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Agency

Salmonella in animals and feed in Great Britain

2024

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APHA is an Executive Agency of the Department for Environment, Food and Rural Affairs and also works on behalf of the Scottish Government, Welsh Government and Food Standards Agency to safeguard animal and plant health for the benefit of people, the environment and the economy.

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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 *Salmonella* in Broiler Flocks Order
CSPO	Control of *Salmonella* in Poultry Order
CSTO	Control of *Salmonella* in Turkey Flocks Order
DT	Definitive Phage Type of *S.* Typhimurium 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 *Salmonella* that cannot be serotyped due to autoagglutination
SE	*Salmonella* Enteritidis
SRUC	Scotland's Rural College
STM	*Salmonella* 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
Untypable	A culture which is not suitable for typing
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’
Untyped	Full information unavailable at the time of data collation
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 2024 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, or phage type in the case of *S*. Enteritidis and *S*. Typhimurium. 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 people, 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 amendment in 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 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 combination of a particular *Salmonella*, from an animal, 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* in humans, 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.

Serovar and phage type combinations where the phage type is RDNC were previously not considered to be incidents. This was changed in 2018 and these serovar and phage type combinations are now recorded as incidents. Serovar and phage type combinations where the phage type is UNTY or NOPT are not considered to be incidents. The exception to this is isolations with a phage type of NOPT which have been identified by SRUC. As SRUC no longer carry out phagetyping these isolations are assigned individual incident references.

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 or human foodstuffs of animal origin, 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 all 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 2024 the majority of Salmonella characterisation was by WGS with a small number additionally parallel tested by phenotypic methods.

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, will be reported as “*S.* Idikan (including monophasic variants)”. Historic data has also been reclassified in the 2024 book 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.

Since 2010, only *S*. Typhimurium and *S*. Enteritidis have been routinely phage typed. Cultures are seeded onto special agar plates and a specific set of phages applied to the culture. After incubation, the pattern and degree of lysis is read and a phage type attributed to the isolate (Anderson et al 1977, Ward et al 1987). In the case of *S*. Typhimurium, some phage types are not fully validated as being stable and specific for the serovar. These are referred to as undesignated phage types (U) rather than definitive phage types (DT). In early December 2024, APHA ceased to carry out phage typing of *Salmonella*. This will affect a small number of isolates in the current report as these will be reported in tables and text as phage type NOPT (not phage typed).

Serotyping and phage typing of samples received from premises in England and Wales is carried out by APHA. Mammalian isolates, and some poultry isolates, from Scotland are serotyped and also assessed by PHS using whole genome sequencing. The majority of poultry samples from Scotland are serotyped and phage typed by APHA.

Some phage types are recorded as RDNC (reacts with the phages but does not conform to a recognised phage type). In previous years, where the same RDNC pattern was regularly reported this would be considered by the UK Health Security Agency (UKHSA) and assigned a U type number with a definitive type (DT) designated after further validation. As UKHSA no longer carry out conventional phage typing this activity has not been carried out since 2019, resulting in an increased number of RDNC phage types.

Some phage types may be ‘related variants’ although they are still reported as distinct types. For example, PT4 and PT7 of *S*. Enteritidis and DT12, DT104, DT104b and U302 of *S*. Typhimurium. More than one phage type may sometimes be recovered from a group of animals that is sampled by means of environmental samples. This may result from variations in the attachment of phages to organisms that have been exposed to environmental stress.

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 obtaining a definitive phage type (DT) for the strain or 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* 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).

The serovar formerly known as *Salmonella* Java has now been reclassified, on the basis of genetic similarity studies, as *Salmonella* Paratyphi B variant (var.) Java. It is a group B *Salmonella* and has the same antigenic structure as *Salmonella* Paratyphi B (4,12:b:1,2). *Salmonella* Paratyphi B var. Java and *Salmonella* Paratyphi B are differentiated by the dextro-tartrate test, in which *Salmonella* Paratyphi B var. Java gives a positive acid reaction, whereas *Salmonella* Paratyphi B is negative.

Similarly, *Salmonella* Pullorum is now designated as *S*. Gallinarum biovar Pullorum and some other individual serovars have also been consolidated as variants of a single serovar (for example, *S*. Orion and *S.* Binza).

The serovar previously reported as *S*. Binza is now recorded under the updated nomenclature of *S*. Orion var. 15^+. It is for this reason that the tables of this publication show no reports of *S*. Binza.

The serovar previously reported as *S*. Newbrunswick is now recorded under the updated nomenclature of *S*. Give var. 15^+.

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

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) (England), Public Health Wales and Public Health Scotland (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 2024 alongside the most common serovars isolated from human cases of salmonellosis in Great Britain (Figure 1.1.1). Figures under headings 1.2 and 1.3 provide data for phage types of *S*. Typhimurium and *S*. Enteritidis in livestock. Human data are not shown in these figures as phage typing is no longer carried out by the Public Health reference laboratories, this has been replaced by routine whole genome sequencing as the method for *Salmonella* species characterisation. 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 2024 was the second most commonly reported from dogs in 2024.

In 2024, a total of 10,388 isolations of *Salmonella* from humans in England were reported to UKHSA. A marked impact on national surveillance for the major gastrointestinal pathogens was observed in 2020 and 2021 coinciding with the SARS-CoV-2 (COVID-19) pandemic therefore data for 2020 and 2021 should not be compared to data from previous or subsequent years.

Likewise, 2020 and 2021 saw a reduction in submissions to Animal and Plant Health Agency (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 and 2024 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 2024 (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 2024, the total number of *Salmonella* isolation reports from cattle, sheep, pigs and poultry decreased by 16.2% compared with 2023 (3,043 isolations versus 3,630 isolations) and decreased by 12.1% compared with 2022 (3,461 isolations) (Table 1.1). Trends were also variable across serovars, for example, reports of both *S*. Indiana and *S.* Newport were almost 3 times that of 2023. However, reports of *S*. Infantis were 68.8% less in 2024 compared to 2023 and reports of *S*. Montevideo were 44.3% fewer in 2024 compared to 2023. Reports of *S*. Senftenberg fell by 44.0% in 2024 in comparison to 2023.

The most important factor which may bias the number of *Salmonella* reports from species not covered by NCPs (that is species other than 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 1.7% in 2024 compared with 2023. This decrease was seen for cattle, pigs, miscellaneous species and other birds with the greatest decrease being in miscellaneous species (19.4%). The number of submissions increased for sheep, goats, poultry and game birds, with the greatest increase seen in goats (13.7%). As the majority of the isolations from species other than poultry relate to clinical investigations (although the *Salmonella* found may not always be the primary cause of the illness), 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 shown in this publication (Chapter 10).

There were 3,725 isolations of *Salmonella* in livestock and dogs in 2024 which represents a decrease of 18.0% compared with 2023 (4,541 isolations). This comprised 3,604 isolations from species covered by the statutory reporting requirements of the Zoonoses Order 1989 (1,961 isolations from chickens, 482 isolations from dogs, 366 isolations from cattle, 311 isolations from pigs, 196 isolations from ducks, 108 isolations from turkeys, 101 isolations from sheep, 53 isolations from horses, 22 isolations from pigeons, 2 isolations each from deer and goats), plus 121 isolations from non-statutory species (for example, cats and reptiles, which are not reported in detail in this publication).

Relative to 2023, in 2024 there were fewer isolations from chickens (1,961 versus 2,633 isolations) and cattle (366 versus 436 isolations). In contrast, there were more isolations from ducks (196 versus 96 isolations) and pigs (311 versus 258 isolations). Isolations stayed relatively stable in sheep and turkeys in 2024 (101 versus 98 isolations and 108 versus 109 isolations, respectively).

The surveillance data for 2024 shows that 23.0% of the isolations of *Salmonella* reported to APHA resulted from samples taken due to clinical disease in livestock. This is lower than during 2023, where 33.2% of isolations were from clinical disease investigations, and higher than 2022 where 20.2% of isolations were from clinical disease investigations. This contrasts with data for *Salmonella* in humans where reports usually originate from cases of clinical disease.

The majority of the isolations reported from chicken and turkey flocks (98.1% and 91.7%, respectively) during 2024 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 2024, 99.5% of the *Salmonella* isolations from ducks resulted from voluntary surveillance.

Reports of *S*. Enteritidis in 2024 were similar to that in 2023 (13 versus 11 isolations) and were around half that seen in 2022 (25 isolations). As in previous years, the majority of *S*. Enteritidis isolations in 2024 were reported from chickens (12 of 13 isolations), and there was also one isolation from cattle. This is similar to 2023 when most isolations of *S*.

Enteritidis came from chickens (9 of 11), with one isolation each from cattle and ducks (Figure 1.4). As in most years since 2019, PT8 was the most common *S.* Enteritidis phage type isolated.

The total number of *S*. Typhimurium isolations from cattle, sheep, pigs and poultry fell by 1.2% in 2024 (254 isolations) relative to 2023 (257 isolations). There was an increase in the number of isolations of this serovar in 2 sectors relative to the previous year; isolations from pigs increased by 12.2% (156 versus 139) and isolations from turkeys also increased (13 versus 1) (Figure 1.5). Isolations of *S*. Typhimurium in cattle decreased by 24.4% in 2024 compared to 2023 (62 versus 82 isolations). Isolations of *S*. Typhimurium in sheep fell by 50.0% in 2024 relative to 2023 (6 versus 12 isolations). Isolations of *S*. Typhimurium in chickens decreased by 19.0 % in 2024 compared to 2023 (17 versus 21 isolations). There were no isolations of *S.* Typhimurium from ducks in 2024, compared to one isolation in 2023. There has also been a notable change in *S.* Typhimurium phage type distribution in recent years with the emergence of DT105 and DT75 across most species, particularly in ruminants, which displaced DT104 from being the previously most commonly identified phage type of *S*. Typhimurium.

Total isolations of monophasic *Salmonella* Typhimurium decreased by 10.7% in 2024 compared to 2023 (75 versus 83 isolations, Figure 1.6). There was an increase in isolations of monophasic *S.* Typhimurium in pigs in 2024 compared to 2023 (70 versus 61 isolations). Isolations of monophasic *S*. Typhimurium fell in cattle and chickens in 2024 compared to 2023 (3 versus 14 isolations and 1 versus 6 isolations, respectively).

Highlights

Cattle

Isolations of *Salmonella* from cattle in 2024 were 16.0% lower than during 2023 (366 versus 436 isolations) and 14.9% lower than during 2022 (430 isolations).

As in previous years, *S*. Dublin remained the most common serovar identified in cattle (215 isolations, 58.7% of total cattle isolations). The number of isolations of *S*. Dublin decreased by 14.7%, compared with 2023 and by 18.9%, compared with 2022.

There were 62 isolations of *S.* Typhimurium from cattle in 2024, which is a decrease of 24.4% compared with 2023. The relative number of *Salmonella* Typhimurium isolations fell in 2024 and this serovar was the second most commonly isolated serovar from cattle (62 isolations, 16.9% of total cattle isolations) and *S*. Mbandaka was the third most commonly isolated (45 isolations, 12.3% of total cattle isolations). This is the same as during 2023, but a change from 2022, 2021 and 2020 where *S*. Mbandaka was the second most commonly isolated serovar and *Salmonella* Typhimurium was the third most commonly isolated (Figure 2.2).

There were only 3 phage types of *S*. Typhimurium reported from cattle during 2024, these were DT75 (28 isolations, 45.2% of isolations), DT105 (19 isolations, 30.6% of isolations) and DT1 (1 isolation, 1.6% of isolations).

There were 3 isolations of monophasic *S*. Typhimurium (0.8% of total cattle isolations) during 2024 compared with 14 isolations during 2023, and 3 isolations during 2022. In 2024 one isolation was phage type DT120 and 2 isolations were not phage typed.

There was one isolation of *S.* Enteritidis (NOPT) from cattle during 2024 this is the same as in 2023 which also had one isolation.

Small ruminants

Isolations of *Salmonella* from sheep in 2024 were 3.1% higher than during 2023 (101 versus 98 isolations) and 7.4% higher than during 2022 (94 isolations) (Table 3.1).

Salmonella enterica subspecies *diarizonae* serovar 61(k):1,5,(7) remained the most common serovar isolated from sheep (65 isolations, 64.4% of total sheep isolations).

Salmonella Dublin and *S*. Montevideo were the joint second most commonly isolated serovars from sheep in 2024, with 14 isolations each (13.9% of total isolations each). In 2023 *S*. Montevideo was also the second most commonly isolated serovar, with 13 isolations (13.3% of total isolations). *S*. Dublin was the fourth most commonly isolated serovar in 2023, with 4 isolations (4.1% of total isolations).

Salmonella Typhimurium was the fourth most commonly isolated serovar from sheep in 2024 (6 isolations, 5.9% of total isolations), half the number of isolations recorded in 2023 (12 isolations, 12.2% of total sheep isolations). The phage types reported during 2024 were DT75 (4 isolations) and DT193 (one isolation) with one isolation not phage typed.

There were 2 isolations from goats in 2024 (*S. enterica* subspecies *diarizonae* 61:k:1,5,(7) and *S*. Dublin) compared to one isolation from goats in 2023 (*S. enterica* subspecies *diarizonae* 61:(k):1,5,(7)) and 2 isolations during 2022 (both *S. enterica* subspecies *diarizonae* 61:(k):1,5,(7)).

Pigs

There were 311 *Salmonella* isolations from pigs in 2024 which was 20.5% higher compared to 2023 (258 isolations) and 45.3% higher than during 2022 (214 isolations) (Table 4.1).

Salmonella Typhimurium and monophasic *S*. Typhimurium were together responsible for 72.7% of all isolations from pigs in 2024 (226 isolations). This is similar to previous years. As has been the case since 2020, the number of *S*. Typhimurium isolations exceeded isolations of monophasic *S*. Typhimurium.

The most common phage type of *S*. Typhimurium isolated from pigs in 2024 was DT193 (54 isolations, 34.6% of total *S*. Typhimurium isolations in pigs), followed by DT32 (50 isolations, 32.1% of total *S*. Typhimurium isolations in pigs). Most typable isolations of monophasic *S*. Typhimurium from pigs in 2024 were phage type DT193 (52 isolations, 74.3% of total monophasic *S*. Typhimurium isolations) but there were also single isolations of DT104 and DT194.

Deer, horses and rabbits

There were 2 isolations of *Salmonella* from deer during 2024 (monophasic *S*. Typhimurium (NOPT) and *S.* Typhimurium (RDNC)), this is compared to one isolation of *S*. Typhimurium (DT105) during 2023 and no isolations in 2022, 2021 and 2020 (Table 5.1).

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

There were 53 isolations of *Salmonella* from horses during 2024, 3.6% lower than during 2023 (55 isolations) and 11.7% lower than during 2022 (60 isolations) (Table 5.3).

Salmonella Typhimurium was the most common serovar isolated from horses in 2024 (24 isolations, 45.3% of total horse isolations). This is similar to the number of isolations in 2023 and 2022 (20 and 18, respectively). The most common phage type of *S*. Typhimurium in 2024 was DT75 (4 isolations, 16.7% of *S*. Typhimurium isolations).

Salmonella Enteritidis was the second most commonly reported serovar from horses during 2024 (8 isolations, 15.1% of total horse isolations), which represents a large increase compared to 2023 (1 isolation) and is double the number of isolations seen in 2022 (4 isolations).

There was one isolation of monophasic *S.* Typhimurium (DT193) in horses in 2024 compared to one isolation in 2023 (DT193), and 2 isolations (both DT104) during 2022.

Chickens

Including both NCP and non-statutory surveillance data, there were 1,961 isolations of *Salmonella* from chickens in 2024. This is a decrease of 25.5% compared with 2023 (2,633 isolations) and a decrease of 18.4% compared with 2022 (2,404 isolations) (Table 6.1).

The most commonly reported serovars were:

- *S.* Idikan (including monophasic variants 13,23: i:-) (679 isolations, 34.6% of total chicken isolations)
- *S*. Kedougou (382 isolations, 19.5% of total chicken isolations)
- *S*. Montevideo (308 isolations, 15.7% of total chicken isolations)
- *S*. Mbandaka (168 isolations, 8.6% of total chicken isolations)
- *S*. Agona (136 isolations, 6.9% of total chicken isolations)

There were 12 isolations of *S*. Enteritidis in 2024 compared with 9 isolations during 2023 and 23 isolations during 2022. The most commonly reported phage type in 2024 was PT8 (5 isolations).

There were 17 isolations of *S*. Typhimurium compared with 21 isolations in 2023. The most commonly reported phage types were DT75 (7 isolations) and DT1 and DT105 (3 isolations each). There was one isolation of monophasic *S*. Typhimurium in 2024 (DT193), compared with 6 isolations in 2023.

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, 2% for layers and 1% for broilers, with Great Britain prevalences estimated at 0.35% for breeders, 0.24% for layers and 0.03% 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 chapters for devolved administration prevalences.

Turkeys

Including both NCP and non-statutory surveillance data, there were 108 isolations of *Salmonella* from turkeys in 2024. This is similar to 2023 when there were 109 isolations and a decrease of 43.2% compared within 2022 (190 isolations) (Table 7.1).

During 2024 the most common serovars isolated from turkeys were *S*. Anatum and *S.* Kedougou (21 isolations each, 19.4% of total turkey isolations each), the third most common serovar was *S.* Agona (20 isolations, 18.5% of total turkey isolations) and the fourth most common was *S.* Typhimurium (13 isolations, 12.0% of total turkey isolations).

There were 13 isolations of *S*. Typhimurium during 2024 (DT75 x9, DT99 x1, DT104 x1, DT105 x1 and DT193 x1), compared with 2 isolations during 2023 (both DT193) and one isolation during 2022 (DT99). There were no isolations of monophasic *S.* Typhimurium during 2024, compared with one isolation during 2023 and 4 isolations during 2022.

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 0.32% for turkey fatteners and 0.67% for turkey breeders, with all devolved nations coming in below the national targets of 1% for each of these turkey production sectors. 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 196 isolations of *Salmonella* from ducks in 2024. This is more than double compared to 2023 (96 isolations) and a 62.0% increase compared within 2022 (121 isolations) (Table 8.1). This upturn was influenced by an increase in voluntary surveillance testing carried out by the duck industry, resulting in a higher number of isolations in 2024.

The most commonly isolated serovars from ducks in 2024 were *S.* Indiana (147 isolations, 75.0% of total duck isolations), *S.* Newport (20 isolations, 10.2% of total duck isolations), *S.* Kottbus (12 isolations, 6.1% of total duck isolations), *S.* Give (5 isolations, 2.6% of total duck isolations) and *S.* Give var. 15^+ (3 isolations, 1.5% of total duck isolations each).

There had been a declining trend in the number of isolations of *S.* Hadar from ducks in recent years resulting in the lowest number of isolations of this serovar reported from ducks in 2021 (one isolation) since 2011 (when there was also a single isolation). The declining trend ended in 2022 where there were 17 isolations however decreased again during 2023 (6 isolations) and 2024 (2 isolations).

There were no isolations of *S*. Typhimurium from ducks in 2024. This compared to one isolation during 2023 (DT1) and no isolations during 2022 and 2021 when for the first time

S. Typhimurium was not recorded from ducks in Great Britain since 2001. There were no isolations of *S*. Enteritidis from ducks in 2024 compared with one isolation during 2023 (PT9) and no isolations during 2022.

There was one isolation of *Salmonella* (*S.* Typhimurium) from geese in 2024, compared to no isolations during 2023 and 2022.

Other statutory birds (as specified in the Zoonoses Order)

There were no isolations of *Salmonella* from game birds in 2024, which is a decrease from 2023 (4 isolations) and 2021 (1 isolation). Game birds include guinea fowl, partridges, pheasants and quail.

In 2024 there were no isolations of *Salmonella* from pheasants, compared to 2 isolations in 2023 and one isolation in 2022. In 2024 there were no isolations of *Salmonella* from partridges, compared to 2 isolations in 2023 and no isolations in 2022. There were no isolations of *Salmonella* in quail of guinea fowl in 2024, 2023 or 2022.

There were 22 *Salmonella* isolations from pigeons in 2024, which is slightly higher than in 2023 and 2022 (18 and 17 isolations, respectively). Of the isolations in 2024, 21 were *S*. Typhimurium and one was *S*. Braenderup.

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 482 isolations of *Salmonella* from dogs in 2024, a decrease of 30.0% compared to 2023 (689 isolations). The majority of these isolations (98.5%) were from reports of clinical disease. The most common serovars reported were *S*. Typhimurium (77 isolations, 16.0% of total isolations from dogs), *S.* Infantis (39 isolations, 8.1% of isolations from dogs) and *S.* Newport (30 isolations, 6.1% of isolations from dogs). All of these were in the top 5 human serovars in 2024.

The most common phage types of *S*. Typhimurium from dogs during 2024 were DT105 and RDNC (15 isolations each, 19.5% of isolations each), DT75 (13 isolations, 16.9% of isolations) and DT2 (10 isolations, 13.0% of isolations). There were also 19 isolations of monophasic *S*. Typhimurium (78.9% of which were DT193).

There were 17 isolations of *S*. Enteritidis from dogs during 2024. The most common phage types were PT8 and PT11 (2 isolations each).

Wildlife

There were 14 isolations of *Salmonella* from wildlife during 2024. Of these, 6 isolations were from hedgehogs (4 isolations of *S*. Enteritidis PT11 and one isolation each of *S*. Enteritidis PT9a and *S*. Enteritidis NOPT), 3 isolations of *S*. Typhimurium from gulls (DT193 x1, NOPT x1 and RDNC x1), 2 isolations from badgers of *S.* Eboko and *Salmonella* 4,5,12:b:-, one isolation of *S*. Typhimurium (DT2) from a fox, one isolation of *Salmonella* 4,12:a:- from a porpoise and one isolation of *S*. Typhimurium (DT75) from a seal. This is higher than in 2023 where there were 9 isolations and also higher than 2022 when there were 2 isolations of *Salmonella* from wildlife.

Feeding stuffs

There were 795 isolations of *Salmonella* from feeding stuffs during 2024, including 69 isolations from compound feeds (Tables 12.3 to 12.6) and 726 from feed ingredients or products associated with testing under Animal By-Products Regulations (ABPR). This is a decrease of 11.4% compared with 2023 (897 isolations) and an increase of 13.2% compared with 2022 (702 isolations).

There were 190 isolations of regulated *Salmonella* serovars from animal feeding stuffs and related products during 2024. Regulated serovars are key serovars of public health importance targeted by the NCPs. This is 28.3% fewer than in 2023 (265 isolations) and 1.6% higher than in 2022 (187 isolations). There were 84 isolations of *S*. Infantis, 57 isolations of *S.* Typhimurium, 28 isolations of *S.* Enteritidis, 20 isolations of monophasic *S.* Typhimurium, and one isolation of *S*. Virchow.

There were 290 reports of *Salmonella* from raw meat pet food (Table 12.8b). This is lower than during 2023 (331 reports) and 2022 (406 reports). The most common serovars reported in raw pet food during 2024 were *S.* Infantis (38 isolations), *S.* Indiana (36 isolations), and *S.* Typhimurium (28 isolations). Overall, there were 95 isolations of regulated serovars from raw meat pet food in 2024. This is a decrease of 4.0% compared with 2023 (99 isolations) and 22.8% lower than in 2022 (123 isolations).

The isolation rate of *Salmonella* from domestic processed animal protein in 2024 was 1.7%, which is higher than in 2023 when it was 1.2%.

No batches of imported processed animal protein were tested during 2024, which is the same as during 2023 and 2022.

Antimicrobial resistance

Of the 4,705 *Salmonella* isolates examined during 2024, 73.3% were susceptible to all 16 antimicrobial compounds tested against. This is the same as 2023, when 73.3% of isolates were also susceptible to all 16 antimicrobials.

A total of 246 isolates of *S*. Dublin were examined in 2024, of which 91.5% were susceptible to all the antimicrobials tested against. This is lower than in 2023 when 96.3% were susceptible to all antimicrobials tested against.

A total of 569 isolates of *S.* Typhimurium were examined in 2024, of which 54.3% were susceptible to all the antimicrobials tested against which is similar to 2023 (55.0%), and higher than in 2022 (47.8%).

A total of 140 isolates of monophasic *S*. Typhimurium were examined in 2024, of which 4.3% were susceptible to all the antimicrobials tested against. This is lower than in 2023 when 7.4% were susceptible to all antimicrobials tested against.

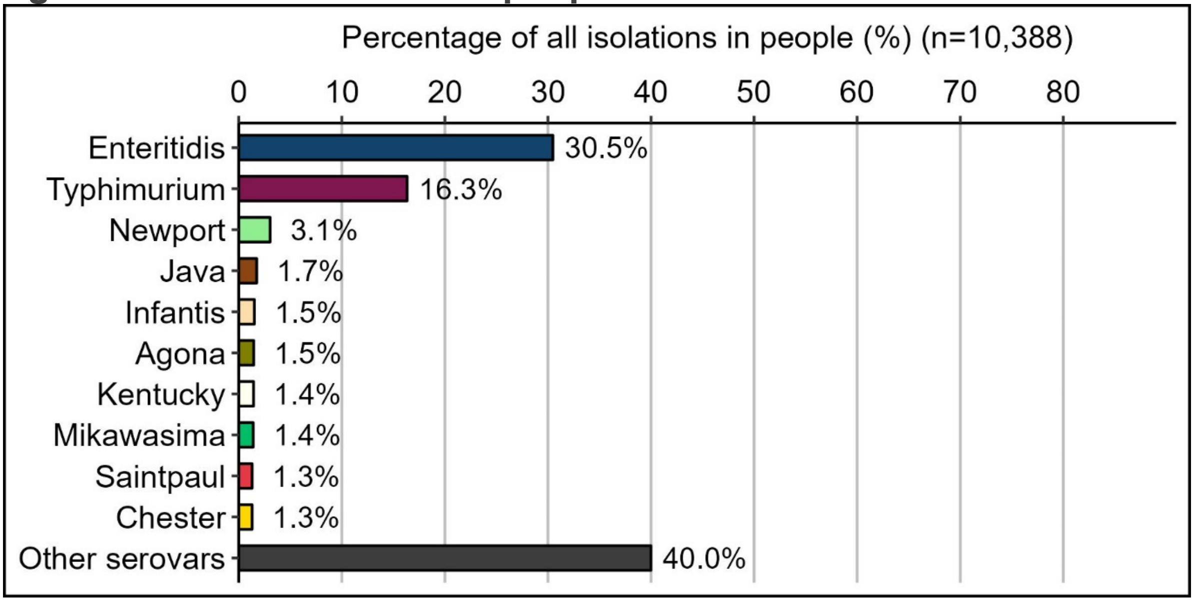
In total, 3,890 isolates of serovars other than *S*. Dublin or *S*. Typhimurium were tested in 2024 and 74.9% of these were sensitive to all the antimicrobials tested against. This is similar to 2023 when 73.9% of isolates were fully sensitive.

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 2024 was 0.7%. Cefotaxime or ceftazidime resistance was not detected in *S*. Infantis from animals in 2023. Cefotaxime and ceftazidime resistance remained stable in 2024 at 0.1% (5 isolates) with 3 *Salmonella* isolates from dogs.

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

Figure 1.1: Isolations of the most common serovars in livestock and people in England in 2024

Figure 1.1.1: Isolations from people

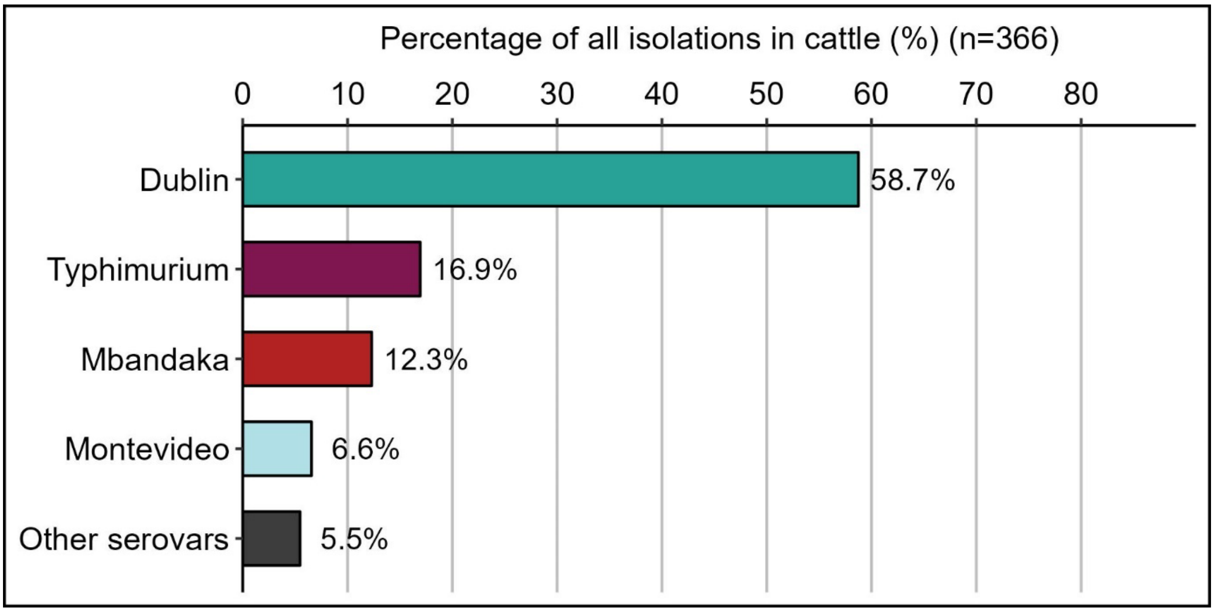


Horizontal bar graph showing the percentage of the top *Salmonella* isolations in people in 2024. The most commonly reported *Salmonella* serovar in people in 2024 was *S.* Enteritidis, accounting for 30.5% of total isolations, followed by *S.* Typhimurium (16.3%), *S.* Newport (3.1%) and *S.* Java (1.7%).

S. Typhimurium isolates in people include monophasic strains.

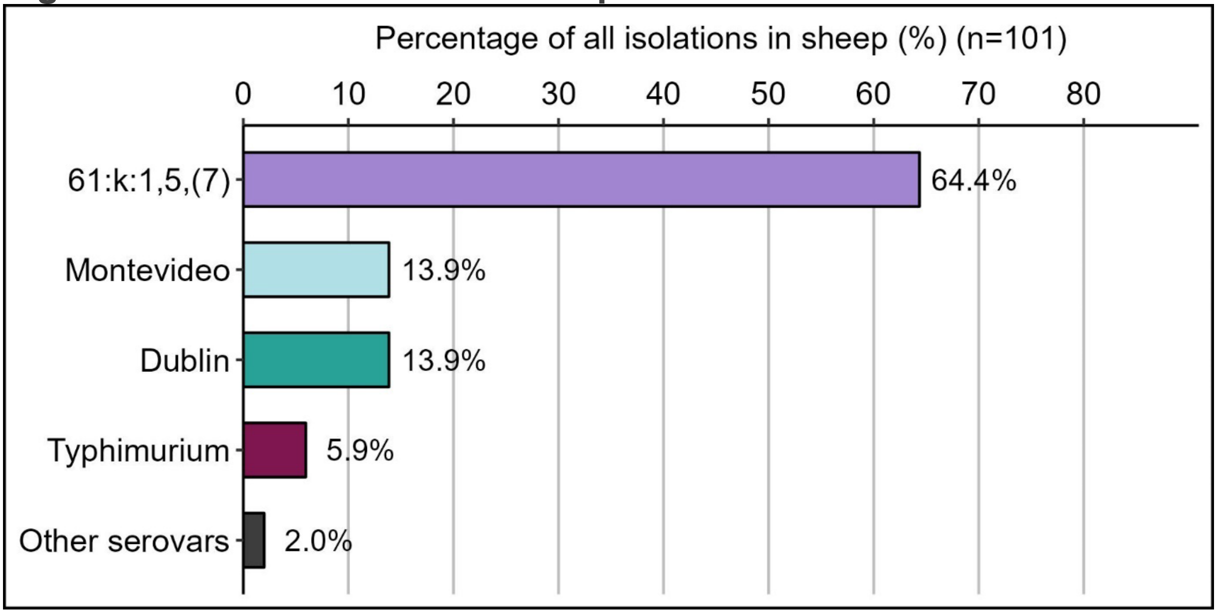
Data on human isolates in England was provided by UK Health Security Agency (UKHSA). The UKHSA Second-Generation System (SGSS) is a live laboratory reporting system therefore numbers are subject to change and may not be directly comparable with data reported in previous years.

Figure 1.1.2: Isolations from cattle



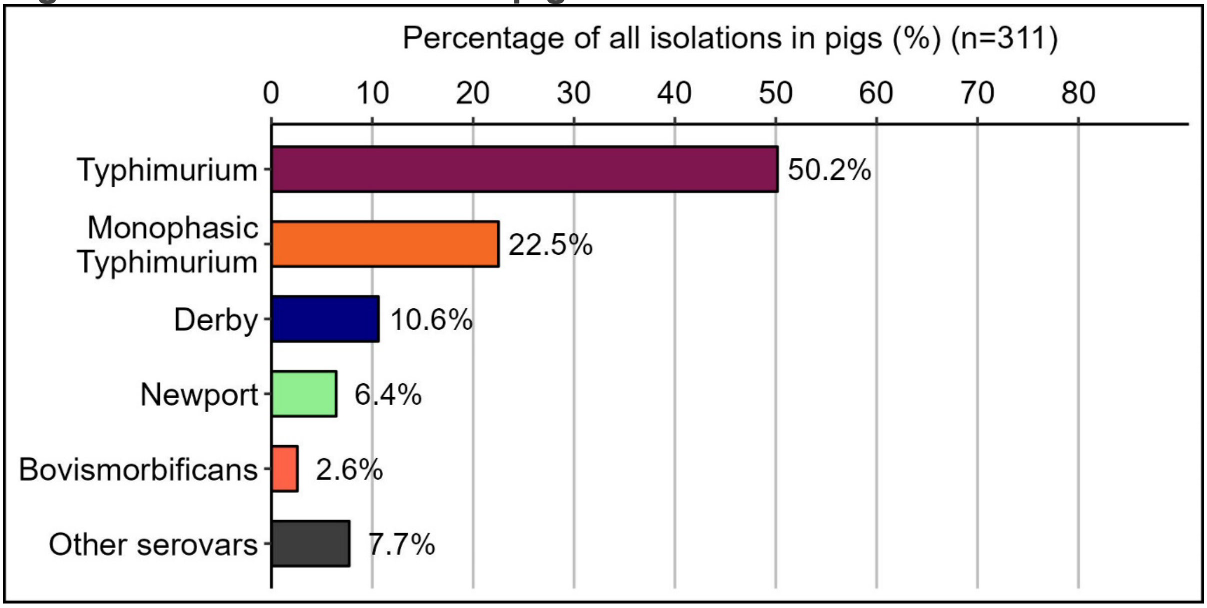
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in cattle in 2024. The most common *Salmonella* serovar in cattle in 2024 was *S.* Dublin (58.7% of total isolations), followed by *S.* Typhimurium (16.9%) and *S.* Mbandaka (12.3%).

