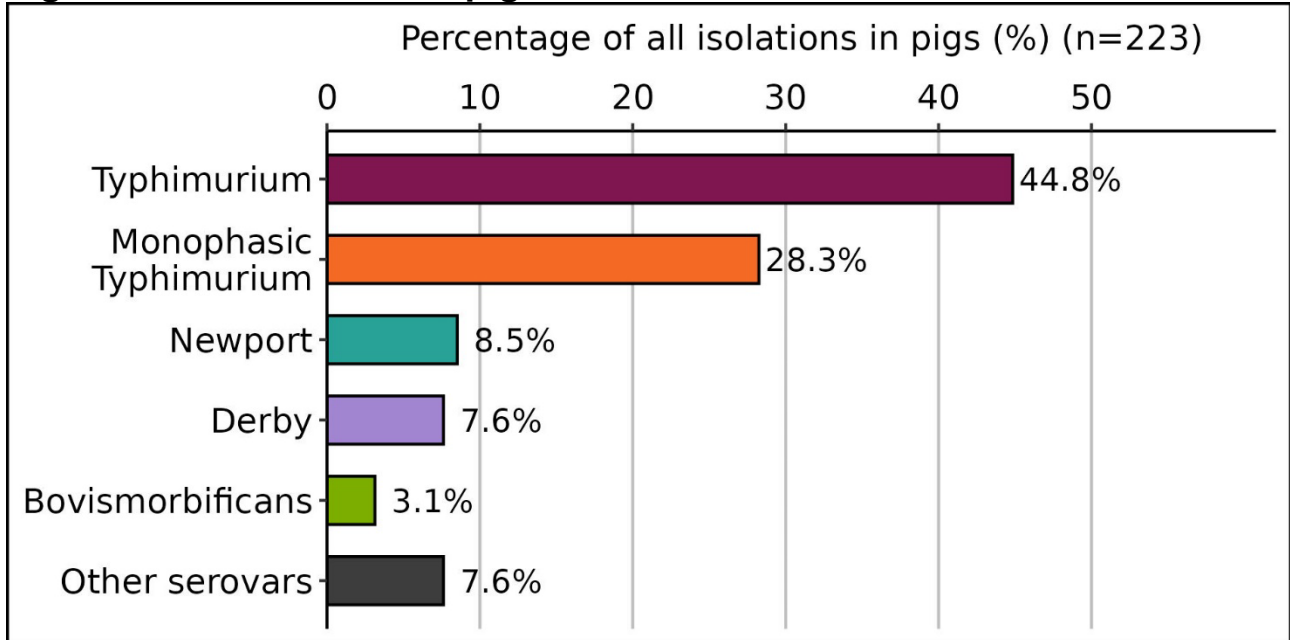
Table 4.1: Isolations and incidents of *Salmonella* in pigs on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Bovismorbificans	7	6	2	2	2	2	8	8	5	5
Braenderup	0	0	0	0	0	0	0	0	1	1
Cerro	0	0	0	0	1	1	0	0	1	1
Chester	0	0	0	0	1	1	0	0	0	0
Derby	17	16	15	13	17	16	33	30	33	30
Dublin	1	1	0	0	0	0	1	1	1	1
Hessarek	0	0	0	0	0	0	1	1	0	0
Indiana	2	1	0	0	0	0	0	0	0	0
Kedougou (incl. monophasic variants)	1	1	3	2	3	3	5	5	6	6
Livingstone	1	1	0	0	0	0	0	0	1	1
London	5	5	7	6	2	2	1	1	2	2
London var 15⁺	0	0	1	1	0	0	0	0	0	0
Monophasic Typhimurium	63	57	51	44	61	59	70	68	61	58
Newport	19	18	20	19	18	16	20	20	16	16
Panama	4	4	10	9	10	10	7	7	9	9
Reading	2	2	3	3	2	2	7	7	10	10

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Rissen	0	0	0	0	2	2	1	1	1	1
Typhimurium	100	93	100	97	139	124	156	141	106	99
rough strains	1	1	0	0	0	0	0	0	0	0
untypable strains	0	0	2	2	0	0	1	1	0	0
Total	223	206	214	198	258	238	311	291	253	240

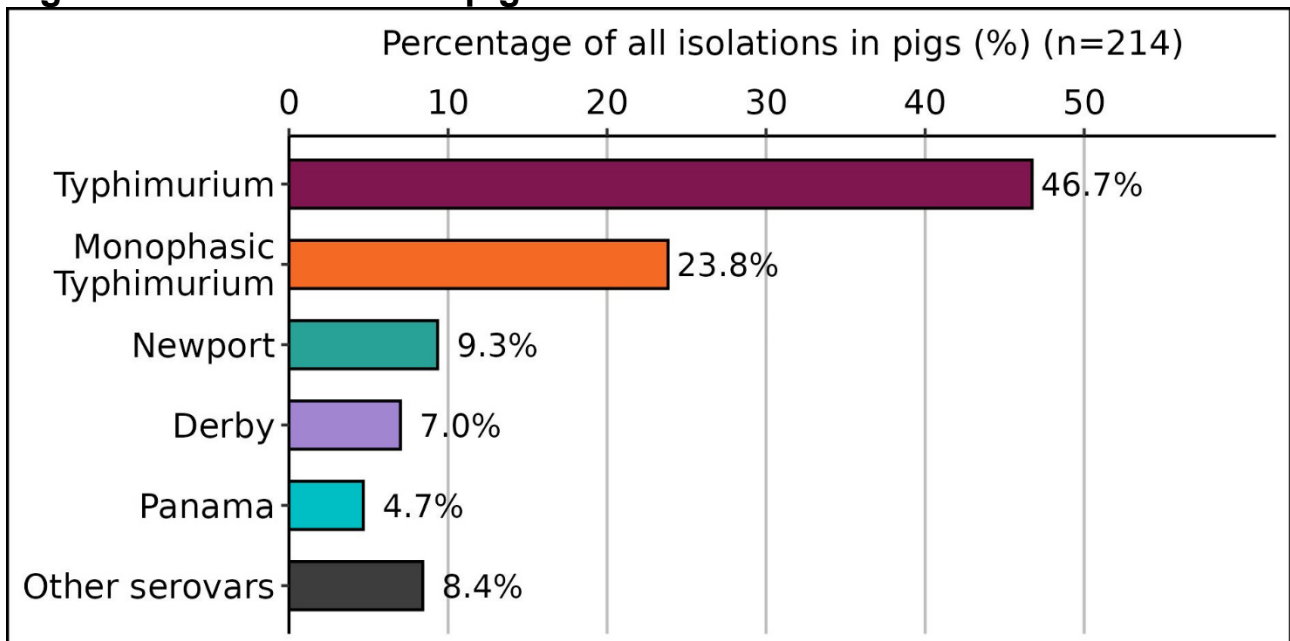
Figure 4.2: Isolations of the most common *Salmonella* serovars in pigs in Great Britain 2021 to 2025

Figure 4.2.1: Isolations in pigs in 2021



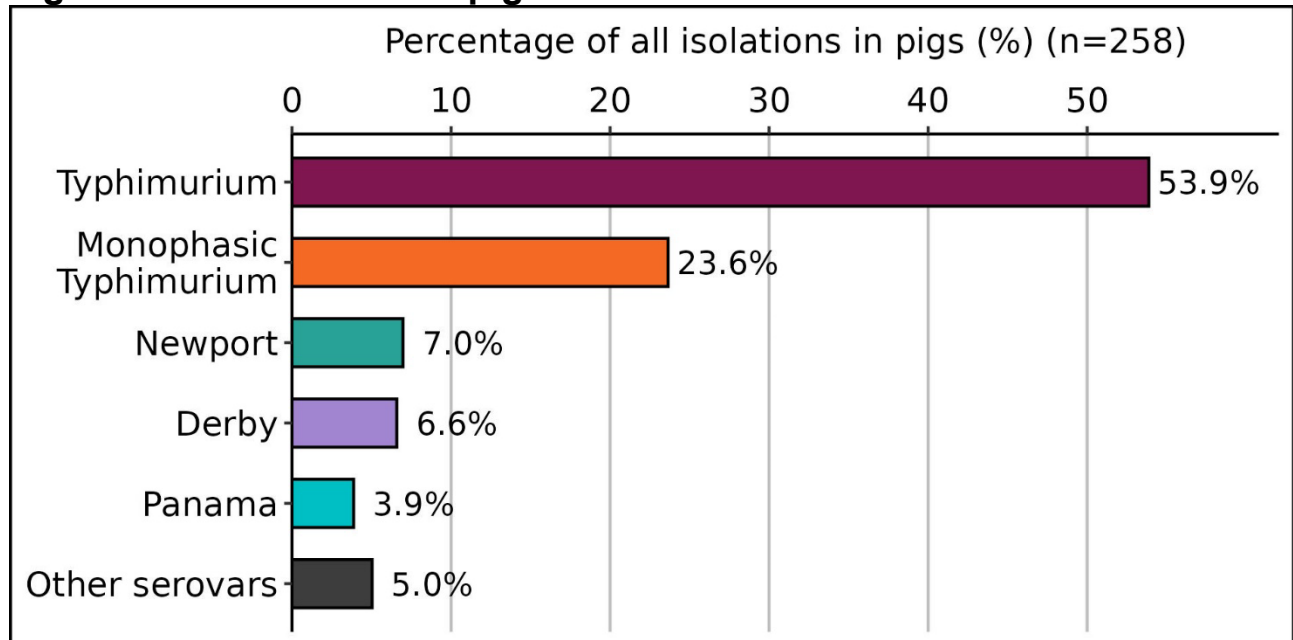
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in pigs in 2021. The most common serovar in pigs in 2021 was *S. Typhimurium* (44.8% of isolations), followed by monophasic *S. Typhimurium* (28.3% of isolations) and *S. Newport* (8.5% of isolations).

Figure 4.2.2: Isolations in pigs in 2022



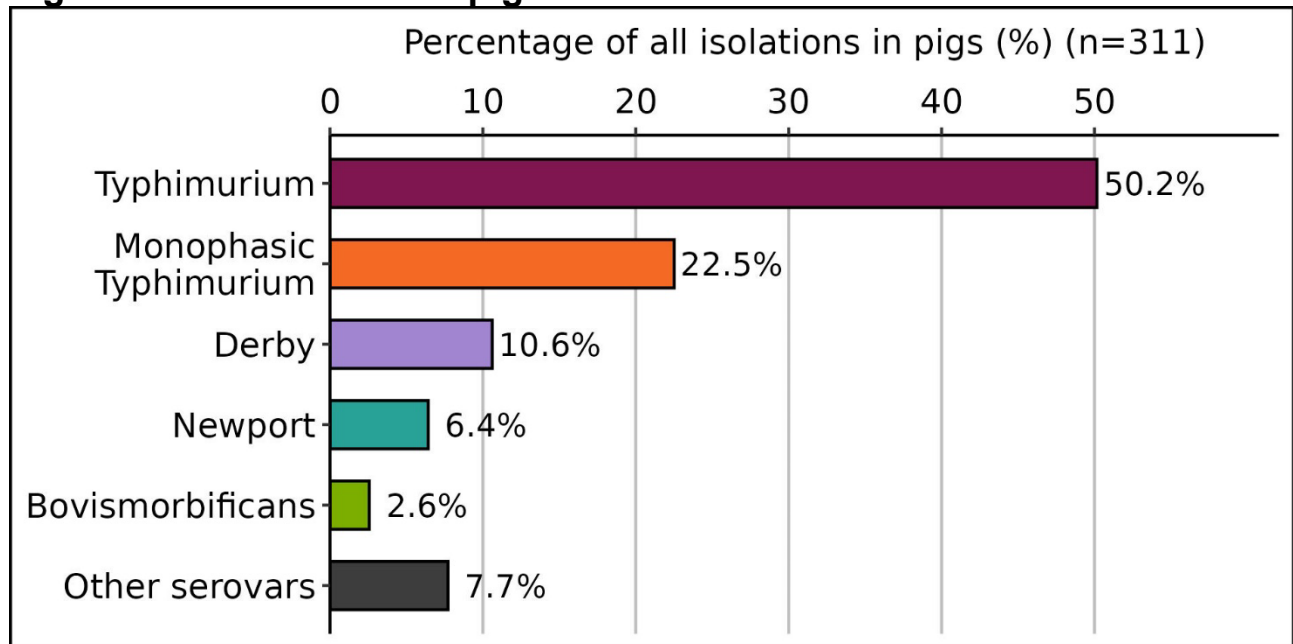
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in pigs in 2022. The most common serovar in pigs in 2022 was *S. Typhimurium* (46.7% of isolations), followed by monophasic *S. Typhimurium* (23.8% of isolations) and *S. Newport* (9.3% of isolations).

Figure 4.2.3: Isolations in pigs in 2023



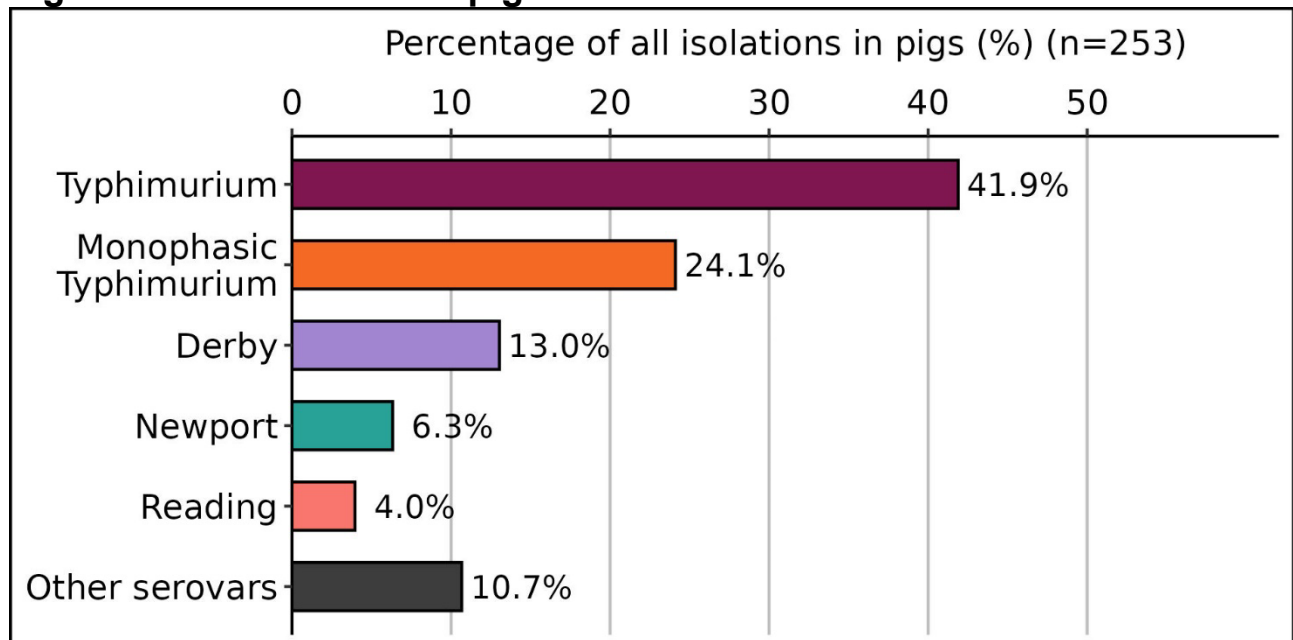
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in pigs in 2023. The most common serovar in pigs in 2023 was *S. Typhimurium* (53.9% of isolations), followed by monophasic *S. Typhimurium* (23.6% of isolations) and *S. Newport* (7.0% of isolations).

Figure 4.2.4: Isolations in pigs in 2024



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in pigs in 2024. The most common serovar in pigs in 2024 was *S. Typhimurium* (50.2% of isolations), followed by monophasic *S. Typhimurium* (22.5% of isolations) and *S. Derby* (10.6% of isolations).

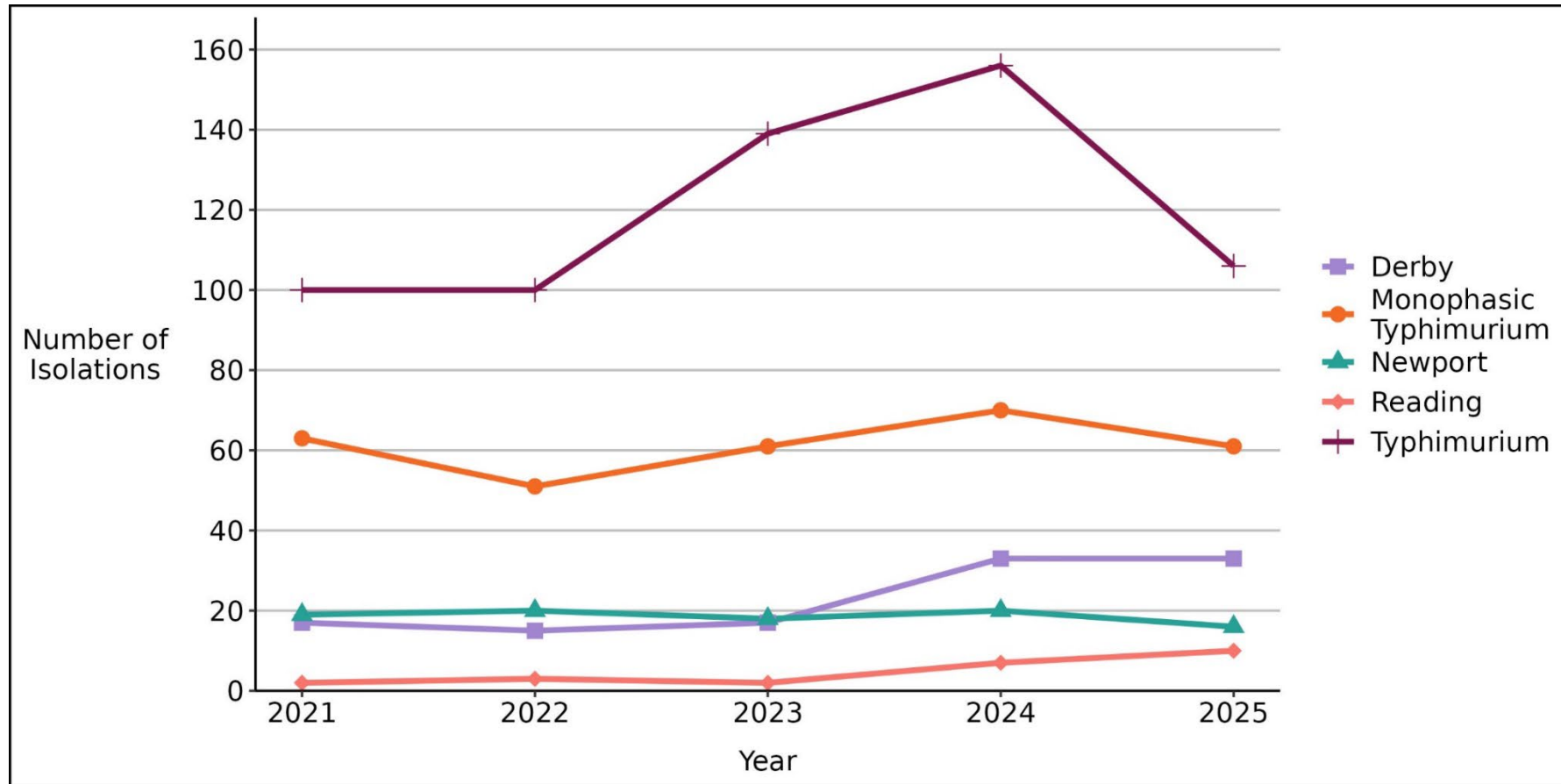
Figure 4.2.5: Isolations in pigs in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in pigs in 2025. The most common serovar in pigs in 2025 was *S. Typhimurium*

(41.9% of isolations), followed by monophasic *S. Typhimurium* (24.1% of isolations), *S. Derby* (13.0% of isolations) and *S. Newport* (6.3% of isolations).

Figure 4.3: The 5 most common *Salmonella* serovars in pigs in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in pigs from 2021 to 2025. The figure shows the most common serovars in pigs for all years was *S. Typhimurium* peaking at 156 isolations in 2024. The number of isolations of the monophasic *S. Typhimurium* decreased

from 2021 to 2022 but then increased to 70 isolations in 2024 before a decrease to 61 isolations in 2025. Isolations of S. Derby increased in 2024 to 33 and remained at 33 in 2025, when numbers had varied between 15 and 17 from 2021 to 2023.

Table 4.2: Sequence types of S. Typhimurium isolations in pigs in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	135	152	102
34	0	3	1
568	0	1	0
8336	0	0	1
No ST data	4	0	2
Total	139	156	106

Table 4.3: Sequence types of monophasic S. Typhimurium isolations in pigs in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	0	1	1
34	59	69	60
No ST data	2	0	0
Total	61	70	61

Chapter 5: Reports of *Salmonella* in deer, horses and rabbits

Isolations of *Salmonella* from deer, horses and rabbits are reportable. Some individuals of these species may be slaughtered for human consumption.

Where *Salmonella* is isolated from diagnostic submissions to APHA, it is recorded as a salmonellosis diagnosis in the [Veterinary Investigation Diagnoses Analysis \(VIDA\) database](#). Surveillance data, including clinical signs, age and presenting signs are also recorded.

Deer

There was one *Salmonella* isolation, *S. Coeln*, from deer during 2025 (Table 5.1). This is compared to 2 isolations during 2024 (one each of monophasic *S. Typhimurium* and *S. Typhimurium*), one isolation during 2023 (*S. Typhimurium*) and no isolations during 2022 or 2021. *Salmonella* Coeln has never previously been reported from deer in Great Britain. APHA received 83 diagnostic submissions from deer in 2025, a 23.9% decrease compared to the 109 received in 2024.

Horses

The number of horses recorded as being kept in Great Britain at the June 2025 Agricultural Survey was 189,428, which is a decrease of 4.4% compared to 2024 (198,087 animals).

There were 71 isolations of *Salmonella* from horses during 2025 (Table 5.3). This represents a 34.0% increase compared to the total number of isolations recorded from horses during 2024 (53 isolations) and a 29.1% increase compared to 2023 (55 isolations). As companion animals, horses are a potential source of infection to their keepers and the zoonotic implications of salmonellosis in horses, as well as prevention and control measures (Martelli et al, 2018), must be considered.

The most commonly isolated serovars from horses during 2025 were *S. Typhimurium* (30 isolations, 42.3% of total horse isolations), *S. Enteritidis* (12 isolations, 16.9% of total horse isolations), *S. Agama* (8 isolations, 11.3% of total horse isolations) and *S. Newport* (5 isolations, 7.0% of total horse isolations) (Figure 5.1). During 2024 the most common serovars were *S. Typhimurium* (24 isolations, 45.3% of total horse isolations), *S. Enteritidis* (8 isolations, 15.1% of total horse isolations), *S. Newport* (5 isolations, 9.4% of total horse isolations) and *S. Oslo* (3 isolations, 5.7% of total horse isolations).

The number of *S. Typhimurium* isolations during 2025 was 25.0% higher than that reported in 2024 (30 versus 24 isolations) and 50.0% higher than in 2023 (20 isolations)

(Table 5.4). The 30 isolations of *S. Typhimurium* reported from horses during 2025 comprised 3 different sequence types. The most common sequence type was ST19 (27 isolations). There was also one isolation each of ST8336 and ST8937, and one isolation where the sequence type could not be determined. In 2023 and 2024, the majority of *S. Typhimurium* isolations were also ST19. There were 3 isolations of monophasic *S. Typhimurium* (ST34 x2 and ST19 x1)) in 2025, compared to one isolation during both 2024 and 2023 (both ST34) (Table 5.5).

There were 12 isolations of *S. Enteritidis* in 2025 (Table 5.6), an increase compared to 8 isolations (ST8943 x2, ST10467 x2, ST11 x1, ST183 x1, ST5492 x1 and ST6086 x1)) seen in 2024 and a notable increase compared to 2023 when there was one isolation (ST183 x1). The sequence types reported in 2025 were ST8943 (x6), ST11 (x5) and ST10467 (x2).

During 2025 there were also 2 isolations each of *S. Coeln* and *S. Heidelberg*, and one isolation each of *S. Bonn*, *S. Bovismorbificans*, *S. Durham*, *S. Fulica*, *S. Hessarek*, *S. Kentucky* and *S. Kottbus*. Neither *S. Coeln* nor *S. Heidelberg* have been reported in horses previously in Great Britain.

There were 7 isolations of *S. Typhimurium* and one isolation of *S. Colindale* in 2025 from horses imported from the Republic of Ireland. All 8 isolations resulted from clinical disease investigations, though information on clinical signs were not available. These isolations are not reported in the tables and figures of this report.

Antimicrobial susceptibility in horses

A total of 59 *Salmonella* isolates from horses were tested against a panel of 16 antimicrobials in 2025. The proportion of fully susceptible isolates was 75.0%, compared to 78.0% in 2024. Nine isolates (9.8%) were MDR: three *S. Typhimurium*, three monophasic *S. Typhimurium*, two *S. Heidelberg*, and one *S. Agama*.

Four isolates were resistant to cefotaxime and ceftazidime; three of these isolates were *S. Typhimurium*, and one isolate was *S. Agama*. Two isolates were resistant to nalidixic acid alone; both were *S. Typhimurium*. No isolates showed resistance to ciprofloxacin in 2025.

Rabbits

APHA received 5 diagnostic submissions from rabbits in 2025. *Salmonella* was not isolated from any of them. The last isolations from rabbits were in 2022 (one isolation each of *S. Fluntern* and *S. Newport*) (Table 5.2). Prior to that there was a single isolation in 2016 (*Salmonella* 21:g,t:-).

Table 5.1: Isolations and incidents of *Salmonella* in deer on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Coeln	0	0	0	0	0	0	0	0	1	1
Monophasic Typhimurium	0	0	0	0	0	0	1	1	0	0
Typhimurium	0	0	0	0	1	1	1	1	0	0
Total	0	0	0	0	1	1	2	2	1	1

Table 5.2: Isolations and incidents of *Salmonella* in rabbits on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Fluntern	0	0	1	1	0	0	0	0	0	0
Newport	0	0	1	1	0	0	0	0	0	0
Total	0	0	2	2	0	0	0	0	0	0

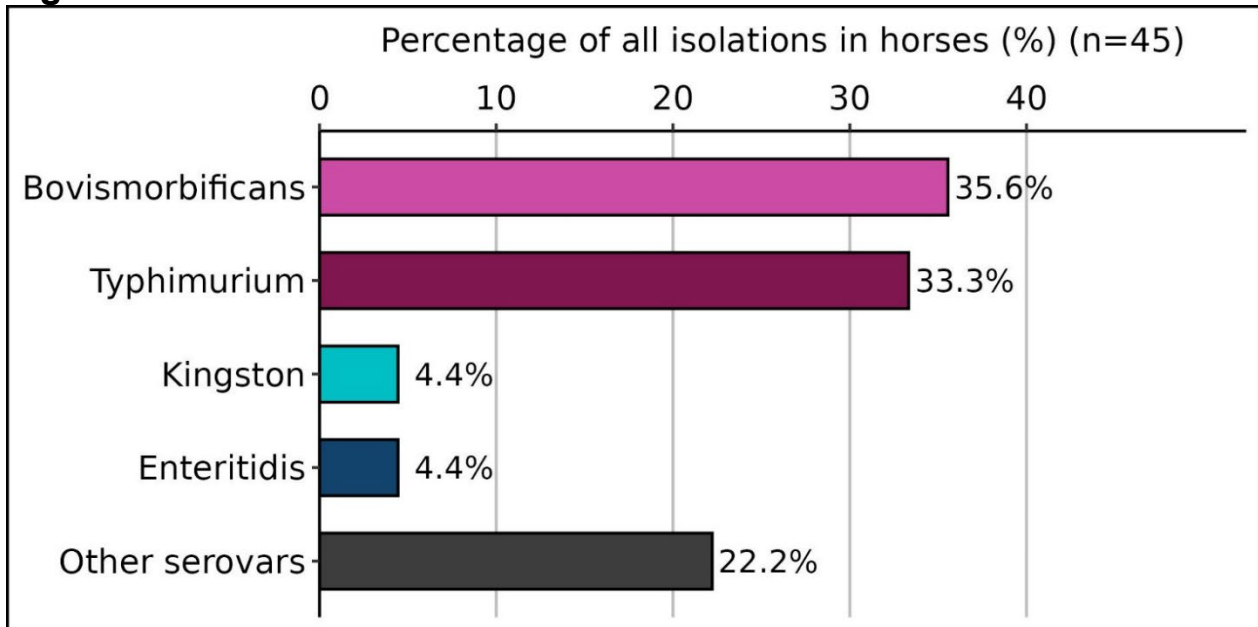
Table 5.3: Isolations and incidents of *Salmonella* in horses on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Agama	0	0	4	4	0	0	2	2	8	8
Agona	1	1	0	0	0	0	0	0	0	0
Anatum	0	0	1	1	2	2	1	1	0	0
Birkenhead	0	0	0	0	1	1	0	0	0	0
Blockley	0	0	0	0	0	0	1	1	0	0
Bonn	0	0	0	0	0	0	1	1	1	1
Bovismorbificans	16	10	4	4	3	3	1	1	1	1
Braenderup	0	0	1	1	1	1	0	0	0	0
Coeln	0	0	2	2	1	1	0	0	2	2
Concord	1	1	0	0	6	5	1	1	0	0
Dublin	1	1	2	2	0	0	0	0	0	0
Durham	0	0	1	1	0	0	0	0	1	1
Eastbourne	0	0	0	0	0	0	1	1	0	0
Eboko	0	0	3	3	0	0	0	0	0	0
Enteritidis	2	2	4	4	1	1	8	8	12	6
Fulica	0	0	0	0	0	0	2	2	1	1
Heidelberg	0	0	0	0	0	0	0	0	2	2
Hessarek	0	0	0	0	0	0	0	0	1	1
Infantis	0	0	0	0	3	2	0	0	0	0

Salmonella serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Kentucky	0	0	0	0	0	0	0	0	1	1
Kingston	2	2	3	2	3	3	1	1	0	0
Kottbus	1	1	3	3	1	1	0	0	1	1
Monophasic Typhimurium	0	0	2	1	1	1	1	1	3	3
Montevideo	1	1	0	0	0	0	0	0	0	0
Newport	1	1	6	6	7	7	5	5	5	5
Oslo	1	1	4	4	2	1	3	3	0	0
Paratyphi B var. Java	1	1	0	0	1	1	0	0	0	0
Sanga	0	0	0	0	1	1	0	0	0	0
Stanleyville	1	1	0	0	0	0	1	1	0	0
Typhimurium	15	12	18	17	20	20	24	23	30	27
untypable strains	1	1	2	2	1	1	0	0	2	2
Total	45	36	60	57	55	52	53	52	71	62

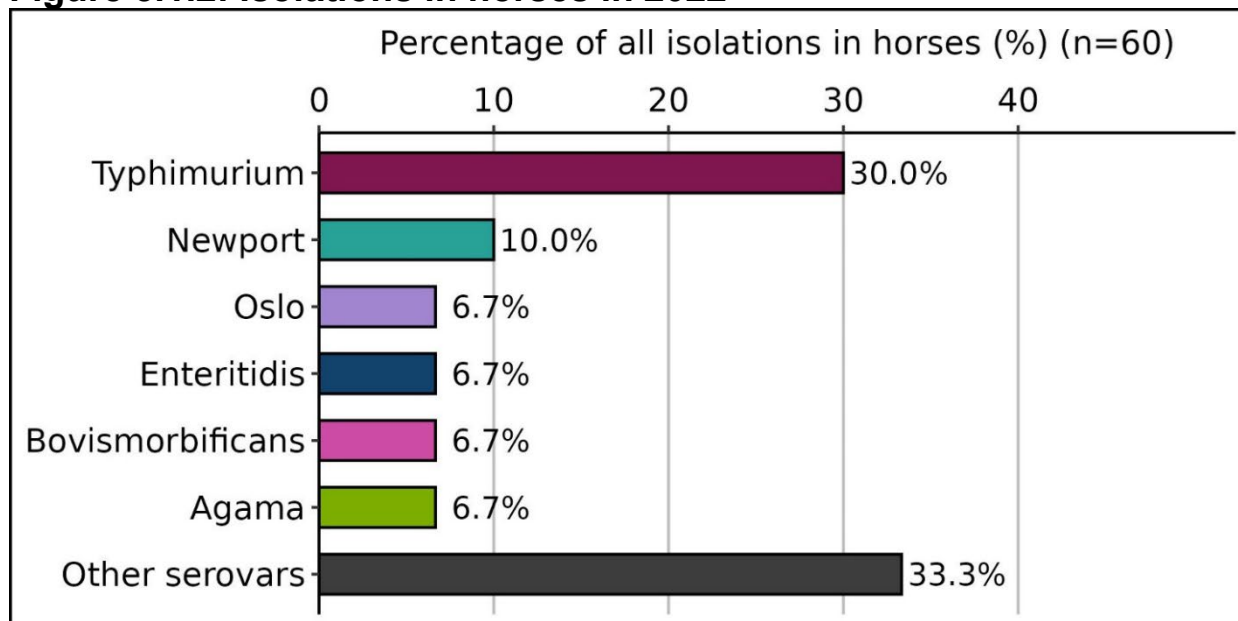
Figure 5.1: Isolations of the most common *Salmonella* serovars in horses in Great Britain 2021 to 2025

Figure 5.1.1: Isolations in horses in 2021



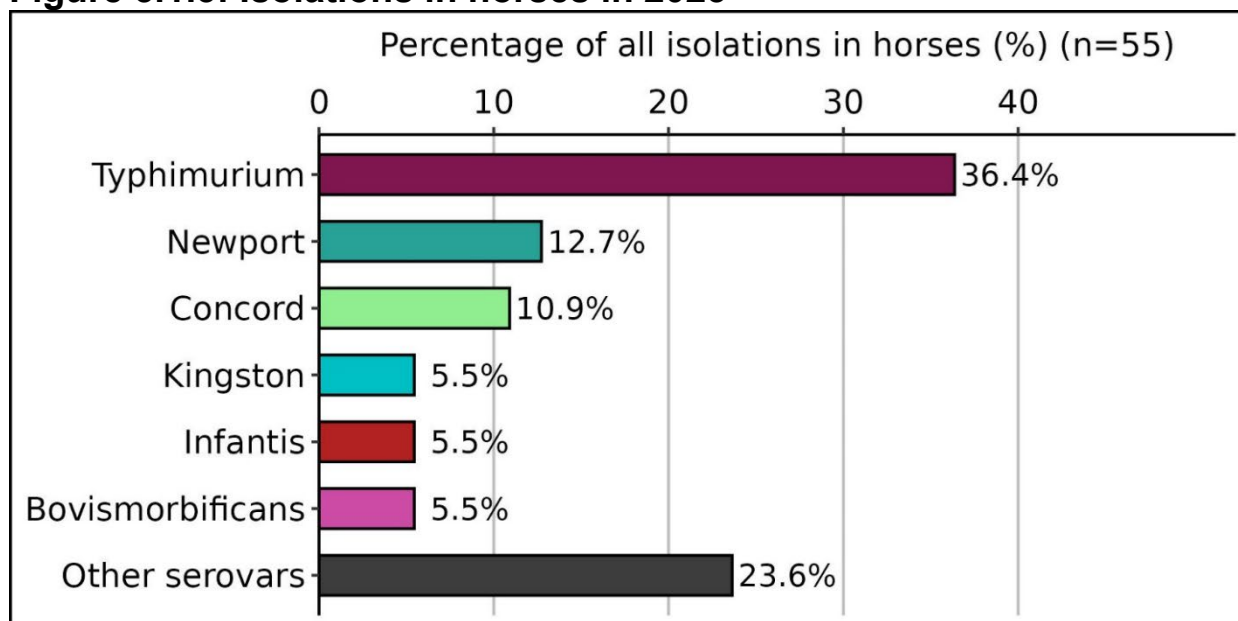
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in horses in 2021. The most common serovar in horses in 2021 was *S. Bovismorbificans* (35.6% of isolations), followed by *S. Typhimurium* (33.3% of isolations), *S. Enteritidis* and *S. Kingston* (4.4% of isolations each).

Figure 5.1.2: Isolations in horses in 2022



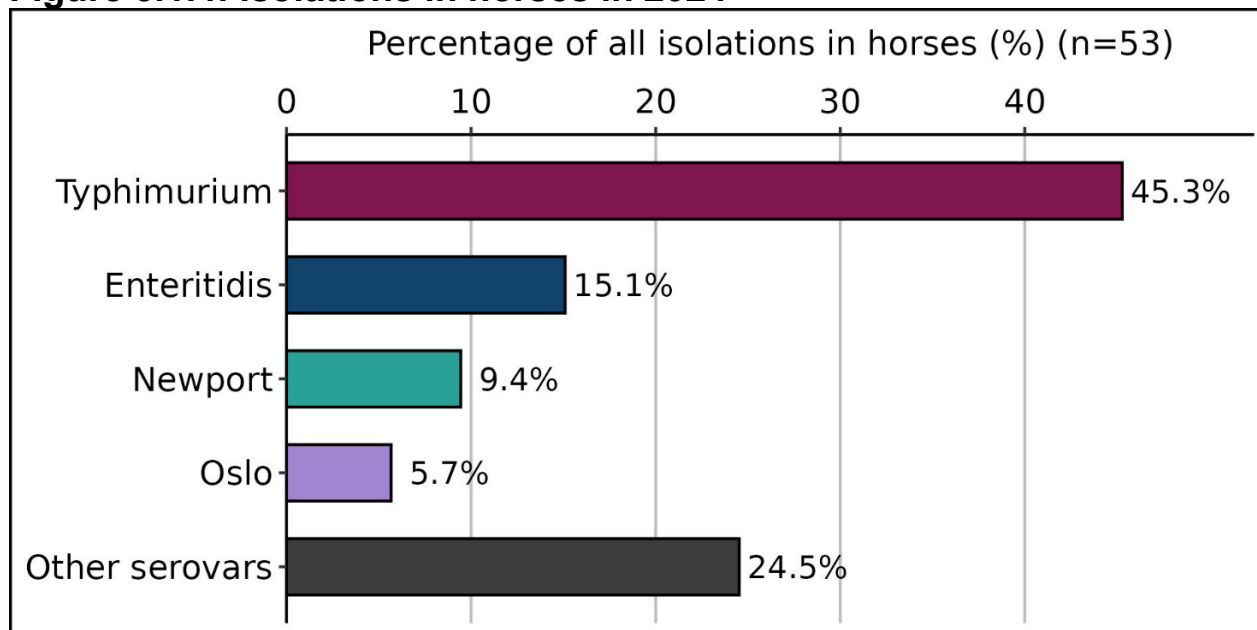
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in horses in 2022. The most common serovar in horses in 2022 was *S. Typhimurium* (30.0% of isolations), followed by *S. Newport* (10.0% of isolations), *S. Agama*, *S. Bovismorbificans*, *S. Enteritidis* and *S. Oslo* (6.7% of isolations each).

Figure 5.1.3: Isolations in horses in 2023



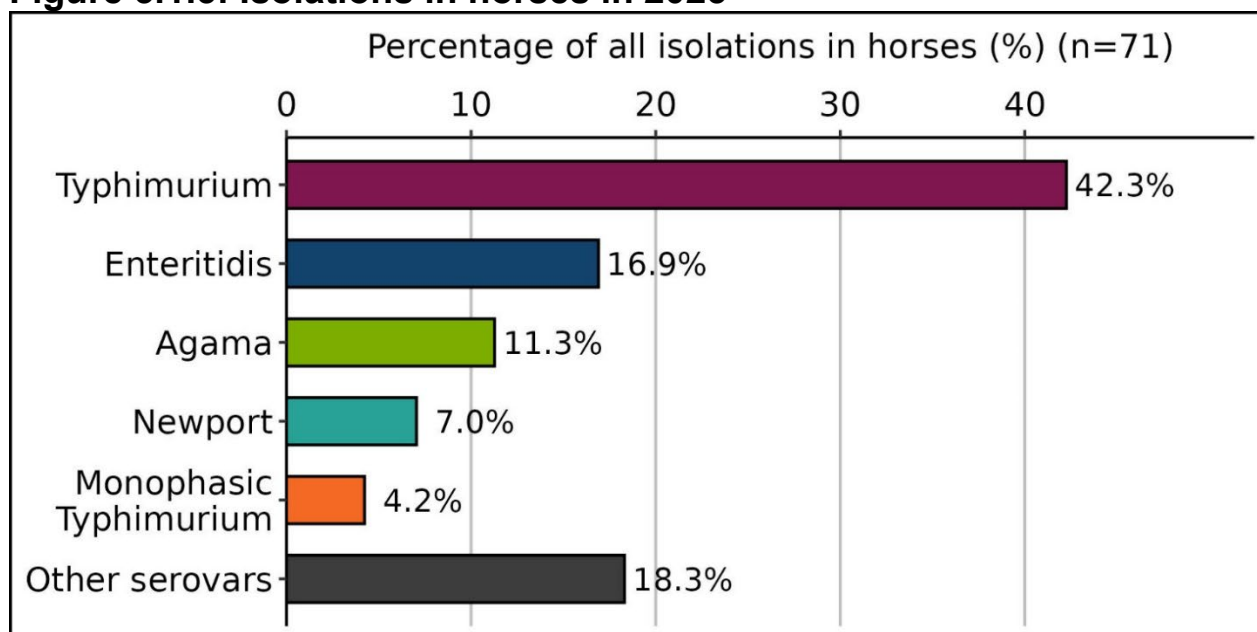
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in horses in 2023. The most common serovar in horses in 2023 was *S. Typhimurium* (36.4% of isolations), followed by *S. Newport* (12.7 % of isolations), *S. Concord* (10.9% of isolations), *S. Bovismorbificans*, *S. Infantis* and *S. Kingston* (5.5% of isolations each).

Figure 5.1.4: Isolations in horses in 2024



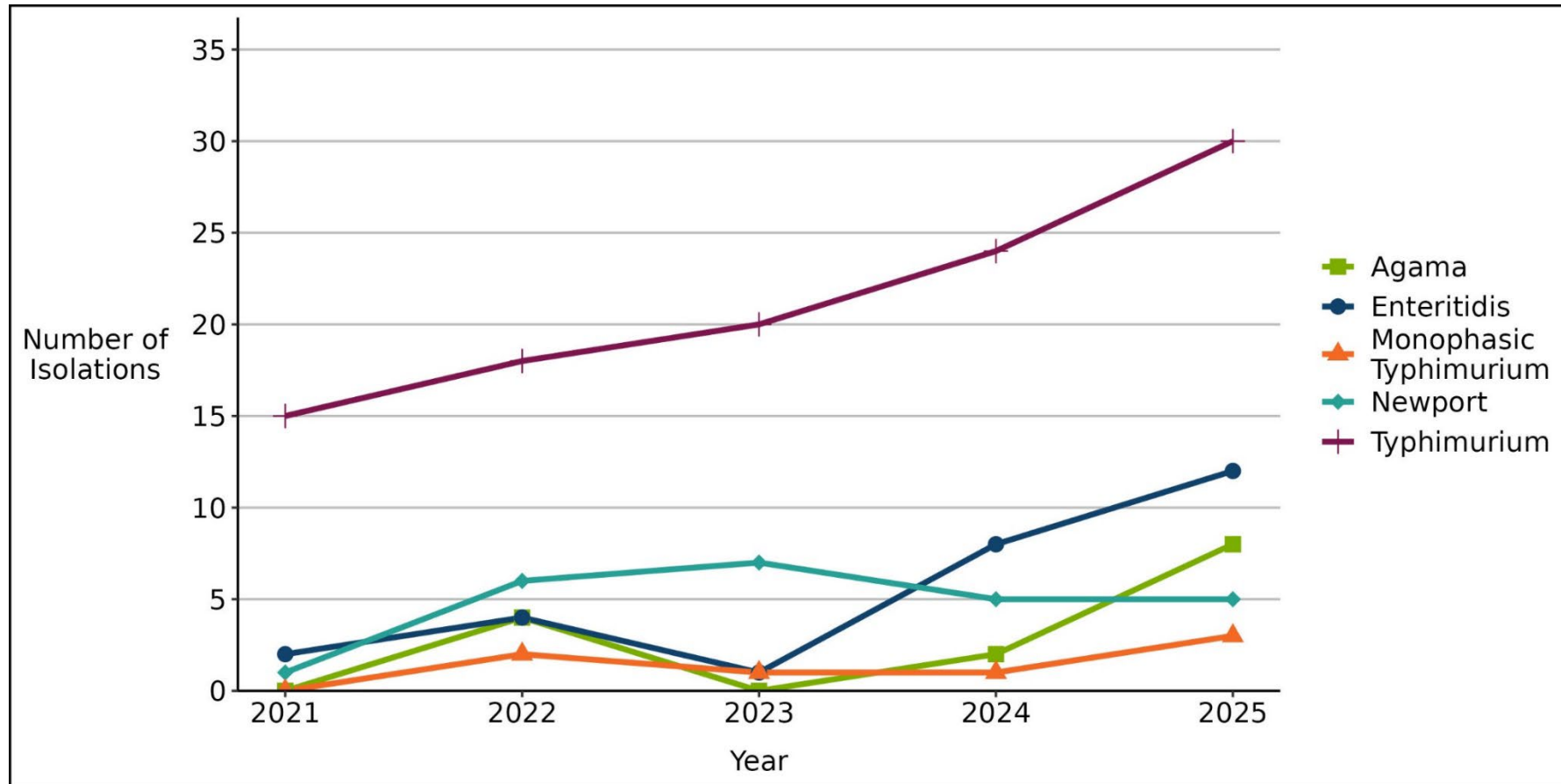
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in horses in 2024. The most common serovar in horses in 2024 was *S. Typhimurium* (45.3% of isolations), followed by *S. Enteritidis* (15.1 % of isolations), *S. Newport* (9.4% of isolations) and *S. Oslo* (5.7% of isolations).

Figure 5.1.5: Isolations in horses in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in horses in 2025. The most common serovar in horses in 2025 was *S. Typhimurium* (42.3% of isolations), followed by *S. Enteritidis* (16.9 % of isolations), *S. Agama* (11.3% of isolations), *S. Newport* (7.0% of isolations) and monophasic *S. Typhimurium* (4.2% of isolations).

Figure 5.2: The 5 most common *Salmonella* serovars in horses in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in horses from 2021 to 2025. The figure shows that *S. Typhimurium* remains the top serovar in horses with 30 isolations in 2025 and has been steadily increasing from 15 in 2021. *S. Enteritidis*, the second most common

serovar in 2025, has increased overall from two isolations in 2021 to 12 in 2025. The third most common serovar in 2025 was *S. Agama* which has fluctuated and seen an overall increase since 2021. *S. Newport* was the fourth most common serovar in 2025, which has also fluctuated though seen an overall increase since 2021. The fifth most common serovar in 2025 was monophasic *S. Typhimurium* which has stayed at low levels across all years rising gradually from 0 in 2021 to 3 isolations in 2025.

Table 5.4: Sequence types of *S. Typhimurium* isolations in horses in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	20	21	27
34	0	1	0
568	0	2	0
8336	0	0	1
8937	0	0	1
No ST data	0	0	1
Total	20	24	30

Table 5.5: Sequence types of monophasic *S. Typhimurium* isolations in horses in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	0	0	1
34	1	1	2
Total	1	1	3

Table 5.6: Sequence types of *S. Enteritidis* isolations in horses in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
11	0	1	5
183	1	1	0
5492	0	1	0
6086	0	1	0
8943	0	2	6
10467	0	2	2
Total	1	8	12

In 2025, one isolation yielded two sequence types (ST11 and ST10467), but is only counted once in the overall number of isolations.

Chapter 6: Reports of *Salmonella* in chickens

From early 2022 and every year since there has been significant disruption to the poultry industry due to national outbreaks of Avian Influenza affecting all industry sectors. This resulted in increased culling of infected flocks, altered management and biosecurity measures which will have likely impacted submission numbers, though statutory surveillance through NCP sampling remains a requirement. During 2020 and 2021 there was also a reduction in submissions for non-statutory surveillance and a reduction in diagnostic submissions in many species as a consequence of the Covid-19 pandemic and associated lockdown measures. This should therefore be borne in mind when comparing 2020 to 2025 data with previous years.

According to the June Agricultural Survey, the total number of chickens held in Great Britain was 149.5 million birds in 2025, comprising approximately 42.1 million breeding and laying hens, and 107.4 million broiler chickens (Figure 6.1). This compares to 143.6 million chickens in 2024, an increase of 4.1%, which is largely attributable to the broiler sector.

Two different systems of reporting are used in this chapter, which should be taken into account when interpreting the results. The first part of this chapter describes isolations of *Salmonella*, including samples originating from statutory surveillance, voluntary surveillance, investigations into clinical disease and investigations carried out under the Zoonoses Order. If 2 submissions from the same group of animals on different dates give the same serovar, this is reported as 2 isolations.

The second part of this chapter describes results obtained within the National Control Programmes (NCPs), comprising results only from statutory surveillance of chicken flocks. The *Salmonella* serovars considered to be of particular public health significance under the assimilated EU regulations (the regulated serovars) form a small proportion of the total isolates reported in Great Britain. Results from the NCPs are reported in a way that ensures that every flock with a *Salmonella*-positive result is counted only once. Numbers of positive flocks reported within the NCP are, therefore, expected to differ from the number of reported isolations. For example, some flocks may be positive for more than one serovar, in which case they are still only counted once as positive flocks for the NCP.

There was a total of 4,671 chicken diagnostic and monitoring submissions received by APHA and SRUC laboratories and partner post-mortem providers in 2025, an 8.7% decrease, compared to 5,115 in 2024. However, APHA does not have information on the number of non-statutory submissions submitted to private laboratories that do not result in a positive culture of *Salmonella*, as the negative results are not reportable under the Zoonoses Order.

There were 2,407 isolations of *Salmonella* from chickens in 2025 (Table 6.1) an increase of 22.7% compared with 2024 (1,961 isolations). This is fewer than in 2023 (2,633

isolations) when isolations were at their highest since before 2009. *Salmonella* isolations from chickens increased substantially between 2018-2020 compared to the previous years (approximately 50% year on year), primarily as a result of increased isolations of non-regulated serovars in the broiler sector. Notably, there has been an increase in the broiler population in the last year.

The total number of isolations reported in this chapter includes samples from statutory surveillance, voluntary surveillance, diagnostic submissions and investigations of clinical disease. It should be noted that there is substantial statutory surveillance of *Salmonella* in chickens and turkeys, which differs from all other food animal species in Great Britain.

The total number of isolations in 2025 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 2,242 (93.1%)
- voluntary surveillance: 165 (6.9%)
- clinical disease: 0 (0.0%)

The percentage of *Salmonella* isolations reported through statutory surveillance in 2025 was lower than in 2024 when 98.1% of total chicken isolations arose from statutory surveillance and only 1.9% arose from voluntary surveillance. These figures are known to vary year on year.

Forty-seven different *Salmonella* serovars were isolated in 2025, accounting for 2,399 of the 2,407 isolations. Eight isolations involved untypable *Salmonella* isolates (these were typed though did not produce a serotype name) which are reported as antigenic structures, and there were no rough strains. Table 6.1 shows the *Salmonella* serovars isolated from chickens between 2021 and 2025. Figure 6.2 shows the relative percentages of the most common serovars isolated from chickens between 2021 and 2025.

The 4 most common serovars isolated from chickens in 2025 is consistent with 2021 to 2024, however the relative contribution of each serovar varied (Figure 6.3). The increase in isolations from 2024 to 2025 is largely the result of an increase in *S. Idikan* (including monophasic variants) isolations.

Consistent with 2018 to 2024, *S. Idikan* (including monophasic variant 13,23:i:-) was the most frequently isolated serovar in 2025 (909 isolations) accounting for 37.8% of all chicken isolations, consistent with 2024 in terms of percentage of isolations (34.6% in 2024) but a greater number of isolations (679 isolations in 2024). Prior to 2025, isolations of this serovar had peaked in 2020 with 716 isolations but had decreased both in real and relative terms in recent years. In previous years the majority of isolations of this serovar comprised were of the monophasic variant *S. 13,23:i:-*, which can be associated with contaminated feed mills and can also become established and persistent in hatcheries and on poultry farms (Gosling *et al.*, 2022).

Salmonella Kedougou (including monophasic variants) accounted for 423 isolations in 2025 having consistently been one of the most common serovars to be isolated from chickens in Great Britain for many years (Table 6.1, Figure 6.3). Isolations of *S. Kedougou* (including monophasic variants) had been rising steadily until 2021 when they almost halved (217 versus 430 isolations in 2020) but rose again to a peak in 2023 (537 isolations) before dropping to 382 isolations in 2024. The relative proportion of flocks with this serovar increased from 11.5% in 2022 to 20.4% in 2023 but has since been declining (19.5% in 2024, 17.6% in 2025).

With 341 isolations, *S. Montevideo* was the third most common serovar isolated in 2025 accounting for 14.2% of all chicken isolations. This is consistent with 2024 when it was also the third most common serovar (308 isolations, 15.7% of all chicken isolations) (Figure 6.2). Isolations of this serovar decreased from 2023 (591 isolations) to 2024 otherwise isolations had been increasing year-on-year (Figure 6.3). Although isolations in 2025 increased compared to 2024, the number of flocks these isolations were associated with decreased from 286 in 2024 to 234 flocks in 2025.

Isolations of *Salmonella* Mbandaka have been fluctuating in recent years. There were 237 isolations in 2025 (9.8% of all chicken isolations). This represents an increase from 2024 (168 isolations, 8.6% of all chicken isolations). In 2022 this serovar was the most frequently isolated serovar with 695 isolations, (28.9% of all chicken isolations) having increased by over 2-fold compared to 294 isolations in 2021. Isolations of *S. Mbandaka*, which can be a feed related serovar associated with soya products, had been generally increasing since 2010, peaking in 2018 at 472 isolations when it was the most frequently isolated serovar. This was followed by a decline in isolations until 2020 after which isolations increased in 2021 and 2022 when isolations were at their highest since before 2009 (Figure 6.3).

There were 7 *S. Typhimurium* isolations from chickens in 2025 originating from 6 flocks, accounting for 0.3% of all *Salmonella* isolations. This is the lowest number of isolations since 2017 when there were 5 isolations of *S. Typhimurium* and represents a 58.8% decrease compared to 2024 (17 isolations). There was also an associated reduction in the number of flocks testing positive and percentage of isolations compared to recent years; 16 flocks, 0.9% in 2024, 13 flocks, 0.6% in 2023. There were 2 different sequence types identified in 2025, ST19 and 8937 (Table 6.2). Sequence type 8937 was not identified in 2023 or 2024.

There were 15 isolations of *S. Enteritidis* in 2025 representing a 25.0% increase compared to 2024 (12 isolations). This is the second consecutive year there has been an increase in this serovar but is still considerably lower than 2022 when isolations were at a 3-year high (23 isolations). Isolations in 2025 were associated with 10 flocks on 4 holdings, compared to 11 flocks on 8 holdings in 2024 and 8 flocks on 5 holdings in 2023. There was similar diversity of sequence types of *S. Enteritidis* isolated in 2025 compared to 2024 with most

isolations associated with ST10 (Table 6.4), also the most common sequence type in 2024 and 2023. Three isolations yielded three sequence types (all three isolations yielded ST11, ST6086 and ST10467) and two isolations yielded two sequence types (one isolation yielded ST6086 and ST10467 and one isolation yielded ST11 and ST10467). Refer to the introduction chapter for the definition of an isolation. There were 7 isolations of ST10467 in 2025 which was also isolated as the second most common sequence type in 2024 and 2023.

Monophasic strains of *S. Typhimurium* were first reported from chickens in 2010, when both *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- were isolated. In 2025, there were 4 isolations of monophasic *S. Typhimurium* compared with 1 isolation in 2024 and 6 isolations in 2023. Monophasic *S. Typhimurium* is often associated with pigs and all isolations in chickens since 2023 have been sequence type ST34 which is also the most common sequence type in pigs (Table 4.3, Chapter 4).

Salmonella Agama, a serovar often associated with badgers, was reported in 12 isolations in 2025 compared to 1 isolation in 2024. This represents the highest number of isolations of this serovar since before 2012 compared to a previous maximum of 10 isolations in 2017. This serovar has most often been associated with single isolations in recent years (2021, 2022 and 2023).

The number of isolations of *S. Ohio* almost doubled in 2025 compared to the previous year (83 isolations in 2025 compared to 44 isolations in 2024). There have been fluctuations in the number of reports of this serovar over recent years, which is most likely to be associated with contaminated feed. Isolations of this serovar peaked in 2018 with 94 isolations.

This is the third consecutive year there has been decreasing isolations of *S. Derby* (6 isolations in 2025). A serovar often associated with pigs and turkeys, isolations peaked in 2019 with 44 isolations, declining to 3 isolations in 2020 before gradually increasing in 2021 and 2022, increasing to second smaller peak of 14 isolations in 2023.

There were notable increases in some other serovars isolated from chickens in 2025 compared with 2024 including *S. Give* (10 versus 0 isolations) and *S. Orion* var. 15⁺ (72 versus 50).

In 2025 there were single isolations of 4 serovars never previously reported from chickens in Great Britain; *S. Altona*, *S. Grumpensis*, *S. Richmond* and *S. Uganda*. Other unusual serovars included *S. Meleagridis* (last reported from chickens in 2017), *S. Nima* (last reported from chickens in 2019), *S. Ouakam* (last reported from chickens in 2010), *S. Paratyphi B Variant Java* (last reported in chickens in 2017), *S. Schwarzengrund* (last reported in chickens in 2020) and *S. Virchow* (last reported in chickens in 2013).

There were no reported isolations of *Salmonella* from chickens imported into Great Britain in 2025. This is consistent with 2024 and 2023 and compares to one report in 2022.

National Control Programme for *Salmonella* in chickens

The [Regulation \(EC\) No 2160/2003](#) of the European Parliament and of the Council of 17 November 2003 on the control of *Salmonella* and other specified food-borne zoonotic agents, which came into force on 21 December 2003, aims to reduce the prevalence of certain zoonotic infections at the primary production level, by requiring the implementation of species-specific *Salmonella* National Control Programmes (NCPs). The *Salmonella* NCPs for chickens (*Gallus gallus*) in Great Britain cover breeding flocks, laying flocks and broiler flocks and since exit from the EU in 2021 each devolved nation in Great Britain has had its own individual target for each sector.

For all the NCPs, the results are reported in terms of positive flocks. A flock is counted as positive only once regardless of the number of separate isolations reported from that flock or the number of different serovars identified. If more than one positive flock is identified on a holding within the year, these are counted separately.

National Control Programme for *Salmonella* in breeding flocks of chickens

The NCP for breeding flocks of chickens implements the monitoring and controls that are required in order to meet the target for reduction in *Salmonella* prevalence that has been set in [Regulation \(EU\) No. 200/2010](#) and [Regulation \(EU\) No. 517/2011](#) (amended in 2019 by [Regulation \(EU\) 2019/268](#)). Following the EU exit, these regulations were incorporated into UK law and references to EU legislations throughout this chapter are references to those as assimilated in UK law. The target is for a maximum of 1% of adult breeding flocks testing positive for regulated *Salmonella* serovars annually within each devolved nation of Great Britain. The regulated serovars are *S. Enteritidis*, *S. Typhimurium*, monophasic strains of *Salmonella* Typhimurium with the antigenic formula *Salmonella* 1,4,[5],12:i:- (the somatic antigen 1 can only be determined after lysogeny so is not normally tested for. The somatic antigen 5 may or may not be present in different strains of *S. Typhimurium* or its monophasic variants), *S. Infantis*, *S. Virchow* and *S. Hadar*.

The NCPs for *Salmonella* in breeding flocks includes all holdings with 250 or more birds (for further information see [Salmonella: test your breeding chickens - GOV.UK](#)). The NCPs across Great Britain are enforced by separate, equivalent Control of *Salmonella* in Poultry Orders (CSPO) in [England](#), [Scotland](#) and [Wales](#). The assimilated targets for reduction is only concerned with regulated serovars in adult breeding flocks. However, the CSPOs set out sampling and recording requirements for both in-rear and adult flocks, and APHA monitors the results from testing in both age categories.

Positive breeding flocks identified in the NCP in 2025

In 2025, 11 adult breeding flocks, on 8 separate holdings, tested positive for *Salmonella* spp. under the statutory testing programme. This is comparable to 2024 (10 positive flocks) and 2023 (9 positive flocks) and a decrease from 2022 (17 positive flocks). Since 2013, there has been a generally increasing trend in the proportion of adult breeding flocks testing positive for *Salmonella* in Great Britain, though the proportion has been more stable in recent years (Figure 6.4).

Two adult breeding flocks tested positive for a regulated *Salmonella* serovar in 2025 (Table 6.5) compared to 4 in 2024. Both flocks were broiler breeder flocks and tested positive for *Salmonella* Typhimurium monophasic variants *Salmonella* 4,12:i (x1) and *Salmonella* 4,5,12:i (x1). The last time monophasic strains of *S. Typhimurium* were isolated from breeder flocks as part of the NCP was 2014. Broiler breeder flocks account for 89.6% of registered breeder flocks in Great Britain. One flock was identified through annual official sampling and one flock through operator sampling. This is the second consecutive year that *S. Infantis* has not been isolated in breeding flocks as part of the NCP, having first been isolated in 2021. No breeder flocks tested positive for *S. Typhimurium* in 2025. The number of flocks testing positive for *Salmonella* Typhimurium has increased in recent years from 2 flocks in 2022 to 4 flocks in 2023 and 2024. *Salmonella* Enteritidis, *S. Hadar* and *S. Virchow* have never been detected in breeding chickens as part of the NCP.

Nine adult breeding flocks, on 6 separate holdings, were positive for non-regulated *Salmonella* serovars. This included 2 broiler breeder flocks on the same holding which tested positive for *S. Idikan* (including monophasic variants *S. 13,23:i:-*). This is similar to 2024 when 2 flocks also tested positive but slightly less than in both 2023 (3 flocks) and 2022 (5 flocks). This serovar can be a resident strain in some hatcheries and feed mills, and can become resident on affected farms. (*S. Idikan* (including monophasic variants) was one of four serovars isolated from compound poultry feed in 2025-see Chapter 12) Until 2021, *S. 13,23:i:-* had been the most commonly reported serovar in adult breeding flocks each year since 2016, reaching a peak in 2018 (9 positive flocks). The low number of positive flocks in 2025 continues a decreasing trend in occurrence of this serovar in breeding flocks in recent years.

Three immature (in-rear) breeding flocks tested positive for a non-regulated *Salmonella* spp. *S. Orion* var 15+ (Binza), *S. Idikan* (including monophasic variants) and *S. Montevideo* were identified in three separate in-rear broiler breeder flocks. The last time immature breeding flocks tested positive for *Salmonella* spp. was in 2021.

A comparison of the serovars identified in adult breeding flocks testing positive under the NCP between 2021 and 2025 is shown in Table 6.5 and Figure 6.5. Data for years prior to this are available in the *Salmonella* in Livestock Production reports from the relevant year. There is no clear trend in the occurrence of different *Salmonella* serovars in adult chicken

breeding flocks year on year and numbers are low. *S. Idikan* or its monophasic variant 13,23:i:-, which are now reported together, has been identified every year since 2013 (and always in broiler breeder flocks).

In Great Britain, a total of 1,087 adult breeding flocks on 235 premises (those with more than 250 birds) were registered in 2025, and a total of 1,076 flocks were subject to *Salmonella* testing via routine annual official sampling visits. This represents a shortfall of approximately 1% in the number of flocks subject to annual official sampling, which is less than in 2024 (5%) and in 2023 (6%) when resources had to be diverted in order to respond to outbreaks of Avian Influenza and Bluetongue. Using the number of registered flocks as the denominator population, the estimated prevalence of *Salmonella* spp. in adult breeding flocks in Great Britain, tested within the NCP was 1.01% (11 of 1,087) in 2025. The prevalence of *Salmonella* spp. in adult breeding flocks in England was 1.39% (11/793), in Wales was 0.00% (0/57) and in Scotland was 0.00% (0/237). The prevalence of regulated serovars in Great Britain was 0.18% (Table 6.5, Figure 6.4). The prevalence of regulated serovars in adult breeding flocks in England was 0.25% (2/793), in Wales was 0.00% (0/57), and in Scotland was 0.00% (0/237). Each devolved nation is well below their 1% target for regulated serovars.

National Control Programme for *Salmonella* in laying hen flocks

The NCP for commercial laying flocks of chickens implements the monitoring and controls that are required in order to meet the target for reduction in *Salmonella* prevalence that has been set in the assimilated regulations: [Regulation \(EU\) No. 517/2011](#), amended in 2019 by [Regulation \(EU\) 2019/268](#). The target is for a maximum of 2% of adult laying hen flocks testing positive for regulated *Salmonella* serovars annually. In Great Britain this applies to each devolved nation individually. The regulated serovars are *S. Enteritidis* and *S. Typhimurium*, including monophasic strains of *S. Typhimurium*.

The NCP for *Salmonella* in laying flocks includes all commercial egg laying holdings with 350 or more birds (for further information see [Laying hens and flocks: poultry testing for *Salmonella* - GOV.UK](#)). The NCPs are enforced by separate, equivalent Control of *Salmonella* in Poultry Orders (CSPO) in [England](#), [Scotland](#), and [Wales](#). The EC target for reduction is only concerned with regulated serovars in adult laying flocks, however, the CSPO sets out sampling and recording requirements for both in-rear and adult flocks, and APHA monitors the results from testing in both age categories.

Positive laying flocks identified in the NCP in 2025

During 2025, a total of 46 adult laying hen flocks, originating from 32 separate holdings, tested positive for *Salmonella* spp. under the statutory testing programme. This is 31.3% fewer than the number of flocks testing positive in 2008 when the NCP was first

implemented (67 positive flocks), and an increase of 39.4% compared to 2024 (33 positive flocks) (Table 6.6).

A total of 16 adult flocks, from 8 separate holdings, tested positive for regulated *Salmonella* serovars during 2025, more than in 2024 (9 positive flocks from 5 holdings). Prior to 2024, there had been a generally decreasing trend in number of flocks positive for regulated *Salmonella* serovars since a peak in 2019 (16 positive flocks) (Table 6.6 and Figure 6.6).

Ten adult flocks from 4 separate holdings tested positive for *S. Enteritidis* in 2025. Seven flocks originated from one holding where two flocks tested positive via operator sampling. Five further flocks were identified via follow-on official sampling. Two further flocks tested positive following operator sampling and one flock through annual official sampling. This is an increase in *S. Enteritidis* positive flocks compared to 2024 (2 adult flocks from two separate holdings) and 2023 (3 adult flocks from the same holding). Prior to 2025, there had been a decreasing trend in isolation of *S. Enteritidis* since 2019 (14 flocks from 5 holdings), when the highest numbers of flocks tested positive for *S. Enteritidis* since the implementation of the NCP in 2008 (49 positive flocks).

Six adult flocks, from 4 separate holdings, tested positive for *S. Typhimurium* in 2025. This is a slight decrease from 7 flocks from 3 holdings in 2024 and 2 flocks in 2023. Prior to 2024 there had been a decreasing trend seen in recent years in the number of flocks testing positive for this serovar following a small peak of 6 positive flocks in 2021 (Table 6.6). Before 2018, *S. Typhimurium* had not been isolated from NCP samples collected from adult laying flocks since 2012, when 2 flocks on 2 different holdings tested positive.