Figure 1.1.3: Isolations from sheep



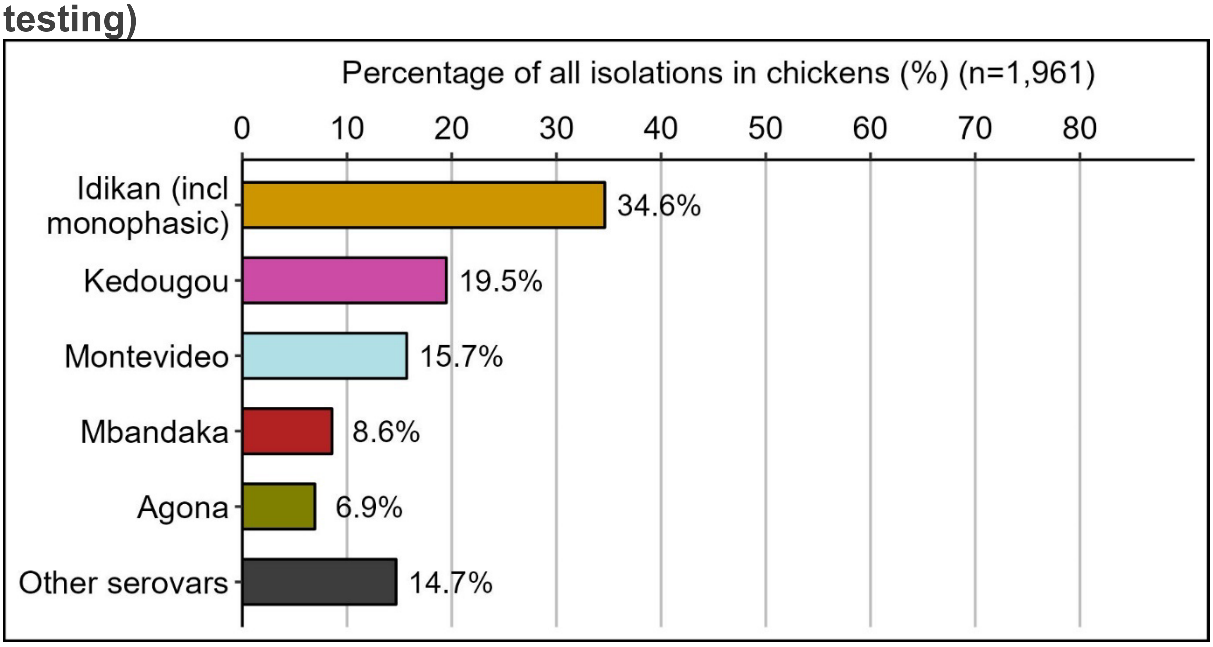
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in sheep in 2024. The most common *Salmonella* serovar in sheep in 2024 was *S.* 61:k:1,5,(7) which includes *S. enterica diarizonae* and variants (64.4% of total isolations), followed by *S.* Dublin and *S.* Montevideo (13.9%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

Figure 1.1.4: Isolations from pigs



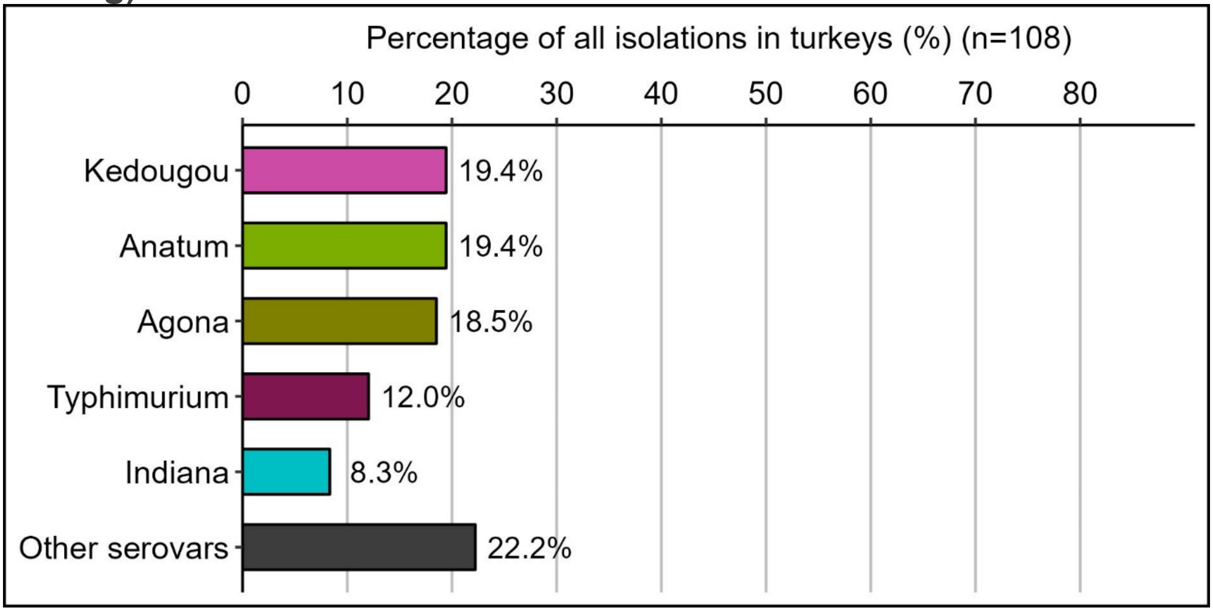
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in pigs in 2024. The most common *Salmonella* serovar in pigs in 2024 was *S.* Typhimurium (50.2% of total isolations), followed by monophasic *S*. Typhimurium (22.5%) and *S.* Derby (10.6%).

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



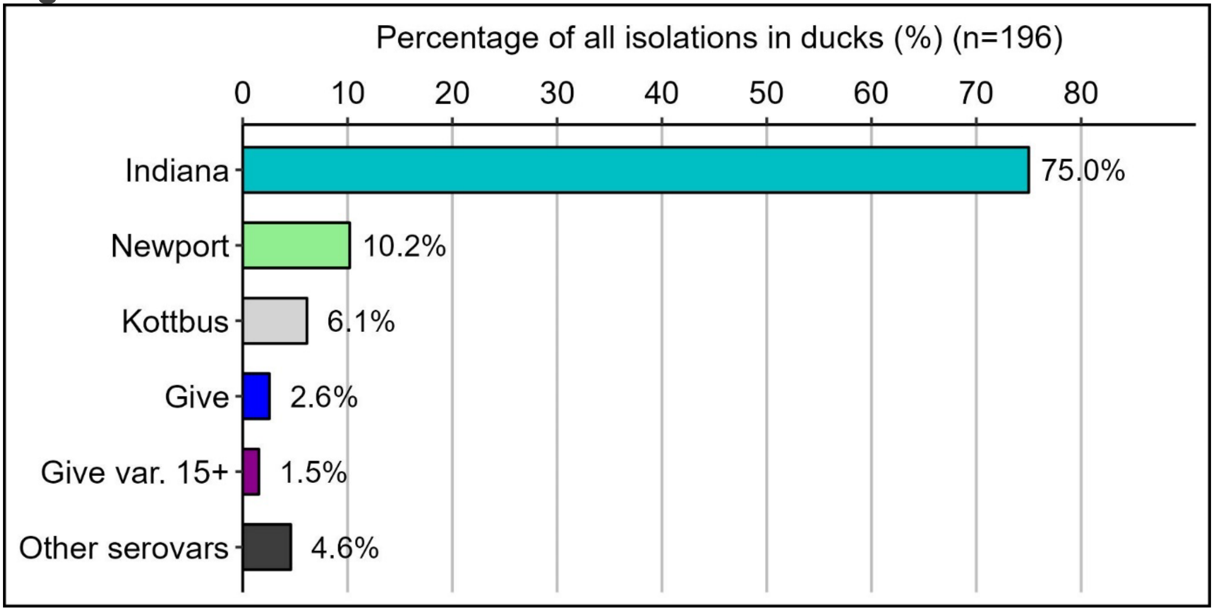
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in chickens in 2024. The most common *Salmonella* serovar in chickens in 2024 was *S.* Idikan (incl monophasic) (34.6% of total isolations), followed by *S.* Kedougou (19.5%), *S.* Montevideo (15.7%) and *S*. Mbandaka (8.6%).

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



Horizontal bar graph showing the percentage of the top *Salmonella* isolations in turkeys in 2024. The most common *Salmonella* serovars in turkeys in 2024 were *S.* Anatum and *S.* Kedougou (19.4% of total isolations each), followed by *S.* Agona (18.5%), *S.* Typhimurium (12.0%) and *S.* Indiana (8.3%).

Figure 1.1.7: Isolations from ducks



Horizontal bar graph showing the percentage of the top *Salmonella* isolations in ducks in 2024. The most common *Salmonella* serovar in ducks in 2024 was *S.* Indiana (75.0% of total isolations), followed by *S.* Newport (10.2%) and *S.* Kottbus (6.1%).

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 2020 to 2024. Poultry includes chickens, turkeys and ducks.

The data includes statutory and non-statutory results.

***Salmonella* serovar**	**2020 isolations**	**2021 isolations**	**2022 isolations**	**2023 isolations**	**2024 isolations**
61:k:1,5,(7)	50	74	71	75	73
Agama	7	5	3	3	2
Ago	0	0	0	0	1
Agona	103	42	139	208	156
Ajiobo	0	1	0	1	0
Amsterdam	0	0	0	1	0
Anatum	52	42	70	25	32
Bardo	14	10	5	0	0
Bareilly	0	1	0	0	0
Berta	1	0	2	1	1
Bovismorbificans	43	30	18	3	8
Braenderup	1	2	2	5	2
Brandenburg	0	0	1	0	0
Bredeney	3	1	0	0	1
Cerro	0	0	0	1	0
Chester	1	0	0	3	2
Chomedey	0	0	0	1	0
Coeln	3	1	4	7	3
Corvallis	0	0	3	0	1
Cubana	0	0	0	1	0
Derby	39	49	40	35	45
Dublin	235	321	274	258	230
Durham	0	0	0	1	0
Eboko	1	0	1	0	0
Enteritidis	34	11	25	11	13
Essen	0	1	0	0	0
Ferruch	0	2	0	0	0
Fresno	0	0	0	1	0
Gaminara	0	1	1	0	0
Give	9	6	3	14	5
Give var. 15+	36	23	23	5	3
Glostrup	1	0	0	0	0
Goldcoast	0	1	0	0	0
Hadar	21	1	17	6	2
Havana	1	2	6	0	1
Hessarek	0	0	0	0	1

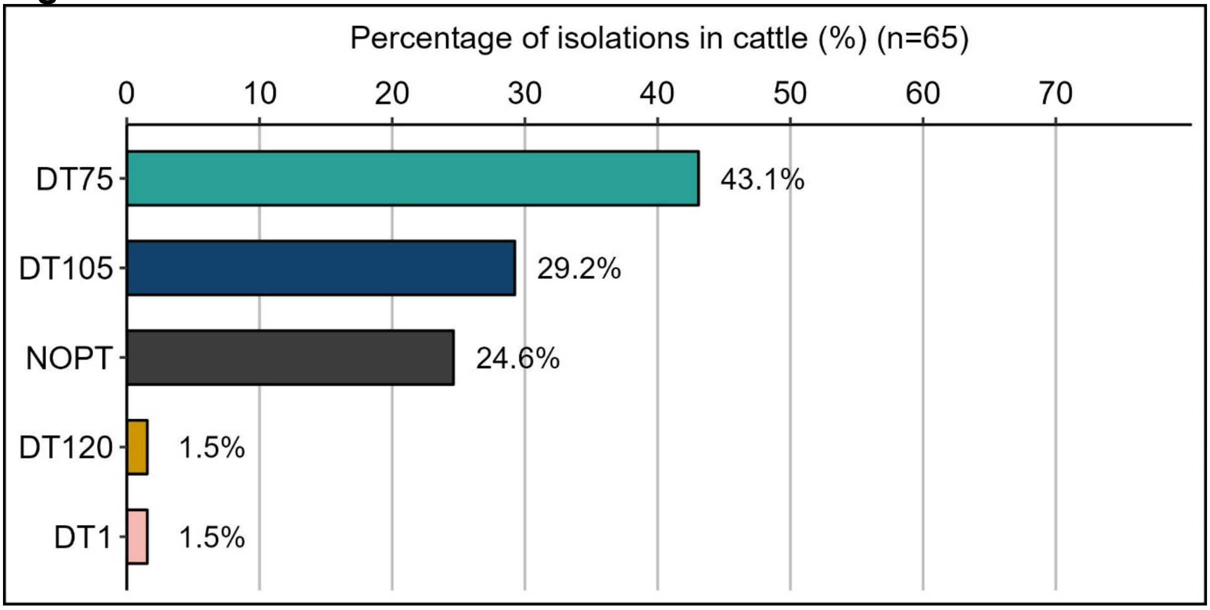
Salmonella serovar	2020 isolations	2021 isolations	2022 isolations	2023 isolations	2024 isolations
Idikan (incl monophasic)	739	288	390	686	684
Indiana	65	44	40	57	166
Infantis	1	42	98	64	20
Isangi	0	3	0	0	0
Javiana	0	0	0	0	2
Kedougou	499	235	310	583	410
Kentucky	1	0	4	1	18
Kingston	6	2	6	4	4
Kottbus	13	15	7	15	16
Lexington	7	10	9	8	1
Liverpool	2	0	1	0	0
Livingstone	13	18	3	14	8
London	6	12	14	2	2
London var 15+	0	0	1	0	0
Mbandaka	326	369	754	351	213
Menston	0	2	0	0	0
Mikawasima	1	0	0	0	0
Minnesota	0	1	0	0	0
Molade	0	1	0	0	0
Monophasic Typhimurium	95	100	79	83	75
Monschaui	2	0	0	0	0
Montevideo	540	908	982	1242	692
Muenchen	8	4	9	5	27
Muenster	0	0	0	3	0
Newport	66	62	33	25	69
Nottingham	0	7	4	0	1
Odozi	0	4	0	0	0
Ohio	1	0	1	1	0
Ohio	33	55	49	36	44
Orion	0	0	0	0	1
Orion	0	0	1	0	0
Orion	16	12	2	2	2
Orion	0	0	0	1	0
Orion	16	12	3	3	3
Orion var. 15+	44	47	80	77	56
Oslo	6	3	0	4	4
Oxford	0	0	0	1	0
Panama	0	0	1	1	0
Panama	2	5	12	10	8
Paratyphi B var. Java	2	0	0	0	0
Poona	1	0	0	1	1
Ramatgan	1	0	0	0	0
Reading	3	3	4	2	7

Salmonella serovar	**2020 isolations**	**2021 isolations**	**2022 isolations**	**2023 isolations**	**2024 isolations**
Rissen	0	0	1	2	1
Saintpaul	1	0	0	0	0
Schwarzengrund	1	0	0	2	0
Senftenberg	96	63	37	22	10
Senftenberg	15	21	26	3	4
Stanley	0	0	1	0	0
Stanleyville	1	0	1	0	0
Stourbridge	1	3	1	0	0
Takoradi	0	0	1	0	0
Tennessee	1	0	1	0	0
Typhimurium	159	200	185	257	254
Wangata	0	0	0	1	0
Yoruba	0	0	0	2	0
rough strains	37	33	32	2	0
untypable strains	86	64	57	17	9
Total	**3568**	**3275**	**3948**	**4256**	**3394**

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.

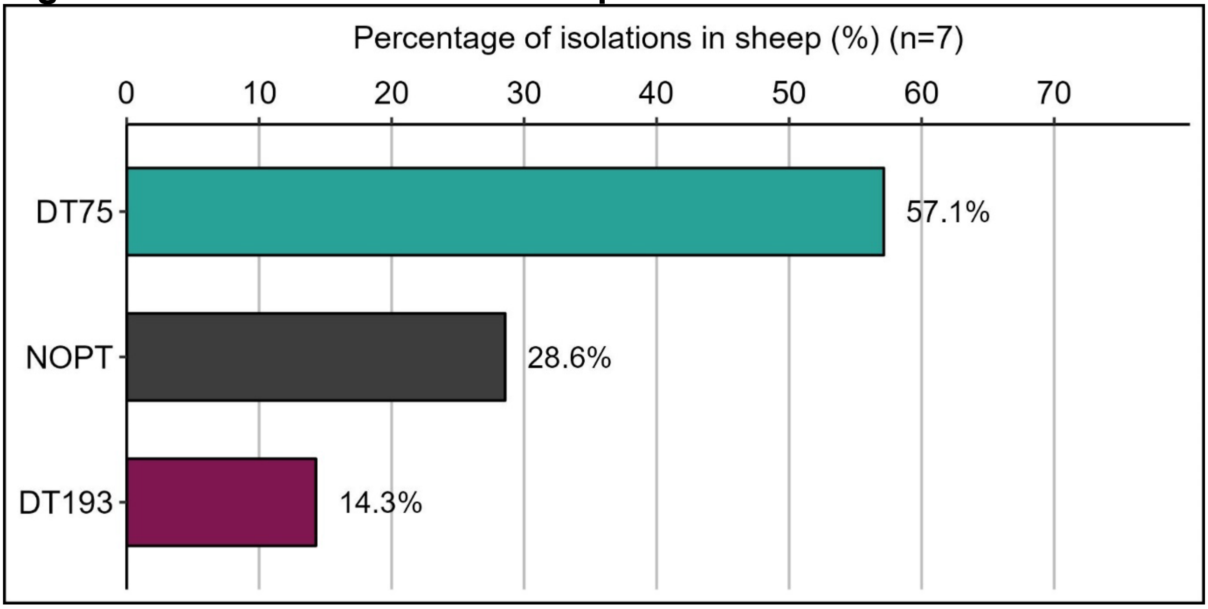
Figure 1.2: Isolations of the most common *S.* Typhimurium phage types (including monophasic strains) in livestock in 2024

Figure 1.2.1: Isolations from cattle



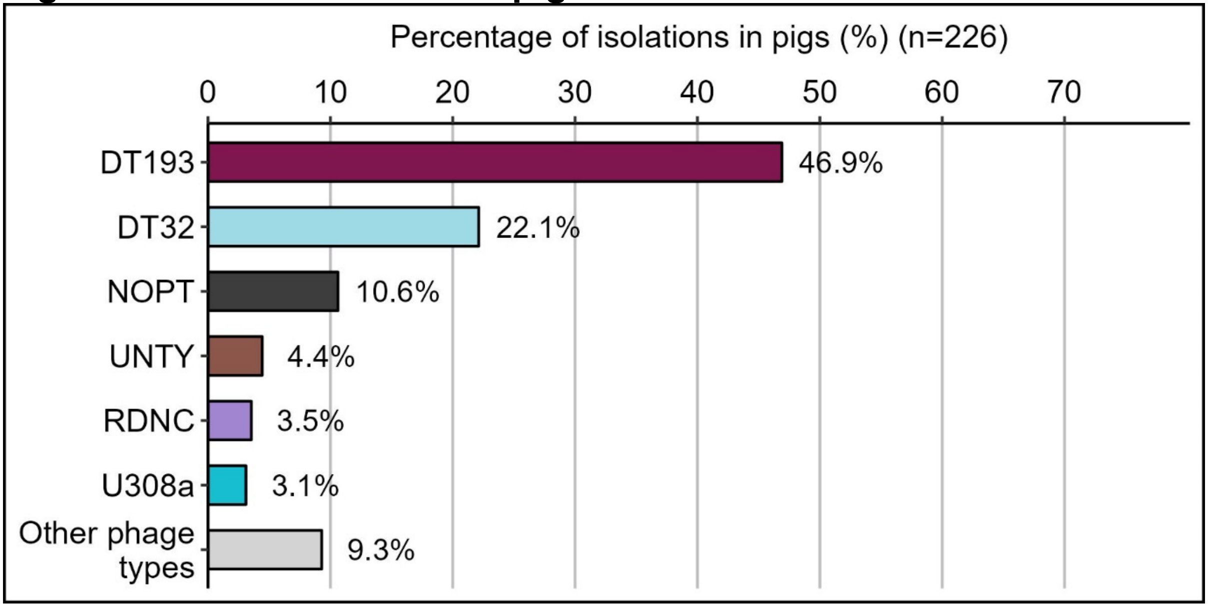
Horizontal bar graph showing the percentage of isolations of the most common *Salmonella* Typhimurium (including monophasic strains) phage types in cattle in 2024. The most common *S.* Typhimurium phage type in cattle in 2024 was DT75 (43.1% of all cattle isolations), followed by DT105 (29.2%), NOPT (24.6%), DT120 and DT1 (1.5% each).

Figure 1.2.2: Isolations from sheep



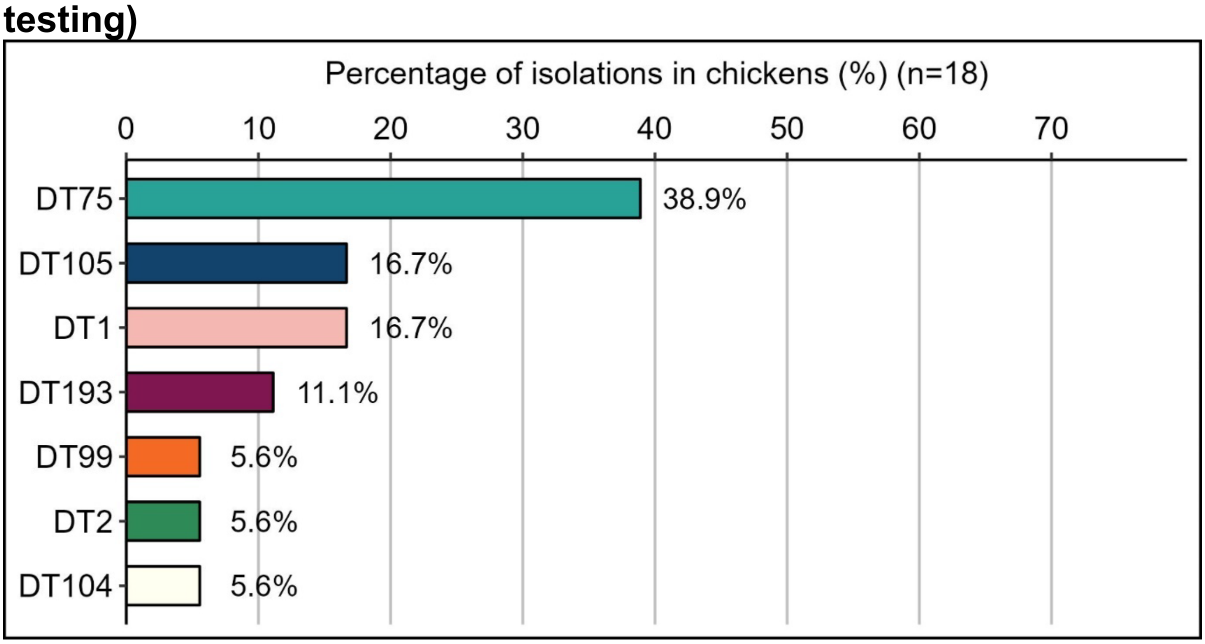
Horizontal bar graph showing the percentage of isolations of the most common *Salmonella* Typhimurium (including monophasic strains) phage types in sheep in 2024. The most common *S.* Typhimurium phage type in sheep in 2024 were DT75 (57.1% of all sheep isolations) and DT193 (14.3%). 28.6% of isolates were not phage typed (NOPT).

Figure 1.2.3: Isolations from pigs



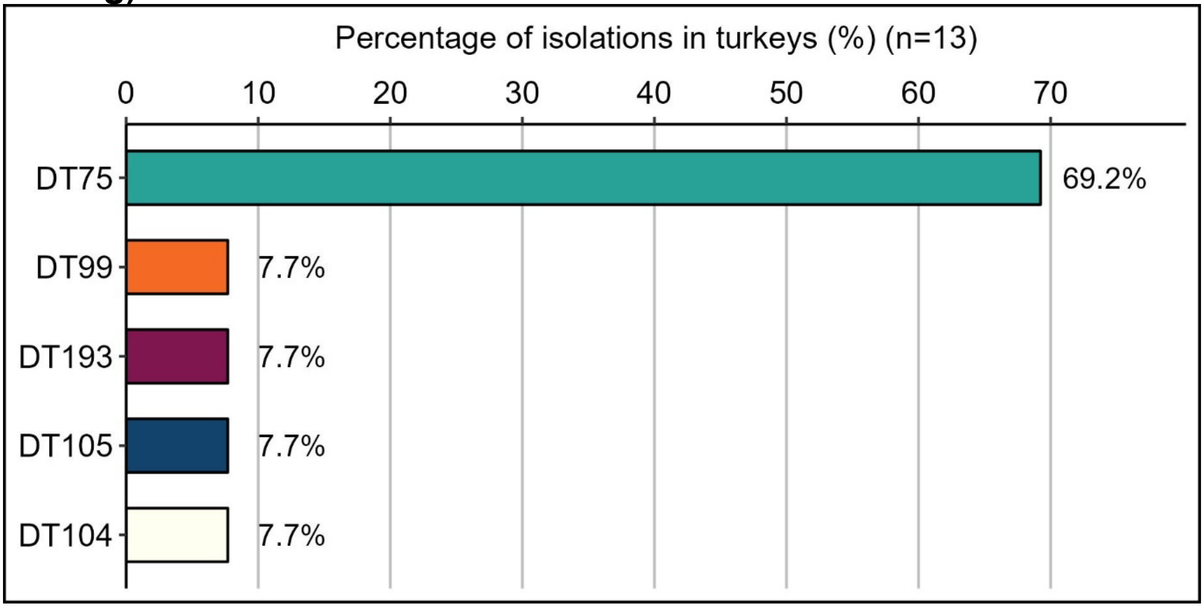
Horizontal bar graph showing the percentage of isolations of the most common *Salmonella* Typhimurium (including monophasic strains) phage types in pigs in 2024. The most common *S.* Typhimurium phage type in pigs in 2024 was DT193 (46.9% of all pig isolations), followed by DT32 (22.1%) and NOPT (10.6%).

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



Horizontal bar graph showing the percentage of isolations of the most common *Salmonella* Typhimurium (including monophasic strains) phage types in chickens in 2024. The most common *S.* Typhimurium phage type in chickens in 2024 was DT75 (38.9% of all chicken isolations), followed by DT1 and DT105 (16.7% each) and DT193 (11.1%).

Figure 1.2.5: Isolations from turkeys (statutory and non-statutory testing)



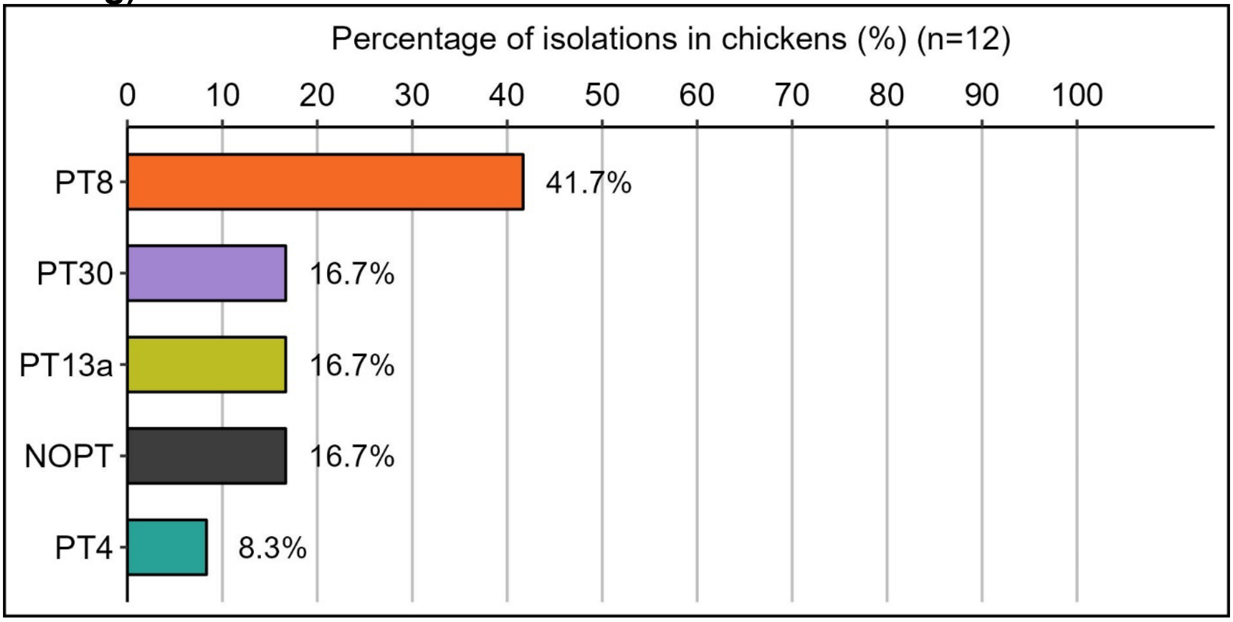
Horizontal bar graph showing the percentage of isolations of the most common *Salmonella* Typhimurium (including monophasic strains) phage types in turkeys in 2024. The most common *S.* Typhimurium phage type in turkeys in 2024 was DT75 (69.2% of all turkey isolations).

There were no isolations of *S*. Typhimurium in ducks in 2024.

Figure 1.3: Isolations of the most common *S*. Enteritidis phage types in livestock in 2024

No isolates of *S*. Enteritidis in cattle were phage typed in 2024.

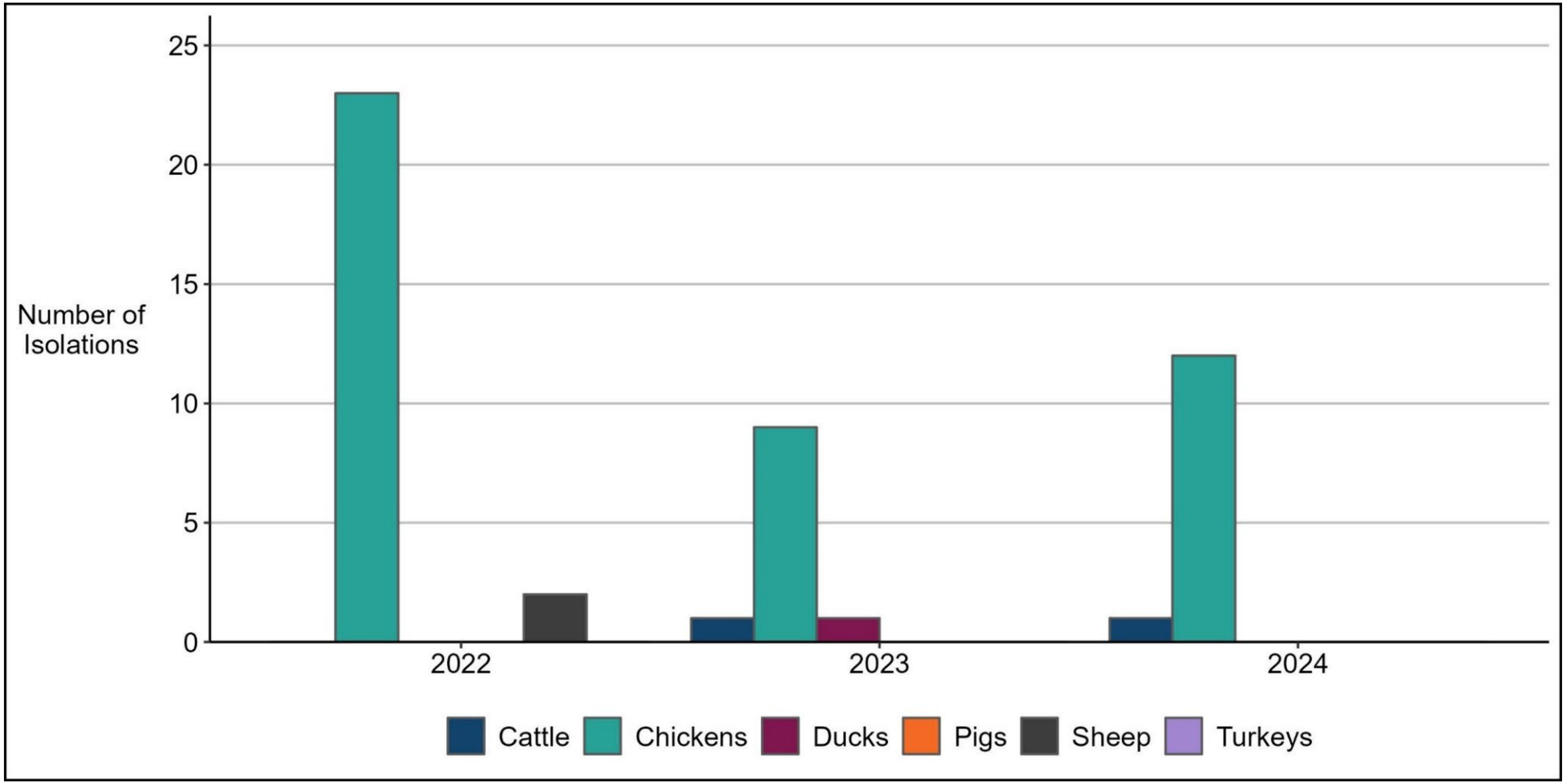
Figure 1.3.2 Isolations from chickens (statutory and non-statutory testing)



Horizontal bar graph showing the percentage of isolations of the most common *Salmonella* Enteritidis phage types in chickens in 2024. The most common *S*. Enteritidis phage types in chickens in 2024 were PT8 (41.7% of all chicken isolations) and PT13a, PT30 and NOPT (16.7% each).

There were no isolations of *S*. Enteritidis in pigs, sheep, turkeys or ducks in 2024.

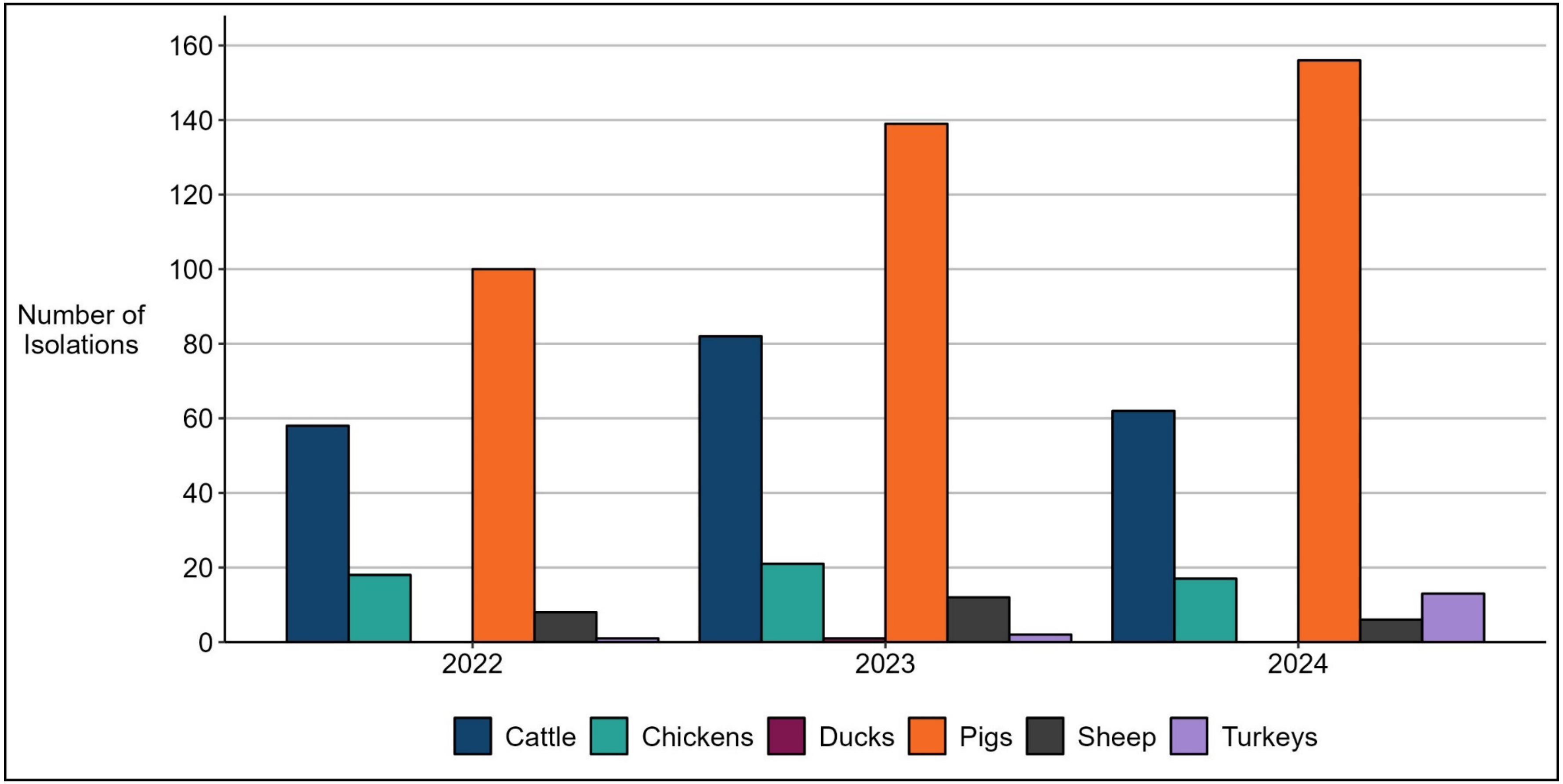
Figure 1.4: Isolations of *S*. Enteritidis in livestock in Great Britain 2022 to 2024



Vertical bar graph showing the number of isolations of *Salmonella* Enteritidis isolated in cattle, chickens, ducks, pigs, sheep and turkeys in 2024. The figure shows *Salmonella* Enteritidis was most commonly isolated from chickens during 2024, and in fewer numbers from cattle. This compares to chickens also being the most commonly isolated species in 2023 and 2022. *S*. Enteritidis was isolated from ducks in 2022, though not in 2021. *S*. Enteritidis was not isolated in pigs or turkeys in 2022, 2023 or 2024.

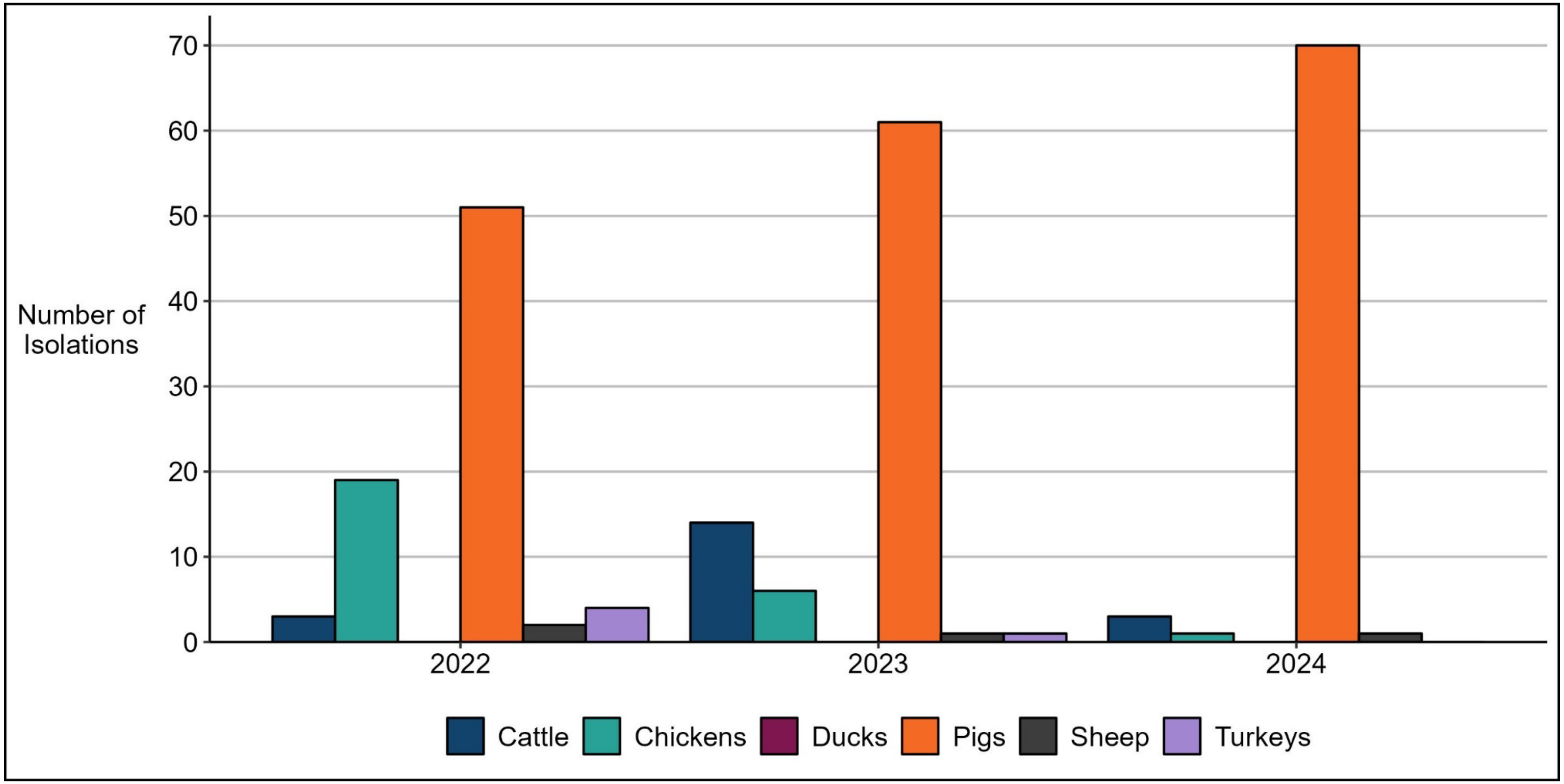
Data for chickens and turkeys include both statutory and non-statutory testing.

Figure 1.5: Isolations of S. Typhimurium in livestock in Great Britain 2022 to 2024



Vertical bar graph showing the number of isolations of *Salmonella* Typhimurium isolated in cattle, chickens, ducks, pigs, sheep and turkeys in 2024. *Salmonella* Typhimurium was most commonly isolated from pigs amongst livestock species during 2024, and in lesser numbers from cattle, chickens, sheep and turkeys. This compares to pigs also being the most commonly isolated species in 2023 and 2022. *S*. Typhimurium was also isolated from cattle, chickens, ducks, sheep and turkeys in 2023. 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 2022 to 2024



Vertical bar graph showing the number of isolations of monophasic *Salmonella* Typhimurium isolated in cattle, chickens, ducks, pigs, sheep and turkeys in 2024. Monophasic *S*. Typhimurium was most commonly isolated from pigs among livestock species during 2024, and in lesser numbers from cattle, chickens and sheep. This compares to pigs also being the most commonly isolated species in 2023 and 2022. Monophasic *S*. Typhimurium was also isolated from cattle, chickens, sheep and turkeys in 2023 and 2022. 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 on agricultural holdings in Great Britain was just under 7.74 million in 2024 according to the agricultural census, a decrease of 1.8% compared to 2023. With the exception of 2022, there has been a gradual decline in the cattle population since 2016 (Figure 2.1). There has also been a steady decline in the number of commercial cattle holdings in Great Britain since 2016, to just over 52,000 in 2024.

On the Veterinary Investigation Diagnoses Analysis (VIDA) database there were 16,530 submissions recorded from cattle in 2024, which was a decrease of 7.7% compared to 2023 (17,910). There is no active monitoring for *Salmonella*e in bovines, with nearly all isolations arising from diagnostic submissions (animals with clinical disease). Surveillance data, including clinical signs, age and country information, associated with diagnoses of salmonellosis in cattle can be accessed at Cattle Dashboard | Tableau Public.

There were 366 *Salmonella* isolations from cattle in 2024, a decrease of 16.1% from 2023 when there were 436 isolations (Table 2.1). This represents a continued decline from the 2021 figure when a total of 521 isolations were recorded. The 3 commonest 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). The number of *S.* Dublin isolations, the commonest serovar in cattle, fell by 14.7% from 252 isolations in 2023 to 215 isolations in 2024. The proportion of *S*. Dublin isolations in relation to the total number of *Salmonella* isolations from cattle changed little from 57.8% in 2023 to 58.7% in 2024. There was a marked reduction of 24.4% in isolations of *S.* Typhimurium in 2024, from 82 isolations to 62 isolations in 2023. Isolations of *S.* Mbandaka did not vary significantly from 2023.

Salmonella Dublin

The most common serovar isolated from cattle in Great Britain was *Salmonella* Dublin for the 2fifth successive year. There were 215 isolations of *Salmonella* Dublin, representing 58.7% of the total 366 *Salmonella* isolations from cattle.

As in previous years, the number of isolations peaked in the autumn (Figure 2.4). Alimentary tract disease was the most common presentation, 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

The number of isolations of monophasic *S*. Typhimurium fell from 14 in 2023 to 3 in 2024, with only one phage type represented, DT120, the 2 other isolates were not phage typed (NOPT) (Table 2.3).

As stated, the second most common serovar isolated from cattle submissions was *S.* Typhimurium, although the number of isolations reduced by 24.4% with 62 isolations in 2024 compared to 82 in 2023. The proportion of *Salmonella* Typhimurium in respect to total *Salmonella* isolations fell slightly from 18.8% in 2023 to 16.9% in 2024.

Only 3 phage types were identified in 2024 compared to 7 in 2023 (Table 2.2). The most common was DT75 with 28 isolations, the same number as 2023. This phage type was first identified in 2022, having previously never being isolated from cattle in Great Britain. There was a marked reduction in DT105, with the number of isolations falling from 33 in 2023 to 19 in 2024. There were again no isolations of *S*. Typhimurium UNTY in 2024.

Salmonella Mbandaka

The third most common serovar in cattle was *S.* Mbandaka with 45 isolations representing 12.3% of the cattle isolations. This compared to 46 isolations in 2023 when it represented 10.6% of the isolations.

Other serovars

The number of *Salmonella* Montevideo isolations, the fourth most common serovar in cattle in 2024 rose from 16 isolations in 2023 to 24 in 2024 (3.7% of total isolations in cattle to 6.6% in 2024).

Reports of non-Great Britain origin

There were 3 reports of *S*. Dublin from cattle of non-GB origin. One arising from cattle imported from the Republic of Ireland, one from cattle imported from an unspecified country in the EU and the third in cattle imported from Denmark.

There were 2 reports of *S*. Typhimurium DT105 in cattle imported from the Netherlands. These reports are excluded from the tables and figures of this publication.

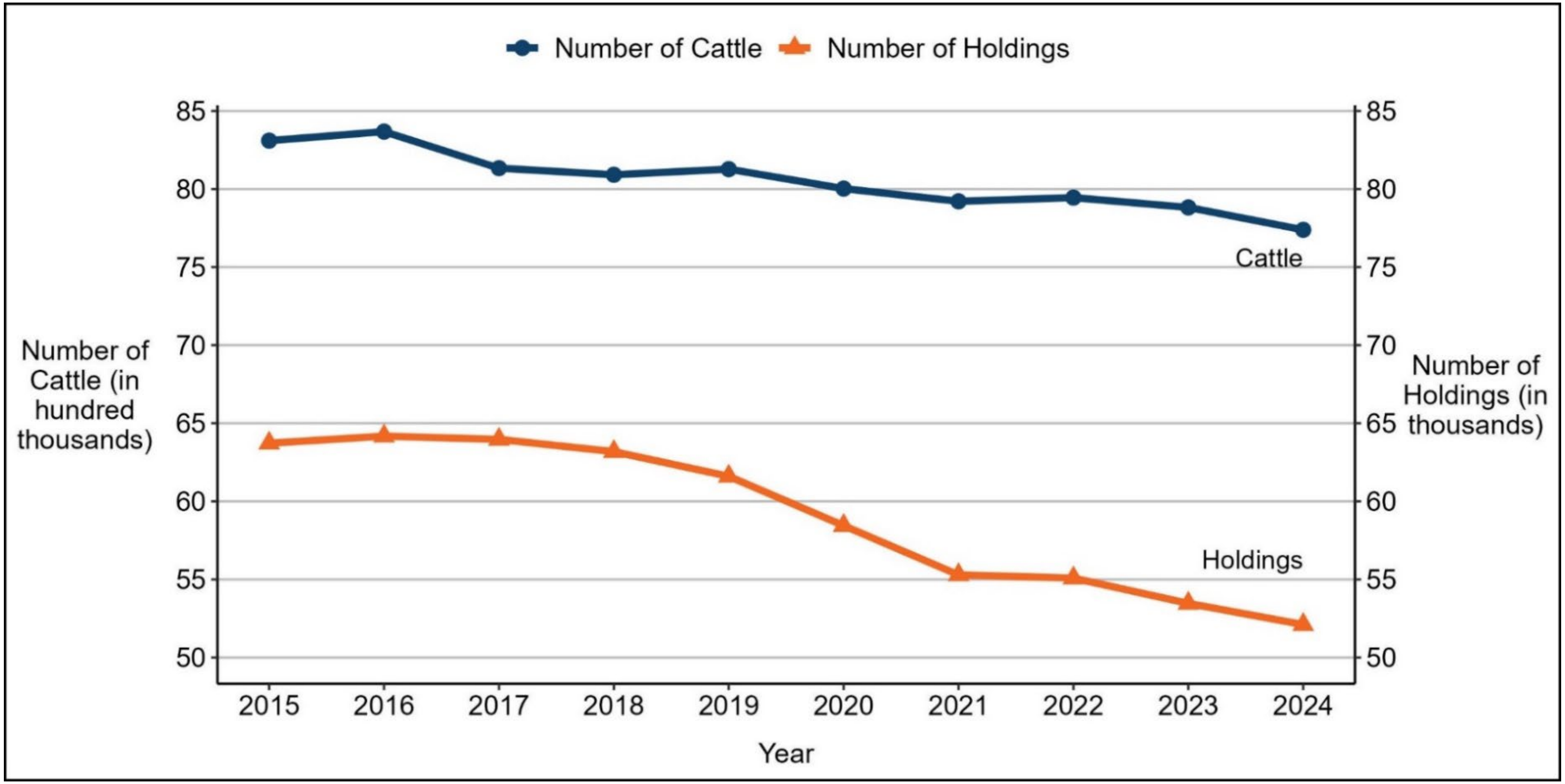
Antimicrobial susceptibility in cattle

A total of 346 isolates from cattle were tested against a panel of 16 antimicrobials in 2024. Fully susceptible isolates accounted for 89.6%, a stable figure compared to 2023. Only 2 isolates (0.6%) were multidrug-resistant (MDR; resistant to 4 or more antimicrobials), a decrease from the previous year (3.2%, n=471).

S. Dublin (n=20) and *S.* Typhimurium (n=7) were the most frequently resistant serovars. However, *S.* Dublin isolates were almost exclusively resistant to only one antimicrobial, while the 2 MDR isolates belonged to the serovars *S.* Mbandaka and monophasic *S.* Typhimurium. Resistance patterns mainly included streptomycin (6.1%), tetracycline (3.2%), and sulphonamides (2.6%), all at low and stable levels. A decrease in ampicillin resistance was detected between 2023 (4.5%) and 2024 (0.6%). Resistance to nalidixic acid was observed in one monophasic *S*. Typhimurium 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).

Figure 2.1: Cattle population and numbers of commercial holdings with cattle in Great Britain 2015 to 2024



A line graph showing the cattle population and number of commercial holdings from 2015 to 2024. There was a steady decline in the number of cattle holdings since 2015 and while the number of cattle has also declined there was a small upturn in 2022 before declining again 2023.

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

Number of holdings in 2020 is estimated.

Source: June 2024 Agricultural Census. For the definition of a commercial holding in the agricultural census, see the survey methodology

Table 2.1: Isolations and incidents of *Salmonella* in cattle on all premises in Great Britain 2020 to 2024

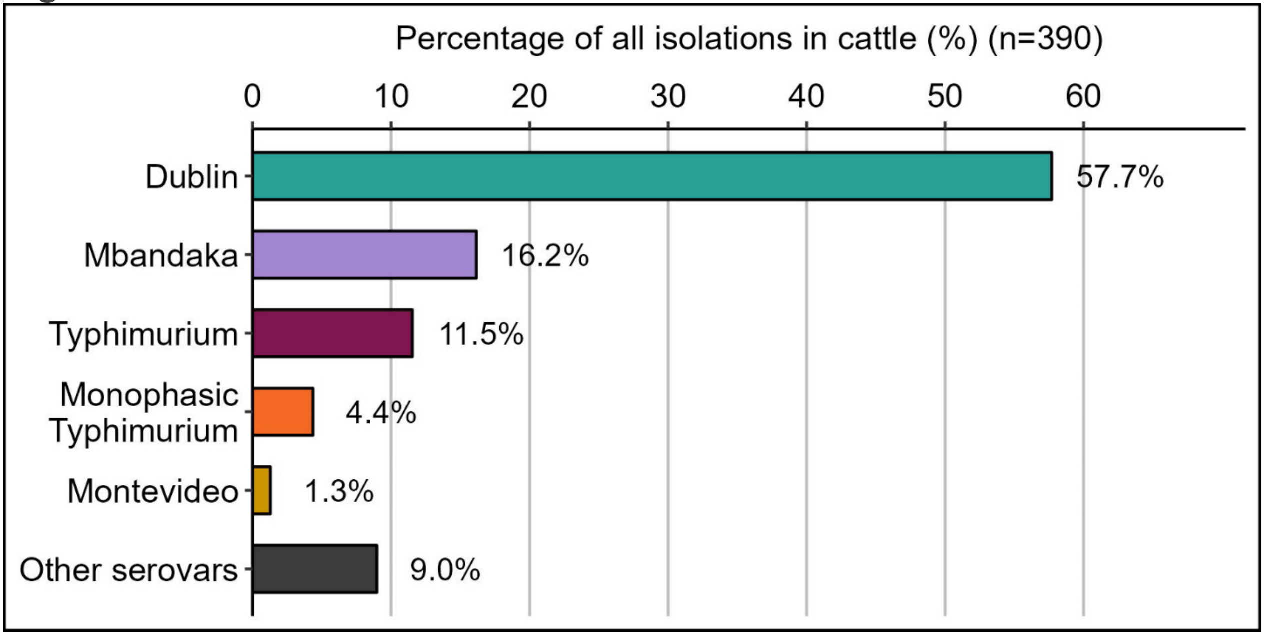
Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Agama	1	1	1	1	0	0	0	0	0	0
Anatum	2	2	5	4	1	1	1	1	1	1
Bovismorbificans	1	1	0	0	0	0	0	0	0	0
Bredeney	2	2	1	1	0	0	0	0	0	0
Chester	1	1	0	0	0	0	1	1	0	0
Coeln	0	0	1	1	0	0	3	2	2	1
Derby	1	1	0	0	0	0	1	1	0	0
Dublin	225	199	306	253	265	219	252	217	215	181
Eboko	1	1	0	0	0	0	0	0	0	0
Enteritidis	2	2	1	1	0	0	1	1	1	1
Gaminara	0	0	1	1	1	1	0	0	0	0
Glostrup	1	1	0	0	0	0	0	0	0	0
Indiana	1	1	0	0	1	1	0	0	3	3
Infantis	0	0	0	0	0	0	1	1	0	0
Kingston	0	0	1	1	0	0	1	1	0	0
Kottbus	2	2	6	6	0	0	0	0	0	0
London	1	1	0	0	0	0	0	0	1	1
Mbandaka	63	56	73	64	59	54	46	42	45	40
Menston	0	0	2	2	0	0	0	0	0	0
Monophasic Typhimurium	17	10	15	14	3	3	14	12	3	3

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Montevideo	5	4	23	19	18	17	16	13	24	21
Muenster	0	0	0	0	0	0	1	1	0	0
Newport	2	2	2	2	0	0	3	3	3	3
Orion	0	0	0	0	0	0	0	0	1	1
Oslo	1	1	1	1	0	0	3	2	0	0
Panama	0	0	0	0	1	1	1	1	0	0
Paratyphi B var. Java	2	2	0	0	0	0	0	0	0	0
Saintpaul	1	1	0	0	0	0	0	0	0	0
Typhimurium	45	35	65	46	58	48	82	73	62	49
61:k:1,5,(7)	5	5	5	5	6	6	8	8	0	0
untypable strains	7	5	9	9	12	12	1	1	5	4
rough strains	1	1	3	3	5	5	0	0	0	0
Total	**390**	**337**	**521**	**434**	**430**	**368**	**436**	**381**	**366**	**309**

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.

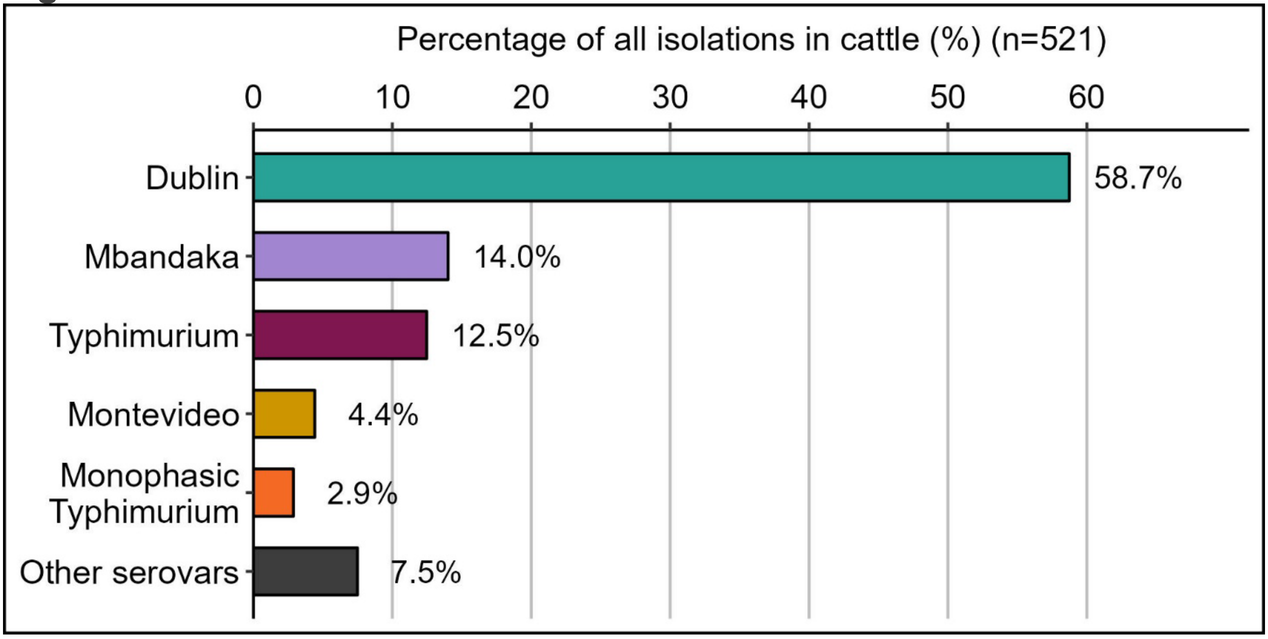
Figure 2.2: Isolations of the most common serovars in cattle in Great Britain 2020 to 2024

Figure 2.2.1: Isolations in cattle in 2020



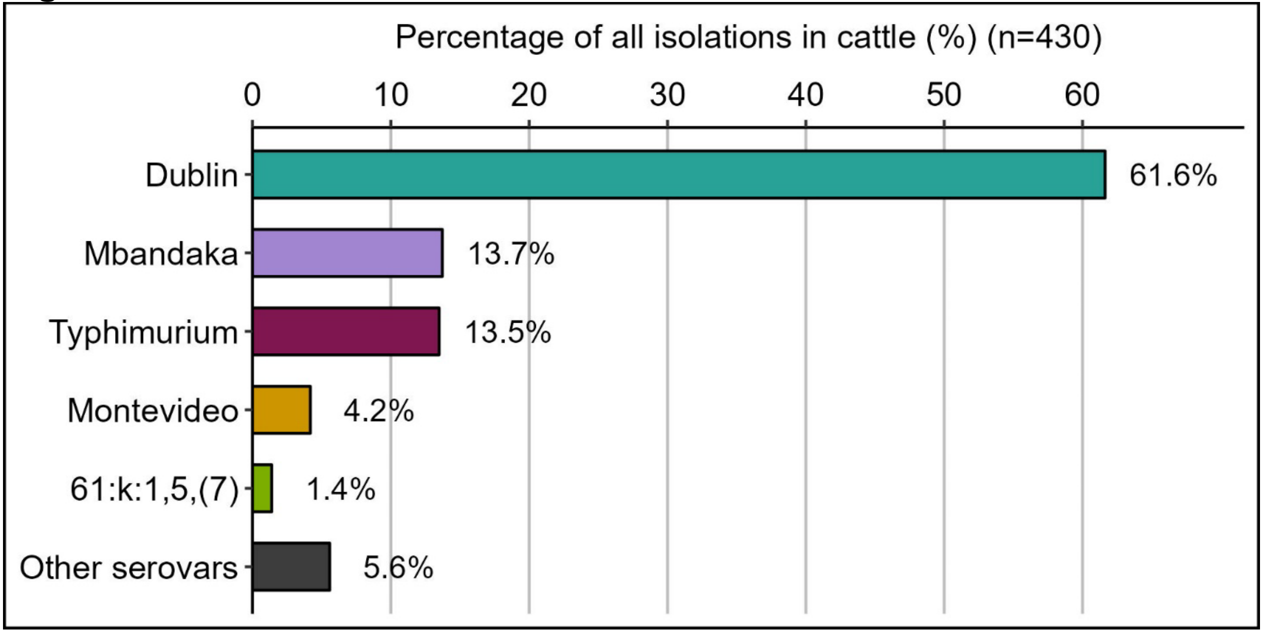
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in cattle in 2020. The most common serovar in cattle in 2020 was *S.* Dublin (57.7% of isolations), followed by *S.* Mbandaka (16.2% of isolations), *S*. Typhimurium (11.5% of isolations) and monophasic *S.* Typhimurium (4.4% of isolations).

Figure 2.2.2: Isolations in cattle in 2021



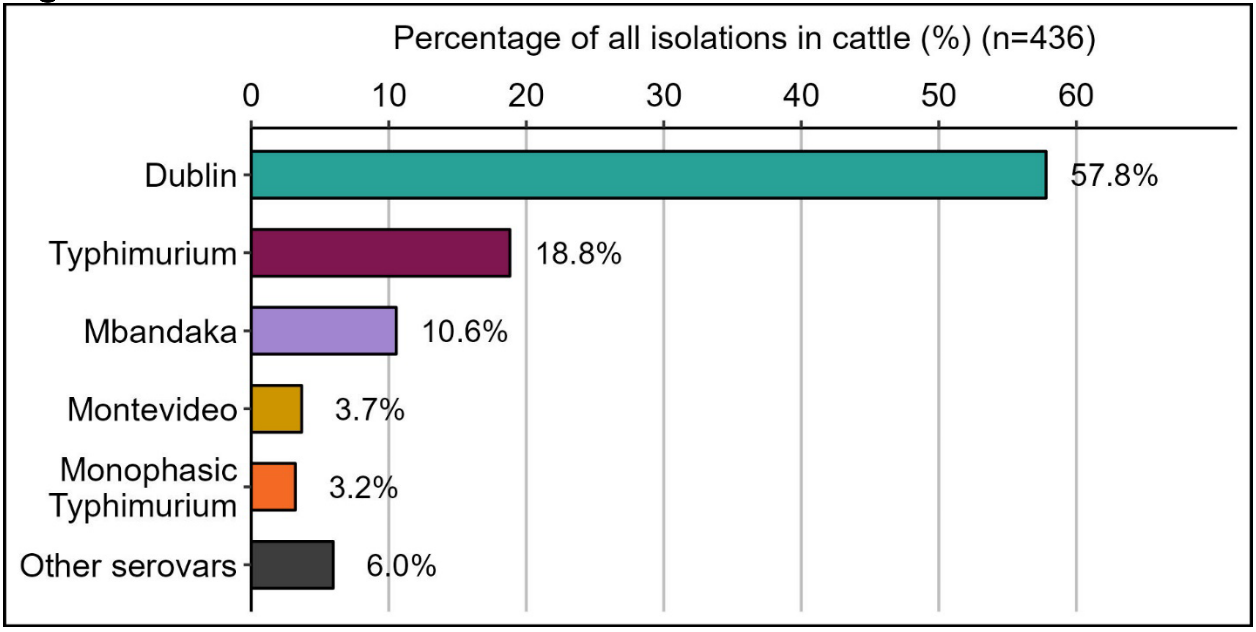
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in cattle in 2021. The most common serovar in cattle in 2021 was *S.* Dublin (58.7% of isolations), followed by *S.* Mbandaka (14.0% of isolations), *S*. Typhimurium (12.5% of isolations) and *S.* Montevideo (4.4% of isolations).

Figure 2.2.3: Isolations in cattle in 2022



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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).

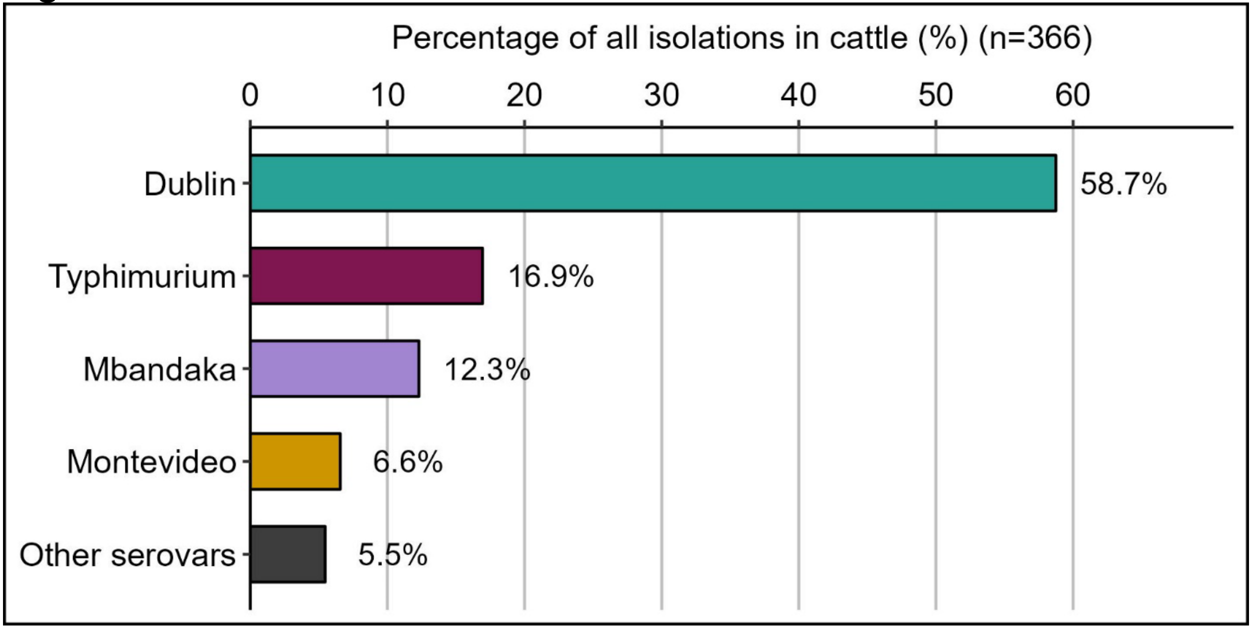
Figure 2.2.4: Isolations in cattle in 2023



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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).

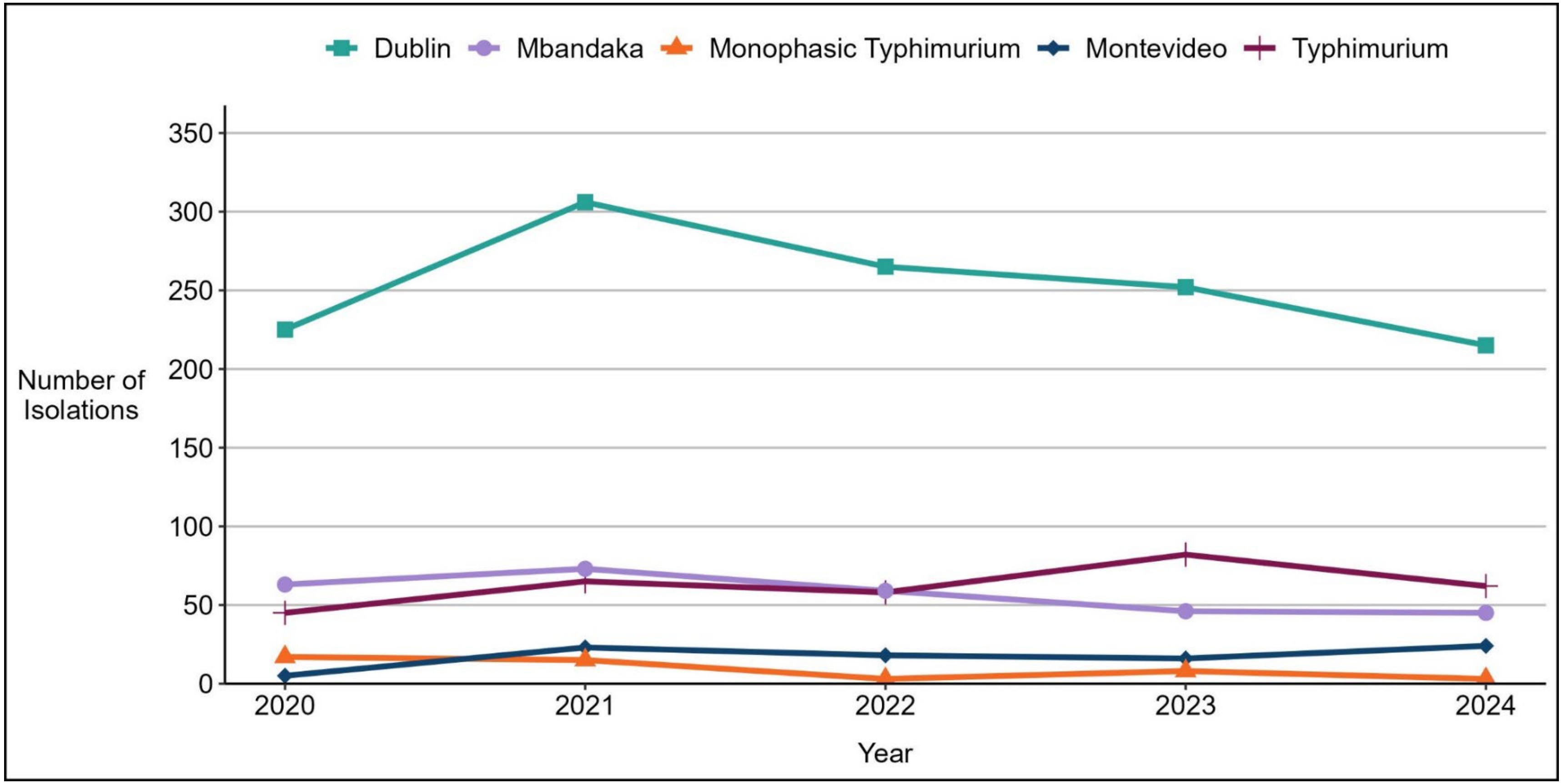
Figure 2.2.5: Isolations in cattle in 2024



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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).

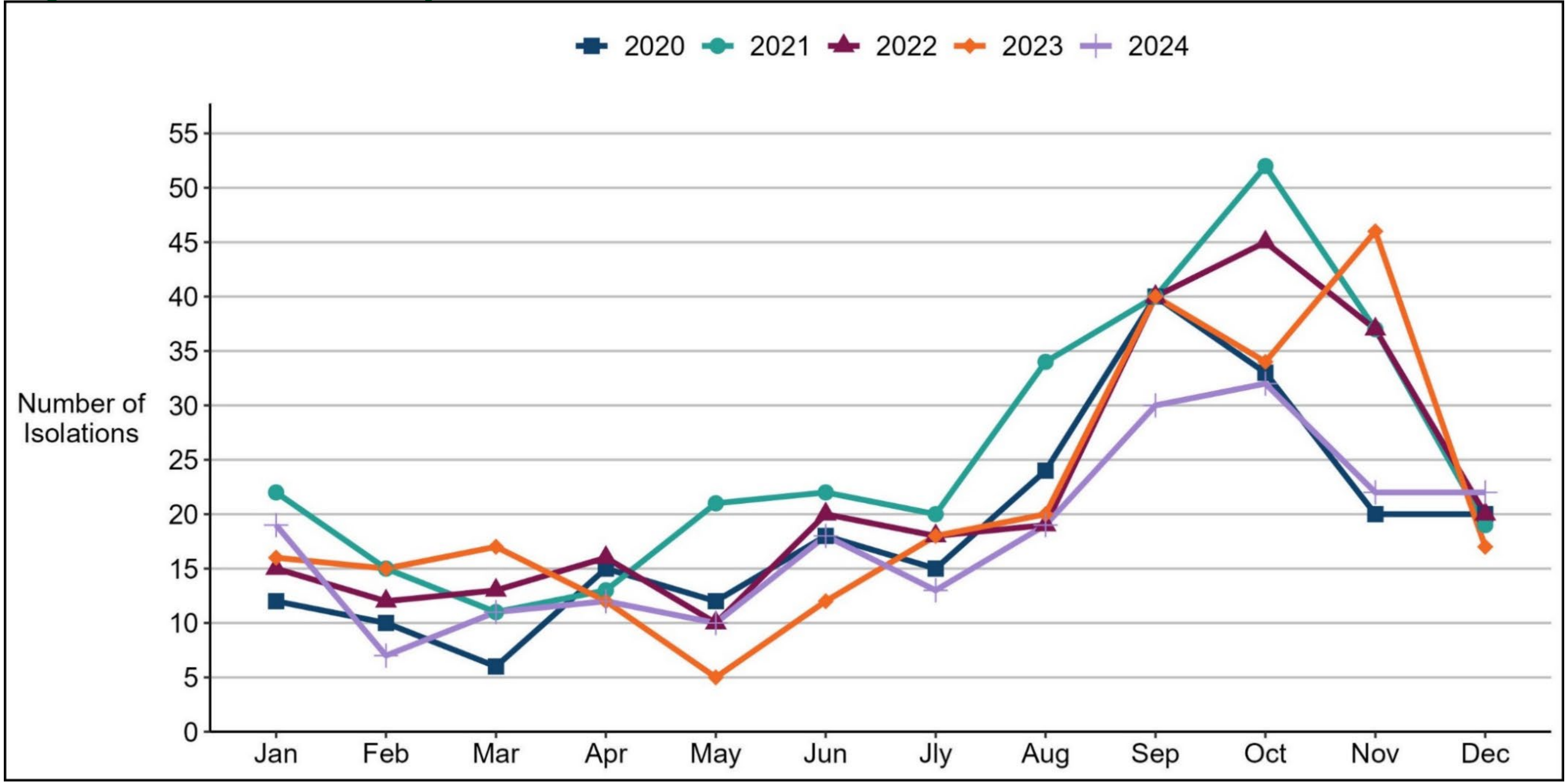
All isolations of 61:k:1,5(7) are variants of *Salmonella* enterica subspecies diarizonae.