No adult flocks of laying hens were positive for monophasic *S. Typhimurium* in 2025 or 2024 which compares to one flock positive for *S. 4,12:i:-* in 2023. This was the first instance of a laying flock testing positive for this monophasic strain of *S. Typhimurium* since 2015. The last isolation of *S. 4,5,12:i:-* was in 2019 when one flock tested positive. This continues a generally low prevalence of these monophasic strains of *S. Typhimurium* in adult laying flocks.

A comparison of the serovars identified in adult laying flocks in the NCP between 2021 and 2025 is shown in Table 6.6 and Figure 6.7. Data for years prior to this are available in the *Salmonella* in Livestock Production reports from the relevant year.

In total, 19 different non-regulated serovars were identified from adult laying chickens in 2025, from 30 flocks on 25 separate holdings, compared to 24 flocks from 22 holdings in 2024. One flock tested positive for 2 different non-regulated serovars, *S. Cubana* and *S. Senftenberg*. The most common serovars were *Salmonella* 61:k:1,5,(7), which was isolated from 6 flocks on 4 different holdings, and *S. Mbandaka*, which was isolated from 5 flocks on 5 different holdings. *Salmonella* 61:k:1,5,(7) (*enterica* subspecies *diarizonae*), last detected in 2024 but prior to that 2014, is considered to be a sheep adapted strain and

is the most commonly isolated *Salmonella* from scanning surveillance samples of sheep. *S. Mbandaka* was the most common non-regulated serovar in layers in 2022 and is often amongst the most common serovar isolated from broiler NCP samples.

In 2025, one serovar (*S. Grumpensis*) was isolated from adult laying flocks in the NCP for the first time.

Four in-rear (immature) flocks tested positive for *Salmonella* in 2025 in Great Britain. This compares to no positive flocks during 2024, and 3 positive flocks during both 2022 and 2023. Two in-rear flocks on different holdings tested positive for a regulated serovar in 2025 (*S. Enteritidis* (x1) and *S. Typhimurium* (x1)). One adult flock at the same holding also tested positive for *S. Enteritidis*. Prior to 2025, the last time an in-rear layer flock tested positive for a regulated serovar was in 2019 when a flock tested positive for *S. Typhimurium*.

Using the number of NCP-eligible adult flocks of laying hens in production in Great Britain during 2025 as the denominator population, the estimated prevalence of *Salmonella* spp. in laying flocks was 1.23% (46 of 3,755) in 2025. NCP-eligible flocks include those with over 350 birds or whose eggs are not for private domestic use only. This is an increase compared to 2024 (0.89% (33 of 3,700) (Figure 6.6). The prevalence of *Salmonella* spp. in England was 1.34%, in Wales was 0.89% and in Scotland was 0.96%.

The estimated prevalence of regulated *Salmonella* serovars in 2025 in adult laying flocks was 0.43% (16 of 3,755). This represents an increase compared to 2024 (0.24%). The prevalence of regulated serovars in England was 0.52%, in Wales was 0.45% and there were no flocks positive for regulated serovars in Scotland. Therefore, for all devolved nations, the prevalence of regulated serovars in laying hens was well below the target of 2.00%. Overall, the prevalence of *Salmonella* in adult laying hens in Great Britain remains considerably lower than in 2004 and 2005 when the EU baseline survey was carried out. Whilst the results of the baseline survey are not directly comparable to the NCP monitoring results, due to different sampling methods and denominator data, this nevertheless demonstrates continued successful control of *Salmonella* in the egg industry.

National Control Programme for *Salmonella* in broiler flocks

The NCP for commercial broiler flocks of chickens implements the monitoring and controls that are required in order to meet the targets for reduction in *Salmonella* prevalence that has been set in the assimilated EU regulations: [Regulation \(EU\) No. 200/2012](#), amended in 2019 by the retained [Regulation \(EU\) 2019/268](#). The targets, which apply to each devolved nation individually, are set for a maximum of 1% of broiler flocks testing positive for regulated *Salmonella* serovars annually. The regulated serovars are *S. Enteritidis* and *S. Typhimurium*, including monophasic variants of *S. Typhimurium*.

The NCPs for *Salmonella* in broiler flocks includes all commercial broiler holdings with 2,000 or more birds. The NCPs are enforced by separate, equivalent Control of *Salmonella* in Broiler Orders (CSBO) in [England](#), [Scotland](#) and [Wales](#).

Positive flocks identified in the NCP for broiler flocks in 2025

During 2025, a total of 2,082 broiler flocks from 419 separate holdings tested positive for *Salmonella* under NCP testing with an estimated prevalence of 4.50%. This represents an increase of 17.3% relative to 2024 (1,775 flocks) but an 8.2% decrease relative to 2023 (2,268 flocks). With the exceptions of 2024 and 2021, this follows a generally increasing trend in positive flocks since 2017 (Table 6.7 and Figure 6.8). The increase seen in 2025 compared to 2024 is mostly attributable to a 36.5% increase in *S. Idikan* (including monophasic variants), a 36.3% increase in *S. Mbandaka* and a 14.6% increase in *S. Kedougou* (including monophasic variants) (Table 6.7).

Two broiler flocks, on 2 separate holdings, tested positive for regulated serovars in 2025 which is a marked reduction compared to recent years, 2024, 2023, 2022 and 2021 (14 flocks, 16 flocks, 15 flocks and 15 flocks respectively) (Table 6.7 and Figure 6.8).

There were no reports of *S. Enteritidis* positive flocks in 2025 compared to 9 flocks in 2024 and 5 flocks in 2023 (Table 6.7). This is similar to levels seen in 2021 and 2022 (2 and one positive flock(s), respectively), and remains considerably lower than 2015, where 50 flocks tested positive for this serovar after an outbreak related to imported hatching eggs, which also happened in 2018 to a lesser extent.

There were 2 reports of monophasic *Salmonella* Typhimurium variant *S. 4,12:i:-* in 2025, an increase compared to 2024, 2023 and 2022, where no positive flocks were reported, and similar to 2021 (3 positive flocks).

No flocks were positive for monophasic *S. Typhimurium* variant *S. 4,5,12:i:-* in 2025, the same as 2024, but a decrease compared to the number of reports seen in 2023 (4 flocks), 2022 (10 flocks), and 2021 (6 flocks).

There were no reports of *S. Typhimurium* positive flocks in 2025, compared to 5 positive flocks in 2024, 7 in 2023, and 4 in 2022 and 2021.

A comparison of the serovars identified in broiler flocks in the NCP between 2021 and 2025 is shown in Table 6.7 and Figure 6.9. Data for years prior to this are available in the *Salmonella* in Livestock Production reports from the relevant year. There were 2,080 broiler flocks positive for non-regulated *Salmonella* serovars in 2025, including 7 flocks that tested positive for more than one non-regulated serovar. The 4 most common serovars isolated from broiler chickens in 2025 was consistent across all years since 2019 (including *S. 13,23:i:-* as a monophasic variant of *S. Idikan*).

The occurrence of *S. Idikan* (including monophasic variants) has in previous years been comprised largely by the monophasic variant *S. 13,12;i:-*. This serovar began increasing in 2018 until 2020, it then decreased significantly in 2021, but has since been rising again, and was the most frequently isolated serovar in 2025, with 857 flocks (Table 6.7). *S. 13,23;i:-* in particular is associated with some hatcheries and feed mills and can become resident on farm. It has been commonly observed in broiler flocks since 2013. In 2025, *S. Idikan* (including monophasic variants) was identified on 206 premises, of which 119 (57.8%) were repeatedly positive for the same serovar in subsequent flocks. Repeated incidents of *S. Idikan* (including monophasic variants), defined as at least one positive flock placed on the premises in a particular month, were observed on individual premises. Of the 206 premises which had at least one flock positive for *S. Idikan* (including monophasic variants), 24.3% had 2 incidents of *S. Idikan* (including monophasic variants), whilst 9.7%, 11.2%, 5.8%, and 3.9%, had 3, 4, 5, and 6 incidents of this serovar in 2025, respectively. The maximum number of incidents of *S. Idikan* (including monophasic variants) on one premises in 2025 was 7.

As seen in 2024, *Salmonella* Kedougou (including monophasic variants) was the second most frequently reported serovar in 2025 (392 flocks). This is similar to the level observed in 2023 and 2024 (421 and 342 flocks, respectively) and remains higher than 2022 and 2021 where *S. Kedougou* (including monophasic variants) was observed in 232 and 192 flocks, respectively (Table 6.7). *S. Kedougou* (including monophasic variants) is associated with feed mill environments and can be found in ingredients such as oilseed meals (for further detail see Chapter 12). In 2025, *S. Kedougou* (including monophasic variants) was identified on 89 premises, of which 45 (50.6%) were repeatedly positive for the same serovar in subsequent flocks. Repeated incidents of *S. Kedougou* (including monophasic variants) were observed on individual premises. Of the 89 premises which had at least one flock positive for *S. Kedougou*, 15.7% (14/89) had 2 incidents, whilst 12.4% (11/89), 5.6% (5/89), 5.6% (5/89), and 10.1% (9/89) had 3, 4, 5, and 6 incidents of this serovar in 2025. The maximum number of incidents of *S. Kedougou* (including monophasic variants) on one premises in 2025 was 7 (1.1%, 1/89).

Despite a 17.9% decrease compared to 2024 (285 flocks), *Salmonella* Montevideo remained the third most frequently reported serovar from broiler flocks in 2025 (234 flocks). Reports of the serovar increased each year from 2015 (19 flocks) to 2023 (545 flocks), with the decline in 2025 marking the second consecutive annual decrease (Table 6.7). *S. Montevideo* was identified on 89 premises in 2025, of which 39 (43.8%) were repeatedly positive for the same serovar in subsequent flocks. Multiple incidents of *S. Montevideo* were observed on individual premises; 18.0% (16) of the 89 premises which had at least one positive flock for *S. Montevideo* had 2 incidents of this serovar in 2025. Up to 6 incidents of *S. Montevideo* were observed on one premises (1.1%), with 11.2% (10/89), 11.2% (10/89) and 2.2% (2/89) of premises having 3, 4 and 5 incidents respectively.

Other notable increases in the number of broiler flocks testing positive in 2025 compared to 2024 include: *S. Give* (5 flocks versus 0 flocks) *S. Mbandaka* (214 versus 157 flocks) and *S. Ohio* (73 versus 41 flocks).

Notable decreases in the number of flocks testing positive in 2025 compared to 2024 include: *S. Agona* (120 versus 135) and *S. Derby*, often associated with pigs and turkeys (6 versus 9 flocks). *Salmonella* *Infantis* is not commonly isolated from food producing animals in Great Britain, but has been associated with imported feed ingredients, as well as raw meat pet food and dogs, and showed an increase in number of affected broiler flocks in recent years (27 positive flocks in 2025, 19 positive flocks in 2024, 50 positive flocks in 2023). There were no *S. Infantis* positive flocks in 2019 or 2020 and one positive flock in 2018. It is one of the most frequently isolated serovars in broiler chickens across mainland Europe.

An estimated 46,298 broiler flocks were tested in Great Britain according to the requirements of the *Salmonella* NCP during 2025. Using this as the denominator population, the estimated prevalence of *Salmonella*-positive broiler flocks was 4.50% (2,082 of 46,298). This is an increase compared to 4.05% in 2024 but a decrease compared to 5.33% in 2023 (highest prevalence since inception of NCP) (Table 6.7, Figure 6.8).

The estimated Great Britain prevalence of regulated *Salmonella* serovars in NCP-eligible broiler flocks in Great Britain during 2025 was 0.004% (2 of 46,298). This is lower than in 2024 and 2023 (0.03% and 0.04%, respectively) (Table 6.7, Figure 6.8) and is consistent with the ongoing maintenance of a low prevalence of regulated serovars in this sector. Unfortunately, accurate denominator data for each devolved nation is not available to estimate country level prevalence to compare against national targets. One broiler premises in Wales and one broiler premises in England tested positive for regulated serovars. For non-regulated serovars 2025 *Salmonella* positive flocks were in England, 53 flocks were in Wales and 2 flocks were in Scotland.

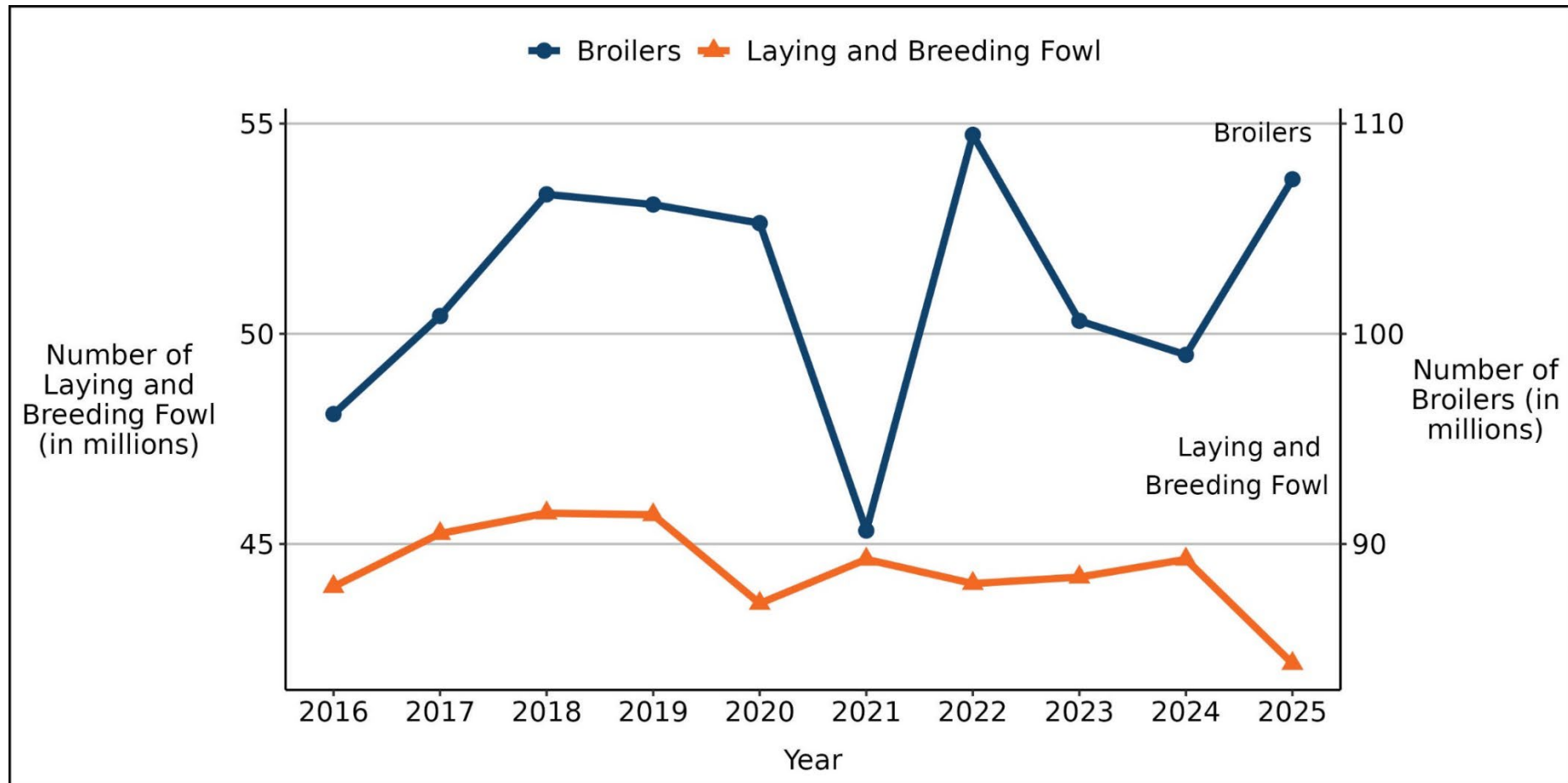
Antimicrobial susceptibility in chickens

A total of 1,778 *Salmonella* isolates from chickens were tested against a panel of 16 antimicrobials in 2025. The majority of isolates (78.7%) were fully susceptible, while 4.9% were classified as MDR.

Resistance remained low across most antibiotic classes and often involved the sulphamethoxazole and trimethoprim combination (10.0%) and sulphonamides (17.3%). The main resistant serovars were *S. Kedougou* (including monophasic variants) (n=152), *S. Ohio* (n=69), *S. Enteritidis* (n=34), and *S. Idikan* (including monophasic variants) (n=30). Ciprofloxacin resistance was identified in 2 isolates, which were both also resistant to nalidixic acid. These 2 isolates did not show resistance to third-generation cephalosporins.

Forty-four isolates were resistant to nalidixic acid overall. No isolates were simultaneously resistant to ciprofloxacin, streptomycin, and neomycin. In 2025, 7 isolates from chicken had resistance to apramycin (0.4%), whereas no isolates showed apramycin resistance in 2024. Four apramycin resistant isolates were detected from chickens in 2023, and 6 were detected in 2022.

Figure 6.1: Chicken population in Great Britain 2016 to 2025



A line graph showing the chicken population for broilers and laying and breeding fowl from 2016 to 2025. The figure shows that the number of broiler, laying and breeding fowl in Great Britain increased steadily from 2016 to 2018, peaking at just over 106 million broilers

and 45 million laying and breeding fowl in 2018. After this there has been a slight decline in the number of layers to between 44 and 45 million birds for the last 3 years while the number of broilers increased sharply to 109 million in 2022 but declined to slightly below 100 million in 2024. There was a decline in laying and breeding fowl in 2025 to just above 40 million birds which is the lowest number of birds since 2016 but the number of broiler birds has risen sharply to approximately 108 million birds.

Source: June 2025 Agricultural Survey.

Table 6.1: *Salmonella* in chickens on all premises in Great Britain (positive flocks from statutory testing, isolations from both statutory and non-statutory testing)

<i>Salmonella</i> serovar	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations	2025 flocks	2025 isolations
Agama	1	1	1	1	3	3	1	1	9	12
Agona	33	34	117	128	191	200	135	136	122	133
Altona	0	0	0	0	0	0	0	0	0	1
Ajiobo	0	0	0	0	1	1	0	0	0	0
Amsterdam	0	0	0	0	1	1	0	0	0	0
Anatum	4	5	2	3	5	5	10	10	2	4
Bareilly	1	1	0	0	0	0	0	0	0	0
Bardo	5	10	3	5	0	0	0	0	0	0
Berta	0	0	1	1	0	0	1	1	0	0
Bovismorbificans	7	21	0	0	1	1	0	0	0	0
Braenderup	2	2	2	2	5	5	2	2	1	1
Bredeney	0	0	0	0	0	0	1	1	0	0
Chester	0	0	0	0	0	0	2	2	2	2
Chomedey	0	0	0	0	1	1	0	0	0	0
Coeln	0	0	4	4	4	4	1	1	0	0
Corvallis	0	0	2	3	0	0	1	1	0	0
Cubana	0	0	0	0	1	1	0	0	1	1
Derby	8	9	11	12	14	14	9	9	6	6
Dublin	0	0	4	4	1	1	0	0	0	0
Durham	0	0	0	0	1	1	0	0	0	0

Salmonella serovar	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations	2025 flocks	2025 isolations
Eboko	0	0	1	1	0	0	0	0	0	0
Enteritidis	5	9	6	23	8	9	11	12	10	15
Essen	0	1	0	0	0	0	0	0	0	0
Ferruch	2	2	0	0	0	0	0	0	0	0
Fresno	0	0	0	0	1	1	0	0	0	0
Give	0	0	0	0	4	4	0	0	8	10
Give var. 15⁺	6	16	8	8	5	5	0	0	0	0
Goldcoast	1	1	0	0	0	0	0	0	0	0
Grumpensis	0	0	0	0	0	0	0	0	1	1
Havana	2	2	5	6	0	0	1	1	0	0
Idikan (incl. monophasic variants)	258	284	347	388	610	681	630	679	859	909
Indiana	0	0	1	1	5	5	6	7	4	4
Infantis	24	42	81	98	54	62	19	20	27	27
Isangi	1	3	0	0	0	0	0	0	2	2
Kedougou (incl. monophasic variants)	192	217	233	277	421	537	344	382	394	423
Kentucky	0	0	4	4	0	1	17	18	5	5
Kingston	0	0	2	2	1	1	1	1	3	3
Kottbus	0	0	1	1	0	0	4	4	4	5
Lexington	1	1	0	0	0	0	0	0	0	0
Liverpool	0	0	1	1	0	0	0	0	0	0

Salmonella serovar	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations	2025 flocks	2025 isolations
Livingstone	4	17	2	3	12	14	3	6	0	4
London	1	1	2	2	0	0	0	0	1	1
Mbandaka	240	294	586	695	273	305	160	168	219	237
Meleagridis	0	0	0	0	0	0	0	0	0	1
Minnesota	0	1	0	0	0	0	0	0	0	1
Molade	1	1	0	0	0	0	0	0	0	0
Monophasic Typhimurium	9	12	10	19	5	6	0	1	4	4
Montevideo	332	403	411	460	547	591	286	308	234	341
Muenchen	4	4	9	9	5	5	23	27	20	20
Muenster	0	0	0	0	1	2	0	0	0	0
Newport	10	37	10	12	4	4	24	26	14	17
Nottingham	0	7	2	4	0	0	1	1	0	0
Nima	0	0	0	0	0	0	0	0	1	1
Odozi	2	4	0	0	0	0	0	0	0	0
Ohio	54	55	44	49	35	36	41	44	73	83
Orion	0	0	1	1	0	0	0	0	2	2
Orion var. 15⁺	33	34	55	60	57	61	50	50	67	72
Oslo	2	2	0	0	1	1	2	2	4	4
Ouakam	0	0	0	0	0	0	0	0	1	1
Oxford	0	0	0	0	1	1	0	0	0	0
Panama	1	1	1	2	0	0	1	1	1	1

Salmonella serovar	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations	2025 flocks	2025 isolations
Paratyphi B Variant Java	0	0	0	0	0	0	0	0	1	1
Poona	0	0	0	0	1	1	1	1	0	0
Reading	1	1	0	1	0	0	0	0	0	0
Richmond	0	0	0	0	0	0	0	0	1	1
Rissen	0	0	1	1	0	0	0	0	1	2
Schwarzengrund	0	0	0	0	0	0	0	0	1	2
Senftenberg	29	63	19	37	17	22	10	10	12	15
Stanley	0	0	1	1	0	0	0	0	0	0
Stanleyville	0	0	0	1	0	0	0	0	1	1
Stourbridge	2	2	1	1	0	0	0	0	0	0
Takoradi	0	0	0	1	0	0	0	0	0	0
Tennessee	0	0	0	1	0	0	0	0	2	2
Typhimurium	10	15	11	18	13	21	16	17	6	7
Uganda	0	0	0	0	0	0	0	0	1	1
Virchow	0	0	0	0	0	0	0	0	3	3
Wangata	0	0	0	0	0	1	0	0	0	1
Yoruba	0	0	0	0	0	2	0	0	0	0
61:k:1,5,(7)	0	0	0	0	1	2	7	8	9	9
untypable strains	27	28	32	35	10	13	3	3	8	8
rough strains	1	27	0	18	0	1	0	0	0	0
Total	1,302	1,670	2,019	2,404	2,306	2,633	1,818	1,961	2,139	2,407

Flocks testing positive for more than one serovar

In 2021 14 flocks were positive for more than one serovar.

In 2022 16 flocks were positive for more than one serovar.

In 2023 15 flocks were positive for more than one serovar.

In 2024 6 flocks were positive for more than one serovar.

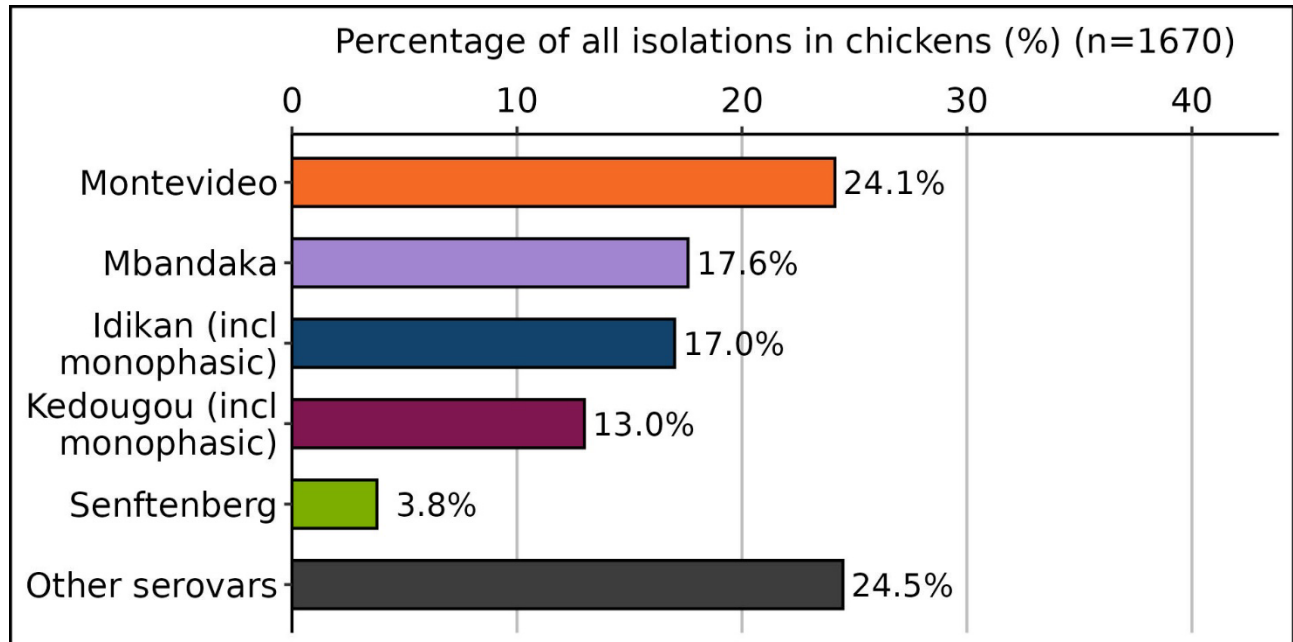
In 2025 8 flocks were positive for more than one serovar.

All flocks positive for more than one serovar are included in the table under both serovars, but only once in the overall total.

All serovars are *Salmonella* enterica subspecies enterica, with the exception of isolates of 61:k:1,5,(7), which are variants of *Salmonella* enterica subspecies diarizonae.

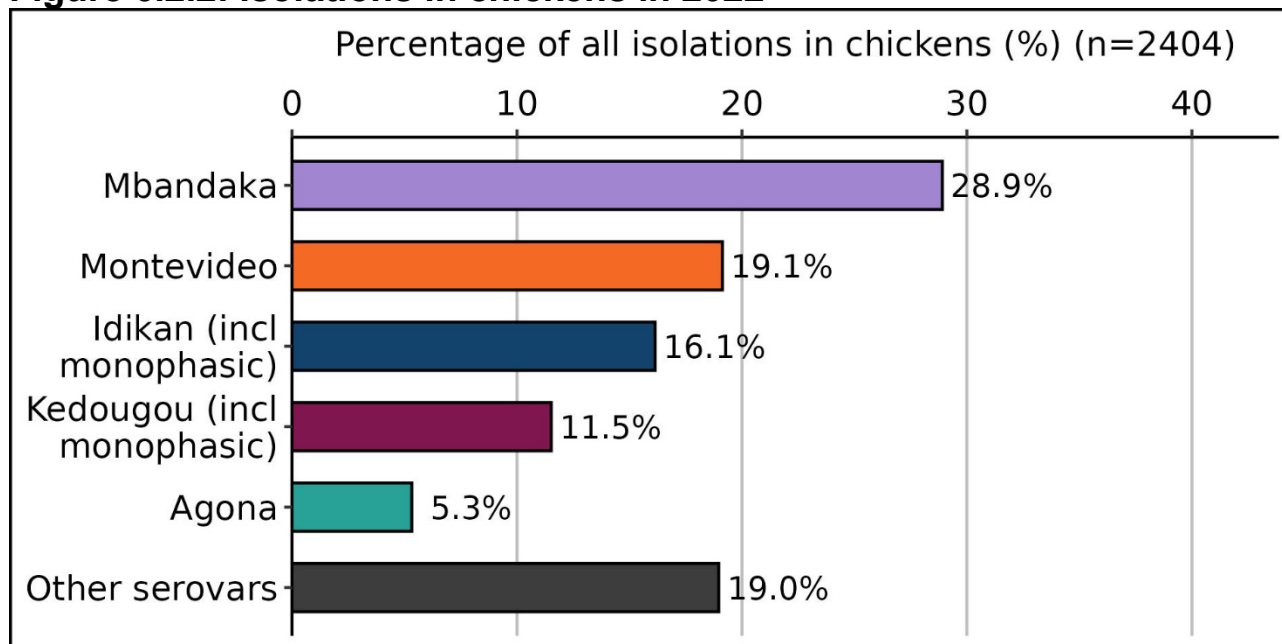
Figure 6.2: Isolations of the most common *Salmonella* serovars in chickens in Great Britain 2021 to 2025 (statutory and non-statutory testing)

Figure 6.2.1: Isolations in chickens in 2021



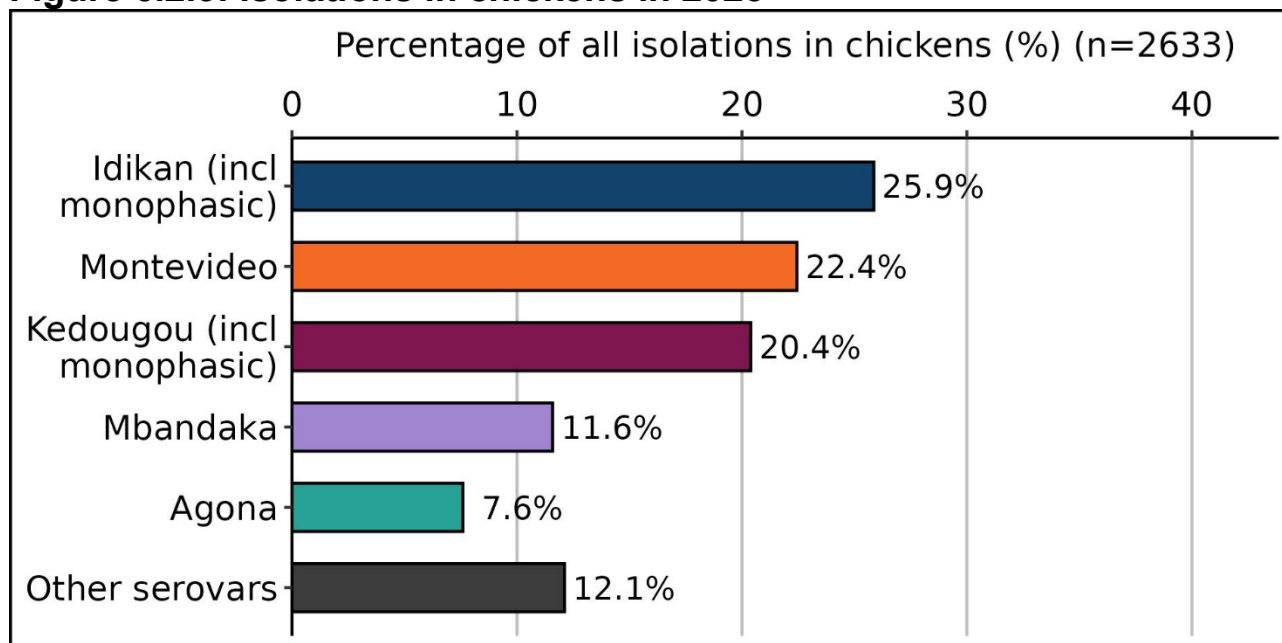
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in chickens in 2021. The most common serovar in chickens in 2021 was *S. Montevideo*, accounting for 24.1% of total isolations, followed by *S. Mbandaka* (17.6%), *S. Idikan* (including monophasic variants) (17.0%) and *S. Kedougou* (including monophasic variants) (13.0%).

Figure 6.2.2: Isolations in chickens in 2022



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in chickens in 2022. The most common serovar in chickens in 2022 was *S. Mbandaka* accounting for 28.9% of total isolations, followed by *S. Montevideo* (19.1%), *S. Idikan* (including monophasic variants) (16.1%) and *S. Kedougou* (including monophasic variants) (11.5%).

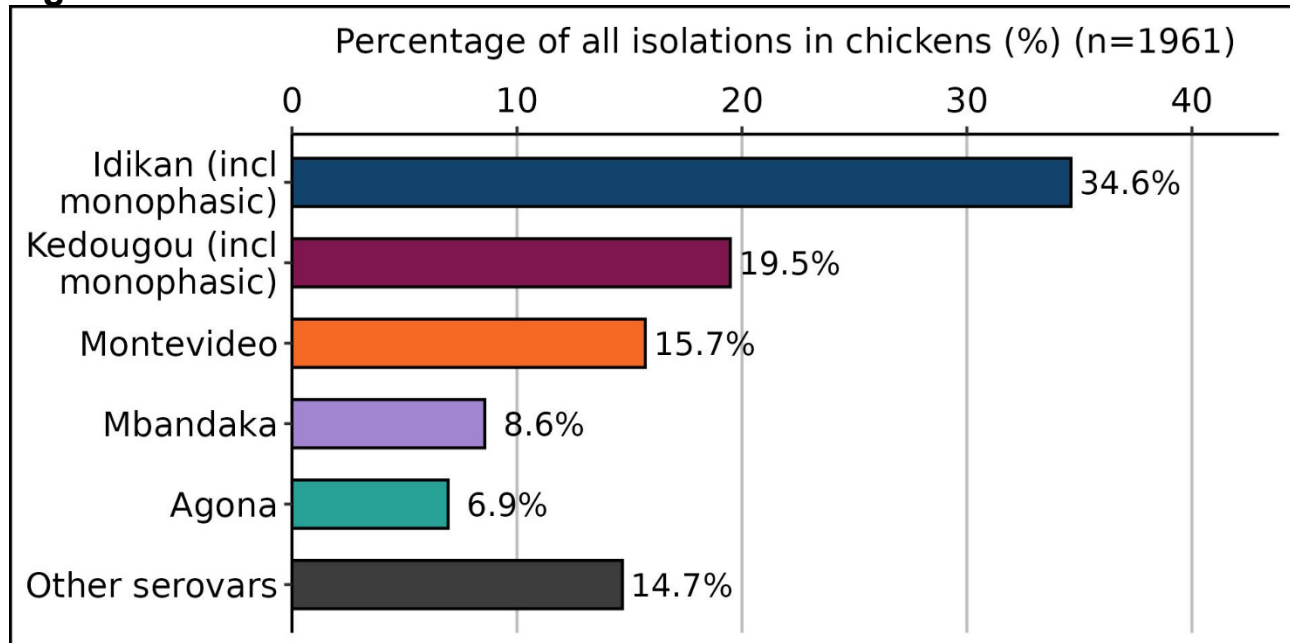
Figure 6.2.3: Isolations in chickens in 2023



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in chickens in 2023. The most common serovar in chickens in 2023 was *S. Idikan*

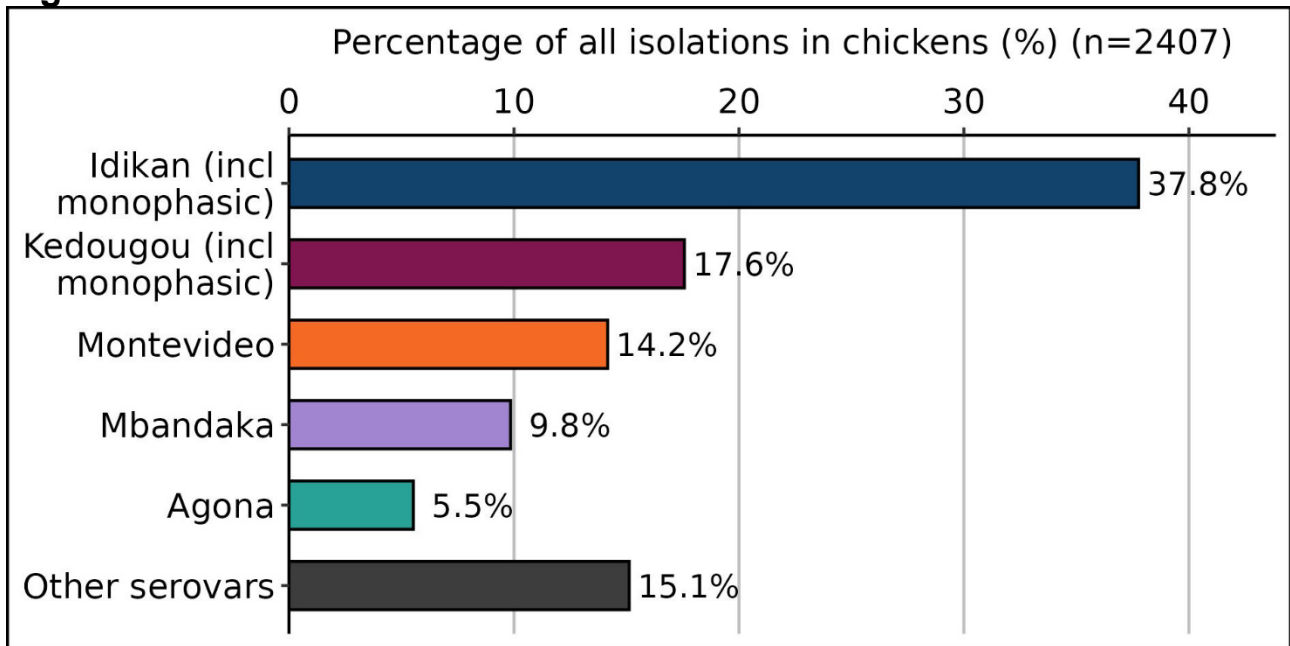
(including monophasic variants), accounting for 25.9% of total isolations, followed by *S. Montevideo* (22.4%), *S. Kedougou* (including monophasic variants) (20.4%) and *S. Mbandaka* (11.6%).

Figure 6.2.4: Isolations in chickens in 2024



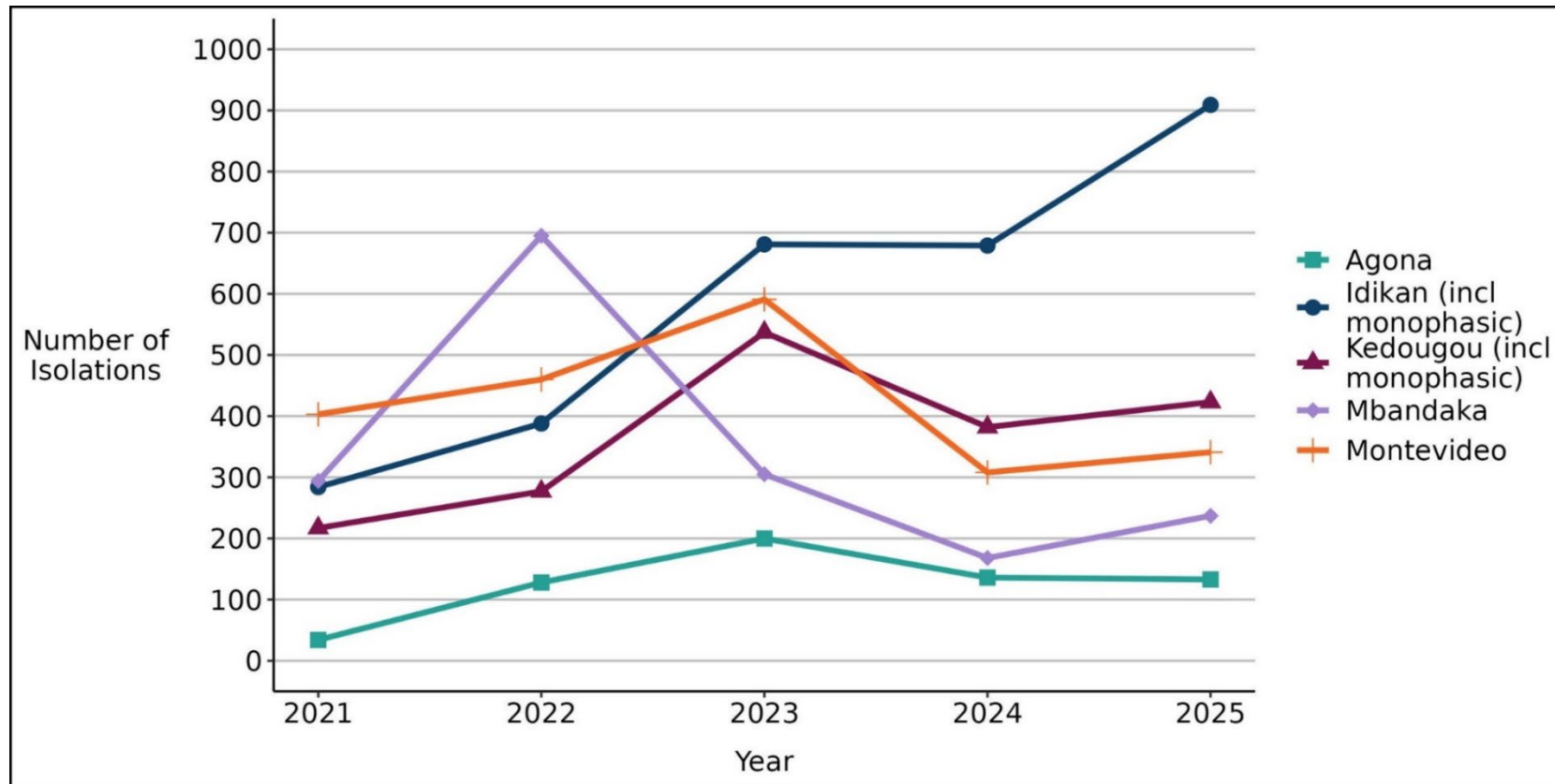
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars chickens in 2024. The most common serovar in chickens in 2024 was *S. Idikan* (including monophasic variants), accounting for 34.6% of total isolations, followed by *S. Kedougou* (including monophasic variants) (19.5%), *S. Montevideo* (15.7%) and *S. Mbandaka* (8.6%).

Figure 6.2.5: Isolations in chickens in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in chickens in 2025. The most common serovar in chickens in 2025 was *S. Idikan* (including monophasic variants), accounting for 37.8% of total isolations, followed by *S. Kedougou* (including monophasic variants) (17.6%), *S. Montevideo* (14.2%) and *S. Mbandaka* (9.8%).

Figure 6.3: The 5 most common *Salmonella* serovars in chickens in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in chickens from 2021 to 2025. The figure illustrates that isolations of *S. Idikan* (including monophasic variants) have been increasing since 2021 and in the last 3 years it has been the most common serovar isolated

from chickens (909 isolations in 2025). Isolations have increased from 343 isolations in 2022 to 681 isolations in 2023 and 679 isolations in 2024. Isolations of *S. Mbandaka*, which was the fourth most frequently isolated serovar in 2025, were consistent with 2024 and 2023. Isolations of *S. Mbandaka* and *S. Kedougou* (including monophasic variants) isolations have fluctuated over recent years and show no consistent trend. *S. Kedougou* (including monophasic variants) was the second most frequently isolated serovar in 2025 (423 isolations) consistent to 2024 (382 isolations). *S. Montevideo* had been steadily increasing between 2020 and 2023 when it was the second most common serovar with 591 isolations. In 2024 isolations of this serovar declined to 308 isolations increasing to 341 isolations in 2025 making it the third most common serovar. *S. Agona* remains the fifth most commonly isolated serovar with 133 isolations in 2025.

Table 6.2: Sequence types of *S. Typhimurium* isolations in chickens in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	16	17	6
568	1	0	0
8336	1	0	0
8937	0	0	1
No ST data	3	0	0
Total	21	17	7

This data includes isolations from both statutory and non-statutory testing.

Table 6.3: Sequence types of monophasic *S. Typhimurium* isolations in chickens in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
34	6	1	4
Total	6	1	4

This data includes isolations from both statutory and non-statutory testing.

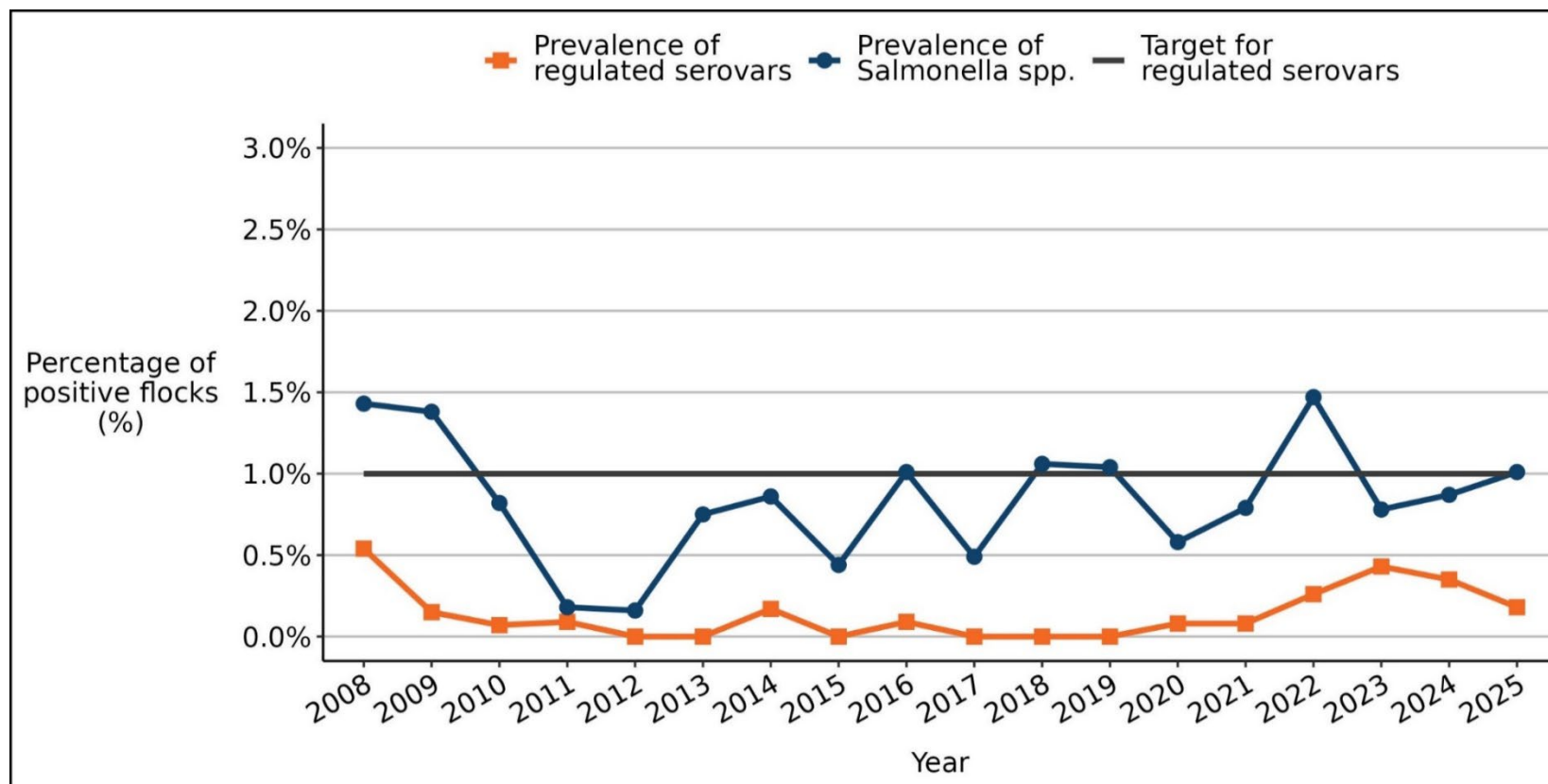
Table 6.4: Sequence types of *S. Enteritidis* isolations in chickens in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
11	7	7	10
6086	0	1	6
8943	0	1	0
10467	2	3	7
Total	9	12	15

In 2025 3 isolations yielded 3 sequence types (all 3 isolations yielded ST11, ST6086 and ST10467) and 2 isolations yielded 2 sequence types (one isolation yielded ST6086 and ST10467 and one isolation yielded ST11 and ST10467). These are counted only once in the total number of isolations.

This data includes isolations from both statutory and non-statutory testing.

Figure 6.4: Prevalence of *Salmonella* in breeding chicken flocks tested under NCP in Great Britain 2008 to 2025



A line graph showing the prevalence of *Salmonella* in chicken breeding flocks tested under the NCP from 2008 to 2025. The figure shows a variable prevalence of *Salmonella* spp. in breeding chicken flocks of between 0.16% and 1.47% but a more constant, lower prevalence of regulated serovars of between 0.0% and 0.54% which does not exceed the target of 1% prevalence.

Table 6.5: Chicken breeding flocks in Great Britain. Number of flocks reported positive with each *Salmonella* serovar, NCP testing 2021 to 2025

The following table shows the number of chicken breeding flocks reported positive with each *Salmonella* serovar from 2021 to 2025 and serovar rank in that year.

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Give	0	0	0	0	0	0	0	0	1	2
Kedougou (incl. monophasic variants)	0	0	0	0	0	0	0	0	1	2
Idikan (incl. monophasic variants)	2	1	1	6	2	3	2	2	1	2
Monophasic Typhimurium	0	0	0	0	0	0	0	0	1	2
Agona	0	0	2	2	0	0	0	0	2	1
Anatum	0	0	3	1	3	1	0	0	2	1
Newport	2	1	0	0	0	0	0	0	2	1
Corvallis	0	0	3	1	0	0	0	0	0	0
Give var. 15⁺	1	5	2	2	0	0	0	0	0	0
Infantis	2	1	3	1	3	1	0	0	0	0
Livingstone	0	0	0	0	0	0	3	1	0	0
London	2	1	0	0	0	0	0	0	0	0
Mbandaka	2	1	3	1	0	0	3	1	0	0
Ohio	0	0	3	1	0	0	0	0	0	0

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Orion var. 15⁺	0	0	3	1	0	0	0	0	0	0
Senftenberg	0	0	0	0	0	0	3	1	0	0
Typhimurium	0	0	2	2	1	4	1	4	0	0
61:k:1,5,(7)	0	0	0	0	0	0	3	1	0	0

For details of chicken breeding flocks reported positive in 2014 to 2020, see the [2020 edition of *Salmonella* in livestock production in Great Britain](#).

Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2021	0.79%	0.08%
2022	1.47%	0.26%
2023	0.78%	0.43%
2024	0.87%	0.35%
2025	1.01%	0.18%

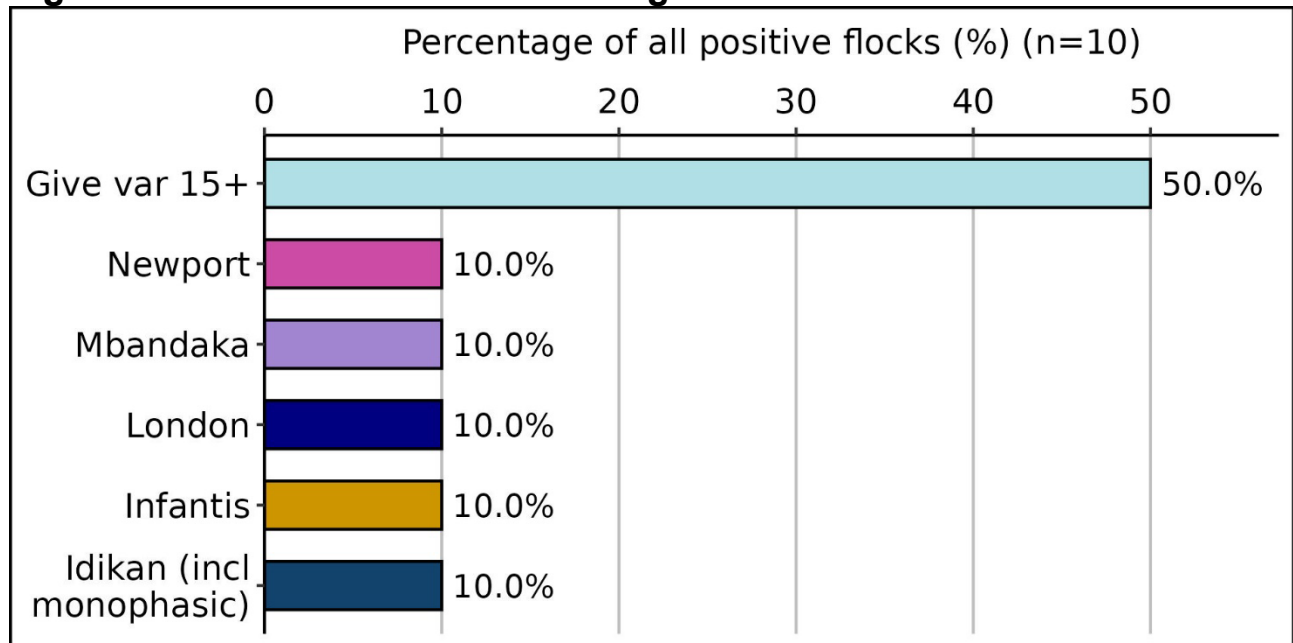
Flocks testing positive for more than one serovar

Some flocks tested positive for more than one serovar. Each flock was counted only once in the overall figure to calculate prevalence.

In 2022 one flock tested positive for *S. Agona* and *S. Give* var. 15⁺.

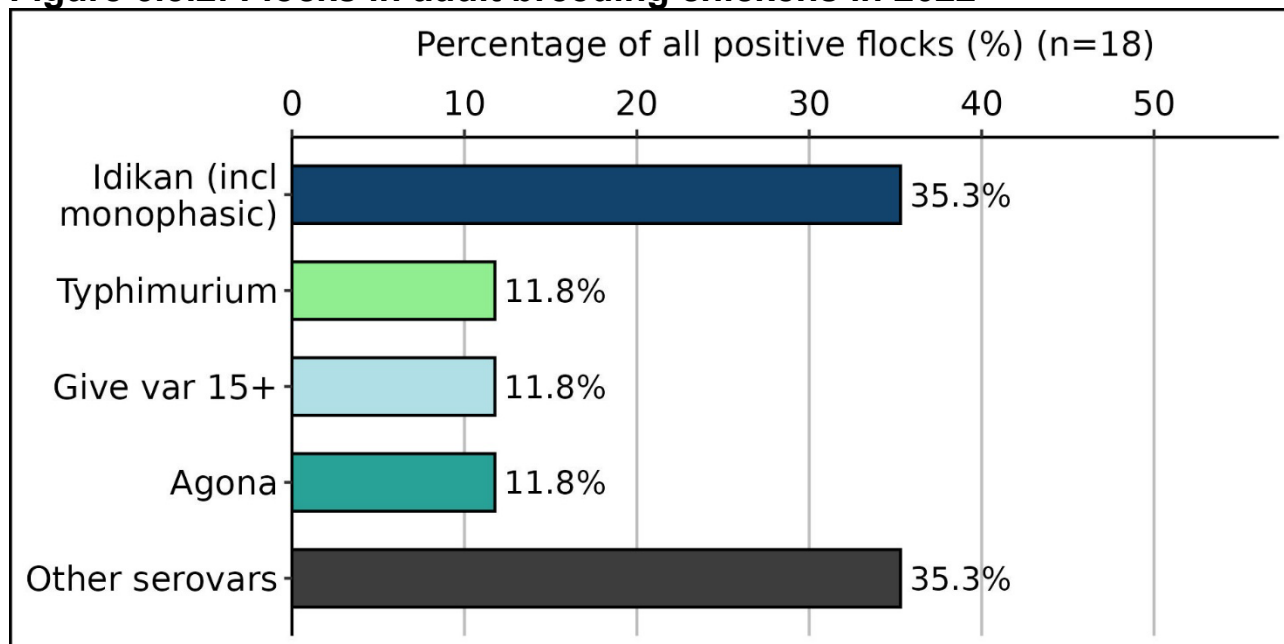
Figure 6.5: The most common *Salmonella* serovars identified in adult chicken breeding flocks in Great Britain 2021 to 2025 reported from NCP testing

Figure 6.5.1: Flocks in adult breeding chickens in 2021



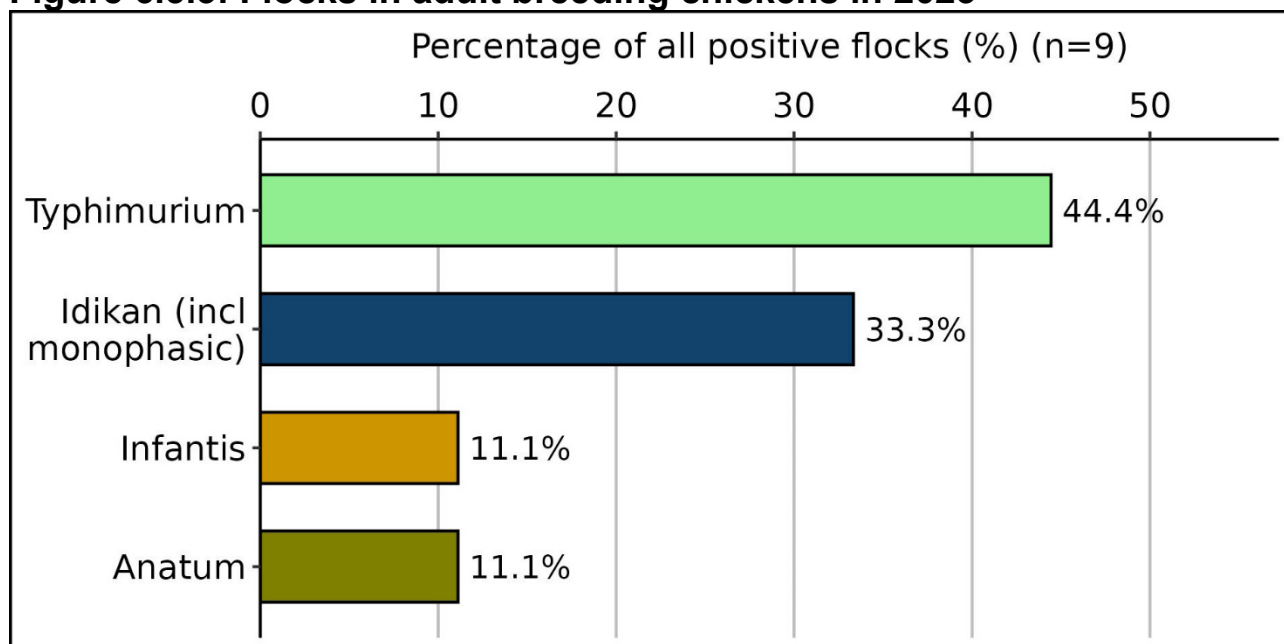
Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult breeding chickens in 2021. In 2021, the most common *Salmonella* serovar in all positive flocks was *S. Give var. 15⁺*, accounting for 50.0% of total flocks. Each of the other 5 serovars recorded, accounted for 10.0% of total flocks.

Figure 6.5.2: Flocks in adult breeding chickens in 2022



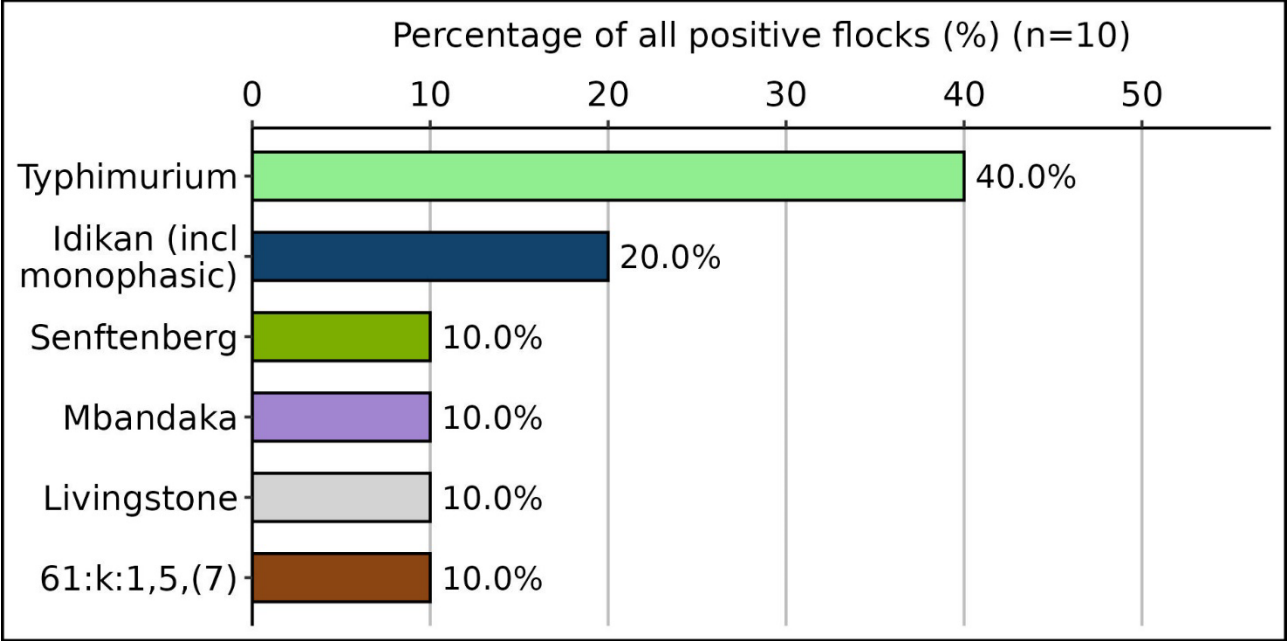
Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult breeding chickens in 2022. In 2022, the most common *Salmonella* serovar in all positive flocks was *S. Idikan* (including monophasic variants), accounting for 35.3% of total positive flocks, followed by *S. Agona* (11.8%), *S. Typhimurium* (11.8%) and *S. Give var. 15⁺* (11.8%). All other serovars made up the remaining 35.3%. In 2022 one flock tested positive for 2 serovars plotted (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

Figure 6.5.3: Flocks in adult breeding chickens in 2023



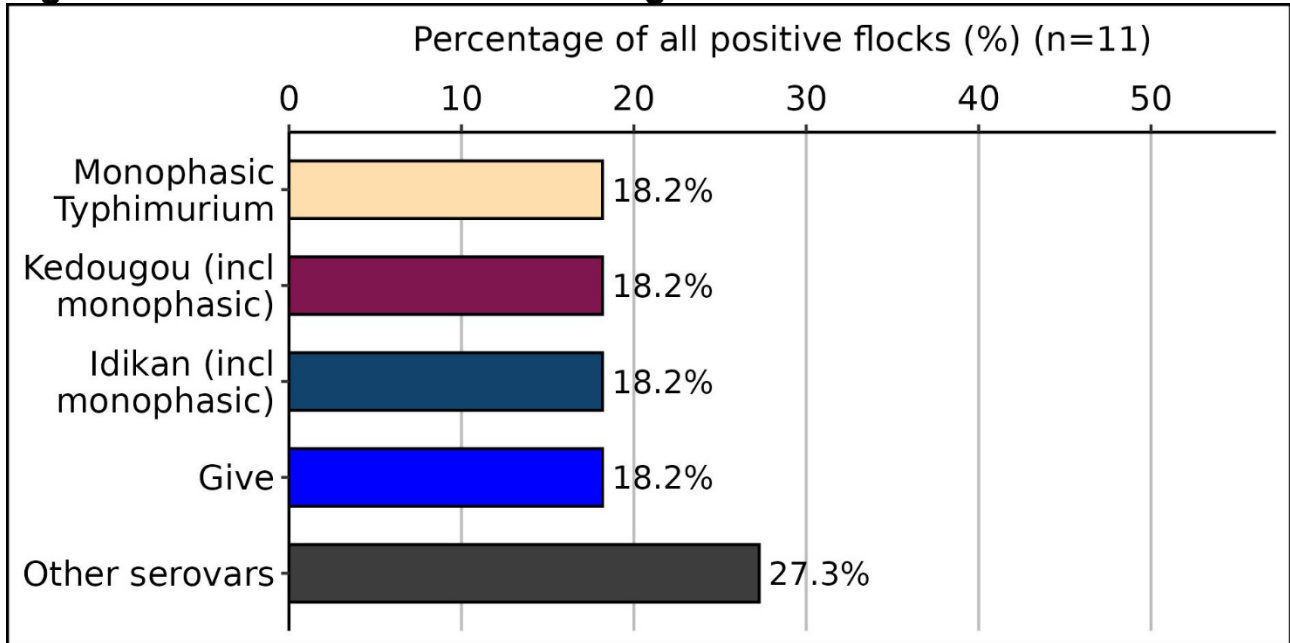
Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult breeding chickens in 2023. In 2023, the most common *Salmonella* serovar in all positive flocks was *S. Typhimurium*, accounting for 44.4% of total flocks, followed by *S. Idikan* (including monophasic variants) (33.3%), *S. Infantis* (11.1%) and *S. Anatum* (11.1%).

Figure 6.5.4: Flocks in adult breeding chickens in 2024



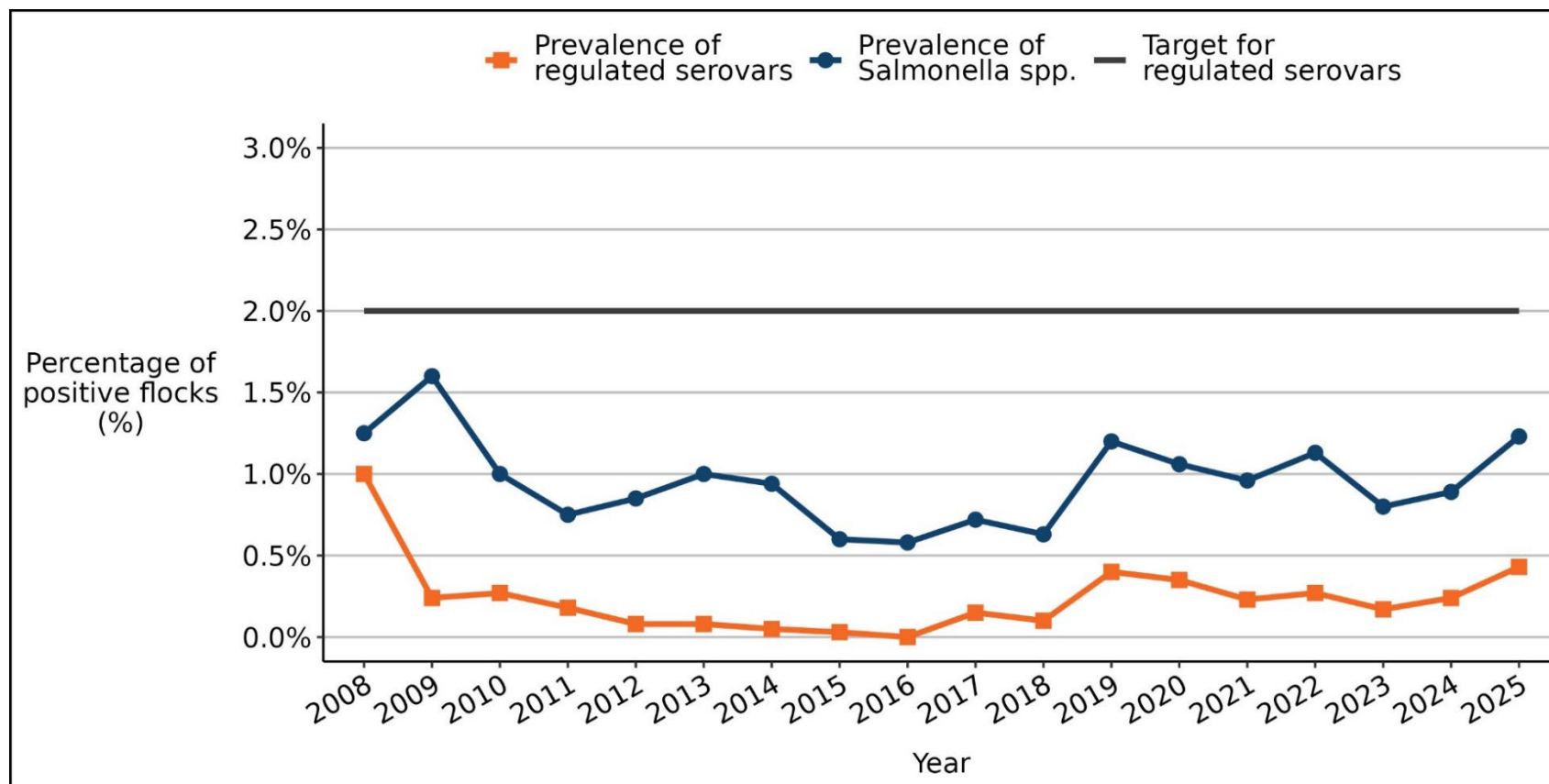
Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult breeding chickens in 2024. In 2024, the most common *Salmonella* serovar in all positive flocks was *S. Typhimurium*, accounting for 40.0% of total flocks, followed by *S. Idikan* (including monophasic variants) (20.0%), *S. Senftenberg*, *S. Mbandaka*, *S. Livingstone*, and *Salmonella* 61:k:1,5,(7) (each accounting for 10.0% of total positive flocks).