Figure 2.3: The 5 most common *Salmonella* serovars in cattle in Great Britain in 2024 and their trends over time since 2020



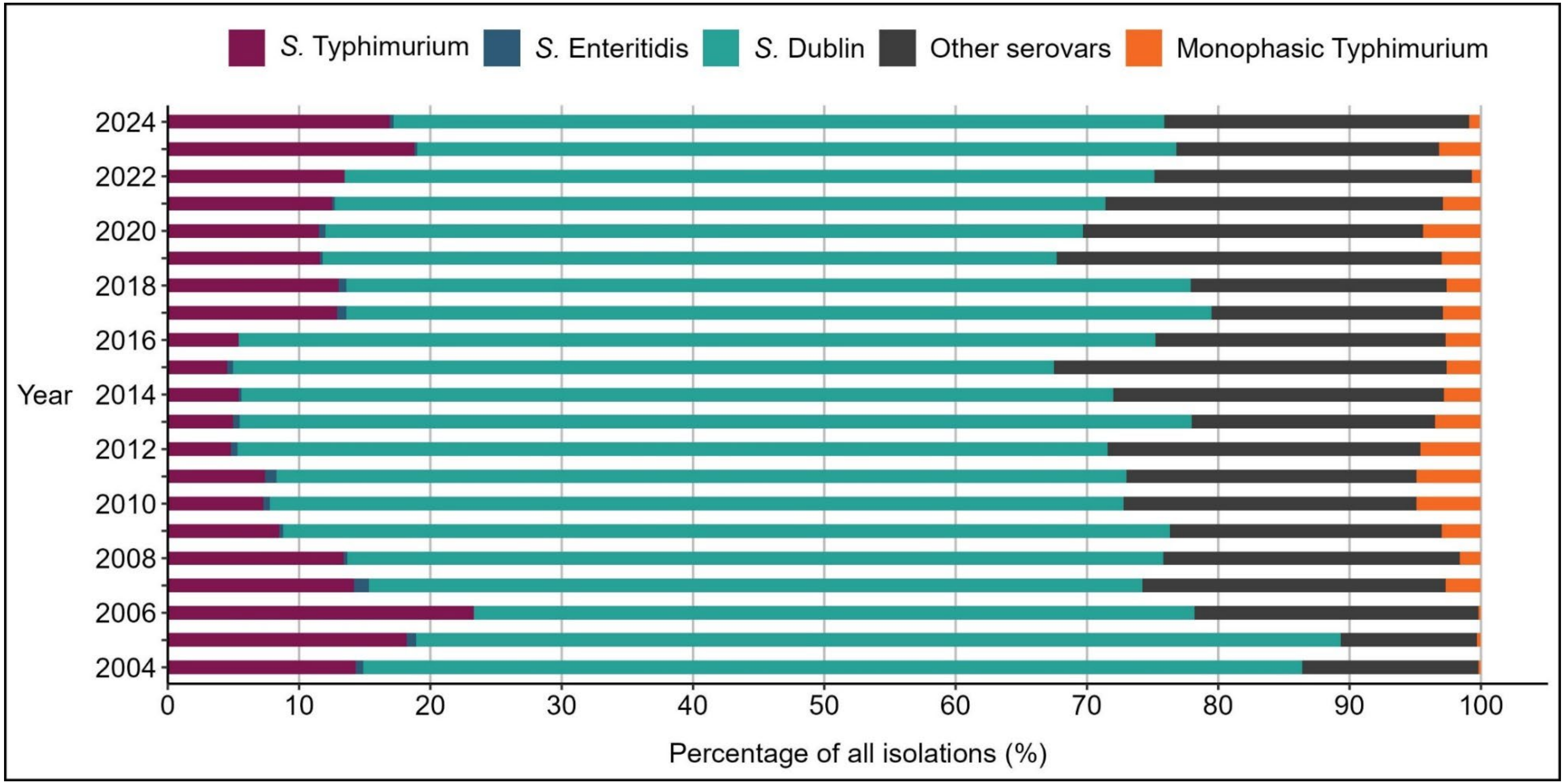
A line graph showing the 5 most common serovars in cattle from 2020 to 2024. The figure shows the most common serovar in cattle for all years was *S.* Dublin with above 215 isolations in all years. There was a dip in isolations in 2020 and following a peak in 2021 isolations have been decreasing since. The number of isolations of *S.* Mbandaka, *S.* Typhimurium, *S.* Montevideo and monophasic *S.* Typhimurium have shown less fluctuation and were consistently less than 100.

Figure 2.4: Seasonality of *Salmonella* Dublin in cattle in Great Britain 2020 to 2024



A line graph showing the number of isolations of *Salmonella* Dublin each month in 2020 to 2024. It shows a marked seasonality in *S.* Dublin in all years peaking in September to November, dropping to lower levels in January to June.

Figure 2.5: *S*. Dublin, *S*. Enteritidis, *S*. Typhimurium and monophasic *S*. Typhimurium as a proportion of all isolations in cattle in Great Britain 2004 to 2024



A stacked horizontal bar graph showing *S*. Dublin, *S*. Enteritidis, S. Typhimurium and monophasic *S*. Typhimurium as a proportion of all isolations in cattle from 2004 to 2024. The figure shows that as a proportion of all isolations in cattle in Great Britain between 2004 and 2024:

- *S.* Dublin accounted for the greatest proportion of isolations in all years, with rates at between 50% to 80% of all isolations in cattle
- *S.* Enteritidis was consistently low across the years with a high of 1.1% in 2007 and low of 0.0% in 2022
- *S.* Typhimurium accounted for 23.3% of isolations in 2006 but has since declined until 2016. Since then rates have increased and made up 16.9% in 2024
- Monophasic *S.* Typhimurium varied over the years but have remained at less than 5% of isolations
- Other serovars have accounted for between 17% and 30% since 2006 with large fluctuations year on year

Figure 2.5: Table of data

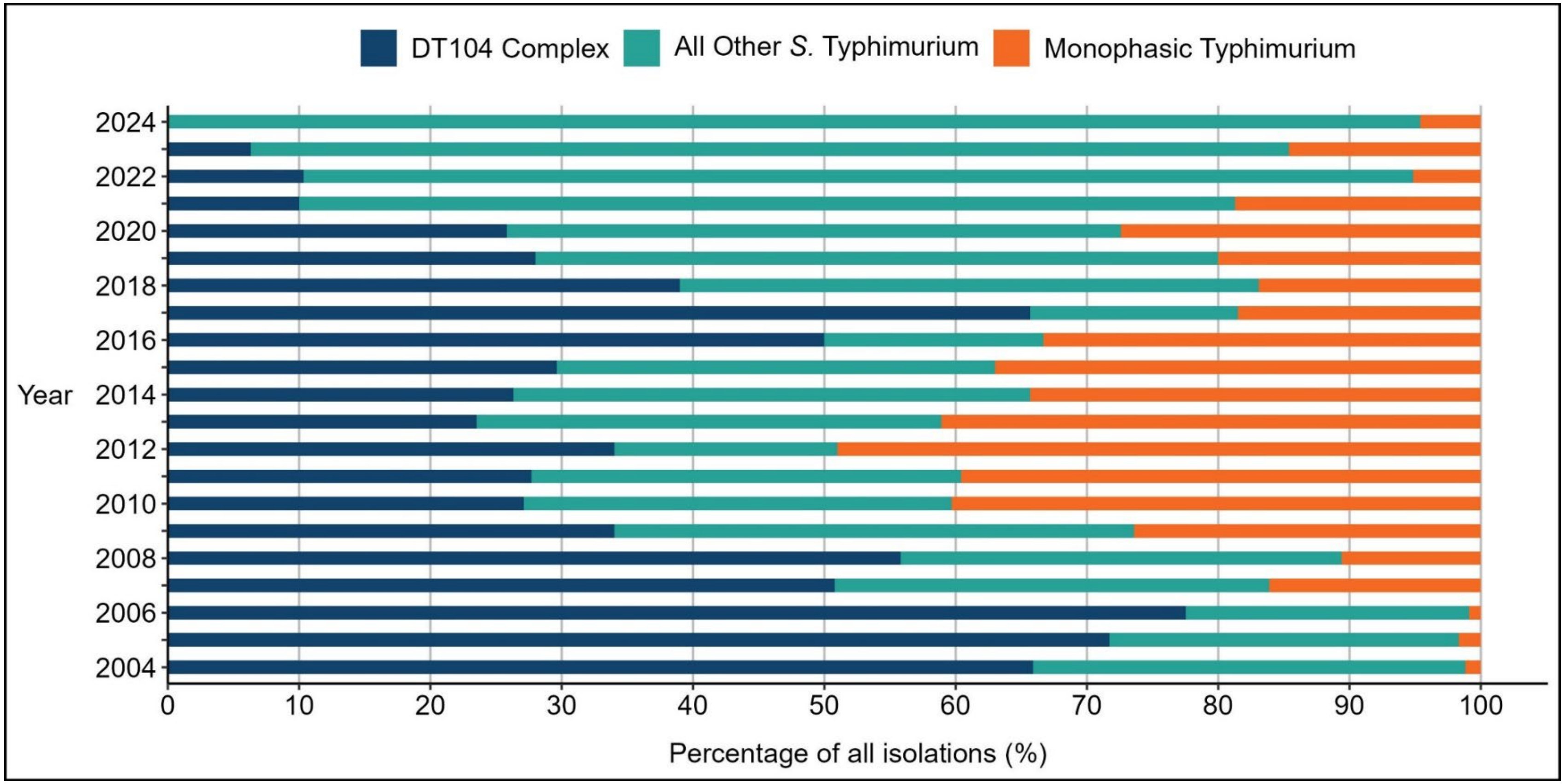
Year	*S.* Dublin	*S.* Enteritidis	Monophasic Typhimurium	*S.* Typhimurium	Other serovars
2004	71.5%	0.6%	0.2%	14.3%	13.4%
2005	70.4%	0.7%	0.3%	18.2%	10.4%
2006	54.9%	0.0%	0.2%	23.3%	21.6%
2007	58.9%	1.1%	2.7%	14.2%	23.1%
2008	62.1%	0.3%	1.6%	13.4%	22.6%
2009	67.5%	0.3%	3.0%	8.5%	20.7%
2010	65.0%	0.5%	4.9%	7.3%	22.3%
2011	64.7%	0.9%	4.9%	7.4%	22.1%
2012	66.3%	0.5%	4.6%	4.8%	23.8%
2013	72.5%	0.5%	3.5%	5.0%	18.5%
2014	66.4%	0.2%	2.8%	5.4%	25.2%
2015	62.5%	0.5%	2.6%	4.5%	29.9%
2016	69.8%	0.0%	2.7%	5.4%	22.1%
2017	65.9%	0.7%	2.9%	12.9%	17.6%
2018	64.3%	0.6%	2.6%	13.0%	19.5%
2019	55.9%	0.2%	3.0%	11.6%	29.3%

Year	*S.* Dublin	*S.* Enteritidis	Monophasic Typhimurium	*S.* Typhimurium	Other serovars
2020	57.7%	0.5%	4.4%	11.5%	25.9%
2021	58.7%	0.2%	2.9%	12.5%	25.7%
2022	61.6%	0.0%	0.7%	13.5%	24.2%
2023	57.8%	0.2%	3.2%	18.8%	20.0%
2024	58.7%	0.3%	0.8%	16.9%	23.2%

Table 2.2: *S.* Typhimurium phage types in cattle in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT1	0	0	0	0	0	0	1	1	1	1
DT2	1	1	6	4	2	2	1	1	0	0
DT9	1	1	0	0	0	0	0	0	0	0
DT11	0	0	1	1	0	0	0	0	0	0
DT36	0	0	1	1	0	0	0	0	0	0
DT41b	1	1	0	0	0	0	0	0	0	0
DT46	0	0	1	1	0	0	0	0	0	0
DT75	0	0	0	0	11	10	28	25	28	20
DT104	15	10	8	6	6	6	6	4	0	0
DT105	0	0	1	1	22	17	33	31	19	17
DT109	0	0	0	0	0	0	1	1	0	0
DT116	10	5	4	3	4	3	0	0	0	0
DT120	0	0	1	1	0	0	0	0	0	0
DT189	1	1	0	0	1	1	0	0	0	0
DT193	2	2	6	3	3	2	5	4	0	0
DT204b	1	1	0	0	0	0	0	0	0	0
U289	0	0	0	0	1	1	0	0	0	0
U300	0	0	2	2	0	0	0	0	0	0
U302	1	1	0	0	0	0	0	0	0	0
U308	1	1	14	11	0	0	0	0	0	0
NOPT	10	10	9	5	6	4	3	2	14	11
RDNC	1	1	11	7	2	2	4	4	0	0
UNTY	0	0	0	0	0	0	0	0	0	0
Total	**45**	**35**	**65**	**46**	**58**	**48**	**82**	**73**	**62**	**49**

Figure 2.6: *Salmonella* Typhimurium DT104 and related strains as a proportion of all isolations of *S*. Typhimurium and monophasic *S*. Typhimurium in cattle in Great Britain 2004 to 2024



A stacked horizontal bar graph showing *Salmonella* Typhimurium DT104 and related strains as a proportion of all isolations of *S*. Typhimurium and monophasic *S*. Typhimurium in cattle from 2004 to 2024. The figure shows the proportion of all isolations of *S.*

Typhimurium DT104 (and related strains), other *S.* Typhimurium strains and monophasic *S.* Typhimurium in cattle in Great Britain between 2004 and 2024:

- There was a fluctuating but overall decline in the proportion of DT104 complex (including DT104, DT104b, DT12 and U302) across the years with the lower rates in 2021, 2022 and 2023 (approx. 10% of all isolations) and none in 2024
- All other non-DT104 *S.* Typhimurium strains showed an increase from 2017 onwards, with the highest proportion of 95.4% in 2024
- Monophasic *S.* Typhimurium showed wide ranging proportions with a general decline since rising to a high of 49.0% in 2012

Figure 2.6: Table of data

Year	DT104 complex	All other *S.* Typhimurium	Monophasic Typhimurium
2004	65.9%	32.9%	1.2%
2005	71.7%	26.6%	1.7%
2006	77.5%	21.6%	0.9%
2007	50.8%	33.1%	16.1%
2008	55.8%	33.6%	10.6%
2009	34.0%	39.6%	26.4%
2010	27.1%	32.6%	40.3%
2011	27.7%	32.7%	39.6%
2012	34.0%	17.0%	49.0%
2013	23.5%	35.4%	41.1%
2014	26.3%	39.4%	34.3%
2015	29.6%	33.4%	37.0%
2016	50.0%	16.7%	33.3%
2017	65.7%	15.8%	18.5%
2018	39.0%	44.1%	16.9%

Year	DT104 complex	All other *S.* Typhimurium	Monophasic Typhimurium
2019	28.0%	52.0%	20.0%
2020	25.8%	46.8%	27.4%
2021	10.0%	71.3%	18.7%
2022	9.8%	80.3%	4.9%
2023	6.3%	79.2%	14.6%
2024	0.0%	95.4%	4.6%

DT104 complex includes DT104, DT104b, DT12 and U302.

Table 2.3: Monophasic S. Typhimurium phage types in cattle in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT1	0	0	0	0	0	0	1	1	0	0
DT191	0	0	0	0	0	0	1	1	0	0
DT120	0	0	1	1	0	0	0	0	1	1
DT193	11	7	11	10	3	3	7	5	0	0
DT194	3	1	0	0	0	0	0	0	0	0
U311	2	1	0	0	0	0	0	0	0	0
NOPT	0	0	0	0	0	0	1	1	2	2
RDNC	0	0	1	1	0	0	0	0	0	0
UNTY	1	1	2	2	0	0	4	4	0	0
Total	**17**	**10**	**15**	**14**	**3**	**3**	**14**	**12**	**3**	**3**

Table 2.4: S. Enteritidis phage types in cattle in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
PT5	0	0	0	0	0	0	1	1	0	0
PT8	0	0	0	0	0	0	0	0	0	0
PT11	1	1	0	0	0	0	0	0	0	0
NOPT	1	1	1	1	0	0	0	0	1	1
Total	**2**	**2**	**1**	**1**	**0**	**0**	**1**	**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 2024, from 29.8 million animals in 2023 to 29.0 million animals in 2024 according to the June agricultural census (Figure 3.1).

There were 6,040 diagnostic submissions recorded from sheep in Great Britain in 2024 compared to 5,979 diagnostic submissions in 2023, an increase of 1.0%. This differs to the previous decreasing trend in submission numbers seen since 2016 (with the exception of 2021 when submissions increased compared to 2020). 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.

Surveillance data, including clinical signs, age, and country information, associated with diagnoses of salmonellosis in sheep can be accessed at Sheep Dashboard | Tableau Public.

A total of 101 isolations of *Salmonella* were reported from sheep in 2024. This figure is comparable to 2023 (98 isolations) (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 2024 (Figure 3.2.5). There were 65 isolations in 2024, the same as in the 2 preceding years and within the annual range of 37 to 109 isolations seen since 2008. *Salmonella* Montevideo (14 isolations), *S.* Dublin (14 isolations), and *S.* Typhimurium (6 isolations) were the next most commonly isolated serovars. Although the number of isolations of these 3 serovars fluctuates year on year, they regularly appear within the top 4 most frequently isolated serovars from sheep. *S.* Dublin showed increased isolations compared to 2023, whereas *Salmonella* Montevideo was comparable, and isolation numbers were within the typical range seen for each of these 2 serovars in previous years. *S.* Typhimurium showed half as many isolations compared to 2023, and isolation numbers were lower than the preceding 4 years.

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 2024 there were 65 isolations, accounting for 64.4% of the total isolations obtained from sheep samples (Figure 3.2.5). This is comparable to the percentage contribution of this serovar in 2023 (66.3%) and 2022 (69.1%), but higher than the 2 years preceding those. *S. enterica* subspecies *diarizonae* 61:k:1,5,(7) (and associated incompletely typable strains) 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 2024, predominant clinical signs recorded included abortion, sudden death, and malaise.

Salmonella Montevideo

Salmonella Montevideo was the second equal most commonly isolated serovar from sheep in 2024, alongside *S.* Dublin, with a total of 14 isolations accounting for 13.9% 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 14 isolations of *Salmonella* Dublin in sheep in 2024, representing 13.9% of the total sheep *Salmonella* isolations (Figure 3.2.5), making it the second most common serovar, alongside *S.* Montevideo. This was a marked increase compared to 2023 (4 isolations), which represented 4.1% of total sheep *Salmonella* isolations for that year (Figure 3.2.4). Isolation numbers were equal to the upper end of the range seen for this serovar over the preceding 4 years (4 to 14 isolations). Although typically a cattle adapted strain, infection in sheep was predominately associated with abortion, diarrhoea and sudden deaths, with malaise also recorded in 2024.

Salmonella Typhimurium and monophasic *Salmonella* Typhimurium

Salmonella Typhimurium was the fourth most common serovar isolated from sheep in 2024, representing 5.9% of the total *Salmonella* isolations (Figure 3.2.5). Isolations were lower this year compared to 2023 (6 versus 12) and were lower than the range seen for this serovar over the preceding 4 years (8 to 17 isolations). This year, the most common reasons for submission were diarrhoea or sudden death. Other clinical signs recorded were malaise and wasting.

Phage typing was carried out on 5 of the 6 *S.* Typhimurium isolations from sheep in 2024 (Table 3.3). Phage-type DT75 predominated (4 isolations) with DT193 being the only other identified phage type (1 isolation). DT193 was last reported from sheep in GB in 2017.

There were no records of the previously reported predominant phage types DT104 and U308 in 2024, which was comparable to 2023. One isolation was not phage typed (NOPT).

There was one isolation of monophasic *S.* Typhimurium in 2024 which was not phage typed (NOPT). This is comparable to other single monophasic variant isolations in 2021 and 2023 (both NOPT).

Other serovars

There was a single isolation of *Salmonella* Agama in 2024, causing abortion in an adult ewe. This was comparable to 2020, 2021 and 2022 when single isolations were made each year. This serovar is typically associated with badgers.

There were no other serovars isolated in sheep during 2024.

Salmonella isolations from non-clinical submissions

In 2023 FSA commissioned a survey to determine the microbial contamination on sheep carcases in abattoirs in England and Wales as the last survey of healthy sheep at slaughter in England and Wales was undertaken 20 years ago. This project was run in conjunction with surveys funded by Defra and the PATH-SAFE research programme aimed at determining prevalence of caecal carriage of pathogens and levels of antimicrobial resistance in sheep at slaughter. Twelve out of 132 abattoirs in England and Wales were recruited, covering 28% of the annual national sheep slaughterhouse throughput. In total,1282 carcase swab samples were collected over a 12-month period from February 2023 to January 2024. All samples were tested for the isolation and quantification of *Salmonella*. *Salmonella* was only detected in 7 (0.55%) of carcase swabs. Five isolates were confirmed as *S*. enterica subsp. diarizonae serotype 61:k:1:5, a sheep-adapted type with no confirmed association with human disease. The other 2 isolates were confirmed as *S*. Typhimurium. This work suggests that slaughtering processes are effective in reducing carcases being contaminated with pathogens. The full report can be accessed here FSA-Survey of the microbiological contamination of sheep carcases

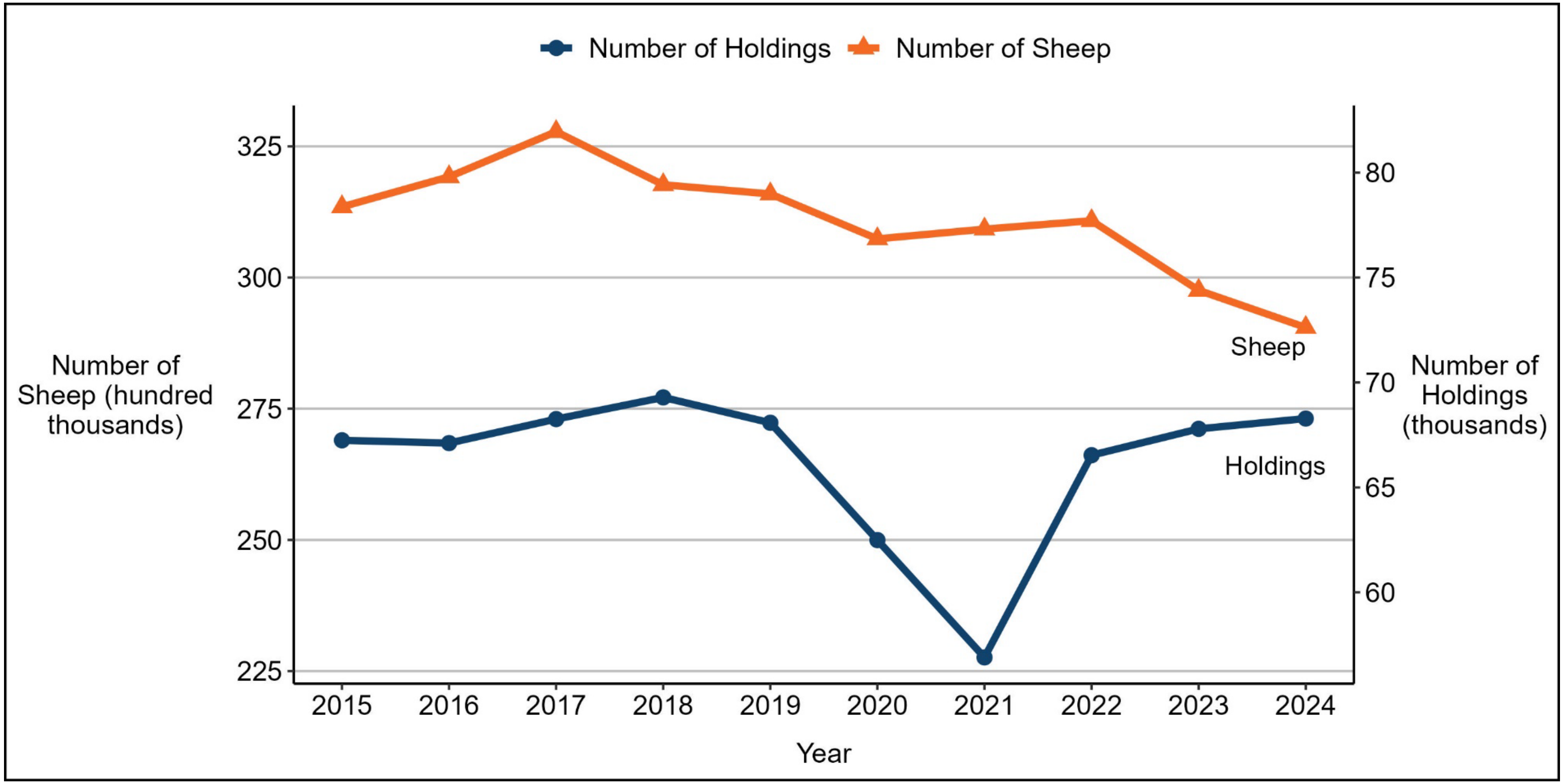
Goats

The Great Britain goat population fell slightly in 2024 to 106,716 compared to 109,534 in 2023 (June 2024 Agricultural Census).

There were 505 diagnostic submissions recorded from goats in 2024 compared to 444 diagnostic submissions in 2023, an increase of 13.7%.

*Salmonella*e are seldom isolated from goats, in most years single or zero isolations are reported. There were 2 isolations of *Salmonella* in goats during 2024. One was *Salmonella enterica* subspecies *diarizonae* 61:k:1,5,(7) which has been isolated from goats in previous years. The other was *S.* Dublin which was comparable to 2020 and 2021 where a single isolation was made each year. This isolation of *S.* Dublin was associated with systemic infection causing malaise and deaths in neonatal goat kids.

Figure 3.1: Sheep population and number of commercial holdings with sheep in Great Britain 2015 to 2024



A line graph showing the pig population and number of commercial holdings from 2015 to 2024 in Great Britain. There was a relatively constant level of sheep holdings until 2019 when it starts to decline but with an upturn in 2022, 2023 and 2024 to 68,281 holdings in 2024. 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 and 2024 declined to approximately 29,050,000 in 2024.

Scotland (animals and holdings) 2021 census data used for 2022.
Source: June 2024 Agricultural Census. For the definition of a commercial holding in the agricultural census, see the survey methodology.

Table 3.1: Isolations and incidents of *Salmonella* in sheep on all premises in Great Britain 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Agama	1	1	1	1	1	1	0	0	1	1
Ajiobo	0	0	1	1	0	0	0	0	0	0
Anatum	0	0	1	1	0	0	0	0	0	0
Berta	1	1	0	0	0	0	0	0	0	0
Derby	0	0	1	1	1	1	1	1	0	0
Dublin	10	9	14	12	5	4	4	4	14	13
Enteritidis	0	0	0	0	2	2	0	0	0	0
Indiana	0	0	1	1	0	0	0	0	0	0
Infantis	0	0	0	0	0	0	1	1	0	0
Kingston	0	0	0	0	1	1	0	0	0	0
Mbandaka	0	0	1	1	0	0	0	0	0	0
Monophasic Typhimurium	0	0	1	1	2	2	1	1	1	1
Montevideo	3	3	28	18	5	5	13	10	14	12
Newport	1	1	0	0	0	0	0	0	0	0
Ohio	1	1	0	0	1	1	1	1	0	0
Stourbridge	0	0	1	1	0	0	0	0	0	0
Typhimurium	8	5	17	13	8	8	12	11	6	6
61:k:1,5,(7)	45	45	69	66	65	61	65	64	65	64
untypable strains	7	5	8	8	1	1	0	0	0	0
rough strains	0	0	0	0	2	2	0	0	0	0
Total	**77**	**71**	**144**	**125**	**94**	**89**	**98**	**93**	**101**	**97**

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*.

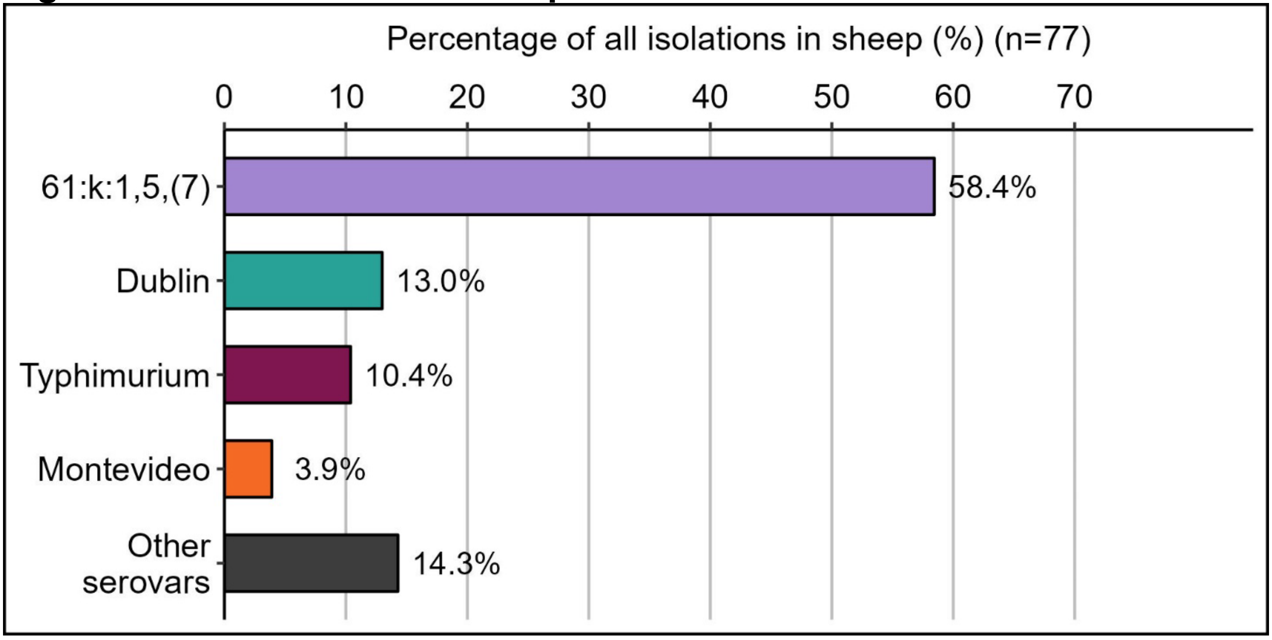
Table 3.2: Isolations and incidents of *Salmonella* in goats on all premises in Great Britain 2020 to 2024

***Salmonella* serovar**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**	**2024 isolations**	**2024 incidents**
Dublin	1	1	1	1	0	0	0	0	1	1
61:k:1,5,(7)	0	0	1	1	2	2	1	1	1	1
Total	**1**	**1**	**2**	**2**	**2**	**2**	**1**	**1**	**2**	**2**

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*

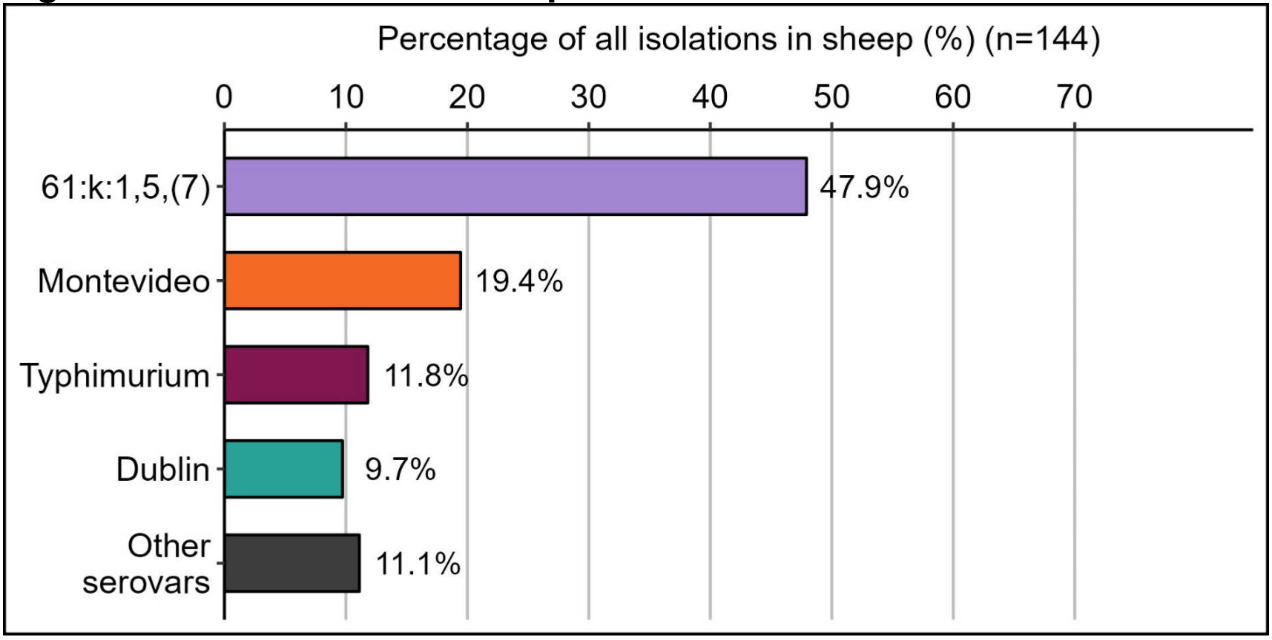
Figure 3.2: Isolations of the most common serovars in sheep in Great Britain 2020 to 2024

Figure 3.2.1: Isolations in sheep in 2020



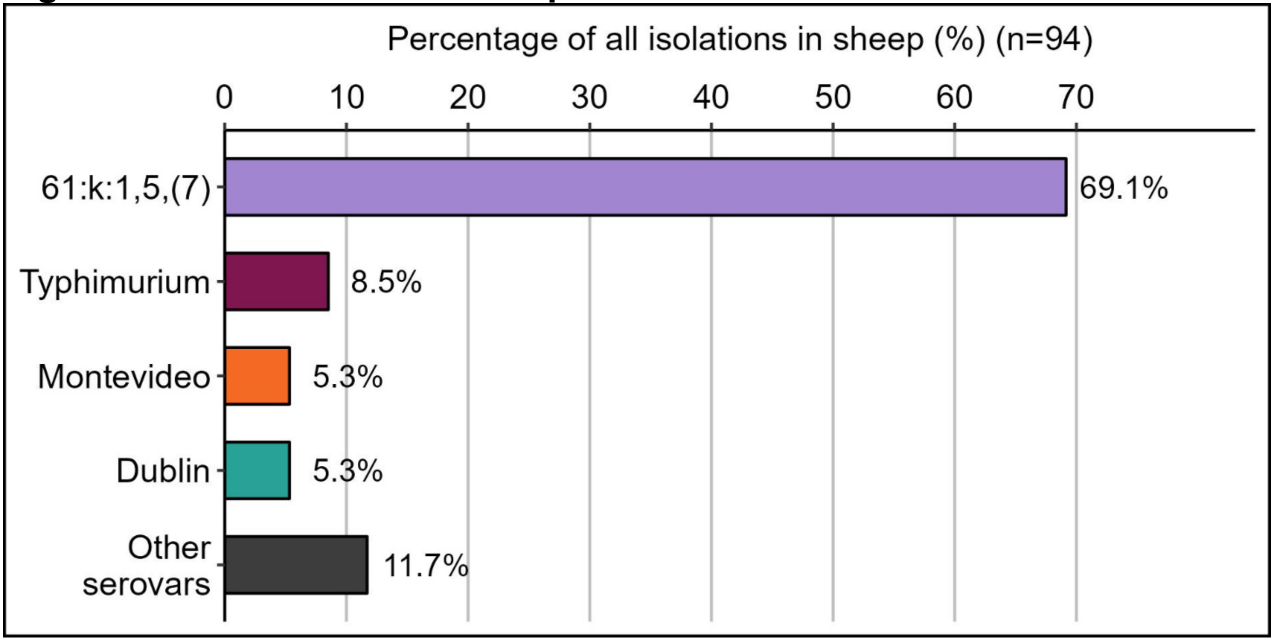
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in sheep in 2020. The most common serovar in sheep in 2020 was *Salmonella* 61:k:1,5,(7) (58.4% of isolations), followed by *S*. Dublin (13.0% of isolations), *S*. Typhimurium (10.4% of isolations) and *S*. Montevideo (3.9% of isolations).