Figure 6.5.5: Flocks in adult breeding chickens in 2025



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult breeding chickens in 2025. In 2025, the most common *Salmonella* serovars in all positive flocks were monophasic *S. Typhimurium*, *S. Kedougou* (including monophasic variants), *S. Give* and *S. Idikan* (including monophasic variants) each accounting for 18.2.% of total flocks.

Figure 6.6: Prevalence of *Salmonella* in laying hen flocks tested under NCP in Great Britain 2008 to 2025



A line graph showing the prevalence of *Salmonella* in chicken laying flocks tested under the NCP from 2008 to 2025. The figure shows a variable prevalence of *Salmonella* spp. in laying hen flocks of between 0.58% and 1.60% and a similar trend in the prevalence of regulated serovars of between 0.0% and 1.0% which does not exceed 2% prevalence across all years.

Table 6.6: Laying hen flocks in Great Britain. Number of flocks reported positive with each *Salmonella* serovar, NCP testing 2021 to 2025

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Enteritidis	4	3	2	5	1	3	4	2	1	10
Typhimurium	2	6	2	5	2	2	1	7	2	6
61:k:1,5,(7)	0	0	0	0	3	1	2	6	2	6
Mbandaka	6	1	1	6	3	1	4	2	3	5
Isangi	6	1	0	0	0	0	0	0	4	2
Oslo	6	1	0	0	0	0	5	1	4	2
Tennessee	0	0	0	0	0	0	0	0	4	2
Agama	6	1	6	1	3	1	5	1	5	1
Agona	0	0	6	1	0	0	0	0	5	1
Cubana	0	0	0	0	3	1	0	0	5	1
Give	0	0	0	0	1	3	0	0	5	1
Grumpensis	0	0	0	0	0	0	0	0	5	1
Indiana	0	0	6	1	3	1	5	1	5	1
London	0	0	0	0	0	0	0	0	5	1
Nima	0	0	0	0	0	0	0	0	5	1
Ouakam	0	0	0	0	0	0	0	0	5	1
Paratyphi B var. Java	0	0	0	0	0	0	0	0	5	1
Rissen	0	0	0	0	0	0	0	0	5	1
Schwarzengrund	0	0	0	0	0	0	0	0	5	1
Senftenberg	0	0	6	1	0	0	5	1	5	1

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Stanleyville	0	0	0	0	0	0	0	0	5	1
Amsterdam	0	0	0	0	3	1	0	0	0	0
Anatum	6	1	0	0	0	0	5	1	0	0
Bardo	3	5	4	3	0	0	0	0	0	0
Bareilly	6	1	0	0	0	0	0	0	0	0
Bovismorbificans	4	3	0	0	0	0	0	0	0	0
Chester	0	0	0	0	0	0	5	1	0	0
Coeln	0	0	0	0	3	1	0	0	0	0
Corvallis	0	0	0	0	0	0	5	1	0	0
Derby	6	1	3	4	0	0	0	0	0	0
Dublin	0	0	3	4	3	1	0	0	0	0
Havana	6	1	0	0	0	0	5	1	0	0
Infantis	6	1	4	3	1	3	0	0	0	0
Kedougou (incl. monophasic variants)	0	0	6	1	0	0	4	2	0	0
Kentucky	0	0	6	1	0	0	0	0	0	0
Kingston	0	0	0	0	3	1	0	0	0	0
Kottbus	0	0	0	0	0	0	5	1	0	0
Lexington	6	1	0	0	0	0	0	0	0	0
Livingstone	0	0	6	1	3	1	0	0	0	0
Molade	6	1	0	0	0	0	0	0	0	0
Monophasic Typhimurium	0	0	0	0	3	1	0	0	0	0

Salmonella serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Montevideo	5	2	5	2	2	2	5	1	0	0
Muenster	0	0	0	0	3	1	0	0	0	0
Newport	1	7	4	3	2	2	3	4	0	0
O rough:z₃₈:-	6	1	0	0	0	0	0	0	0	0
Odozi	5	2	0	0	0	0	0	0	0	0
Orion var 15⁺	0	0	0	0	3	1	0	0	0	0
Poona	0	0	0	0	3	1	0	0	0	0
Stourbridge	6	1	6	1	0	0	0	0	0	0
Yoruba	0	0	0	0	0	0	0	0	0	0
4,12:b:-	0	0	0	0	0	0	0	0	0	0
6,7:-:enz₁₅	6	1	0	0	0	0	0	0	0	0

For details of laying flocks reported positive in 2015 to 2020, see the [2020 edition of *Salmonella* in livestock production in Great Britain](#).

Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2021	0.96%	0.23%
2022	1.13%	0.27%
2023	0.80%	0.17%
2024	0.89%	0.24%
2025	1.23%	0.43%

Flocks testing positive for more than one serovar

Some flocks tested positive for more than one serovar. Each flock was counted only once in the overall figure to calculate prevalence.

In 2021 3 flocks tested positive for S. Newport and S. Bardo and one flock that tested positive for S. Derby and S. Oslo.

In 2022 one flock tested positive for S. Bardo and S. Newport.

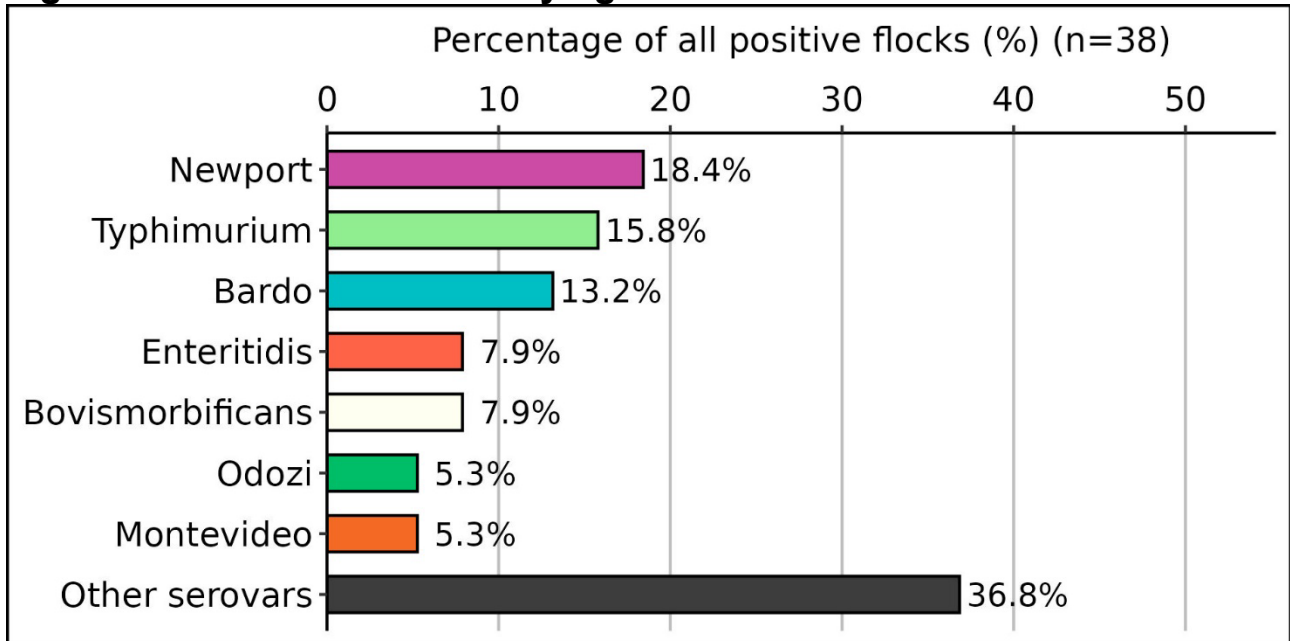
In 2023 no flocks tested positive for two different serovars.

In 2024 no flocks tested positive for two different serovars.

In 2025 one flock tested positive for S. Cubana and S. Senftenberg.

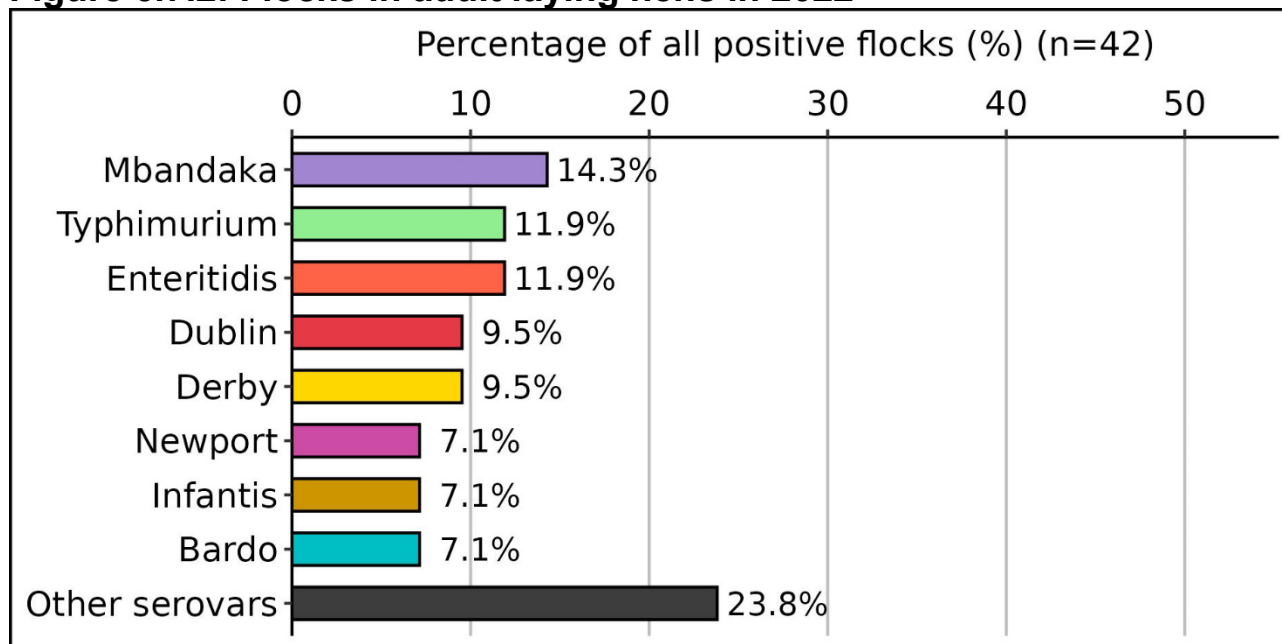
Figure 6.7: The most common *Salmonella* serovars identified in adult laying hen flocks in Great Britain 2021 to 2025 reported from NCP testing

Figure 6.7.1: Flocks in adult laying hens in 2021



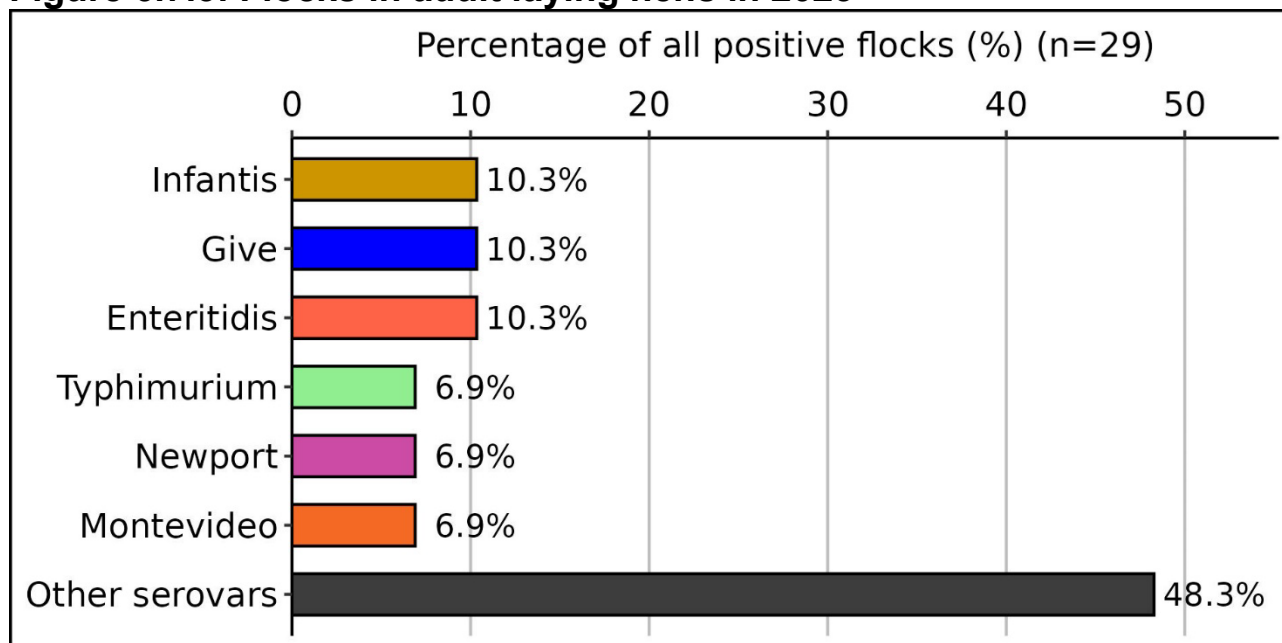
Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult laying chickens in 2021. In 2021, the most common *Salmonella* serovar in adult laying hen flocks was *S. Newport* accounting for 18.4% of total positive flocks, followed by *S. Typhimurium* (15.8%) and *S. Bardo* (13.2%).

Figure 6.7.2: Flocks in adult laying hens in 2022



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult laying chickens in 2022. In 2022, the most common *Salmonella* serovar in adult laying hen flocks was *S. Mbandaka* accounting for 14.3% of total positive flocks, followed by *S. Enteritidis* (11.9%) and *S. Typhimurium* (11.9%). In 2022 1 flock was positive for 2 serovars (counted once in total). Summed percentages of all serovars therefore exceeds 100%.

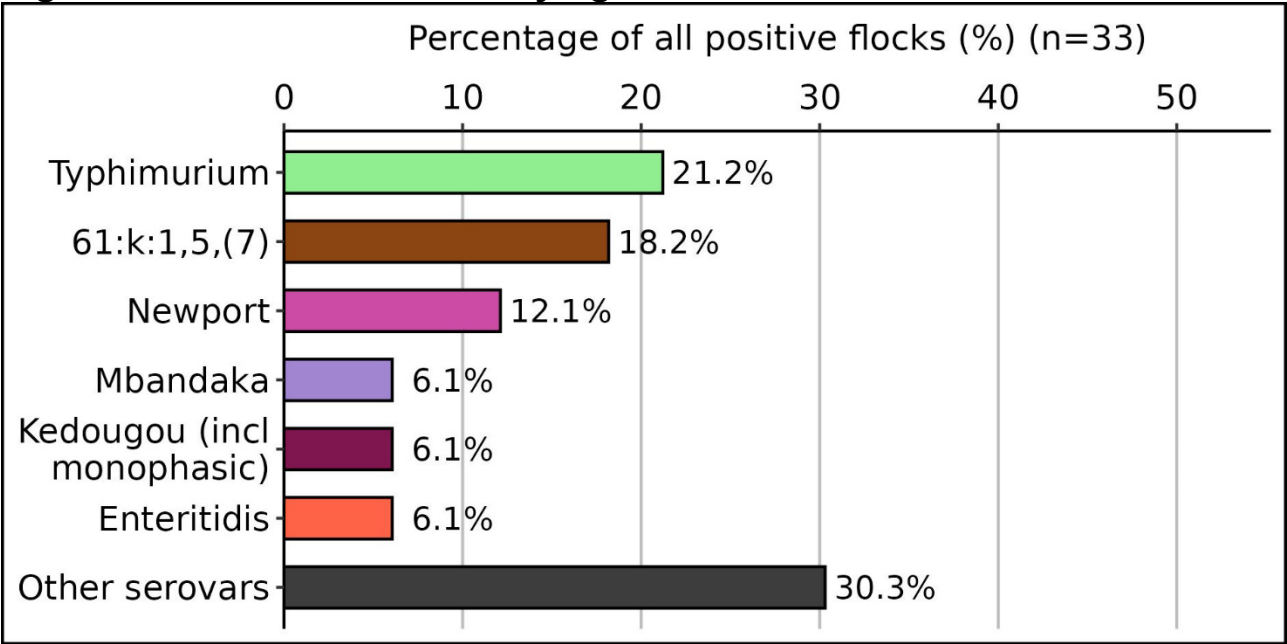
Figure 6.7.3: Flocks in adult laying hens in 2023



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult laying chickens in 2023. In 2023, the most common *Salmonella* serovars in adult laying hen

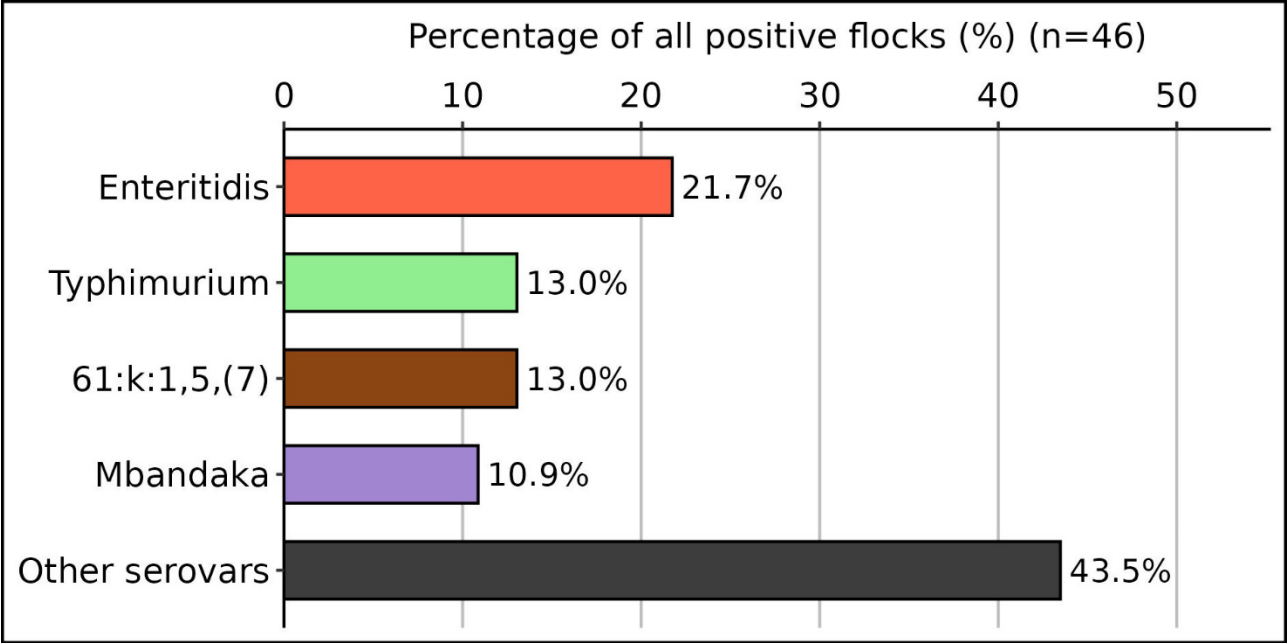
flocks were *S. Enteritidis*, *S. GIVE* and *S. Infantis*, each accounting for 10.3% of total positive flocks, followed by *S. Typhimurium*, *S. Montevideo* and *S. Newport* at 6.9% each.

Figure 6.7.4: Flocks in adult laying hens in 2024



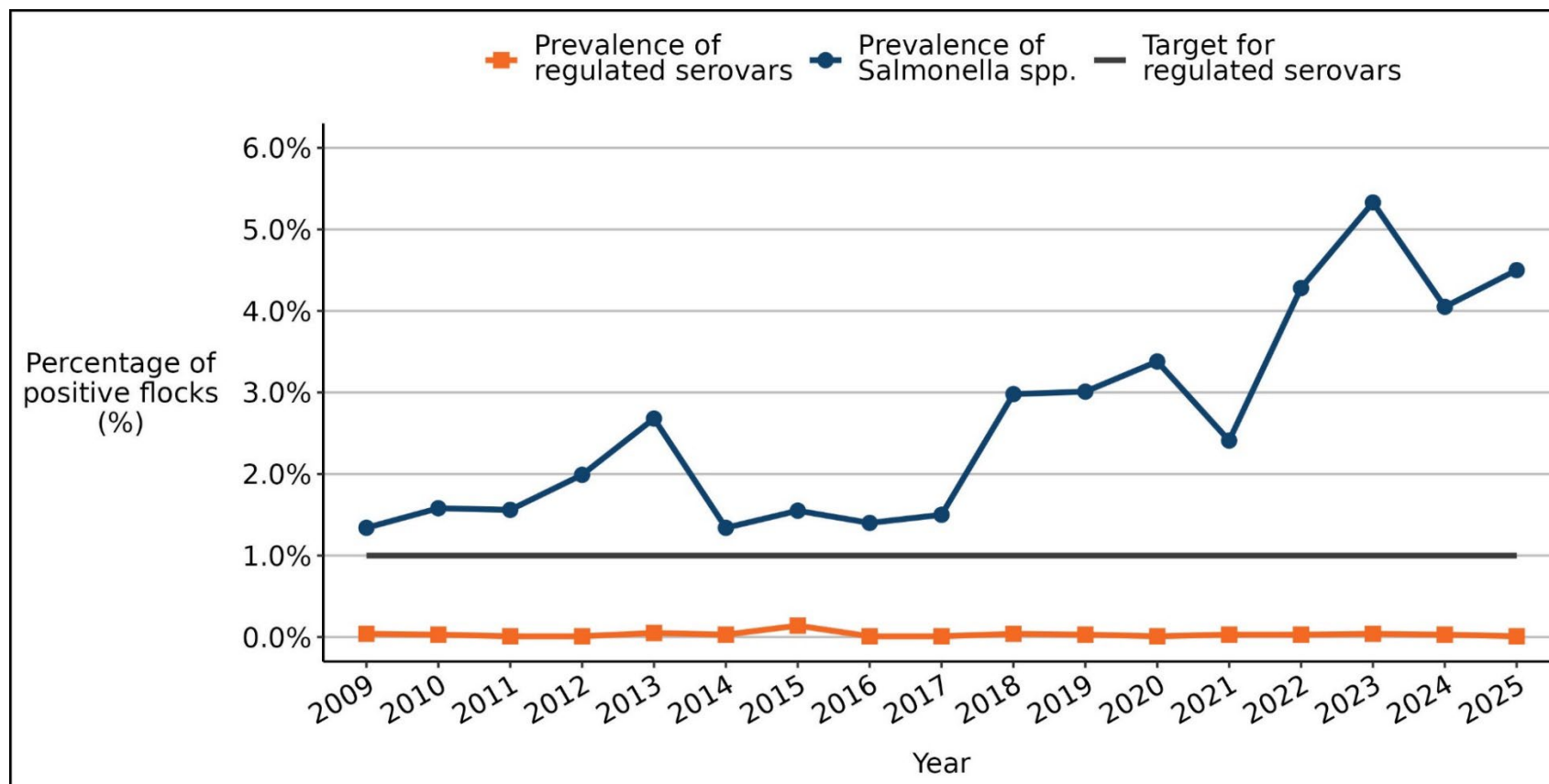
Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult laying chickens in 2024. In 2024, the most common *Salmonella* serovar in adult laying hen flocks was *S. Typhimurium*, accounting for 21.2% of total positive flocks, followed by *Salmonella* 61:k:1,5,(7) (18.2%), and *S. Newport* (12.1%).

Figure 6.7.5: Flocks in adult laying hens in 2025



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in adult laying chickens in 2025. In 2025, the most common *Salmonella* serovar in adult laying hen flocks was *S. Enteritidis*, accounting for 21.7% of total positive flocks, followed by *Salmonella* 61:k:1,5,(7), and *S. Typhimurium* (each with 13.0%).

Figure 6.8: Prevalence of *Salmonella* in broiler chicken flocks tested under NCP in Great Britain 2009 to 2025



A line graph showing the prevalence of *Salmonella* in chicken broiler flocks tested under the NCP from 2009 to 2025. The figure shows a variable prevalence of *Salmonella* spp. in broiler chicken flocks rising from 1.34% in 2009 to a peak of 5.33% in 2023 but a lower prevalence of regulated serovars of between 0.01% and 0.14% which does not exceed 1% prevalence.

Table 6.7: Broiler chicken flocks in Great Britain. Number of flocks positive for each *Salmonella* serovar, NCP testing 2021 to 2025

The following table shows the number of broiler chicken flocks reported positive with each *Salmonella* serovar from 2021 to 2025 and the rank within that year. This data comes from NCP testing.

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Idikan (incl. monophasic variants)	2	257	3	341	1	607	1	628	1	857
Kedougou (incl. monophasic variants)	4	192	4	232	3	421	2	342	2	392
Montevideo	1	330	2	409	2	545	3	285	3	234
Mbandaka	3	238	1	579	4	272	4	157	4	214
Agona	6	33	5	114	5	191	5	135	5	120
Ohio	5	54	8	43	8	35	7	41	6	73
Orion var. 15⁺	6	33	7	54	6	56	6	50	7	67
Infantis	9	22	6	77	7	50	10	19	8	27
Muenchen	12	4	12	9	14	5	8	23	9	20
Newport	14	2	13	7	17	2	9	20	10	13
Senftenberg	7	29	10	18	9	17	13	8	11	11
Agama	0	0	0	0	17	2	0	0	12	8
Derby	11	7	13	7	10	14	12	9	13	6
Give	0	0	0	0	18	1	0	0	14	5
Kentucky	0	0	17	3	0	0	11	17	14	5

Salmonella serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Kottbus	0	0	19	1	0	0	15	3	15	4
Indiana	0	0	0	0	15	4	14	5	16	3
Kingston	0	0	18	2	0	0	17	1	16	3
Virchow	0	0	0	0	0	0	0	0	16	3
4,12:d:-	15	1	18	2	17	2	16	2	16	3
4,5,12:b:-	0	0	0	0	0	0	0	0	16	3
61:k:1,5,(7)	0	0	0	0	0	0	0	0	16	3
Chester	0	0	0	0	0	0	17	1	17	2
Monophasic Typhimurium	10	9	11	10	15	4	0	0	17	2
Orion	0	0	19	1	0	0	0	0	17	2
Oslo	15	1	0	0	18	1	17	1	17	2
Anatum	13	3	19	1	15	4	12	9	18	1
Braenderup	14	2	18	2	14	5	16	2	18	1
Panama	15	1	19	1	0	0	17	1	18	1
Richmond	0	0	0	0	0	0	0	0	18	1
Uganda	0	0	0	0	0	0	0	0	18	1
untypable strains	0	0	0	0	0	0	0	0	18	1
13,23:-:-	0	0	0	0	0	0	0	0	18	1
Ajiobo	0	0	0	0	18	1	0	0	0	0
Berta	0	0	19	1	0	0	17	1	0	0
Bovismorbificans	12	4	0	0	18	1	0	0	0	0
Bredeney	0	0	0	0	0	0	17	1	0	0

Salmonella serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Chomedey	0	0	0	0	18	1	0	0	0	0
Coeln	0	0	16	4	16	3	17	1	0	0
Corvallis	0	0	19	1	0	0	0	0	0	0
Durham	0	0	0	0	18	1	0	0	0	0
Eboko	0	0	19	1	0	0	0	0	0	0
Enteritidis	14	2	19	1	14	5	12	9	0	0
Ferruch	14	2	0	0	0	0	0	0	0	0
Frenso	0	0	0	0	18	1	0	0	0	0
Give var 15⁺	15	1	14	6	14	5	0	0	0	0
Goldcoast	15	1	0	0	0	0	0	0	0	0
Havana	15	1	15	5	0	0	0	0	0	0
Liverpool	0	0	19	1	0	0	0	0	0	0
Livingstone	12	4	19	1	11	11	16	2	0	0
London	0	0	18	2	0	0	0	0	0	0
Oxford	0	0	0	0	18	1	0	0	0	0
Nottingham	0	0	18	2	0	0	17	1	0	0
Poona	0	0	0	0	0	0	17	1	0	0
Reading	15	1	0	0	0	0	0	0	0	0
Rissen	0	0	19	1	0	0	0	0	0	0
Stanley	0	0	19	1	0	0	0	0	0	0
Stourbridge	15	1	0	0	0	0	0	0	0	0
Typhimurium	12	4	16	4	12	7	14	5	0	0
3,19: - : -	14	2	0	0	0	0	0	0	0	0

Salmonella serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
4,5,12:a:-	0	0	0	0	18	1	0	0	0	0
4,12:i,v:-	0	0	0	0	18	1	0	0	0	0
6,7:d:-	0	0	19	1	0	0	0	0	0	0
6,7:z₁₀:-	8	23	9	21	13	6	0	0	0	0
6,7:-:enz₁₅	0	0	0	0	0	0	17	1	0	0
6,7:-:-	0	0	14	6	0	0	0	0	0	0
6,8:d: -	0	0	19	1	0	0	0	0	0	0
47:z₄,z₂₃: -	0	0	19	1	0	0	0	0	0	0

For details of broiler chicken flocks reported positive in 2015 to 2020, see the [2020 edition of *Salmonella* in livestock production in Great Britain](#).

Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2021	2.41%	0.03%
2022	4.28%	0.03%
2023	5.33%	0.04%
2024	4.05%	0.03%
2025	4.50%	<0.01%

Flocks testing positive for more than one serovar

Some flocks tested positive for more than one serovar. Each flock was counted only once in the overall figure to calculate prevalence.

In 2021:

- 3 flocks tested positive for both *S. Mbandaka* and *S. 6,7:z10:-*
- 2 flocks tested positive for both *S. Montevideo* and *S. Idikan* (including monophasic variants)
- 1 flock tested positive for both *S. Mbandaka* and *S. Montevideo*
- 1 flock tested positive for both *S. Idikan* (including monophasic variants) and *S. Orion* var. 15⁺
- 1 flock tested positive for both *S. Kedougou* (including monophasic variants) and *S. Mbandaka*
- 1 flock tested positive for both *S. Idikan* (including monophasic variants) and *S. Agona*
- 1 flock tested positive for both *S. Typhimurium* and *S. Newport*

In 2022:

- 3 flocks tested positive for *S. Mbandaka* and *S. Montevideo*
- 2 flocks tested positive for *S. Idikan* (including monophasic variants) and *S. Infantis*
- 2 flocks tested positive for *S. Idikan* (including monophasic variants) and *S. Idikan*
- 1 flock tested positive for the following combinations of multiple serovars: *S. Mbandaka* and *S. Kedougou*, *S. Montevideo* and *S. Kedougou* (including monophasic variants), *S. Agona* and *S. Orion* var. 15⁺, *S. Mbandaka* and *S. 6,7:d:-*, *S. Agona* and *S. Kedougou* (including monophasic variants), *S. Idikan* (including monophasic variants) and *S. Montevideo* x1, *S. 6,7:-:-* and *S. Ohio*

In 2023:

- 4 flocks tested positive for *S. Idikan* (including monophasic variants) and *S. Agona*.
- 2 flocks tested positive for *S. Idikan* (including monophasic variants) and *S. Kedougou*(including monophasic variants)
- 2 flocks tested positive for *S. Infantis* and *S. Kedougou*
- 1 flock tested positive for *S. Idikan* (including monophasic variants) and *S. Muenchen*

- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Montevideo
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Orion var 15+
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Infantis,
- 1 flock tested positive for S. Montevideo and S. Mbandaka
- 1 flock tested positive for S. Orion var 15+ and S. Infantis
- 1 flock tested positive for S. Give and S. Give var 15+
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Agona in Official (routine annual) sampling
- 1 flock tested positive for S. Kedougou(including monophasic variants) in both operator and official (replacement flocks) sampling

In 2024:

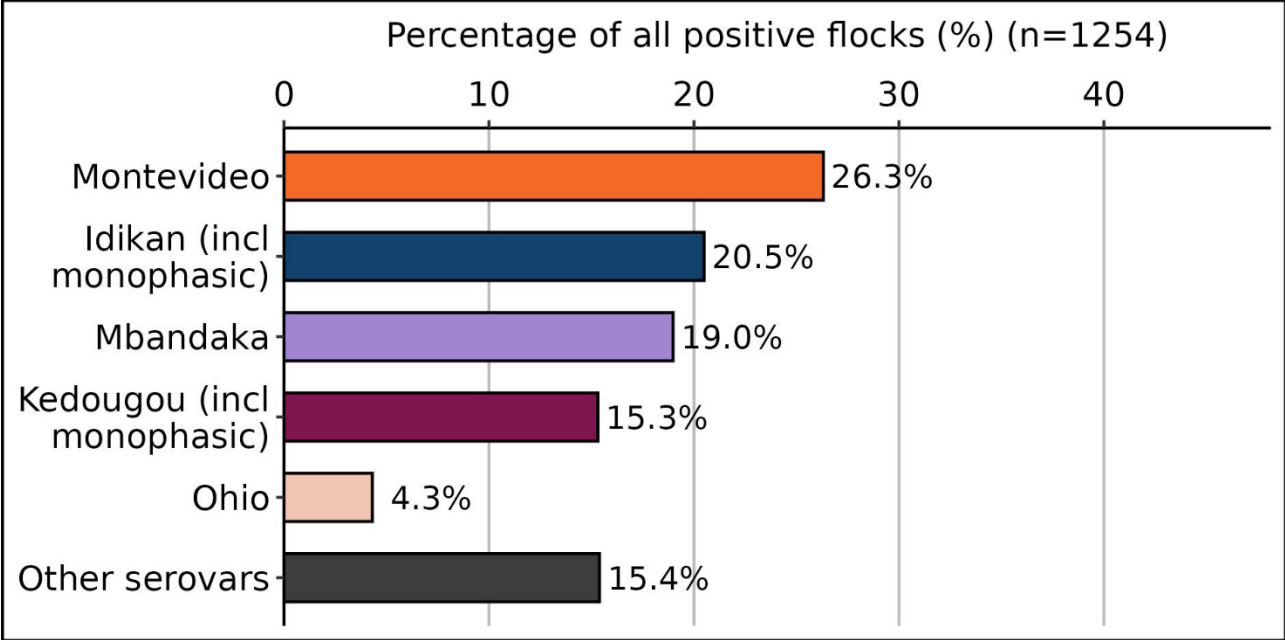
- 1 flock tested positive for S. Montevideo and S. Agona
- 1 flock tested positive for S. Montevideo and S. Orion var 15+ (Binza),
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Infantis
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Kedougou(including monophasic variants)
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Mbandaka
- 1 flock tested positive for S. Montevideo and S. Mbandaka in both operator and official (replacement flocks) sampling

In 2025:

- 2 flocks tested positive for S. Idikan (including monophasic variants) and S. Orion var 15+
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Mbandaka
- 1 flock tested positive for S. Idikan (including monophasic variants) and S. Agona
- 1 flock tested positive for S. Agona and S. Montevideo
- 1 flock tested positive for S. Agona and S. Give
- 1 flock tested positive for S. Kedougou (including monophasic variants) and S. Mbandaka

Figure 6.9: The most common *Salmonella* serovars identified in broiler chicken flocks in Great Britain 2021 to 2025 reported from NCP testing

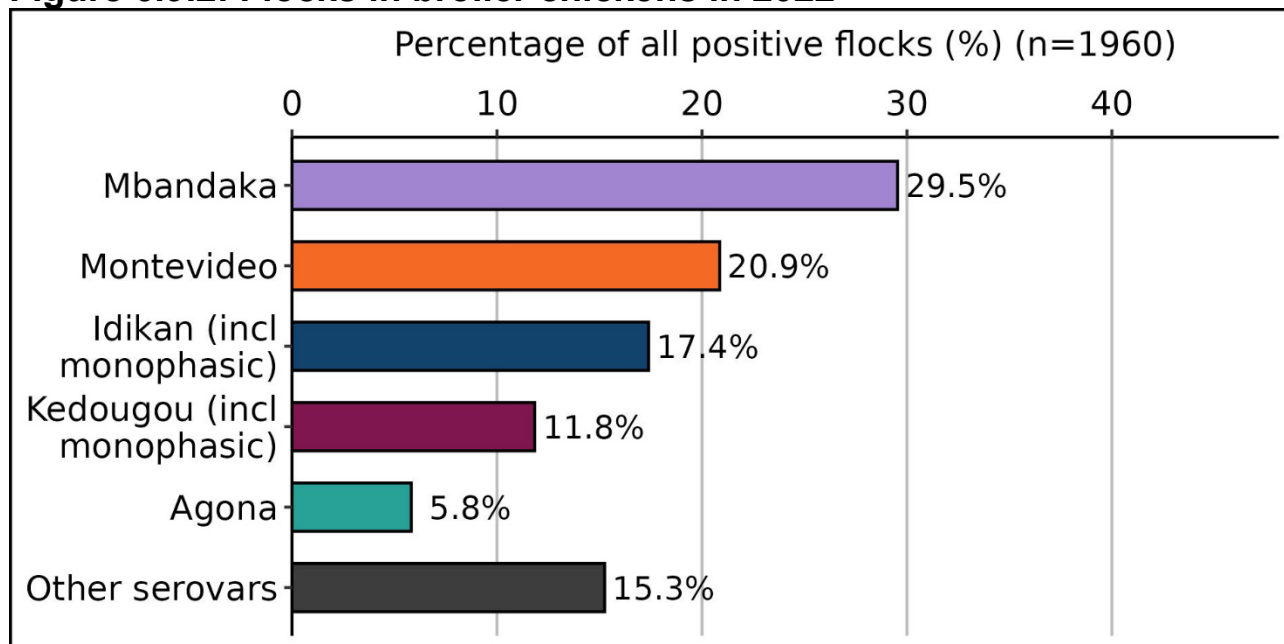
Figure 6.9.1: Flocks in broiler chickens in 2021



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in broiler chickens in 2021. In 2021 the most common *Salmonella* serovar in broiler flocks was S. Montevideo accounting for 26.3% of total positive flocks, followed by S. Idikan (including monophasic variants) (20.5%), S. Mbandaka (19.0%) and S. Kedougou (including monophasic variants) (15.3%).

In 2021, 10 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

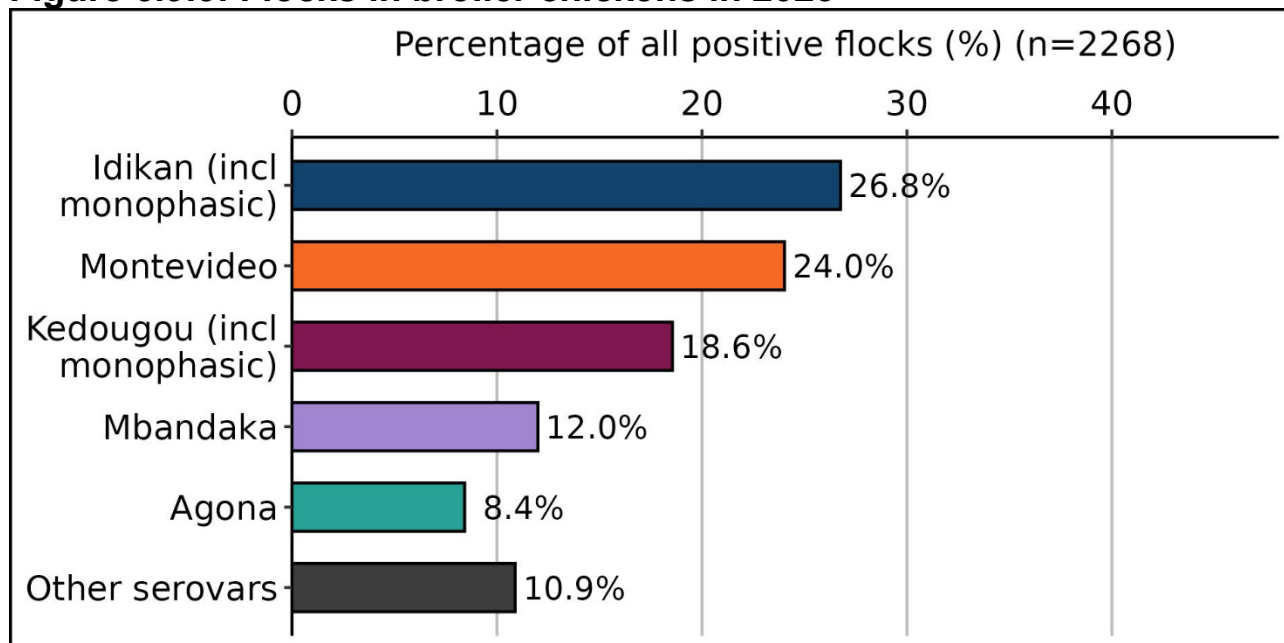
Figure 6.9.2: Flocks in broiler chickens in 2022



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in broiler chickens in 2022. In 2022, the most common *Salmonella* serovar in broiler flocks was *S.* Mbandaka, accounting for 29.5% of total positive flocks, followed by *S.* Montevideo (20.9%), *S.* Idikan (including monophasic variants) (17.4%) and *S.* Kedougou (including monophasic variants) (11.8%).

In 2022 14 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

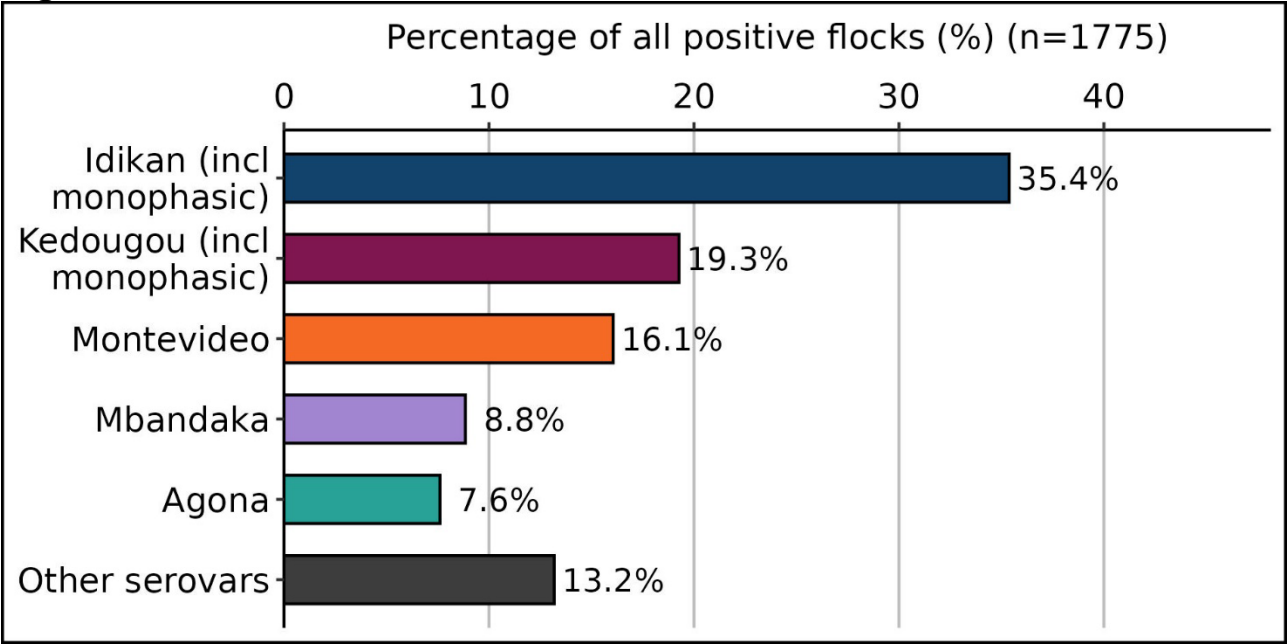
Figure 6.9.3: Flocks in broiler chickens in 2023



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in broiler chickens in 2023. In 2023 the most common *Salmonella* serovar in broiler flocks was S. Idikan (including monophasic variants), accounting for 26.8% of total positive broiler flocks, followed by S. Montevideo (24.0%), S. Kedougou (including monophasic variants) (18.6%) and S. Mbandaka (12.0%).

In 2023, 15 flocks were positive for 2 serovars (each counted only once in total); summed percentages of all serovars therefore exceeds 100%.

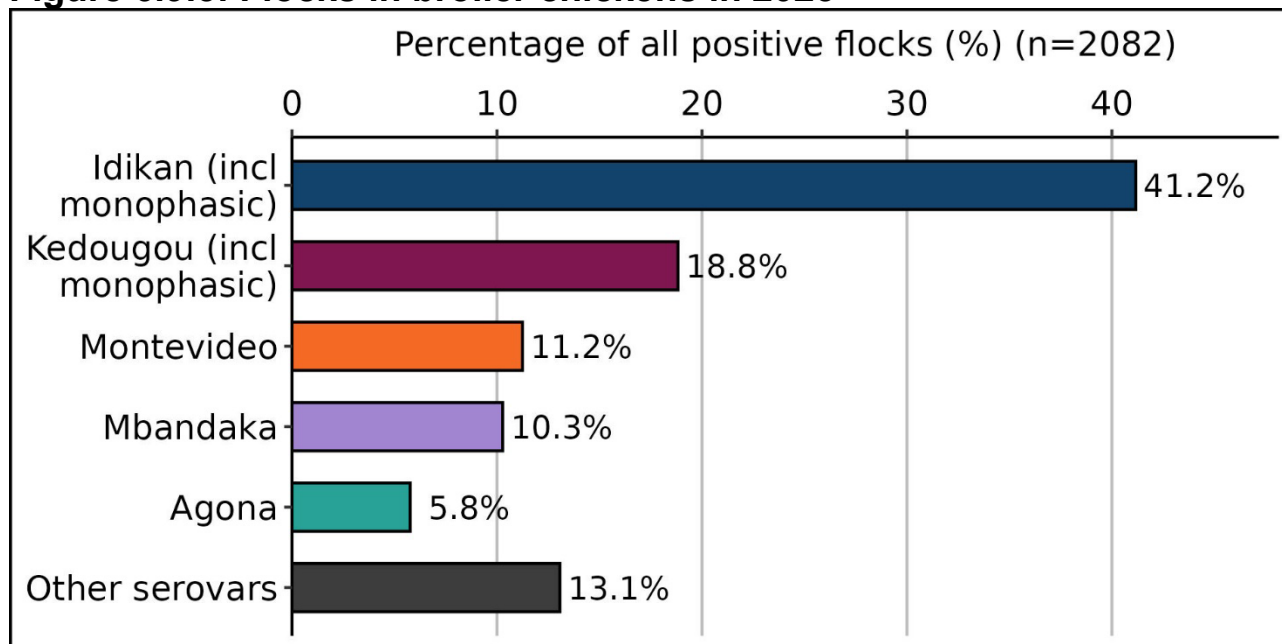
Figure 6.9.4: Flocks in broiler chickens in 2024



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in broiler chickens in 2024. In 2024, the most common *Salmonella* serovar in positive broiler flocks was S. Idikan (including monophasic variants), accounting for 35.4% of total positive flocks, followed by S. Kedougou (including monophasic variants) (19.3%), S. Montevideo (16.1%), and S. Mbandaka (8.8%).

In 2024, 6 flocks were positive for 2 serovars (each counted only once in total); summed percentages of all serovars therefore exceeds 100%.

Figure 6.9.5: Flocks in broiler chickens in 2025



Horizontal bar graph showing the percentage of *Salmonella* positive flocks in broiler chickens in 2025. In 2025, the most common *Salmonella* serovar in positive broiler flocks was *S. Idikan* (including monophasic variants), accounting for 41.2% of total positive flocks, followed by *S. Kedougou* (including monophasic variants) (18.8%), *S. Montevideo* (11.2%), and *S. Mbandaka* (10.3%).

In 2025, 7 flocks were positive for 2 serovars (each counted only once in total); summed percentages of all serovars therefore exceeds 100%.

Chapter 7: Reports of *Salmonella* in turkeys

From early 2022 and every year since there has been significant disruption to the poultry industry due to national outbreaks of Avian Influenza affecting all industry sectors. This resulted in culling of infected flocks, altered management and biosecurity measures which will have likely impacted non-statutory submission numbers, though statutory surveillance through NCP sampling remained a requirement. During 2020 and 2021 there was also a reduction in levels of non-statutory surveillance and clinical diagnosis submissions in many species as a direct consequence of the Covid-19 pandemic and associated lockdown measures. These circumstances should therefore be borne in mind when comparing 2020 to 2025 data with previous years.

According to the June Agricultural Survey, there were 2.78 million turkeys in Great Britain in 2025 compared with 3.17 million in 2024, 2.48 million in 2023 and 3.73 million in 2022.

In January 2010, the National Control Programme (NCP) to control *Salmonella* in turkeys was implemented across the European Union. Breeding turkey farms with more than 250 adult birds on the holding at any time in a 12-month period and fattening turkey farms with more than 500 birds are required to participate in *Salmonella* testing under the NCP (for further information see [Salmonella: test your breeding turkeys - GOV.UK](#) or [Salmonella: test your fattening turkeys - GOV.UK](#)) This is a mix of mostly testing undertaken by operators and some official NCP sampling of flocks, although some smaller turkey fattening farms can be granted an exemption from operator testing. Since 2010, *Salmonella* reports from turkeys have largely originated from samples taken under the NCP, so data cannot be compared with previous years.

As described in Chapter 6 for chickens, 2 different systems of reporting are also used in this chapter and results should be interpreted accordingly. The first part of this chapter describes all isolations of *Salmonella*, including samples originating from statutory surveillance, voluntary surveillance, investigations into clinical disease and investigations carried out under the Zoonoses Order. If two submissions from the same group of birds on different dates give the same serovar, this is reported as two isolations.

The second part of this chapter describes results obtained within the National Control Programmes (NCPs), comprising results from statutory surveillance only. Results from the NCPs are reported in a way that ensures that every flock with a *Salmonella* positive result is counted only once.

Numbers of positive flocks reported within the NCP are expected to differ from the number of reported isolations. Some flocks may be positive for more than one serovar, in which case, they are still only counted once as positive flocks under the NCP but are counted as more than one isolation.

There were 271 turkey diagnostic and monitoring submissions made to APHA and SRUC laboratories in 2025. This compares to 277 in 2024, representing a decrease of 2.2%. In comparison, during 2009, before the introduction of the NCP for *Salmonella* in turkeys, the number of submissions was lower (240 submissions). However, APHA does not have information on the number of non-statutory submissions submitted to private laboratories that do not result in a positive culture of *Salmonella*, as these are not reportable under the Zoonoses Order.

A total of 33 *Salmonella* isolations were reported from turkeys in 2025 (Table 7.1), a 69.4% decrease compared to 2024 (108 isolations) and the lowest number of isolations since the inception of the NCP in turkeys in 2010. With the exception of 2022, when isolations briefly increased, there had been a decreasing trend in isolations since 2015.

In 2009, before the introduction of the NCP, 88 isolations were reported from turkeys. The considerable increase in isolations in subsequent years can be explained by more sensitive and regular statutory testing of turkey flocks under the NCP. This has led to the identification of positive flocks that otherwise might not have been detected through voluntary surveillance alone. Isolations peaked in 2012 (789 isolations) but then declined substantially by 2014 (193 isolations). Isolations subsequently increased again in 2015 (619 isolations) and 2016 (607 isolations), mainly due to increased isolation of *S. Derby*. Subsequently the overall number of isolations from turkeys has declined each year up to 2021 (Table 7.1), which was primarily attributable to a decrease in *S. Derby* isolations. Isolations of *Salmonella* in turkeys increased in 2022 (188 isolations) which were not attributable to an increase in *S. Derby* isolations (increased isolations were reported for *S. Anatum*, *S. Kedougou* and *S. Senftenberg*),

The total number of isolations in 2025 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 31 (93.9%)
- voluntary surveillance: 2 (6.1%)
- investigations of clinical disease: 0 (0.0%)

Eight different serovars of *Salmonella* were isolated in 2025, accounting for all of the isolations (no rough or untypable strains). Table 7.1 shows the absolute number of isolations of each *Salmonella* serovar from turkeys, from 2021 to 2025, and Figure 7.1 shows the relative percentages of the most common serovars.

Salmonella Kedougou (including monophasic variants) (10 isolations, 30.3% of all isolations), a feed related serovar, was the most common serovar in 2025. This represents a 52.4% decrease in the number of isolations compared with 2024 (21 isolations). *S. Kedougou* (including monophasic variants) has regularly featured among the top 3 most common serovars isolated from turkeys since at least 2004 (Figure 7.1 and 7.2). *S. Kedougou* (including monophasic variants) is associated with feed mill environments and can be found in ingredients such as oilseed meals (for further detail see Chapter 12).

There were 5 isolations (15.2% of all isolations) of *S. Agona* in 2025, which represents a four-fold decrease from 2024 (20 isolations, 18.5% of all isolations). The proportion of isolations associated with this serovar have been increasing in recent years with 5.9% in 2022 and 7.3% in 2023 (Figure 7.1 and 7.2).

In 2025 there were no isolations of regulated serovars from turkey flocks compared to 13 isolations in 2024. All isolations in 2024 were of *S. Typhimurium*, an 84.6% increase in this serovar compared to 2023. In 2024, seven turkey fattening flocks, on three sites, tested positive for *S. Typhimurium*. All three sites were epidemiologically linked. Prior to 2024, there had been low numbers of isolations of *S. Typhimurium* in turkeys (2 isolations in 2023, 1 isolation in 2022). The occurrence of *S. Typhimurium* had reduced considerably over the last decade, having once been the most commonly reported serovar in turkeys (accounting for 20.7% of isolations in 2006). Sequence types of *S. Typhimurium* and monophasic *S. Typhimurium* isolated from turkeys between 2023 and 2025 are shown in Table 7.2 and 7.3, respectively. There were no isolations of *S. Typhimurium* reported in 2025 but all isolations in 2024 and 2023 were ST19. There was one isolation of monophasic *S. Typhimurium* ST34 in 2023.

Notably, *S. Goldcoast* (5 isolations from statutory testing) was last reported from turkeys in Great Britain in 2003 before statutory testing was introduced. *S. Uganda* (3 isolation from statutory testing) has not previously been reported from turkeys in Great Britain.

Salmonella Anatum has often been amongst the top 3 most common serovars isolated from turkeys. In 2025 there was one isolation compared with 21 isolations in 2024. This is the lowest number of isolations since 2017 when there were no isolations associated with this serovar. Isolations had increased dramatically since 2019 (4 isolations), peaking in 2022 with 66 isolations (Figure 7.1). *S. Anatum* was one of four serovars identified in *Salmonella* positive compound poultry feed (see Chapter 12).

In 2025 there were no isolations of *Salmonella* Derby, the first time this serovar has been absent since the implementation of the NCP in turkeys in 2010. Isolations have been reducing over recent years with 3 isolations in 2024, (2.8% of all isolations) and 2 isolations in 2023 (1.8% of all isolations) (Figure 7.1). Historically, *S. Derby* has been associated with high numbers of isolations from turkeys in Great Britain, representing the most common serovar isolated from turkeys from 2007 to 2019. Isolations of *S. Derby* peaked in 2016 with 501 isolations and have been generally decreasing since. This reduction follows improved control of *S. Derby* in adult turkey breeding flocks and hatcheries and gradual resolution of persistent contamination of some fattening farms.

Salmonella Newport had been among the most common serovars isolated in turkeys since at least 2004 and there was concern that it had become established in the turkey industry. However, since 2015, *S. Newport* reporting levels have been low with 2 and 3 isolations in 2020 and 2021, respectively. There have been no isolations of this serovar since 2022.

There were no isolation of *S. Typhimurium* in turkeys in 2025. This is compared to 13 isolations in 2024 and 2 isolations in 2023.

There were no isolations of monophasic strains of *S. Typhimurium* in 2025, similar to 2024 which was the first time that these two strains had been absent in turkeys since 2020. Monophasic strains of *S. Typhimurium* are often associated with pigs.

There were no isolations of *S. Enteritidis* in turkeys in 2025. This serovar was last isolated from turkey flocks in 2017.

There were no reported cases of *Salmonella* from turkeys imported into Great Britain in 2025.

National Control Programme for *Salmonella* in fattening and breeding turkeys

The NCP for *Salmonella* in fattening and breeding turkeys came into effect within EU member countries on 1 January 2010 and has been implemented to comply with [Regulation \(EC\) No. 2160/2003](#) and [Regulation \(EC\) No. 1190/2012](#). These regulations, which are now assimilated into UK law, aim to protect public health, through a reduction in levels of *Salmonella* in turkey flocks. All references to EU legislations throughout this chapter are references to those as assimilated in UK law.

All holdings with 250 or more breeding turkeys over the course of a 12 month period and all holdings with 500 or more fattening turkeys are included in the NCP. However turkey fattening flocks may be exempted from operator sampling if able to meet the criteria in assimilated Regulation (EC) No. 2160/2003 under Article 1.3, that is less than 10,000 fattening birds per year produced for private domestic consumption, or where there is direct supply of small quantities of product to the final consumer or to local retail establishments that directly supply the primary products to the final consumer.

The NCP is enforced by The [Control of *Salmonella* in Turkey Flocks Order 2009 \(CSTO\)](#) in England, by [The Control of *Salmonella* in Turkey Flocks \(Wales\) Order 2010](#) in Wales and by [The Control of *Salmonella* in Turkey Flocks \(Scotland\) Order 2009](#) in Scotland.

Positive flocks identified in the NCP for breeding turkeys 2025

No adult turkey breeding flock tested positive for *Salmonella* in 2025. This is fewer than in recent years with one positive flock in each of 2024 and 2023 and compares to 7 positive flocks in 2020 (Table 7.4).

A total of 146 adult turkey breeding flocks were in production in Great Britain in 2025 and were included in the NCP if they had more than 250 birds. Therefore, the estimated Great

Britain prevalence for regulated serovars was 0% (0 of 146). This is well below the national targets of 1% of flocks positive for *S. Enteritidis* and/or *S. Typhimurium* (including monophasic strains) and lower than in 2024 when the prevalence of regulated serovars was 0.67% (one positive flock). The estimated Great Britain prevalence for all *Salmonella* serovars in 2025 was 0% (0 of 149) which is lower than in recent years; 0.67% in 2024, 0.58% in 2023 and 1.97% in 2022. Therefore, the prevalence of *Salmonella* serovars in all devolved nations was 0%, below the target of a maximum of 1% of flocks positive for regulated serovars in all devolved nations, Figure 7.3 shows the change in *Salmonella* prevalence of turkey breeder flocks in Great Britain testing positive for *Salmonella* serovars since 2015. The absolute number of breeder flocks eligible for NCP testing and positive for *Salmonella* is relatively small and should be borne in mind when interpreting the trend in Figure 7.3.

The last time no regulated serovars were isolated from breeding turkeys as part of the NCP was in 2022. One turkey breeding flock tested positive for a regulated serovar, *Salmonella* Typhimurium, in 2024 and 2023. Prior to this, 2019 was the last time a regulated serovar has been identified in turkey breeder flocks when 2 flocks from one site tested positive for the monophasic strain of *S. Typhimurium* 4,[5],12:i:-. The first isolation of regulated serovars from breeder turkey flocks in the NCP was in 2018 when 6 positive flocks (all under the same ownership) tested positive for *S. Typhimurium* monophasic variant 4,[5],12:i:-.

No adult turkey breeding flocks tested positive for non-regulated serovars in 2025 (Table 7.4). Since the NCP started for breeding turkeys in 2010, this is the third consecutive year that no non-regulated serovars have been detected in breeding turkey flocks, the first being in 2023.

No immature breeding flocks tested positive for *Salmonella* under the NCP in 2025. This is consistent with 2024 and 2023, when no flocks tested positive and compares to 6 positive flocks in 2022 and 7 flocks in 2021.

For comparison, the serovars identified in the adult turkey breeder NCP between 2021 and 2025 are shown in Table 7.4. Figure 7.4 shows the relative percentages of the serovars in the turkey breeder NCP from 2021 to 2025.

Positive flocks identified in the NCP for fattening turkeys in 2025

In total, 24 fattening turkey flocks (on 17 different holdings) were positive for *Salmonella* in 2025. This represents a 64.7% decrease from 2024 (68 positive flocks on 37 different holdings) (Table 7.5).

A total of 1,690 turkey fattening flocks were in production in Great Britain in 2025 and were included in the NCP if they had more than 500 birds. This represented a reduction from 2,191 turkey fattening flocks in production in 2024, primarily reflecting management

changes in some of the larger poultry companies, alongside the loss of flocks due to avian influenza and a shift towards broiler production.

The estimated Great Britain prevalence of all *Salmonella* spp. in 2025 was 1.42% (24 of 1,690). There were no positive flocks identified in Scotland or Wales. and the prevalence of *Salmonella* spp. in England was 1.43% (24/1,679). This is a decrease from 3.10% in 2024 and 3.38% in 2023. With the exception of 2022 when there was a 3.2% increase on the previous year, there has been a year-on-year decreasing trend in the number of turkey fatteners positive for *Salmonella* spp, since 2016. Figure 7.5 shows the change in *Salmonella* prevalence of turkey fattening flocks in Great Britain testing positive for *Salmonella* since 2015.

No flocks tested positive for regulated serovars in 2025 and therefore the prevalence of regulated serovars in GB was 0% (0/1,690), below the target of a maximum of 1% of flocks positive for regulated serovars. This is lower than in 2024 when the prevalence of regulated serovars was 0.32% (seven flocks, on three sites, tested positive for *S. Typhimurium*) and 2023 when it was 0.05% (three flocks tested positive for *S. Typhimurium* and one flock for monophasic ST strain *S. 4,12:i:-*). The detection of regulated serovars in 2021 followed two years in which no flocks tested positive for regulated serovars. 2019 was the first year since the NCP began in 2010 that no regulated serovars were isolated from turkey fattening flocks, although only one was isolated in both 2012 and 2013.

The most common serovar isolated in 2025 was *S. Kedougou* (including monophasic variants), with seven flocks testing positive for this serovar. This is a decrease from 15 flocks testing positive for this serovar in 2024, 32 flocks in 2023 and 21 in 2022 (Table 7.5). The proportion of positive flocks with this serovar in 2025 was 29.2% which is slightly higher than in 2024 when it was 22.1% but lower than 2023 when it was 42.1%. *S. Kedougou* (including monophasic variants) is associated with feed mill environments and can be found in ingredients such as oilseed meals (for further detail see Chapter 12). The relative percentages of the most common serovars from turkey fattening flocks each year from 2021 to 2025 are shown in Figure 7.6.

The joint second most common serovar isolated in 2025, alongside *S. Goldcoast*, was *S. Agona* with four flocks testing positive. This was a decrease from eleven flocks in 2024 but comparable to the four flocks in 2023. This followed an increase from two flocks in 2020 to four in 2021 and then to seven in 2022. The proportion of positive flocks represented by this serovar has increased slightly to 16.7% in 2025 from 16.2% in 2024 both of which are higher than in 2023 when it was 5.3% (Table 2).

Notably, four flocks across two holdings tested positive for *S. Goldcoast* and three flocks across three holdings tested positive for *S. Uganda* in 2025. This is the first time that these two serovars have been isolated from turkey fatteners since the inception of the NCP.

Two flocks tested positive for *S. Give* in 2025 compared to no flocks in 2024 and represented 8.3% of positive flocks. This is an increase in the relative proportion of positive flocks from when the serovar was first isolated in turkey fattener flocks in 2023 and represented 1.3% of positive flocks.

Two flocks tested positive for *S. Senftenberg* in 2025 which represented 8.3% of positive flocks. This compares to no flocks in 2024. This serovar was last isolated in 2023 in one flock (1.3% of positive flocks). In 2019, 21 flocks tested positive for this serovar which decreased to six in 2020 and three in 2021 before increasing to five in 2022. Prior to this there were year on year increases in the number of flocks positive for *S. Senftenberg* from 2016 to 2019. *Salmonella* Senftenberg is a known hatchery contaminant (Mueller-Doblies et al., 2013).

One flock tested positive for *S. Anatum* in 2025 which represented 4.2% of positive flocks. It was the most frequently isolated serovar in 2024 with 19 flocks testing positive, a small increase from 18 flocks in 2023. No flocks were positive for *S. Anatum* from 2015 to 2017, but the number steadily increased from two flocks in 2018 to a peak of 40 flocks in 2022. The proportion of positive flocks with this serovar increased from 0.7% in 2018 to 41.3% in 2022, when there followed a decrease in 2023 to 23.7% and an increase in 2024 to 27.9%. This serovar is thought to be associated with contaminated feed and was one of four serovars isolated from poultry compound feed in 2025 (see Chapter 12 for more detail).

Antimicrobial susceptibility in turkeys

A total of 26 *Salmonella* isolates from turkeys were tested against a panel of 16 antimicrobials in 2025. Susceptibility in 2025 decreased notably to 34.6%, compared to 53.8% in 2024. Seven isolates were classified as MDR. This increase will have been influenced by the MDR *S. Goldcoast* isolates (see textbox in Chapter 13).

The serovars most commonly showing resistance were *S. Kedougou* (n=6), *S. Goldcoast* (n=4), and *S. Senftenberg* (n=4). Tetracycline resistance increased to 50.0% in 2025, compared to 19.8% in 2024 and 44.7% in 2023. There were seven isolates resistant to nalidixic acid, including three of the four *S. Goldcoast* isolates which were also resistant to cefotaxime, ceftazidime, and ciprofloxacin. Four *S. Senftenberg* isolates were resistant to nalidixic acid but had no other resistances detected. Resistance to sulphonamides remained among the most frequently detected (50.0%), alongside streptomycin (34.6%). The number of isolates showing ampicillin resistance decreased from 18 isolates (19.8%) in 2024, to 4 isolates (15.4%) in 2025.