Figure 3.2.2: Isolations in sheep in 2021



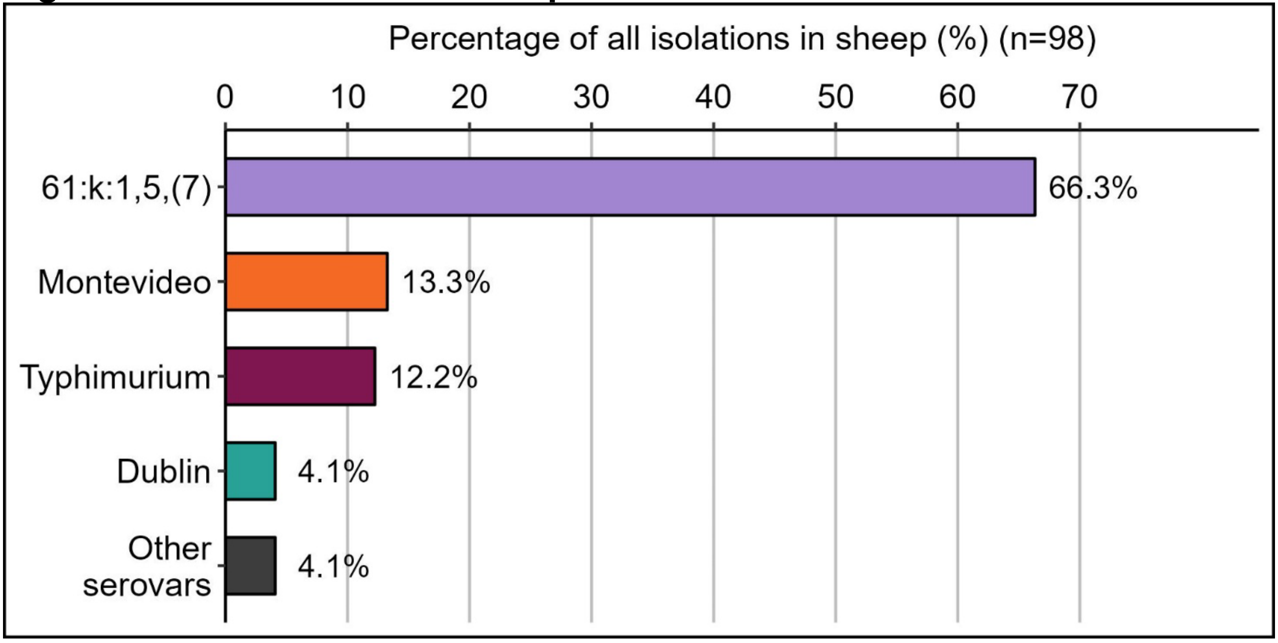
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in sheep in 2021. The most common serovar in sheep in 2021 was *Salmonella* 61:k:1,5,(7) (47.9% of isolations), followed by *S*. Montevideo (19.4% of isolations), *S*. Typhimurium (11.8% of isolations) and *S*. Dublin (9.7%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

Figure 3.2.3: Isolations in sheep in 2022



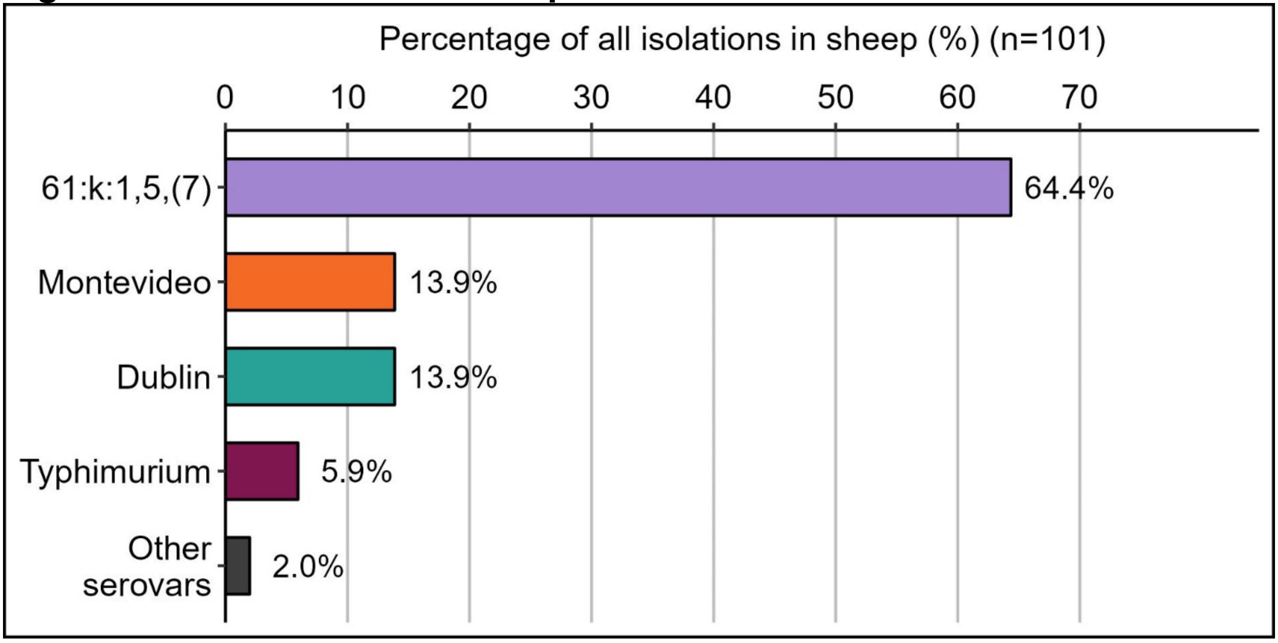
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in sheep in 2022. The most common serovar in sheep in 2022 was *Salmonella* 61:k:1,5,(7) (69.1% of isolations), followed by *S*. Typhimurium (8.5% of isolations), *S*. Dublin and *S*. Montevideo (5.3% of isolations each).

Figure 3.2.4: Isolations in sheep in 2023



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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).

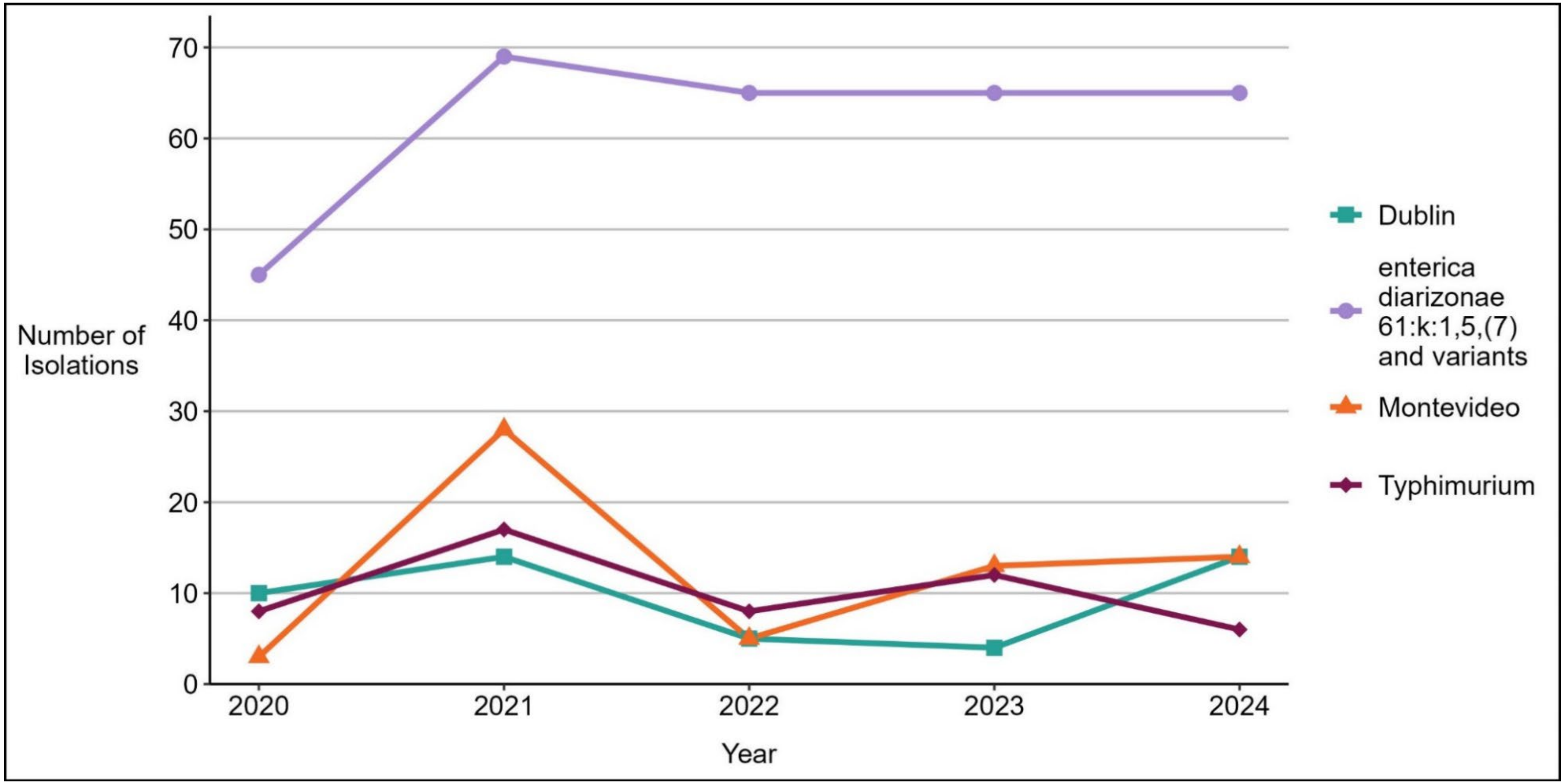
Figure 3.2.5: Isolations in sheep in 2024



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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).

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 2024 and their trends over time since 2020



A line graph showing the 5 most common serovars in sheep from 2020 to 2024. 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 65 isolations in 2022, 2023 and 2024. *Salmonella* Montevideo and

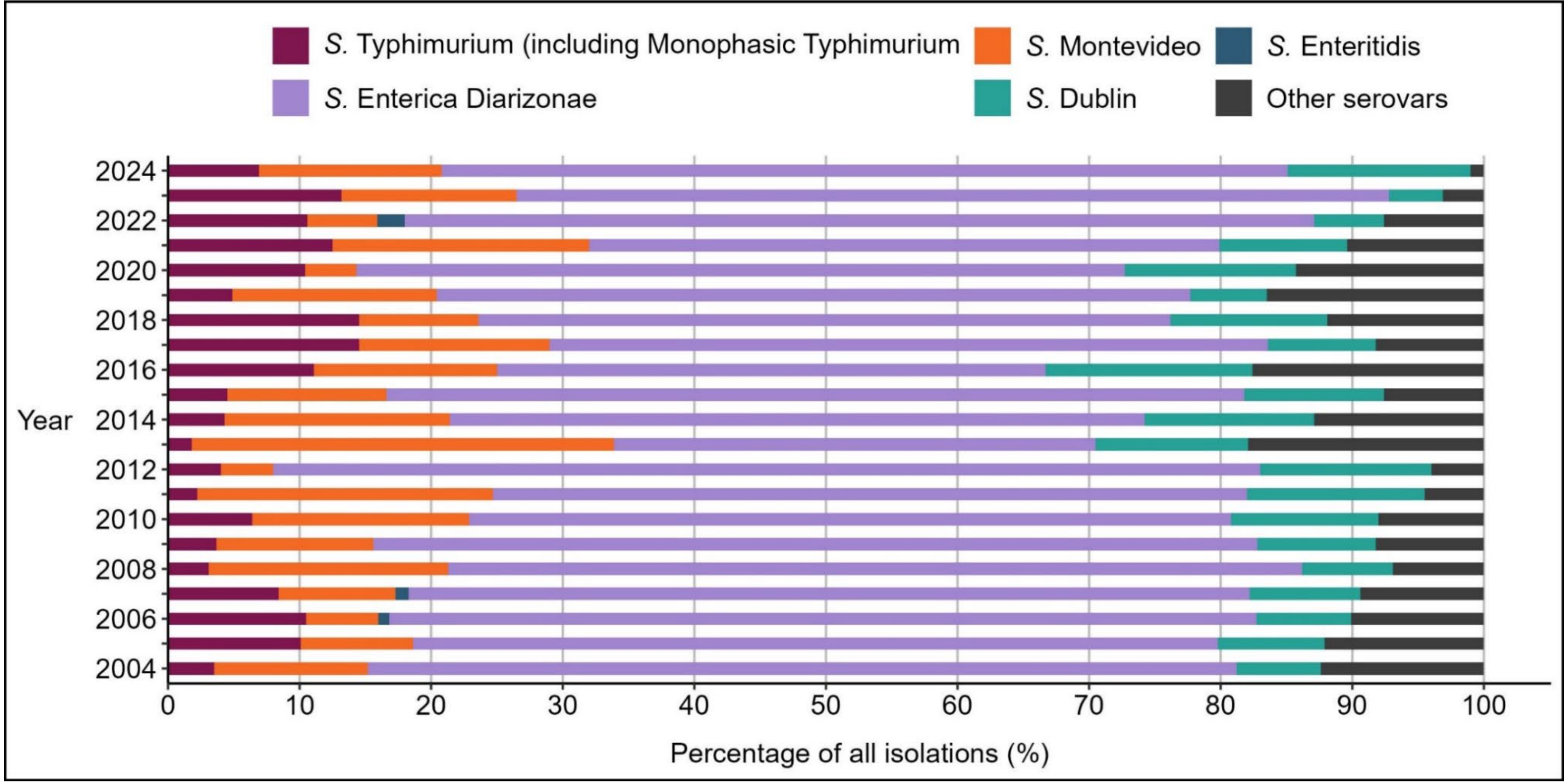
S. Dublin were the joint second most common serovar isolated in 2024 with 14 isolations each, followed by *S.* Typhimurium with 6 isolations in 2024.

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

Table 3.3: S. Typhimurium phage types in sheep in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT2	2	1	0	0	0	0	0	0	0	0
DT75	0	0	0	0	2	2	5	5	4	4
DT104	4	3	3	2	1	1	0	0	0	0
DT105	0	0	0	0	2	2	4	3	0	0
DT116	0	0	2	2	0	0	0	0	0	0
DT193	0	0	0	0	0	0	0	0	1	1
U288	0	0	0	0	0	0	1	1	0	0
U289	0	0	0	0	1	1	0	0	0	0
U300	0	0	1	1	0	0	0	0	0	0
U308	0	0	10	7	1	1	0	0	0	0
U320	0	0	0	0	0	0	0	0	0	0
NOPT	0	0	1	1	0	0	2	2	1	1
RDNC	2	1	0	0	1	1	0	0	0	0
Total	**8**	**5**	**17**	**13**	**8**	**8**	**12**	**11**	**6**	**6**

Figure 3.4: *S*. Dublin, *S. enterica diarizonae*, *S*. Enteritidis, *S*. Montevideo, *S*. Typhimurium (including monophasic *S*. Typhimurium) as a proportion of all isolations in sheep in Great Britain 2004 to 2024



A stacked horizontal bar graph showing *S*. Dublin, *S. enterica diarizonae*, *S*. Enteritidis, *S*. Montevideo, *S*. Typhimurium (including monophasic *S*. Typhimurium) as a proportion of all isolations in sheep from 2004 to 2024. The figure shows the proportion of all isolations of *S*. Dublin, *S*. *enterica diarizonae*, *S*. Enteritidis, *S*. Montevideo, *S*. Typhimurium and monophasic *S.* Typhimurium in sheep in Great Britain between 2004 and 2024:

- *S*. *enterica diarizonae* accounted for the greatest proportion of isolations but rates remained stable across most years at around 60%
- *S*. Montevideo was far more variable across the years with a high of 32.1% in 2013 and low of 3.9% in 2020
- *S*. Dublin accounted for 13.9% of isolations in 2024, the highest proportion seen since 2016
- *S*. Typhimurium (including monophasic variants) had risen to 13.2% in 2023 but decreased in 2024 to 6.9%
- *S*. Enteritidis was consistently very low at 2.1% or less and was only isolated in 2006, 2007 and 2022
- Other serovars have accounted for between 1.0% and 17.9% with fluctuations year on year

Figure 3.4: Table of data

Year	*S.* Dublin	*S. enterica diarizonae*	*S.* Enteritidis	*S.* Montevideo	*S.* Typhimurium (including monophasic Typhimurium)	Other serovars
2004	6.4%	66.0%	0.0%	11.7%	3.5%	12.4%
2005	8.1%	61.2%	0.0%	8.5%	10.1%	12.1%
2006	7.2%	65.9%	0.8%	5.5%	10.5%	10.1%
2007	8.4%	63.9%	1.0%	8.9%	8.4%	9.4%
2008	6.9%	64.9%	0.0%	18.2%	3.1%	6.9%
2009	9.0%	67.2%	0.0%	11.9%	3.7%	8.2%
2010	11.2%	57.9%	0.0%	16.5%	6.4%	8.0%
2011	13.5%	57.3%	0.0%	22.5%	2.2%	4.5%
2012	13.0%	75.0%	0.0%	4.0%	4.0%	4.0%

Year	*S.* Dublin	*S. enterica diarizonae*	*S.* Enteritidis	*S.* Montevideo	*S.* Typhimurium (including monophasic Typhimurium)	Other serovars
2013	11.6%	36.6%	0.0%	32.1%	1.8%	17.9%
2014	12.9%	52.8%	0.0%	17.1%	4.3%	12.9%
2015	10.6%	65.2%	0.0%	12.1%	4.5%	7.6%
2016	15.7%	41.7%	0.0%	13.9%	11.1%	17.6%
2017	8.2%	54.6%	0.0%	14.5%	14.5%	8.2%
2018	11.9%	52.6%	0.0%	9.1%	14.5%	11.9%
2019	5.8%	57.3%	0.0%	15.5%	4.9%	16.5%
2020	13.0%	58.4%	0.0%	3.9%	10.4%	14.3%
2021	9.7%	47.9%	0.0%	19.5%	12.5%	10.4%
2022	5.3%	69.1%	2.1%	5.3%	10.6%	7.6%
2023	4.1%	66.3%	0.0%	13.3%	13.2%	3.1%
2024	13.9%	64.3%	0.0%	13.9%	6.9%	1.0%

Chapter 4: Reports of *Salmonella* in pigs

Compared with 2023, there was a slight increase in the total Great Britain pig herd in 2024 to over 4 million animals according to the 2024 agricultural census (Figure 4.1). This was after a decrease of 10.7% in 2023. The number of commercial pig holdings in 2024 decreased to just over 9500, compared to just over 9800 in 2023.

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 derive from diagnostic submissions, in which *Salmonella* may be the causal pathogen, or a secondary incidental finding. Where it is considered the cause of disease in submissions to the Great Britain scanning surveillance network, it is recorded as a diagnosis 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 at Great Britain disease surveillance dashboard.

There was an increase (7.1%) in the total number of pig submissions (all types) from Great Britain to the Great Britain scanning surveillance network (APHA and SRUC laboratories) during 2024 (4,089 submissions) compared to 2023 (3,818 submissions). Similarly, there was an increase (16.8%) in diagnostic pig submissions during 2024 (2,024 submissions) compared to 2023 (1,732 submissions).

There were 311 isolations of *Salmonella* in pigs in 2024. This is higher than in recent years (2020 to 2023) in which the number of isolations ranged from 189 to 258. The number of incidents of *Salmonella* as a proportion of the total pig submissions to the GB scanning surveillance network was 7.1% in 2024, versus 6.2% in 2023. The number of diagnoses of salmonellosis made through the GB scanning surveillance network in pigs was 169 in 2024, which was the same number as in 2023 but higher than in 2022 (125). The number of diagnoses of salmonellosis in pigs as a proportion of diagnosable submissions for salmonellosis was lower in 2024 (11.8%) than 2023 (13.9%) and 2022 (12.0%). The number of diagnoses does not equate with the number of incidents from diagnostic scanning surveillance submissions because only a proportion of isolations are deemed to be clinically significant.

The number and type of diagnostic submissions are affected by many factors and it is likely that several contributed to the increase in diagnostic pig submissions in 2024 which included an increase in diagnostic submissions with diarrhoea as a main presenting sign. These factors may include increased use of diagnostics for post-weaning diarrhoea by veterinarians seeking evidence-based and disease-specific control measures and alternatives to zinc oxide and antibiotics.

The different serovars isolated are detailed in Table 4.1 and Figure 4.2.

Salmonella Typhimurium and monophasic S. Typhimurium

As in previous years, isolations of *S*. Typhimurium and its monophasic variants together accounted for the majority of isolations of *Salmonella* from pigs in 2024 (72.7% of all isolations from pigs, Figures 4.2, 4.3 and 4.4). This was lower than in 2023 (77.5%) but higher than in 2022 (70.5%). As has been the case since 2020, the number of *S*. Typhimurium isolations exceeded isolations of monophasic *S.* Typhimurium.

As in previous years, the most common serovar isolated from pigs in 2024 was *S*. Typhimurium (156 [50.1% of] isolations). This increased from 2023 (139 isolations) and is also higher than the 3 previous years 2020 to 2022 (Table 4.1).

Phage type DT193 was the most commonly isolated phage type of *S*. Typhimurium in 2024, which increased from 31 isolations in 2023 to 54 isolations in 2024 (Table 4.2). The second most commonly isolated *S.* Typhimurium phage type was DT32 (50 isolations versus 22 in 2023). Interestingly, there were only 7 isolations of *S.* Typhimurium U308a, which was the third most common phage type isolated in 2024. Phage type U308a was the most commonly isolated phage type of *S*. Typhimurium in 2023 (46 isolations), after having been first reported from surveillance in pigs in Great Britain in 2021. Two *S.* Typhimurium phage types identified in 2024, namely DT75 and DT116, have not been recorded previously in pigs in Great Britain.

The next most common *Salmonella* serovar isolated from pigs in 2024 was monophasic *S.* Typhimurium (70 isolations) which represents 22.5% of total pig isolations n 2024. Isolations of monophasic *S*. Typhimurium increased in 2023 and 2024 (Figure 4.2 and 4.3).

Of the monophasic *S.* Typhimurium isolations that could be phage typed in 2024, 96.3% (52 of 54) were DT193 (Table 4.3). Phage type DT193 represents the ‘epidemic’ strain that emerged in Europe from 2006 and has been dominant amongst monophasic strains of *S.* Typhimurium in pigs in Great Britain. The 2 non-DT193 phage types of monophasic *S*. Typhimurium isolations were DT104 and DT194. Monophasic *S*. Typhimurium DT104 has never previously been isolated from pigs in GB.

Other serovars

Other frequently isolated serovars from pigs in 2024 were *S*. Derby (33 isolations – up from 17 isolations in 2023) and *S*. Newport (20 isolations – up from 18 isolations in 2023 –

Table 4.1 and Figure 4.2). *S*. Bovismorbificans was isolated 8times, which was an increase on the 2 isolations of this serovar in 2023.

Twelve different serovars were identified in 2024 which accounted for 310 isolations (one untypeable strain, Table 4.1). One serovar, *S*. Hessarek, was detected in 2024 but has never previously been identified in pigs in Great Britain. There were no isolations of *S*. Enteritidis in 2024, which was last isolated on one occasion in pigs in 2019 (phage type 11).

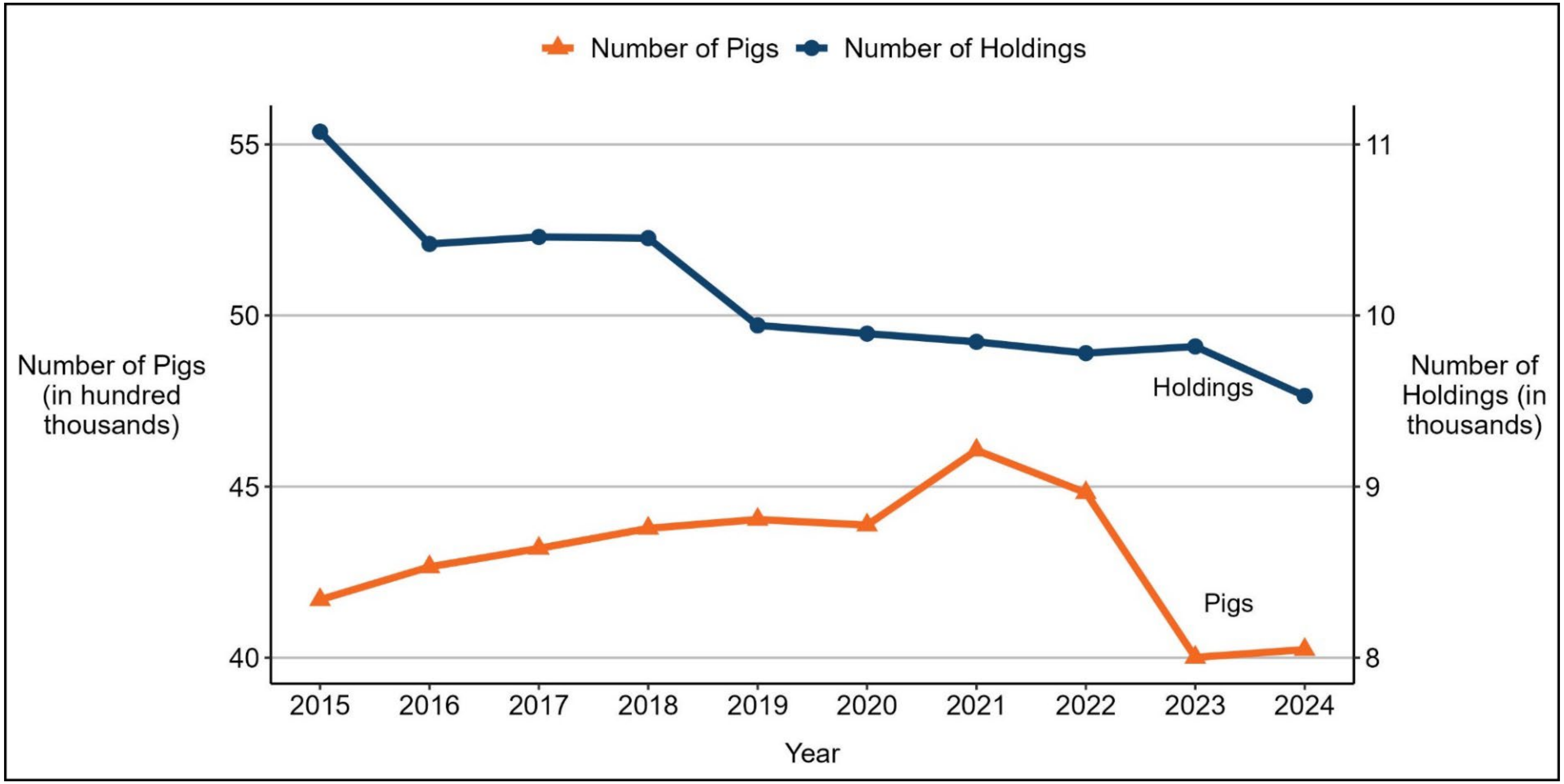
Antimicrobial susceptibility in pigs

A total of 404 *Salmonella* isolates from pigs were tested against a panel of 16 antimicrobials in 2024. In this species, antimicrobial resistance remained high, with 17.3% of fully susceptible isolates and 74.8% of isolates classified as multidrug-resistant (MDR; resistant to 4 or more antimicrobials). The main serovars associated with resistance were *S.* Typhimurium (n=212) and monophasic *S.* Typhimurium (n=91).

Resistance to ampicillin (77.2%) and sulphonamides (76.7%) remained widespread. Patterns with resistance to the sulphamethoxazole and trimethoprim combination (62.4%), tetracycline, and chloramphenicol (59.7%) also showed consistly high levels. Although resistance trends for most antibiotics remained stable compared to 2023, resistance to amikacin emerged in 12 *S.* Typhimurium isolates, increasing from 0% in 2023 to 3.0% in 2024. All amikacin resistant isolates also displayed neomycin and gentamicin resistance. Among resistant pig isolates (n=334), 36.2% showed resistance to at least one aminoglycoside, and 18.3% were resistant to up to 4 (typically apramycin, gentamicin, neomycin, and streptomycin). Nalidixic acid resistance was observed in 2 MDR S. Typhimurium isolates.

Importantly, none of the *Salmonella* isolates from pigs exhibited resistance to third generation cephalosporins or fluoroquinolones, which are classified as “highest priority critically important antibiotics” (HP-CIAs)

Figure 4.1: Pig population and number of commercial holdings with pigs in Great Britain 2015 to 2024



A line graph showing the sheep population and number of commercial holdings from 2015 to 2024 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 9,530 in 2024. The number of pigs in Great Britain increased until 2021 after which there was a decline in 2022 and 2023, before an increase in 2024 to 4,023,578.

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

The number of holdings in 2020 is estimated.

Source: June 2024 Agricultural Census. For the definition of a commercial holding in the agricultural census, see the survey methodology

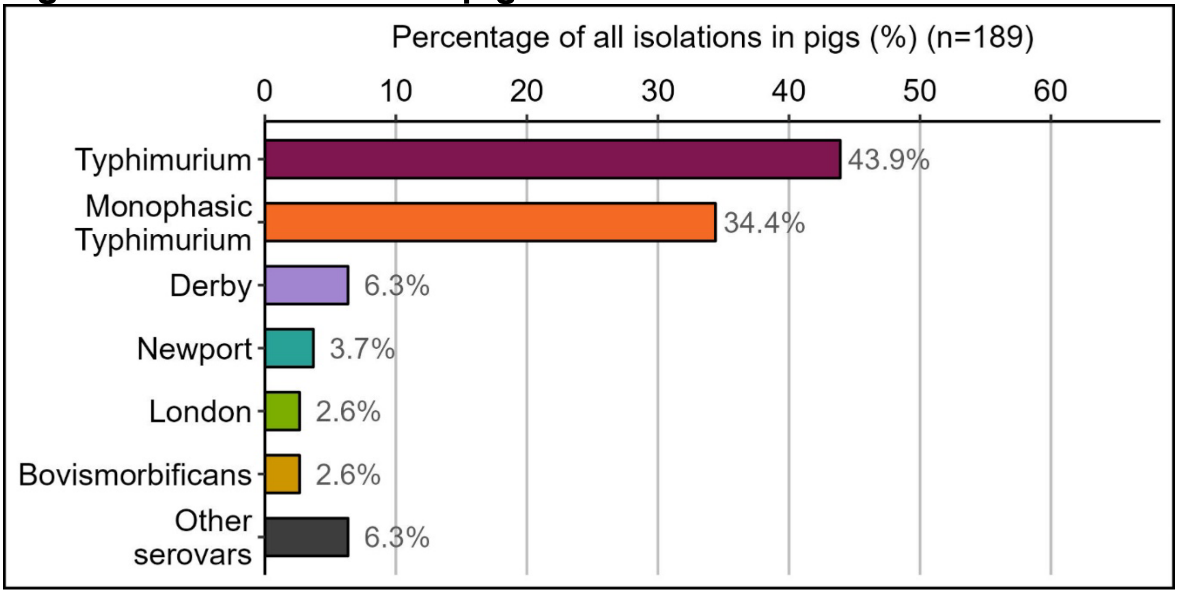
Table 4.1: Isolations and incidents of *Salmonella* in pigs on all premises in Great Britain 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Bardo	1	1	0	0	0	0	0	0	0	0
Bovismorbificans	5	5	7	6	2	2	2	2	8	8
Cerro	0	0	0	0	0	0	1	1	0	0
Chester	0	0	0	0	0	0	1	1	0	0
Derby	12	11	17	16	15	13	17	16	33	30
Dublin	0	0	1	1	0	0	0	0	1	1
Hessarek	0	0	0	0	0	0	0	0	1	1
Indiana	1	1	2	1	0	0	0	0	0	0
Kedougou	1	1	1	1	3	2	3	3	5	5
Livingstone	0	0	1	1	0	0	0	0	0	0
London	5	5	5	5	7	6	2	2	1	1
London var 15$^+$	0	0	0	0	1	1	0	0	0	0
Monophasic Typhimurium	65	62	63	57	51	44	61	59	70	68
Newport	7	7	19	18	20	19	18	16	20	20
Panama	2	2	4	4	10	9	10	10	7	7
Reading	2	2	2	2	3	3	2	2	7	7
Rissen	0	0	0	0	0	0	2	2	1	1
Typhimurium	83	76	100	93	100	97	139	124	156	141
rough strains	3	3	1	1	0	0	0	0	0	0

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
untypable strains	2	2	0	0	2	2	0	0	1	1
Total	**189**	**178**	**223**	**206**	**214**	**198**	**258**	**238**	**311**	**291**

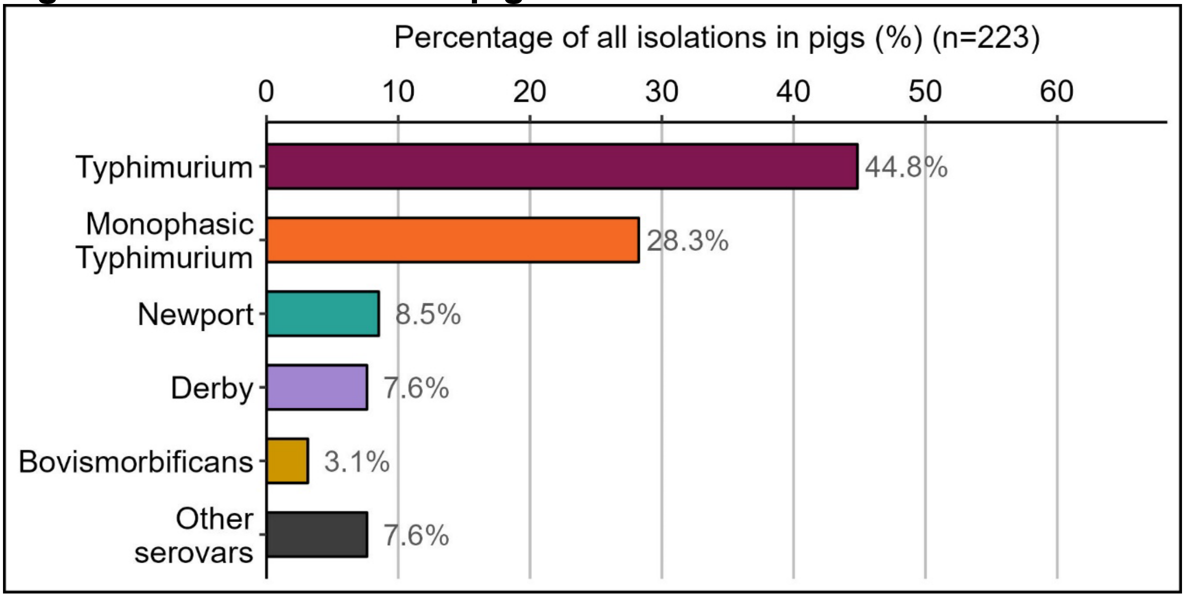
Figure 4.2: Isolations of the most common serovars in pigs in Great Britain 2020 to 2024

Figure 4.2.1: Isolations in pigs in 2020



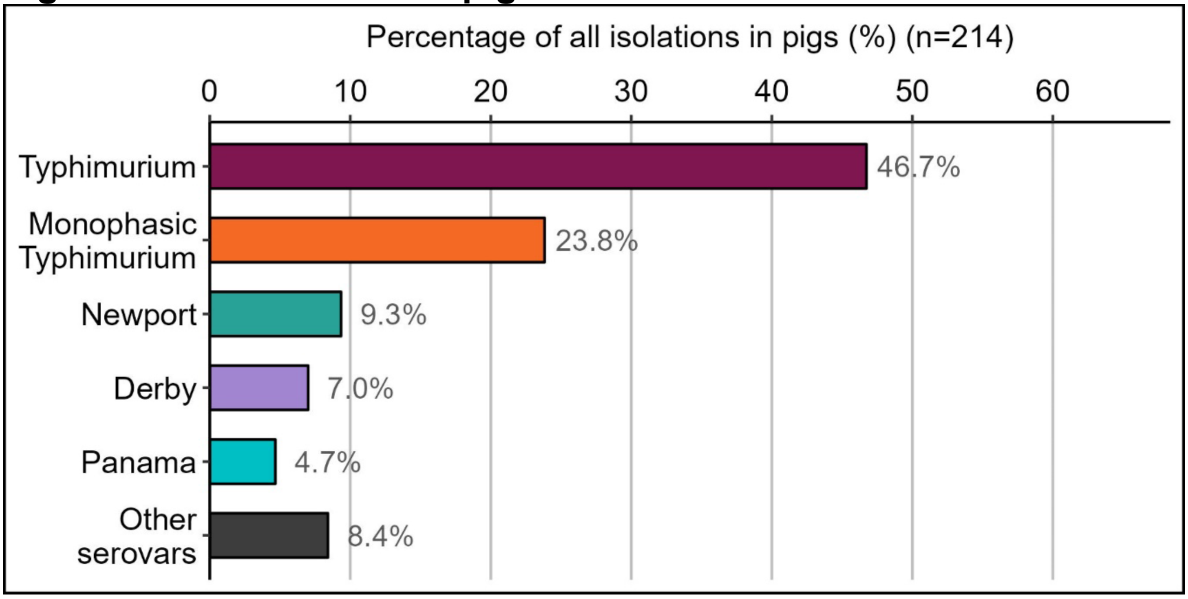
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in pigs in 2020. The most common serovar in pigs in 2020 was *S.* Typhimurium (43.9% of isolations), followed by monophasic *Salmonella* Typhimurium (34.4% of isolations) and *S.* Derby (6.3% of isolations).

Figure 4.2. 2: Isolations in pigs in 2021



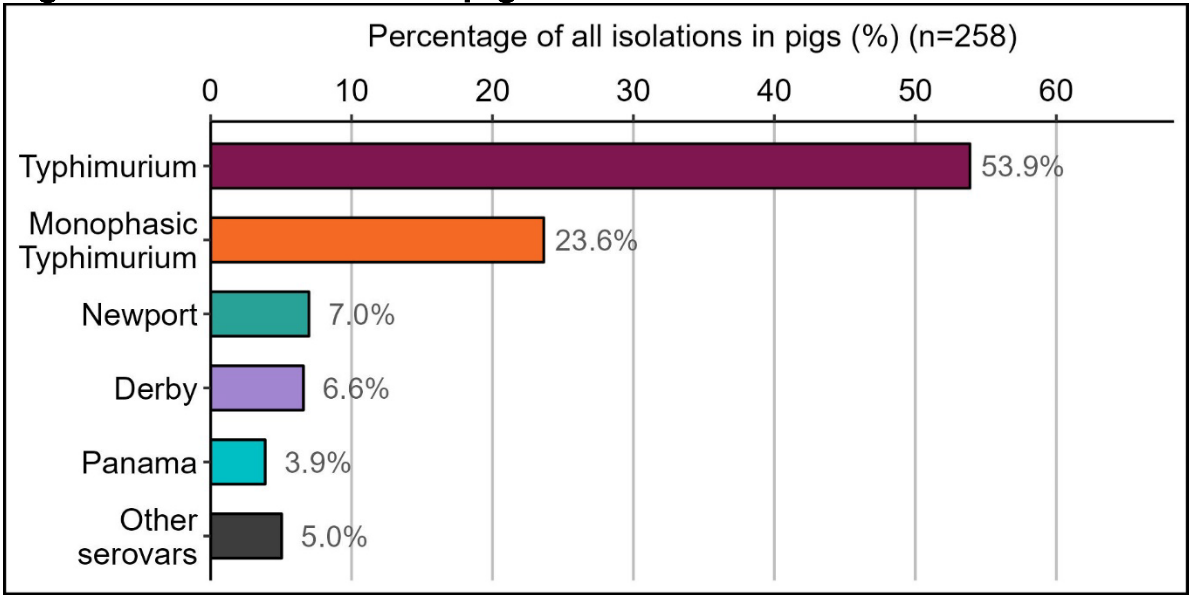
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in pigs in 2021. The most common serovar in pigs in 2021 was *S.* Typhimurium (44.8% of isolations), followed by monophasic *Salmonella* Typhimurium (28.3% of isolations) and *S.* Newport (8.5% of isolations).

Figure 4.2.3: Isolations in pigs in 2022



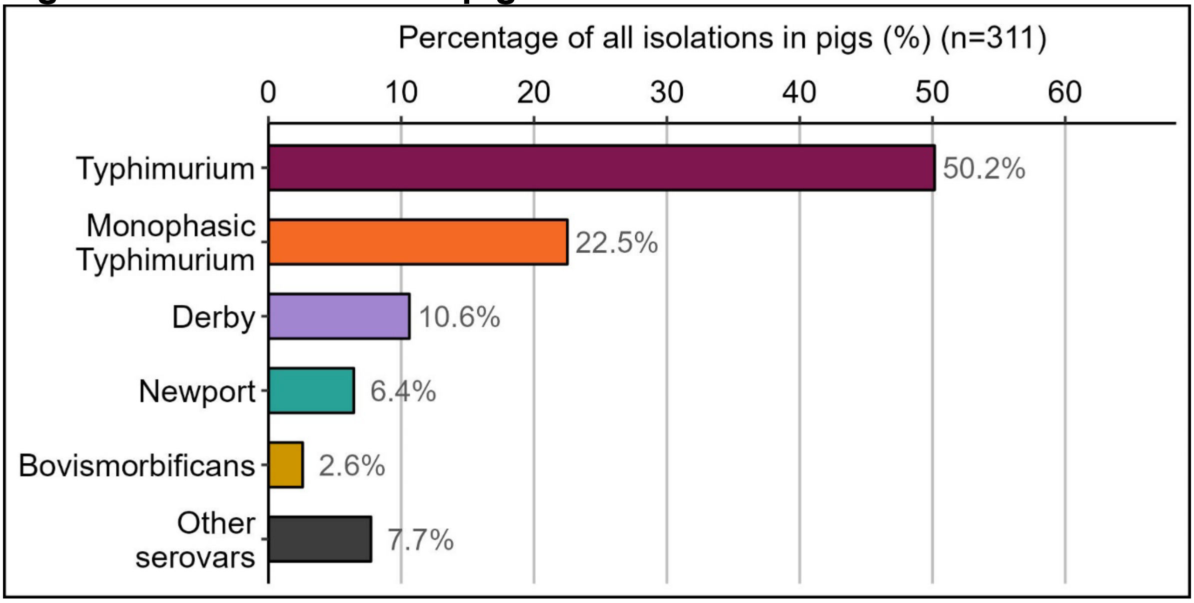
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in pigs in 2022. The most common serovar in pigs in 2022 was *S.* Typhimurium (46.7% of isolations), followed by monophasic *Salmonella* Typhimurium (23.8% of isolations) and *S.* Newport (9.3% of isolations).

Figure 4.2.4: Isolations in pigs in 2023



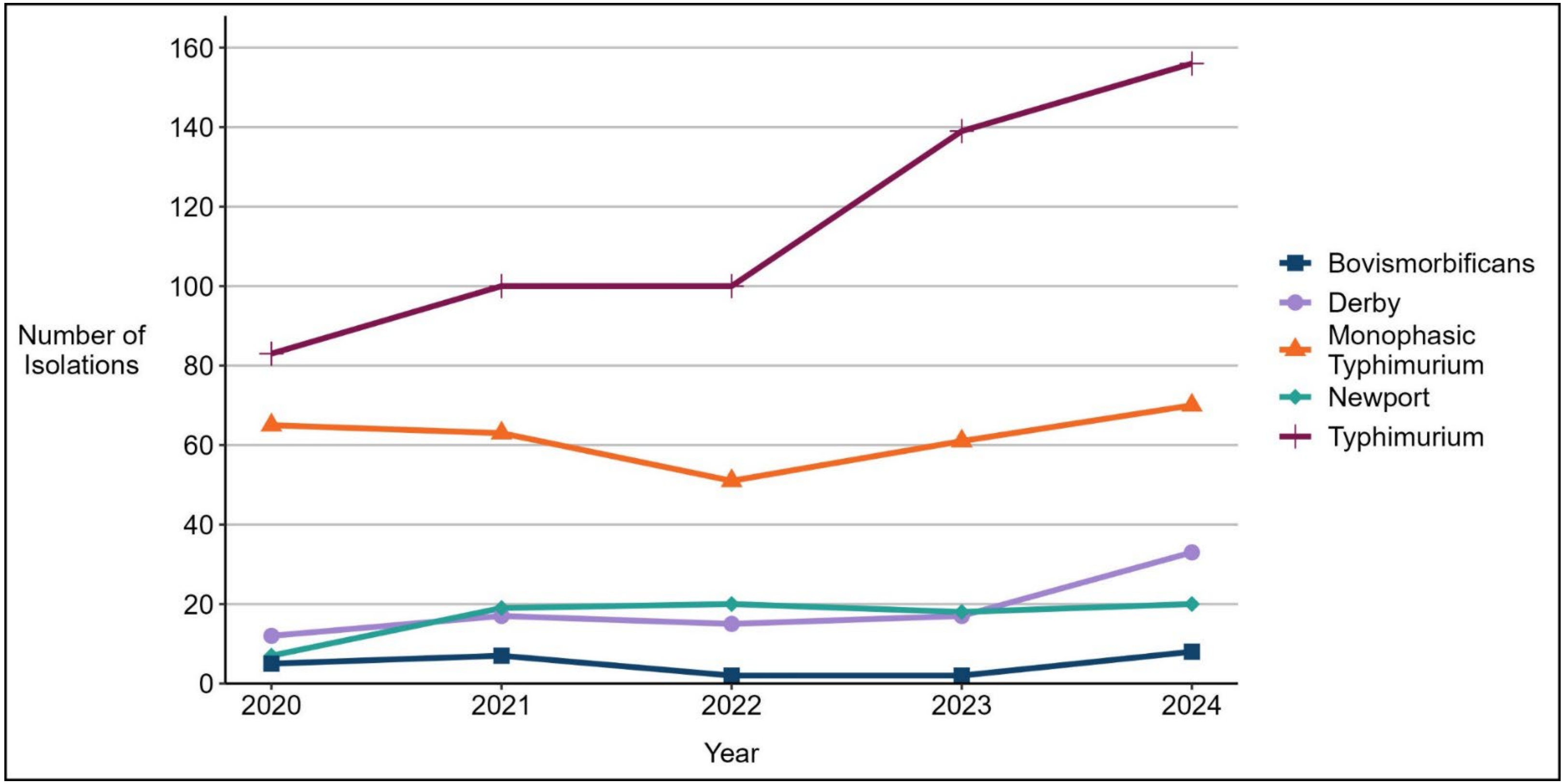
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in pigs in 2023. The most common serovar in pigs in 2023 was *S.* Typhimurium (53.9% of isolations), followed by monophasic *Salmonella* Typhimurium (23.6% of isolations) and *S.* Newport (7.0% of isolations).

Figure 4.2.5: Isolations in pigs in 2024



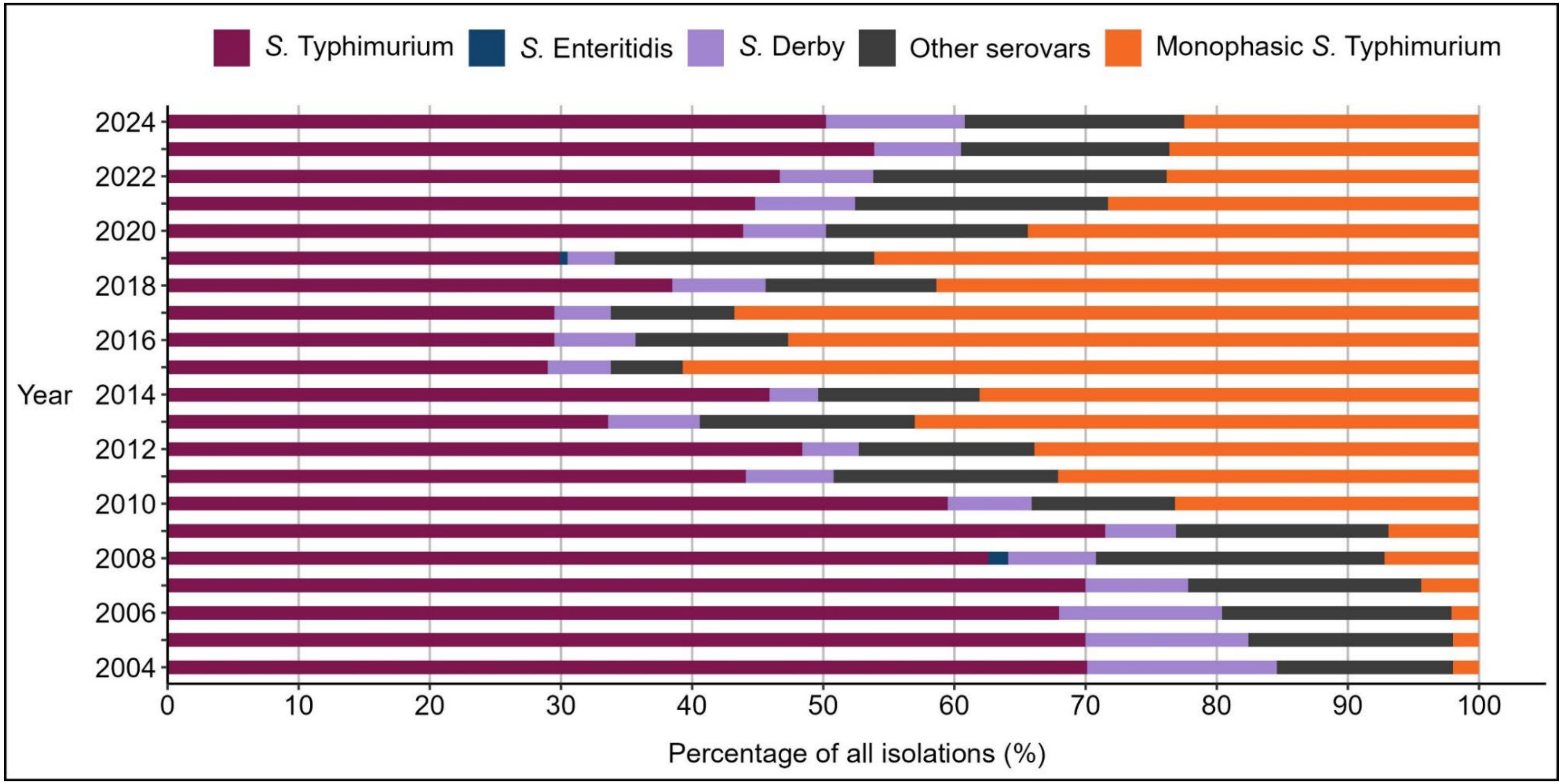
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in pigs in 2024. The most common serovar in pigs in 2024 was *S.* Typhimurium (50.2% of isolations), followed by monophasic *Salmonella* Typhimurium (22.5% of isolations) and *S.* Derby (10.6% of isolations).

Figure 4.3: The 5 most common *Salmonella* serovars in pigs in Great Britain in 2024 and their trends over time since 2020



A line graph showing the 5 most common serovars in pigs from 2020 to 2024. 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 until 2022 but increased to 61 isolations in 2023 and 70 isolations in 2024. Isolations of *S.* Derby increased in 2024 to 33 when numbers had varied between 12 and 17 from 2020 to 2023.

Figure 4.4: *S.* Derby, *S.* Enteritidis, *S.* Typhimurium and monophasic *S.* Typhimurium as a proportion of all isolations in pigs in Great Britain 2004 to 2024



A stacked horizontal bar graph showing *S*. Derby, *S*. Enteritidis, *S*. Typhimurium and monophasic *S.* Typhimurium as a proportion of all isolations in pigs from 2004 to 2024. The figure shows that as a proportion of all isolations in pigs in Great Britain between 2004 and 2024:

- *S.* Typhimurium accounted for the greatest proportion of isolations in most years and varied across the years from 29% to 72%
- Monophasic *S.* Typhimurium - accounted for 60.7% of isolations in 2015 but have since declined and made up 22.5% in 2024
- Isolations of *S.* Derby decreased as a proportion of the total from a high of 14.5% in 2004 to 10.6% in 2024
- With the exception of 2008 and 2019 *S.* Enteritidis has not been isolated from pigs
- Other serovars have accounted for between 5.5% and 22.4% since 2004 with fluctuations year on year

Figure 4.4: Table of data

Year	Monophasic *S.* Typhimurium	*S.* Typhimurium	*S.* Enteritidis	*S.* Derby	Other serovars
2004	2.0%	70.1%	0.0%	14.5%	13.4%
2005	2.0%	70.0%	0.0%	12.4%	15.6%
2006	2.1%	68.0%	0.0%	12.4%	17.5%
2007	4.4%	70.0%	0.0%	7.8%	17.8%
2008	7.2%	62.6%	1.5%	6.7%	22.0%
2009	6.9%	71.5%	0.0%	5.4%	16.2%
2010	23.2%	59.5%	0.0%	6.4%	10.9%
2011	32.1%	44.1%	0.0%	6.7%	17.1%
2012	33.9%	48.4%	0.0%	4.3%	13.4%
2013	43.0%	33.6%	0.0%	7.0%	16.4%
2014	38.1%	45.9%	0.0%	3.7%	12.3%
2015	60.7%	29.0%	0.0%	4.8%	5.5%
2016	52.7%	29.5%	0.0%	6.2%	11.6%
2017	56.8%	29.5%	0.0%	4.3%	9.4%
2018	41.4%	38.5%	0.0%	7.1%	13.0%
2019	46.1%	29.9%	0.6%	3.6%	19.8%

Year	Monophasic *S.* Typhimurium	*S.* Typhimurium	*S.* Enteritidis	*S.* Derby	Other serovars
2020	34.4%	43.9%	0.0%	6.3%	15.4%
2021	28.3%	44.8%	0.0%	7.6%	19.3%
2022	23.8%	46.7%	0.0%	7.1%	22.4%
2023	23.7%	53.9%	0.0%	6.6%	15.9%
2024	22.5%	50.2%	0.0%	10.6%	16.7%

Table 4.2: *S.* Typhimurium phage types in pigs in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT4	5	5	5	4	6	6	2	2	4	4
DT8	0	0	1	1	0	0	0	0	0	0
DT9	0	0	2	2	4	3	0	0	0	0
DT20	0	0	0	0	0	0	3	3	0	0
DT11	0	0	0	0	0	0	1	1	0	0
DT32	0	0	2	2	16	16	22	16	50	48
DT52	0	0	1	1	1	1	0	0	0	0
DT75	0	0	0	0	0	0	0	0	1	1
DT104	4	4	0	0	1	1	5	5	5	5
DT105	0	0	0	0	2	2	7	6	2	2
DT116	0	0	0	0	0	0	0	0	1	1
DT118	0	0	0	0	1	1	0	0	0	0
DT120	0	0	1	1	2	2	5	5	1	1
DT181	0	0	0	0	1	1	3	3	1	1
DT193	26	26	27	27	27	25	31	30	54	46
DT204b	1	1	0	0	0	0	0	0	0	0
U288	36	33	36	35	6	6	4	4	0	0
U302	1	1	0	0	0	0	0	0	0	0
U308	1	1	8	6	3	3	8	8	4	2
U308a	0	0	7	7	18	18	46	39	7	7
U323	1	1	0	0	0	0	0	0	0	0
NOPT	2	0	2	1	0	0	0	0	18	15
RDNC	5	3	8	6	12	12	2	2	8	8

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
UNTY	1	1	0	0	0	0	0	0	0	0
Total	**83**	**76**	**100**	**93**	**100**	**97**	**139**	**124**	**156**	**141**

Table 4.3: Monophasic *S.* Typhimurium phage types in pigs in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT7	0	0	1	1	0	0	0	0	0	0
DT104	0	0	0	0	0	0	0	0	1	1
DT120	0	0	3	2	1	1	1	1	0	0
DT193	56	53	48	44	45	39	43	42	52	50
DT194	0	0	0	0	0	0	1	1	1	1
DT208	0	0	1	1	0	0	0	0	0	0
U302	0	0	0	0	0	0	1	1	0	0
U311	0	0	1	1	1	1	0	0	0	0
NOPT	3	3	2	2	0	0	4	3	6	6
RDNC	2	2	2	2	0	0	2	2	0	0
UNTY	4	4	5	4	4	3	9	9	10	10
Total	**65**	**62**	**63**	**57**	**51**	**44**	**61**	**59**	**70**	**68**

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 were 2 *Salmonella* isolations from deer during 2024, one each of monophasic *S*. Typhimurium (NOPT) and *Salmonella* Typhimurium (RDNC) (Table 5.1). This is compared to one isolation of *S*. Typhimurium (DT105) during 2023 and no isolations between 2020 and 2022. Monophasic *S*. Typhimurium has never previously been reported from deer in Great Britain. APHA received 109 diagnostic submissions from deer in 2024, similar to the 115 received in 2023.

Horses

The number of horses recorded as being kept in Great Britain at the June 2024 Agricultural Census was 198,087, which is a decrease of 5.2% compared to 2023 (209,058 animals).

There were 53 isolations of *Salmonella* from horses during 2024 (Table 5.3). This represents a 3.6% decrease compared to the total number of isolations recorded from horses during 2023 (55 isolations) and an 11.7% decrease compared to 2022 (60 isolations). As companion animals, horses are a potential source of infection to their keepers and the zoonotic implications of salmonellosis in horses must be considered.

The most commonly isolated serovars from horses during 2024 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) (Figure 5.1). During 2023 the most common serovars were *S*. Typhimurium (20 isolations, 36.4% of total horse isolations), *S*. Newport (7 isolations, 12.7% of total horse isolations) and *S*. Concord (6 isolations, 10.9% of total horse isolations).

The number of *S.* Typhimurium isolations during 2024 was slightly higher than that reported in 2023 (24 versus 20 isolations) and 2022 (18 isolations) (Table 5.4). There was one isolation of monophasic *S.* Typhimurium (DT193) in both 2024 and 2023, compared to 2 isolations (both DT104) in 2022 (Table 5.5).

The 24 isolations of *S*. Typhimurium reported from horses during 2024 comprised 6 different phage types (excluding NOPT and RDNC). The most common phage type was DT75 (4 isolations). There were 3 isolations of DT193, and one isolation each of DT36, DT99, DT116 and U323. Phage types DT36 and U323 have never previously been reported in horses in Great Britain.

There were 8 isolations of *S*. Enteritidis in 2024 (Table 5.6), a notable increase compared to one isolation (PT8) seen in 2023 and double that of 2022 when there were 4 isolations (PT9a x2, PT8 x1 and PT13a x1). The phage types reported in 2024 were PT3 (x3), PT8 (x1), PT9a (x1) and PT36 (x1) with 2 isolations not phage typed (NOPT). PT3 and PT36 have never been reported in horses previously in Great Britain.

There were 2 isolations each of *S.* Agama and *S*. Fulica in 2024 and single isolations each of *S*. Anatum, *S*. Blockley, *S*. Bonn, *S*. Bovismorbificans, *S*. Concord, *S*. Eastbourne, *S*. Kingston, monophasic *S*. Typhimurium and *S*. Stanleyville. *Salmonella* Blockley, *S*. Bonn nor *S.* Fulica have not previously been reported in horses in Great Britain.

Antimicrobial susceptibility in horses

A total of 59 *Salmonella* isolates from horses were tested against a panel of 16 antimicrobials in 2024. The proportion of fully susceptible isolates dropped to 78.0%, from 91.9% in 2023 (n=62). Multidrug resistance (MDR; resistance to 4 or more antimicrobials) remained low and limited to 2 isolates: one *S.* Typhimurium and one monophasic *S.* Typhimurium.

A limited number of isolates exhibited resistance (n=16) and belonged to different serovars. Emerging resistance to nalidixic acid was observed in 5 *S.* Oslo isolates, all resistant only to this compound - a trend not seen in 2023. Resistance to tetracycline (10.2%) and streptomycin (10.2%) was also noted in isolates from other serovars.

None of the *Salmonella* isolates from horses showed resistance to third generation cephalosporins or fluoroquinolones, which are considered "highest priority critically important antibiotics" (HP-CIAs).

Rabbits

APHA received 8 diagnostic rabbit submissions in 2024. Of these there were no isolations of *Salmonella*. 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 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Monophasic Typhimurium	0	0	0	0	0	0	0	0	1	1
Typhimurium	0	0	0	0	0	0	1	1	1	1
Total	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**1**	**2**	**2**

Table 5.2: Isolations and incidents of *Salmonella* in rabbits on all premises in Great Britain 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Fluntern	0	0	0	0	1	1	0	0	0	0
Newport	0	0	0	0	1	1	0	0	0	0
Total	**0**	**0**	**0**	**0**	**2**	**2**	**0**	**0**	**0**	**0**

Table 5.3: Isolations and incidents of *Salmonella* in horses on all premises in Great Britain 2020 to 2024

***Salmonella* serovar**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**	**2024 isolations**	**2024 incidents**
Agama	4	4	0	0	4	4	0	0	2	2
Agona	0	0	1	1	0	0	0	0	0	0
Anatum	2	2	0	0	1	1	2	2	1	1
Birkenhead	0	0	0	0	0	0	1	1	0	0
Blockley	0	0	0	0	0	0	0	0	1	1
Bonn	0	0	0	0	0	0	0	0	1	1
Bovismorbificans	0	0	16	10	4	4	3	3	1	1
Braenderup	0	0	0	0	1	1	1	1	0	0
Coeln	0	0	0	0	2	2	1	1	0	0
Concord	0	0	1	1	0	0	6	5	1	1
Dublin	0	0	1	1	2	2	0	0	0	0
Durham	0	0	0	0	1	1	0	0	0	0
Eastbourne	0	0	0	0	0	0	0	0	1	1
Eboko	0	0	0	0	3	3	0	0	0	0
Enteritidis	1	1	2	2	4	4	1	1	8	8
Fulica	0	0	0	0	0	0	0	0	2	2
Infantis	0	0	0	0	0	0	3	2	0	0
Javiana	1	1	0	0	0	0	0	0	0	0
Kingston	3	3	2	2	3	2	3	3	1	1
Kottbus	1	1	1	1	3	3	1	1	0	0
Mokola	1	1	0	0	0	0	0	0	0	0

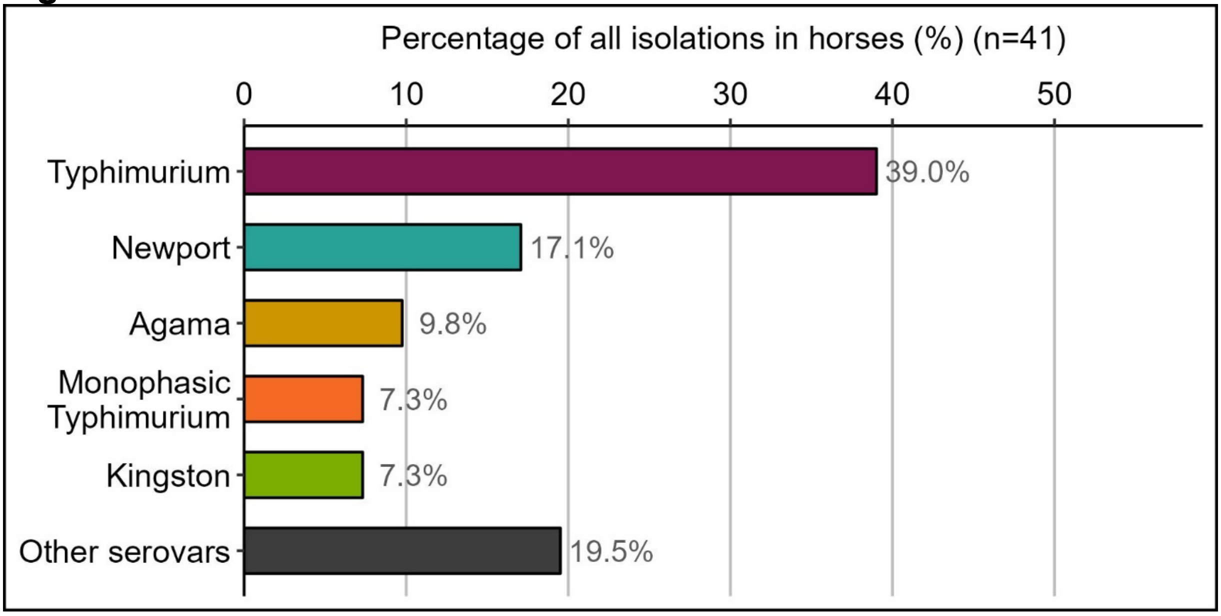
Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Monophasic Typhimurium	3	1	0	0	2	1	1	1	1	1
Montevideo	0	0	1	1	0	0	0	0	0	0
Newport	7	6	1	1	6	6	7	7	5	5
Oslo	1	1	1	1	4	4	2	1	3	3
Paratyphi B var. Java	1	1	1	1	0	0	1	1	0	0
Sanga	0	0	0	0	0	0	1	1	0	0
Stanleyville	0	0	1	1	0	0	0	0	1	1
Typhimurium	16	15	15	12	18	17	20	20	24	23
untypable strains	0	0	1	1	2	2	1	1	0	0
Total	**41**	**37**	**45**	**36**	**60**	**57**	**55**	**52**	**53**	**52**

Table 5.4: *S*. Typhimurium phage types in horses in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT1	1	1	5	5	2	2	2	2	0	0
DT2	0	0	2	2	0	0	2	2	0	0
DT8	0	0	0	0	2	1	0	0	0	0
DT29	0	0	1	1	0	0	0	0	0	0
DT32	0	0	0	0	1	1	0	0	0	0
DT36	0	0	0	0	0	0	0	0	1	1
DT75	0	0	0	0	0	0	5	5	4	4
DT99	0	0	0	0	0	0	2	2	1	1
DT104	0	0	0	0	1	1	1	1	0	0
DT105	0	0	0	0	3	3	1	1	0	0
DT109	0	0	0	0	2	2	0	0	0	0
DT116	5	4	0	0	2	2	0	0	1	1
DT193	2	2	0	0	2	2	1	1	3	3
U302	0	0	1	1	0	0	0	0	0	0
U320	1	1	0	0	0	0	0	0	0	0
U323	0	0	0	0	0	0	0	0	1	1
NOPT	0	0	0	0	0	0	0	0	8	8
RDNC	7	7	6	3	3	3	6	6	5	4
Total	**16**	**15**	**15**	**12**	**18**	**17**	**20**	**20**	**24**	**23**

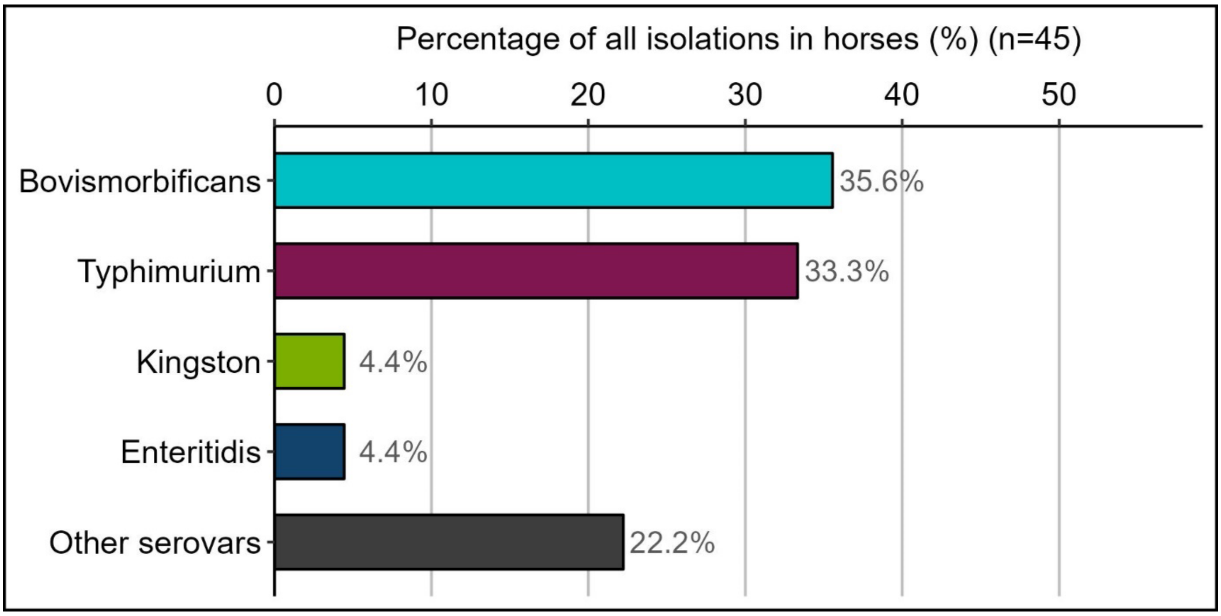
Figure 5.1: Isolations of the most common serovars in horses in Great Britain 2020 to 2024

Figure 5.1.1: Isolations in horses in 2020



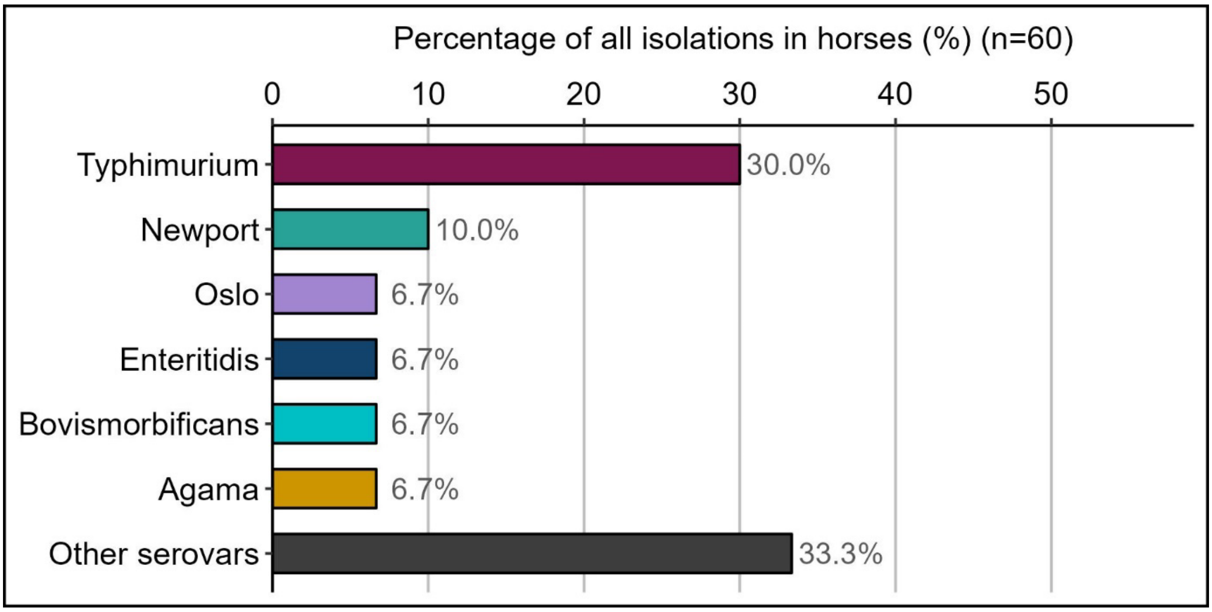
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in horses in 2020. The most common serovar in horses in 2020 was *S.* Typhimurium (39.0% of isolations), followed by *S*. Newport (17.1% of isolations), *S.* Agama (9.8% of isolations), *S.* Kingston and monophasic *Salmonella* Typhimurium (7.3% of isolations each).

Figure 5.1.2: Isolations in horses in 2021



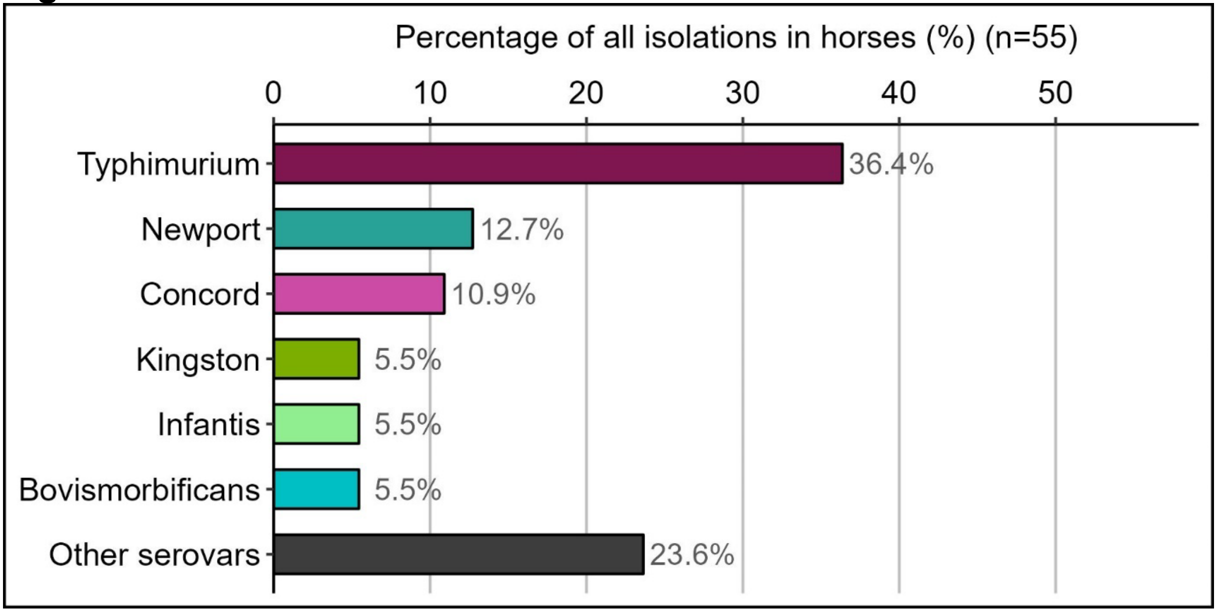
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in horses in 2021. The most common serovar in horses in 2021 was *S.* Bovismorbificans (35.6% of isolations), followed by *S*. Typhimurium (33.3% of isolations), *S.* Enteritidis and *S*. Kingston (4.4% of isolations each).