Table 7.1: *Salmonella* in turkeys on all premises in Great Britain 2021 to 2025 (positive flocks from statutory testing, isolations from both statutory and non-statutory testing)

<i>Salmonella</i> serovar	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations	2025 flocks	2025 isolations
Agama	2	2	0	1	0	0	0	0	0	0
Ago	0	0	0	0	0	0	1	1	0	0
Agona	4	7	7	11	4	8	11	20	4	5
Anatum	31	31	40	66	18	19	19	21	1	1
Berta	0	0	0	1	0	1	0	0	0	0
Bovismorbificans	2	2	0	1	0	0	0	0	0	0
Brandenburg	0	0	1	1	0	0	0	0	0	0
Chester	0	0	0	0	1	1	0	0	0	0
Derby	19	22	7	12	2	2	2	3	0	0
Dublin	0	0	0	0	0	1	0	0	0	0
Give	0	0	0	2	1	1	0	0	2	3
Give var. 15+	1	1	0	0	0	0	0	0	0	0
Goldcoast	0	0	0	0	0	0	0	0	4	5
Idikan (incl. monophasic variants)	2	4	2	2	5	5	4	5	0	0
Indiana	0	0	0	0	0	0	6	9	0	0
Javiana	0	0	0	0	0	0	1	2	0	0
Kedougou (incl. monophasic variants)	9	16	21	30	32	43	15	21	7	10
Kottbus	0	0	0	0	2	3	0	0	0	0

<i>Salmonella</i> serovar	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations	2025 flocks	2025 isolations
Livingstone	0	0	0	0	0	0	0	2	0	0
London	1	6	3	5	0	0	0	0	0	0
Mbandaka	1	1	0	0	0	0	0	0	0	0
Monophasic Typhimurium	9	9	2	4	1	1	0	0	0	0
Montevideo	0	0	3	8	0	1	0	0	0	0
Newport	2	3	1	1	0	0	0	0	0	0
Orion	0	0	0	0	1	1	0	0	1	2
Orion var. 15+	4	5	3	5	6	11	2	5	0	0
Oslo	0	0	0	0	0	0	0	2	0	0
Schwarzengrund	0	0	0	0	1	2	0	0	0	0
Senftenberg	3	20	9	26	1	3	0	4	2	4
Typhimurium	3	3	0	1	1	2	8	13	0	0
Uganda	0	0	0	0	0	0	0	0	3	3
untypable strains	4	6	3	4	0	3	0	0	0	0
rough strains	1	2	2	7	1	1	0	0	0	0
Total	96	140	101	188	71	109	69	108	24	33

Flocks testing positive for more than one serovar

In 2021 2 flocks tested positive for 2 different *Salmonella* serovars. These are included in the table under both serovars but only once in the overall total.

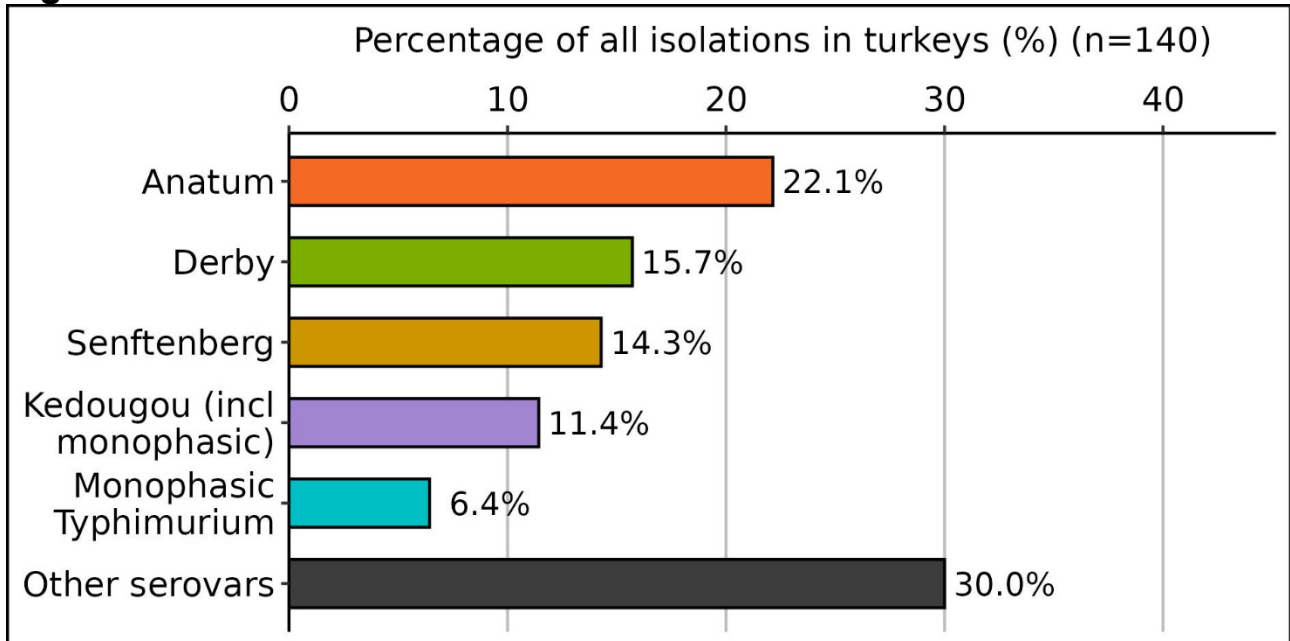
In 2022 3 flocks tested positive for 2 different *Salmonella* serovars. These are included in the table under both serovars but only once in the overall total.

In 2023 6 flocks tested positive for 2 different *Salmonella* serovars. These are included in the table under both serovars but only once in the overall total.

In 2024 and 2025 no flocks tested positive for more than one *Salmonella* serovar.

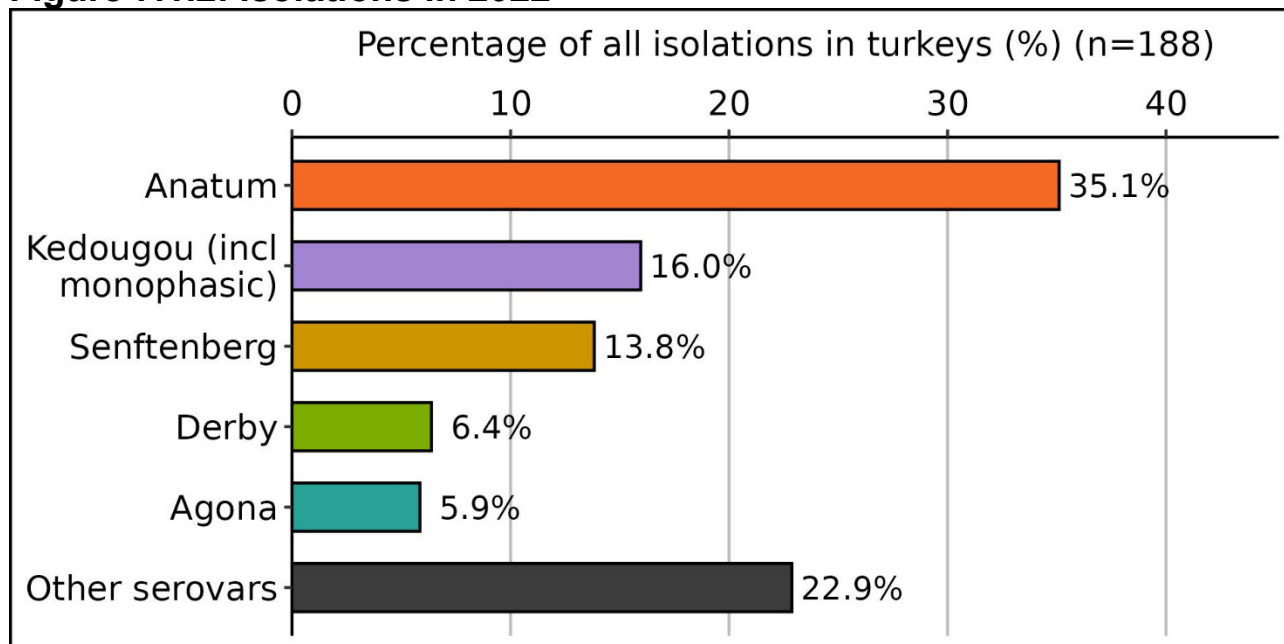
Figure 7.1: The most common *Salmonella* serovars in turkeys by number of isolations in Great Britain 2021 to 2025 (statutory and non-statutory testing)

Figure 7.1.1: Isolations in 2021



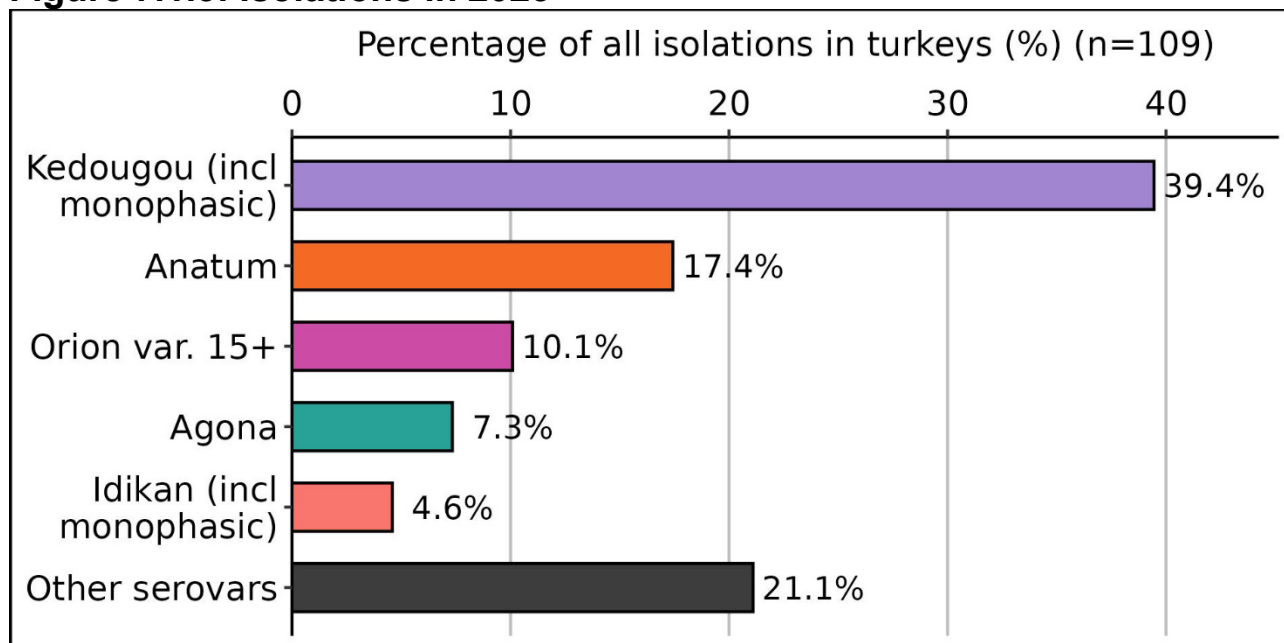
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in turkeys in 2021. The most common *Salmonella* serovar in turkeys in 2021 was *S. Anatum*, accounting for 22.1% of total isolations, followed by *S. Derby* (15.7%), *S. Senftenberg* (14.3%) and *S. Kedougou* (including monophasic variants) (11.4%).

Figure 7.1.2: Isolations in 2022



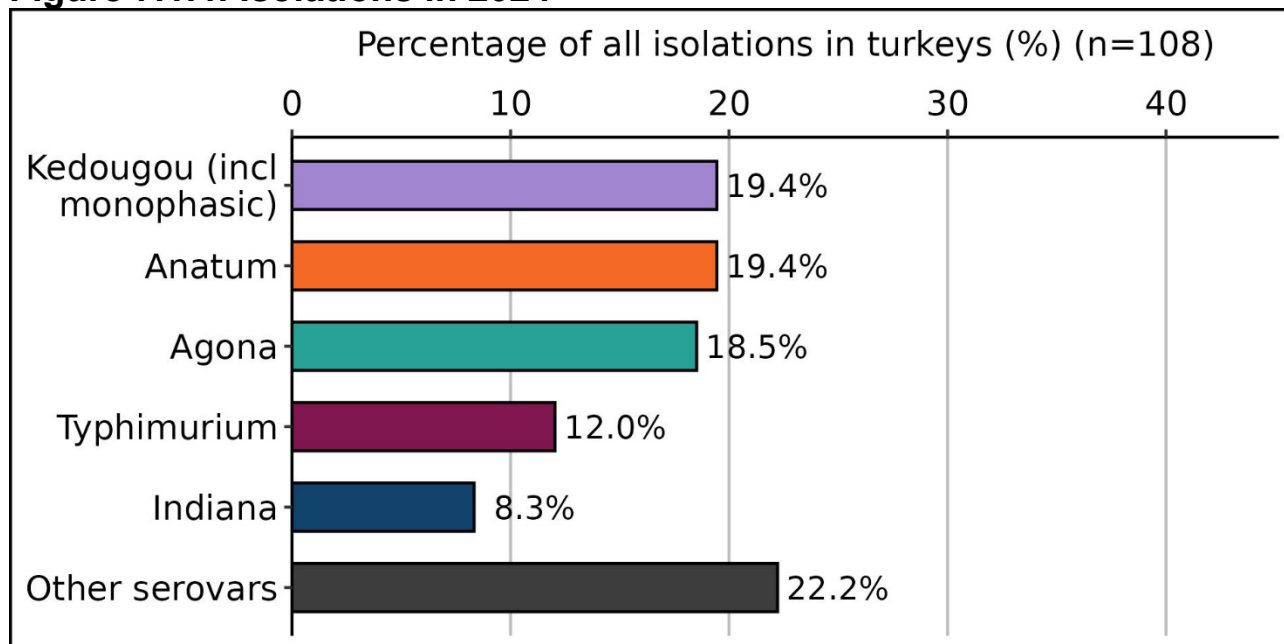
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in turkeys in 2022. The most common *Salmonella* serovar in turkeys in 2022 was S. Anatum, accounting for 35.1% of total isolations, followed by S. Kedougou (including monophasic variants) (16.0%), S. Senftenberg (13.8%) and S. Derby (6.4%).

Figure 7.1.3: Isolations in 2023



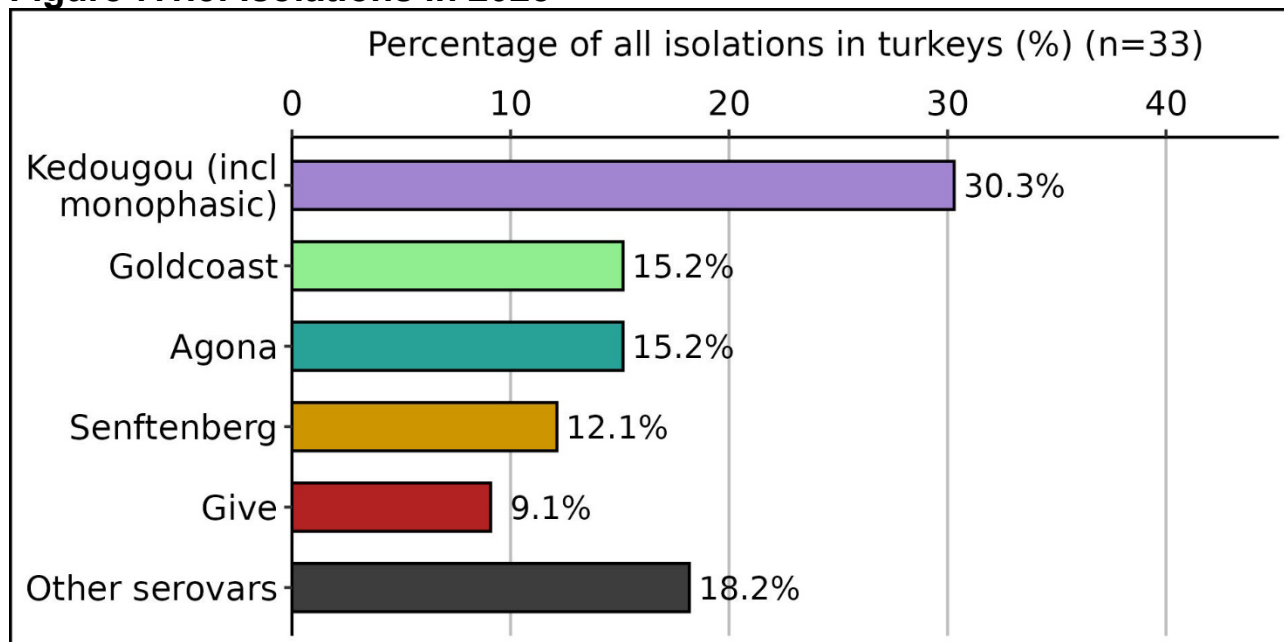
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in turkeys in 2023. The most common *Salmonella* serovar in turkeys in 2023 was S. Kedougou (including monophasic variants), accounting for 39.4% of total isolations, followed by S. Anatum (17.4%), S. Orion var 15+ (10.1%) and S. Agona (7.3%).

Figure 7.1.4: Isolations in 2024



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in turkeys in 2024. The most common *Salmonella* serovars in turkeys in 2024 were *S. Kedougou* (including monophasic variants) and *S. Anatum*, each accounting for 19.4% of total isolations, followed by *S. Agona* (18.5%), and *S. Typhimurium* (12.0%).

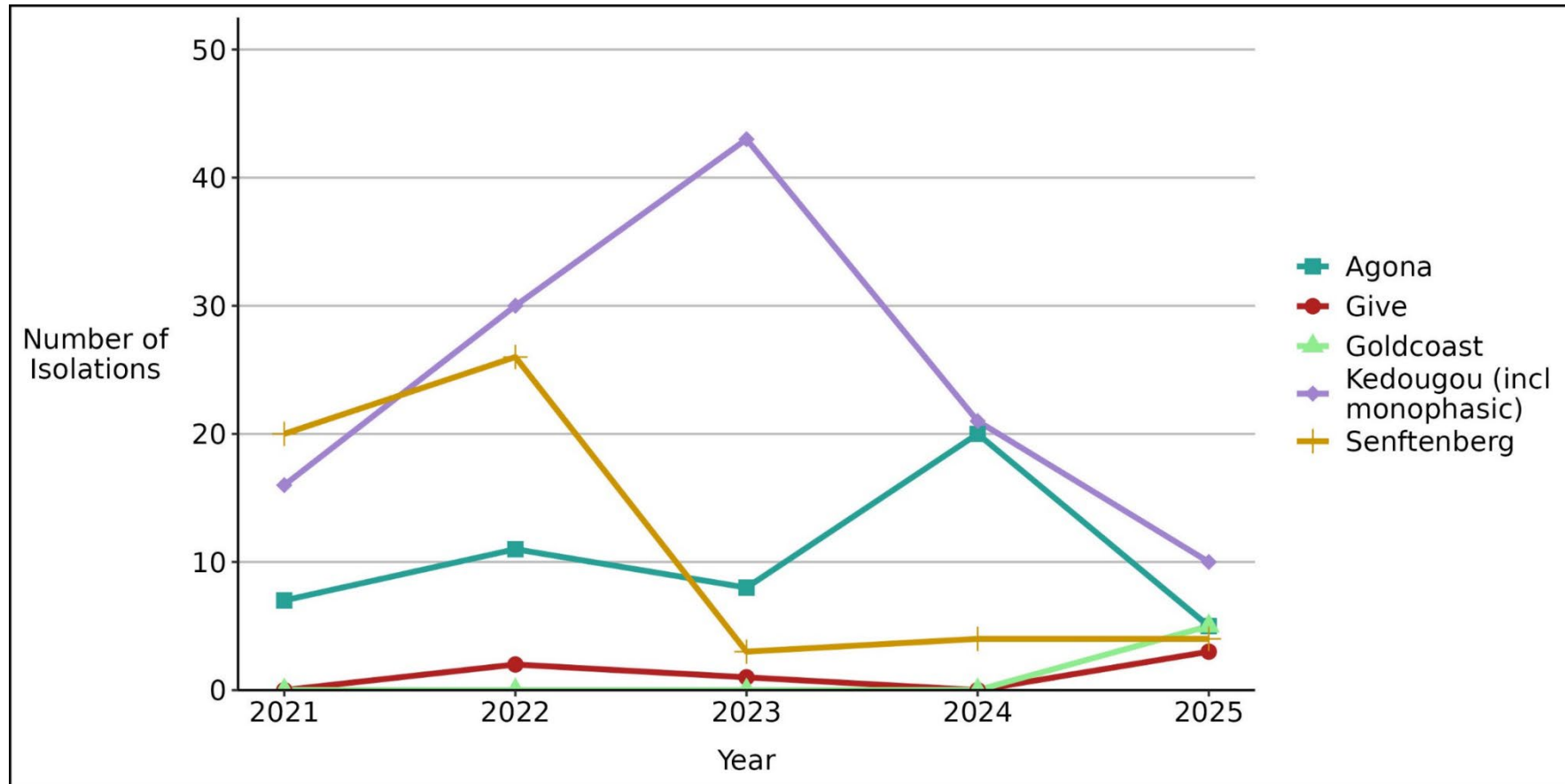
Figure 7.1.5: Isolations in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in turkeys in 2025. The most common *Salmonella* serovar in turkeys in 2025 was *S. Kedougou* (including monophasic variants), accounting for accounting for 30.3% of total

isolations, followed by *S. Goldcoast* and *S. Agona* (15.2% each), and *S. Senftenberg* (12.1%).

Figure 7.2: The 5 most common *Salmonella* serovars in turkeys in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in turkeys from 2021 to 2025. The figure shows that *S. Kedougou* (including monophasic variants) was the most common serovar in turkeys in 2025. The number of isolations of *S. Kedougou* (including monophasic

variants) has been variable with a high in 2023 of 43 isolations, dropping to 21 isolations in 2024 and 10 isolations in 2025. The second most common serovars in 2025 were *S. Agona* and *S. Goldcoast*, with 5 isolations in each. Numbers of *S. Agona* had increased in 2024 to 20 isolations though dropped down again to 5 isolations in 2025. *Salmonella* Senftenberg was the third most common serovar in 2025, which has remained low at between 3 and 4 isolations between 2023 and 2025, though there was a peak of 26 isolations in 2022. The fourth most common serovar in 2025 was *S. Give*, which has remained low to zero over the last 5 years, never exceeding 3 isolations.

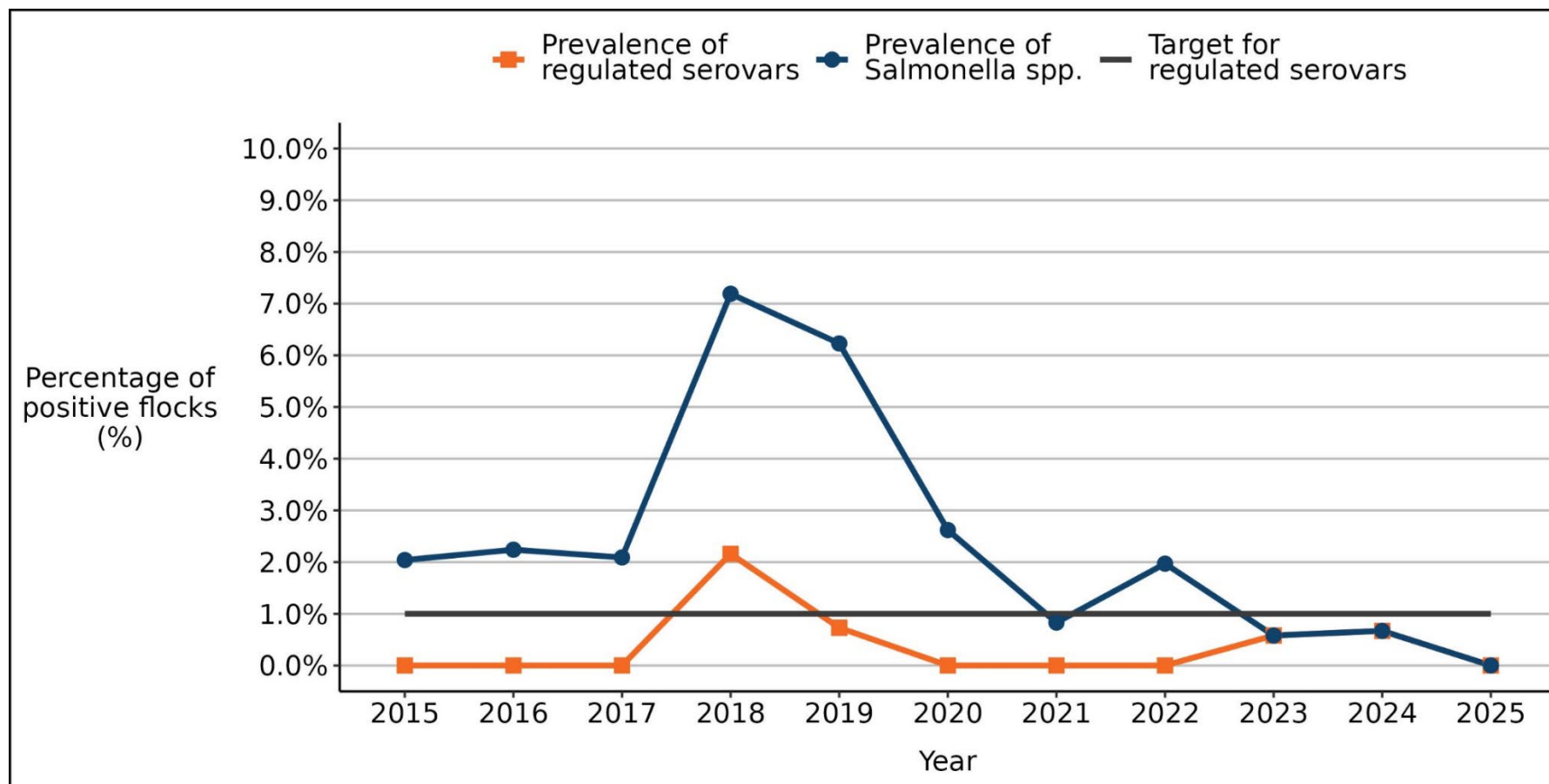
Table 7.2: Sequence types of S. Typhimurium isolations in turkeys in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	2	13	0
Total	2	13	0

Table 7.3: Sequence types of monophasic S. Typhimurium isolations in turkeys in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
34	1	0	0
Total	1	0	0

Figure 7.3: Prevalence of *Salmonella* in adult turkey breeding flocks tested under NCP in Great Britain 2015 to 2025



A line graph showing the prevalence of *Salmonella* in adult turkey breeding flocks tested under the NCP from 2015 to 2025. The figure shows a peak in the prevalence of *Salmonella* spp. in breeding turkey flocks of 7.19% in 2018 but a subsequent decline thereafter to

0.00% in 2025. The prevalence of regulated serovars remains low at 0.00% despite a small peak in 2018 to 2.16% which was above the target of 1% prevalence. The absolute number of breeder flocks eligible for NCP testing and positive for *Salmonella* is relatively small and should thus be borne in mind when interpreting the trends in this figure.

Table 7.4: Turkey breeding flocks in Great Britain (number of adult flocks reported positive for each *Salmonella* serovar, NCP testing 2021 to 2025)

The following table shows the number of turkey breeding flocks reported positive with each *Salmonella* serovar from 2021 to 2025 and the rank within that year. This data comes from NCP testing.

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Typhimurium	0	0	0	0	1	1	1	1	0	0
Agama	1	1	0	0	0	0	0	0	0	0
Mbandaka	1	1	0	0	0	0	0	0	0	0
Senftenberg	0	0	1	4	0	0	0	0	0	0

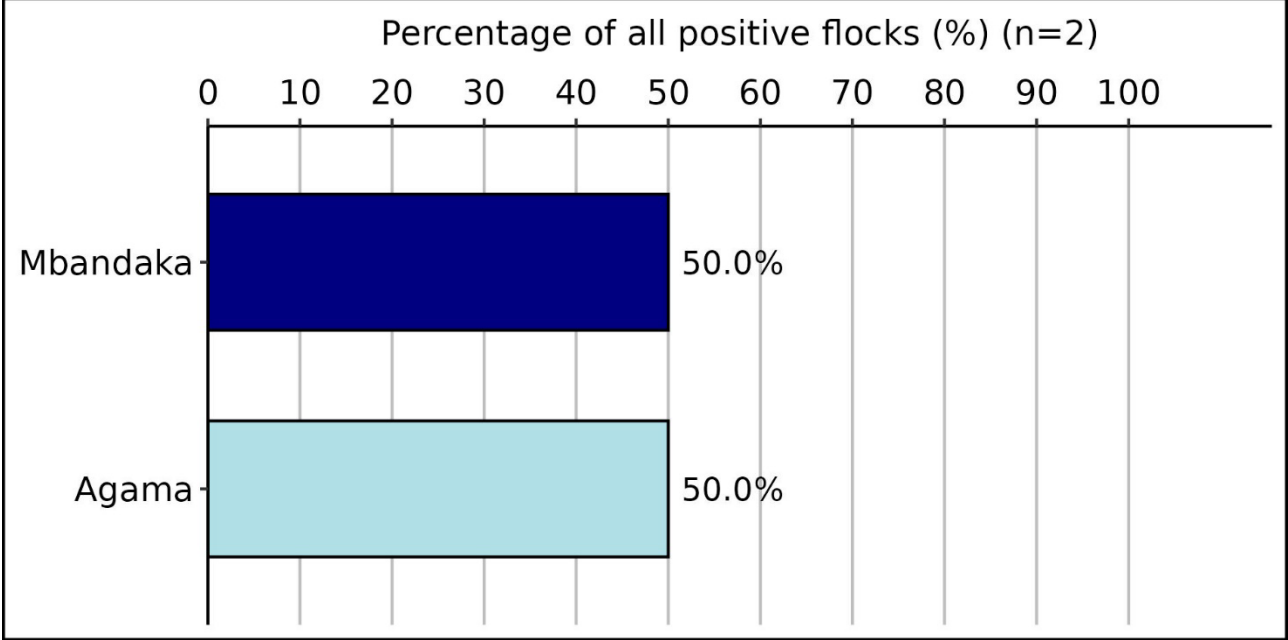
For details of turkey breeding flocks reported positive in 2014 to 2020, see the [2020 edition of *Salmonella* in livestock production in Great Britain](#).

Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2021	0.83%	0.00%
2022	1.97%	0.00%
2023	0.58%	0.58%
2024	0.67%	0.67%
2025	0.00%	0.00%

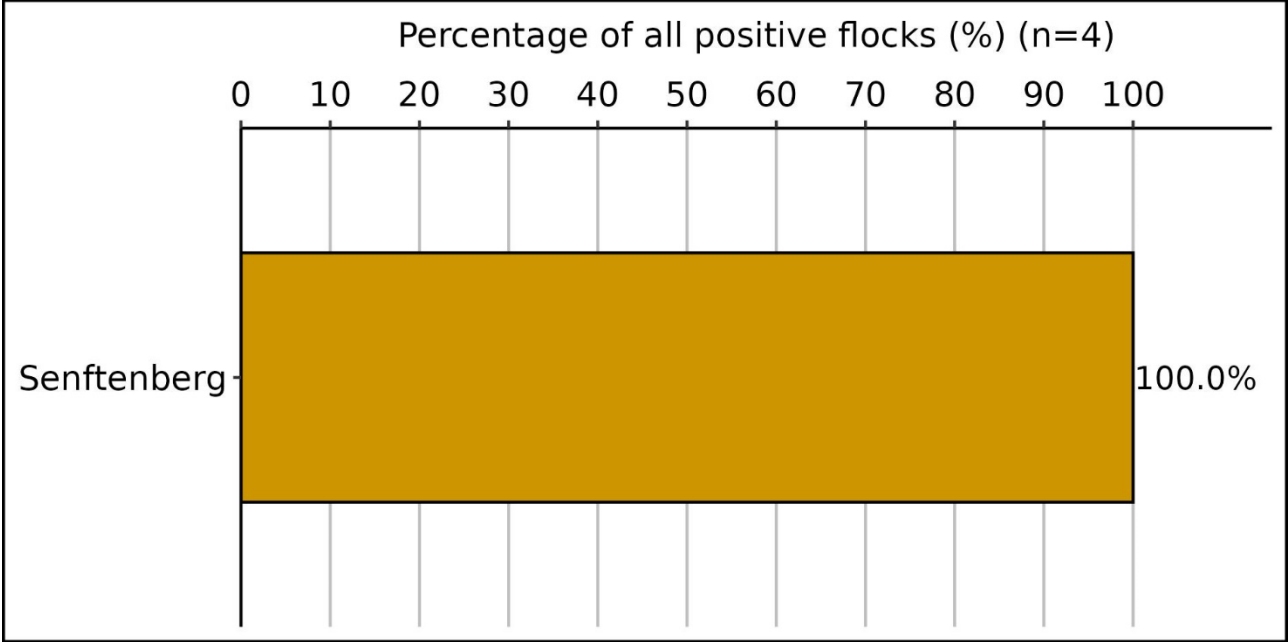
Figure 7.4: *Salmonella* serovars identified in adult turkey breeding flocks in Great Britain 2021 to 2025 reported from NCP testing

Figure 7.4.1: Flocks in adult breeding turkeys in 2021



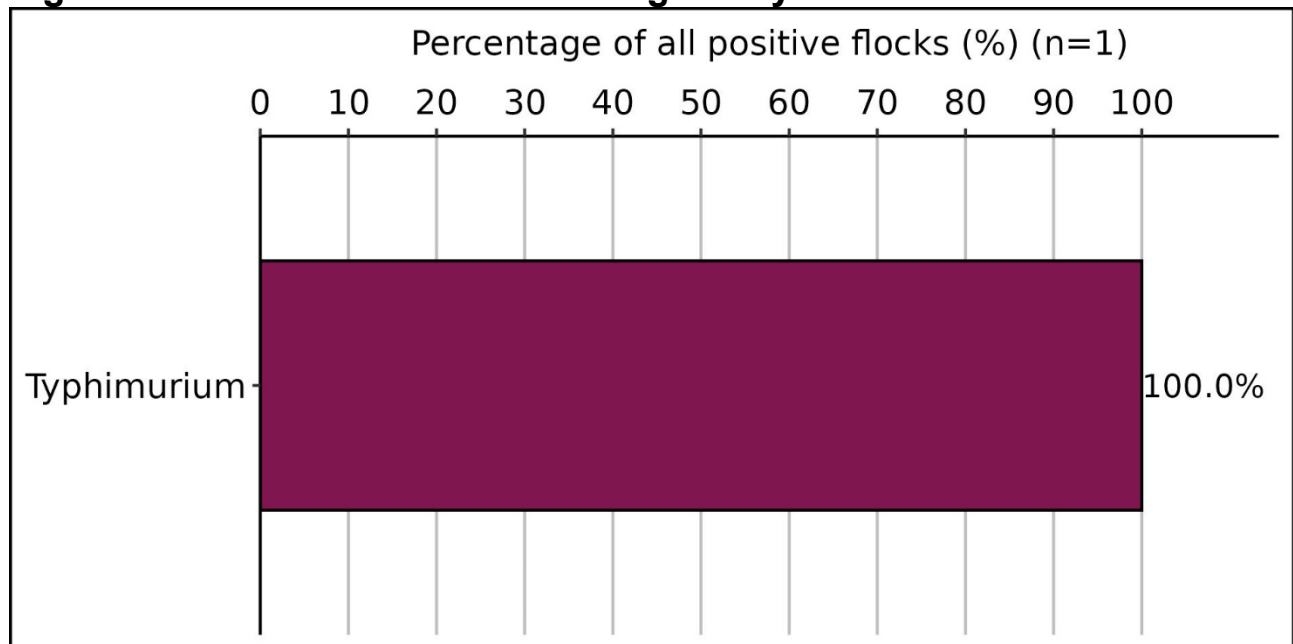
In 2021 the most common *Salmonella* serovars in breeding turkey flocks were *S. Agama* and *S. Mbandaka*, each accounting for 50.0% of total isolations.

Figure 7.4.2: Flocks in adult breeding turkeys in 2022



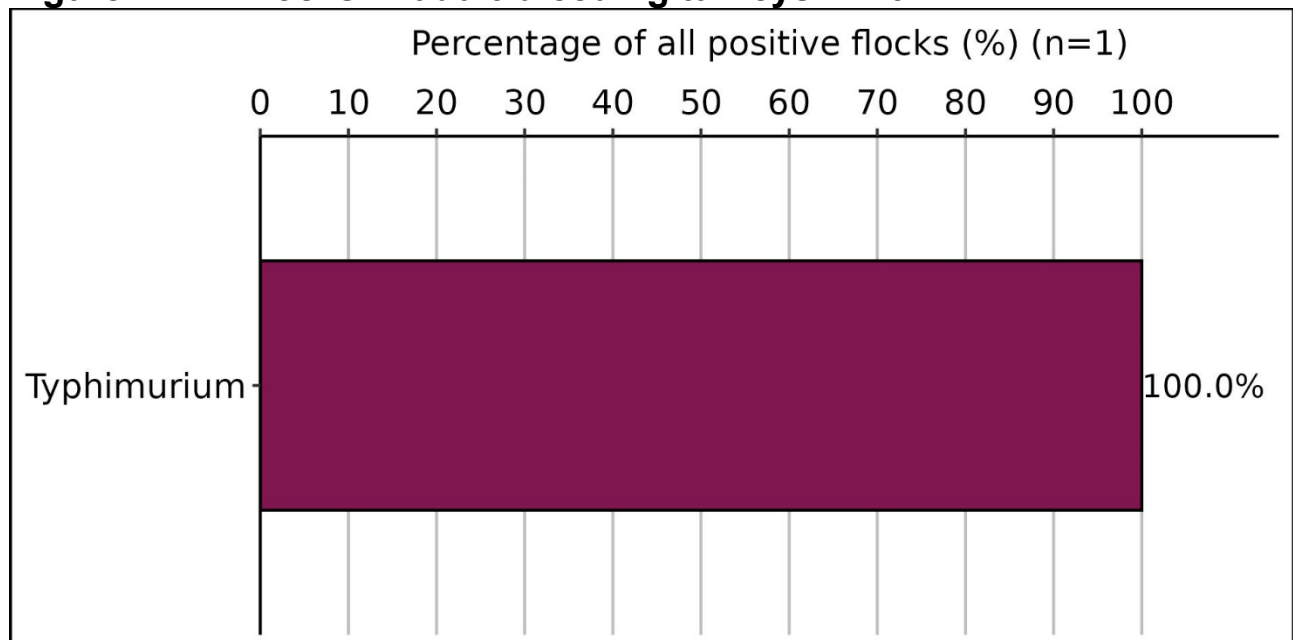
In 2022 the only *Salmonella* serovar in breeding turkey flocks was *S. Senftenberg* accounting for 100% of all isolations.

Figure 7.4.3: Flocks in adult breeding turkeys in 2023



In 2023 the only *Salmonella* serovar isolated in breeding turkey flocks was *S. Typhimurium*, accounting for 100% of all isolations.

Figure 7.4.4: Flocks in adult breeding turkeys in 2024

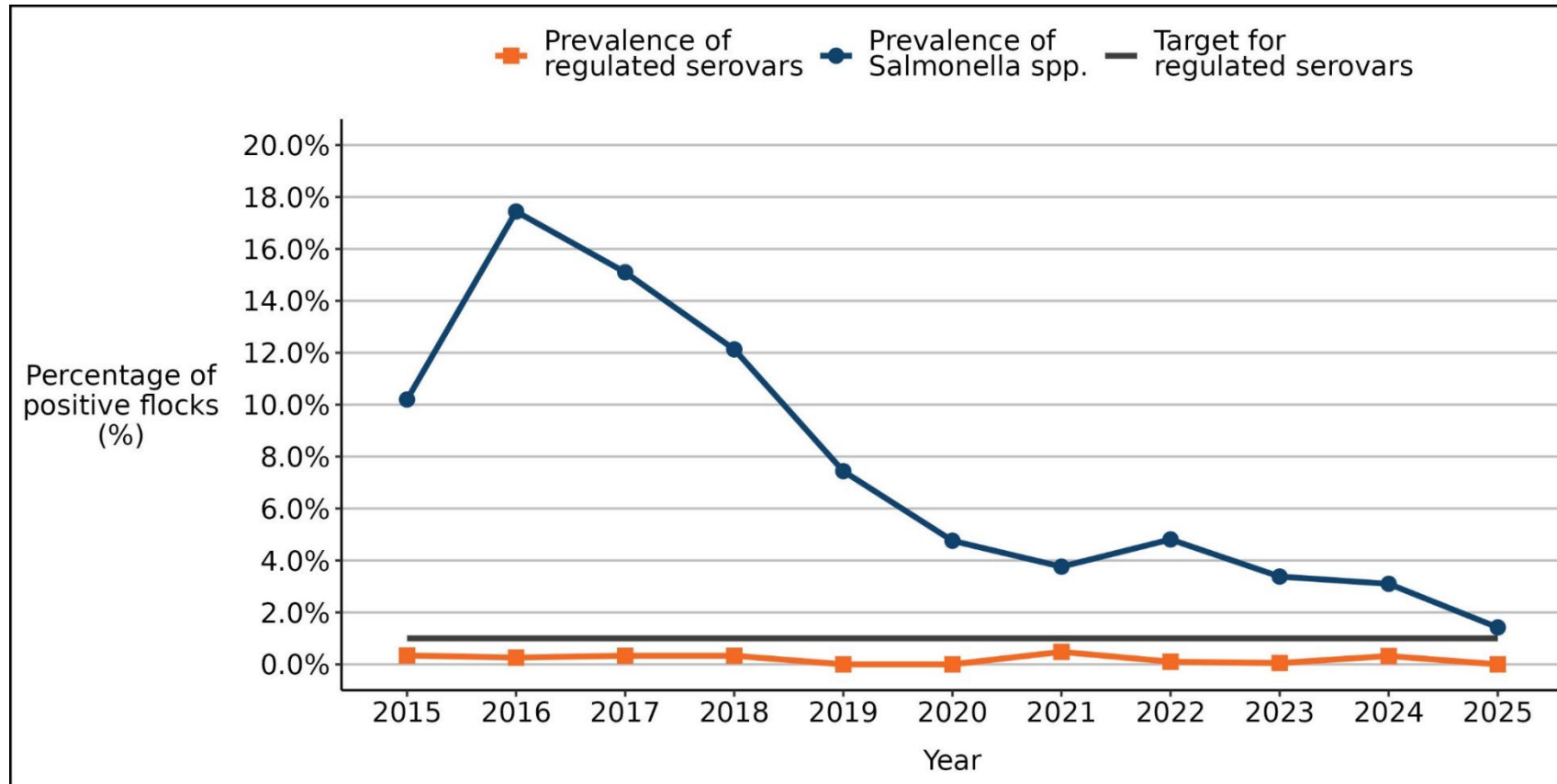


In 2024 the only *Salmonella* serovar isolated in breeding turkey flocks was *S. Typhimurium*, accounting for 100% of all isolations.

Figure 7.4.5: Flocks in adult breeding turkeys in 2025

There were no isolations of *Salmonella* in adult breeding turkey flocks in 2025.

Figure 7.5: Prevalence of *Salmonella* in turkey fattening flocks tested under NCP in Great Britain 2015 to 2025



A line graph showing the prevalence of *Salmonella* in adult turkey fattening flocks tested under the NCP from 2015 to 2025. The figure shows a peak in the prevalence of *Salmonella* spp. in fattening turkey flocks of 17.4% in 2016 but a subsequent decline thereafter to 1.4% in 2025. The prevalence of regulated serovars remains very low and below 1% prevalence across all years.

Table 7.5: Turkey fattening flocks in Great Britain (number of flocks reported positive for each *Salmonella* serovar, NCP testing 2021 to 2025)

The following table shows the number of turkey fattening flocks reported positive with each *Salmonella* serovar from 2021 to 2025 and the rank within that year. This data comes from NCP testing.

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Kedougou (incl. monophasic variants)	3	9	2	21	1	32	2	15	1	7
Agona	4	4	3	7	5	4	3	11	2	4
Goldcoast	0	0	0	0	0	0	0	0	2	4
Uganda	0	0	0	0	0	0	0	0	3	3
Give	0	0	0	0	7	1	0	0	4	2
Senftenberg	5	3	4	5	7	1	0	0	4	2
Anatum	1	31	1	40	2	18	1	19	5	1
Orion	0	0	0	0	7	1	0	0	5	1
Agama	7	1	0	0	0	0	0	0	0	0
Ago	0	0	0	0	0	0	8	1	0	0
Bovismorbificans	6	2	0	0	0	0	0	0	0	0
Brandenburg	0	0	7	1	0	0	0	0	0	0
Chester	0	0	0	0	7	1	0	0	0	0
Derby	2	19	3	7	6	2	7	2	0	0
Give var. 15⁺	7	1	0	0	0	0	0	0	0	0
Indiana	0	0	0	0	0	0	5	6	0	0
Idikan (incl. monophasic variants)	6	2	6	2	4	5	6	4	0	0

<i>Salmonella</i> serovar	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024	Rank 2025	Flocks 2025
Kottbus	0	0	0	0	6	2	0	0	0	0
Javiana	0	0	0	0	0	0	8	1	0	0
London	7	1	5	3	0	0	0	0	0	0
Mbandaka	0	0	0	0	0	0	0	0	0	0
Monophasic Typhimurium	3	9	6	2	7	1	0	0	0	0
Montevideo	0	0	5	3	0	0	0	0	0	0
Newport	6	2	7	1	0	0	0	0	0	0
Orion var. 15⁺	4	4	5	3	3	6	7	2	0	0
Schwarzengrund	0	0	0	0	7	1	0	0	0	0
Typhimurium	5	3	0	0	0	0	4	7	0	0
3,10:e,h:-	5	3	6	3	0	0	0	0	0	0
3,19:rough:-	7	1	7	1	7	1	0	0	0	0
6,8:e,h:-	7	1	7	1	0	0	0	0	0	0

For details of turkey fattening flocks reported positive in 2014 to 2020, see the [2020 edition of *Salmonella* in livestock production in Great Britain](#).

Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2021	3.76%	0.48%
2022	4.81%	0.10%
2023	3.38%	0.05%
2024	3.10%	0.32%
2025	1.42%	0.00%

Flocks testing positive for more than one serovar

In 2021:

- 1 flock tested positive for *S. Derby* and *S. Newport*
- 1 flock tested positive for *S. Give* var. 15⁺ and *S. Orion* var. 15⁺

In 2022:

- 2 flocks tested positive for both *Salmonella* 3,10:e,h:- and *S. Anatum*
- 1 flock tested positive for both *Salmonella* 3,10:e,h:- and *S. Kedougou* (including monophasic variants)

In 2023:

- 4 flocks tested positive for both *S. Kedougou* (including monophasic variants) and *S. 13,23:i:-*
- 1 flock tested positive for both *S. Kedougou* (including monophasic variants) and *S. Anatum*
- 1 flock tested positive for both *S. Orion* and *S. Orion* var 15⁺

In 2024:

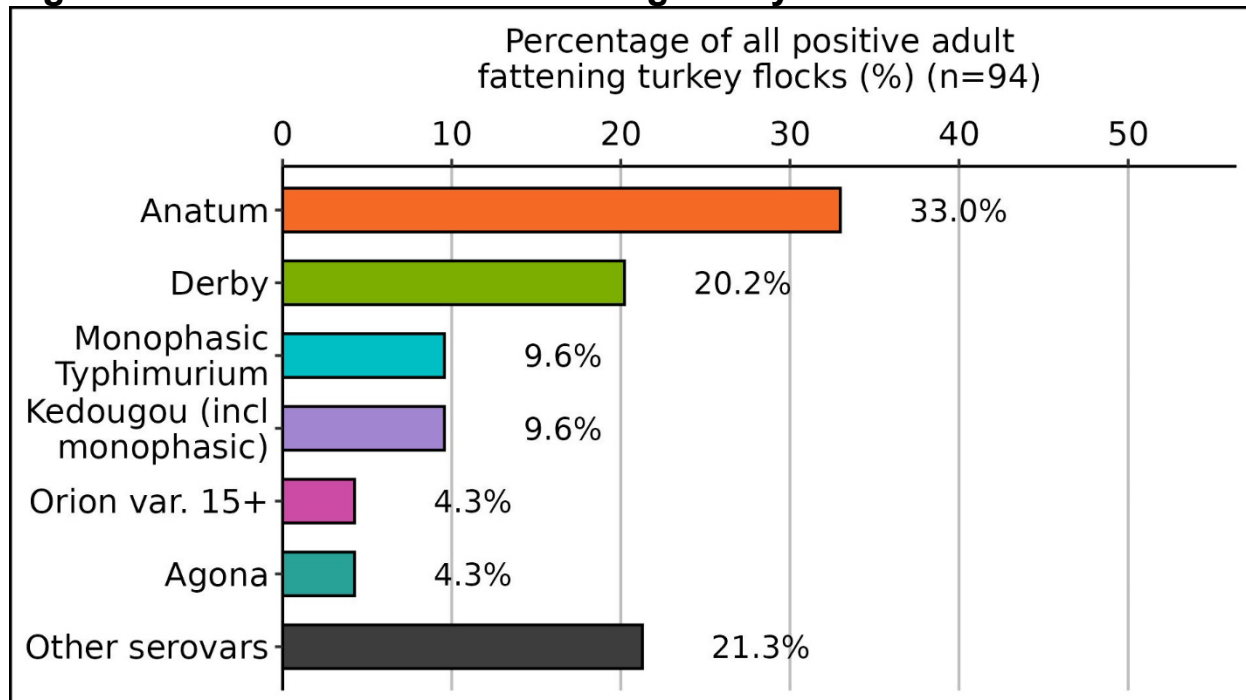
- 0 flocks tested positive for more than one serovar.

In 2025:

- 0 flocks tested positive for more than one serovar.

Figure 7.6: The most common *Salmonella* serovars identified in turkey fattening flocks in Great Britain 2021 to 2025 reported from NCP testing

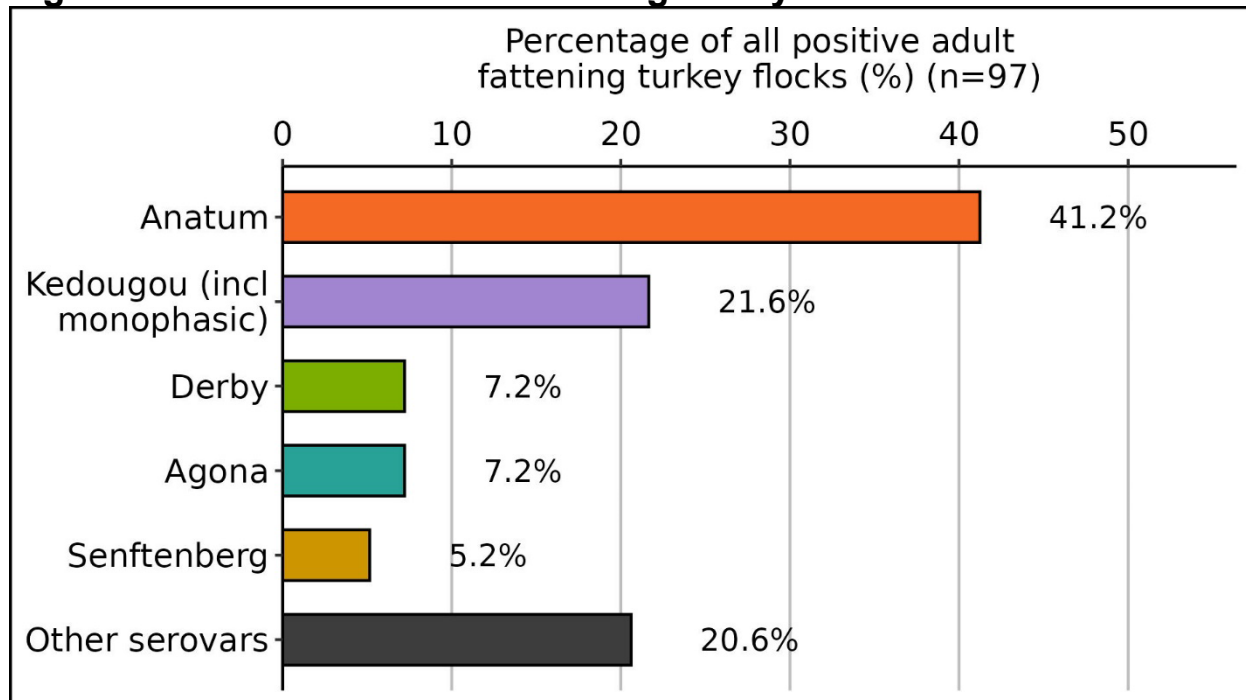
Figure 7.6.1: Flocks in adult fattening turkeys in 2021



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult fattening turkeys in 2021. In 2021 the most common *Salmonella* serovar in fattening turkey flocks was *S. Anatum*, accounting for 33.0% of total isolations, followed by *S. Derby* (20.2%), *S. Kedougou* (including monophasic variants) (9.6%) and monophasic *S. Typhimurium* (9.6%).

In 2021 2 flocks were positive for 2 serovars (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

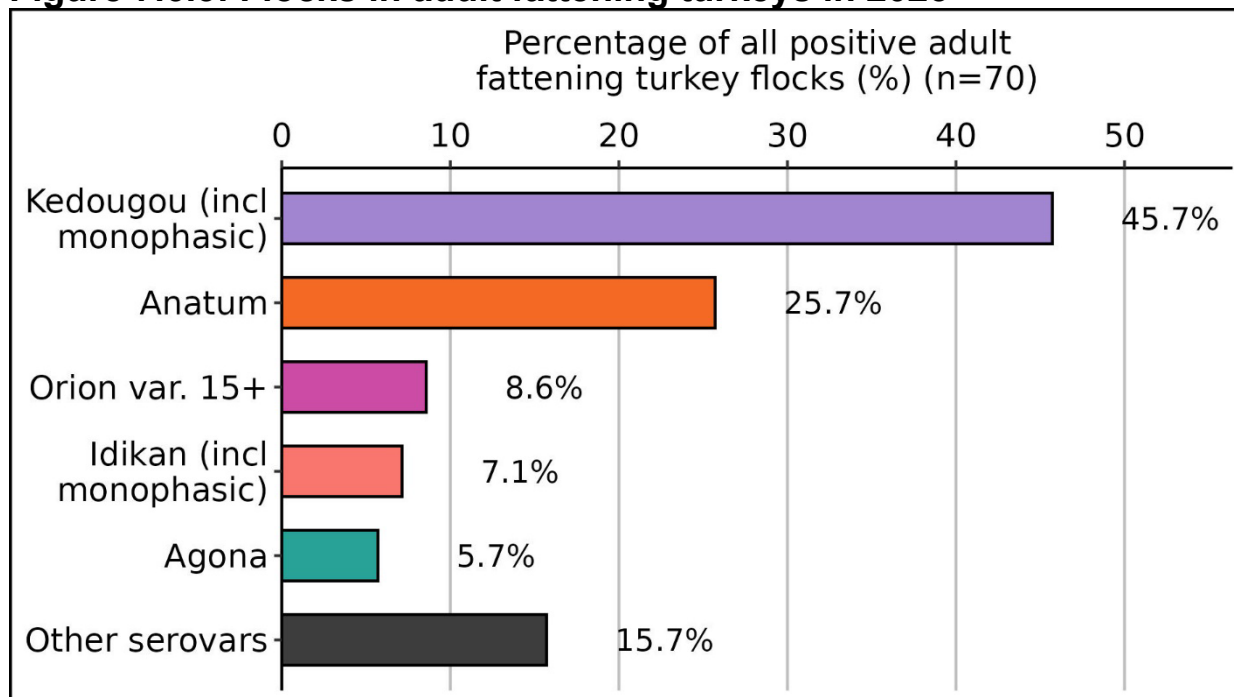
Figure 7.6.2: Flocks in adult fattening turkeys in 2022



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult fattening turkeys in 2022. In 2022 the most common *Salmonella* serovar in fattening turkey flocks was *S. Anatum*, accounting for 41.2% of total isolations, followed by *S. Kedougou* (including monophasic variants) (21.6%), *S. Derby* (7.2%) and *S. Agona* (7.2%).

In 2022 3 flocks were positive for 2 serovars (each counted only in the total). Summed percentages of all serovars therefore exceeds 100%.

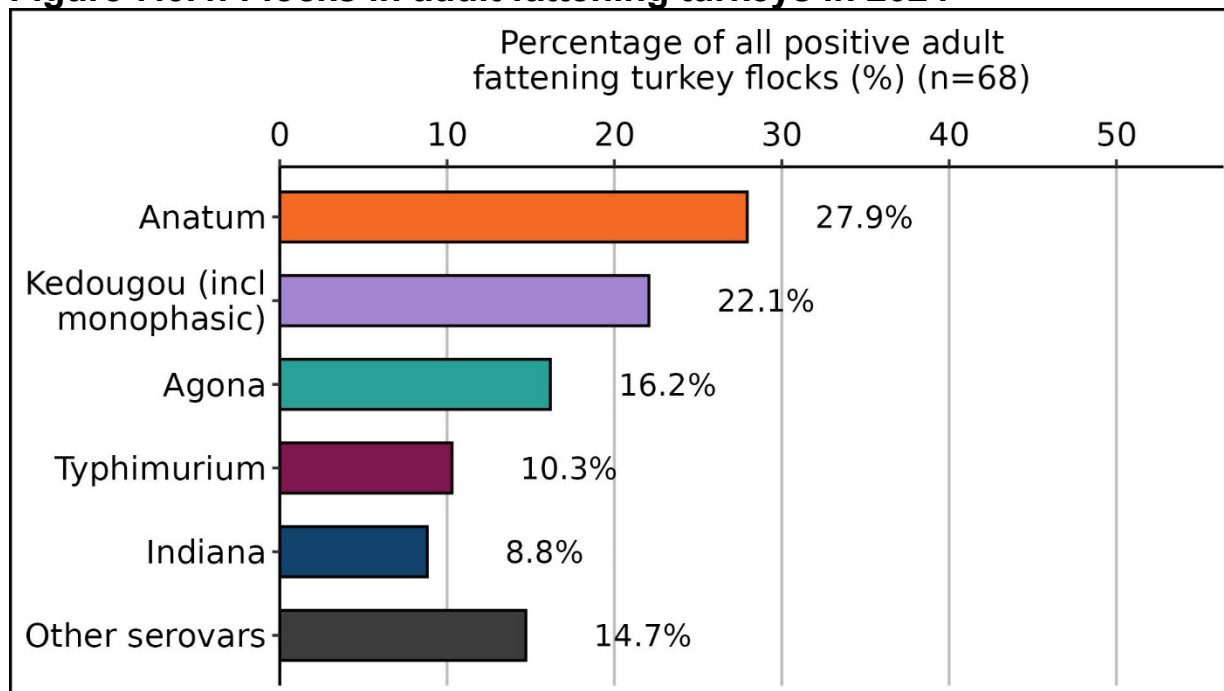
Figure 7.6.3: Flocks in adult fattening turkeys in 2023



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult fattening turkeys in 2023. In 2023 the most common *Salmonella* serovar in fattening turkey flocks was *S. Kedougou* (including monophasic variants), accounting for 45.7% of total isolations, followed by *S. Anatum* (25.7%), *S. Orion* var 15⁺ (8.6%) and *S. Idikan* (including monophasic variants) (7.1%).

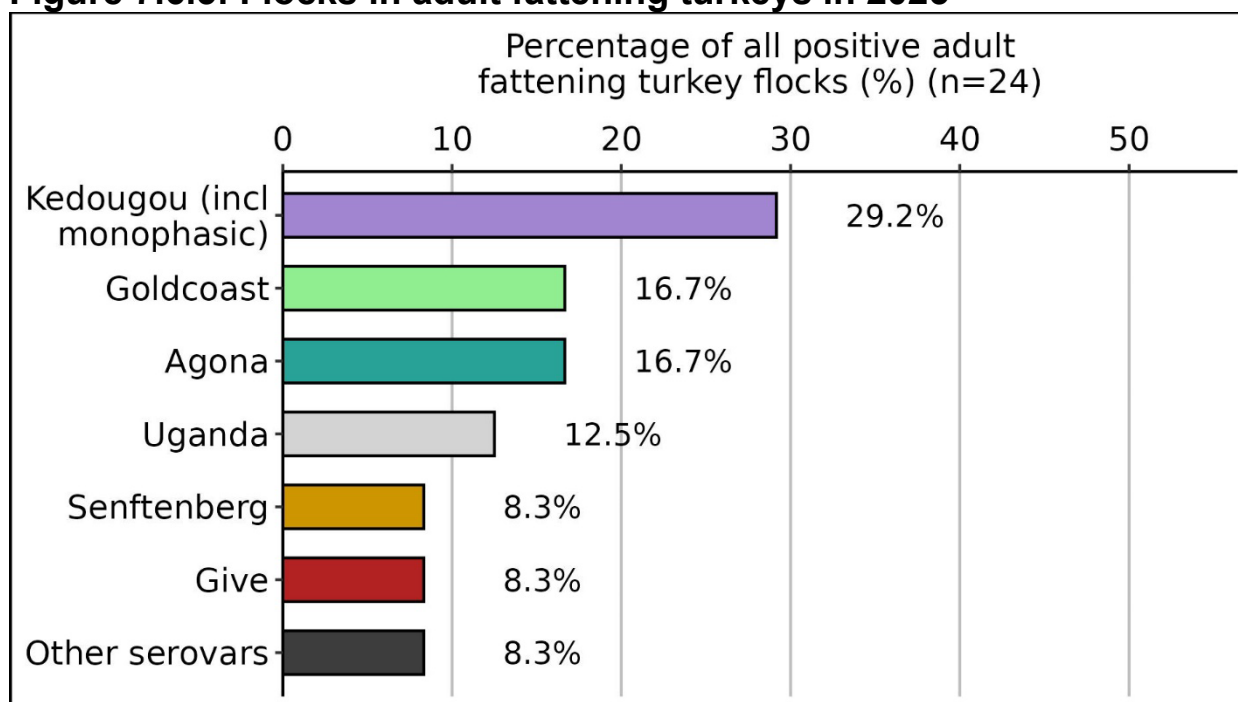
In 2023 6 flocks were positive for 2 serovars (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

Figure 7.6.4: Flocks in adult fattening turkeys in 2024



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult fattening turkeys in 2024. In 2024 the most common *Salmonella* serovar in fattening turkey flocks was *S. Anatum*, accounting for 27.9% of total isolations, followed by *S. Kedougou* (22.1%), *S. Agona* (16.2%), and *S. Typhimurium* (10.3%).

Figure 7.6.5: Flocks in adult fattening turkeys in 2025



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult fattening turkeys in 2025. In 2025 the most common *Salmonella* serovar in fattening turkey flocks was *S. Kedougou* (including monophasic variants), accounting for 29.2% of total isolations, followed by *S. Goldcoast* (16.7%), *S. Agona* (16.7%), and *S. Uganda* (12.5%).

Chapter 8: Reports of *Salmonella* in ducks and geese

Whilst there is a voluntary Duck Assurance Scheme in place in Great Britain, there are no statutory monitoring requirements for *Salmonella* in farmed ducks or geese although *Salmonella* is reportable in both farmed and wild ducks and geese. The tables and figures of this chapter, therefore, include isolations and incidents of *Salmonella* from both farmed and wild birds although the majority of submissions each year are from farmed birds.

Ducks

In 2025 there were 211 diagnostic submissions from ducks recorded on the VIDA database in Great Britain compared to 92 in 2024. The VIDA database records both farmed and wild ducks.

During 2025 there were 113 isolations of *Salmonella* from ducks in Great Britain, which is a 42.3% decrease compared to 2024 (196 isolations), and a 17.7% increase compared to 2023 (96 isolations) (Table 8.1). The majority of isolations arose from voluntary surveillance (112 isolations) with the remaining one isolation from clinical disease investigation. An increase in voluntary surveillance testing in the duck industry resulted in higher numbers of isolations in 2024.

The most common serovars isolated from ducks during 2025 were *S. Indiana* (78 isolations, 69.0% of duck isolations), *S. Give* (11 isolations, 9.7% of duck isolations), *S. Lexington* (8 isolations, 7.1% of duck isolations), *S. Newport* and *S. Kottbus* (7 isolations of each serovar, 6.2% of duck isolations each). Together these serovars accounted for 98.2% of all *Salmonella* isolations from ducks (Figure 8.1). In contrast, during 2024 the most common serovars were *S. Indiana* (147 isolations, 75.0% of duck isolations), *S. Newport* (20 isolations, 10.2% of duck isolations), *S. Kottbus* (12 isolations, 6.1% of duck isolations), *S. Give* (5 isolations, 2.6% of duck isolations) and *S. Give* var. 15⁺ (3 isolations, 1.5% of duck isolations).

Salmonella Indiana remained the most commonly reported serovar from ducks during 2025 (78 isolations). This was a decrease of 46.9% compared to 2024 (147 isolations) and an increase of 50.0% compared to 2023 (52 isolations). This serovar accounted for 69.0% of total isolations from ducks in 2025, a decrease compared to 75.0% in 2024 (Figure 8.1).

The second most commonly reported serovar in 2025 was *S. Give*, with 11 isolations. This is the highest number of isolations of this serovar seen since 2019 (11 isolations) but was still lower than in the period 2014 to 2018 when there were more than 20 isolations each year. This serovar accounted for a larger proportion of total isolations in 2025 (9.7% of isolations) compared to 2024 (2.6% of isolations) and 2023 (9.4% of isolations).

There were 8 isolations of *S. Lexington* from ducks in 2025, an increase compared to 2024 (1 isolation) and consistent with 2023 (8 isolations). *S. Lexington* isolations accounted for 7.1% of total isolations from ducks in 2025 and was the third most common serovar.

There were 7 isolations of *S. Newport* in 2025, a decrease of 65.0% compared to 2024 (20 isolations). Isolations of this serovar had been low in previous years with no isolations in 2022 or 2023 and one isolation in 2021.

There were 7 isolations of *S. Kottbus* in 2025, a decrease compared to 2023 and 2024 (12 isolations in each year). *Salmonella* Kottbus has been isolated from ducks every year since 2013 and prior to 2023, there had been a generally declining trend in the number of isolations since 2018.

There was one isolation of *S. Orion* var. 15⁺ during 2025, the same as in 2024 and a decrease compared to 2023 (5 isolations) and 2022 (15 isolations).

There were no isolations of the serovars *S. Hadar* and *S. Orion* in 2025 which is the first time these serovars have not been reported in ducks since before 2013. In 2022, *S. Hadar* was the second most common serovar isolated from ducks. Isolations of this serovar peaked in 2018 (44 isolations) and have since been in general decline. Isolations of *S. Orion* peaked in 2014 with 38 isolations but have been declining since 2018 when there were 36 isolations.

There was one isolation of *S. Typhimurium* (ST19) from ducks in 2025 an increase compared to 2024 (no isolations) and the same as 2023 where there was one isolation (Table 8.3). Isolations of *S. Typhimurium* from ducks have decreased substantially since 2010 when there were 119 isolations representing 60.4% of total isolations. It is thought that this overall reduction may be associated with the inception of the voluntary duck assurance scheme in 2010, which requires control measures including post cleaning and disinfection swabbing of infected houses. There were no isolations of *S. Enteritidis* from ducks in 2025, compared to no isolations in 2024 and one isolation in 2023 (ST814) (Table 8.4). There were no isolations of monophasic *S. Typhimurium* in ducks during 2025, consistent with 2021 to 2024.

Antimicrobial susceptibility in ducks

A total of 118 *Salmonella* isolates from ducks were tested against a panel of 16 antimicrobials in 2025. Overall, 90.7% were fully susceptible to all antimicrobials tested. This was a decrease from 2024 (96.6%) but was higher than 2023 (84.3%). Eleven isolates displayed resistance: the most common resistant serovar was *S. Give* (n=6).

None of the *Salmonella* isolates from ducks showed resistance to third-generation cephalosporins or fluoroquinolones, which are considered highest priority critically important antibiotics.

Geese

There were no isolations of *Salmonella* from geese in 2025. This compares to one isolation of *S. Typhimurium* (ST19) in 2024 and no isolations between 2021 and 2023. The annual number of *Salmonella* isolations from geese in Great Britain is generally low, with the highest number in recent years being 6 isolations in 2017. In 2025 there were 586 diagnostic submissions from geese recorded on the VIDA database in Great Britain compared to 119 in 2024. The VIDA database records both farmed and wild geese.

Table 8.1: Isolations and incidents of *Salmonella* in ducks on all premises in Great Britain 2021 to 2025

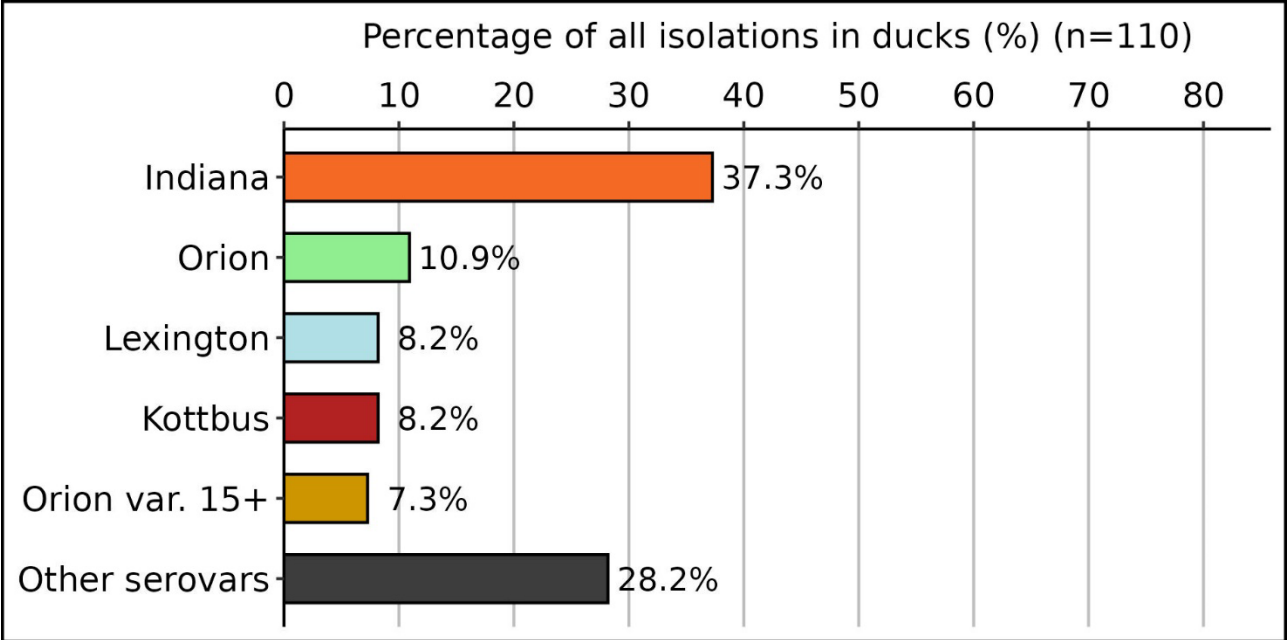
<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Agona	1	1	0	0	0	0	0	0	0	0
Bovismorbificans	0	0	15	3	0	0	0	0	0	0
Enteritidis	1	1	0	0	1	1	0	0	0	0
Give	6	5	1	1	9	9	5	5	11	8
Give var. 15⁺	6	5	15	13	0	0	3	1	0	0
Hadar	1	1	17	10	6	5	2	2	0	0
Indiana	41	33	38	28	52	28	147	100	78	54
Kedougou (incl. monophasic variants)	1	1	0	0	0	0	2	2	0	0
Kingston	0	0	0	0	0	0	1	1	0	0
Kottbus	9	9	6	5	12	10	12	10	7	6
Lexington	9	7	9	8	8	6	1	1	8	7
Newport	1	1	0	0	0	0	20	16	7	4
Orion	12	11	2	2	2	2	2	1	0	0
Orion var. 15⁺	8	6	15	8	5	2	1	1	1	1
Senftenberg	1	0	0	0	0	0	0	0	0	0
Typhimurium	0	0	0	0	1	1	0	0	1	1
untypable strains	13	13	3	3	0	0	0	0	0	0
Total	110	94	121	81	96	64	196	140	113	81

Table 8.2: Isolations and incidents of *Salmonella* in geese on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Typhimurium	0	0	0	0	0	0	1	1	0	0
Total	0	0	0	0	0	0	1	1	0	0

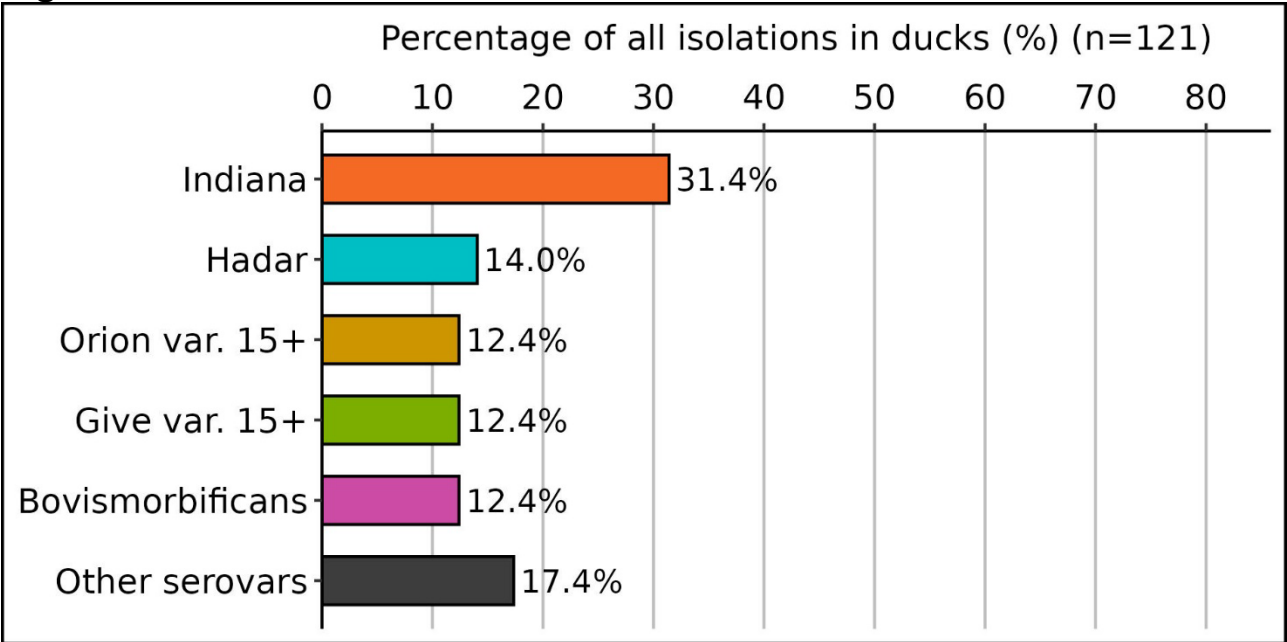
Figure 8.1: Isolations of the most common *Salmonella* serovars in ducks in Great Britain 2021 to 2025

Figure 8.1.1: Isolations in ducks in 2021



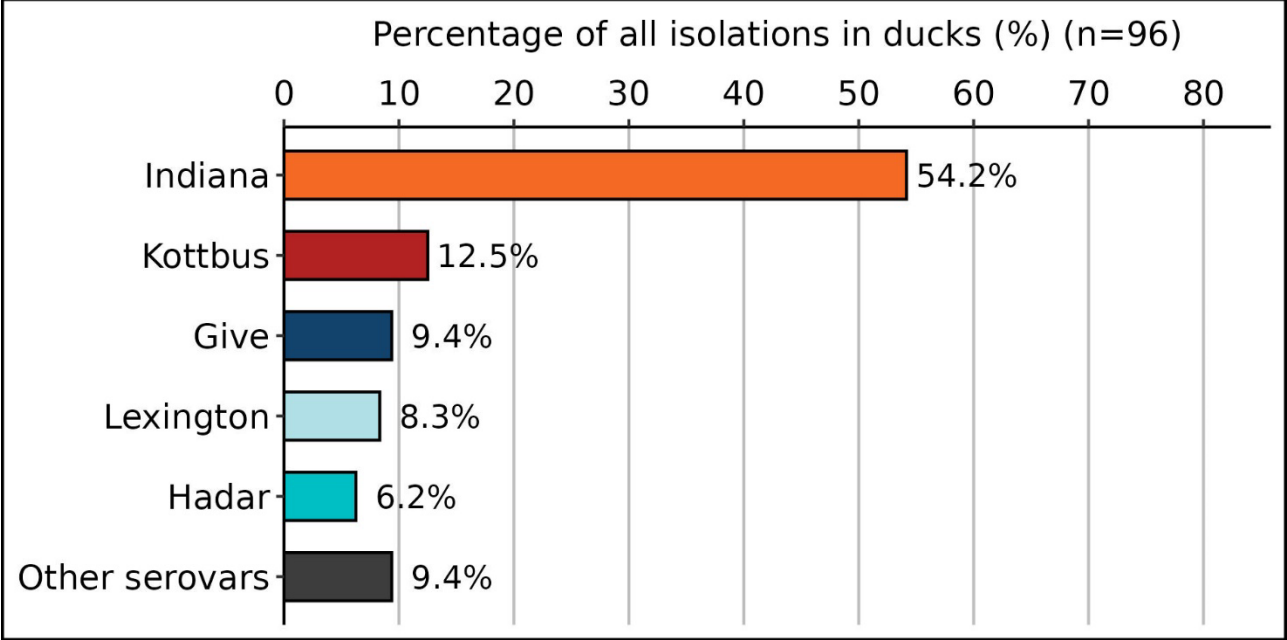
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in ducks in 2021. The most common *Salmonella* serovar in ducks in 2021 was *S. Indiana*, accounting for 37.3% of total isolations, followed by *S. Orion* (10.9%), *S. Kottbus* and *S. Lexington* (8.2% each) and *S. Orion var. 15+* (7.3%).

Figure 8.1.2: Isolations in ducks in 2022



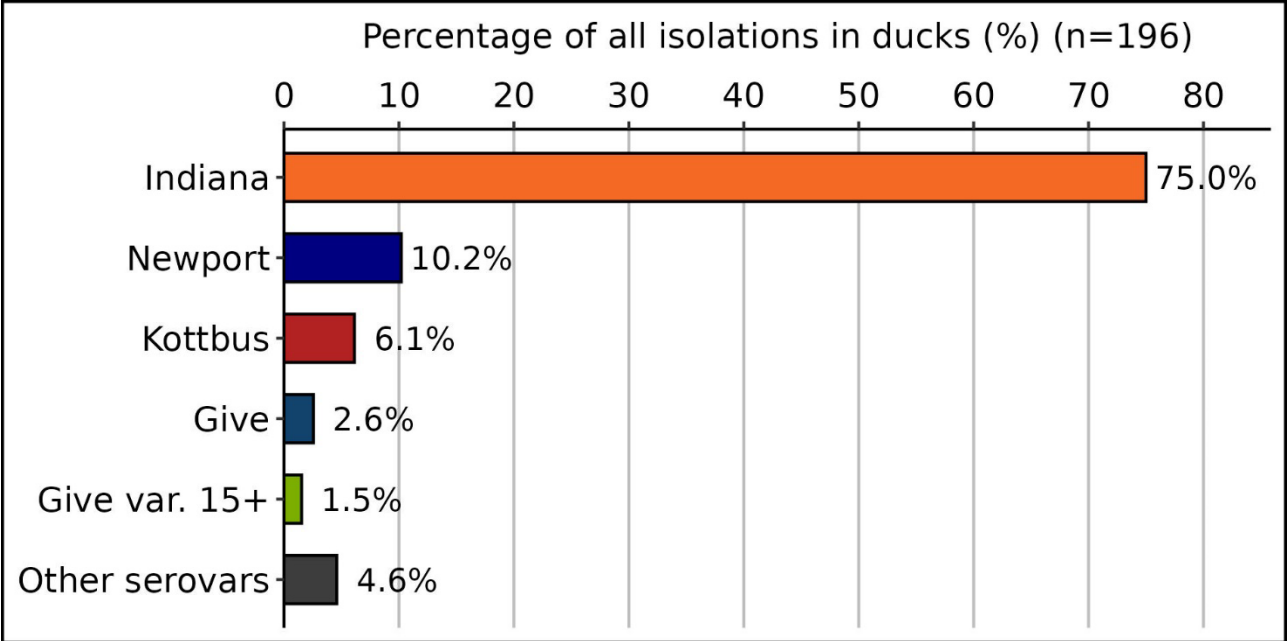
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in ducks in 2022. The most common *Salmonella* serovar in ducks in 2022 was S. Indiana, accounting for 31.4% of total isolations, followed by S. Hadar (14.0%), S. Bovismorbificans, S. Give var. 15⁺ and S. Orion var. 15⁺ (all 12.4% each).

Figure 8.1.3: Isolations in ducks in 2023



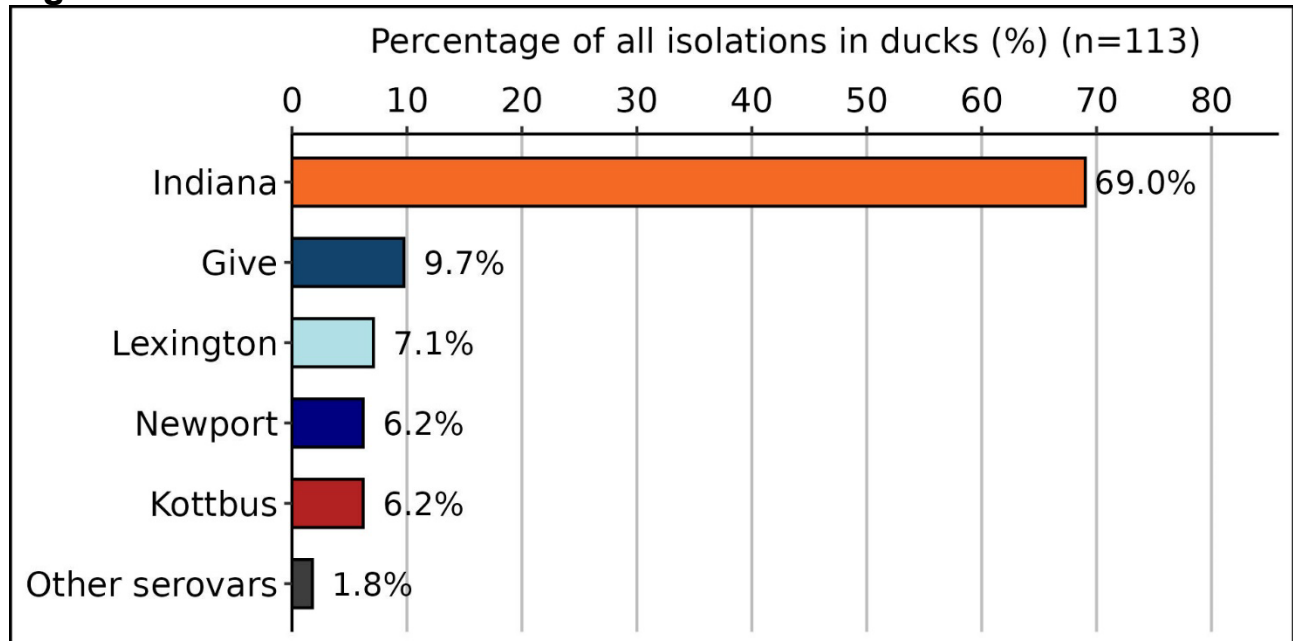
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in ducks in 2023. The most common *Salmonella* serovar in ducks in 2023 was S. Indiana, accounting for 54.2% of total isolations, followed by S. Kottbus (12.5%), S. Give (9.4%), S. Lexington (8.3%) and S. Hadar (6.2%).

Figure 8.1.4: Isolations in ducks in 2024



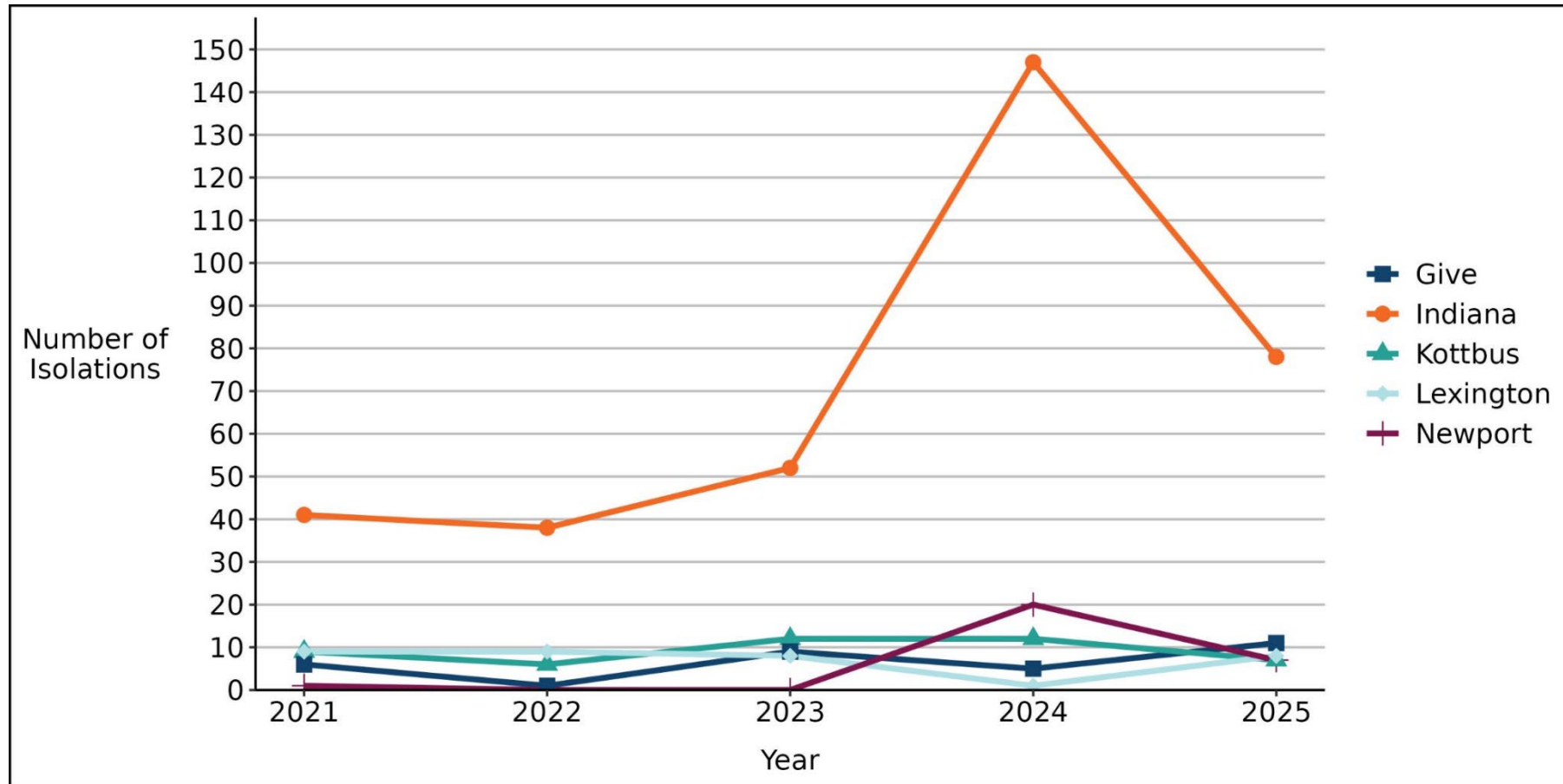
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in ducks in 2024. The most common *Salmonella* serovar in ducks in 2024 was S. Indiana, accounting for 75.0% of total isolations, followed by S. Newport (10.2%), S. Kottbus (6.1%), S. Give (2.6%) and S. Give var. 15⁺ (1.5%).

Figure 8.1.5: Isolations in ducks in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in ducks in 2025. The most common *Salmonella* serovar in ducks in 2025 was S. Indiana, accounting for 69.0% of total isolations, followed by S. Give (9.7%), S. Lexington (7.1%), S. Newport (6.2%) and S. Kottbus (6.2%).

Figure 8.2: The 5 most common *Salmonella* serovars in ducks in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in ducks from 2021 to 2025. The figure shows that *S. Indiana* remains the most common serovar isolated from ducks, although there was a decrease from 147 isolations in 2024 to 78 in 2025. *S. Give* was the second

most common serovar in 2025 and isolations increased to 11 in 2025, compared to years 2021 to 2024 when isolations ranged from 1 to 9. *S. Lexington* was the third most common serovar in 2025 with 8 isolations which was similar to 2021 to 2023, though an increase compared to one isolation in 2024. *S. Kottbus* has remained relatively stable in recent years with 7 isolations in 2025 and was the joint fourth most common serovar in 2025. Isolations of *S. Newport* have ranged from 0 in 2022 and 2023, to 20 in 2024, with a decrease to 7 isolations in 2025, making it the joint fourth most common serovar in the year.

Table 8.3: Sequence types of *S. Typhimurium* isolations in ducks and geese in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	0	1	1
No ST data	1	0	0
Total	1	1	1

One isolation in this table was reported from geese, ST19 in 2024. The further 2 isolations in the table were reported from ducks.

Table 8.4: Sequence types of *S. Enteritidis* isolations in ducks and geese in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
814	1	0	0
Total	0	0	0

One isolation reported from ducks. There were no isolations of *S. Enteritidis* from geese between 2023 and 2025.

Chapter 9: Reports of *Salmonella* in other statutory birds

Other statutory birds comprise guinea fowl, partridges, pheasants, pigeons and quail. In these species isolation of *Salmonella* is also reportable. A total of 15 isolations of *Salmonella* were reported from these species during 2025 which is decrease compared to 2024 (22 isolations) and 2023 (22 isolations).

Game birds

The total number of VIDA submissions from game birds (grouse (not a statutory species for reporting under the Zoonoses Order, but included in this chapter as a gamebird species), guinea fowl, partridges, pheasants, quail and other game) to APHA and SRUC increased by 26.1% to 203 submissions in 2025, compared to 161 submissions in 2024. As in previous years, the greatest number of submissions were from pheasants, with an increase of 51.6% compared to 2024 (144 versus 95 submissions). During 2025 there were also 27 submissions from partridges which was similar to 2024 (26 submissions) and 5 submissions from grouse, which was a decrease of 75.0% compared with 2024 (20 submissions).

During 2025, 23 quail submissions were received, compared to 8 submissions in 2024. Four guinea fowl submissions were received in 2025 compared to 2 submissions in 2024. There were no submissions from birds reported as “other game” in 2025 whereas there were 10 submissions in 2024.

There is no statutory *Salmonella* monitoring of game birds in Great Britain and the majority of submissions in 2025 were for diagnostic purposes (85.7%), which is more than during 2024 (78.9%). In 2025 there were 3 *Salmonella* isolations in game birds (all from pheasants), compared to no isolations in 2024 and 4 isolations in 2023. In recent years there has been a decreasing trend in the number of *Salmonella* isolations from game birds, across all species.

Pheasants

There were 3 isolations of *Salmonella* from pheasants in 2025, 2 of which were *S. Senftenberg* and one *S. Typhimurium*. This compares to no isolations in 2024 and 2 isolations in 2023 (*S. Senftenberg* and *S. Typhimurium*) (Table 9.1). The *S. Typhimurium* isolation in 2025 was sequence type 19 (Table 9.4).

The serovar most commonly associated with pheasants in previous years has been *S. Senftenberg*.

Partridges

There were no isolations of *Salmonella* in partridges in 2025, which is comparable to 2024 (no isolations), and a decrease compared to 2023 when there were 2 isolations. There were also no isolations in 2022 and 2021 (Table 9.2).

Quail

There were no isolations of *Salmonella* from quail in 2025. The last reported isolation from this category of game birds was 5 isolations in 2019.

Guinea fowl

There were no isolations from guinea fowl in 2025. The last time *Salmonella* was isolated from guinea fowl was in 2015 when there was one isolation.

Pigeons

There were 167 VIDA submissions from pigeons to APHA and SRUC in 2025 which is a 57.5% increase compared to 2024 (106 submissions) and over double the submissions received in 2023 (68 submissions).

There were 12 *Salmonella* isolations from pigeons in 2025, which is a 45.5% decrease compared to 2024 (22 isolations) and a 33.3% decrease compared to 2023 (18 isolations) (Table 9.3). Four of these isolations were from clinical disease investigations with death and weight loss being the presenting sign for one isolation, limping and blindness being the presenting sign for another isolation and no available presenting signs for the other two isolations. The other 8 isolations were from voluntary surveillance submissions. All isolations from pigeons in 2025 were *S. Typhimurium*, which is consistently the most commonly isolated serovar from pigeons. Among these, 5 isolations were ST128, 4 were ST19 and 3 were ST8937 (Table 9.6).

Table 9.1: Isolations and incidents of *Salmonella* in pheasants on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Dublin	0	0	1	1	0	0	0	0	0	0
Monophasic Typhimurium	1	1	0	0	0	0	0	0	0	0
Orion	1	1	0	0	0	0	0	0	0	0
Senftenberg	4	3	0	0	1	1	0	0	2	2
Typhimurium	1	1	0	0	1	1	0	0	1	1
Total	7	6	1	1	2	2	0	0	3	3

Table 9.2: Isolations and incidents of *Salmonella* in partridges on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Senftenberg	0	0	0	0	1	1	0	0	0	0
Typhimurium	0	0	0	0	1	1	0	0	0	0
Total	0	0	0	0	2	2	0	0	0	0

Table 9.3: Isolations and incidents of *Salmonella* in pigeons on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Braenderup	0	0	0	0	0	0	1	1	0	0
Enteritidis	1	1	0	0	0	0	0	0	0	0
Typhimurium	6	6	17	17	18	18	21	20	12	12
untypable strains	1	1	0	0	0	0	0	0	0	0
Total	8	8	17	17	18	18	22	21	12	12

Table 9.4: Sequence types of *S. Typhimurium* isolations in pheasants in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	0	0	1
No ST data	1	0	0
Total	1	0	1

Table 9.5: Sequence types of *S. Typhimurium* isolations in partridges in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	1	0	0
Total	1	0	0

Table 9.6: Sequence types of *S. Typhimurium* isolations in pigeons in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	5	3	4
128	10	15	5
8937	3	3	3
Total	18	21	12

Chapter 10: Reports of *Salmonella* in dogs

Salmonella in dogs became reportable following amendments to the Zoonoses Order in early 2021. The statutory reporting of *Salmonella* in dogs was introduced in England from 22 February 2021 and in Scotland and Wales from 21 April 2021. This 2025 annual summary therefore represents the fourth full year of receiving statutory data on *Salmonella* isolates in dogs. Prior to these amendments, *Salmonella* notifications (and isolates) in dogs were received on a voluntary basis. It is therefore advisable to consider this change when comparing data from before and after the legislation amendment. APHA continues to receive more isolates from dogs than in previous years when reporting was optional.

In January 2026, the [UK dog population was estimated to be around 15.5 million](#), with 41% of UK households owning one or more dogs. This is an increase compared to the 2024 estimate of 13.5 million. Estimates of the total dog population in Great Britain are not available, so the estimate given here is for the UK. However, the text, tables, and figures of this chapter refer to *Salmonella* in Great Britain.

There were 416 *Salmonella* isolations from dogs in 2025 (Table 10.1). This is a decrease of 13.7% compared to 2024 (482 isolations), and a decrease of 39.6% compared to 2023 (689 isolations). In total, 71 different serovars were reported (excluding untypable and rough strains), which is higher than 2024 (62 serovars) and lower than 2023 (79 serovars). The majority of isolations (413 isolations, 99.3%) arose from clinical investigations with the remainder from voluntary surveillance (3 isolations, 0.7%).

The most commonly reported serovar from dogs in 2025 was *S. Typhimurium* (61 isolations, 14.7% of all isolations). *Salmonella Typhimurium* has been the most commonly reported serovar for the past 4 years (77 isolations in 2024, 90 isolations in 2023, 116 isolations in 2022, 97 isolations in 2021). The second most commonly reported serovar was monophasic *S. Typhimurium* (32 isolations, 7.7% of all isolations). Other commonly reported serovars were *S. Infantis* (29 isolations), *S. Dublin* (29 isolations), *S. Derby* (17 isolations), *S. Indiana* (15 isolations), and *S. Enteritidis* (15 isolations) (Table 10.1, Figure 10.1.5).

Salmonella Typhimurium and monophasic *Salmonella Typhimurium*

There were 61 isolations of *S. Typhimurium* during 2025 comprising 3 different sequence types (Table 10.2). Sequence type data replaced phage type at the end of 2024. The vast majority of isolations were sequence type 19 (51 isolations, 83.6% of all *S. Typhimurium* in dogs). Other sequence types were 313 (9 isolations, 14.8% of all *S. Typhimurium* in dogs), and 34 (1 isolation, 1.6% of all *S. Typhimurium* in dogs). This compares to 2024 when the most common sequence types were 19 (60 isolations, 77.9% of all *S. Typhimurium* in

dogs), 313 (13 isolations, 16.9% of all *S. Typhimurium* in dogs), 36 (2 isolations, 2.6% of all *S. Typhimurium* in dogs), and 568 (2 isolations, 2.6% of all *S. Typhimurium* in dogs).

There were 32 isolations of monophasic *S. Typhimurium* reported from dogs during 2025 comprising 3 different sequence types. The most common sequence type was 34 (30 isolations, 93.8% of all monophasic *S. Typhimurium* in dogs) (Table 10.3).

Other notable serovars

In 2025, the number of *Salmonella* Infantis isolations from dogs was 29, a decrease from 39 isolations in 2024, 79 isolations in 2023, 109 isolations in 2022 and 51 isolations in 2021 (Table 10.1 and Figure 10.2). *Salmonella* Enteritidis was isolated 15 times from dogs in 2025, a decrease from 2024 (17 isolations). The most common sequence types of *S. Enteritidis* were 11 and 10467 (Table 10.4).

Serovars not previously reported

Isolations in 2025 which had never previously been reported in dogs from Great Britain included: *S. Alpenquai* (1 isolation), *S. Baildon* (1 isolation), *S. Choleraesuis* (1 isolation), *S. Gaminara* (1 isolation), *S. Heidelberg* (1 isolation), *S. Manhattan* (1 isolation), *S. Mapo* (3 isolations) and *S. Toulon* (1 isolation).

Public health significance

The change to make *Salmonella* in dogs reportable was made to improve the protection of public health. In 2025, *Salmonella* isolations in dogs accounted for 10.7% of *Salmonella* isolations from all animals. The most common serovars isolated included those which are important causes of human disease. *Salmonella* Typhimurium, *S. Enteritidis* and *S. Newport* were the 3 most commonly reported serovars isolated in humans in England in 2025 (see Chapter 1).

Notably, while dogs and cats may become clinically ill when infected with *Salmonella* (Morley et al., 2006), they are often asymptotically infected and can shed these bacteria (Finley et al., 2007). Therefore, while the vast majority of dog isolations this year arose from clinical investigations (99.3%), it is likely that the true public health burden of infection in this companion animal population is greater than what is captured in this report. Close contact with dogs, especially those with additional risk of exposure to *Salmonella*, may therefore represent an important source of human *Salmonella* infection via infected animals shedding the pathogen into the shared environment.

Moreover, raw meat pet food (RMPF), is known to harbour pathogens including *Salmonella*. *Salmonella* continues to be isolated from RMPF with 234 isolations in 2025 (see Chapter 12, Table 12.8b). Consistent with 2024, *S. Infantis* (14 isolations) and *S. Typhimurium* (25 isolations) were among the top 4 serovars isolated from RMPF in 2025, and overall, more than one quarter of isolations were regulated serovars (key serovars of public health importance targeted by the NCPs). Contaminated RMPF (which does not undergo any heat treatment to deactivate pathogens) may therefore represent a potential source of infection to both the dogs consuming it and people who handle it. By the same extrapolation of lacking a heat treatment step to reduce bacterial load, feeding of raw, including dried, treats should also be considered a potential risk behaviour.

Antimicrobial susceptibility in dogs

A total of 420 *Salmonella* isolates from dogs were tested against a panel of 16 antimicrobials in 2025. Susceptibility levels were 76.0%, slightly lower than in 2024 (83.5%). The proportion of MDR isolates, was 10.5%, a notable increase compared to 2024 (5.1%) and 2023 (8.3%). Most isolates classed as MDR were monophasic *S. Typhimurium*.

Resistance occurred across several serovars, most frequently monophasic *S. Typhimurium* (32 isolates), and *S. Typhimurium* (16 isolates). The most common resistances were seen in streptomycin (14.0%), sulphonamides (14.0%), tetracycline (13.1%), and ampicillin (12.9%). Five isolates were resistant to ciprofloxacin; all of these isolates were also resistant to nalidixic acid, and two of these isolates also showed resistance to cefotaxime and ceftazidime. These were the only 2 isolates showing resistance to cefotaxime and ceftazidime; both were serovar *S. Kentucky*. Twenty-six (6.2%) isolates showed resistance to nalidixic acid. In 2024, there were no isolates which showed resistance to apramycin; in 2025, 3 isolates (0.7%) showed resistance to apramycin.

Table 10.1: Isolations and incidents of *Salmonella* in dogs on all premises in Great Britain 2021 to 2025

<i>Salmonella</i> serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Aarhus	3	3	0	0	0	0	0	0	0	0
Abony	0	0	1	1	0	0	1	1	0	0
Adelaide	0	0	0	0	2	2	3	3	2	1
Agama	14	14	11	11	13	13	9	9	8	7
Agona	16	16	27	27	15	15	15	15	14	14
Ajiobo	4	4	2	2	1	1	1	1	2	2
Albany	0	0	0	0	0	0	0	0	1	1
Alpenquai	0	0	0	0	0	0	0	0	1	1
Altona	0	0	1	1	0	0	0	0	0	0
Amersfoort	1	1	0	0	0	0	0	0	0	0
Anatum	20	20	22	22	32	32	27	27	12	12
Ank	0	0	0	0	4	4	1	1	0	0
Apeyeme	0	0	0	0	1	1	0	0	0	0
Baildon	0	0	0	0	0	0	0	0	1	1
Ball	0	0	1	1	0	0	0	0	1	1
Bardo	0	0	1	1	0	0	0	0	0	0
Bareilly	1	1	1	1	1	1	0	0	2	2
Berta	2	2	1	1	3	3	3	3	0	0
Bonn	1	1	0	0	3	3	0	0	1	1
Bovismorbificans	25	25	9	9	12	12	6	6	1	1
Braenderup	0	0	0	0	0	0	0	0	9	7

Salmonella serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Brancaster	0	0	0	0	0	0	2	2	0	0
Brandenburg	11	11	10	10	4	4	2	2	2	2
Bredeney	3	3	10	10	2	2	1	1	2	2
Budapest	0	0	1	1	0	0	0	0	0	0
Cannstatt	0	0	1	1	0	0	0	0	0	0
Cerro	2	2	5	5	0	0	5	5	1	1
Chailey	0	0	0	0	0	0	1	1	0	0
Chester	0	0	0	0	1	1	0	0	2	2
Choleraesuis	0	0	0	0	0	0	0	0	1	1
Coeln	3	3	11	11	3	3	3	3	7	6
Concord	2	2	1	1	1	1	2	2	1	1
Corvallis	0	0	0	0	1	1	0	0	0	0
Cotham	0	0	0	0	1	1	0	0	0	0
Cubana	1	1	0	0	0	0	0	0	0	0
Derby	26	26	55	55	37	36	19	19	17	15
Dublin	61	61	55	54	35	35	17	17	29	26
Durham	1	1	1	1	0	0	0	0	0	0
Ealing	3	3	8	8	1	1	0	0	0	0
Eboko	1	1	0	0	1	1	0	0	1	1
Enteritidis	26	26	15	15	26	26	17	17	15	13
Fluntern	0	0	1	1	0	0	0	0	0	0
Fresno	0	0	0	0	0	0	1	1	0	0
Fulica	0	0	1	1	1	1	2	2	2	2
Gaminara	0	0	0	0	0	0	0	0	1	1

Salmonella serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Give	4	4	0	0	6	6	4	4	4	4
Give var 15+	0	0	3	3	0	0	0	0	0	0
Goelzau	0	0	0	0	1	1	0	0	0	0
Goldcoast	9	9	2	2	3	3	1	1	0	0
Gueuletapee	0	0	1	1	1	1	0	0	0	0
Hadar	8	8	5	5	2	2	2	2	4	4
Haifa	0	0	2	2	0	0	0	0	0	0
Havana	1	1	3	3	3	3	1	1	0	0
Heidelberg	0	0	0	0	0	0	0	0	1	1
Hessarek	2	2	1	1	3	3	1	1	0	0
Hvittingfoss	0	0	0	0	1	1	0	0	0	0
Idikan (incl. monophasic variants)	0	0	0	0	4	4	0	0	1	1
Indiana	13	13	20	20	7	7	21	20	15	14
Infantis	51	51	109	107	79	78	39	38	29	27
Isangi	1	1	2	2	0	0	0	0	0	0
Javiana	2	2	1	1	1	1	2	2	0	0
Johannesburg	0	0	0	0	0	0	0	0	1	1
Kapemba	0	0	1	1	1	1	0	0	2	2
Kedougou (incl. monophasic variants)	8	8	1	1	9	9	2	2	2	2
Kentucky	0	0	8	8	4	4	17	15	4	4

Salmonella serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Kingston	4	4	1	1	2	2	1	1	2	1
Kisarawe	0	0	20	20	0	0	0	0	0	0
Kottbus	11	11	0	0	12	12	13	12	13	11
Leeuwarden	0	0	0	0	0	0	1	1	0	0
Litchfield	0	0	1	1	0	0	0	0	0	0
Liverpool	0	0	1	1	0	0	1	1	4	4
Livingstone	12	12	14	14	19	19	12	12	8	7
Lome	0	0	0	0	1	1	0	0	0	0
Lomita	1	1	0	0	0	0	0	0	0	0
London	7	7	13	13	5	5	8	8	1	1
Manhattan	0	0	0	0	0	0	0	0	1	1
Mapo	0	0	0	0	0	0	0	0	3	3
Matopeni	1	1	0	0	0	0	0	0	0	0
Mbandaka	7	7	11	11	30	30	7	7	14	14
Meleagridis	1	1	0	0	0	0	1	1	0	0
Miami	1	1	0	0	0	0	0	0	0	0
Mikawasima	0	0	0	0	1	1	0	0	1	1
Mishmarhaem-ek	0	0	0	0	1	1	0	0	0	0
Molade	0	0	0	0	1	1	0	0	0	0
Monophasic Typhimurium	71	71	64	64	42	42	19	19	32	32
Montevideo	17	17	27	26	35	35	10	9	4	3
Muenchen	0	0	2	2	1	1	3	3	1	1
Muenster	2	2	2	2	9	9	8	8	5	5

Salmonella serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Nagoya	0	0	0	0	1	1	0	0	0	0
Newport	43	43	52	52	25	25	30	29	12	12
Ohio	3	3	0	0	1	1	1	1	1	1
Oranienburg	1	1	4	4	4	4	0	0	0	0
Orion	3	3	1	1	3	3	0	0	0	0
Orion var 15+	0	0	0	0	1	1	0	0	0	0
Oslo	6	6	10	10	7	7	7	7	8	7
Panama	5	5	9	9	4	4	1	1	3	3
Paratyphi B var. Java	11	11	9	9	1	1	0	0	3	3
Pomona	1	1	0	0	0	0	0	0	0	0
Poona	0	0	0	0	1	1	1	1	0	0
Putten	1	1	0	0	0	0	0	0	0	0
Reading	1	1	1	1	0	0	2	2	1	1
Rissen	10	9	6	6	3	3	1	1	2	2
Saintpaul	0	0	1	1	1	1	0	0	1	1
Saphra	1	1	0	0	0	0	0	0	0	0
Schwarzengrund	2	2	1	1	1	1	1	1	2	2
Senftenberg	3	3	0	0	0	0	4	4	2	2
Singapore	0	0	0	0	0	0	1	1	0	0
Soerenga	3	3	1	1	0	0	0	0	1	1
Stanley	1	1	10	10	4	4	0	0	0	0
Stanleyville	4	4	0	0	1	1	12	12	10	7
Stendal	0	0	1	1	0	0	0	0	0	0

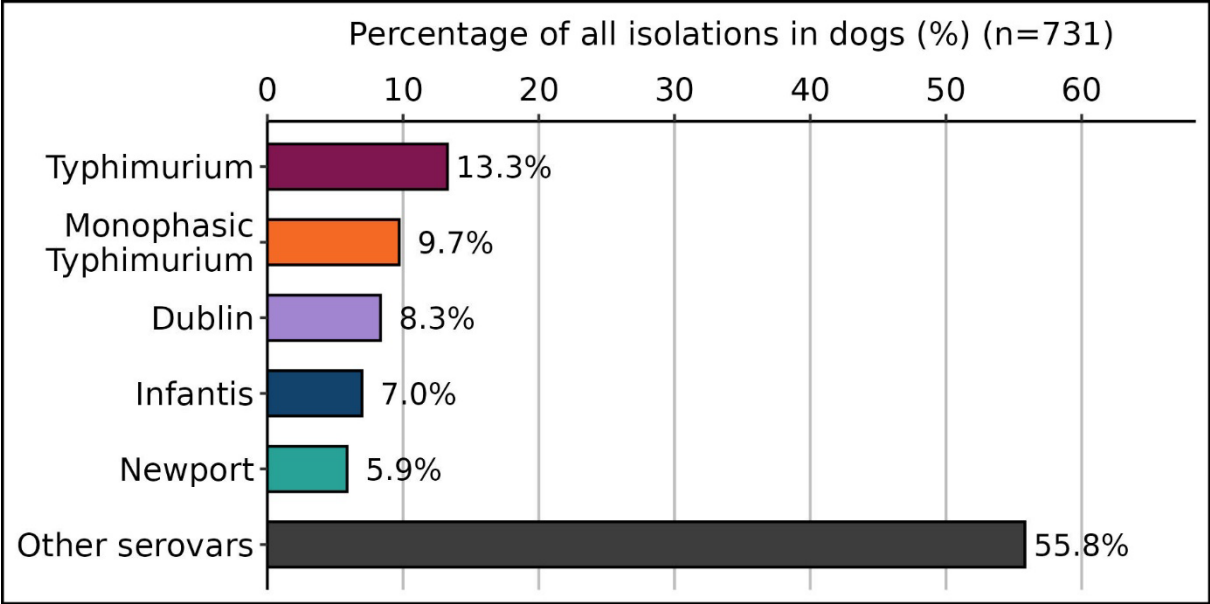
Salmonella serovar	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents	2025 isolations	2025 incidents
Stourbridge	2	2	0	0	1	1	1	1	1	1
Szentes	0	0	0	0	1	1	0	0	0	0
Tennessee	1	1	1	1	0	0	2	2	3	3
Thompson	1	1	0	0	22	20	10	10	3	3
Toulon	0	0	0	0	0	0	0	0	1	1
Typhimurium	97	87	116	116	90	90	77	77	61	60
Uganda	7	7	3	3	1	1	1	1	1	1
Utah	0	0	0	0	1	1	0	0	0	0
Virchow	7	7	3	3	1	1	0	0	1	1
Wangata	1	1	0	0	0	0	0	0	0	0
Yoruba	0	0	0	0	3	3	0	0	1	1
4,5,12:b:-	5	5	2	2	1	1	2	2	1	1
6,7:-:-	17	17	23	23	1	1	0	0	0	0
6,8:-:-	3	3	0	0	2	2	2	2	0	0
61:k:1,5,(7)	0	0	8	7	3	3	1	1	3	3
untypable strains	22	22	19	19	18	18	13	12	6	6
rough strains	8	8	8	8	1	1	0	0	0	0
Total	731	720	857	852	689	685	482	474	416	391

All serovars are *Salmonella enterica* subspecies *enterica*, with the exception of isolates of 61:k:1,5,(7), which are variants of *Salmonella enterica* subspecies *diarizonae*.

Reporting of *Salmonella* in dogs became statutory in early 2021, so not a full year of mandatory reporting that year. In 2020 and earlier reporting was voluntary.

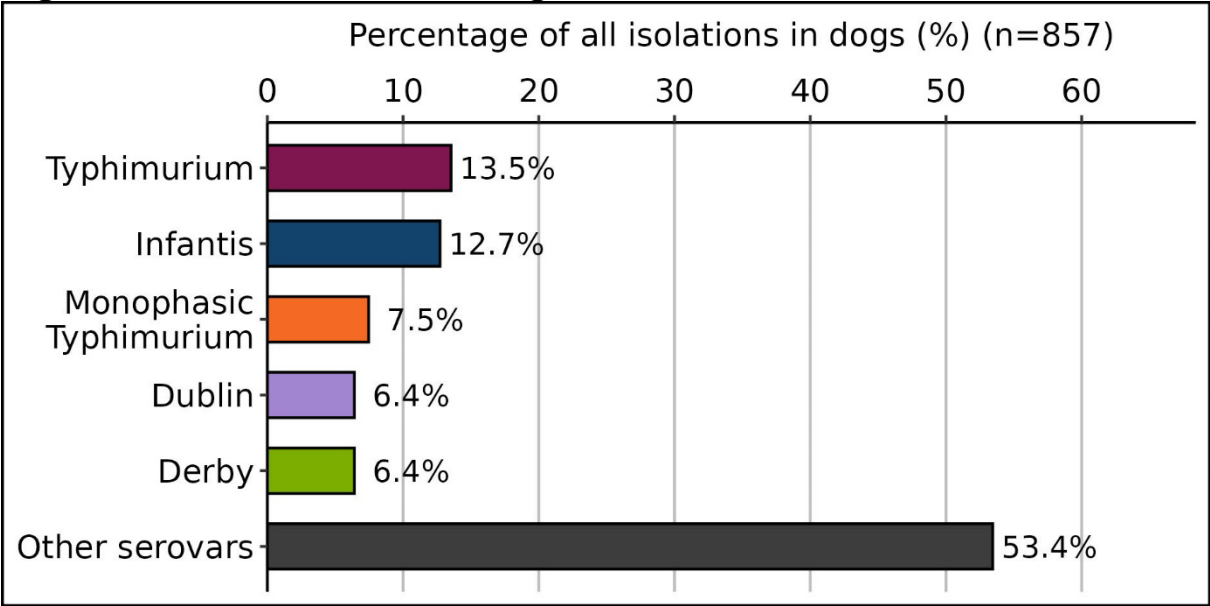
Figure 10.1: Isolations of the most common *Salmonella* serovars in dogs in Great Britain 2021 to 2025

Figure 10.1.1: Isolations in dogs in 2021



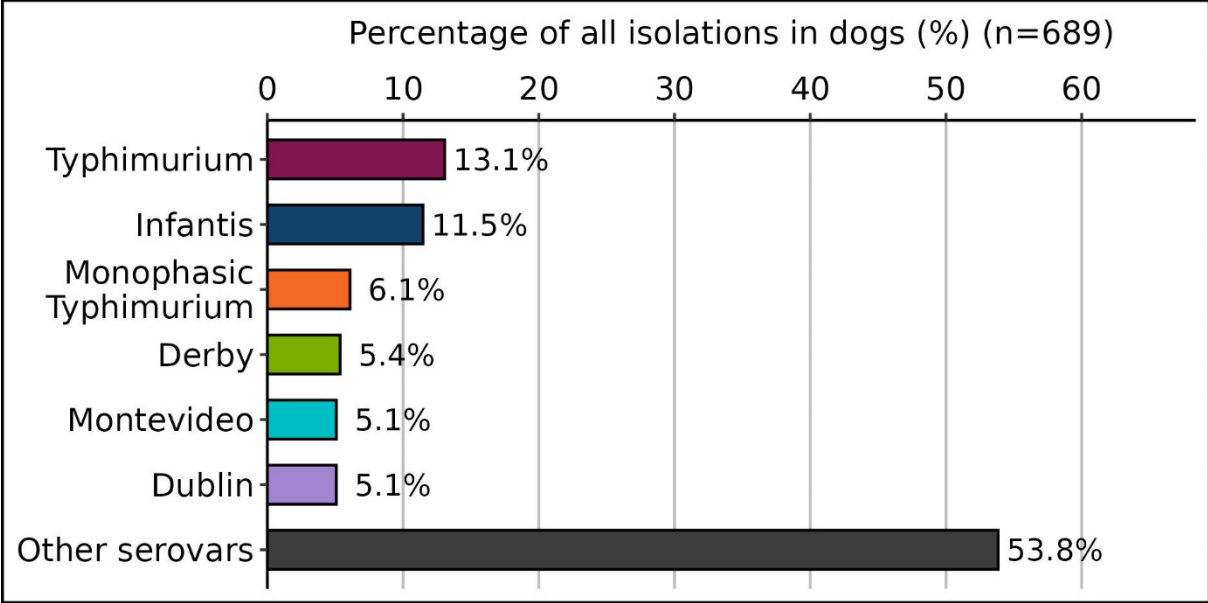
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in dogs in 2021. The most common *Salmonella* serovar in dogs in 2021 was *S.* Typhimurium, accounting for 13.3% of total isolations, followed by monophasic *S.* Typhimurium (9.7%), *S.* Dublin (8.3%) and *S.* Infantis (7.0%).

Figure 10.1.2: Isolations in dogs in 2022



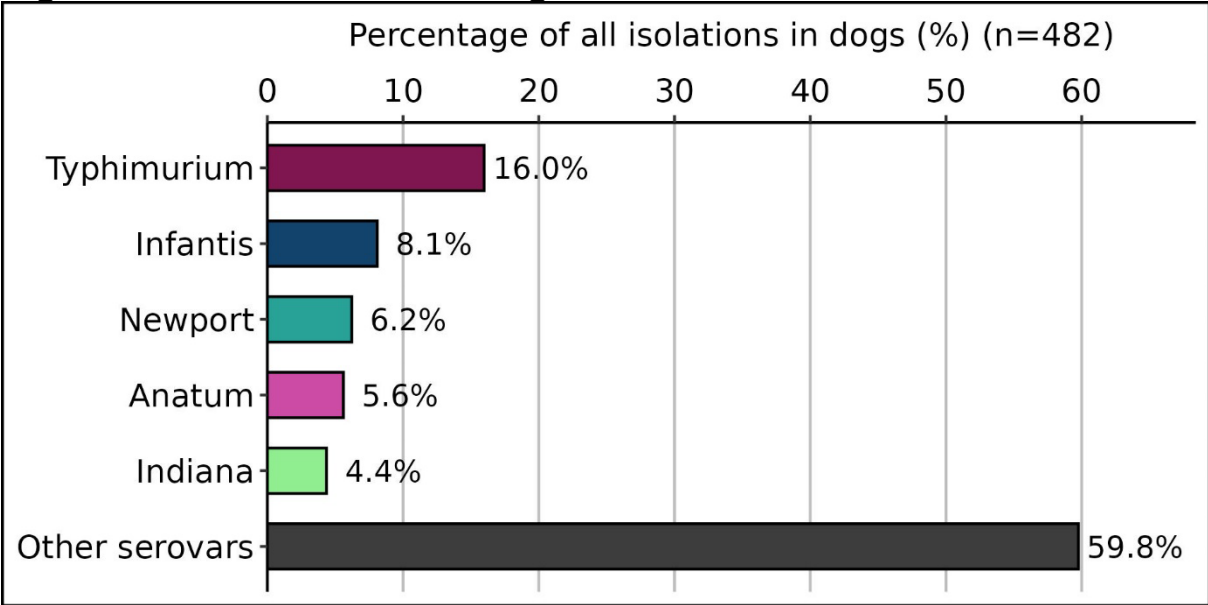
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in dogs in 2022. The most common *Salmonella* serovar in dogs in 2022 was *S.* Typhimurium, accounting for 13.5% of total isolations, followed by *S.* Infantis (12.7%), monophasic *S.* Typhimurium (7.5%), *S.* Derby (6.4%) and *S.* Dublin (6.4%).

Figure 10.1.3: Isolations in dogs in 2023



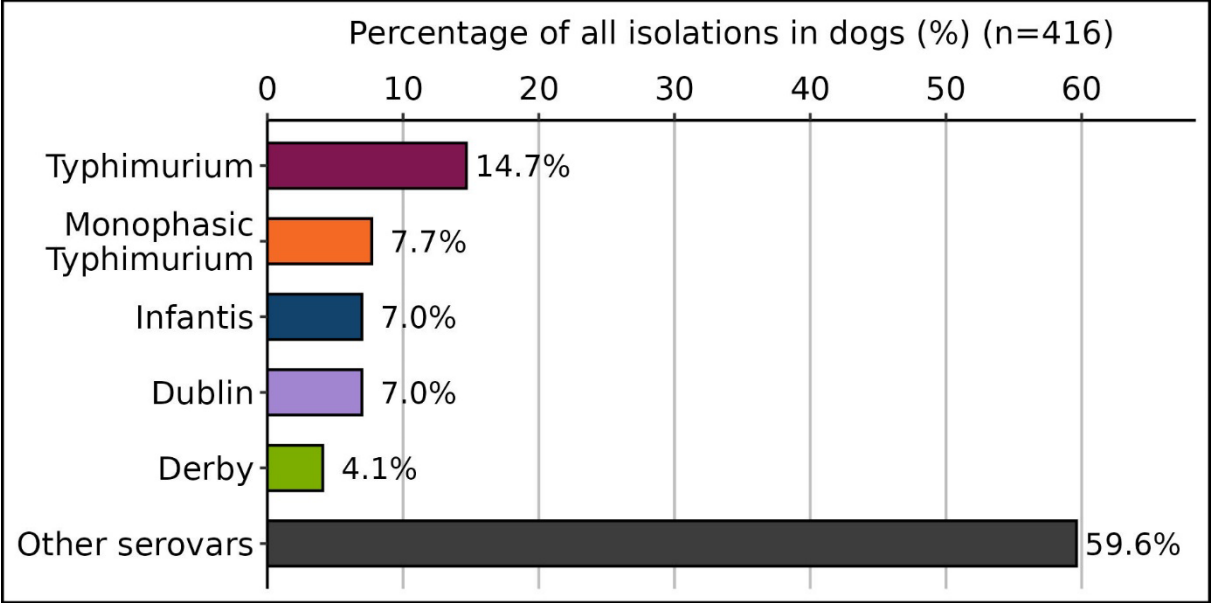
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in dogs in 2023. The most common *Salmonella* serovar in dogs in 2023 was *S.* Typhimurium, accounting for 13.1% of total isolations, followed by *S.* Infantis (11.5%), monophasic *S.* Typhimurium (6.1%), *S.* Derby (5.4%), *S.* Dublin (5.1%) and *S.* Montevideo (5.1%).

Figure 10.1.4: Isolations in dogs in 2024



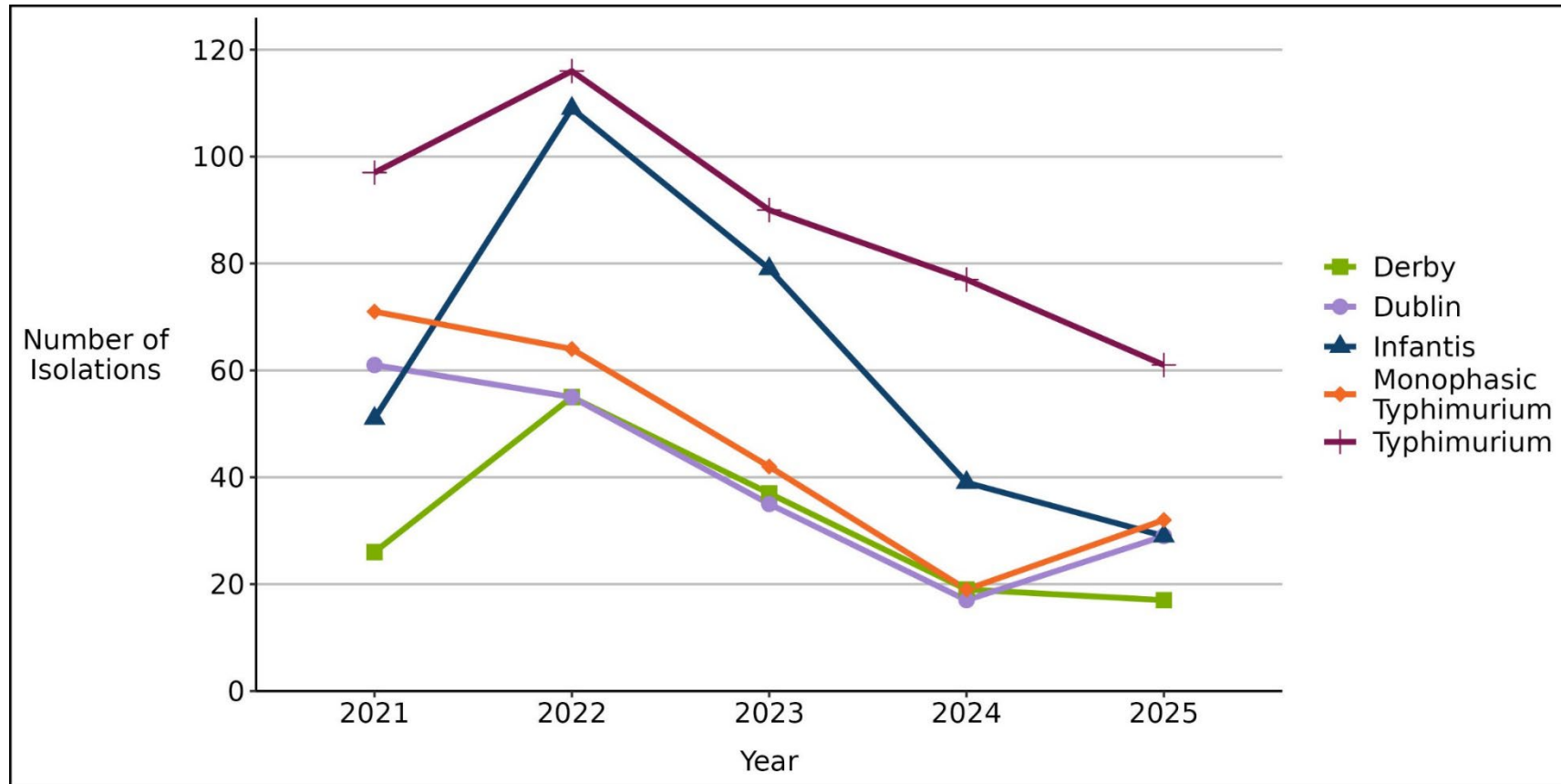
Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in dogs in 2024. The most common *Salmonella* serovar in dogs in 2024 was *S. Typhimurium*, accounting for 16.0% of total isolations, followed by *S. Infantis* (8.1%), *S. Newport* (6.2%) and *S. Anatum* (5.6%).

Figure 10.1.5: Isolations in dogs in 2025



Horizontal bar graph showing the percentage of isolations belonging to the top *Salmonella* serovars in dogs in 2025. The most common *Salmonella* serovar in dogs in 2025 was *S. Typhimurium*, accounting for 14.7% of total isolations, followed by monophasic *S. Typhimurium* (7.7%), *S. Infantis* (7.0%) and *S. Dublin* (7.0%).

Figure 10.2: The 5 most common *Salmonella* serovars in dogs in Great Britain in 2025 and their trends over time since 2021



A line graph showing the 5 most common serovars in dogs from 2021 to 2025. Isolations of the 5 most common serovars in 2025 peaked in 2022, with overall decreases in all 5 serovars since then. *S. Typhimurium* was the most common serovar in 2025 (61 isolations), followed by monophasic *S. Typhimurium* (32 isolations), *S. Infantis* and *S. Dublin* (29 isolations in each) and *S. Derby* (17 isolations).

Table 10.2: Sequence types of *S. Typhimurium* isolations in dogs in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	76	60	51
34	0	0	1
36	0	2	0
313	8	13	9
568	2	2	0
8937	1	0	0
No ST data	3	0	0
Total	90	77	61

Table 10.3: Sequence types of monophasic *S. Typhimurium* isolations in dogs in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
19	3	0	1
34	38	19	30
36	0	0	1
3430	1	0	0
Total	42	19	32

Table 10.4: Sequence types of *S. Enteritidis* isolations in dogs in Great Britain 2023 to 2025

Sequence Type	2023 isolations	2024 isolations	2025 isolations
11	8	4	7
183	11	7	2
6005	1	0	0
6086	0	1	0
8353	0	0	1
8943	1	1	1
10467	5	4	4
Total	26	17	15

Chapter 11: Reports of *Salmonella* in wildlife

The APHA is the reference laboratory for *Salmonella* isolation and serotyping. There is a [legal requirement to report suspected *Salmonella*](#) detection in species covered by the Zoonoses Order. The Zoonoses Order does not include wildlife, however APHA encourages voluntary reporting. There is no routine monitoring for *Salmonella* in wild birds or wild mammals. Therefore, isolates are typically from clinical cases and investigations, although *Salmonella* may often not be the primary cause of disease. There were 17 cases of *Salmonella* detected in wildlife in Great Britain during 2025.

Wild mammals

Hedgehogs

Salmonella Enteritidis was reported in 5 European hedgehogs (*Erinaceus europaeus*) and *Salmonella* Typhimurium was reported in 2 European hedgehogs.

S. Enteritidis Sequence Type (ST)183 was isolated from 4 hedgehogs and ST3750 was isolated from one hedgehog. One juvenile hedgehog admitted to a rescue centre presented with dehydration and hypothermia and died despite supportive treatment. Post-mortem examination (PME) at Starcross Veterinary Investigation Centre (VIC) revealed liquid intestinal contents and markedly enlarged mesenteric lymph nodes, consistent with enteritis. Bacterial culture of intestinal contents and lymph nodes confirmed *S. Enteritidis* ST183. Histopathology supported a diagnosis of salmonellosis. A heavy burden of *Capillaria* spp. eggs was also detected, suggesting that endoparasitism may have contributed to its death.

Three cases involved immature male hedgehogs sampled at different rescue centres, in which *S. Enteritidis* ST183 was isolated from two and ST3750 was isolated from one hedgehog. No further clinical or pathological data is available for these hedgehogs. *Salmonella* infection, including *S. Enteritidis*, has previously been reported in free-living hedgehogs from Great Britain and continental Europe (Keymer and others, 1991; Krawczyk and others, 2015; Lawson and others, 2018; Nauerby and others, 2000). Notably, *S. Enteritidis* ST183 was identified in 27% of hedgehog carcasses (n=170 carcasses) and 3% of faecal samples (n=208) during a national surveillance programme conducted between August 2012 and December 2015 (Lawson and others, 2018). However, there is a lack of published literature on *S. Enteritidis* ST3750 in hedgehogs so its detection may represent a sporadic infection or exposure from an unknown environmental source.

Salmonella Typhimurium ST19 was isolated from 2 hedgehogs sampled at different rescue centres. No further clinical or pathological data is available for these hedgehogs. A study to

characterise *Salmonella* spp. isolates from faecal samples taken from European Hedgehogs held in wildlife rehabilitation centres in Italy, identified *S. Typhimurium* (36.7%) being the second most prevalent.

Otters

Salmonella Typhimurium was isolated from a pooled sample from 2 otters submitted to Carmarthen VIC that had died due to severe trauma caused by road traffic accidents. Faecal samples were taken for surveillance purposes that led to the isolation of *S. Typhimurium*. *Salmonella* spp. isolates have been obtained from different otter species at rehabilitation centres and in the wild: infection may be subclinical or are sometimes associated with serious illnesses, such as enterotoxemia (Kimber and Kollias, 2000) and renal tubular necrosis (Hoover and Tyler, 1986). For wild Eurasian otters (*Lutra lutra*), several *Salmonella* spp. have been isolated from their faecal samples in Portugal that were resistant to multiple antimicrobials (Oliveira and others, 2010) suggestive of environmental exposure.

Badgers

S. Typhimurium ST36 was isolated from 2 badgers (*Meles meles*) sampled at a single rescue centre and sent to Starcross VIC. No further clinical or pathological data is available for these badgers. A passive surveillance study of wildlife in north-west Italy conducted between 2002 and 2010 showed that *S. Typhimurium* was the most identified serotype in badgers (Botti and others, 2013).

Wild birds

Gulls

S. Typhimurium was identified in a Herring gull (*Larus argentatus*) and a Lesser Black-backed gull (*Larus fuscus*) from samples submitted to Penrith and Bury St Edmunds VICs respectively.

In one case *S. Typhimurium* ST19 was isolated from lung tissue of an immature Herring gull that had died from aspergillosis-related lung lesions. *S. Typhimurium* ST19 was also isolated from a lung sample for bacterial culture submitted to Penrith. Gulls are known carriers of a wide range of *Salmonella* serotypes, including those found in humans (including *S. Typhimurium*). Exposure is often linked to feeding at coastal untreated sewage outfalls (Butterfield and others, 1983).

Buzzard

Salmonella Arizonae was isolated from the alimentary tract of an adult female buzzard (*Buteo buteo*) submitted to SRUC Veterinary Services. PME found a swollen spleen suggestive of an infectious condition and faecal staining around the vent led to suspicion of

enteric disease and systemic infection. Enteric salmonellosis due to an infection with *S. Arizonae* serotype 50:z₁₀:z was considered likely to have contributed to the death of this bird.

Corvid species

Salmonella Hessarek ST5723 was isolated from carcasses of corvid species submitted to Bury St Edmunds VIC from four separate mortality incidents between February and August 2025. Two mortality incidents in February and July involved small numbers of rooks (*Corvus frugilegus*). Hepatopathy was found at PME in both submissions. Histopathology from the July submission demonstrated bacteraemia affecting the liver, kidneys, and pancreas. In August there were two larger mass mortality incidents of corvids involving rooks, carrion crows (*Corvus corone*) and jackdaws (*Coloeus monedula*). Although severe autolysis of multiple carcasses limited the examination to only one carcass from one submission, multiple carcasses (crows and jackdaw) from the other were found to have a necrotising myositis, pneumonia, hepatitis, and thrombosis consistent with septicaemia. *S. Hessarek* was cultured from lung and liver tissues.

Salmonella Hessarek is a recognised cause of sporadic mortality events in wild birds across the UK and continental Europe, having been reported in species such as song thrushes (*Turdus philomelos*), common starlings (*Sturnus vulgaris*) and great spotted woodpeckers (*Dendrocopos major*) (Dakman and others, 2017 Velarde and others, 2012, Wilkinson and others, 2019). The reservoir or source of *S. Hessarek* infection in wild birds remains unknown and associated lesions can vary (Wilkinson and others, 2019). These findings further highlight its pathogenic potential in wild avian populations, though it should be noted that further examination and differential testing was limited in these investigations.