Figure 5.1.3: Isolations in horses in 2022



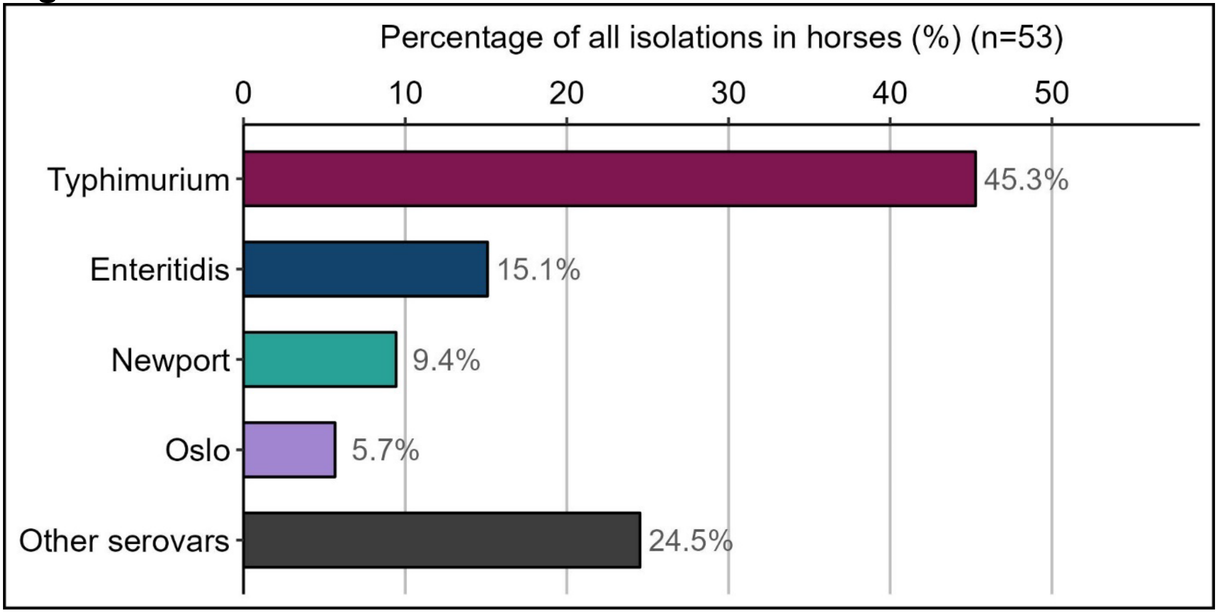
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in horses in 2022. The most common serovar in horses in 2022 was *S.* Typhimurium (30.0% of isolations), followed by *S*. Newport (10.0% of isolations), *S.* Agama, *S*. Bovismorbificans, *S*. Enteritidis and *S*. Oslo (6.7%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

Figure 5.1.4: Isolations in horses in 2023



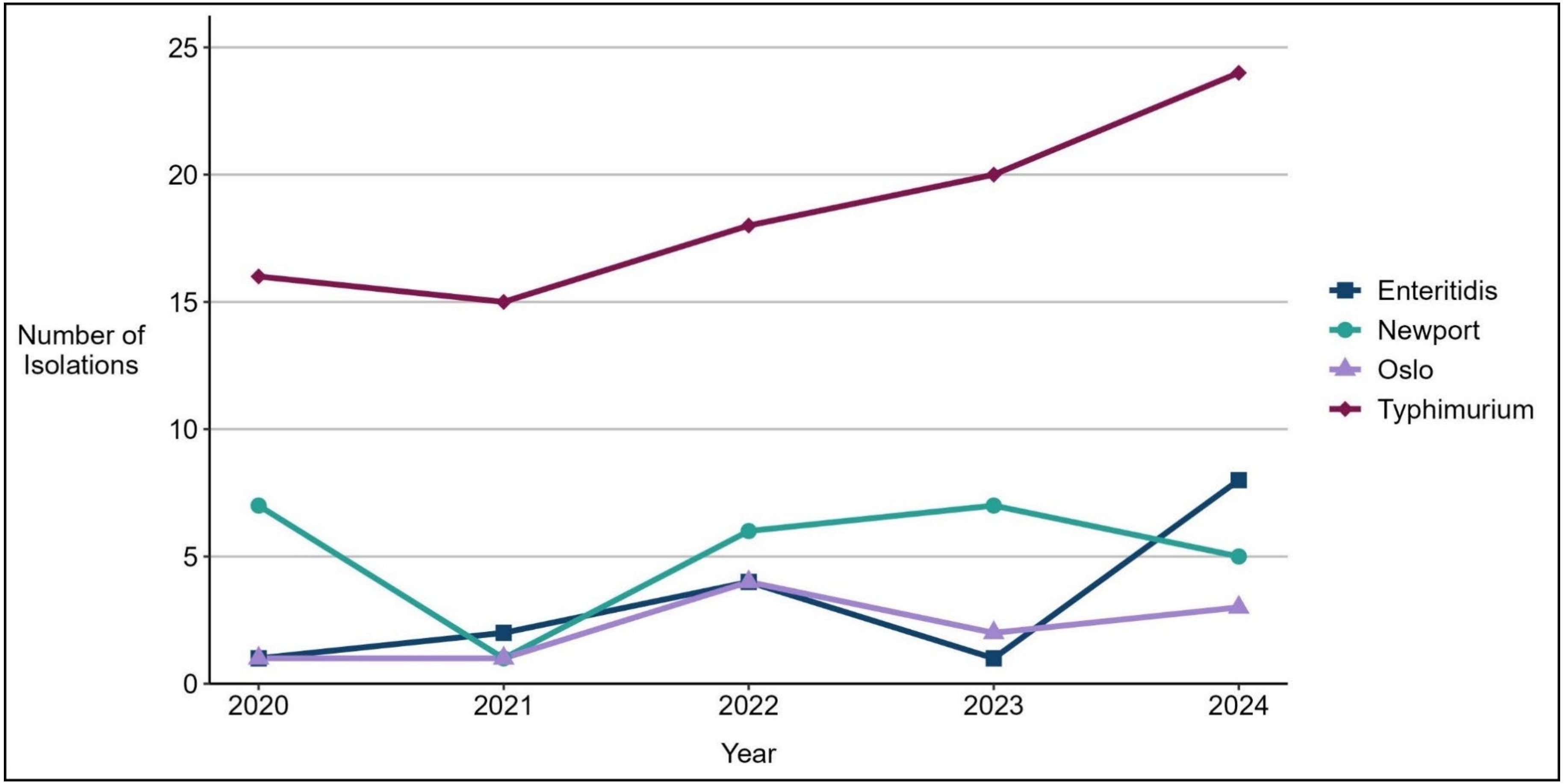
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in horses in 2023. The most common serovar in horses in 2023 was *S.* Typhimurium (36.4% of isolations), followed by *S.* Newport (12.7 % of isolations), *S.* Concord (10.9% of isolations), *S.* Bovismorbificans, *S.* Infantis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

Figure 5.1.5: Isolations in horses in 2024



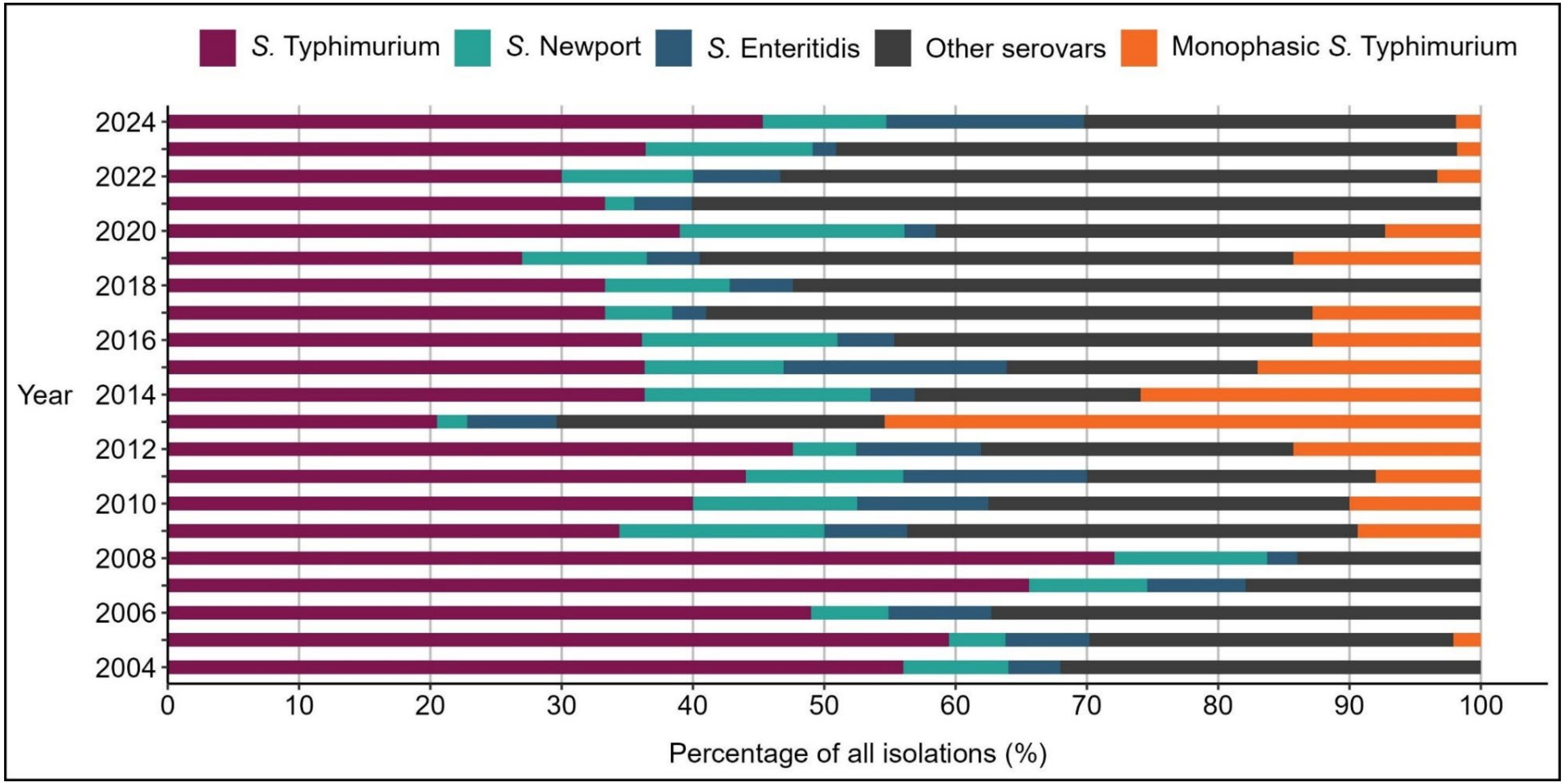
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in horses in 2024. The most common serovar in horses in 2024 was *S.* Typhimurium (45.3% of isolations), followed by *S.* Enteritidis (15.1 % of isolations), *S.* Newport (9.4% of isolations) and *S.* Oslo (5.7% of isolations).

Figure 5.2: The 4 most common *Salmonella* serovars in horses in Great Britain in 2024 and their trends over time since 2020



A line graph showing the 4 most common serovars in horses from 2020 to 2024. The figure shows that *S*. Typhimurium remains the top serovar in horses with 24 isolations in 2024 and has been steadily increasing since 2021. *S.* Enteritidis, the second most common serovar in 2024, has increased from one isolation in 2020 to 8 in 2024. The third most common serovar in 2024 was *S*. Newport which has fluctuated and seen an overall decrease since 2020. *S.* Oslo was the fourth most common serovar in 2024, which has also fluctuated though seen an overall increase since 2020.

Figure 5.3: *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and monophasic *S.* Typhimurium as a proportion of all isolations in horses in Great Britain 2004 to 2024



A stacked horizontal bar graph showing *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and monophasic *S.* Typhimurium as a proportion of all isolations in horses from 2004 to 2024. The figure shows the proportion of all isolations of *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and monophasic *S*. Typhimurium in horses in Great Britain between 2004 and 2024:

- *S*. Typhimurium accounted for the greatest proportion of individual serovar isolations in all years apart from 2013.

Monophasic *S*. Typhimurium as a proportion of all isolations peaked in 2013 at 45.4% but has since returned to lower levels at 1.9% in 2024.

- *S*. Newport accounted for a high of 17.2% of isolations in 2014, with variable numbers across other years.
- *S*. Enteritidis was also more variable between 17.0% in 2015 and a low of 1.8% in 2023. In 2024 *S*. Enteritidis accounted for 15.1% of all isolations.
- Other serovars have accounted for between 14.0% and 60.1% during the time period, with the proportion in 2024 at 28.3% being the lowest seen since 2015.

Figure 5.3: Table of data

Year	Other serovars	*S.* Enteritidis	*S.* Newport	*S.* Typhimurium	Monophasic *S.* Typhimurium
2004	32.0%	4.0%	8.0%	56.0%	0.0%
2005	27.7%	6.4%	4.3%	59.5%	2.1%
2006	37.3%	7.8%	5.9%	49.0%	0.0%
2007	17.9%	7.5%	9.0%	65.6%	0.0%
2008	14.0%	2.3%	11.6%	72.1%	0.0%
2009	34.3%	6.3%	15.6%	34.4%	9.4%
2010	27.5%	10.0%	12.5%	40.0%	10.0%
2011	22.0%	14.0%	12.0%	44.0%	8.0%
2012	23.8%	9.5%	4.8%	47.6%	14.3%
2013	25.0%	6.8%	2.3%	20.5%	45.4%

Year	Other serovars	*S.* Enteritidis	*S.* Newport	*S.* Typhimurium	Monophasic *S.* Typhimurium
2014	17.2%	3.4%	17.2%	36.3%	25.9%
2015	19.1%	17.0%	10.6%	36.3%	17.0%
2016	31.9%	4.3%	14.9%	36.1%	12.8%
2017	46.2%	2.6%	5.1%	33.3%	12.8%
2018	52.4%	4.8%	9.5%	33.3%	0.0%
2019	45.2%	4.0%	9.5%	27.0%	14.3%
2020	34.2%	2.4%	17.1%	39.0%	7.3%
2021	60.1%	4.4%	2.2%	33.3%	0.0%
2022	50.0%	6.7%	10.0%	30.0%	3.3%
2023	47.3%	1.8%	12.7%	36.4%	1.8%
2024	28.3%	15.1%	9.4%	45.3%	1.9%

Table 5.5: Monophasic S. Typhimurium phage types in horses in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT104	0	0	0	0	2	1	0	0	0	0
DT193	3	1	0	0	0	0	1	1	1	1
Total	**3**	**1**	**0**	**0**	**2**	**1**	**1**	**1**	**1**	**1**

Table 5.6: S. Enteritidis phage types in horses in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
PT3	0	0	0	0	0	0	0	0	3	3
PT8	1	1	0	0	1	1	1	1	1	1
PT9a	0	0	0	0	2	2	0	0	1	1
PT13a	0	0	1	1	1	1	0	0	0	0
PT36	0	0	0	0	0	0	0	0	1	1
NOPT	0	0	1	1	0	0	0	0	2	2
Total	**1**	**1**	**2**	**2**	**4**	**4**	**1**	**1**	**8**	**8**

Chapter 6: Reports of *Salmonella* in chickens

During the early months of the years 2022 to 2024 there was significant disruption to the poultry industry due to national outbreaks of Avian Influenza affecting all industry sectors. This resulted in altered management and biosecurity measures. Although the biosecurity measures would not have impacted the need to comply with NCP sampling, it is likely to have impacted submission numbers. 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 2024 data with previous years.

According to the June Agricultural Census, the total number of chickens kept in Great Britain was 143.6 million birds in 2024, comprising approximately 44.6 million breeding and laying hens, and 98.9 million broiler chickens (Figure 6.1). This compares to 144.8 million chickens in 2023, a decrease of 0.8%.

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. This also applies if there is a long interval between positive tests from the same flock.

There was a total of 5,115 chicken diagnostic and monitoring submissions received by APHA and SRUC laboratories and partner post-mortem providers in 2024, a decrease of 1.8% compared to 5,210 in 2023. 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.

Total *Salmonella* isolations

A total of 1,961 *Salmonella* isolations were reported from chickens in 2024 (Table 6.1), a decrease of 25.5% compared with 2023 (2,633 isolations) when the highest number of isolations since before 2009 were reported. *Salmonella* isolations from chickens increased substantially between 2018 and 2020 compared to the previous years (approximately 50% year on year). This overall rise was primarily the result of increased isolations in the broiler sector.

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 2024 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 1,923 (98.1%)
- voluntary surveillance: 37 (1.9%)
- clinical disease: 1 (0.05%)

The percentage of *Salmonella* isolations reported through statutory surveillance in 2024 was higher than in 2023 when 95.3% of total chicken isolations arose from statutory surveillance and only 4.6% arose from voluntary surveillance.

Thirty-four different *Salmonella* serovars were isolated in 2024, accounting for 1,958 of the 1,961 isolations*.* Three isolations involved un-typable *Salmonella* isolates (no rough strains). Table 6.1 shows the *Salmonella* serovars isolated from chickens between 2020 and 2024. Figure 6.2 shows the relative percentages of the most common serovars isolated from chickens between 2020 and 2024.

The 4 most common serovars isolated from chickens in 2024 are consistent with 2019 to 2023, however the relative contribution of each serovar varied (Figure 6.3). The decrease in isolations from 2023 to 2024 is largely the result of decreases in isolations of 2 of the most common serovars, *S*. Montevideo and *S.* Kedougou.

Consistent with 2018 to 2023, *S*. Idikan (including monophasic variant 13,23:i:-) was the most frequently isolated serovar in 2024 (679 isolations) accounting for 34.6% of all chicken isolations, consistent with 2023 in terms of isolations (681 isolations) but accounting for a greater percentage of isolations (25.9% in 2023). Isolations of this serovar peaked in 2020 with 716 isolations representing 32.6% of all *Salmonella* isolations but have decreased both in real and relative terms in recent years. In previous years the majority of isolations of this serovar comprised of the monophasic variant *S.* 13,23:i:-, which is associated with contaminated feed mills and can also become established and persistent in hatcheries and on poultry farms (Gosling *et al.,* 2022).

Salmonella Kedougou accounted for 382 isolations in 2024 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 had been rising steadily until 2021 when they almost halved (217 vs 430 isolations) but rose again to a peak in 2023 (537 isolations) before dropping again in 2024. The relative proportion of flocks with this serovar increased from 11.5% in 2022 to 20.4% in 2023 and remains elevated in 2024 at 19.5%.

With 308 isolations, *S*. Montevideo was the third most common serovar isolated in 2024 accounting for 15.7% of all chicken isolations. This represents a 47.9% decrease in this serovar compared to 2023 (591 isolations, 22.4% of all chicken isolations) (Figure 6.2). This is the first reported decrease since 2015 (31 isolations), after which isolations had been increasing year-on-year (Figure 6.3).

Isolations of *Salmonella* Mbandaka have markedly decreased in 2024 to 168 isolations (8.6% of all chicken isolations), from 305 isolations in 2023 (11.6% 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).

Isolations of *S*. Agona from chickens have also decreased in 2024 by 32.0%, to 136 isolations compared to 200 in 2023. This was the highest number of isolations of this serovar ever reported. Since 2018 there has been large fluctuations in numbers of this serovar which is usually associated with feed contamination.

Other notable increases in serovars isolated from chickens in 2024 compared with 2023 included *S.* Anatum (10 versus 5 isolations), *S.* Kentucky (18 versus 1 isolations), *S.* Muenchen (27 versus 5 isolations), *S.* Newport (26 versus 4 isolations), *S.* Ohio (44 versus 36 isolations) and *S*. 61:k:1,5,(7) (8 versus 2 isolations).

There were 17 *S.* Typhimurium isolations from chickens in 2024 originating from 16 flocks, accounting for 0.9% of all *Salmonella* isolations and consistent with recent years when it accounted for 0.8% of all *Salmonella* isolations in 2023 (21 isolations) and 0.7% of all *Salmonella* isolations in 2022 (18 isolations). There were 7 different phage types identified in both 2024 and 2023 (Table 6.2), however the phage types isolated varied. The most common phage type in 2024, as in 2023, was DT75 (7 isolations), first isolated from chickens in 2022. *Salmonella* Typhimurium DT105 was isolated on 3 occasions from 3 flocks but prior to 2023 (6 flocks and 4 isolations) had not been reported from chickens in

Great Britain. There were 3 isolations from 3 flocks of DT1, and single isolations of the phage types DT2, DT99, DT104 and DT193.

There were 12 isolations of *S.* Enteritidis in 2024 representing a 33.3% increase compared to 2023 (9 isolations). This is considerably lower than 2022 when isolations were at a 3-year high (23 isolations). Isolations in 2024 were associated with 11 flocks (2 of which were from the layer sector) on 8 holdings, compared with 5 holdings in 2023 and 6 holdings in 2022. There was similar diversity of phage types of *S.* Enteritidis isolated in 2024 compared to 2023 with 5 of the 12 isolations in 2024 belonging to PT8 (Table 6.4), also the most common phage type in 2022, 2020 and 2019. Phage type PT30 was associated with 2 isolations (one statutory sample and one voluntary sample) from a single flock and has never previously been reported from chickens in Great Britian. The remaining phage types isolated in 2024 were PT4 (which is frequently reported from chickens in Great Britain) and PT13a which is rarely isolated from chickens in Great Britain.

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 2024, there was one isolation of monophasic *S.* Typhimurium compared with 6 isolations in 2023 and 19 isolations in 2022. The single isolation was phage type DT193 (Table 6.3). This has been the only phage type isolated since 2020. The cases of monophasic *S.* Typhimurium are likely to be associated with contamination originating from pig herds.

There has been an increase in isolations of *S*. Infantis in chickens in recent years with a marked increase in the broiler sector in 2022 (98 isolations compared with 42 isolations in 2021 and one isolation in 2020). Isolations in 2023 decreased by 35.7% to 62 isolations and in 2024 have decreased once again by 67.7% to 20 isolations. *Salmonella* Infantis is often associated with imported feed ingredients, as well as raw meat pet food and dogs and is one of the most frequently isolated serovars in mainland Europe. There have been associated human outbreaks of *S*. Infantis in recent years.

Salmonella Senftenberg isolations from chickens have been highly variable in recent years but the recent trend in decreasing isolations of this serovar continued in 2024 with 10 isolations compared to 22 isolations in 2023. Isolations of *Salmonella* Senftenberg peaked in 2017 (238 isolations) and are often related to hatchery contamination.

In 2024 *S.* Chester was isolated from chickens in Great Britain for the first time with 2 isolations from 2 flocks. Other unusual serovars included *S*. Berta (last reported from chickens in 2022), *S*. Bredeney (last reported from chickens in 2020), *S.* Corvallis (last reported from chickens in 2022).

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

National Control Programme for *Salmonella* in chickens

The assimilated 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. 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 (including 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. 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 2024

In 2024, 10 adult breeding flocks, on 9 separate holdings, tested positive for *Salmonella* spp. under the statutory testing programme. This is comparable to 2023 (9 positive flocks) and 2021 (10 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 fluctuated in more recent years (Figure 6.4).

Four adult breeding flocks tested positive for a regulated *Salmonella* serovar in 2024 (Table 6.5) compared to 5 in 2023. All 4 flocks were broiler breeder flocks and tested positive for *S.* Typhimurium (DT75, DT193, DT2 and DT99), 3 identified through operator sampling, the other through annual official sampling. This is the first year since 2020 that *S*. Infantis has not been isolated in breeding flocks as part of the NCP, having first been isolated in 2021. 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. Prior to this, *S*. Typhimurium was last identified in one breeder flock as part of the NCP in 2020, from a broiler breeding flock. *Salmonella* Enteritidis has never been detected in breeding chickens as part of the NCP.

Six adult breeding flocks, on 5 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) via operator samples. This is 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. Until 2021, *Salmonella* 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 small number of positive flocks in 2024 continues a decreasing trend in occurrence of this serovar in breeding flocks in recent years.

No immature (in-rear) breeding flocks tested positive for *Salmonella* spp. during 2024 consistent recent years and compares with one in 2021 and 2 in 2020.

A comparison of the serovars identified in adult breeding flocks testing positive under the NCP between 2020 and 2024 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. However, it is noteworthy that the number of flocks testing positive for *Salmonella* Typhimurium has increased in recent years (4 flocks in 2023 and 2024). The monophasic variant of *S.* Idikan, 13,23:i:-, which are now reported together with *S.* Idikan, has been identified every year since 2013 (and always in broiler breeder flocks).

In Great Britain, a total of 1,155 adult breeding flocks on 249 premises were registered in 2024, and a total of 1,102 flocks were subject to *Salmonella* testing via routine annual official sampling visits. In 2024 there was a shortfall of approximately 5% in the number of flocks subject to annual official sampling, which is less than in 2023 (6%) and considerably less than in 2022 (13%). The shortfall in 2022 was largely due to the large Avian Influenza outbreak which impacted the number of official sampling visits that could take place in that year. Although the Avian Influenza outbreak of 2023 had an effect on testing this was limited to the early part of the year. 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 0.87% (10 of 1,155) in 2024 and the prevalence of regulated serovars 0.35% (Table 6.5, Figure 6.4), with each devolved nation coming in below their 1% target for regulated serovars. The estimated prevalence of regulated serovars in 2024 in England was 0.36%, Wales was 0.00%, and Scotland was 0.39%.

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. 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 2024

During 2024, a total of 33 adult laying hen flocks, originating from 27 separate holdings, tested positive for *Salmonella* under the statutory testing programme. This is 50.7% lower than the number of flocks testing positive in 2008 when the NCP was first implemented (67 positive flocks), and an increase of 13.8% compared to 2023 (29 positive flocks) (Table 6.6).

A total of 9 adult flocks, from 5 separate holdings, tested positive for regulated *Salmonella* serovars during 2024, more than in 2023 (7 positive flocks from 4 holdings) but less than in 2022 (10 positive flocks from 8 separate holdings). Although a small increase there is 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).

Two adult flocks from 2 holdings tested positive for *S.* Enteritidis via official sampling (PT30 (x1) and NOPT (x1)) in 2024. This is a decrease in the number of flocks compared to 2023 (3 positive flocks on one holding), and a large reduction compared to 2019 (14 flocks from 5 holdings), when the highest number of flocks tested positive for *S*. Enteritidis as part of the NCP which was implemented in 2008. The large number of positive flocks in 2020 was influenced by an outbreak on a single large farm which resulted in 7 of the flocks on the same site testing positive. In 2019, the number of positive flocks was influenced by the occurrence of risk-based enhanced sampling by APHA and the British Egg Industry Council (BEIC) on some premises that were linked via egg packing centres.

Seven adult flocks, from 3 separate holdings, tested positive for *S.* Typhimurium (DT75 (x6), DT105 (x1)) in 2024. This is an increase from 2 flocks in 2023 and 5 flocks in 2022. 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). Prior to 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 2024 compared to one flock in 2023. 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 2020 and 2024 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, 14 different non-regulated serovars were identified from adult laying chickens in 2024, from 24 flocks on 22 separate holdings (23 flocks from 21 holdings in 2023). No flocks tested positive for 2 different non-regulated serovars. The most common serovars were *Salmonella* 61:k:1,5,(7), which was isolated from 6 flocks on 6 different holdings, and *S*. Newport, which was isolated from 4 flocks on 4 different holdings. *Salmonella* 61:k:1,5,(7) *(enterica* subspecies *diarizonae)*, last detected in 2014, is considered to be a sheep adapted strain and is the most commonly isolated *Salmonella* from scanning surveillance samples of sheep. *S.* Newport was the most common non-regulated serovar in 2021 and isolations of this serovar typically occur every year.

There was a decrease in the number of different serovars isolated as part of the NCP in 2024 (14 versus 17 in 2023). Isolations of *S.* Infantis decreased in 2024 (no flocks) compared to 3 flocks in 2023 and 2022. For the fourth consecutive year, no adult flocks tested positive for *S.* Idikan or the partially typeable monophasic variant *Salmonella* 13,23:i:-. This represents a continued reduction in the prevalence of this feed-associated serovar in laying flocks compared to 2018, when the number of flocks testing positive was much higher than in any previous year since the implementation of the NCP in 2008 (5 flocks from 4 different holdings tested positive in 2018).

In 2024, 3 different serovars were isolated from adult laying flocks in the NCP for the first time. These were *S*. Chester, *S*. Corvallis (although this serovar was isolated from an immature laying flock in 2008) and *S*. Havana, which is isolated most years from broiler flocks under NCP.

No in-rear (immature) flocks tested positive for *Salmonella* in 2024 in Great Britain. This is a decrease compared to recent years when 3 flocks tested positive in 2023 and 2022 and continues the recent low numbers of positive holdings compared to 2021 (14 positive flocks from 12 holdings) and 2020 (25 positive flocks from 23 holdings). Prior to 2019, the number of in-rear flocks testing positive for *Salmonella* each year was 8 or fewer.

No in-rear layer flocks tested positive for regulated serovars in 2024. The last time an in-rear layer flock tested positive for a regulated serovar was in 2018, when a flock tested positive for *S*. Typhimurium. This was the first time since 2010 that a regulated serovar had been detected in NCP samples from an immature flock.

Using the number of NCP-eligible adult flocks of laying hens in production in Great Britain during 2024 as the denominator population, the estimated prevalence of *Salmonella* spp. in laying flocks was 0.89% (33 of 3,700) in 2024. This is comparable to the prevalence in 2023 (0.80% (29 of 3,372) and a decrease in prevalence from 2022 (1.13% (42 of 3,721)) (Figure 6.6). The estimated prevalence of regulated *Salmonella* serovars in 2024 in adult laying flocks was 0.24% (9 of 3,700). This represents an increase compared to 2023 (0.17%) but comparable to 2022 when 0.27% of flocks tested positive (10 of 3,721). For all devolved nations, the prevalence or regulated serovars in laying hens was below the target of 2.00%. The prevalence of regulated serovars in England was 0.26%, Wales was 0.46%, and in Scotland was 0.00%.

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 strains 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 2024

During 2024, a total of 1,775 broiler flocks from 446 separate holdings tested positive for *Salmonella* under NCP testing with an estimated prevalence of 4.05%. This represents a decrease of 21.7% relative to 2023 (2,268 flocks). This decrease follows a generally increasing trend (with exception of 2021) in positive flocks since 2017 (Table 6.7 and Figure 6.8). The decrease in 2024 is mostly attributable to a 47.7% decrease in *S.* Montevideo compared to 2023, a 42.3% decrease in *S.* Mbandaka compared to 2023, an 18.8% decrease in *S.* Kedougou compared to 2023, and a 29.3% decrease in *S.* Agona compared to 2023 (Table 6.7).

Fourteen broiler flocks, on 9 separate holdings, tested positive for regulated serovars in 2024 which is consistent with years 2023, 2022 and 2021 (16 flocks, 15 flocks and 15 flocks respectively) but a 5-fold increase in the number identified in 2020 (3 flocks positive) (Table 6.7 and Figure 6.8). Although a similar number of flocks tested positive for regulated serovars in 2024 relative to 2023 the proportion of each regulated serovar varied.

Five broiler flocks from 3 separate holdings tested positive for *S.* Typhimurium (DT1 (x3), DT104 (x1), and DT105 (x1)) in 2024 compared to 7 flocks from 6 holdings in 2023 (Table 6.7). These phage types have been isolated previously in broiler flocks as part of the NCP.

The number of flocks testing positive for *S.* Enteritidis increased in 2024, with 9 positive flocks (from 6 holdings) compared to 5 flocks (from 4 holdings) in 2023, one flock in 2022 and 2 flocks in 2021. Phage types reported were PT8 (x5), PT13a (x2), PT4 (x1) and NOPT (x1), this is the first report of PT13a in broiler flocks (from two distinct holdings) as part of the NCP. Although an increase compared to recent years these 9 positive flocks represent a considerable decrease compared to 2015, when 50 flocks tested positive for this serovar after an outbreak related to imported hatching eggs, which also happened in 2018 to a lesser extent. Fortunately, *S.* Enteritidis and *S.* Typhimurium can be readily eliminated from hatcheries as they do not persist for long within incubators (unlike several non-regulated serovars) but can survive in dust that has settled in inaccessible areas.

No flocks tested positive for monophasic *S*. Typhimurium in 2024, compared to 4 flocks in 2023, 10 flocks in 2022, and 9 flocks in 2021.

A comparison of the serovars identified in broiler flocks in the NCP between 2020 and 2024 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 1,761 broiler flocks positive for non-regulated *Salmonella* serovars in 2024, including 6 flocks that tested positive for more than one non-regulated serovar. The 4 most common serovars isolated from broiler chickens in 2024 was consistent across all years since 2019 (including *S.* 13,23:i:- as a monophasic variant of *S*. Idikan).

The occurrence of *Salmonella* Idikan (incl. monophasic variants) has in previous years been comprised largely of the monophasic variant *S.* 13,23:i:-. This serovar began increasing in 2018 but following a decrease in 2021, has since been rising, and is the most frequently isolated serovar in 2024, with 628 flocks (Table 3). *Salmonella* 13,23:i:- in particular is associated with some hatcheries and feed mills and has been commonly observed in broiler flocks since 2013. In 2024, *S.* Idikan (incl. monophasic variants) was identified on 190 premises, of which 98 (51.6%) were repeatedly positive for the same serovar in subsequent flocks. Repeated incidents of *S.* Idikan (incl. monophasic variants), defined as at least one positive flock placed on the premises in a particular month, were observed on individual premises. Of the 190 premises which had at least one flock positive for *S*. Idikan (incl. monophasic variants), 20.5% had 2 incidents, while 12.6%, 9.5%, 6.3%, and 1.1%, had 3, 4, 5 and 6 incidents of this serovar in 2024, respectively. The highest number of incidents of *S.* Idikan (incl. monophasic variants) in 2024 was 7. Further laboratory analysis of these chicken isolates revealed that the vast majority, greater than 99%, were the monophasic variant *S.* 13,23:i:-.

Salmonella Montevideo was the third most frequently reported serovar from broiler flocks in 2024 (285 flocks). Reports of the serovar increased every year between 2015 (19 flocks) to 2023 (545 flocks), with the 47.2% decrease between 2023 and 2024 marking the first annual decline since 2015. *S.* Montevideo was identified on 117 premises in 2024, of which 45 (38.5%) were repeatedly positive for the same serovar in subsequent flocks. Multiple incidents of *S.* Montevideo were observed on individual premises; 16.2% (19) of the 167 premises which had at least one positive flock for *S.* Montevideo had 2 incidents of this serovar in 2024. Up to 7 incidents of *S.* Montevideo were observed on 2 premises (1.7%), with 14.5% (17/117), 3.4% (4/117), 2.6% (3/117) and 0.9% (1/117) of premises having 3, 4, 5 and 6 incidents respectively.

Despite a 18.8% decrease compared to 2023 (421 flocks), *Salmonella* Kedougou was the second most frequently reported serovar in 2024 (342 flocks). This is similar to the level observed in 2020 (339 flocks) but remains higher than 2022 and 2021, where *S.* Kedougou was observed in 232 and 192 flocks, respectively (Table 3). *S*. Kedougou is associated with feed mill environments and can be found in ingredients such as oilseed meals. In 2024, *S.* Kedougou was identified on 93 premises, of which 49 (52.7%) were repeatedly positive for the same serovar in subsequent flocks.

Other notable increases in the number of broiler flocks testing positive in 2024 compared to 2023 include: *S*. Anatum (9 versus 4 flocks), *S*. Kentucky (17 versus 0 flocks), *S*. Muenchen (23 versus 5 flocks), *S*. Newport (20 versus 2 flocks).

Notable decreases in the number of flocks testing positive in 2024 compared to 2023 include *S*. Agona, often associated with feed contamination (135 versus 191 flocks), *S*. Derby, often associated with pigs and turkeys (9 versus 14 flocks), *S.* Give var 15+ (Newbrunswick) (0 versus 5 flocks), *S.* Infantis (19 versus 50 flocks), *S*. Livingstone (2 versus 11 flocks), *S*. Senftenberg (8 versus 17 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, but showed an increase in number of affected broiler flocks in recent years. It is one of the most frequently isolated serovars in broiler chickens across mainland Europe.

Salmonella Chester is rarely isolated as part of the NCP and was last isolated in chickens in 2019.

An estimated 43,802 broiler flocks were tested in Great Britain according to the requirements of the *Salmonella* NCP during 2024. Using this as the denominator population, the estimated prevalence of *Salmonella*-positive broiler flocks was 4.05% (1,775 of 43,802). This is a decrease compared to 5.33% in 2023 (highest prevalence since inception of NCP) and 4.28% in 2022 (Table 6.7, Figure 6.8).

The estimated Great Britain prevalence of regulated *Salmonella* serovars in broiler flocks in Great Britain during 2024 was 0.03% (14 of 43,802). This is slightly lower than in 2023 (0.04%) but the same as in 2022 and 2021 (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. Of the 14 broiler flocks that tested positive for regulated serovars, 9 were in Scotland and 5 were in England.