Table 11.1: Isolations of *Salmonella* in wild mammals in Great Britain 2021 to 2025

Species	<i>Salmonella</i> Serovar	2021	2022	2023	2024	2025
Badger	Agama	1	0	1	0	0
Badger	Anatum	0	0	1	0	0
Badger	Berta	0	0	1	0	0
Badger	Eboko	0	0	0	1	0
Badger	Newport	1	0	1	0	0
Badger	Typhimurium	0	0	0	0	2
Badger	4,5,12:b:-	0	0	0	1	0
Fox	Typhimurium	0	0	0	1	0
Hedgehog	Enteritidis	11	1	2	6	5
Hedgehog	Typhimurium	0	0	0	0	2
Otter	Typhimurium	0	0	0	0	1
Porpoise	4,12:-:-	0	1	0	0	0
Porpoise	4,12:a:-	0	0	0	1	0
Seal	Typhimurium	0	0	0	1	0
Squirrel	Typhimurium	0	0	1	0	0
Total	Not applicable	13	2	7	11	10

Table 11.2: Isolations of *Salmonella* in wild birds in Great Britain 2021 to 2025

Species	<i>Salmonella</i> Serovar	2021	2022	2023	2024	2025
Buzzard	Typhimurium	0	0	1	0	0
Buzzard	50:Z ₁₀ :Z	0	0	0	0	1
Finch	Typhimurium	2	0	0	0	0
Gull	Typhimurium	0	0	1	3	2
Heron	Typhimurium	1	0	0	0	0
Jackdaw	Hessarek	0	0	0	0	1
Mixed species	Typhimurium	1	0	0	0	0
Rook	Hessarek	0	0	0	0	3
Swan	Typhimurium	2	0	0	0	0
Total	Not applicable	6	0	2	3	7

Chapter 12: *Salmonella* in animal feeding stuffs and products tested under ABPR

From 2020 onwards, the total number of samples of animal feeding stuffs and ingredients tested by private laboratories was no longer recorded centrally. It is therefore not possible to compare the number of tests carried out since 2020 with previous years. Due to the absence of denominator data, care should be taken when interpreting trends in these data.

There were 798 isolations of *Salmonella* from animal feeding stuffs and products associated with the [Animal By-Products Regulations](#) (ABPR) in 2025 (Table 12.7), including 60 isolations from compound feeds (Tables 12.3 to 12.6), 178 from feed ingredients (Table 12.8a) and 560 from other products associated with testing under ABPR (Table 12.8b). Total isolations increased by 0.4% compared with 2024 (795 isolations) and decreased by 11.0% compared with 2023 (897 isolations).

The number of regulated serovars (those considered by the retained EU legislation as having particular public health significance and targeted in the NCPs) isolated from animal feeding stuffs and products tested under the ABPR decreased by 27.9% in 2025 compared with 2024 (137 isolations versus 190 isolations) and by 48.3% compared with 2023 (265 isolations) (Table 12.1). In 2025, these comprised 56 isolations of *S. Infantis*, 46 isolations of *S. Typhimurium*, 17 isolations of monophasic *S. Typhimurium*, 11 isolations of *S. Enteritidis*, 5 isolations of *S. Hadar*, and 2 isolations of *S. Virchow*. See Tables 12.1 and 12.2 for further details.

Isolations from compound animal feed

Details of *Salmonella* isolations reported from compound ruminant, pig and poultry feed are given in Tables 12.3, 12.4 and 12.5 respectively. *Salmonella* was also isolated from compound feeds intended for feeding other species, including dogs, cats, mixed avian species and unspecified. Details of these isolations are given in Table 12.6.

There were no isolations of *Salmonella* from compound ruminant feed during 2025, remaining unchanged from 2024 (no isolations) and a decrease from 2023 (8 isolations).

There were no isolations of *Salmonella* from compound pig feed during 2025, which continues the declining trend from 14 isolations in 2022, one isolation in 2023, and no isolations in 2024.

There were 4 isolations from compound poultry feed during 2025, a 75.0% decrease compared to 2024 (16 isolations) and a 55.6% decrease compared to 2023 (9 isolations) (Table 12.5). Four different serovars were reported – *S. Amager*, *S. Anatum*, *S. Idikan* (including monophasic variants), and *S. Oslo* (one isolation each, each accounting for

25.0% of total isolations). A comparison of the serovars recorded from compound poultry feed and the most common serovars found in chicken and turkey flocks tested under the NCP in 2025 is shown in Figure 12.6. *Salmonella* Idikan (including monophasic variant S. 13,23:i:-) was the most commonly isolated *Salmonella* serovar in broiler chicken flocks in 2025, accounting for 41.2% of total broiler flocks. This serovar was also isolated from chicken breeder flocks and has in recent years been predominantly comprised of the monophasic variant S. 13,23:i:, which has been shown to be associated with low level contamination of poultry feed mills. There were no isolations of S. Poona or S. Falkensee in poultry in 2025. There is a more direct relationship between feed contaminants and poultry isolates than for other livestock species, for which animal movements and environmental exposures are considered the predominant ongoing sources. However, feed may also be a means of the initial movement of a *Salmonella* strain into an animal breeding pyramid. The voluntary and statutory monitoring programmes for poultry, unlike in the case of other animal species, will also detect subclinical infection, which accounts for the majority of poultry submissions.

Isolations from feeding stuff ingredients

During 2025, there was a total of 178 *Salmonella* isolations arising from 13 different feeding stuff ingredient types (Table 12.8a). The number of *Salmonella* isolations have increased by 223% compared to 2024 (55 isolations) and have increased by 305% since 2023 (44 isolations). This increase was primarily driven by an increase in isolations from poultry meal. *Salmonella* was most commonly isolated from poultry meal (139 isolations), followed by soya (11 isolations), pork meal (8 isolations), rapeseed (5 isolations), fishmeal and stow malt (3 isolations each), feather meal and wheat (2 isolations each), and antler powder, barley, oilseeds, palm kernel, and plant material (one isolation each).

There were 139 isolations from poultry meal in 2025, compared to no isolations during 2024 and 2023. In 2025, there were 8 isolations from pork meal compared to no isolations during 2024 and 2023. Isolations from stow malt increased from no isolations in 2024 and 2023, to 3 isolations in 2025. Isolations of soya and wheat have remained largely constant since 2023. *Salmonella* isolations from oilseeds in 2025 decreased by 90.9% compared to 2024 (one versus 11 in 2024) and by 50.0% compared to 2023 (2 isolations). There were 5 isolations from rapeseed in 2025, a 68.8% reduction compared to 2024 (16 isolations), but a 25.0% increase compared to 2023 (4 isolations). There were no isolations of feed additives, guar protein, maize, and soya bean meal in 2025. There have been no isolations of separated fibre since 2023. Data provision with submissions has allowed greater discrimination of sample source. this has influenced the relative numbers of isolates from identified sources rather than 'raw other' as reported in previous editions.

The most commonly isolated serovars from feeding stuff ingredients during 2025 were S. Montevideo (67 isolations), S. Infantis (31 isolations), S. Havana (17 isolations), and S.

Senftenberg (15 isolations) (Table 12.8a). During 2025, *S. Montevideo* was isolated from poultry meal (65 isolations) and feather meal (2 isolations). In contrast, in 2024 there were 6 isolations of *S. Montevideo* from fish meal, and 3 isolations in 2023 (2 from fish meal and 1 from mixed vegetables). During 2025, *S. Infantis* was isolated from poultry meal (31 isolations). This contrasts to one isolation of this serovar from soya bean meal in 2024, and 2 isolations in 2023 from feed additive and oilseeds (one isolation each). All 17 isolations of *S. Havana* were from poultry meal. This serovar was not isolated from feeding stuff ingredients during 2024 or 2023. During 2025, *S. Senftenberg* was isolated from poultry meal (10 isolations), soya and pork meal (2 isolations each), and fish meal (one isolation). In 2024, *S. Senftenberg* was isolated from soya (3 isolations) and oilseeds (one isolation), and from soya and palm kernel during 2023 (one isolation each) (Table 12.8a).

Isolations from products associated with ABPR

During 2025, there were 560 *Salmonella* isolations arising from 10 different product types tested under ABPR plus feed mill environments in Great Britain (Table 12.8b). This is a 16.5% decrease in the number of isolations from 2024 (671 isolations) and a 26.2% decrease compared to 2023 (759 isolations). The highest number of isolations was from raw meat pet food (234 isolations), followed by feed mill environmental samples (177 isolations), other raw materials (46 isolations), and manure (32 isolations).

Compared with 2024, there was an increase in the number of *Salmonella* isolations from other raw materials (46 versus 15 isolations), manure (32 versus no isolations), processed animal protein (20 versus one isolation), compost (17 versus 8 isolations), blood products (9 versus one isolation), feeder chick (2 versus no isolations), and dog chews (one versus no isolations). Compared with 2024, there was a decrease in the number of isolations from raw meat pet food (234 versus 290 isolations), feed mill environment (177 versus 267 isolations), digestate (21 versus 35 isolations), and slurry (1 versus 12 isolations). (Table 12.8b).

The most commonly isolated serovars from products tested under the ABPR were *S. Kedougou* (including monophasic variants, 83 isolations), *S. Ohio* (51 isolations), *S. Typhimurium* (39 isolations), and *S. Indiana* (31 isolations) (Table 12.8b). The majority of *S. Kedougou* (including monophasic variants) isolations were from samples collected from feed mill environments (79 isolations) and are likely to indicate resident contamination within some mills. Likewise, 92.0% of *S. Ohio* isolations (47 out of 51 isolations) were from feed mill environments. *S. Indiana* isolations were predominantly from raw meat pet food (83.9%, 26 out of 31 isolations). *S. Typhimurium* isolations were from a variety of sources including 25 isolations (64.1%) from raw pet food, 10 isolations from feed mill environments (25.6%), 3 isolations from other raw materials (7.7%), and one isolation from compost (2.6%) (Table 12.8b).

Isolations from raw meat pet food

During 2025 there were 234 reports of *Salmonella* from raw meat pet food (Table 12.8b and Figure 12.7). This is 19.3% lower than during 2024 (290 isolations) and 29.3% lower than during 2023 (331 isolations). The most common serovars isolated from raw meat pet food during 2025 were *S. Indiana* (26 isolations), *S. Typhimurium* (25 isolations), *S. London* (16 isolations), and *S. Derby*, *S. Infantis* and *S. Senftenberg* (14 isolations of each) (Figure 12.7.1). Similarly, *S. Indiana*, *S. Infantis*, and *S. Typhimurium* were the three most commonly isolated serovars in 2024. In comparison, *S. Typhimurium*, monophasic *S. Typhimurium*, and *S. Infantis* and *S. Dublin* were the four most commonly isolated serovars in dogs in 2025 (Figure 12.7.2 and Chapter 10).

There were 62 isolations of regulated serovars from raw meat pet food in 2025 (Table 12.2) which was 34.7% lower than in 2024 (95 isolations) and 37.4% lower than in 2023 (99 isolations). Regulated serovars comprise *S. Enteritidis*, *S. Hadar*, *S. Infantis*, monophasic *S. Typhimurium*, *S. Typhimurium* and *S. Virchow*. These included 25 isolations of *S. Typhimurium*, 14 isolations of *S. Infantis*, 11 isolations of monophasic *S. Typhimurium*, 6 isolations of *S. Enteritidis*, 5 isolations of *S. Hadar*, and one isolation of *S. Virchow* (Table 12.2, Figure 12.2.3). The sequence types for each serovar are provided in Table 12.2.

Regulated serovars originating from raw meat pet food during 2025 accounted for 45.3% of total regulated serovars isolated from all feeding stuffs and products associated with the ABPR (Table 12.2). This is a lower proportion than during 2024 (50.0%) but a higher proportion than during 2023 (37.4% of total regulated serovars).

Testing of processed animal protein

A total of 473 batches of domestically produced processed animal protein were tested during 2025. This is a 3.1% increase compared with 2024 (459 batches) and a 46.4% increase compared with 2023 (323 batches) (Table 12.9 and Figure 12.8). Sixteen batches tested positive for *Salmonella* in 2025 (3.4%), which is double that of 2024 (8 positive batches; 1.7%) and four times that of 2023 (4 positive batches; 1.2%).

There were 20 positive *Salmonella* isolations during 2025 (4.19% of total isolations). Thirteen different serovars were isolated in 2025 including *S. Montevideo* (6 isolations), *S. Infantis* (3 isolations), *Salmonella* 4,12:d:-, *Salmonella* 4,5,12:b:- monophasic Java, *S. Agona*, *S. Anatum*, *S. Cerro*, *S. Enteritidis*, *S. Indiana*, *S. Kedougou* (including monophasic variants), *S. Livingstone*, *S. London*, and *S. Senftenberg* (one isolation each) (Table 12.10).

No batches of imported animal protein were tested during 2025, which is the same as during both 2024 and 2023. The last batches of imported animal protein testing positive for *Salmonella* were reported during 2009.

Antimicrobial susceptibility in feeds

A total of 1177 *Salmonella* isolates from feed were tested against a panel of 16 antimicrobials in 2025. Overall, 75.9% were fully susceptible, while 5.0% were classified as MDR.

The serovars with the greatest number of isolates showing resistance to at least one antimicrobial were *S. Ohio* (n=86), *S. Kedougou* (including monophasic variants) (n=58), and *S. Indiana* (n=46). However, MDR cases were mostly linked to monophasic *S. Typhimurium* (n=24) and *S. Infantis* (n=14). Resistance trends remained mostly stable compared to 2024, with patterns often involving resistance to sulphonamides (17.4%) and tetracycline (17.4%).

Nalidixic acid resistance was observed in 68 isolates, of which 4 were also resistant to ciprofloxacin (one of each *S. Albany*, *S. Agona*, *S. Infantis*, and *S. Kottbus*). These were the only 4 isolates showing ciprofloxacin resistance. Three of these isolates were resistant to ciprofloxacin, neomycin and streptomycin. There were no feed isolates showing ceftazidime resistance in 2025. One isolate (*S. Montevideo*) showed cefotaxime resistance and also had gentamicin resistance. Two MDR isolates showed apramycin resistance in 2025 (one *S. Ohio* and one monophasic *S. Typhimurium*).

Table 12.1: Regulated *Salmonella* serovars in animal feeding stuffs in Great Britain 2023 to 2025

<i>Salmonella</i> serovar	2023 Finished feed	2023 Vegetable material	2023 Misc.	2024 Finished feed	2024 Vegetable material	2024 Misc.	2025 Finished Feed	2025 Vegetable Material	2025 Misc.
Enteritidis ST10467	1	0	2	0	0	15	0	0	6
Enteritidis ST11	0	0	10	0	0	8	0	0	5
Enteritidis ST183	0	0	2	0	0	0	0	0	0
Enteritidis ST6005	0	0	1	0	0	0	0	0	0
Enteritidis ST6086	0	0	0	0	0	5	0	0	0
Enteritidis No ST data	0	0	3	0	0	0	0	0	0
Hadar ST33	1	0	11	0	0	0	0	0	5
Hadar No ST data	0	0	2	0	0	0	0	0	0
Infantis ST1032	0	0	0	0	0	0	0	0	6
Infantis ST2283	0	0	1	0	0	0	0	0	0
Infantis ST32	10	1	120	5	2	77	0	0	49
Infantis No ST data	0	0	0	0	0	0	0	0	1
Monophasic Typhimurium ST19	0	0	0	0	0	0	0	0	2
Monophasic Typhimurium ST34	2	1	25	0	0	20	2	0	13
Monophasic Typhimurium ST8486	0	0	1	0	0	0	0	0	0
Typhimurium ST19	5	10	48	1	6	46	2	3	36
Typhimurium ST34	0	0	3	0	0	1	0	0	1

<i>Salmonella</i> serovar	2023 Finished feed	2023 Vegetable material	2023 Misc.	2024 Finished feed	2024 Vegetable material	2024 Misc.	2025 Finished Feed	2025 Vegetable Material	2025 Misc.
Typhimurium ST36	0	0	0	0	0	0	0	0	1
Typhimurium ST376	0	0	2	0	0	0	0	0	0
Typhimurium ST4358	0	0	0	0	0	0	0	0	1
Typhimurium ST513	0	0	0	1	0	0	0	0	0
Typhimurium ST568	0	0	1	0	0	0	0	0	0
Typhimurium ST8937	0	0	0	1	1	0	0	1	1
Typhimurium No ST data	0	0	1	0	0	0	0	0	0
Virchow ST16	0	0	1	0	0	0	0	0	1
Virchow ST303	0	0	0	0	0	1	0	0	1
Total	19	12	234	8	9	173	4	4	129

Miscellaneous includes pet food (raw).

Table 12.2: Isolations of *Salmonella* serovars considered to be of special public health importance from products monitored in Great Britain under the Defra Codes of Practice, 2025

<i>Salmonella</i> serovar	Feeding stuff	N
Enteritidis ST10467	Other raw materials	1
Enteritidis ST10467	Pet food (raw)	4
Enteritidis ST10467	Poultry meal	1
Enteritidis ST11	Pet food (raw)	2
Enteritidis ST11	Poultry meal	2
Enteritidis ST11	Processed animal protein	1
Hadar ST33	Pet food (raw)	5
Infantis ST1032	Other raw materials	2
Infantis ST1032	Poultry meal	4
Infantis ST32	Blood products	1
Infantis ST32	Compost	1
Infantis ST32	Digestate	1
Infantis ST32	Feed mill environment	1
Infantis ST32	Manure	1
Infantis ST32	Other raw materials	1
Infantis ST32	Pet food (raw)	13
Infantis ST32	Poultry meal	27
Infantis ST32	Processed animal protein	3
Infantis No ST data	Pet food (raw)	1
Monophasic Typhimurium ST19	Pet food (raw)	2
Monophasic Typhimurium ST34	Compound unknown species feed	2
Monophasic Typhimurium ST34	Digestate	1
Monophasic Typhimurium ST34	Feed mill environment	1
Monophasic Typhimurium ST34	Other raw materials	2
Monophasic Typhimurium ST34	Pet food (raw)	9
Typhimurium ST19	Compound cat feed	1
Typhimurium ST19	Compound unknown species feed	1
Typhimurium ST19	Feed mill environment	10
Typhimurium ST19	Fish meal	1
Typhimurium ST19	Other raw materials	2
Typhimurium ST19	Pet food (raw)	23
Typhimurium ST19	Rapeseed	1
Typhimurium ST19	Soya	1

<i>Salmonella</i> serovar	Feeding stuff	N
Typhimurium ST19	Wheat	1
Typhimurium ST34	Pet food (raw)	1
Typhimurium ST36	Compost	1
Typhimurium ST4358	Pet food (raw)	1
Typhimurium ST8937	Other raw materials	1
Typhimurium ST8937	Soya	1
Virchow ST16	Pet food (raw)	1
Virchow ST303	Compost	1
Total	Not applicable	137

Figure 12.1: Number of isolations of regulated *Salmonella* serovars in animal feeding stuffs and products associated with the ABPR, 2021 to 2025

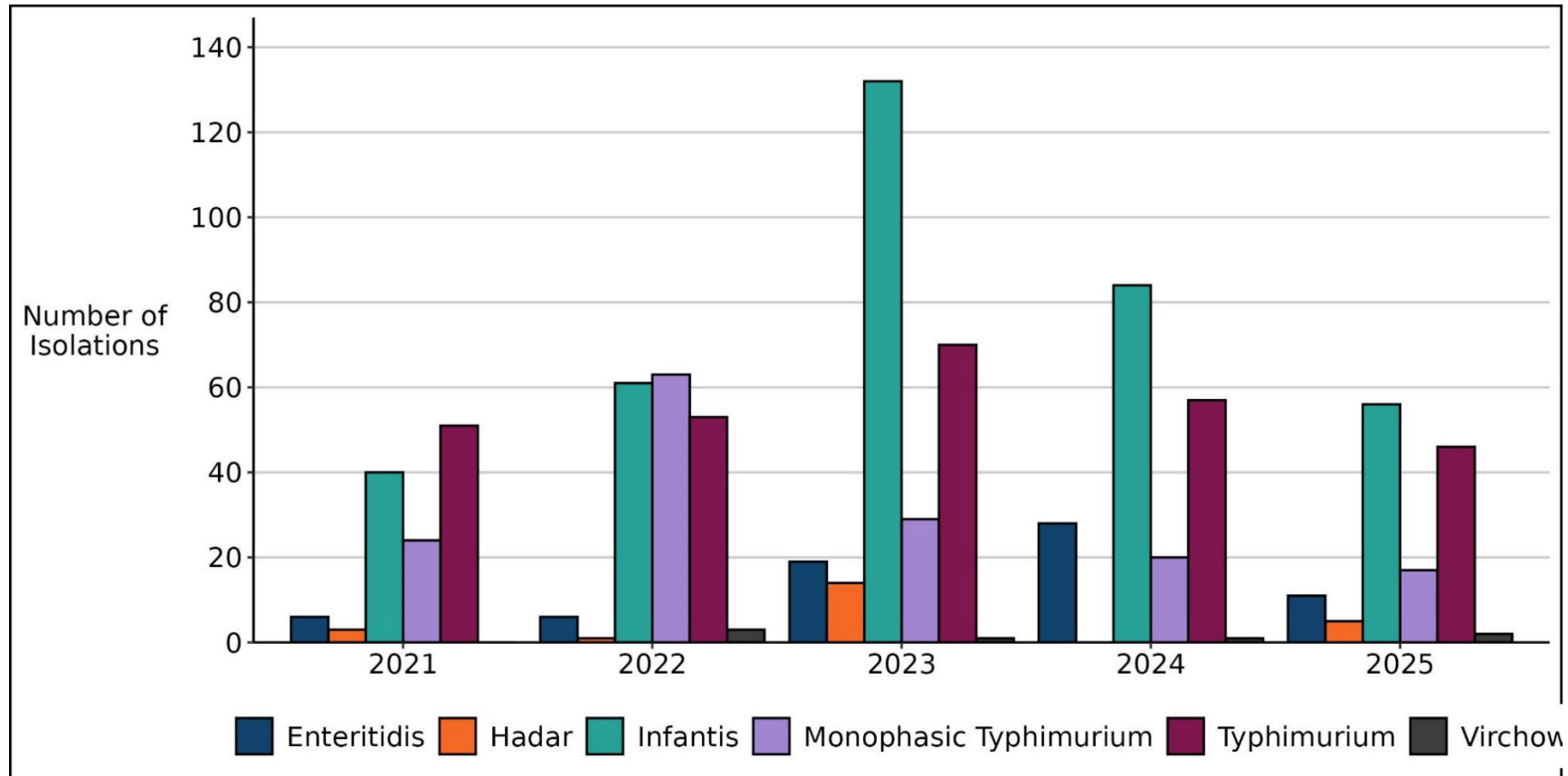
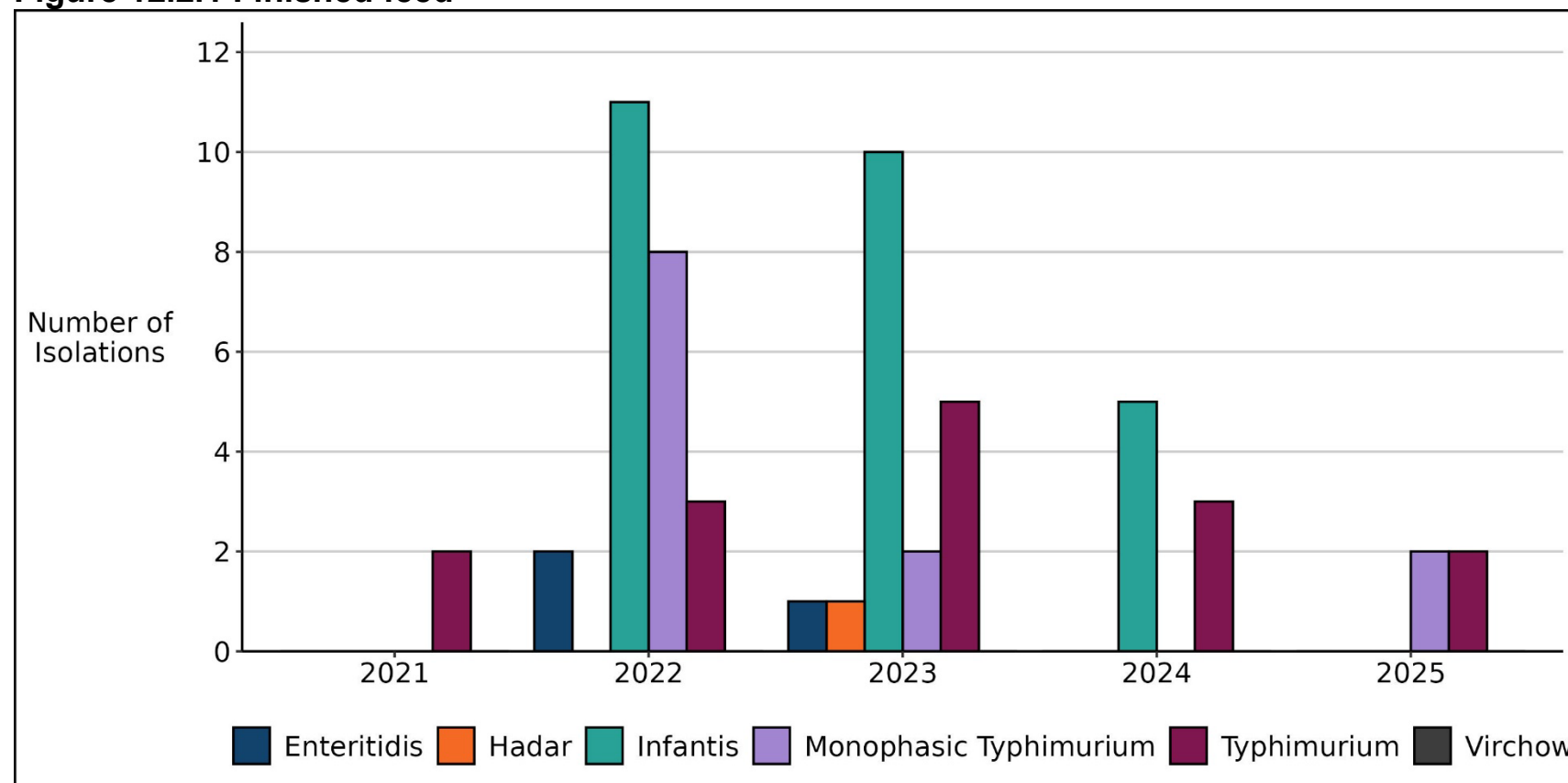


Figure 12.1 shows the number of isolations of monophasic *S. Typhimurium* have decreased since 2022. Isolations of *S. Typhimurium* have increased since 2020 from 38 to 57 isolations in 2024 but have since decreased to 46 in 2025. Isolations of *S. Infantis* have increased since 2020 from 29 isolations to 132 in 2023 but have since decreased to 56 in 2025. *S. Enteritidis* isolations have increased

since 2020 from 3 to 28 in 2024, dropping to 11 in 2025. There were 5 *S. Hadar* isolations during 2025, compared to 0 in 2024 and 14 isolations in 2023. Isolations of *S. Virchow* have remained very low in all years.

Figure 12.2: Number of isolations of regulated *Salmonella* serovars in animal feeding stuffs and products associated with the ABPR, 2021 to 2025 by type of feeding stuff

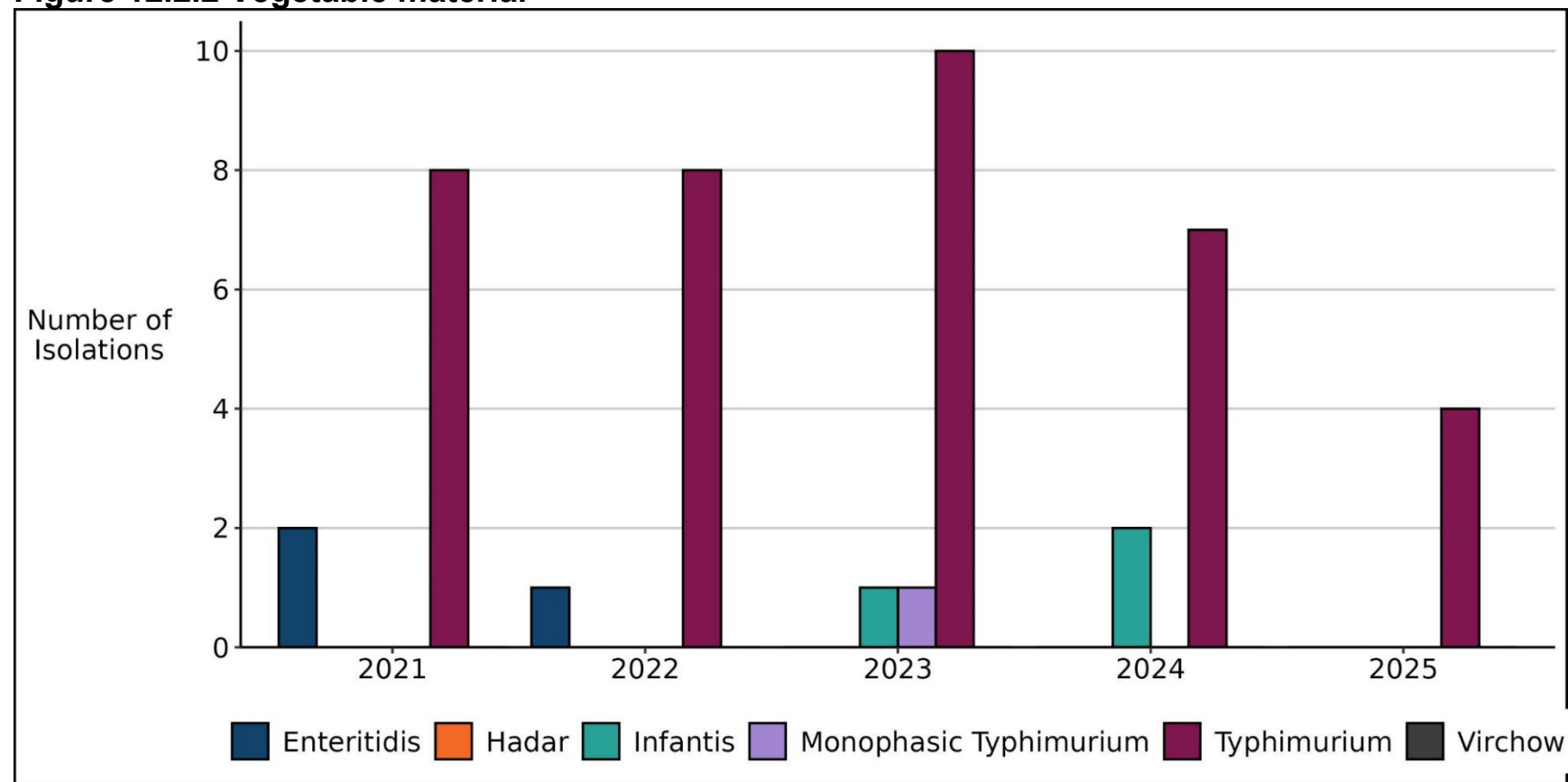
Figure 12.2.1 Finished feed



There were 4 isolations of regulated serovars from finished feed during 2025, down from 8 isolations in 2024. There were 2 isolations of monophasic *S. Typhimurium* in 2025, an increase from no isolations during 2024 but the same as in 2023. The number of isolations of

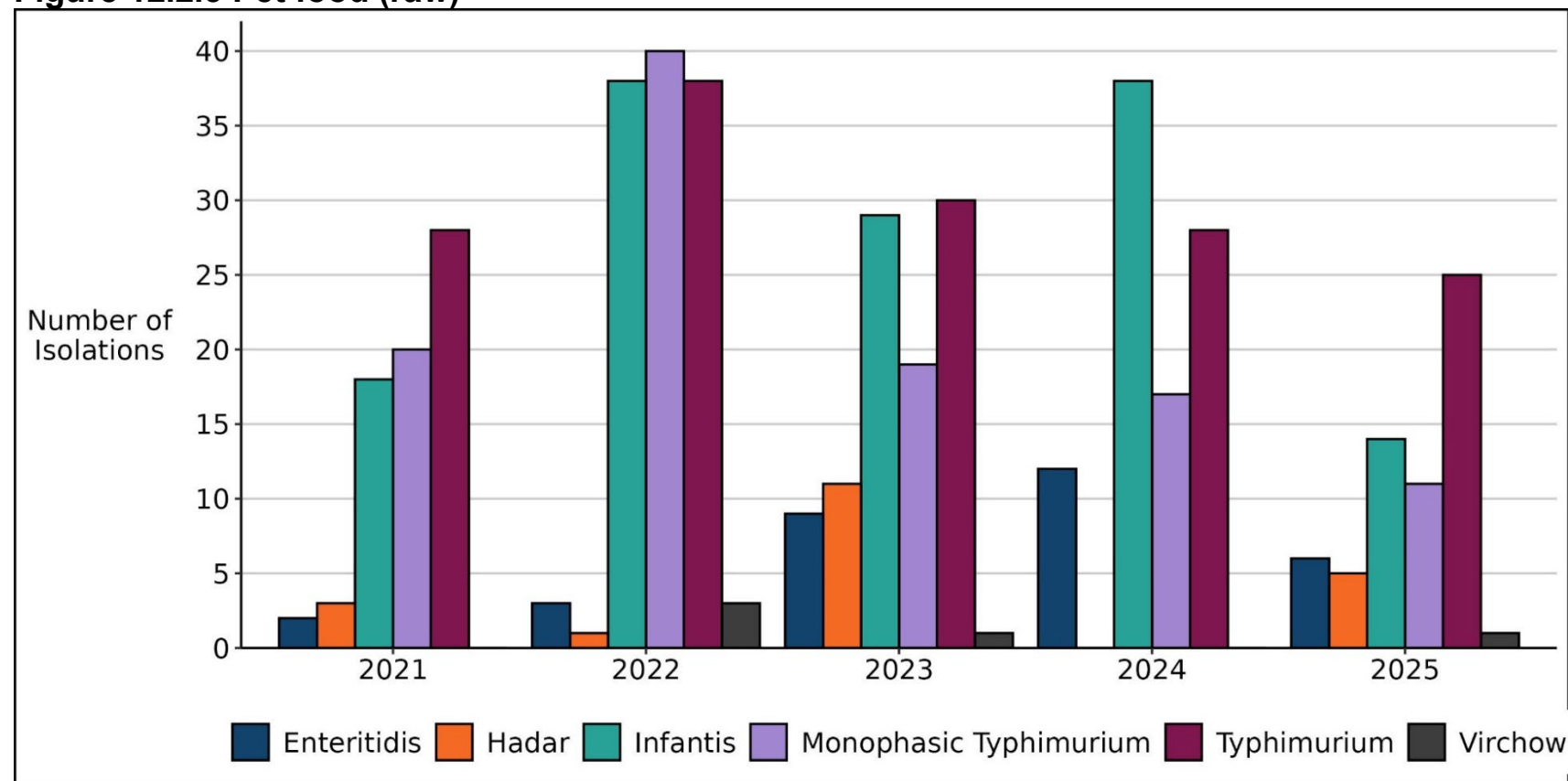
the regulated serovar *S. Typhimurium* from finished feed increased between 2019 and 2023, however isolations have followed a decreasing trend since 2023, to 2 isolations during 2025. Isolations of *S. Infantis* have continued to decrease from a peak of 11 isolations in 2022 to 5 isolations in 2024, and 0 isolations in 2025. There were no isolations of *S. Enteritidis* in 2025 or 2024 compared to 1 isolation in 2023, after being isolated for the first time in 2022. There have been no isolations of *S. Virchow* in finished feed.

Figure 12.2.2 Vegetable material



S. Infantis was isolated from vegetable material in 2020 (6 isolations), 2023 (1 isolation), and 2024 (2 isolations), but there were no isolations in 2025. *S. Enteritidis* has not been isolated from vegetable material since 2022. *S. Typhimurium* has decreased from a peak of 10 isolations in 2023 to 4 isolations in 2025. Neither *S. Hadar* nor *S. Virchow* have been isolated in vegetable material between 2020 and 2025. There were no isolations of monophasic *S. Typhimurium* in 2025 or 2024, compared to one isolation in 2023 and 2020.

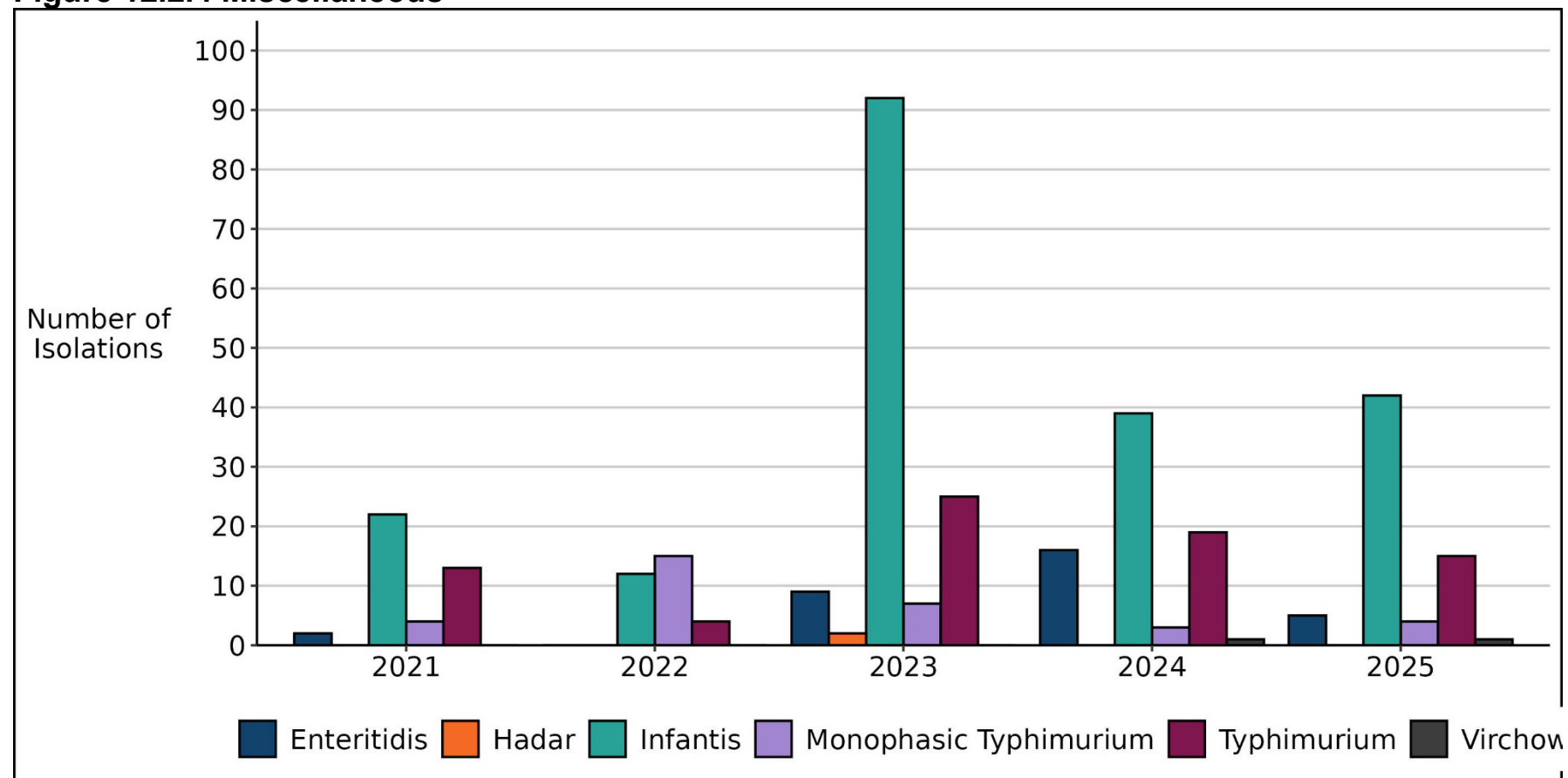
Figure 12.2.3 Pet food (raw)



S. Typhimurium, monophasic *S. Typhimurium* and *S. Infantis* have been the most frequently isolated serovars from raw pet food across all years since 2020. The numbers of all three rose steadily and peaked in 2022 but dropped in 2023. Isolations of monophasic *S. Typhimurium* and *S. Typhimurium* have continued to decline since 2022, to 11 isolations and 25 isolations respectively in 2025. Isolations of *S. Infantis* have fluctuated between 2021 and 2025, with the highest number of isolations (38 isolations) in 2022 and 2024. There were 14 isolations of *S. Infantis* in 2025. *S. Virchow* is infrequently isolated from raw pet food, with one isolation in 2025 and 2023,

and three isolations in 2022. There were 5 isolations of *S. Hadar* during 2025, an increase from no isolations during 2024. Isolations of *S. Enteritidis* were steady at less than 5 between 2020 and 2022, peaking in 2024 (12 isolations), before decreasing to 6 isolations in 2025.

Figure 12.2.4 Miscellaneous



The number of isolations of *S. Enteritidis* remained relatively stable between 2020 and 2022 with between 0 and 2 isolations per year but increased to 9 in 2023 and 16 in 2024, before decreasing to 5 isolations in 2025. Isolations of *S. Infantis* increased in miscellaneous feed stuffs from 12 in 2020 to 92 in 2023 but decreased to 39 isolations in 2024 and 41 isolations in 2025. *S. Typhimurium* isolations increased

between 2022 and 2023 (25 versus 4 in 2022) but decreased in 2024 to 18 isolations and 15 isolations in 2025. There was one isolation of *S. Virchow* in 2024 and 2025. Isolations of monophasic *S. Typhimurium* have decreased since 2023, from 7 to 4 in 2025.

Figure 12.3: Number of isolations of *Salmonella* in compound animal feeding stuffs, 2021 to 2025

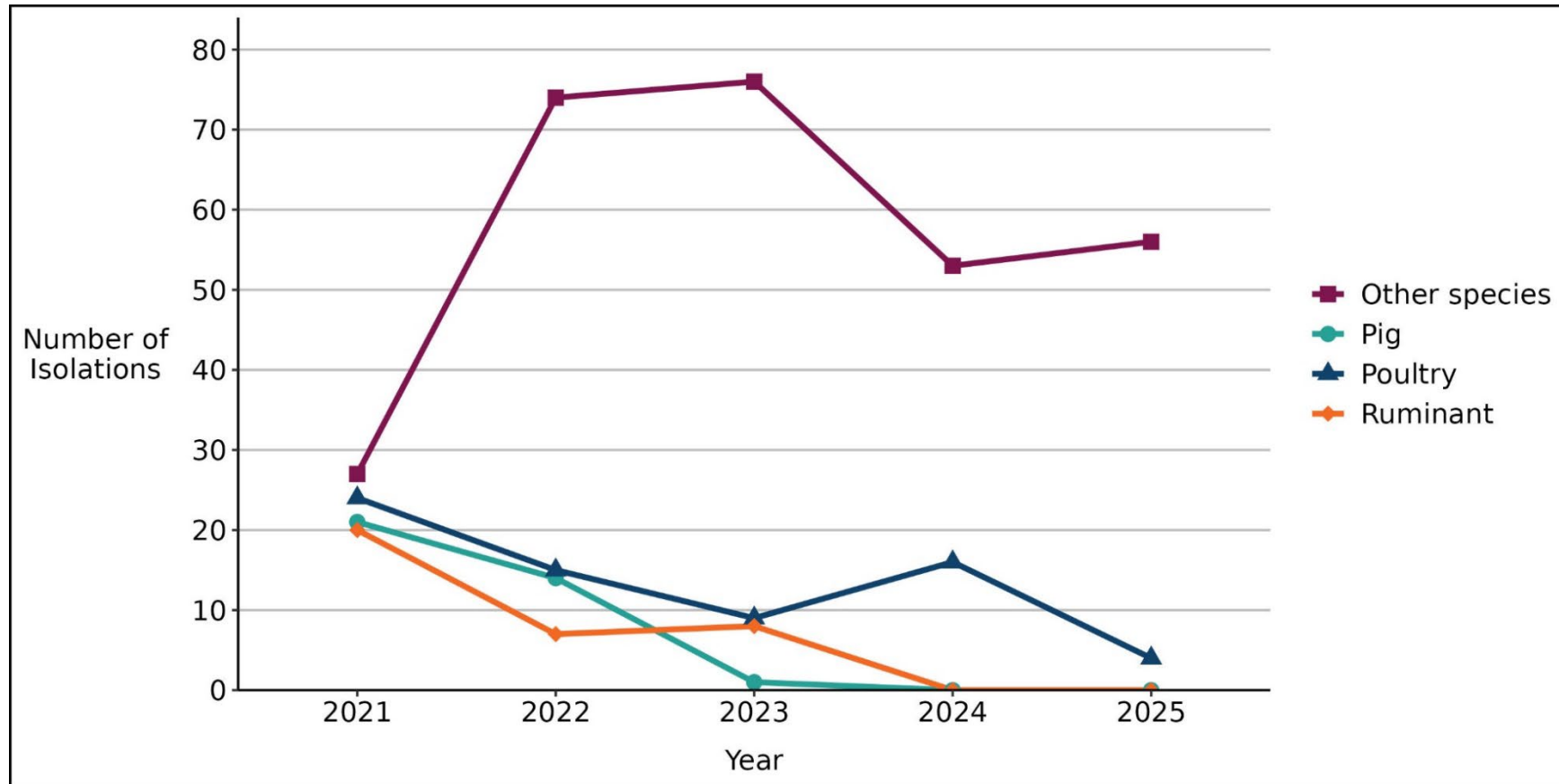


Figure 12.3 shows an overall decreasing trend in the number of isolations of *Salmonella* in compound pig feed and compound ruminant feed, with no isolations of either feed type in 2024 or 2025. Isolations in compound poultry feed have followed a decreasing trend since 2020, however the number of isolations increased from 9 in 2023 to 16 in 2024, before declining to 4 isolations in 2025. There were 56

isolations in compound feed from other species or un-specified species in 2025, an increase from 2024 (53 isolations) but a decline from 2023 (76 isolations).

Table 12.3: Serovars of *Salmonella* isolated from compound ruminant feed in Great Britain in 2025, compared with the previous 2 years

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Molade	1	0	0
Tennessee	7	0	0
Total	8	0	0

Figure 12.4: Isolations of the most common serovars in compound ruminant feed in Great Britain in 2025

Figure 12.4.1: Isolations from compound ruminant feed

There were no isolations of compound ruminant feed in 2025.

Table 12.4: Serovars of *Salmonella* isolated from compound pig feed in Great Britain in 2025, compared with the previous 2 years

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Derby	1	0	0
Total	1	0	0

Figure 12.5: Isolations of the most common *Salmonella* serovars in compound pig feed in Great Britain in 2025

Figure 12.5.1: Isolations from compound pig feed

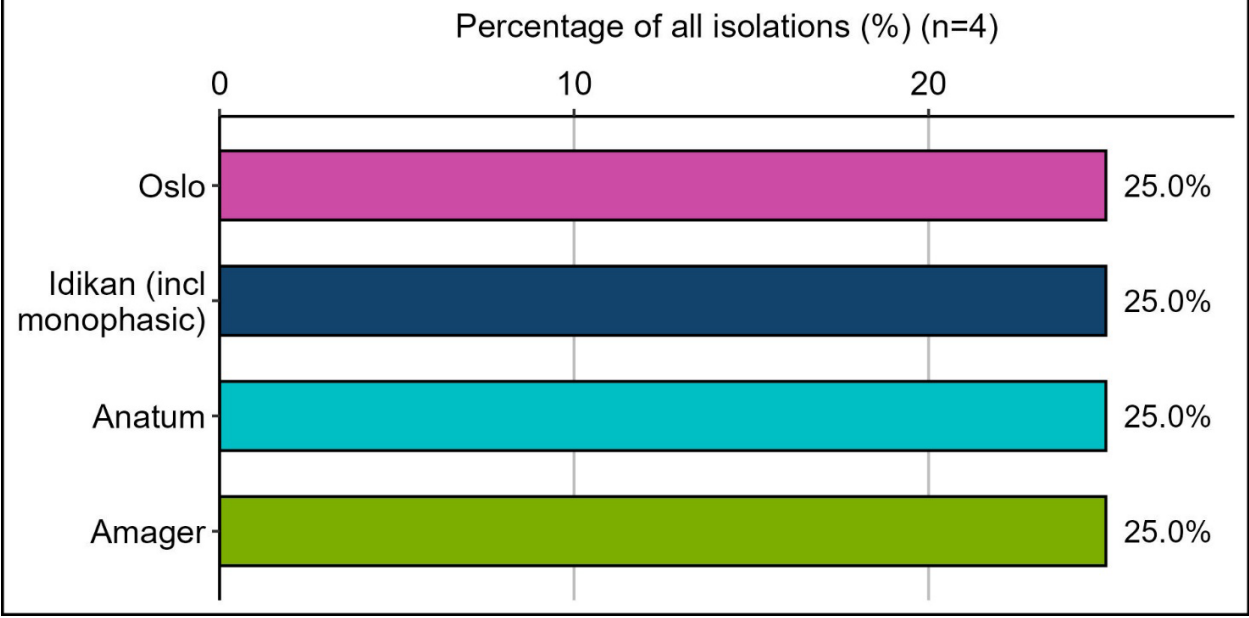
There were no isolations of *Salmonella* in compound pig feed in 2025.

Table 12.5: Serovars of *Salmonella* isolated from compound poultry feed in Great Britain in 2025, compared with the previous 2 years

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
4,12:b:-	1	0	0
Agama	0	1	0
Agona	0	1	0
Amager	0	1	1
Anatum	0	0	1
Cubana	1	0	0
Falkensee	0	2	0
Idikan (incl. monophasic variants)	0	2	1
Kentucky	0	1	0
Kingston	0	1	0
Mbandaka	0	1	0
Newport	0	1	0
Ohio	0	1	0
Oslo	0	0	1
Poona	0	2	0
Rissen	0	1	0
Senftenberg	1	0	0
Typhimurium	5	0	0
Utah	1	0	0
Yoruba	0	1	0
Total	9	16	4

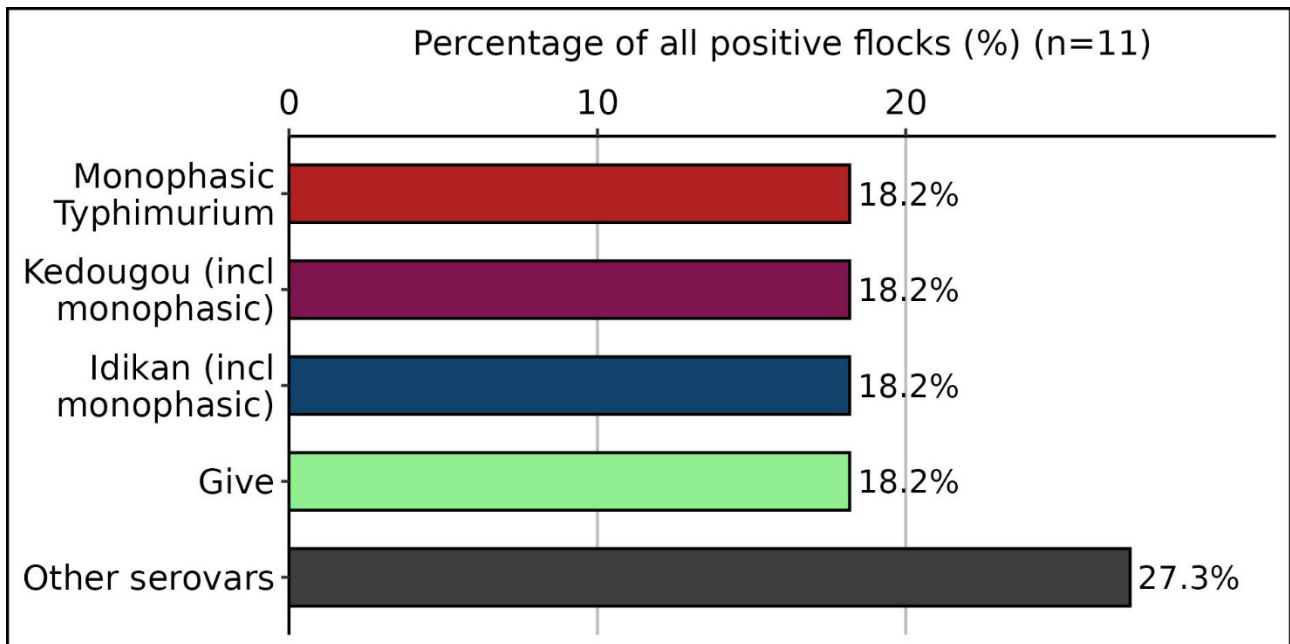
Figure 12.6: Isolations of the most common *Salmonella* serovars in compound poultry feed and positive flocks of chickens and turkeys from NCP testing in Great Britain in 2025

Figure 12.6.1: Isolations from compound poultry feed



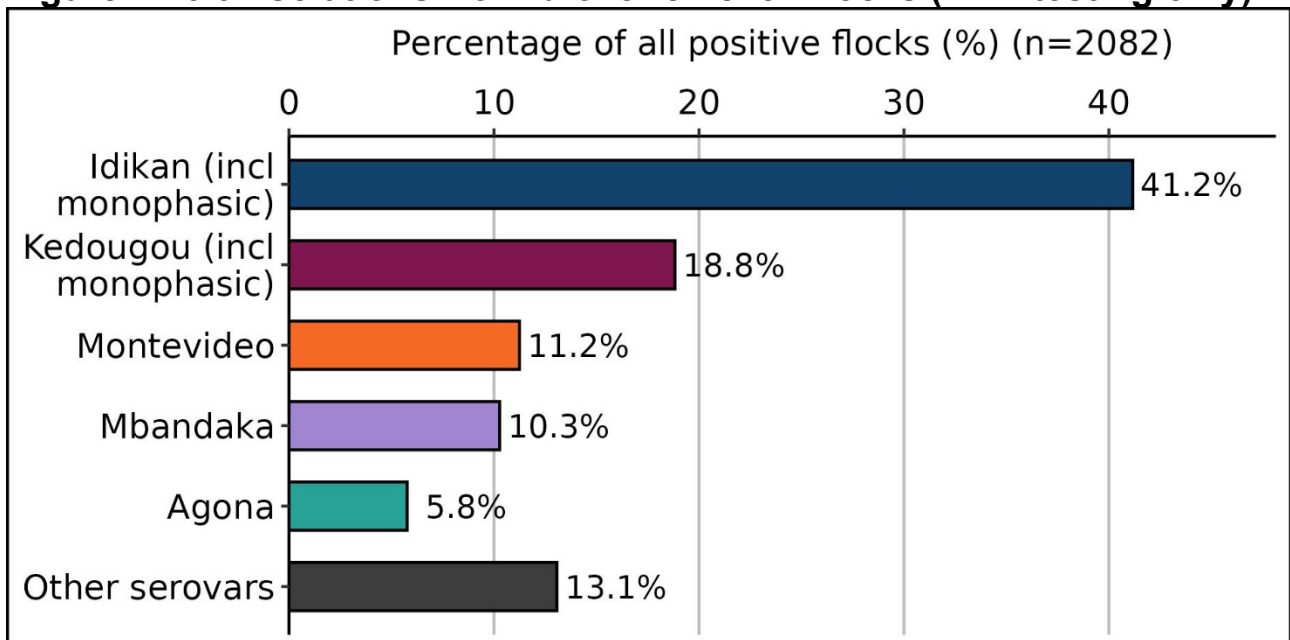
In 2025, the four serovars isolated from compound poultry feed were *S. Anatum*, *S. Amager*, *S. Idikan* (including monophasic variants), and *S. Oslo* (1 isolation each, each representing 25.0% of total positive isolations).

Figure 12.6.2: Isolations from (adult) breeder chicken flocks (NCP testing only)



The most common *Salmonella* serovars in (adult) breeder chicken flocks were *S. Give*, *S. Idikan* (including monophasic variants), *S. Kedougou* (including monophasic variants), and monophasic *S. Typhimurium* - each accounting for 18.2% of total positive flocks. Other serovars accounted for 27.3% of total *Salmonella* isolations from adult breeder flocks.

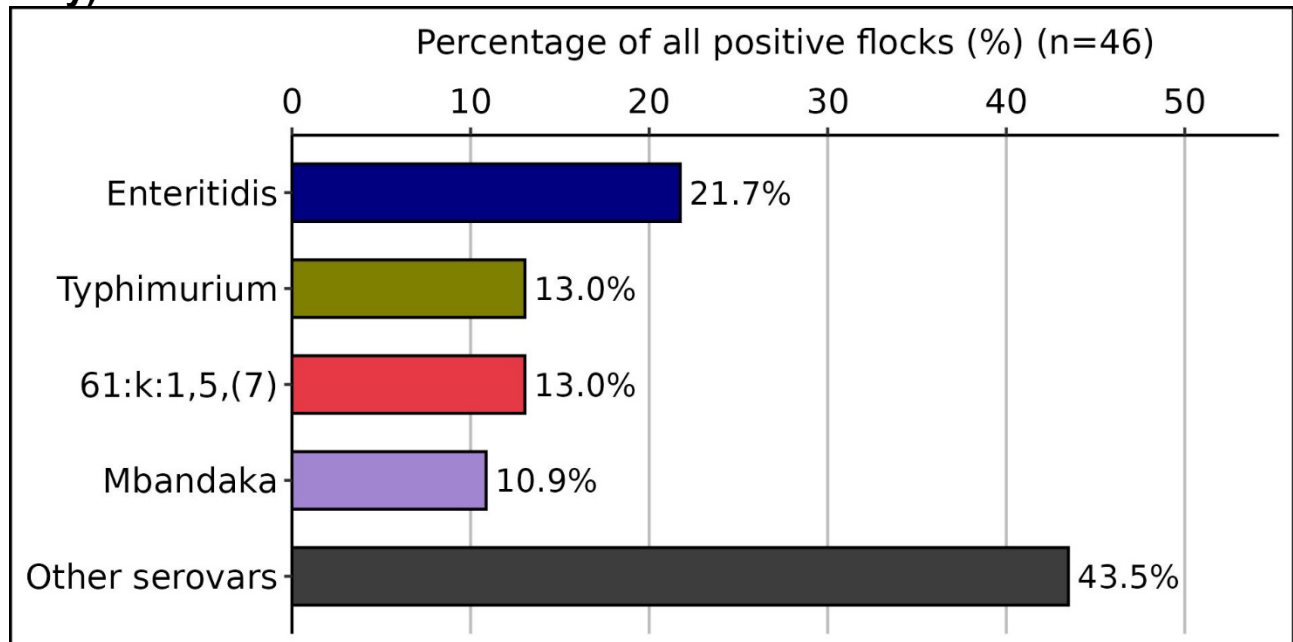
Figure 12.6.3: Isolations from broiler chicken flocks (NCP testing only)



The most common *Salmonella* serovar in broiler chicken flocks was *S. Idikan* (including monophasic variants), accounting for 41.2% of total flocks, followed by *S. Kedougou*

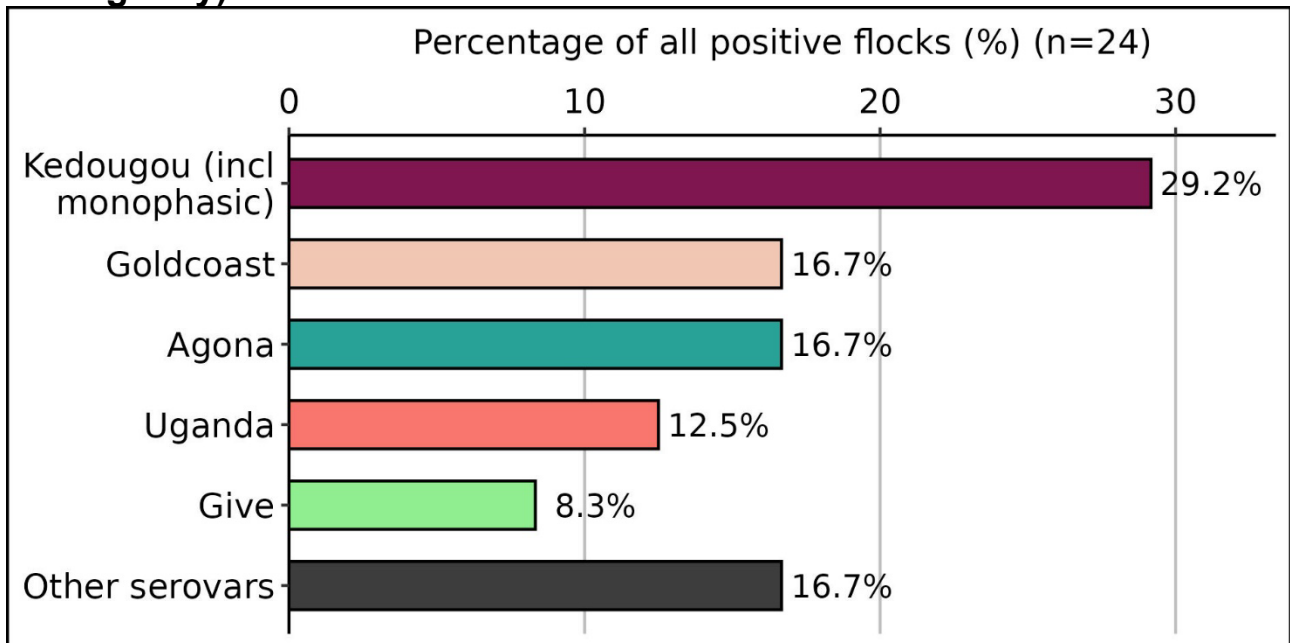
(including monophasic variants, 18.8%), *S. Montevideo* (11.2%), *S. Mbandaka* (10.3%), and *S. Agona* (5.8%). Other serovars accounted for 13.1% of total *Salmonella* isolations from broiler chicken flocks.

Figure 12.6.4: Isolations from (adult) layer chicken flocks (NCP testing only)



The most common serovar in adult chicken layer flocks in 2025 was *S. Enteritidis* (21.7% of total flocks), followed by *Salmonella* 61:k:1,5,(7) and *S. Typhimurium* (each isolated from 13.0% of total flocks), and *S. Mbandaka* (10.9%). Other serovars accounted for 43.5% of total *Salmonella* isolations from adult chicken layer flocks.

Figure 12.6.5: Isolations from breeder and fattening turkey flocks (NCP testing only)



In 2025, the most common *Salmonella* serovar in breeder and fattening turkey flocks was *S. Kedougou* (including monophasic variants), accounting for 29.2% of total flocks, followed by *S. Agona* and *S. Goldcoast* (each isolated from 16.7% of total flocks), *S. Uganda* (12.5%), and *S. Give* (8.3%). Other serovars accounted for 16.7% of total *Salmonella* isolations from breeder and fattening turkey flocks.

Table 12.6: Serovars of *Salmonella* isolated from compound feed for other species feed in Great Britain in 2025, compared with the previous 2 years

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
13,23:i:-	2	0	0
3,10:-:1,5	1	0	0
Agona	1	4	1
Anatum	0	0	2
Bolton	0	0	1
Bovismorbificans	0	1	0
Cerro	0	0	1
Coeln	0	1	0
Cubana	0	1	1
Derby	9	6	0
Duisburg	1	0	0
Durham	0	0	1
Enteritidis	1	0	0
Give	1	1	0
Grumpensis	0	0	1
Hadar	1	0	0
Havana	1	0	1
Idikan (incl. monophasic variants)	0	1	1
Indiana	4	0	0
Infantis	10	5	0
Isangi	0	1	0
Kedougou (incl. monophasic variants)	2	2	2
Kentucky	1	0	0
Leeuwarden	0	0	1
Lexington	1	0	0
Liverpool	0	1	0
London	1	0	0
Mbandaka	0	2	16
Mississippi	0	0	1
Molade	0	0	1
Monophasic Typhimurium	2	0	2

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Montevideo	4	1	2
Morbihan	1	0	0
Muenster	1	0	0
Newport	3	2	0
Nottingham	1	0	0
Ohio	6	0	0
Ouakam	0	0	1
Panama	0	1	0
Poona	1	0	1
Putten	2	0	0
Riggil	0	1	0
Rissen	0	10	7
Senftenberg	13	3	2
Soerenga	3	0	2
Tennessee	1	0	3
Thompson	0	1	0
Typhimurium	0	3	2
Uganda	0	5	2
Worthington	1	0	0
Yoruba	0	0	1
Total	76	53	56

Other species in 2025 were cat (1 isolation), dogs (4 isolations), mixed avian (2 isolations), and unspecified (49 isolations).

Table 12.7: *Salmonella* serovars reported from animal feeding stuff ingredients and products associated with the ABPR in Great Britain, 2023 to 2025

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Adelaide	0	0	1
Agama	4	9	8
Agona	13	29	23
Albany	0	0	1
Amager	0	1	1
Amsterdam	0	1	0
Anatum	10	12	9
Bareilly	0	0	1
Bolton	0	0	1
Bonn	1	0	1
Bovismorbificans	4	2	3
Brandenburg	1	1	2
Bredeney	2	1	1
Cerro	5	2	2
Chester	0	0	5
Coeln	1	2	7
Corvallis	0	1	0
Cubana	1	2	1
Derby	57	27	20
Dublin	5	12	13
Duisburg	1	0	0
Durban	0	0	1
Durham	0	0	2
Ealing	0	4	11
Eastbourne	1	0	0
Enteritidis	19	28	0
Falkensee	0	2	0
Fresno	2	0	0
Fulica	0	0	1
Give	13	3	8
Give var 15+ (Newbrunswick)	1	0	0
Goldcoast	0	1	5
Grumpensis	0	0	2

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Hadar	14	0	5
Haifa	0	0	5
Havana	3	7	20
Heidelberg	1	0	0
Idikan (incl. monophasic variants)	3	10	15
Indiana	53	37	31
Infantis	132	84	56
Isangi	2	13	1
Jerusalem	0	0	1
Johannesburg	0	0	2
Kaapstad	0	1	0
Kassel	0	1	0
Kedougou (incl. monophasic variants)	94	103	85
Kentucky	6	7	2
Kiambu	1	0	0
Kingston	1	1	0
Kottbus	12	14	6
Leeuwarden	0	0	1
Lexington	2	1	2
Litchfield	3	0	0
Liverpool	0	1	11
Livingstone	9	3	5
London	3	3	18
Mbandaka	13	30	42
Meleagridis	1	0	8
Miami	1	0	0
Mississippi	0	0	1
Molade	1	4	2
Monophasic Typhimurium	29	20	17
Montevideo	26	19	95
Morbihan	1	0	0
Morehead	1	0	0
Muenchen	1	1	2
Muenster	6	3	5
Nagoya	1	0	0
Neunkirchen	1	0	0
Newport	32	14	9

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Nottingham	19	3	0
Ohio	82	114	51
Oranienburg	1	0	4
Orion	2	0	0
Orion var 15⁺	1	0	1
Oslo	1	1	8
Ouakam	0	0	1
Panama	5	2	5
Paratyphi B var. Java	5	0	0
Paris	0	0	1
Pomona	0	0	1
Poona	1	2	1
Putten	2	0	0
Reading	2	1	2
Richmond	0	1	0
Ridge	0	0	2
Riggil	0	1	0
Rissen	8	29	13
Riuru	0	0	1
Saintpaul	0	3	1
Schwarzengrund	1	1	0
Senftenberg	41	19	42
Singapore	0	0	2
Soerenga	3	0	4
Stanley	2	1	0
Stanleyville	1	2	0
Szentes	0	1	0
Taksony	0	0	1
Telaviv	0	1	0
Tennessee	12	2	4
Thompson	1	2	2
Typhimurium	70	57	46
Uganda	3	8	6
Umbilo	0	1	0
Utah	1	0	0
Virchow	1	1	2
Wilhelmsberg	2	0	0

<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Worthington	1	0	0
Yoruba	0	2	1
Zehlendorf	0	1	0
3,10:b:-	0	0	1
3,10:-:-	0	1	0
3,10:-:1,5	1	0	0
3,15:b:-	0	0	1
4,5,12:b:- monophasic Java	0	0	1
4,12:b:-	3	0	4
4,12:d:-	0	0	2
13,23:i:-	15	0	0
17:b:-	1	0	0
42:b:e,n,x,z15	1	0	0
47:z4,z23:-	1	0	1
48:z4,z23:-	0	2	0
50:z52:1,5,7	0	0	1
61:i:z53	0	3	0
61:k:1,5,7	12	16	8
61:-:1,5,7	1	0	0
Total	897	795	798

Table 12.8a: Serovars of *Salmonella* in feeding stuff ingredients in Great Britain, 2023 to 2025

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Antler powder	50:z52:1,5,7	0	0	1
Barley	Derby	0	0	1
Feather meal	Montevideo	0	0	2
Feather meal	Tennessee	0	1	0
Feed additive	Derby	4	0	0
Feed additive	Infantis	1	0	0
Feed additive	Nottingham	1	0	0
Fishmeal	Livingstone	0	1	1
Fishmeal	Montevideo	2	6	0
Fishmeal	Senftenberg	0	0	1
Fishmeal	Tennessee	0	1	0
Fishmeal	Typhimurium	0	0	1
Guar protein	Cubana	0	1	0
Maize	Typhimurium	4	2	0
Malt	Agama	3	0	0
Minerals	Hadar	1	0	0
Mixed vegetables	Derby	2	0	0
Mixed vegetables	Indiana	2	0	0
Mixed vegetables	Monophasic Typhimurium	1	0	0
Mixed vegetables	Montevideo	1	0	0
Oilseeds	Agama	0	2	0
Oilseeds	Agona	0	1	0
Oilseeds	Infantis	1	1	0
Oilseeds	Kentucky	0	1	0
Oilseeds	Ohio	0	1	0
Oilseeds	Rissen	1	4	1
Oilseeds	Senftenberg	0	1	0
Palm kernel	Rissen	0	0	1
Palm kernel	Senftenberg	1	0	0
Plant material	Anatum	0	1	0
Plant material	Idikan (incl. monophasic variants)	0	0	1
Pork meal	Jerusalem	0	0	1
Pork meal	Liverpool	0	0	5
Pork meal	Senftenberg	0	0	2

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Poultry meal	Agona	0	0	9
Poultry meal	Enteritidis	0	0	3
Poultry meal	Havana	0	0	17
Poultry meal	Infantis	0	0	31
Poultry meal	Liverpool	0	0	1
Poultry meal	Mbandaka	0	0	2
Poultry meal	Montevideo	0	0	65
Poultry meal	Muenster	0	0	1
Poultry meal	Senftenberg	0	0	10
Rapeseed	Agona	1	1	0
Rapeseed	Ealing	0	3	0
Rapeseed	Idikan (incl. monophasic variants)	0	0	1
Rapeseed	Kedougou (incl. monophasic variants)	1	1	0
Rapeseed	Kentucky	0	1	1
Rapeseed	Mbandaka	0	1	0
Rapeseed	Rissen	0	7	2
Rapeseed	Tennessee	1	0	0
Rapeseed	Typhimurium	1	2	1
Separated fibre	Agona	1	0	0
Soya	Agona	1	0	0
Soya	Anatum	0	0	1
Soya	Fresno	1	0	0
Soya	Havana	1	0	0
Soya	Idikan (incl. monophasic variants)	0	0	1
Soya	Lexington	0	1	0
Soya	Livingstone	1	0	1
Soya	Mbandaka	1	2	3
Soya	Molade	0	0	1
Soya	Rissen	0	1	0
Soya	Senftenberg	1	3	2
Soya	Tennessee	1	0	0
Soya	Typhimurium	5	2	2
Soya	Yoruba	0	1	0
Soya bean meal	Infantis	0	1	0
Soya bean meal	Mbandaka	0	1	0

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Stow malt	Coeln	0	0	3
Wheat	Idikan (incl. monophasic variants)	0	1	1
Wheat	Kedougou (incl. monophasic variants)	1	0	0
Wheat	Kingston	1	0	0
Wheat	Ohio	0	1	0
Wheat	Typhimurium	0	1	1
Total	Not applicable	44	55	178

Table 12.8b: Serovars of *Salmonella* in other products associated with the ABPR in Great Britain, 2023 to 2025

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Aeration tank	Infantis	4	1	0
Beef concentrate	Isangi	1	0	0
Biogas	Infantis	1	0	0
Biogas	Typhimurium	1	0	0
Blood products	Derby	0	0	3
Blood products	Havana	0	0	1
Blood products	Infantis	0	0	1
Blood products	London	0	0	1
Blood products	Monophasic Typhimurium	0	1	0
Blood products	Montevideo	0	0	1
Blood products	Panama	0	0	1
Blood products	Tennessee	0	0	1
Centrate liquor	Infantis	13	2	0
Compost	Anatum	0	1	0
Compost	Bovismorbificans	0	0	1
Compost	Chester	0	0	2
Compost	Durban	0	0	1
Compost	Durham	0	0	1
Compost	Indiana	0	0	1
Compost	Infantis	2	2	1
Compost	Kentucky	0	1	0
Compost	London	0	0	1
Compost	Montevideo	0	0	1
Compost	Muenster	0	1	0
Compost	Newport	0	2	0
Compost	Oranienburg	0	0	2
Compost	Oslo	0	0	2
Compost	Pomona	0	0	1
Compost	Typhimurium	0	1	1
Compost	Virchow	0	0	1
Compost	4,5,12:b:- monophasic Java	0	0	1
Compost	13,23:i:-	1	0	0

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Digestate	Agona	1	5	0
Digestate	Anatum	0	1	0
Digestate	Bareilly	0	0	1
Digestate	Bovismorbificans	1	0	0
Digestate	Derby	0	1	1
Digestate	Eastbourne	1	0	0
Digestate	Give	0	0	1
Digestate	Haifa	0	0	1
Digestate	Indiana	0	0	3
Digestate	Infantis	22	22	1
Digestate	Isangi	0	0	1
Digestate	Kentucky	1	0	0
Digestate	Kottbus	0	0	2
Digestate	Livingstone	2	0	0
Digestate	Monophasic Typhimurium	1	0	1
Digestate	Montevideo	0	0	1
Digestate	Muenster	0	1	0
Digestate	Newport	1	0	1
Digestate	Nottingham	0	1	0
Digestate	Ohio	2	1	0
Digestate	Oslo	1	0	3
Digestate	Paris	0	0	1
Digestate	Saintpaul	0	1	0
Digestate	Schwarzengrund	0	1	0
Digestate	Taksony	0	0	1
Digestate	Typhimurium	1	1	0
Digestate	4,12:b:-	0	0	1
Digestate	4,12:d:-	0	0	1
Digestate liquor	Infantis	18	0	0
Dog chews	Muenster	0	0	1
Dog treat	Agona	0	1	0
Dog treat	Anatum	0	3	0
Dog treat	Derby	1	1	0
Dog treat	Infantis	1	0	0
Dog treat	Kentucky	0	1	0
Dog treat	Montevideo	1	1	0

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Dog treat	Newport	0	1	0
Dog treat	Nottingham	1	0	0
Dog treat	Senftenberg	0	2	0
Dog treat	Telaviv	0	1	0
Dog treat	Typhimurium	0	2	0
Dog treat	Uganda	0	2	0
Dog treat	Umbilo	0	1	0
Effluent tank	13,23:i:-	1	0	0
Environmental	61:k:1,5,7	0	1	0
Environmental	Indiana	0	1	0
Environmental	Infantis	0	1	0
Environmental	Kedougou (incl. monophasic variants)	0	1	0
Environmental	Kottbus	0	1	0
Environmental	Newport	0	2	0
Environmental	Typhimurium	0	5	0
Feeder chick	Idikan (incl. monophasic variants)	0	0	2
Feeder mice	Enteritidis	0	5	0
Feeder mice	Monophasic Typhimurium	0	1	0
Feed mill environment	Agama	0	6	7
Feed mill environment	Agona	1	3	1
Feed mill environment	Anatum	0	3	0
Feed mill environment	Bonn	1	0	1
Feed mill environment	Bredeney	0	0	1
Feed mill environment	Cerro	3	1	0
Feed mill environment	Derby	5	1	1
Feed mill environment	Ealing	0	1	0
Feed mill environment	Enteritidis	7	11	0
Feed mill environment	Give	1	0	0
Feed mill environment	Grumpensis	0	0	1
Feed mill environment	Hadar	1	0	0
Feed mill environment	Haifa	0	0	1
Feed mill environment	Heidelberg	1	0	0
Feed mill environment	Idikan (incl. monophasic variants)	3	1	4

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Feed mill environment	Infantis	20	8	1
Feed mill environment	Kassel	0	1	0
Feed mill environment	Kedougou (incl. monophasic variants)	82	92	79
Feed mill environment	Kentucky	4	0	1
Feed mill environment	Kiambu	1	0	0
Feed mill environment	Kottbus	1	0	0
Feed mill environment	Livingstone	1	0	1
Feed mill environment	Mbandaka	3	0	5
Feed mill environment	Meleagridis	0	0	1
Feed mill environment	Molade	0	4	0
Feed mill environment	Monophasic Typhimurium	5	1	1
Feed mill environment	Montevideo	7	0	0
Feed mill environment	Morehead	1	0	0
Feed mill environment	Nagoya	1	0	0
Feed mill environment	Neunkirchen	1	0	0
Feed mill environment	Newport	4	0	0
Feed mill environment	Nottingham	16	2	0
Feed mill environment	Ohio	68	110	47
Feed mill environment	Oranienburg	1	0	0
Feed mill environment	Oslo	0	1	1
Feed mill environment	Panama	0	0	1
Feed mill environment	Paratyphi B var. Java	1	0	0
Feed mill environment	Rissen	2	5	1
Feed mill environment	Ruiru	0	0	1
Feed mill environment	Saintpaul	0	1	0
Feed mill environment	Senftenberg	9	0	4
Feed mill environment	Soerenga	0	0	2
Feed mill environment	Stanley	0	1	0
Feed mill environment	Stanleyville	1	1	0
Feed mill environment	Tennessee	1	0	0
Feed mill environment	Typhimurium	20	10	10
Feed mill environment	Uganda	3	1	3
Feed mill environment	Virchow	0	1	0
Feed mill environment	Williamsberg	1	0	0
Feed mill environment	Zehlendorf	0	1	0

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Feed mill environment	6,7:-:-	1	0	0
Feed mill environment	13,23:i:-	8	0	0
Feed mill environment	61:k:1,5,7	1	0	0
Feed mill environment	42:b:e,n,x,z15	1	0	0
Feed mill environment	47:z4,z23:-	1	0	1
Fertilizer - tea fungal additive	Anatum	1	0	0
Landfill	Derby	1	0	0
Liquid waste	Derby	0	1	0
Manure	Adelaide	0	0	1
Manure	Agona	0	0	1
Manure	Albany	0	0	1
Manure	Chester	0	0	1
Manure	Give	0	0	1
Manure	Haifa	0	0	3
Manure	Infantis	0	0	1
Manure	Johannesburg	0	0	2
Manure	Montevideo	0	0	4
Manure	Muenchen	0	0	1
Manure	Muenster	0	0	2
Manure	Newport	0	0	3
Manure	Oranienburg	0	0	1
Manure	Oslo	0	0	1
Manure	Panama	0	0	1
Manure	Ridge	0	0	2
Manure	Senftenberg	0	0	1
Manure	Singapore	0	0	2
Manure	4,12:b:-	0	0	3
Meat and bone	Derby	1	0	0
Other raw materials	Agama	0	0	1
Other raw materials	Agona	0	1	3
Other raw materials	Anatum	0	0	2
Other raw materials	Chester	0	0	1
Other raw materials	Derby	0	1	0
Other raw materials	Enteritidis	0	0	1
Other raw materials	Give	0	0	1
Other raw materials	Havana	0	0	1

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Other raw materials	Indiana	0	0	1
Other raw materials	Infantis	0	0	3
Other raw materials	Isangi	0	12	0
Other raw materials	Kedougou (incl. monophasic variants)	0	0	1
Other raw materials	Livingstone	0	0	1
Other raw materials	Mbandaka	0	0	4
Other raw materials	Meleagridis	0	0	1
Other raw materials	Monophasic Typhimurium	0	0	2
Other raw materials	Montevideo	0	0	8
Other raw materials	Ohio	0	0	2
Other raw materials	Oranienburg	0	0	1
Other raw materials	Panama	0	0	1
Other raw materials	Rissen	0	0	1
Other raw materials	Senftenberg	0	1	3
Other raw materials	Typhimurium	0	0	3
Other raw materials	Uganda	0	0	1
Other raw materials	3,10:b:-	0	0	1
Other raw materials	3,15:b:-	0	0	1
Other raw materials	61:k:1,5,7	0	0	1
Pasteurised liquor	Infantis	4	1	0
Pet food (raw)	Agama	1	0	0
Pet food (raw)	Agona	7	11	7
Pet food (raw)	Amsterdam	0	1	0
Pet food (raw)	Anatum	8	3	3
Pet food (raw)	Bovismorbificans	2	1	2
Pet food (raw)	Brandenburg	1	1	2
Pet food (raw)	Bredeney	1	1	0
Pet food (raw)	Chester	0	0	1
Pet food (raw)	Coeln	0	1	4
Pet food (raw)	Derby	31	16	14
Pet food (raw)	Dublin	5	12	13
Pet food (raw)	Enteritidis	9	12	6
Pet food (raw)	Fulica	0	0	1
Pet food (raw)	Give	10	2	5

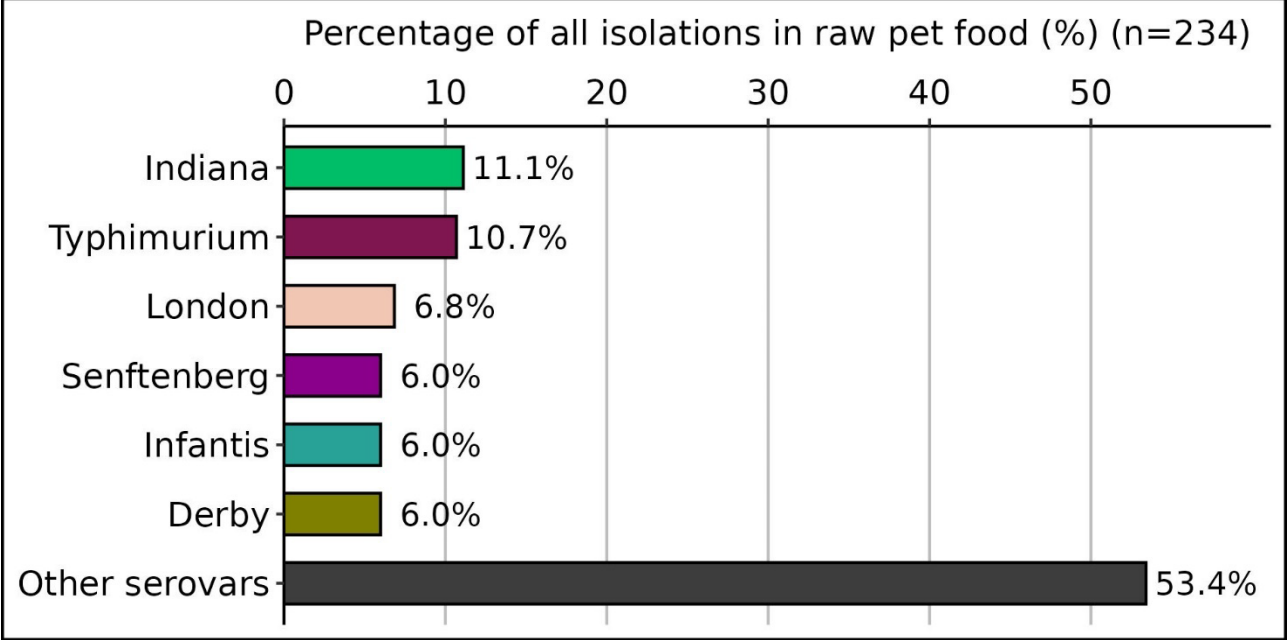
Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Pet food (raw)	Give var 15+ (Newbrunswick)	1	0	0
Pet food (raw)	Goldcoast	0	1	5
Pet food (raw)	Hadar	11	0	5
Pet food (raw)	Havana	1	1	0
Pet food (raw)	Idikan (incl. monophasic variants)	0	5	2
Pet food (raw)	Indiana	46	36	26
Pet food (raw)	Infantis	29	38	14
Pet food (raw)	Isangi	1	0	0
Pet food (raw)	Kaapstad	0	1	0
Pet food (raw)	Kedougou (incl. monophasic variants)	2	7	2
Pet food (raw)	Kentucky	0	2	0
Pet food (raw)	Kottbus	11	13	4
Pet food (raw)	Lexington	1	0	2
Pet food (raw)	Litchfield	3	0	0
Pet food (raw)	Liverpool	0	0	3
Pet food (raw)	Livingstone	3	2	0
Pet food (raw)	London	2	3	16
Pet food (raw)	Mbandaka	8	23	12
Pet food (raw)	Meleagridis	1	0	6
Pet food (raw)	Miami	1	0	0
Pet food (raw)	Monophasic Typhimurium	19	17	11
Pet food (raw)	Montevideo	8	10	5
Pet food (raw)	Muenchen	1	0	1
Pet food (raw)	Muenster	5	1	1
Pet food (raw)	Newport	22	6	5
Pet food (raw)	Ohio	0	0	2
Pet food (raw)	Orion	2	0	0
Pet food (raw)	Orion var. 15+	1	0	1
Pet food (raw)	Panama	4	1	1
Pet food (raw)	Paratyphi B var. Java	3	0	0
Pet food (raw)	Reading	2	0	2
Pet food (raw)	Rissen	4	1	0
Pet food (raw)	Saintpaul	0	1	1

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Pet food (raw)	Senftenberg	13	9	14
Pet food (raw)	Stanley	2	0	0
Pet food (raw)	Szentes	0	1	0
Pet food (raw)	Thompson	0	1	2
Pet food (raw)	Typhimurium	30	28	25
Pet food (raw)	Virchow	1	0	1
Pet food (raw)	Wilhelmsberg	1	0	0
Pet food (raw)	3,10:-:-	0	1	0
Pet food (raw)	4,12:b:-	2	0	0
Pet food (raw)	13,23:i:-	3	0	0
Pet food (raw)	48:z4,z23:-	0	2	0
Pet food (raw)	61:-:1,5,7	1	0	0
Pet food (raw)	61:i:z53	0	3	0
Pet food (raw)	61:k:1,5,7	11	15	7
Process water tank	Infantis	5	2	0
Processed animal protein	4,12:d:-	0	0	1
Processed animal protein	Agona	0	0	1
Processed animal protein	Cerro	0	1	1
Processed animal protein	Enteritidis	0	0	1
Processed animal protein	Infantis	0	0	3
Processed animal protein	Kedougou (incl. monophasic variants)	0	0	1
Processed animal protein	Liverpool (incl. monophasic variants)	0	0	2
Processed animal protein	Livingstone	0	0	1
Processed animal protein	Montevideo	0	0	6
Processed animal protein	Senftenberg	0	0	3
Raw meat	Bovismorbificans	1	0	0
Raw meat	Enteritidis	1	0	0
Raw meat	Indiana	1	0	0
Raw meat	Livingstone	2	0	0

Feeding stuff	<i>Salmonella</i> serovar	Isolations 2023	Isolations 2024	Isolations 2025
Raw meat	Mbandaka	1	0	0
Raw meat	Monophasic Typhimurium	1	0	0
Raw meat	Montevideo	1	0	0
Raw meat	Newport	2	0	0
Raw meat	Paratyphi B var. Java	1	0	0
Raw meat	Schwarzengrund	1	0	0
Slurry	Agona	0	1	0
Slurry	Corvallis	0	1	0
Slurry	Havana	0	6	0
Slurry	Idikan (incl. monophasic variants)	0	0	1
Slurry	Montevideo	0	1	0
Slurry	Reading	0	1	0
Slurry	Richmond	0	1	0
Slurry	Stanleyville	0	1	0
Unspecified	Anatum	1	0	0
Unspecified	Bredeney	1	0	0
Unspecified	Cerro	2	0	0
Unspecified	Coeln	1	0	0
Unspecified	Derby	2	0	0
Unspecified	Enteritidis	1	0	0
Unspecified	Fresno	1	0	0
Unspecified	Give	1	0	0
Unspecified	Infantis	1	0	0
Unspecified	Kedougou (incl. monophasic variants)	6	0	0
Unspecified	Montevideo	2	0	0
Unspecified	Ohio	6	0	0
Unspecified	Panama	1	0	0
Unspecified	Rissen	1	0	0
Unspecified	Senftenberg	3	0	0
Unspecified	Tennessee	1	0	0
Unspecified	Thompson	1	0	0
Unspecified	Typhimurium	3	0	0
Windrow	Muenchen	0	1	0
Total	Not applicable	759	671	560

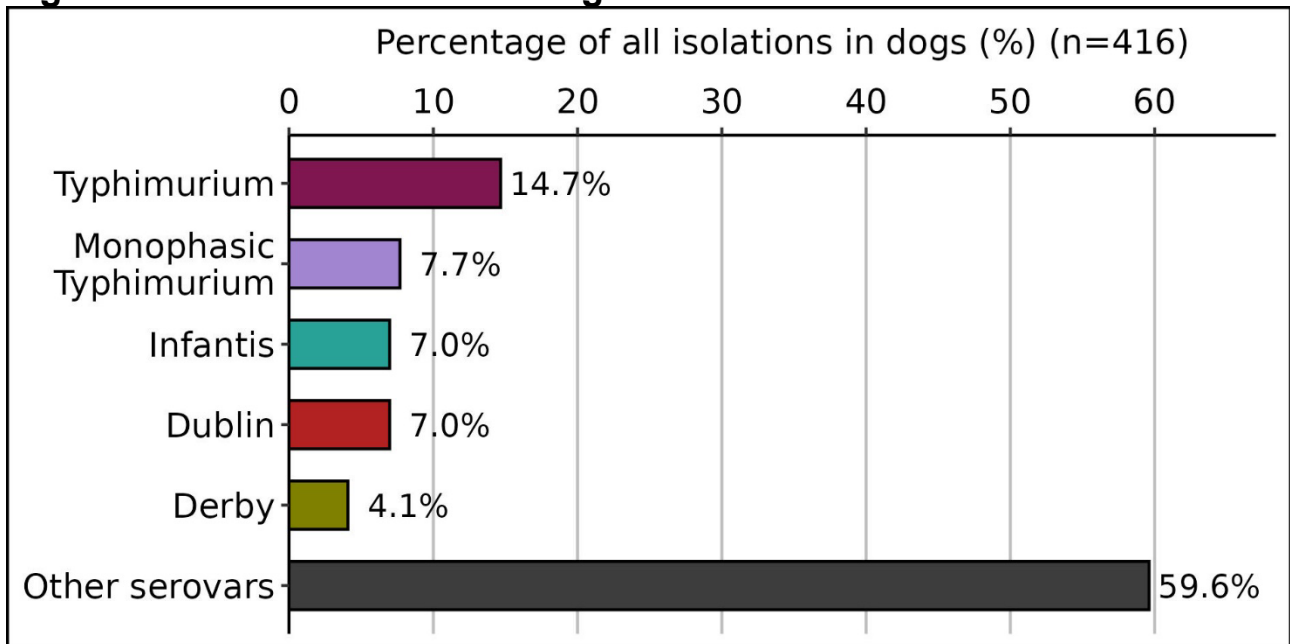
Figure 12.7: Isolations of the most common *Salmonella* serovars in raw pet food and dogs in Great Britain in 2025

Figure 12.7.1: Isolations from raw pet food



The most common *Salmonella* serovar in raw pet food was *S. Indiana*, accounting for 11.1% of total isolations, followed by *S. Typhimurium* (10.7%), *S. London* (6.8%), and *S. Derby*, *S. Infantis*, and *S. Senftenberg* (each accounting for 6.0% of total isolations). Other serovars accounted for 53.4% of total *Salmonella* isolations from raw pet food.

Figure 12.7.2: Isolations from dogs



In 2025 the most common *Salmonella* serovar in dogs was *S. Typhimurium*, accounting for 14.7% of total isolations, followed by monophasic *S. Typhimurium* (7.7%), *S. Infantis* and *S. Dublin* (7.0% each), and *S. Derby* (4.1%). Other serovars accounted for 59.6% of total *Salmonella* isolations in dogs.

Table 12.9: Animal By-Products (Enforcement) Regulations 2013, domestic protein official testing and contamination rates in Great Britain, 2023 to 2025

Sample Type	2023 Batches	2023 number +ve	2023 % +ve	2024 Batches	2024 number +ve	2024 % +ve	2025 Batches	2025 number +ve	2025 % +ve
Blood meal	2	0	0	5	0	0.00	4	0	0.00
Feather meal	9	0	0	12	1	8.33	3	0	0.00
Meat and bone meal	2	0	0	0	0	0.00	2	0	0.00
Poultry offal meal	7	0	0	10	1	10.00	13	0	0.00
Other fish meal	0	0	0	3	0	0.00	0	0	0.00
White fish meal	15	0	0	11	0	0.00	14	0	0.00
Others	288	4	1.39	418	6	1.44	437	16	3.66
Total	323	4	1.24	459	8	1.74	473	16	3.38

This table excludes the results of private testing.

Table 12.10: Animal By-Products (Enforcement) Regulations, 2013. Serovars isolated during 2023 to 2025 from official and private testing of domestic protein and other products associated with the regulations in Great Britain

Serovar	Isolations 2023	Isolations 2024	Isolations 2025
4,12:d:-	0	0	1
4,5,12:b:- monophasic Java	0	0	1
Agona	0	0	1
Anatum	0	1	1
Cerro	0	1	1
Enteritidis	0	0	1
Gueuletapee	1	0	0
Indiana	0	0	1
Infantis	1	0	3
Kedougou (incl. monophasic variants)	0	0	1
Livingstone	0	1	1
London	0	0	1
Montevideo	0	0	6
Nottingham	0	1	0
Senftenberg	0	1	1
Tennessee	0	1	0
Typhimurium	2	2	0
Total	4	8	20

Figure 12.8: *Salmonella* contamination rate for domestic processed animal protein (batches tested) in Great Britain, 2015 to 2025

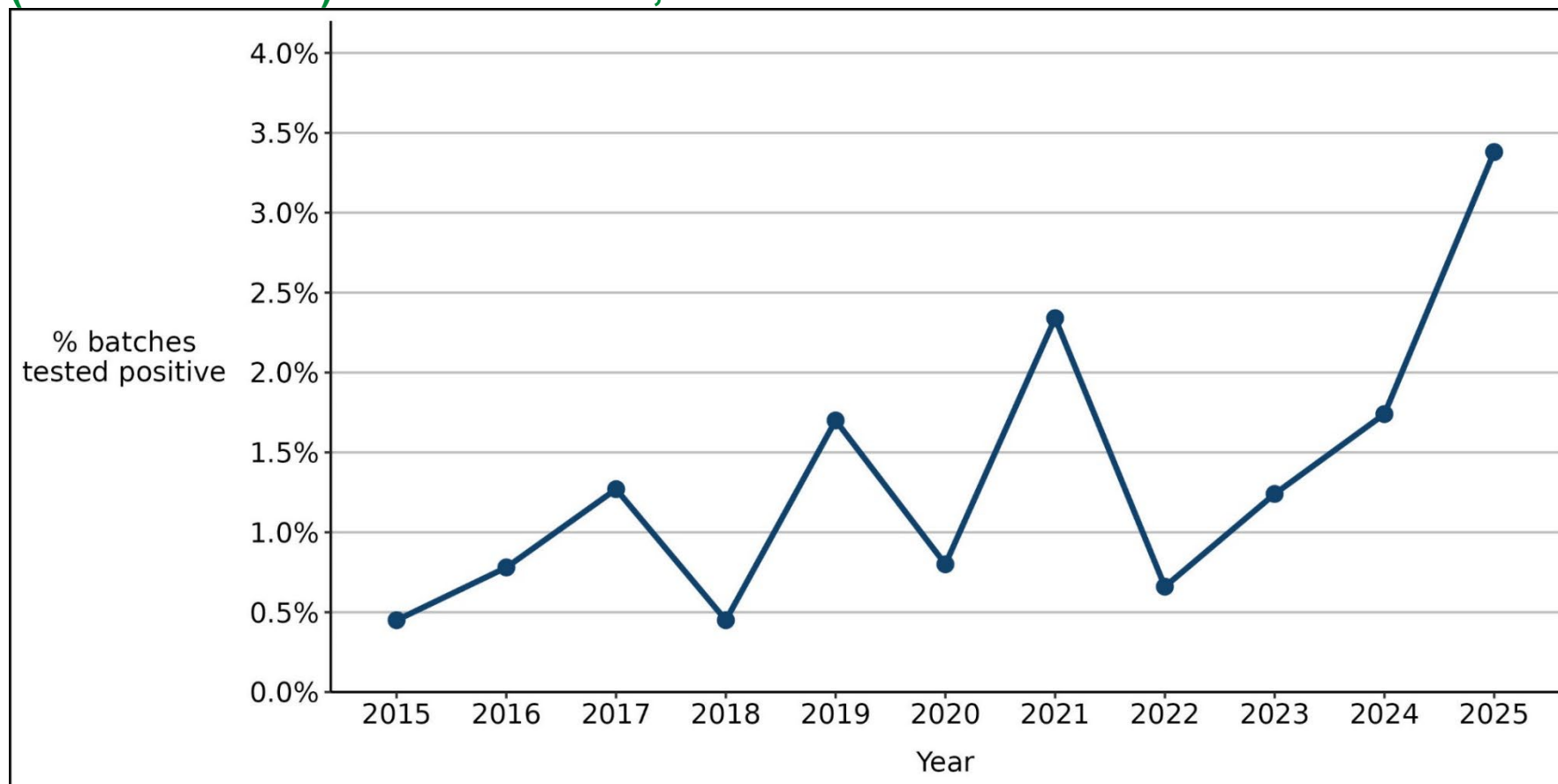


Figure 12.8 shows the proportion of positive batches for domestic processed animal protein had fluctuated year on year with an overall increase in positivity. 2025 saw the highest proportion of contaminated batches (3.38%).

For data prior to 2015, see [Salmonella in livestock production in Great Britain 2014](#).

Chapter 13: Antimicrobial susceptibility in *Salmonella*

Salmonella isolates received for serotyping WGS at APHA Weybridge are tested for their *in vitro* sensitivity to a panel of 16 antimicrobials. The majority of these isolates originate from animals and their environment in England and Wales; however, some isolates (mainly from poultry) originate from Scotland. This chapter also includes isolates that have been recovered under the *Salmonella* National Control Programmes (NCP) which apply to chickens and turkeys. These isolates are derived from premises located throughout Great Britain. AST is carried out for surveillance purposes only.

The choice of antimicrobials included in the sensitivity panel, which is reviewed periodically, is designed to represent a core set of antimicrobial classes that have been used in veterinary practice for many years (Table 13.1). It also includes some antimicrobials which are not authorised for use in food animals in the United Kingdom, but which are relevant to human medicine. For some of the antimicrobials selected, specific resistance mechanisms are invariably identified but, for others, a range of genes (not always species specific, sometimes plasmids are important too) can contribute, interact or do both to achieve a resistance phenotype. Antimicrobial resistance (AMR) patterns can be useful preliminary epidemiological indicators.

All tests are performed using the [British Society for Antimicrobial Chemotherapy](#) (BSAC) disc diffusion technique on Oxoid “Isosensitest” agar and using antimicrobial discs as listed in the table below. BSAC recommendations and clinical breakpoints have been adopted for antimicrobials, for which BSAC breakpoints are available.

Revisions to the methodology have been catalogued in previous reports and include changes made to enhance the detection of resistance to third generation cephalosporins and fluoroquinolones. In 2007, the interpretative criterion was changes for ciprofloxacin from the historical APHA veterinary breakpoint of resistant ≤ 13 mm used in previous years, to the BSAC breakpoint of resistant or intermediate ≤ 19 mm (this breakpoint was that recommended by BSAC on 1 January 2007). Longer term trends in ciprofloxacin resistance should therefore be interpreted considering this change to the breakpoint. Where no BSAC breakpoints are available, then the historical APHA veterinary breakpoint has been used, or a breakpoint has been derived (APHA data on file). The [UK-VARSS Report 2021](#) provides further details in an annex and is available on GOV.UK.

The sole change made to the zone size breakpoints and disc concentrations used over the period 2008 to 2021 related to the ceftazidime disc for which the zone size was reduced from 29mm to 26mm in 2012, in line with BSAC recommendations. The BSAC disc diffusion method is no longer being supported, but the BSAC clinical breakpoints were fully

harmonised with those of the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and will remain valid, unless EUCAST clinical breakpoints for the antimicrobials included in this report are subsequently revised.

Table 13.1: Details of antimicrobials

Antimicrobial	Concentration (µg per ml)	Code	Zone size (R _≤ x mm)
Nalidixic acid	30	NA	13
Tetracycline	10	T	13
Neomycin	10	N	13
Ampicillin	10	AM	14
Furazolidone	15	FR	13
Ceftazidime	30	CAZ	26
Sulphamethoxazole and trimethoprim combination	25	TM	15
Chloramphenicol	30	C	20
Amikacin	30	AK	18
Amoxicillin and clavulanic acid combination	30	AMC	14
Gentamicin	10	CN	19
Streptomycin	10	S	13
Sulphonamide compounds	300	SU	13
Cefotaxime	30	CTX	29
Apramycin	15	APR	13
Ciprofloxacin	1	CIP	16

Prior to 1996, all *Salmonella* isolates received were tested for antimicrobial susceptibility, but since then, only the first isolate of a given serotype or phage type, until phage typing discontinued, from each incident has usually been tested, with the exception of specific investigations. The number of cultures received from a farm varies enormously, especially in the case of those received from poultry premises. Some poultry companies have a continuous monitoring programme and large number of *Salmonella* isolates may be received from a particular company relating to one premises.

Thus, in that situation, the numbers of isolates of a particular serotype and their antimicrobial susceptibility may not reflect the prevalence in the animal population as a whole, but rather the intensity of the monitoring programme on a farm or group of farms. Therefore, to better indicate the prevalence of resistance, normally only the first isolate from each incident has been tested since the start of 1996.

In 2024, APHA discontinued phage typing as a supplementary test for the characterisation of *S. Typhimurium* and *S. Enteritidis*. As APHA no longer performs phage typing for any *Salmonella* isolates, analyses based on phage type are not included in this report, in contrast with previous years.

Salmonella Dublin

A total of 349 *Salmonella* Dublin isolates underwent antimicrobial susceptibility testing in 2025. Overall, 329 isolates (94.3%) were susceptible to all 16 antimicrobials tested.

Resistance to both neomycin and furazolidone decreased to 0.9% in 2025, compared to 2.5% in 2024, after being undetected in 2023 and 2022. Resistance to streptomycin decreased from 4.9% in 2024 to 2.6% in 2025, which is still higher than 2023 (1.9%). Resistance to apramycin, which was detected for the first time after several years in 2023, was identified in 2025 (n=2), following no detections in any of the *S. Dublin* isolates tested in 2024. Of the non-susceptible isolates (n= 20), 17 showed resistance to only one antimicrobial in the panel. 3 isolates exhibited resistance to more than one antimicrobial in the panel, one with 3 resistances, another with 4, and the other with 5.

As in previous years, most *S. Dublin* isolates originated from cattle (303, 86.8%). Among these, 289 isolates (95.4%) were fully susceptible. This represents a statistically significant increase in susceptibility among cattle isolates compared to 90.2% in 2024 and is more like susceptibility levels found in 2022 (96.4%) and 2023 (96.3%) (Table 13.2). *S. Dublin* isolates from species other than cattle were recovered from dogs (n=28), feed (n=14), environmental sources (n=2), one pig, and one sheep. Of these 46 isolates, 87.0% were fully susceptible. Of the 6 isolates exhibiting resistance, 5 showed resistance to only one antimicrobial in the panel, and one isolate showed resistance to 3 antimicrobials in the panel.

The percentage of *S. Dublin* isolates susceptible to all 16 antimicrobials in the panel showed only slight fluctuations between 2006 and 2019. A rise in resistance was observed in 2020 and persisted through 2021. Susceptibility levels then returned to near pre-2020 levels in 2022 and 2023. In 2024, there was a rise in resistance, to similar levels as 2020 and 2021. In 2025, susceptibility levels have returned to levels similar to pre-2020 again. Despite these fluctuations in the last 5 years, the overall majority of *S. Dublin* isolates remain susceptible.

Salmonella Typhimurium

In 2025, 443 isolates of *Salmonella* Typhimurium were tested for antimicrobial susceptibility.

As shown in Table 13.3, the portion of *S. Typhimurium* isolates that were susceptible to all tested antimicrobials decreased slightly in 2025 at 51.1%, compared with 55.0% and 54.3% in 2023 and 2024, respectively. However, it has not dropped to pre-2023 levels.

Over half of all *S. Typhimurium* tested in 2025 originated from pigs, feed, and dogs. Among pig isolates (n=147), 2.7% were susceptible to all antimicrobials in the panels, while 94.6% tested as MDR. In contrast, 75.0% of isolates from dogs (n=64) and 74.6% of from feed (n=67) were susceptible to all antimicrobials in the panel. In previous years' reports, these contrasting resistance patterns have been shown to reflect difference in the phage types associated with each source. As stated previously, APHA no longer carried out phage typing as a supplementary test for the characterisation of *Salmonella* isolates.

Among 61 *S. Typhimurium* isolates from cattle, 90.0% were fully susceptible. Only one isolate was tested as MDR and showed the AmCSSuT pentavalent resistance pattern.

Resistance to the sulphamethoxazole and trimethoprim combination in *S. Typhimurium* was 31.9% in 2025, compared to 36.4% in 2024.

Apramycin resistance in *S. Typhimurium* was 6.6% in 2025, with 93.1% of resistant isolates originating from pigs (Table 13.3). This marks a decrease from 11.1% in 2024 and a change from the consistent rise seen in the previous 3 years.

Neomycin resistance decreased to 13.8% compared to 17.4% in 2024 but remains higher than levels in 2023 (12.5%). From 2022 to 2023, neomycin resistance levels rose to above 10.0% and has remained above since. In 2025, isolates were detected in pigs (n=55), horses (n=2), one from feed, one dog, one in cattle, and one badger.

Eleven *S. Typhimurium* isolates were resistant to nalidixic acid in 2025: 6 from feed, 4 from dogs, and one from a pheasant. One isolate from dogs and the isolate from the pheasant were also resistant to ciprofloxacin. These were the only 2 *S. Typhimurium* isolates showing ciprofloxacin resistance in 2025; these 2 isolates did not show resistance to any other antimicrobials on the panel, other than nalidixic acid and ciprofloxacin.

Monophasic *Salmonella* Typhimurium serovars

A total of 161 isolates of monophasic *S. Typhimurium* were tested in 2025. Most were from pigs (49.7%), dogs (20.5%), and feed (16.8%). Only 1.9% of isolates tested in 2025 were fully susceptible, while 80.7% were MDR. This indicates a decrease in fully susceptible isolates compared to 2024 (4.3%). The proportion of MDR isolates is similar to those observed in 2024.

The AmSuT resistance pattern was found in 75.2% of isolates. This pattern was most frequently accompanied by resistance to streptomycin. It was also frequently accompanied by resistance to neomycin, gentamicin, apramycin, chloramphenicol, and sulphamethoxazole and trimethoprim combination. Resistance was identified in 19.9% of isolates for apramycin, 23.6% for neomycin, and 20.5% for gentamicin. Twenty-one isolates (13.0%) were resistant to all 3 of these aminoglycosides; all these isolates originated from pigs, bar one which was from feed.

No nalidixic acid resistance was observed in monophasic *S. Typhimurium* isolates tested in 2025.

Serovars other than *Salmonella* Dublin and *Salmonella* Typhimurium

Of the 3,976 *Salmonella* isolates tested in 2025, excluding *S. Dublin* and *S. Typhimurium*, 80.2% were susceptible to all antimicrobials in the test panel (Table 13.5). This represents an increase compared to 2024 and is the highest level observed in the past twelve years. Susceptibility in *S. Enteritidis* isolates (n=100) markedly decreased to 58.0% in 2025, compared to 82.4% (n=108) in 2024 and 74.2% (n=66) in 2023. Thirty-four *S. Enteritidis* isolates were MDR, all from chickens.

Resistance to nalidixic acid was identified in 145 isolates (3.6%) of serovars other than *S. Dublin* and *S. Typhimurium*. The majority of these originated from feed (n=63). The majority of serovars other than *S. Dublin* and *S. Typhimurium* that were resistant to nalidixic acid belonged to serovars *S. Indiana* (n=48) and *S. Enteritidis* (n=37). Other main sources of nalidixic acid resistant isolates were chickens (n=44) and dogs (n=20). Among the 42 non-susceptible *S. Enteritidis* isolates, 37 showed resistance to nalidixic acid. The majority of these isolates were from chickens (n=35), with 2 from horses and one from a dog.

Ciprofloxacin resistance was detected in 15 isolates. This included 4 isolates from feed (1 *S. Albany*, 1 *S. Agona*, 1 *S. Infantis*, 1 *S. Kottbus*), 4 isolates from turkeys (all *S. Goldcoast*), 4 from dogs (2 *S. Kentucky*, 1 *S. Infantis*, 1 *S. Newport*), 2 isolates from chickens (1 *S. Infantis*, 1 untyped), and 1 environmental isolate (*S. Infantis*).

Seven isolates were resistant to both cefotaxime and ceftazidime. These included 4 isolates from turkeys (all *S. Goldcoast*), 2 isolates from dogs (both *S. Kentucky*), and one isolate from a horse (*S. Agama*).

MDR was observed in 161 isolates (4.0%). These included 34 *S. Enteritidis* (all from chickens), 25 *S. Infantis* (14 from feed, 6 from chickens, 4 from dogs, one from the environment), and 16 *S. Idikan* (14 from chickens, 2 from the environment).

Of the 130 *S. Infantis* isolates tested, 78.5% were fully susceptible, while 19.2% were MDR. The main sources of *S. Infantis* isolates were feed (n=73), dogs (n=29), and chickens (n=27). Of the isolates from feed, 57 were susceptible to all antimicrobials tested, and 14 were MDR. In dogs, 25 isolates were susceptible and 4 were MDR. Among *S. Infantis* isolates from chickens, 20 were fully susceptible and 14 were MDR.

Individual antimicrobials

Of the 4,929 *Salmonella* isolates tested in 2025, 76.0% were susceptible to all antimicrobials tested (Table 13.6). This is a slight increase in susceptibility in comparison to 2024 (73.3% of 4,705 isolates) and 2023 (73.3% of 5,513 isolates) and is in line with the levels recorded in 2022 (75.7% of 5,562 isolates).

Overall, resistance to most antimicrobials in the testing panel remained stable between 2024 and 2025. Ampicillin resistance was 10.7% in 2025 across all sources, which is in line with 2024 (10.9%). However, within individual sources, there were decreases in pigs (77.2% in 2024, 70.1% in 2025) and turkeys (19.8% in 2024, 15.4% in 2025), and increases in ducks (1.0% in 2024, 7.6% in 2025), horses (3.4% in 2024, 9.8% in 2025), and dogs (5.7% in 2024, 12.9% in 2025). No resistance was found to ampicillin in other avian species in 2024; 6.3% isolates showed resistance to ampicillin from other avian species in 2025 – this represented 2 out of 32 isolates.

Considering all *Salmonella* serovars tested in 2025, a modest decline was detected for resistance to sulphamethoxazole and trimethoprim combination, which decreased from 11.6% in 2024 to 9.6% in 2025. Resistance to apramycin (1.8%), streptomycin (11.5%), gentamicin (2.1%), and neomycin (4.0%) all slightly decreased to levels observed in 2024. Amikacin resistance was observed in 3 isolates in 2025. This was a decrease from 2024 (13 isolates); there was no detection of amikacin resistance in *Salmonella* isolates in 2023. *Salmonella* isolates from pigs (n=328), contributed most to the overall figures of resistance to aminoglycosides, with 49.1% of pig isolates showing resistance to streptomycin, 30.8% to neomycin, 21.6% to gentamicin, 21.3% to apramycin, and 0.6% to amikacin. Forty-five isolates from pigs were resistant to streptomycin, apramycin, neomycin and gentamycin and the serovars showing this resistance pattern were mostly *S. Typhimurium* and monophasic *S. Typhimurium*. Two *S. Typhimurium* isolates from pigs showed resistance to neomycin, gentamycin and amikacin; these were the only 2 isolates from pigs showing resistance to amikacin.

In 2025, 3.3% of isolates were resistant to nalidixic acid, in line with results from the previous year. Overall, 44.4% of isolates resistant to nalidixic acid (n=162) originated from feed, mostly involving the serovar *S. Indiana*. In turkeys isolates resistant to nalidixic acid belonged to the serovars *S. Senftenberg* (n=4) and *S. Goldcoast* (n=3). In chickens,

nalidixic acid resistance was detected in *S. Enteritidis* (34 of 39), *S. Infantis* (6 of 27), *S. Kedougou* (1 of 208), *S. Muenchen* (1 of 20), *S. Senftenberg* (1 of 13), 13,23:i:- (1 of 3).

Resistance to ciprofloxacin was 0.3% in 2025, compared to 0.7% in 2024. In 2025, ciprofloxacin resistance was observed in 5 isolates from dogs (2 *S. Kentucky*, one *S. Newport*, one *S. Infantis*, one *S. Typhimurium*), 4 from turkeys (4 *S. Goldcoast*), 4 from feed (one *S. Kottbus*, one *S. Infantis*, one *S. Agona*, one *S. Albany*), 2 from chickens (one 13,23:i:-, one *S. Infantis*), one *S. Infantis* from an environmental sample and one *S. Typhimurium* from a pheasant. All but one ciprofloxacin resistant isolates were also resistant to nalidixic acid.

Resistance to cefotaxime and ceftazidime remained stable in 2025 (0.2% each) and it was detected in 4 horse isolates (3 *S. Typhimurium* and one *S. Agama*), 4 turkey isolates (all *S. Goldcoast*), 2 dog isolates (both *S. Kentucky*), one *S. Enteritidis* from a chicken and one *S. Montevideo* from a feed sample. All but one of the isolates were MDR, with 8 showing a resistance pattern that involved 10 or more antimicrobials, including the 2 *S. Kentucky* isolates, the 4 *S. Goldcoast* isolates and 2 of the *S. Typhimurium* isolates from horses.

Public health considerations

Antimicrobial susceptibility patterns have been useful in conjunction with the *Salmonella* serovar to investigate the epidemiology of *Salmonella* infections. However, genome sequencing has replaced older methods of *Salmonella* typing for human isolates and is also being increasingly used to characterise and compare isolate from animals and humans. Ongoing liaison takes place between the Agencies concerned in relation to the strains detected and their resistance.

Among the antimicrobials considered in this report, resistance to third-generation cephalosporins and fluoroquinolones is of greatest public health concern, as these agents are critical for treating severe or invasive cases of human salmonellosis. Nonetheless, most non-typhoidal *Salmonella* infections in humans are self-limiting and confined to the gastrointestinal tract and therefore do not require antimicrobial therapy.

In 2025, MDR isolates (n=453) were mostly from pigs, accounting for 50.6% of the total. None of the MDR isolates from pigs showed resistance to ciprofloxacin or third-generation cephalosporins. In contrast, although chickens, feed, and dogs contributed fewer MDR isolates overall (19.2%, 12.8%, and 9.7%, respectively) they included strains resistant to critically important antimicrobials. Of the 189 MDR isolates from these 3 sources, 26 (13.8%) showed resistance to ciprofloxacin or third-generation cephalosporins. Of these 26 isolates, 20 belonged to the serovar *S. Infantis* (76.9%).

In addition to interagency collaboration, APHA offers a veterinary advisory visit and a range of support when cases of *Salmonella* infection in food-producing animals with resistance to highly important antimicrobials such as third-generation cephalosporins or ciprofloxacin are detected, both to explain the significance of the findings and to provide appropriate advice on control.

***Salmonella* Goldcoast isolates**

In 2025, 5 *Salmonella* Goldcoast isolates were recovered from turkeys under the National Control Programme (NCP) for *Salmonella*. One isolate was fully sensitive to all antimicrobials tested, while the other 4 were MDR, including resistance to ciprofloxacin and third-generation cephalosporins. Synergy with ceftazidime/clavulanate and cefotaxime/clavulanate confirmed an extended-spectrum β -lactamase (ESBL) phenotype. Whole genome sequencing identified *bla*_{CTX-M-55} and *qnrS13* genes, accounting for the cephalosporin and fluoroquinolone resistances, respectively. The IncHI-2 plasmid replicon was also identified.

Third-generation cephalosporins and fluoroquinolones are highest priority critically important antimicrobials (HPClAs). The genetic profile of these isolates closely resembles the MDR *S. Goldcoast* strains previously reported in the UK and Taiwan, including the ST358 clone (Liao et al., 2019). IncHI2 plasmids from Taiwanese *S. Goldcoast* strains have also been reported in a Canadian study investigating raw meat-based diets for dogs (Bernaquez et al., 2025).

APHA undertook epidemiological investigations and worked with affected farms to conduct additional sampling and implement *Salmonella* control measures, including enhanced cleaning, disinfection and biosecurity protocols. The source of the MDR *S. Goldcoast* could not be definitely determined. Ongoing surveillance and horizon scanning for AMR continue at APHA, in close collaboration with the FSA, VMD, and UKHSA.

In addition to these cases, 12 further *S. Goldcoast* isolates were identified in 2025 from feed samples; all were fully sensitive to all antimicrobials tested.

Table 13.2: *Salmonella* Dublin in cattle: antimicrobial susceptibility monitoring 2016 to 2025

The table below shows the percentage of *S. Dublin* isolates from cattle resistant to each of the antimicrobials from 2016 to 2025. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
AM	0.4%	0.0%	0.0%	0.0%	1.2%	1.1%	0.0%	0.4%	0.0%	0.7%
C	0.4%	0.0%	0.3%	0.4%	2.3%	1.1%	0.4%	0.0%	0.5%	0.7%
NA	1.2%	0.0%	2.2%	0.0%	1.6%	0.7%	0.0%	0.4%	0.0%	1.3%
S	1.6%	0.0%	0.3%	0.4%	0.8%	0.7%	3.2%	1.9%	4.9%	2.3%
APR	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%	0.7%
CN	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
N	0.0%	0.0%	0.3%	0.0%	5.1%	2.6%	0.0%	0.0%	2.5%	0.3%
FR	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	2.5%	0.0%
SU	0.0%	0.0%	0.3%	0.4%	0.8%	0.4%	0.8%	0.0%	0.0%	0.7%
TM	0.0%	0.0%	0.0%	0.7%	0.8%	0.4%	0.4%	0.0%	0.0%	0.0%
T	0.4%	0.0%	0.3%	0.4%	3.9%	6.0%	0.0%	0.0%	0.0%	0.3%
Susceptible to all 16 antimicrobials	96.3%	100.0%	96.2%	99.6%	88.9%	88.3%	96.4%	96.3%	90.2%	95.4%
Total isolates tested	245	272	320	269	256	267	250	270	203	303

Table 13.3: *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2016 to 2025

The table below shows the percentage of *S. Typhimurium* isolates that were resistant to each of the antimicrobials over the last 10 years. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
AM	60.2%	58.3%	30.1%	46.1%	50.0%	43.0%	39.7%	36.6%	38.7%	39.1%
C	57.8%	53.5%	29.9%	44.1%	45.2%	37.0%	32.4%	31.2%	35.7%	37.3%
NA	0.0%	1.6%	0.4%	0.0%	3.0%	8.8%	4.4%	2.9%	2.1%	2.5%
S	63.9%	57.1%	40.7%	40.2%	49.7%	34.3%	37.2%	31.4%	30.4%	28.7%
APR	2.4%	0.0%	1.8%	0.8%	0.9%	1.5%	4.4%	6.8%	11.1%	6.6%
N	0.6%	0.0%	1.8%	0.8%	7.8%	9.9%	7.3%	12.5%	17.4%	13.8%
FR	0.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
SU	66.3%	62.6%	44.0%	46.1%	58.4%	47.1%	43.9%	40.3%	42.7%	43.9%
TM	28.9%	19.8%	15.7%	24.0%	33.7%	25.3%	22.9%	30.5%	36.4%	31.9%
T	61.4%	54.5%	36.3%	42.1%	50.6%	39.0%	36.4%	30.3%	29.2%	34.6%
Susceptible to all 16 antimicrobials	30.1%	34.2%	54.4%	49.2%	39.9%	44.3%	47.8%	55.0%	54.3%	51.1%
Total isolates tested	166	187	504	254	340	467	494	558	569	443

Table 13.4: Sulphamethoxazole and trimethoprim combination resistance in *Salmonella* Typhimurium from domestic livestock in 2016 to 2025

The following table outlines the number of *S. Typhimurium* isolates tested in different species of livestock between 2016 and 2025 and the percentages of these that were resistant to sulphamethoxazole and trimethoprim combination.

Year	Cattle (%)	Sheep (%)	Pigs (%)	Chickens (%)	Turkeys (%)	Ducks (%)
2016	23 (8.7)	12 (0.0)	47 (87.2)	8 (0.0)	0 (0.0)	1 (0.0)
2017	52 (0.0)	25 (0.0)	39 (82.1)	5 (0.0)	0 (0.0)	5 (0.0)
2018	92 (2.2)	175 (0.0)	79 (87.3)	10 (0.0)	6 (0.0)	10 (0.0)
2019	51 (1.9)	4 (0.0)	58 (98.3)	12 (0.0)	0 (0.0)	2 (0.0)
2020	61 (8.2)	8 (0.0)	111 (84.7)	28 (3.6)	1 (100.0)	1 (0.0)
2021	75 (4.0)	16 (0.0)	118 (83.9)	23 (0.0)	3 (0.0)	0 (0.0)
2022	69 (0.0)	9 (11.1)	125 (82.4)	20 (0.0)	1 (0.0)	0 (0.0)
2023	93 (1.1)	10 (10.0)	176 (91.5)	21 (0.0)	2 (0.0)	1 (0.0)
2024	60 (1.7)	8 (0.0)	214 (95.3)	18 (0.0)	13 (0.0)	0 (0.0)
2025	61 (1.6)	7 (0.0)	147 (90.0)	7 (0.0)	0 (0.0)	1 (0.0)

Table 13.5: *Salmonella* other than *Salmonella* Dublin and *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2016 to 2025

The following table outlines the number *Salmonella* isolates other than *S. Dublin* and *S. Typhimurium* tested between 2016 and 2025 and the percentages of these that were resistant to the antimicrobials tested against. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
AM	11.1	10.3	7.7	7.4	10.3	11.2	9.8	7.3	7.5	5.4
C	2.6	2.0	1.5	2.1	2.4	2.6	1.9	2.4	2.3	1.1
NA	2.6	5.8	1.4	2.7	3.3	5.5	3.9	3.4	3.8	3.6
S	16.0	13.1	11.7	15.0	11.4	13.4	10.2	9.8	10.1	7.7
APR	2.0	1.6	0.8	1.3	1.2	2.4	1.2	1.2	1.1	0.6
N	2.2	2.0	1.8	2.6	3.0	5.2	2.3	2.1	3.5	2.4
FR	1.4	1.6	1.2	1.6	1.0	2	0.8	1.0	1.5	0.8
SU	23.7	19.0	15.7	20.2	19.8	16.2	13.3	17.8	16.5	13.6
TM	10.4	6.2	5.3	10.2	11.7	6.4	6.7	10.9	8.7	7.2
T	22.9	19.6	14.9	20.2	19.3	18.5	11.8	14.6	12.8	9.6
Percentage susceptible to all 16 antimicrobials	68.9	71.2	77.7	71.9	69.5	68.5	77.2	73.9	74.9	80.2
No of isolates	1,986	5,652	3,589	4,010	3,617	3,665	4,735	4,638	3,890	3,976

Table 13.6: All *Salmonella*: antimicrobial susceptibility in 2025 and resistances to individual antimicrobials

The tables below show the percentage of isolates resistant to each antimicrobial in 2025 from different sources, split into livestock and sources other than livestock. For a key to the antimicrobials used see table 13.1.

Isolations from livestock

Antimicrobial	Cattle	Sheep	Pigs	Chickens	Turkeys	Ducks	Total livestock	Total (livestock and non-livestock)
AM	1.3 %	0.0 %	70.1 %	5.6 %	15.4 %	7.6 %	12.6 %	10.7 %
AMC	0.2 %	0.0 %	0.0 %	0.1 %	0.0 %	0.0 %	0.1 %	0.1 %
CAZ	0.0 %	0.0 %	0.0 %	0.0 %	15.4 %	0.0 %	0.1 %	0.2 %
CTX	0.0 %	0.0 %	0.0 %	0.1 %	15.4 %	0.0 %	0.2 %	0.2 %
C	0.7 %	0.0 %	53.4 %	0.8 %	15.4 %	0.0 %	7.1 %	5.2 %
NA	0.9 %	0.0 %	0.6 %	2.5 %	26.9 %	0.0 %	2.1 %	3.3 %
CIP	0.0 %	0.0 %	0.0 %	0.1 %	15.4 %	0.0 %	0.2 %	0.3 %
S	4.4 %	3.3 %	49.1 %	8.4 %	34.6 %	0.8 %	12.4 %	11.5 %
APR	0.7 %	0.0 %	21.3 %	0.4 %	0.0 %	0.0 %	2.9 %	1.8 %
CN	0.2 %	0.0 %	21.6 %	0.7 %	15.4 %	0.0 %	3.2 %	2.1 %
N	0.4 %	3.3 %	30.8 %	1.7 %	26.9 %	0.8 %	5.2 %	4.0 %
FR	0.0 %	0.0 %	0.0 %	0.6 %	0.0 %	0.0 %	0.4 %	0.7 %
SU	3.3 %	1.7 %	72.0 %	17.3 %	50.0 %	5.9 %	21.0 %	18.0 %
TM	0.2 %	0.0 %	54.3 %	10.0 %	19.2 %	5.9 %	13.3 %	9.6 %
T	3.5 %	3.3 %	57.6 %	7.8 %	50.0 %	1.7 %	13.1 %	13.6 %

Antimicrobial	Cattle	Sheep	Pigs	Chickens	Turkeys	Ducks	Total livestock	Total (livestock and non-livestock)
Percentage susceptible to all 16 antimicrobials	93.6%	91.7%	21.6%	78.7%	34.6%	90.7%	74.8%	76.0%
No of isolates	456	60	328	1,778	26	118	2,766	4,929

Isolations from sources other than livestock

Antimicrobial	Horses	Dogs	Other non-avian species	Other avian species	Feed	Environment	Total non-livestock	Total (livestock and non-livestock)
AM	9.8 %	12.9 %	4.6 %	6.3 %	8.6 %	2.2 %	8.3 %	10.7 %
AMC	0.0 %	0.7 %	0.6 %	0.0 %	0.0 %	0.0 %	0.2 %	0.1 %
CAZ	4.3 %	0.5 %	0.0 %	0.0 %	0.0 %	0.0 %	0.3 %	0.2 %
CTX	4.3 %	0.5 %	0.0 %	0.0 %	0.1 %	0.0 %	0.3 %	0.2 %
C	6.5 %	5.2 %	2.3 %	6.3 %	1.7 %	1.1 %	2.6 %	5.2 %
NA	2.2 %	6.2 %	0.0 %	3.1 %	5.9 %	2.6 %	4.9 %	3.3 %
CIP	0.0 %	1.2 %	0.0 %	3.1 %	0.3 %	0.4 %	0.5 %	0.3 %
S	22.8 %	14.0 %	11.5 %	18.8 %	8.8 %	5.2 %	10.3 %	11.5 %
APR	0.0 %	0.7 %	1.1 %	3.1 %	0.2 %	0.0 %	0.4 %	1.8 %
CN	4.3 %	1.2 %	1.1 %	3.1 %	0.3 %	0.0 %	0.7 %	2.1 %
N	5.4 %	2.9 %	2.3 %	3.1 %	2.3 %	1.9 %	2.5 %	4.0 %
FR	0.0 %	1.2 %	1.7 %	0.0 %	1.2 %	0.7 %	1.1 %	0.7 %
SU	21.7 %	14.0 %	4.6 %	6.3 %	17.4 %	5.2 %	14.2 %	18.0 %
TM	6.5 %	4.0 %	2.3 %	3.1 %	6.1 %	1.5 %	4.8 %	9.6 %
T	21.7 %	13.1 %	5.2 %	6.3 %	17.4 %	7.1 %	14.3 %	13.6 %

Antimicrobial	Horses	Dogs	Other non-avian species	Other avian species	Feed	Environment	Total non-livestock	Total (livestock and non-livestock)
Percentage susceptible to all 16 antimicrobials	75.0%	76.0%	80.5%	71.9%	75.9%	87.3%	77.6%	76.0%
No of isolates	92	420	174	32	1,177	268	2,163	4,929

Other non-avian species included alpaca, badger, cat, cheetah, deer, elephant, frog, giraffe, hedgehog, leopard, lion, lizard, meerkat, other mammal, primate, reptile/amphibian, seal, snake, tortoise and zebra. Other avian species included bird of prey, budgerigar, crow, falcon, gull, lorikeet, owl, penguin, pheasant, pigeon and rhea.

Annexe

From 1 January 2023 whole genome sequencing (WGS)-based typing replaced phenotypic serotyping as the primary method of characterisation of *Salmonella* isolates from submissions to APHA. The below tables present the seven-gene multi-locus sequence typing (MLST) sequence types (STs) for all isolations of each serovar included in the above Chapters 2 to 12. Where no ST data is available this is usually due to the presence of novel sequence variants at one or more of the seven MLST genes and hence of a novel seven-gene MLST profile, thus resulting in no ST being assigned by the in silico *Salmonella* typing pipeline. All novel STs were checked against Enterobase for matches and updated where possible.

Table A1: Sequence types of *Salmonella* isolations in cattle in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type (ST)	2024 isolations	2025 isolations
4,5,12:-:-	34	2	0
4,5,12:a:-	1063	1	0
6,7:z10:-	413	2	1
61:k:1,5,(7)	432	0	6
Agona	10	0	1
Anatum	64	1	0
Bovismorbificans	377	0	1
Coeln	1995	2	0
Derby	682	0	1
Dublin	10	213	304
Dublin	8819	0	1
Dublin	No ST data	2	9
Enteritidis	11	1	1
Indiana	17	3	0
Kottbus	212	0	1
London	No ST data	1	0
Mbandaka	13	0	2
Mbandaka	413	44	48
Mbandaka	5078	1	3
Mbandaka	No ST data	0	1
Monophasic Typhimurium	34	3	5
Montevideo	138	23	17
Montevideo	No ST data	1	1
Newport	45	2	3
Newport	166	1	1
Orion	639	1	0

<i>Salmonella</i> serovar	Sequence Type (ST)	2024 isolations	2025 isolations
Stanleyville	1986	0	1
Typhimurium	19	62	58
Total	not applicable	366	466

Table A2: Sequence types of *Salmonella* isolations in sheep in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
61:k:1,5,(7)	432	64	57
61:k:1,5,(7)	No ST data	1	0
Agama	2223	1	0
Chester	1954	0	1
Dublin	10	12	5
Dublin	8819	2	0
Monophasic Typhimurium	34	1	0
Montevideo	195	14	6
Typhimurium	19	6	12
Urbana	512	0	1
Total	not applicable	101	82

Table A3: Sequence types of *Salmonella* isolations in goats in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
61:k:1,5,(7)	432	1	0
Dublin	10	1	0
Total	not applicable	2	0

Table A4: Sequence types of *Salmonella* isolations in pigs in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
4,5,12:-:-	34	1	0
Bovismorbificans	142	7	5
Bovismorbificans	377	1	0
Braenderup	22	0	1
Cerro	1593	0	1
Derby	39	1	0
Derby	40	7	10
Derby	682	25	23
Dublin	10	1	1
Hessarek	5723	1	0

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Kedougou (including monophasic variants)	1543	5	6
Livingstone	457	0	1
London	682	0	1
London	2124	1	0
London	No ST data	0	1
Monophasic Typhimurium	19	1	1
Monophasic Typhimurium	34	69	60
Newport	166	20	16
Panama	48	7	8
Panama	No ST data	0	1
Reading	1628	2	5
Reading	No ST data	5	5
Rissen	469	1	1
Typhimurium	19	151	102
Typhimurium	34	3	1
Typhimurium	568	1	0
Typhimurium	8336	0	1
Typhimurium	No ST data	1	2
Total	not applicable	311	253

Table A5: Sequence types of *Salmonella* isolations in horses in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
4,12:b:-	No ST data	0	1
4,5,12:b:-	42	0	1
Agama	19	0	2
Agama	885	1	5
Agama	2223	1	0
Agama	2267	0	1
Anatum	64	1	0
Blockley	52	1	0
Bonn	19	0	1
Bonn	2636	1	0
Bovismorbificans	377	1	0
Bovismorbificans	1499	0	1
Coeln	1995	0	2
Concord	3937	1	0
Durham	2225	0	1
Eastbourne	93	1	0
Enteritidis	11	1	5

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Enteritidis	183	1	0
Enteritidis	5492	1	0
Enteritidis	6086	1	0
Enteritidis	8943	2	6
Enteritidis	10467	2	2
Fulica	1063	2	1
Heidelberg	15	0	1
Heidelberg	19	0	1
Hessarek	19	0	1
Kentucky	314	0	1
Kingston	2005	1	0
Kottbus	212	0	1
Monophasic Typhimurium	19	0	1
Monophasic Typhimurium	34	1	2
Newport	45	4	5
Newport	614	1	0
Oslo	1370	3	0
Stanleyville	97	1	0
Typhimurium	19	21	27
Typhimurium	34	1	0
Typhimurium	568	2	0
Typhimurium	8336	0	1
Typhimurium	8937	0	1
Typhimurium	No ST data	0	1
Total	not applicable	53	71

In 2025, one isolation of *S. Enteritidis* yielded two sequence types (ST11 and ST10467); this is only counted once in the total number of isolations.

Table A6: Sequence types of *Salmonella* isolations in deer in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Monophasic Typhimurium	34	1	0
Typhimurium	19	1	0
Total	not applicable	2	0

Table A7: Sequence types of *Salmonella* isolations in rabbits in 2024 and 2025

There were no *Salmonella* isolations in rabbits in 2024 or 2025.

Table A8: Sequence types of *Salmonella* isolations in chickens in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
4,12:d:-	279	2	3
4,5,12:b:-	679	0	2
4,5,12:b:-	No ST data	0	1
6,7:-:enz15	413	1	0
13,23:-:-	No ST data	0	1
61:k:1,5,(7)	432	8	9
Agama	885	1	11
Agama	1666	0	1
Agona	13	135	133
Agona	No ST data	1	0
Altona	1549	0	1
Anatum	64	10	4
Berta	435	1	0
Braenderup	22	2	1
Bredeney	897	1	0
Chester	411	1	0
Chester	1954	1	2
Coeln	2015	1	0
Corvallis	1541	1	0
Cubana	286	0	1
Derby	40	1	1
Derby	71	8	4
Derby	682	0	1
Enteritidis	11	7	10
Enteritidis	6086	1	6
Enteritidis	8943	1	0
Enteritidis	10467	3	7
Give	516	0	7
Give	524	0	3
Grumpensis	2060	0	1
Havana	1524	1	0
Idikan (incl. monophasic variants)	1891	677	899
Idikan (incl. monophasic variants)	No ST data	2	10
Indiana	17	7	4
Infantis	32	20	27
Isangi	216	0	1
Isangi	1994	0	1
Kedougou (incl. monophasic variants)	1543	381	416

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Kedougou (incl. monophasic variants)	No ST data	1	7
Kentucky	314	18	5
Kingston	2005	1	3
Kottbus	212	4	5
Livingstone	457	4	4
Livingstone	638	2	0
London	155	0	1
Mbandaka	413	168	233
Mbandaka	1611	0	2
Mbandaka	No ST data	0	2
Meleagridis	463	0	1
Minnesota	548	0	1
Monophasic Typhimurium	34	1	4
Montevideo	138	1	3
Montevideo	316	307	335
Montevideo	No ST data	0	3
Muenchen	82	27	20
Newport	45	5	1
Newport	166	7	1
Newport	614	14	15
Nima	520	0	1
Nottingham	1640	1	0
Ohio	329	44	83
Orion	639	0	2
Orion var 15+ (Binza)	639	50	72
Oslo	1370	2	4
Ouakam	No ST data	0	1
Panama	48	1	1
Paratyphi B var. Java	127	0	1
Poona	812	1	0
Richmond	2007	0	1
Rissen	469	0	2
Schwarzengrund	96	0	2
Senftenberg	14	9	14
Senftenberg	185	1	1
Stanleyville	97	0	1
Tennessee	319	0	2
Typhimurium	19	17	6
Typhimurium	8937	0	1
Uganda	684	0	1
Untypable	No ST data	0	1

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Virchow	303	0	3
Wangata	5281	0	1
Total	not applicable	1,961	2,407

In 2025 3 isolations of *S. Enteritidis* yielded 3 sequence types (all 3 isolations yielded ST11, ST6086 and ST10467) and 2 isolations of *S. Enteritidis* yielded 2 sequence types (one isolation yielded ST6086 and ST10467 and one isolation yielded ST11 and ST10467). These are counted only once in the total number of isolations.

Table A9: Sequence types of *Salmonella* isolations in turkeys in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Ago	2565	1	0
Agona	13	20	5
Anatum	64	21	1
Derby	71	3	0
Give	524	0	3
Goldcoast	358	0	5
Idikan (incl. monophasic variants)	1891	5	0
Indiana	17	9	0
Javiana	24	2	0
Kedougou (incl. monophasic variants)	1543	21	10
Livingstone	457	2	0
Orion	639	0	2
Orion var 15+ (Binza)	639	5	0
Oslo	1370	2	0
Senftenberg	14	4	4
Typhimurium	19	13	0
Uganda	684	0	3
Total	not applicable	108	33

Table A10: Sequence types of *Salmonella* isolations in ducks in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Give	524	5	11
Give var 15+ (Newbrunswick)	524	3	0
Hadar	33	2	0
Indiana	17	146	78
Indiana	No ST data	1	0

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Kedougou (incl. monophasic variants)	1543	2	0
Kingston	2005	1	0
Kottbus	582	12	7
Lexington	247	1	8
Newport	166	0	6
Newport	614	20	2
Orion	639	2	0
Orion var 15+ (Binza)	639	1	1
Typhimurium	19	0	1
Total	not applicable	196	113

In 2025, one isolation of *S. Newport* yielded two sequence types (ST166 and ST614); this is only counted once in the total number of isolations.

Table A11: Sequence types of *Salmonella* isolations in geese in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Typhimurium	19	1	0
Total	not applicable	1	0

Table A12: Sequence types of *Salmonella* isolations in pigeons in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Braenderup	22	1	0
Typhimurium	19	3	4
Typhimurium	128	15	5
Typhimurium	8937	3	3
Total	not applicable	22	12

Table A13: Sequence types of *Salmonella* isolations in pheasants in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Senftenberg	14	0	2
Typhimurium	19	0	1
Total	not applicable	0	3

Table A14: Sequence types of *Salmonella* isolations in dogs in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
4,12:b:-	42	0	1
4,12:b:-	53	1	0
4,12:b:-	679	1	0
4,12:d:-	279	1	0
4,12:z:-	No ST data	1	0
4,5,12:b:-	42	0	1
4,5,12:b:-	679	2	0
4,[5],12,[27]:b:e,n,x	53	1	0
6,8:-:-	8767	2	0
9,12:l,v:-	20	1	0
9,12:z29:1,5	No ST data	0	1
21:g,f,t:-	6970	5	0
38:Z10:-	9407	0	1
42:k:z35	876	0	1
48:z4,z23:-	2811	1	1
61:k:1,5,(7)	432	1	3
Abony	1583	1	0
Adelaide	4024	3	2
Agama	885	6	8
Agama	2223	2	0
Agama	2267	1	0
Agona	13	15	14
Ajiobo	2017	1	0
Aijobo	4349	0	2
Albany	292	0	1
Alpenquai	5704	0	1
Anatum	64	27	12
Ank	8073	1	0
Baildon	2166	0	1
Ball	3502	0	1
Bareilly	362	0	2
Berta	435	3	0
Bonn	2636	0	1
Bovismorbificans	142	5	1
Bovismorbificans	377	1	0
Brancaster	9048	2	0
Braenderup	311	0	9
Brandenburg	65	2	2
Bredeney	306	0	2
Bredeney	897	1	0

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Cerro	367	1	0
Cerro	1593	4	1
Chailey	582	1	0
Chester	1954	0	2
Choleraesuis	145	0	1
Coeln	1995	1	5
Coeln	2015	2	2
Concord	3937	2	1
Derby	39	1	1
Derby	40	3	3
Derby	71	7	3
Derby	682	8	10
Dublin	10	16	29
Dublin	8819	1	0
Eboko	5470	0	1
Enteritidis	11	4	7
Enteritidis	183	7	2
Enteritidis	6086	1	0
Enteritidis	8353	0	1
Enteritidis	8943	1	1
Enteritidis	10467	4	4
Fresno	649	1	0
Fulica	1063	2	2
Gaminara	239	0	1
Give	516	1	2
Give	524	3	2
Goldcoast	358	1	0
Hadar	33	2	4
Havana	588	1	0
Heidelberg	15	0	1
Hessarek	5723	1	0
Idikan (incl. monophasic variants)	1891	0	1
Indiana	17	21	15
Infantis	32	39	29
Javiana	24	2	0
Johannesburg	515	0	1
Kampemba	490	0	1
Kapemba	5104	0	1
Kedougou (incl. monophasic variants)	1543	2	2
Kentucky	198	2	2

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Kentucky	314	15	2
Kingston	2005	1	2
Kottbus	212	9	12
Kottbus	582	4	0
Kottbus	8767	0	1
Leeuwarden	No ST data	1	0
Liverpool	1959	1	4
Livingstone	457	0	1
Livingstone	543	1	1
Livingstone	1941	11	6
London	155	4	1
London	No ST data	4	0
Manhattan	18	0	1
Mapo	6262	0	3
Mbandaka	413	5	11
Mbandaka	1611	0	1
Mbandaka	5078	1	1
Mbandaka	9414	0	1
Mbandaka	No ST data	1	0
Meleagridis	463	1	0
Mikawasima	1815	0	1
Monophasic Typhimurium	19	0	1
Monophasic Typhimurium	34	19	30
Monophasic Typhimurium	36	0	1
Montevideo	195	4	1
Montevideo	316	6	3
Muenchen	82	3	1
Muenster	321	8	5
Newport	31	0	2
Newport	45	11	4
Newport	118	1	0
Newport	164	1	0
Newport	166	11	5
Newport	614	6	1
Ohio	329	1	1
Oslo	1370	7	8
Panama	48	1	3
Paratyphi B var. Java	28	0	1
Paratyphi B var. Java	88	0	2
Poona	812	1	0
Reading	93	1	0

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Reading	1628	1	0
Reading	No ST data	0	1
Rissen	469	0	2
Rissen	11431	1	0
Saintpaul	No ST data	0	1
Schwarzengrund	96	1	2
Senftenberg	14	3	1
Senftenberg	210	1	0
Senftenberg	217	0	1
Singapore	5213	1	0
Soerenga	1659	0	1
Stanleyville	97	12	5
Stanleyville	1986	0	5
Stourbridge	736	1	0
Stourbridge	3736	0	1
Tennessee	319	0	3
Tennessee	2538	1	0
Tennessee	3288	1	0
Thompson	26	10	3
Toulon	5114	0	1
Typhimurium	19	60	51
Typhimurium	34	0	1
Typhimurium	36	2	0
Typhimurium	313	13	9
Typhimurium	568	2	0
Uganda	684	1	1
Untypable	not applicable	1	1
Virchow	16	0	1
Yoruba	1316	0	1
Total	not applicable	482	416

Table A14: Sequence types of *Salmonella* isolations in wildlife in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
4,12:a:-	416	1	0
4,5,12:b:-	679	1	0
50:z10:z	838	0	1
Eboko	5470	1	0
Enteritidis	183	6	4
Enteritidis	3750	0	1

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Hessarek	5723	0	4
Typhimurium	19	4	5
Typhimurium	36	0	2
Typhimurium	313	1	0
Total	not applicable	14	17

Table A15: Sequence types of *Salmonella* isolations in feeds in 2024 and 2025

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
3,10:-:-	No ST data	1	0
3,10:b:-	No ST data	0	1
3,15:b:-	No ST data	0	1
4,12:b:-	42	0	4
4,12:d:-	279	0	2
4,5,12:b:-	679	0	1
47:z4,z23:-	2023	0	1
48:z4,z23:-	2811	2	0
50:z52:1,5,7	5743	0	1
61:i:z53	4303	3	0
61:k:1,5,(7)	432	16	8
Adelaide	2272	0	1
Agama	885	9	6
Agama	2223	0	1
Agama	No ST data	0	1
Agona	13	29	23
Albany	292	0	1
Amager	293	1	1
Amsterdam	2090	1	0
Anatum	64	12	9
Bareilly	909	0	1
Bolton	No ST data	0	1
Bonn	2636	0	1
Bovismorbificans	142	2	3
Brandenburg	65	1	0
Brandenburg	2577	0	2
Bredeney	306	1	1
Cerro	1593	2	2
Chester	411	0	1
Chester	1954	0	4
Coeln	1995	2	7
Corvallis	1541	1	0

Salmonella serovar	Sequence Type	2024 isolations	2025 isolations
Cubana	286	1	1
Cubana	7940	1	0
Derby	39	1	1
Derby	40	9	4
Derby	71	8	9
Derby	682	8	6
Derby	No ST data	1	0
Dublin	10	12	11
Dublin	No ST data	0	2
Durban	2330	0	1
Durham	3238	0	2
Ealing	2013	4	0
Enteritidis	11	8	5
Enteritidis	6086	5	0
Enteritidis	10467	15	6
Falkensee	3093	2	0
Fulica	1063	0	1
Give	516	0	4
Give	524	3	4
Goldcoast	358	1	5
Grumpensis	2060	0	2
Hadar	33	0	5
Haifa	49	0	1
Haifa	2492	0	3
Haifa	4881	0	1
Havana	872	0	1
Havana	1526	7	18
Havana	No ST data	0	1
Idikan (incl monophasic variants)	1891	10	15
Indiana	17	37	31
Infantis	32	84	49
Infantis	1032	0	6
Infantis	No ST data	0	1
Isangi	216	12	1
Isangi	1994	1	0
Jerusalem	1028	0	1
Johannesburg	471	0	2
Kaapstad	4605	1	0
Kassel	6849	1	0

Salmonella serovar	Sequence Type	2024 isolations	2025 isolations
Kedougou	1543	103	85
Kentucky	314	7	2
Kingston	2005	1	0
Kottbus	212	2	3
Kottbus	582	12	3
Leeuwarden	4347	0	1
Lexington	247	1	2
Liverpool	1959	1	11
Livingstone	457	1	2
Livingstone	543	1	1
Livingstone	1941	1	1
Livingstone	No ST data	0	1
London	155	1	11
London	2124	1	0
London	No ST data	1	7
Mbandaka	413	26	31
Mbandaka	1611	0	5
Mbandaka	5078	3	0
Mbandaka	9414	1	6
Meleagridis	463	0	8
Mississippi	448	0	1
Molade	544	4	2
Monophasic Typhimurium	19	0	2
Monophasic Typhimurium	34	20	15
Montevideo	138	6	3
Montevideo	195	3	4
Montevideo	316	9	85
Montevideo	699	0	1
Montevideo	10441	0	2
Montevideo	12723	1	0
Muenchen	82	0	2
Muenchen	112	1	0
Muenster	321	3	4
Muenster	No ST data	0	1
Newport	31	0	1
Newport	45	4	0
Newport	46	0	1
Newport	164	1	1
Newport	166	7	5

Salmonella serovar	Sequence Type	2024 isolations	2025 isolations
Newport	614	2	1
Nottingham	1640	3	0
Ohio	329	114	51
Oranienburg	174	0	2
Oranienburg	1044	0	1
Oranienburg	11828	0	1
Orion var 15+ (Binza)	639	0	1
Oslo	1370	1	8
Ouakam	No ST data	0	1
Panama	48	2	5
Paris	No ST data	0	1
Pomona	451	0	1
Poona	308	2	0
Poona	No ST data	0	1
Reading	1628	1	1
Reading	No ST data	0	1
Richmond	909	1	0
Ridge	2022	0	2
Riggil	No ST data	1	0
Rissen	469	27	13
Rissen	11431	2	0
Riuru	2668	0	1
Saintpaul	49	1	0
Saintpaul	50	0	1
Saintpaul	2059	1	0
Saintpaul	No ST data	1	0
Schwarzengrund	96	1	0
Senftenberg	14	3	14
Senftenberg	185	7	2
Senftenberg	210	9	24
Senftenberg	No ST data	0	2
Singapore	462	0	2
Soerenga	1659	0	4
Stanley	29	1	0
Stanleyville	97	1	0
Stanleyville	1986	1	0
Szentes	427	1	0
Taksony	2204	0	1
Telaviv	1068	1	0

<i>Salmonella</i> serovar	Sequence Type	2024 isolations	2025 isolations
Tennessee	319	1	3
Tennessee	5018	1	1
Thompson	26	2	2
Typhimurium	19	53	41
Typhimurium	34	1	1
Typhimurium	36	0	1
Typhimurium	513	1	0
Typhimurium	4358	0	1
Typhimurium	8937	2	2
Uganda	684	8	6
Umbilo	2014	1	0
Virchow	16	0	1
Virchow	303	1	1
Yoruba	1316	2	1
Zehlendorf	No ST data	1	0
Total	Not applicable	795	798

References

Anderson EH, Ward L, De Saxe MJ, and DeSa JDH (1977). Bacteriophage – Typing Designations of *S. Typhimurium*. *Journal of Hygiene* **78**, pp. 297–300.

Agricultural Survey references:

- English Government (2025) [Livestock populations in England](#)
- Scottish Government (2025) [Results from the Scottish Agricultural Census: June 2025](#)
- Welsh Government (2025) [Survey of agriculture and horticulture: June 2025](#)

APHA (2022) [Veterinary Investigation Surveillance Annual Report \(VIDA\) 2021.](#)

APHA (2023) [Veterinary Investigation Surveillance Annual Report \(VIDA\) 2022.](#)

APHA (2024) [Veterinary Investigation Surveillance Annual Report \(VIDA\) 2023.](#)

APHA (2025) [Veterinary Investigation Surveillance Annual Report \(VIDA\) 2024.](#)

APHA (2026) [Veterinary Investigation Surveillance Annual Report \(VIDA\) 2025.](#)

Achtman M, Wain J, Weill FX, Nair S, Zhou Z, Sangal V, Krauland MG, Hale JL, Harbottle H, Uesbeck A, Dougan G, Harrison LH, Brisse S; S. Enterica MLST Study Group. Multilocus sequence typing as a replacement for serotyping in *Salmonella enterica*. PLoS Pathog. 2012;8(6):e1002776. doi: 10.1371/journal.ppat.1002776. Epub 2012 Jun 21. Erratum in: PLoS Pathog. 2020 Oct 21;16(10):e1009040. doi: 10.1371/journal.ppat.1009040. PMID: 22737074; PMCID: PMC3380943.

Bernaquez I, Dumaresq J, Picard I, Gaulin C, Dion R, Weaver K, Walker M, Kearney A, Bharat A, Fafard J, Bekal S. Dogs fed raw meat-based diets are vectors of drug-resistant *Salmonella* infection in humans. *Communications Medicine* (London) 2025 Jun 4;5(1):214. doi: [10.1038/s43856-025-00919-2](#). PMID: 40467866; PMCID: PMC12137576.

Botti V, Navillod FV, Domenis L, Orusa R, Pepe E, Robetto S, Guidetti C. [Salmonella spp. and antibiotic-resistant strains in wild mammals and birds in north-western Italy from 2002 to 2010.](#) *Veterinaria Italia* 2013; 49(2):195-202. doi: 10.12834/VetIt.2013.492.201.208

Butterfield J, Coulson JC, Kearsey SV, Monaghan P, McCoy JH, Spain GE. [The herring gull *Larus argentatus* as a carrier of *Salmonella*.](#) *Journal of Hygiene* 1983;**91**(3):429 to 436.

Dakman A , Şahan Yapicier Ö, Yasarer A, Gulec M. [First Isolation of *Salmonella* Hessarek from *Sturnus vulgaris* in Turkey: A Case Report.](#) Kafkas Univ Vet Fak Derg 2017;23(2):343 to 346.

Defra (2007) [UK National Control Programme for *Salmonella* in Layers \(*Gallus gallus*\).](#)

Defra (2008) [UK National Control Programme for *Salmonella* in chickens \(*Gallus gallus*\) reared for meat \(Broilers\).](#)

EEC (2003) Zoonoses Regulations 2160/2003. Official Journal **L325**, pp. 1–15. Regulation (EC) No. 2160/2003 on the control of *Salmonella* and other specified food-borne zoonotic agents.

EEC (2003) European Union Council Directive 2003/99/EC. Official Journal **L325**, pp 31–40. Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC.

EEC (2010) Commission Regulation (EU) No. 200/2010. Official Journal **L61** pp. 1-9. Commission Regulation (EU) No. 200/2010 of 10 March 2010 implementing Regulation (EC) No. 2160/2003 of the European Parliament and of the Council as regards a Union target for the reduction of the prevalence of *Salmonella* serotypes in adult breeding flocks of *Gallus gallus*.

EEC (2011) Commission Regulation (EU) No. 517/2011. Official Journal **L138**, pp. 45-51. EEC (2011) Commission Regulation (EU) No. 517/2011 implementing Regulation (EC) No. 2160/2003 of the European Parliament and of the Council as regards a Union target for the reduction of the prevalence of certain *Salmonella* serotypes in laying hens of *Gallus gallus* and amending Regulation (EC) No. 2160/2003 and Commission Regulation (EU) No. 200/2010.

EEC (2012) Commission Regulation (EU) No. 200/2012. Official Journal **L71**, pp. 31-36. Concerning a Union target for the reduction of *Salmonella* Enteritidis and *Salmonella* Typhimurium in flocks of broilers, as provided for in Regulation (EC) No. 2160/2003 of the European Parliament and of the Council.

EEC (2012) Commission Regulation (EU) No 1190/2012. Official Journal **L340**, pp. 29-34. Concerning a Union target for the reduction of *Salmonella* Enteritidis and *Salmonella* Typhimurium in flocks of turkeys, as provided for in Regulation (EC) No. 2160/2003 of the European Parliament and of the Council.

EEC (2019) Commission Regulation (EU) 2019/268 of 15 February 2019 amending Regulations (EU) No 200/2010, (EU) No 517/2011, (EU) No 200/2012 and (EU) No

1190/2012 as regards certain methods for *Salmonella* testing and sampling in poultry (Text with EEA relevance.)

Finley R, Ribble C, Aramini J, Vandermeer M, Popa M, Litman M and Reid-Smith R (2007). The risk of *Salmonellae* shedding by dogs fed *Salmonella*-contaminated commercial raw food diets. *Can. Vet. J.* **48**, pp. 69-75

Gosling, R., Oastler, C., Nichols, C., Jackson, G., Wales, A.D. and Davies, R.H. (2022) Investigations into *Salmonella* Contamination in Feed Mills Producing Rations for the Broiler Industry in Great Britain. *Vet. Sci*, **9(7)**, 307

Grimont PAD and Weill F-X (2007) Antigenic Formulae of the *Salmonella* Serovars, ninth edition. WHO Collaborating Centre for Reference and Research on *Salmonella*, Institut Pasteur: Paris.

Henderson K, Mason C. [Diagnosis and control of *Salmonella* Dublin in dairy herds.](#) *In Practice* 2017;**39**: 158 to 168.

HMSO (1981) The Importation of Processed Animal Protein Order 1981 (ISBN 0 1101 6677 9).

HMSO (1982) The Importation of Processed Animal Protein (Amendment) Order 1982 (ISBN 0 1102 6459 2).

HMSO (1989) The Zoonoses Order 1989 (ISBN 0 1109 6285 0).

HMSO (1993) The Poultry Breeding Flocks and Hatcheries Order 1993 (ISBN 0 1103 4898 2).

HMSO (2013) The Animal By-Products (Enforcement) (England) Regulations 2013 (ISBN 9780 1111 0626 6).

HMSO (2013) The Animal By-Products (Enforcement) (Scotland) Regulations 2013 (ISBN 9780 1110 2180 4).

HMSO (2014) The Animal By-Products (Enforcement) (Wales) Regulations 2014.

HMSO (2007) The Poultry Breeding Flocks and Hatcheries (England) Order 2007 (ISBN 0 11 075819 6).

HMSO (2007) The Poultry Breeding Flocks and Hatcheries (Wales). Order 2007 (ISBN 0 11 091588 3).

HMSO (2007) The Poultry Breeding Flocks and Hatcheries (Scotland). Order 2007 (ISBN 0 11 072109 8).

- HMSO (2008) The Control of *Salmonella* in Poultry Order 2007.
- HMSO (2008) The Control of *Salmonella* in Poultry (Wales) Order 2008.
- HMSO (2009) The Control of *Salmonella* in Poultry (Breeding, Laying and Broiler Flocks) (Scotland) Order 2009.
- HMSO (2009) The Control of *Salmonella* in Broiler Flocks Order 2009.
- HMSO (2009) The Control of *Salmonella* in Broiler Flocks (Wales) Order 2009.
- HMSO (2009) The Control of *Salmonella* in Turkey Flocks Order 2009.
- HMSO (2009) The Control of *Salmonella* in Turkey Flocks (Scotland) Order 2009.
- HMSO (2010) The Control of *Salmonella* in Turkey Flocks (Wales) Order 2010.
- HMSO (2011) [The Animal By-Products \(Enforcement\) \(England\) Regulations No.2011/881](#).
- Hoover JP and Tyler, RD. [Renal function and fractional clearances of American river otters \(*Lutra canadensis*\)](#). *Journal of Wildlife Diseases* 1986;22:547 to 556.
- Keymer I, Gibson E and Reynolds D. Zoonoses and other findings in hedgehogs (*Erinaceus europaeus*): a survey of mortality and review of the literature. *Veterinary Record* 1991;**128**(11):245 to 249.
- Kimber KR and Kollias GV. [Infectious and parasitic diseases and contaminant-related problems of North American river otters \(*Lontra canadensis*\): A review](#). *Journal of Zoo and Wildlife Medicine* 2000;**31**:452 to 472.
- Krawczyk, AI, van Leeuwen, AD, Jacobs-Reitsma, W. *et al.* [Presence of zoonotic agents in engorged ticks and hedgehog faeces from *Erinaceus europaeus* in \(sub\) urban areas](#). *Parasites Vectors* 2015;**8**:210.
- Lawson B, Franklinos LHV, Rodriguez-Ramos Fernandez J, Wend-Hansen C, Nair S, Macgregor SK, John SK, Pizzi R, Nunez A, Ashton PM, Cunningham AA, de Pinna EM (2018) [Salmonella Enteritidis ST183: emerging and endemic biotypes affecting western European hedgehogs \(*Erinaceus europaeus*\) and people in Great Britain](#). *Scientific Reports* 2018;**8**:2449.
- Liao YS, Chen BH, Hong YP, Teng RH, Wang YW, Liang SY, Liu YY, Tu YH, Chen YS, Chang JH, Tsao CS, Chiou CS. Emergence of Multidrug-Resistant *Salmonella enterica* Serovar Goldcoast Strains in Taiwan and International Spread of the ST358 Clone. *Antimicrobial Agents and Chemotherapy* 2019 Sep 23;**63**(10):e01122-19. doi: [10.1128/AAC.01122-19](#). PMID: 31383653; PMCID: PMC6761502.

Martelli F, Kidd S and Lawes J (2018). [Salmonella and salmonellosis in horses: an overview](#). *Veterinary Record* **182** (23), pp. 659-660.

Morley PS, Strohmeier RA, Tankson JD, Hyatt DR, Dargatz DA and Fedorka-Cray PJ (2006). [Evaluation of the association between feeding raw meat and Salmonella enterica infections at a Greyhound breeding facility](#). *J. Am. Vet. Med. A.* **228**, pp. 1524-1532

Nauerby, B, Pedersen, K, Dietz, HH & Madsen, M. [Comparison of Danish isolates of Salmonella enterica serovar enteritidis PT9a and PT11 from hedgehogs \(Erinaceus europaeus\) and humans by plasmid profiling and pulsed-field gel electrophoresis](#). *Journal of Clinical Microbiology* 2000;**38**(10):3631 to 3635.

Oliveira M, Pedroso NM, Sales-Luís T, Santos-Reis M, Tavares L, Vilela CL. [Antimicrobial-Resistant Salmonella Isolated from Eurasian Otters \(Lutra lutra\) in Portugal](#). *The Journal of Wildlife Diseases*. 2010;**46**(4):1257 to 1261.

[UK Veterinary Antibiotic Resistance and Sales Surveillance 2024](#), UK-VARSS.

UKHSA, 2025. [Non-typhoidal Salmonella data 2016 to 2025 - GOV.UK](#).

Velarde R, Porrero MC, Serrano E, Marco I, García M, Téllez S, Domínguez L, Aymí R, Lavín S. [Septicemic salmonellosis caused by Salmonella Hessarek in wintering and migrating Song Thrushes \(Turdus philomelos\) in Spain](#). *Journal of Wildlife Disease* 2012;**48**(1):113 to 121.

Ward LR, DeSa JDH and Rowe B (1987) A Phage typing Scheme for *Salmonella enteritidis*. *Epidemiology and Infection* **99**, pp. 291-294.

Wilkinson V, Rodriguez-Ramos Fernandez J, Núñez A, Macgregor SK, John SK, Dallman TJ, Cunningham AA, de Pinna EM, Lawson B. [Novel Salmonella Variant Associated with Mortality in Two Great Spotted Woodpeckers \(Dendrocopos major\)](#). *Journal of Wildlife Diseases* 2019;**55**(4):874 to 878.

Further publications of interest

Abrego A, Wiseman B, Gragg SE. (2025) Summarizing the Current knowledge and Existing Knowledge Gaps for Preharvest and Postharvest *Salmonella* Contamination in Pork. [doi: 10.1016/j.jfp.2025.100609](#). *J Food Prot.* **88** (10)

Alba P, Leekitcharoenphon P, Carfora V, Amuruso R, Cordaro G, Di Matteo P, Lanzano A, Iurescia M, Diaconu EL, Engage-EURL-AR Network Study Group, Pedersen SK, Guerra B, Hendriksen RS, Franco A, Battisti A (2020) Molecular epidemiology of *Salmonella* Infantis in Europe: insights into the success of the bacterial host and its parasitic pESI-like megaplasmid.

<https://www.microbiologyresearch.org/content/journal/mgen/10.1099/mgen.0.000365>
Microbial Genomics **6** (5)

Almuzaini AM (2023) Phytochemicals: potential alternative strategy to fight *Salmonella* enterica serovar Typhimurium. <https://doi.org/10.3389/fvets.2023.1188752> *Frontiers in Veterinary Science* **10**

Andres VM, Davies RH (2015) Biosecurity measures to control *Salmonella* and other infectious agents in pig farms: a review. <https://ift.onlinelibrary.wiley.com/doi/10.1111/1541-4337.12137> *Comprehensive Reviews in Food Science and Food Safety* **14** (4), pp. 317-335.

Angell JW, Duncan JS, Hamer K (2025) Salmonellosis in lambing ewes with associated human infection. <https://doi.org/10.1002/vrc2.70085> *Vet Record Case Reports* **13** (3)

Apenteng OO, Arnold ME, Vigre H (2020) Using stochastic dynamic modelling to estimate the sensitivity of current and alternative surveillance program of *Salmonella* in conventional broiler production. <https://www.nature.com/articles/s41598-020-76514-3> *Scientific Reports* **10** (1) Article No. 19441.

APHA (2025) [Salmonella in animals and feed in Great Britain 2024](#)

APHA (2024) [Salmonella in animals and feed in Great Britain 2023](#)

APHA (2023) [Salmonella in animals and feed in Great Britain 2022](#)

APHA (2022) [Salmonella in animals and feed in Great Britain 2021](#) (ISBN 1 8995 1534 8).

APHA (2021) [Salmonella in Livestock Production in Great Britain 2020](#) (ISBN 1 8995 1533 X).

APHA (2020) [Salmonella in Livestock Production in Great Britain 2019](#) (ISBN 1 8995 1532 8).

Arnold M, Lawes J, Davies R H, Evans S (2023). Study of *Salmonella* detection in laying hens using a Bayesian model. <https://doi.org/10.1111/zph.13020> *Zoonoses and Public Health* **70** (3) 248-255.

Arsevska E, Singleton D, Sanchez-Vizcaino F, Williams N, Jones PH, Smythe S, Heayns B, Wardeh M, Radford AD, Dawson S, Noble PJM and Davies RH (2017) Small animal disease surveillance: GI disease and salmonellosis. *Veterinary Record* **181** (9), pp. 228-232.

Azevedo C, Bohning D and Arnold M (2017) A ratio regression approach to estimate the size of the *Salmonella*-infected flock population using validation information. In Bohning D, van der Heijden PGM, Bunge J (eds), *Capture-Recapture Methods for the Social and Medical Sciences*, Boca Raton, Taylor and Francis, pp. 61-78.

- Bawn M, Alikhan N-F, Thilliez G, Kirkwood M, Wheeler NE, Petrovska L, Dallman TJ, Adriaenssens EM, Hall N, Kingsley RA (2020) Evolution of *Salmonella* enterica serotype Typhimurium driven by anthropogenic selection and niche adaptation. <https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1008850> *PLoS Genetics* **16** (6) e1008850.
- Bettridge JM, Snow LC, Tang Y, Petrovska L, Lawes J, Smith RP (2023) Using SNP addresses for *Salmonella* Typhimurium DT104 in routine veterinary outbreak detection. <https://doi.org/10.1017/S0950268823001723> *Epidemiology and Infection*
- Birch C, Davies RH (2016) An in-vitro investigation into the efficacy of disinfectants used in the duck industry against *Salmonella*. *Avian Pathology* **45** (5), pp. 576-581.
- Branchu P, Charity OJ, Bawn M, Thilliez G, Dallman TJ, Petrovska L, Kingsley RA (2019) SGI-4 in monophasic *Salmonella* typhimurium ST34 is a novel ICE that enhances resistance to copper. *Frontiers in Microbiology* **10** Article 1118.
- Bruno-Mcclung E, Mackintosh A, Rawlings M (2024). *Salmonella* species infections in dogs: building the epidemiological picture. <https://doi.org/10.1002/vetr.4988> *Veterinary Record* **195** (11) 449-451
- Card R, Vaughan K, Bagnall M, Spiropoulos J, Cooley W, Strickland T, Davies R, Anjum MF (2016) Virulence characterisation of *Salmonella* enterica isolates of differing antimicrobial resistance recovered from UK livestock and imported meat samples. *Frontiers in Microbiology* **7**, Article 640.
- Carter A, Adams M, La Ragione RM and Woodward MJ (2017) Colonisation of poultry by *Salmonella* enteritidis S1400 is reduced by combined administration of *Lactobacillus salivarius* 59 and *Enterococcus faecium* PXN-33. *Veterinary Microbiology* **199**, pp. 100-107.
- Cawthraw S, Wales A, Guzinski J, Trew J, Ring I, Huby T, Hussaini A, Petrovska L, Martelli F (2025). *Salmonella* Infantis outbreak on six broiler units in Great Britain: investigation, epidemiology, and control. <https://doi.org/10.1093/jambio/lxaf040> *Journal of Applied Microbiology* **136**(3).
- Charity OJD, Thilliez G, Acton L, Kolenda R, Bawn M, Petrovska L, Kingsley RA (2025) Reversible excision of the *wzy* locus in *Salmonella* typhimurium may aid recovery following phage predation. <https://doi.org/10.1371/journal.pgen.1011688> *PLoS Genetics* **21** (5)
- Chousalkar K, Gast R, Martelli F and Pande V (2018) Review of egg-related salmonellosis and reduction strategies in United States, Australia, United Kingdom and New Zealand. *Critical Reviews in Microbiology* **44** (3), pp. 290-303.
- Davies R (2019) Salmonellosis. Manual of diagnostic tests and vaccines for terrestrial animals 2019 pp.1735-1752.

Davies RH, Lawes JR, Wales AD (2019) Raw diets for dogs and cats: a review, with particular reference to microbiological hazards. *Journal of Small Animal Practice* **60** (6) pp. 329-339.

Davies R, Wales A (2019) Antimicrobial resistance on farms: a review including biosecurity and the potential role of disinfectants in resistance selection. *Comprehensive Reviews in Food Science and Food Safety* **18** (3) pp. 753-774.

Davies R, Gosling RJ, Wales AD, Smith RP (2016) Use of an attenuated live *Salmonella* typhimurium vaccine on three breeding pig units: a longitudinal observational field study. *Comparative Immunology. Microbiology and Infectious Diseases* **46**, pp. 7-15.

Davies R, Kingsley RA (2016) Microevolution of monophasic *Salmonella* typhimurium during epidemic, United Kingdom, 2005–2010. *Emerging Infectious Diseases* **22** (4), pp. 617-624.

De Lucia A, Cawthraw S, Davies R, Smith RP, Bianco C, Ostanello F, Martelli F (2020) Correlation of anti-*Salmonella* antibodies between serum and saliva samples collected from finisher pigs. <https://doi.org/10.3389/fvets.2019.00489> *Frontiers in Veterinary Science* **6** Article 489.

De Lucia A, Rabie A, Smith RP, Davies R, Ostanello F, Ajayi D, Petrovska L and Martelli F (2018) Role of wild birds and environmental contamination in the epidemiology of *Salmonella* infection in an outdoor pig farm. *Veterinary Microbiology* **227**, pp. 148-154.

[Salmonella: get your broiler flock chickens tested.](#) (published 2016, last updated 2025)

[Laying hens and flocks: poultry testing for Salmonella.](#) (published 2016, last updated July 2023)

[Chicken breeders: poultry testing for Salmonella.](#) (published 2018, last updated 2025)

[Salmonella: get your fattening turkeys tested.](#) (published 2018, last updated 2025)

[Turkey breeders: poultry testing for Salmonella](#) (published 2019, last updated 2025)

EEC (2011) Commission Regulation (EU) No. 142/2011. Official Journal **L54**, pp. 1-254. Commission Regulation (EU) No. 142/2011 implementing Regulation (EC) No. 1069/2009 of the European Parliament and of the Council laying down health rules as regards animal by-products and derived products not intended for human consumption and implementing Council Directive 97/78/EC as regards certain samples and items exempt from veterinary checks at the border under that Directive.

EFSA Panel on Biological Hazards (BIOHAZ), Koutsoumanis K, Allende A, Alvarez-Ordóñez A, Bolton D, Bover-Cid S, Chemaly M, De Cesare A, Herman L, Hilbert F,

Lindqvist R, Nauta M, Peixe L, Ru G, Simmons M, Skandamis P, Suffredini E, Dewulf J, Hald T, Michel V, Niskanen T, Ricci A, Snary E, Boelaert F, Messens W, Davies R 2019 *Salmonella* control in poultry flocks and its public health impact. *EFSA Journal* **17** (2) e05596.

The EFSA Journal (2007), **96**, 1-46, “Report including a proposal for a harmonized monitoring scheme of antimicrobial resistance in *Salmonella* in fowl (*Gallus gallus*), turkeys, and pigs and *Campylobacter jejuni* and *C. coli* in broilers”.

Fabri ND, Santman-Berends IMGA, Weber MF, Van Schaik G (2024) Risk factors for the introduction of *Salmonella* spp. serogroups B and D into Dutch dairy herds. <https://doi.org/10.1016/j.prevetmed.2024.106313> *Preventive Veterinary Medicine* **232**

Fan G, Zhao Y, Suo X, Li Y, Yang X (2024) Effects of Supplementing Yeast Fermentation Products on Growth Performance, Colonic Metabolism, and Microbiota of Pigs Challenged with *Salmonella* Typhimurium. <https://doi.org/10.3390/ani14243675> *Animals* **14** (24)

Fayyaz A, Fatima J, Mahmood S, Khurram Y, Naz G, Aslam RS, Sarwar A, Sarwar F, Israr Y, Israr A, Ahmad A, Rafay A, Shehzad T (2025) Role of probiotics in the control of *Salmonella* infections in animals and humans. <https://doi.org/10.62310/liab.v5i2.202> *Letters in Animal Biology* **5** (2) 6-16

Figueiredo R, Card RM, Nunez-Garcia J, Mendonca N, Jorge de Silva G, Anjum MF (2019) Multidrug-resistant *Salmonella* enterica isolated from food animal and foodstuff may also be less susceptible to heavy metals. *Foodborne Pathogens and Disease* **16** (3) pp. 166-172.

Gavin C, Simons RRL, Berriman ADC, Moorhouse D, Snary EL, Smith RP and Hill AA (2018) A cost-benefit assessment of *Salmonella*-control strategies in pigs reared in the United Kingdom. *Preventive Veterinary Medicine* **160**, pp. 54-62.

García-Díez J, Moura D, Grispoli L, Cenci-Goga B, Saraiva S, Silva F, Saraiva C, Ausina J (2024) *Salmonella* spp. in Domestic Ruminants, Evaluation of Antimicrobial Resistance Based on the One Health Approach—A Systematic Review and Meta-Analysis. <https://doi.org/10.3390/vetsci11070315> *Veterinary Sciences* **11** (7)

Georganas A, Graziosi G, Catelli E, Lupini C (2024) *Salmonella* enterica Serovar Infantis in Broiler Chickens: A Systematic Review and Meta-Analysis. <https://doi.org/10.3390/ani14233453> *Animals* **14** (23)

Gentile, N., Lorenzo-Rebenaque, L., Marco-Fuertes, A., Montoro-Dasi, L., & Marin, C. (2025). Emerging Challenges in *Salmonella* Control: The Need for Innovative and

Sustainable Disinfection Strategies in Poultry Farming.

<https://doi.org/10.3390/pathogens14090912> *Pathogens*, 14(9), 912.

Gil-Molino M, Gonçalves P, Risco D, Martín-Cano FE, García A, Rey J, Fernández-Llario P, Quesada A (2022) Dissemination of antimicrobial-resistant isolates of *Salmonella* spp. in wild boars and its relationship with management practices.

<https://doi.org/10.1111/tbed.14480> *Transboundary and Emerging Diseases* 69 (5) e1488-e1502

Gosling RJ, Mueller-Doblies D, Martelli F, Nunez-Garcia J, Kell N, Rabie A, Wales AD and Davies RH (2018) Observations on the distribution and persistence of monophasic *Salmonella* typhimurium on infected pig and cattle farms. *Veterinary Microbiology* **227**, pp. 90-96.

Gosling RJ, Mawhinney I, Vaughan K, Davies RH and Smith RP (2017) Efficacy of disinfectants and detergents intended for a pig farm environment where *Salmonella* is present. *Veterinary Microbiology* **204**, pp. 46-53.

Guzinski J, Potter J, Tang Y, Davies R, Teale C, Petrovska L (2024) Geographical and temporal distribution of multidrug-resistant *Salmonella* infantis in Europe and the Americas. <https://doi.org/10.3389/fmicb.2023.1244533> *Frontiers in Microbiology* 14, 1244533

Hameed SS, Al-Ogaili AS, Noori N (2022) Single-stranded DNA aptamer-based rolling circle amplification as anti-chicken *Salmonella* bacteriostatic.

<https://doi.org/10.14202/vetworld.2022.1171-1176> *Veterinary World* 15 (5) 1171-1176

Hateley G and Carson A (2017) *Salmonella* investigations in ruminants. *Veterinary Record* **181** (14), pp. 366-367.

Hayward MR, Petrovska L, Jansen VAA, Woodward MJ (2016) Population structure and associated phenotypes of *Salmonella* enterica serovars Derby and Mbandaka overlap with host range. *BMC Microbiology* 16:15.

Hofer K, Trockenbacher B, Sodoma E, Khol JL, Dünser M, Wittek T (2024) Establishing a surveillance programme for *Salmonella* Dublin in Austrian dairy herds by comparing herd-level vs. individual animal detection methods.

<https://doi.org/10.1016/j.prevetmed.2024.106277> *Preventive Veterinary Medicine* 230

Horton RA, Card R, Randall LP, Teale CJ (2016) Differentiation of UK endemic strains of *Salmonella* enterica serovar Newport from epidemic North American strains by PCR detection of a truncated bapA chromosomal gene. *Research in Veterinary Science* **104**, pp. 113-116.

Horton RA, Wu G, Speed K, Kidd S, Davies R, Coldham NG and Duff JP (2013). Wild birds carry similar *Salmonella enterica* serovar Typhimurium strains to those found in domestic animals and livestock. *Research in Veterinary Science* **95** (1), pp. 45-48.

Jones H, Gilson D, Gosling R J, Oastler C, Davies RH, Smith RP (2022) The effectiveness of short-duration in-feed organic acid use in finisher pigs for *Salmonella* control at slaughter. <https://doi.org/10.1016/j.prevetmed.2022.105772> *Preventive Veterinary Medicine* **209**, 105772.

Kanagarajah S, Waldram A, Dolan G, Jenkins C, Ashton PM, Martin AIC, Davies R, Frost A, Dallman TJ, De Pinna EM, Hawker JI, Grant KA and Elson R (2018) Whole genome sequencing reveals an outbreak of *Salmonella* enteritidis associated with reptile feeder mice in the United Kingdom, 2012-2015. *Food Microbiology* **71**, pp. 32-38.

Kumar S, Akter F, Dutta TK (2025). Salmonellosis: A Major Foodborne Zoonotic Disease Linked to Swine. *Emerging Zoonotic Threats from Swine: A Public Health Perspective*: 161–174.

Lewis SE, Cawthraw SA, Wales AD, Rawlins M, Brown D, Ring I, Huby T, Sandu C, Jinks R, Snow LC, Wyllie S, Mackintosh A, Smith RP, Evans S, Martelli F (2025). *Salmonella* in the slaughter sheep population in England and Wales. *Journal of Applied Microbiology* **136** (10) <https://doi.org/10.1093/jambio/lxaf244>

Marier E, Smith RP, Ellis-Iversen J, Watson E, Armstrong D, Hogeveen H, Cook AJC (2016) Changes in perceptions and motivators that influence the implementation of on-farm *Salmonella* control measures by pig farmers in England. *Preventive Veterinary Medicine* **133**, pp. 22-30.

Marin C, Martelli F, Rabie A and Davies R (2018) Commercial frozen mice used by owners to feed reptiles are highly externally contaminated with *Salmonella* enteritidis PT8. *Vector-Borne and Zoonotic Diseases* **18** (9), pp. 453-457.

Martelli F, Andres VM, Davies R and Smith RP (2018) Observations on the introduction and dissemination of *Salmonella* in three previously low prevalence status pig farms in the United Kingdom. *Food Microbiology* **71**, pp. 129-134.

Martelli F, Kidd S, Lawes J (2019) Surveillance for *Salmonella* in horses in Great Britain. *Veterinary Record* **184** (2) pp. 56-58.

Martelli F, Gosling RJ, Callaby R and Davies R (2017) Observations on *Salmonella* contamination of commercial duck farms before and after cleaning and disinfection. *Avian Pathology* **46** (2), pp. 131-137.

Martelli F, Lambert M, Butt P, Cheney T, Tatone FA, Callaby R, Rabie A, Gosling RJ, Fordon S, Crocker G, Davies RH and Smith RP (2017) Evaluation of an enhanced

cleaning and disinfection protocol in *Salmonella* contaminated pig holdings in the United Kingdom. *PLoS ONE* **12** (6): e0178897.

Martelli F, Wales A and Davies R (2017) Of mice and hens - tackling *Salmonella* in table egg production in the United Kingdom and Europe. In: Ricke SC (ed), Gast RK (ed), Producing safe eggs: microbial ecology of *Salmonella*, Elsevier, London, 2017, pp. 3-23.

Martelli F, Birch C, Davies RH (2016) Observations on the distribution and control of *Salmonella* in commercial duck hatcheries in the UK. *Avian Pathology* **45** (2), pp. 261-266.

Mattock J, Chattaway M A, Hartman H, Dallman T J, Smith A M, Keddy K, Petrovska L, Manners E J, Duze S T, Smouse S, Tau N, Timme R, Baker D J, Mather A E, Wain J, Langridge G C (2024). A One Health perspective on *Salmonella* enterica Serovar infantis, an emerging human multidrug-resistant pathogen. <https://doi.org/10.3201/eid3004.231031> *Emerging Infectious Diseases* **30** (4) 701-710

Mellor KC, Petrovska L, Thomson NR, Harris K, Reid SWJ, Mather AE (2019) Antimicrobial resistance diversity suggestive of distinct *Salmonella* typhimurium sources or selective pressures in food-production animals. *Frontiers in Microbiology* **10** Article No. 708.

Mensah N, Tang Y, Cawthraw S, Abuoun M, Fenner J, Thomson NR, Mather AE, Petrovska-Holmes L (2019) Determining antimicrobial susceptibility in *Salmonella* enterica serovar Typhimurium through whole genome sequencing: a comparison against multiple phenotypic susceptibility testing methods. *BMC Microbiology* **19**, pp. 148.

Merrick R, Pulford C, Rubeshkumar P, Seyan P, Fina L, Sawyer C, Lighthill J, Potter T, Harvey N, Thomas K, Lloyd D, Gherman I, Mackintosh A, Lawes J, Snow L, Waldram A, Larkin L, Balasegaram S, Painset A, McCormick J, Elson R, Browning L, Williams C, Andrew R, Malby S, Thomas D (2024). A genetically related cluster of *Salmonella* typhimurium cases in humans associated with ruminant livestock and related food chains, United Kingdom, August 2021-December 2022. <https://doi.org/10.1017/S095026882400030X> *Epidemiology and Infection* **152**, e89

Morris VK, Carrique-Mas JJ, Mueller-Doblies D, Davies RH, Wales AD, Allen VM (2015) A longitudinal observational study of *Salmonella* shedding patterns by commercial turkeys during rearing and fattening, showing limitations of some control measures. <http://dx.doi.org/10.1080/00071668.2014.991273> *British Poultry Science* **56** (1), pp. 48-57.

Mueller-Doblies, D., Clouting, C. and Davies, R.H. (2013), Investigations of the Distribution and Persistence of *Salmonella* and Ciprofloxacin-Resistant *Escherichia coli* in Turkey Hatcheries in the UK. *Zoonoses and Public Health*, **60**: 296-303. <https://doi.org/10.1111/j.1863-2378.2012.01524.x>

Mueller-Doblies D, Speed KCR, Kidd S and Davies RH (2018) *Salmonella* typhimurium in livestock in Great Britain – trends observed over a 32-year period. *Epidemiology and Infection* **146** (4), pp. 409-422.

Mueller-Doblies D, Mawhinney I, Martelli F, Gosling R, Rabie A and Davies RH (2018) Practical aspects of the suitability of different sampling methods for detecting *Salmonella* infection in duck flocks. *Journal of Applied Poultry Research* **27** (4), pp. 616-626.

Munck N, Leekitcharoenphon P, Litrup E, Kaas R, Meinen A, Guillier L, Tang Y, Malorny B, Palma F, Borowiak M, Gourmelon M, Simon S, Banerji S, Petrovska L, Dallman TJ, Hald T (2020) Four European *Salmonella* typhimurium datasets collected to develop WGS-based source attribution methods. <https://doi.org/10.1038/s41597-020-0417-7> *Scientific Data* **7** Article No. 75.

Naqid IA, Owen JP, Maddison BC, Spiliotopoulos A, Emes RD, Warry A, Flynn RJ, Martelli F, Gosling RJ, Davies RH, La Ragione RM, Gough KC (2016) Mapping B-cell responses to *Salmonella* enterica serovars typhimurium and enteritidis in chickens for the discrimination of infected from vaccinated animals. *Scientific Reports* **6**, Article number: 31186.

Newton K, Gosling B, Rabie A, Davies R (2020) Field investigations of multidrug-resistant *Salmonella* Infantis epidemic strain incursions into broiler flocks in England and Wales. <https://doi.org/10.1080/03079457.2020.1809634> *Avian Pathology* **49** (6) 631-641.

Niine T, Viltrop A, Nurmoja I, Smith RP, Pavoni E, Alborali GL, Ianiro G, Do Bartolo I, Tobias T, Sassu EL, Burow E (2025) Assessment of the biosecurity and slaughter practises in selected European abattoirs with a focus on the control of *Salmonella* and hepatitis E virus contamination. <https://doi.org/10.1016/j.jobb.2025.11.001> *Journal of Biosafety and Biosecurity* **7** (4) 168-179

Oastler CE, Nichols C, Newton K, Cawthraw S, Gosling RJ, Martelli F, Wales AD, Davies RH (2022) Observations on the distribution and control of *Salmonella* in commercial broiler hatcheries in Great Britain. <https://doi.org/10.1111/zph.12938> *Zoonoses and Public Health* **69** (5) 487-498.

Pennycott TW, Park A, Mather HA. Isolation of different serovars of *Salmonella* enterica from wild birds in Great Britain between 1995 and 2003. *Vet Rec.* 2006 Jun 17;158(24):817-20. doi: [10.1136/vr.158.24.817](https://doi.org/10.1136/vr.158.24.817). PMID: 16782854.

Perrin-Guyomard A, Granier SA, Slettemeas JS, Anjum M, Randall L, Abuoun M, Pauly N, Irrgang A, Hammerl JA, Kjeldgaard JS, Hammerum A, Franco A, Skarzynska M, Kaminska E, Wasyl D, Dierikx C, Borjesson S, Geurts Y, Haenni M, Veldman K (2022) Multicentre evaluation of a selective isolation protocol for detection of mcr-positive *E. coli* and *Salmonella* spp. in food-producing animals and meat. <https://doi.org/10.1111/lam.13717> *Letters in Applied Microbiology* **75** (2) 224-233.

Porter S, Strain SAJ, Bagdonaite G, McDowell SW, Bronckaers T, Sherrey M, Devine P, Pascual-Linaza AV, Spence N, Porter R, Guelbenzu-Gonzalo M, Davies RH, Lahuerta-Marin A (2020) Trends in *Salmonella* serovars and antimicrobial resistance in pigs and poultry in Northern Ireland between 1997 and 2016. <http://dx.doi.org/10.1136/vr.105640> *Veterinary Record* **186** (5) 156.

Powell LF, Cheney TEA, Williamson S, Guy E, Smith RP, Davies RH (2016) A prevalence study of *Salmonella* spp., *Yersinia* spp., *Toxoplasma gondii* and porcine reproductive and respiratory syndrome virus in UK pigs at slaughter. *Epidemiology and Infection* **144** (7), pp. 1538-1549.

Queiroz AC, Milanesi M, Queiroz LH, Nunes CM (2023). Occurrence of *Salmonella* spp. in the broiler production chain. <https://doi.org/10.1590/1678-4162-12842> *Arquivo Brasileiro de Medicina Veterinaria e Zootecnia* **75** (5) 902-908

Sevellec Y, Felten A, Radomski N, Granier SA, Le Hello S, Petrovska L, Mistou M-Y, Cadel-Six S (2019) Genetic diversity of *Salmonella* derby from the poultry sector in Europe. *Pathogens* **8** (2) p. 46.

Simons RRL, Hill AA, Swart A, Kelly L, Snary EL (2016) A transport and lairage model for *Salmonella* transmission between pigs applicable to EU member states. *Risk Analysis* **36** (3), pp. 482-497.

Smith RP, Andres V, Cheney TE, Martelli F, Gosling R, Marier E, Rabie A, Gilson D and Davies RH (2018) How do pig farms maintain low *Salmonella* prevalence: a case-control study. *Epidemiology and Infection* **146** (15), pp. 1909-1915.

Smith RP, Andres V, Martelli F, Gosling B, Marco-Jimenez F, Vaughan K, Tchorzewska M and Davies R (2018) Maternal vaccination as a *Salmonella* typhimurium reduction strategy on pig farms. *Journal of Applied Microbiology* **124** (1), pp. 274-285.

Smith RP, Andres V, Dormer L, Gosling R, Oastler C and Davies RH (2017) Study of the impact on *Salmonella* of moving outdoor pigs to fresh land. *Epidemiology and Infection* **145** (10) pp. 1983-1992.

Snary EL, Swart AN, Hald T (2016) Quantitative microbiological risk assessment and source attribution for *Salmonella*: taking it further. *Risk Analysis* **36** (3), pp. 433-436.

SRUC VS (2025). Tickborne fever compounding *Salmonella* abortion storm in dairy heifers. <https://doi.org/10.1002/vetr.5898> *Veterinary Record* **197**(4): 138–140.

Swart AN, Evers EG, Simons RLL, Swanenburg M (2016) Modelling of *Salmonella* contamination in the pig slaughterhouse. *Risk Analysis* **36** (3), pp.498-515.

Tang Y, Davies R, Petrovska L (2019) Identification of genetic features for attenuation of two *Salmonella* enteritidis vaccine strains and differentiation of these from wildtype isolates using whole genome sequencing. *Frontiers in Veterinary Science* **6** Article 447.

Tassinari E, Bawn M, Thilliez G, Charity O, Acton L, Kirkwood M, Petrovska L, Dallman T, Burgess CM, Hall N, Duffy G, Kingsley RA (2020) Whole-genome epidemiology links phage-mediated acquisition of a virulence gene to the clonal expansion of a pandemic *Salmonella* enterica serovar typhimurium clone. *Microbial Genomics* **6** (11).
<https://dx.doi.org/10.1099/mgen.0.000456>

Teunis G, Dallman TJ, Zając M, Skarżyńska M, Petrovska L, Pista A, Silveira L, Clemente L, Thépault A, Bonifait L, Kerouanton A, Chemaly M, Alvarez J, Söderlund R, Møller Nielsen E, Chattaway M, Burgess K, Byrne W, Zomer AL, van den Beld M, Hendrickx APA, Franz E, Pires S, Hald T, Mughini-Gras Lapo (2025) Attributable sources of the five most prevalent non-typhoidal *Salmonella* serovars across ten European countries.
<https://doi.org/10.1016/j.jinf.2025.106632> *Journal of Infection* **91** (5)

Wales A, Davies R (2020) Review of hatchery transmission of bacteria with focus on *Salmonella*, chick pathogens and antimicrobial resistance. *World's Poultry Science Journal* **76** (3) 517-536.
<https://doi.org/10.1080/00439339.2020.1789533>

Wales A, Davies R (2019) Antimicrobial drug resistance in poultry. What do we know about risk factors? *Zootecnica International* 4 September 2019, 1-6.

Wales A; Lawes J (2023). JMM Profile: *Salmonella* enterica serovar Gallinarum, biovars Pullorum and Gallinarum. <https://doi.org/10.1099/jmm.0.001653> *Journal of Medical Microbiology* **72** (2) 001653.

Wales A, Lawes J, Davies R (2019) How to advise clients about raw feeding dogs and cats. *Companion* 2019 **8**, pp. 10-15.

Wales AD and Davies RH (2017) *Salmonella* vaccination in pigs: a review. *Zoonoses and Public Health* **64** (1), pp. 1-13.

Wang D, Su Y, Gao F, Guo S, Yang J, Wu D, Jiang Q, Chen J, Sun J, Fang L, Liao X (2025). Comparison of ST19 *Salmonella* Typhimurium and ST34 *Salmonella* I,4,[5],12:i:-: a trade-off between plasmid-mediated antibiotic resistance and virulence. doi: [10.1016/j.lwt.2025.117868](https://doi.org/10.1016/j.lwt.2025.117868) *LWT* **225**.

Wigley P (2024) *Salmonella* and Salmonellosis in Wild Birds.
<https://doi.org/10.3390/ani14233533> *Animals* **14** (23)

Wilkinson V, Rodriguez-Ramos Fernandez J, Nunez A, Macgregor SK, John SK, Dallman TJ, Cunningham AA, de Pinna EM, Lawson B (2019) Novel *Salmonella* variant associated

with mortality in two Great Spotted Woodpeckers (*Dendrocopos major*). *Journal of Wildlife Diseases* **55** (4) pp. 874-878.

Willis C, Jorgensen F, Cawthraw S, Aird H, Lai S, Kesby M, Chattaway M, Lock I, Quill E, Raykova G (2023). A survey of *Salmonella*, *Escherichia coli*, and antimicrobial resistance in frozen, part-cooked, breaded, or battered chicken products on retail sale in the UK.

<https://doi.org/10.1093/jambio/lxad093> *Journal of Applied Microbiology* 134 (5) lxad093

Withenshaw SM, Lawes JR, Teale C, Davis RH (2020) Industry expansion and *Salmonella* surveillance trends for raw meat pet food in Great Britain over the last 10 years. In: van Schaik G (ed), Brennan M (ed), *Society for Veterinary Epidemiology and Preventive Medicine*: proceedings of a meeting held in Westport, Ireland, 25 to 27 March 2020, 33-45.

Quality statement

Section A

1. Coherence

Reports are obtained by various routes: direct submissions to APHA Veterinary Investigation Centres, reports of *Salmonella* isolations by private laboratories and Scottish submissions to Scotland's Rural College (SRUC).

APHA is responsible for collation of data. Submissions result from cases of clinical disease in livestock, monitoring of healthy livestock and investigations of possible links with a human *Salmonella* outbreak.

All private laboratories submitting reports of *Salmonella* isolates to APHA do so using the standard APHA submission and supplementary forms or customised forms developed for them by APHA. Scottish submissions use the SRUC submission form and supplementary forms which are compatible with the APHA system and interpreted in the same way. All use the same definitions and essential categorisation.

An incident comprises the first isolation and all subsequent isolations of the same serovar or serovar and phage/definitive type combination (if available) of *Salmonella* from an animal, group of animals or their environment on a single premises, within a defined time period (usually 30 days).

An antimicrobial susceptibility test is performed for surveillance purposes against an extended panel of 16 antimicrobials on *Salmonella* isolates sent for serotyping to APHA Weybridge.

Antimicrobial	Concentration (µg per ml)	Code
Nalidixic acid	30	NA
Tetracycline	10	T
Neomycin	10	N
Ampicillin	10	AM
Furazolidone	15	FR
Ceftazidime	30	CAZ
Sulphamethoxazole and trimethoprim combination	25	TM
Chloramphenicol	30	C
Amikacin	30	AK
Amoxicillin and clavulanic acid combination	30	AMC
Gentamicin	10	CN
Streptomycin	10	S
Sulphonamide compounds	300	SU
Cefotaxime	30	CTX
Apramycin	15	APR
Ciprofloxacin	1	CIP

This panel is updated when there is a clear need to detect new or emergent types of resistance or to replace outdated antimicrobials. On specific occasions (for example detection of *Salmonella* vaccine strains, characterisation of third generation cephalosporins resistance) more than 16 antimicrobials are used for susceptibility testing.

From 1 January 2007, some of the breakpoints used in assessing antimicrobial resistance, which were previously set at less than or equal to 13mm, were changed. These new breakpoints were set at: Ceftazidime (CAZ) less than or equal to 27mm, Amikacin (AK) less than or equal to 18mm, Ciprofloxacin (CIP) less than or equal to 19mm and Cefotaxime (CTX) less than or equal to 29mm. This may result in an increased number of isolates resistant to these antimicrobials in 2007 and the subsequent years in comparison with previous years. The breakpoint for all other antimicrobials used remains at less than or equal to 13mm.

In 2008, the disc concentrations for streptomycin and chloramphenicol were changed to adopt the disc concentrations recommended by the British Society for Antimicrobial Chemotherapy (BSAC). In the case of streptomycin, the disc concentration was reduced from 25µg to 10µg. The zone size remained unchanged, so this change would be expected to increase the detection of isolates with lower level streptomycin resistance. Work done at APHA has shown that the 10µg disc provides much better discrimination between resistant and sensitive isolates (defined using the gold standard measure of MIC determination) than the 25µg disc.

The only other change made to the breakpoints and disc concentrations used over the period 2008 to 2020 related to the ceftazidime disc where the zone size was reduced from 29 to 26mm in 2012, in line with BSAC recommendations.

2. Accuracy and precision

Sampling error: Isolations of *Salmonella* from statutory species are required to be reported. However, the level of detection and testing (for species without an NCP) depends on various factors including submission of samples for laboratory investigation by private vets, economic considerations and engagement with veterinary and surveillance services.

Antimicrobial susceptibility test is often performed on representative *Salmonella* isolates before the allocation of an automatic incident reference by the computer system. It is important for the Veterinary Investigation Centres to provide information to the testing laboratory on whether the submitted isolates are considered to comprise new incidents. As some companies perform extensive testing for *Salmonella*, this could skew the overall antimicrobial resistance data leading to the patterns obtained, at least in part, reflecting the intensity of sampling procedure. Also, limited resources may prevent susceptibility testing of all isolates. More than one isolate per incident is usually tested in cases where the resistance pattern of the serovar is likely to be of particular public health relevance in terms of antimicrobial resistance. These include *S. Infantis*, *S. Kentucky*, *S. Newport*, *S. Heidelberg* and *S. Typhimurium*.

Coverage error: The reasons for sample submissions (particularly for non-NCP samples) need to be considered, as sources of error can be dependent on this factor. Also, the ability to isolate *Salmonella* needs to be considered (dependent on factors such as sample type taken, age of sample, storage and transport, culture method used, laboratory staff technical expertise).

Non-response error: Although all *Salmonella* isolations from statutory species are required to be reported, not all data items requested are mandatory under the Zoonoses Order. Different categories of submissions may have different non-response rates for different data items.

Measurement error: Different *Salmonella* culture methods vary in their sensitivity, which varies according to sample type, type of *Salmonella* present and profile of competitive flora in the sample. Data on the APHA and SRUC forms are subject to individual interpretation by the person submitting the information, despite the guidance to authorised personnel.

The requirement of this report is to include as much data as is available. However, only approved submissions are included, although efforts are made to ensure that all submissions are approved before the data is extracted. Data are scrutinised to correct errors in results for strategically important isolates (for example resistant to third generation cephalosporins, resistant to ACSSuT pattern). It is not expected to routinely

see resistance to amikacin, ciprofloxacin, ceftazidime or cefotaxime in any isolate. If any appears, it is followed up at the time of detection and the isolate would normally be re-tested.

The laboratory at APHA Weybridge that perform the expanded susceptibility testing have third party accreditation to ISO17025 provided by UKAS.

Data processing error: It is often difficult to obtain the required information from the sample submitted for non-mandatory data. It is the responsibility of the Nominated Officer to ensure that the data are accurate and complete. A validation exercise is carried out on a weekly basis at the APHA Veterinary Investigation Centres and by DES, and on a quarterly basis for NCP submissions.

As a result of refinements to the method of defining incidents, it may not always be possible to reproduce isolation figures in previously published reports.

3. Timeliness and punctuality

The report includes provisional data (with the exception of the flock-level data for the chicken and turkey NCPs) which are subject to change. The APHA *Salmonella* warehouse is updated every night.

4. Accessibility and clarity

Salmonella data (APHA) have a related metadata profile (see section B).

5. Comparability

Salmonella cases in animals are reported both as isolations and incidents. An incident is defined as the first and all subsequent isolations of the same serovar or serovar and phage type combination, if available, of a particular *Salmonella* from an animal, group of animals or their environment on a holding within a defined time period, which is usually 30 days. An incident report is a herd/ flock (which is the epidemiological group of interest) level outcome.

Changes in the number of *Salmonella* isolations from poultry and pigs over time may reflect changes in the monitoring activity conducted by the livestock industry and not necessarily changes in incidence in *Salmonella* infection. The number of tests carried out by authorised laboratories is collated by Defra.

Sampling error, coverage error and measurement error are minimized for submissions from NCP samples as they follow a robust, harmonized protocol and test method.

Chicken and turkey data are not directly comparable before and after implementation of the NCPs. For example, before 2010 the turkey NCP was not in operation so all turkey submissions were voluntary whereas from the beginning of 2010, most turkey submissions

were from statutory monitoring. Comparisons are more valid for years in which the NCPs have run for a full year previously.

The data on positive findings of *Salmonella* in laying, breeding and broiler chicken flocks, and in turkey flocks is reported as the number of positive flocks, as required by the legislation, as well as the number of positive isolations detected during the year. The number of reported isolations of *Salmonella* detected in chickens and turkeys does not equate directly to the overall number of positive flocks that are detected during the year. A flock is counted as positive only once, irrespective of the number of isolations occurring and the number of serovars identified.

Hatchery isolations not associated with a specific flock

Starting with samples collected from 1 January 2006, any hatchery isolates where there are no supply flock details available are treated as isolations only and not incidents as they cannot be traced back to a specific flock.

SRUC and other isolations or reports without cultures submitted

Submissions received from the Scotland's Rural College (SRUC), and any submissions received without a sample are now allocated an incident reference whereas previously these were not allocated such references. These reports appear in the quarterly reports. This improvement was put in place for all reports on the database in 2008.

No isolates of *S. Typhimurium* from animals received from SRUC are phage typed. As the system does not allocate an incident reference number to a report of *S. Typhimurium* until the phage type result is received, this means that for data prior to 2020 some isolates of *S. Typhimurium* from SRUC will not be allocated an incident reference and therefore the actual number of incidents of *S. Typhimurium* may be higher than the number recorded on the database. From 2020 onwards such isolations have been manually allocated incident numbers.

APHA quality assurance statement

The policy of the Animal and Plant Health Agency (APHA) is to ensure that its products and services fully meet the agreed needs of its customers, including those defined by statutory and regulatory requirements. APHA is committed to good professional practice and aims to support this commitment through the use of management systems that will be reviewed to assess effectiveness and to foster continual improvement.

The laboratory facilities are accredited by BS EN ISO 17025:2017 (Accreditation Lab No 1769) for an extensive range of tests supported by proficiency testing accredited to BS ISO 17043:2010 (Accreditation No. 0004). APHA is certificated to BS EN ISO 9001:2015 for 'the provision of specialist scientific services in animal disease research and surveillance to the Government and other interested parties worldwide, including livestock

and wildlife. The provision of administrative services and control of technical services supporting regulation and enforcement of UK plant and seed directives' (certificate number UK013916). This excludes work relating to field based veterinary surveillance and regional laboratory testing, which is covered by ISO 17025 and ISO 17043. APHA research complies with the requirements of the Joint Code of Practice for Research.

APHA also holds approvals to Good Laboratory Practice and Good Manufacturing Practice and complies with Good Clinical Veterinary Practice (Veterinary).

Section B

Metadata elements and definitions

Creator

Salmonella Surveillance Team, DES, APHA Weybridge, New Haw, Addlestone, Surrey
KT15 3NB

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Quality

See Section A

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Additional report metadata elements and definitions

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Zoonoses, Animal Health

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Approved by:

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Report

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Staff of the Animal and Plant Health Agency processed the data.

The following reference laboratories made or confirmed the majority of isolations:

- Animal and Plant Health Agency, Weybridge
- Gastrointestinal Bacteria Reference Unit, UKHSA Colindale
- Scottish *Salmonella* Reference Laboratory, Glasgow

APHA One Health contributed to the review of the report.

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APHA is an Executive Agency of the Department for Environment, Food and Rural Affairs and was formed on 1 October 2014. Prior to this it was known as AHVLA.