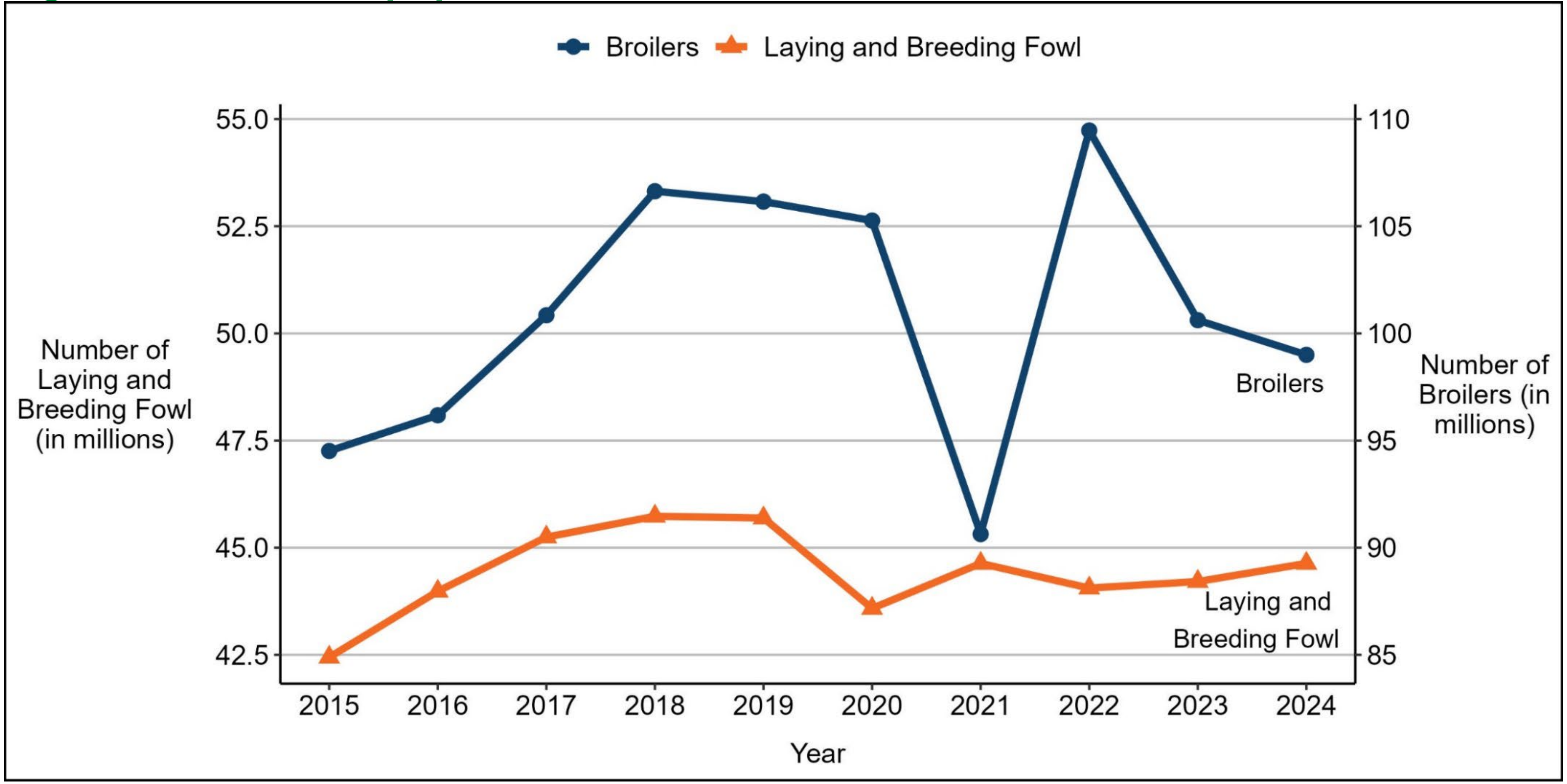
Antimicrobial susceptibility in chickens

A total of 1,523 *Salmonella* isolates from chickens were tested against a panel of 16 antimicrobials in 2024. The majority of isolates (78.6%) were fully susceptible, while 2.8% were classified as multidrug-resistant (MDR; resistant to 4 or more antimicrobials), showing no significant changes in resistance patterns between 2023 and 2024.

Resistance remained low across most antibiotic classes and often involved the sulphamethoxazole and trimethoprim combination (11.7%) and sulphonamides (15.5%). The main resistant serovars were *S.* Kedougou (n=158), *S.* Ohio (n=35), and *S.* Idikan (n=28).

Resistance to “highest priority critically important antibiotics” (HP-CIAs) remained low in 2024. Ciprofloxacin resistance was identified in 7 isolates (4 *S.* Infantis, 2 *S.* Idikan, one *S.* Agona), which were all also resistant to nalidixic acid. Four *S*. Infantis isolates were multidrug-resistant (MDR), all showing co-resistance to fluoroquinolones (ciprofloxacin) and aminoglycosides (streptomycin and neomycin). One MDR *S.* Agona isolate exhibited resistance to fluoroquinolones (ciprofloxacin) and third generation cephalosporins (cefotaxime and ceftazidime).

Figure 6.1: Chicken population in Great Britain 2015 to 2024



A line graph showing the cattle population and number of commercial holdings from 2015 to 2024. The figure shows that the number of broiler, laying and breeding fowl in Great Britain increased steadily from 2015 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 has declined to slightly below 100 million in 2024.

Source: June 2023 Agricultural census.

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)

Salmonella serovar	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
Agama	4	4	1	1	1	1	2	3	1	1
Agona	73	101	33	34	117	128	191	200	135	136
Ajiobo	0	0	0	0	0	0	1	1	0	0
Amsterdam	0	0	0	0	0	0	1	1	0	0
Anatum	6	8	4	5	2	3	5	5	10	10
Bareilly	0	0	1	1	0	0	0	0	0	0
Bardo	1	13	5	10	3	5	0	0	0	0
Berta	0	0	0	0	1	1	0	0	1	1
Bovismorbificans	16	21	7	21	0	0	1	1	0	0
Braenderup	1	1	2	2	2	2	5	5	2	2
Bredeney	1	1	0	0	0	0	0	0	1	1
Chester	0	0	0	0	0	0	0	0	2	2
Chomedey	0	0	0	0	0	0	1	1	0	0
Coeln	2	3	0	0	4	4	4	4	1	1
Corvallis	0	0	0	0	2	3	0	0	1	1
Cubana	0	0	0	0	0	0	1	1	0	0
Derby	4	4	8	9	11	12	14	14	9	9
Dublin	0	0	0	0	4	4	1	1	0	0
Durham	0	0	0	0	0	0	1	1	0	0
Eboko	0	0	0	0	1	1	0	0	0	0
Enteritidis	12	31	5	9	6	23	8	9	11	12

Salmonella serovar	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
Essen	0	0	0	1	0	0	0	0	0	0
Ferruch	0	0	2	2	0	0	0	0	0	0
Fresno	0	0	0	0	0	0	1	1	0	0
Give	2	3	0	0	0	0	4	4	0	0
Give var. 15$^+$	4	4	6	16	8	8	5	5	0	0
Goldcoast	0	0	1	1	0	0	0	0	0	0
Havana	1	1	2	2	5	6	0	0	1	1
Idikan (incl monophasic)	605	724	258	284	347	388	610	681	630	679
Indiana	2	3	0	0	1	1	5	5	6	7
Infantis	0	1	24	42	81	98	54	62	19	20
Isangi	0	0	1	3	0	0	0	0	0	0
Kedougou	342	430	192	217	233	277	421	537	344	382
Kentucky	0	1	0	0	4	4	1	1	17	18
Kingston	2	2	0	0	2	2	1	1	1	1
Kottbus	2	5	0	0	1	1	0	0	4	4
Lexington	0	0	1	1	0	0	0	0	0	0
Liverpool	1	2	0	0	1	1	0	0	0	0
Livingstone	9	11	4	17	2	3	12	14	3	6
London	0	0	1	1	2	2	0	0	0	0
Mbandaka	232	261	240	294	586	695	273	305	160	168
Mikawasima	1	1	0	0	0	0	0	0	0	0
Minnesota	0	0	0	1	0	0	0	0	0	0
Molade	0	0	1	1	0	0	0	0	0	0

Salmonella serovar	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
Montevideo	246	262	332	403	411	460	547	591	286	308
Monophasic Typhimurium	1	13	9	12	10	19	5	6	0	1
Muenchen	6	8	4	4	9	9	5	5	23	27
Muenster	0	0	0	0	0	0	1	2	0	0
Newport	13	52	10	37	10	12	4	4	24	26
Nottingham	0	0	0	7	2	4	0	0	1	1
Odozi	0	0	2	4	0	0	0	0	0	0
Ohio	33	33	54	55	44	49	35	36	41	44
Orion	0	0	0	0	1	1	0	0	0	0
Orion var. 15$^+$	28	30	33	34	55	60	57	61	50	50
Oslo	2	2	2	2	0	0	1	1	2	2
Oxford	0	0	0	0	0	0	1	1	0	0
Panama	0	0	1	1	1	2	0	0	1	1
Poona	1	1	0	0	0	0	1	1	1	1
Ramatgan	1	1	0	0	0	0	0	0	0	0
Reading	1	1	1	1	0	1	0	0	0	0
Rissen	0	0	0	0	1	1	0	0	0	0
Schwarzengrund	1	1	0	0	0	0	0	0	0	0
Senftenberg	53	96	29	63	19	37	17	22	10	10
Stanley	0	0	0	0	1	1	0	0	0	0
Stanleyville	1	1	0	0	0	1	0	0	0	0
Stourbridge	1	1	2	2	1	1	0	0	0	0
Takoradi	0	0	0	0	0	1	0	0	0	0

***Salmonella* serovar**	**2020 flocks**	**2020 isolations**	**2021 flocks**	**2021 isolations**	**2022 flocks**	**2022 isolations**	**2023 flocks**	**2023 isolations**	**2024 flocks**	**2024 isolations**
Tennessee	0	1	0	0	0	1	0	0	0	0
Typhimurium	6	19	10	15	11	18	13	21	16	17
Wangata	0	0	0	0	0	0	0	1	0	0
Yoruba	0	0	0	0	0	0	1	2	0	0
61:k:1,5,(7)	0	0	0	0	0	0	1	2	7	8
untypable strains	38	37	27	28	32	35	11	13	3	3
rough strains	1	26	1	27	0	18	0	1	0	0
Total	**1727**	**2221**	**1302**	**1670**	**2019**	**2404**	**2309**	**2633**	**1818**	**1961**

27 flocks were positive for more than one serovar in 2020.

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

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

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

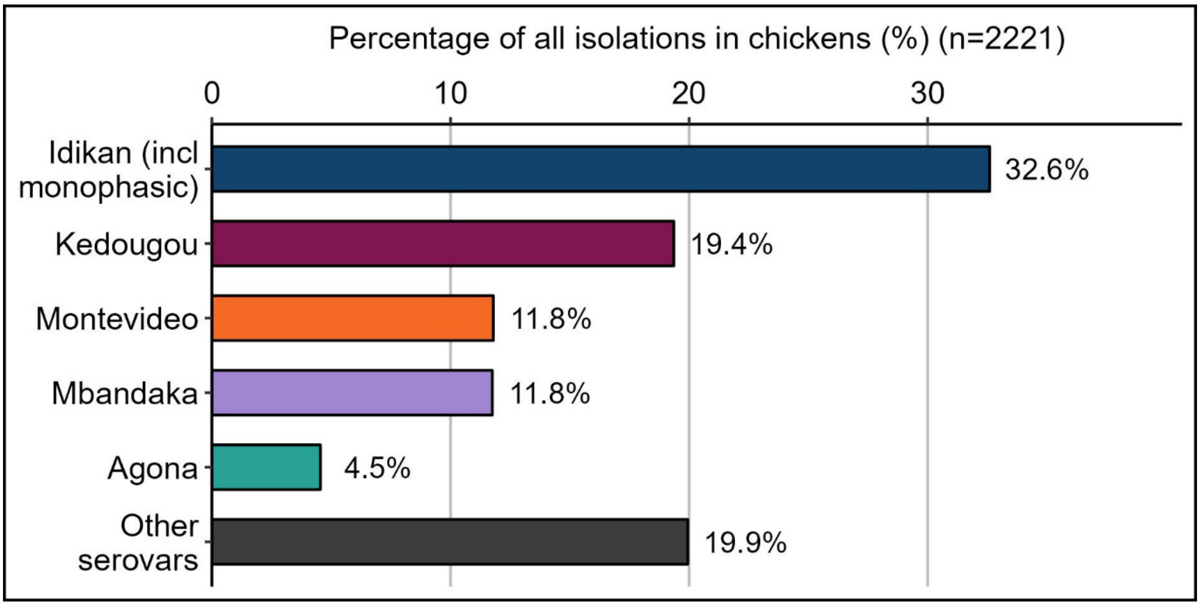
6 flocks were positive for more than one serovar in 2024.

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

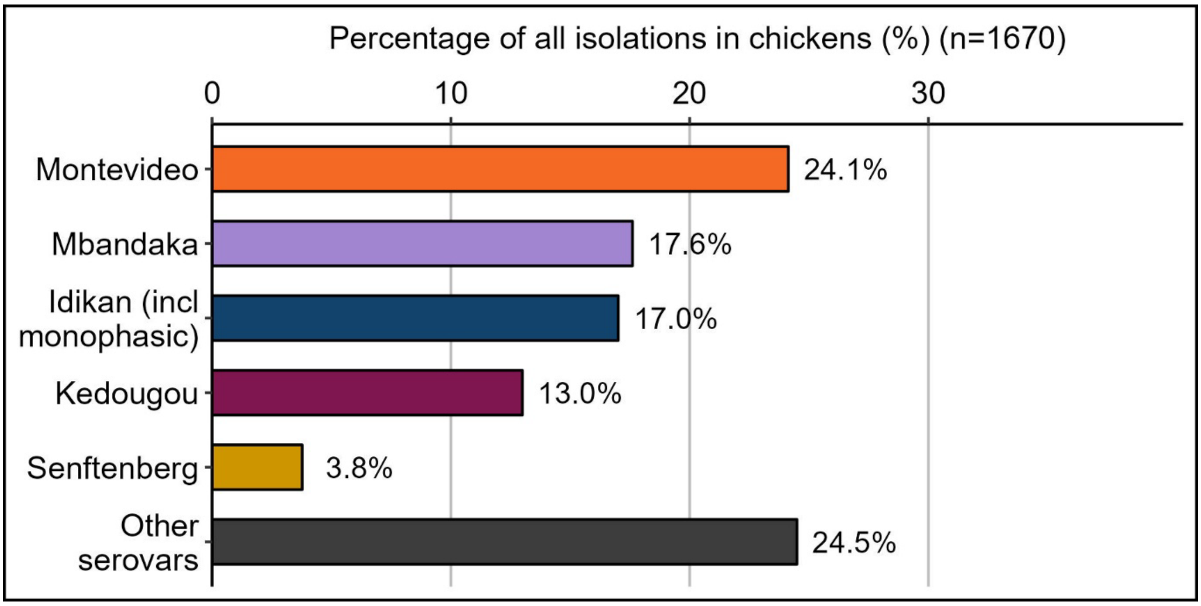
Figure 6.2: Isolations of the most common serovars in chickens in Great Britain 2020 to 2024 (statutory and non-statutory testing)

Figure 6.2.1: Isolations in chickens in 2020



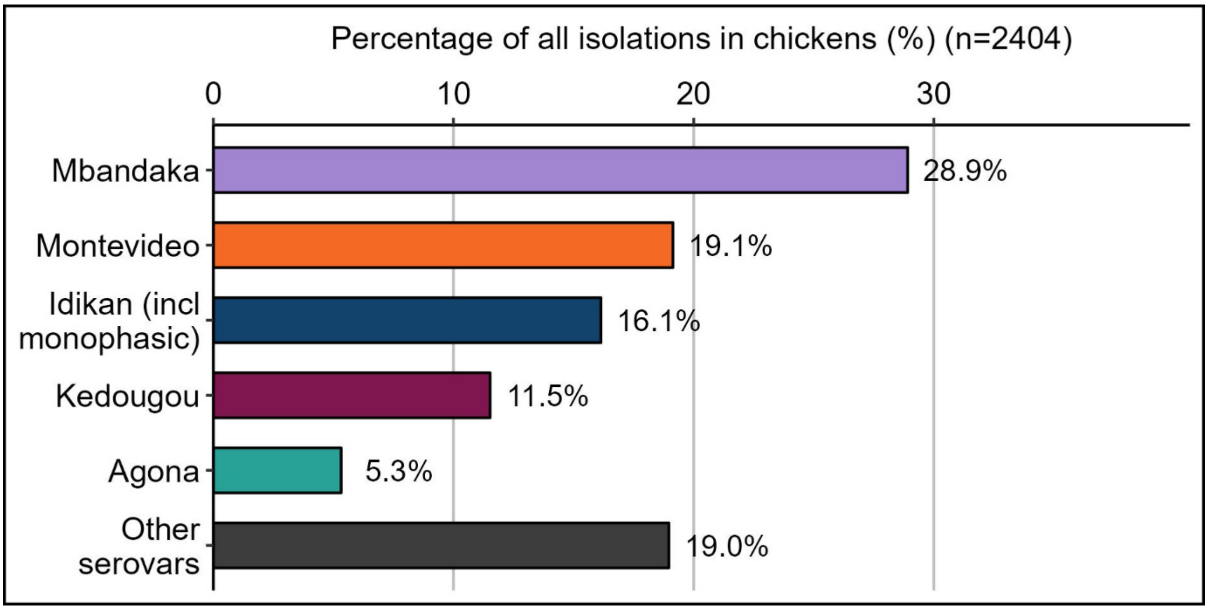
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in chickens in 2020. The most common *Salmonella* serovar in chickens in 2020 was *S.* Idikan (including monophasic variants), accounting for 32.6% of total isolations, followed by *S.* Kedougou (19.4%), *S.* Montevideo (11.8%) and *S.* Mbandaka (11.8%).

Figure 6.2.2: Isolations in chickens in 2021



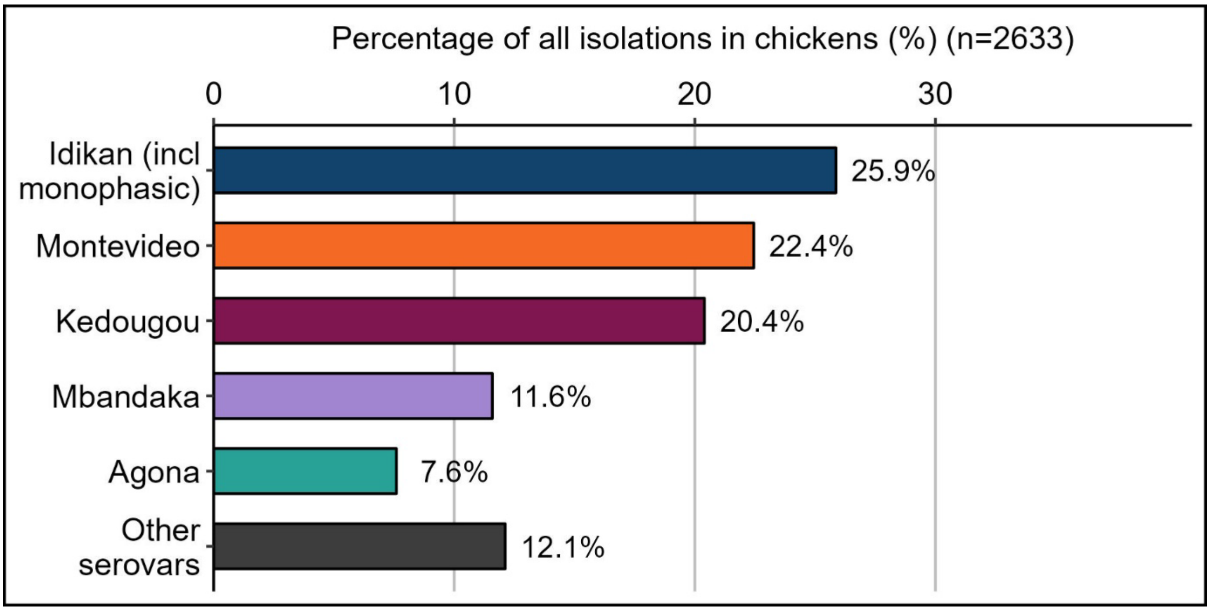
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in chickens in 2021. The most common *Salmonella* serovar in chickens in 2021 was *S.* Montevideo, accounting for 24.1% of total isolations, followed by *S.* Mbandaka (17.6%), *S*. Idikan (including monophasic variants) (17.0%)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

Figure 6.2.3: Isolations in chickens in 2022



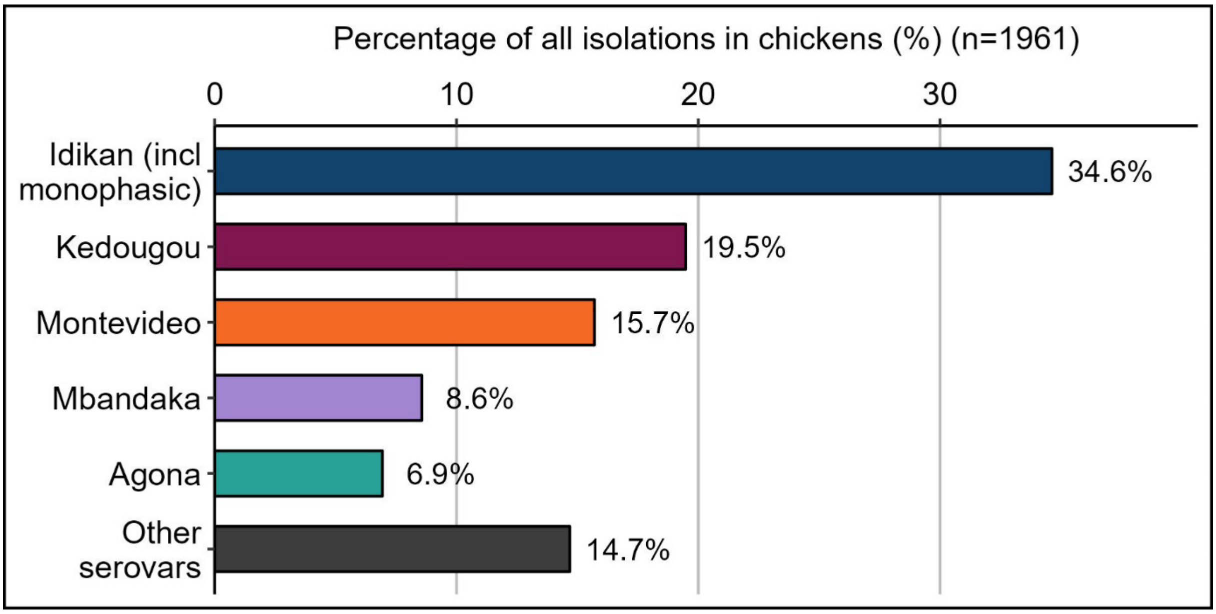
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in chickens in 2022. The most common *Salmonella* serovar in chickens in 2022 was *S.* Mbandaka accounting for 28.9% of total isolations, followed by *S.* Montevideo (19.1%), *S*. Idikan (including monophasic variants) (16.1%)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

Figure 6.2.4: Isolations in chickens in 2023



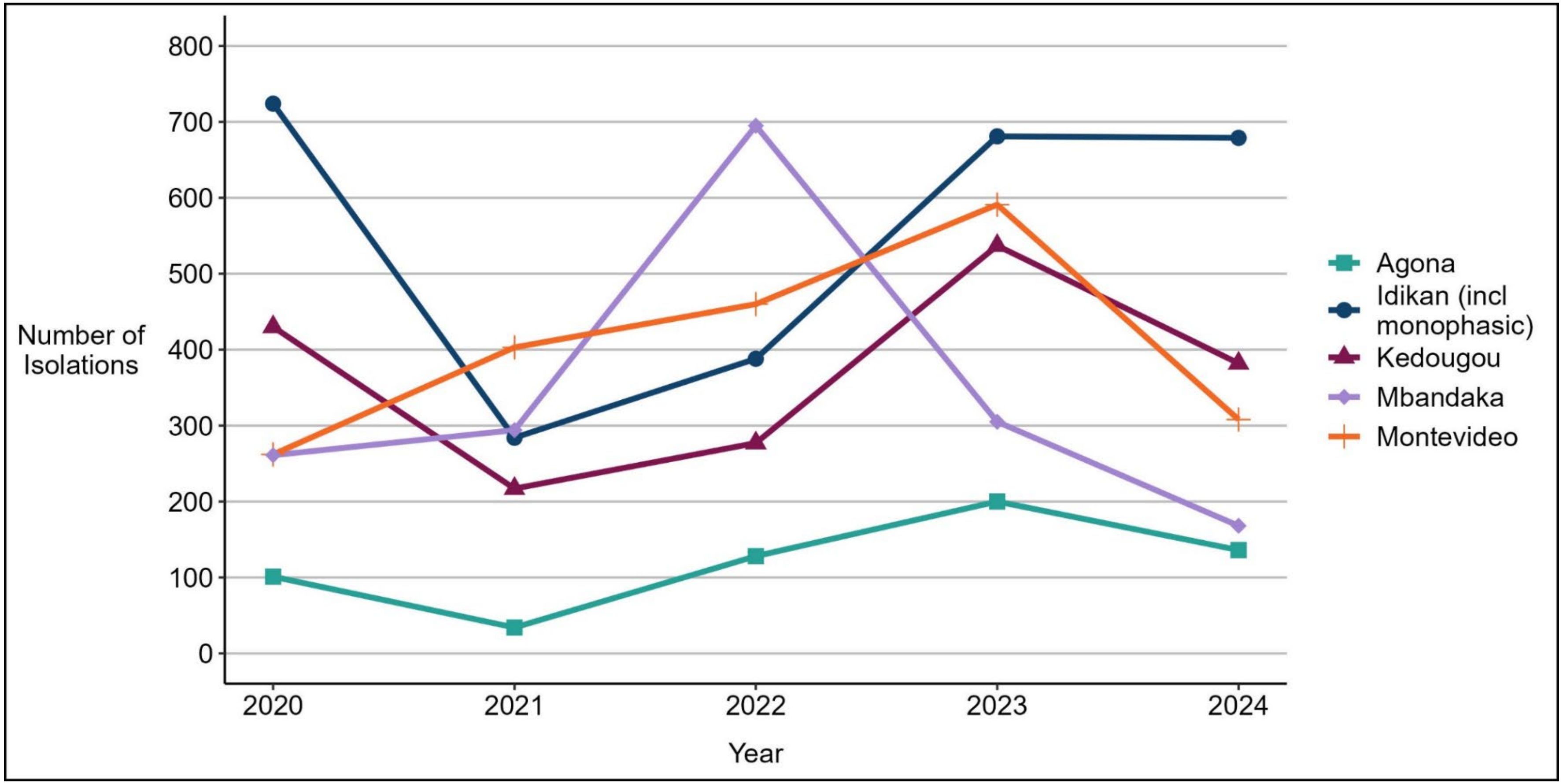
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in chickens in 2023. The most common *Salmonella* serovar in chickens in 2023 was *S.* Idikan (including monophasic variants), accounting for 25.9% of total isolations, followed by *S.* Montevideo (22.4%), *S*. Kedougou (20.4%) and *S.* Mbandaka (11.6%).

Figure 6.2.5: Isolations in chickens in 2024



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

Figure 6.3: The 5 most common *Salmonella* serovars in chickens in Great Britain in 2024 and their trends over time since 2020



A line graph showing the 5 most common serovars in chickens from 2020 to 2024. The figure illustrates that in 2020 *S.* Idikan (including monophasic variants) was the most common serovar isolated from chickens and while it fell to the third most common serovar in 2022

(343 isolations) it increased in 2023 (681 isolations). In 2024 isolations were consistent with the previous year with 679 isolations. *S.* Mbandaka, which has typically been second or third most common dropped to fourth most frequently isolated serovar in 2023 with 305 isolations and remains the fourth most common in 2024 (168 isolations). *S.* Kedougou isolations fluctuate, and it was third most common in 2023 (537 isolations). Despite less isolations in 2024 than in 2023, this year *S*. Kedougou was the second most common serovar isolated. *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 making it the third most common serovar. *S.* Agona remains the fifth most commonly isolated with 136 isolations in 2024.

Table 6.2: *S.* Typhimurium in chickens on all premises in Great Britain

Phage type	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
DT1	0	0	1	2	1	2	1	1	3	3
DT2	3	9	3	4	0	0	0	0	1	1
DT75	0	0	0	0	5	8	2	6	7	7
DT99	0	0	0	0	1	1	4	4	1	1
DT104	0	0	2	2	0	0	0	0	1	1
DT105	0	0	0	0	0	0	4	6	2	3
DT116	0	0	0	1	0	0	0	0	0	0
DT193	2	6	1	1	0	0	0	1	1	1
U308	0	2	0	0	0	0	0	0	0	0
U320	0	0	1	1	0	0	0	0	0	0
NOPT	0	0	0	0	0	0	0	1	0	0
RDNC	1	2	4	4	4	7	2	2	0	0
Total	**6**	**19**	**10**	**15**	**11**	**18**	**13**	**21**	**16**	**17**

In 2021 one flock tested positive for U320, DT193 and RDNC but is included only once in the total.

In 2023 one flock tested positive for *S*. Typhimurium DT193 but was subsequently over-turned via official confirmatory sampling. This is included as an isolation but does not contribute to the numbers of flocks.

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

Table 6.3: Isolations of monophasic *Salmonella* Typhimurium phage types in chickens in Great Britain 2020 to 2024

Phage type	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
DT120	0	0	0	0	0	1	0	0	0	0
DT193	1	12	9	12	10	18	5	6	0	1
RDNC	0	1	0	0	0	0	0	0	0	0
Total	**1**	**13**	**9**	**12**	**10**	**19**	**5**	**6**	**0**	**1**

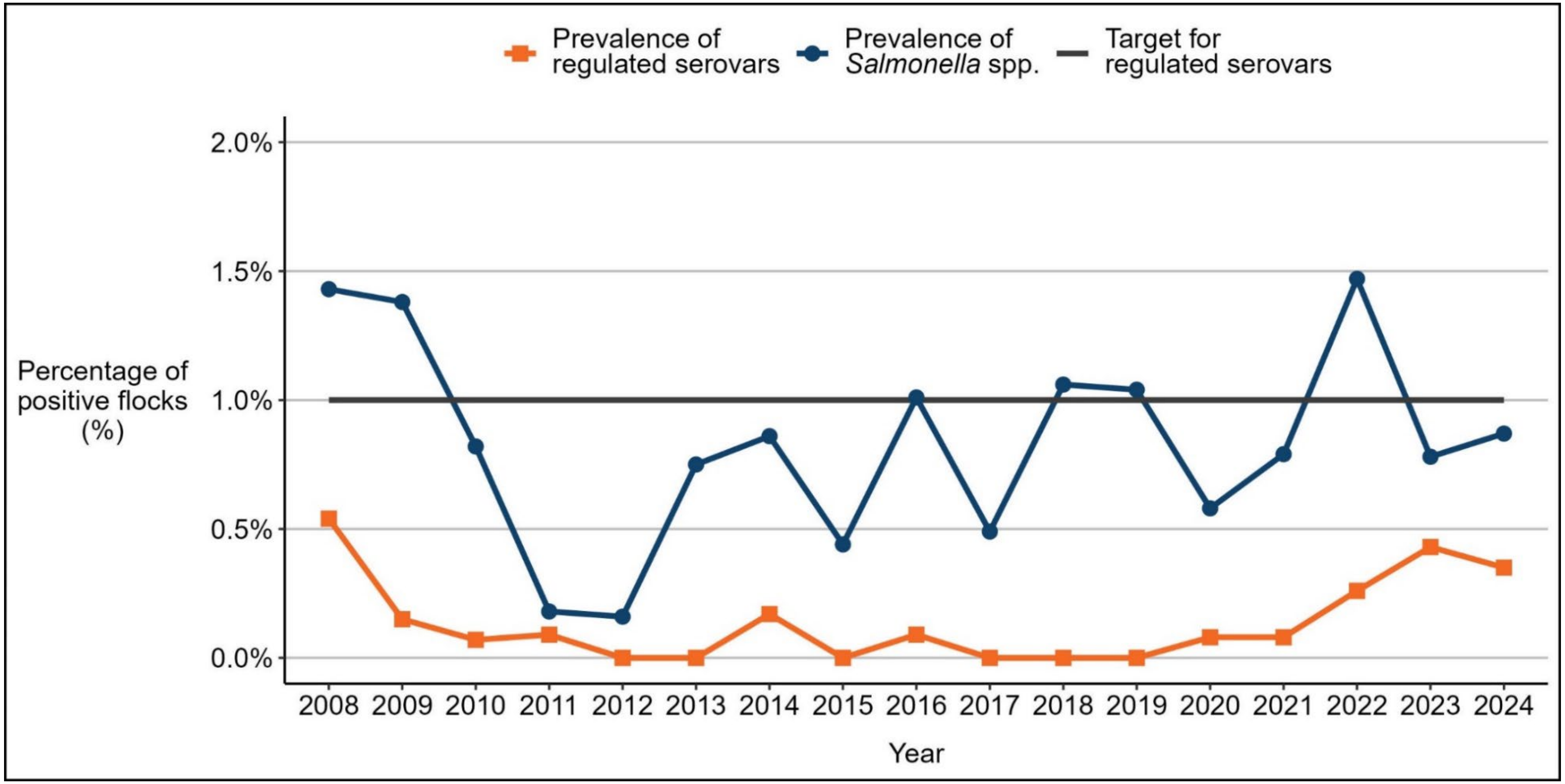
This data includes flocks from statutory testing and isolations from both statutory and non-statutory testing.

Table 6.4: *S*. Enteritidis in chickens on all premises in Great Britain

Phage type	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
PT4	0	2	3	3	0	0	2	2	1	1
PT8	9	22	0	2	3	19	6	7	5	5
PT8a	0	0	1	1	0	0	0	0	0	0
PT9b	0	0	0	1	0	0	0	0	0	0
PT11	0	0	0	0	1	1	0	0	0	0
PT13	3	5	0	0	0	0	0	0	0	0
PT13a	0	0	0	1	0	0	0	0	2	2
PT14b	0	0	0	0	1	1	0	0	0	0
PT20	0	0	1	1	1	1	0	0	0	0
PT30	0	0	0	0	0	0	0	0	1	2
NOPT	0	0	0	0	0	1	0	0	2	2
UNTY	1	2	0	0	0	0	0	0	0	0
Total	**12**	**31**	**5**	**9**	**6**	**23**	**8**	**9**	**11**	**12**

In 2020, one flock tested positive for both PT8 and PT13a but is included only once in the total.

Figure 6.4: Prevalence of *Salmonella* in breeding chicken flocks tested under NCP in Great Britain 2008 to 2024



A line graph showing the prevalence of *Salmonella* in chicken breeding flocks tested under the NCP from 2008 to 2024. 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 2020 to 2024

The following table shows the number of chicken breeding flocks reported positive with each *Salmonella* serovar from 2020 to 2024 and serovar rank in that year.

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Typhimurium	2	1	0	0	2	2	1	4	1	4
Idikan (incl monophasic)	1	2	2	1	4	6	2	3	2	2
Livingstone	0	0	0	0	0	0	0	0	3	1
Mbandaka	2	1	2	1	3	1	0	0	3	1
Senftenberg	0	0	0	0	0	0	0	0	3	1
61:k:1,5,(7)	0	0	0	0	0	0	0	0	3	1
Agona	0	0	0	0	2	2	0	0	0	0
Anatum	0	0	0	0	3	1	3	1	0	0
Bardo	2	1	0	0	0	0	0	0	0	0
Corvallis	0	0	0	0	3	1	0	0	0	0
Give var. 15^{+}	0	0	1	5	2	2	0	0	0	0
Infantis	0	0	2	1	3	1	3	1	0	0
Kedougou	1	2	0	0	0	0	0	0	0	0
London	0	0	2	1	0	0	0	0	0	0
Newport	2	1	2	1	0	0	0	0	0	0
Ohio	0	0	0	0	3	1	0	0	0	0
Orion var. 15^{+}	0	0	0	0	3	1	0	0	0	0
6,8:e,h:-	2	1	0	0	0	0	0	0	0	0

For details of chicken breeding flocks reported positive in 2014 to 2019, see the 2019 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
2020	0.58%	0.08%
2021	0.79%	0.08%
2022	1.47%	0.26%
2023	0.78%	0.43%
2024	0.87%	0.35%

Flocks testing positive for more than one serovar

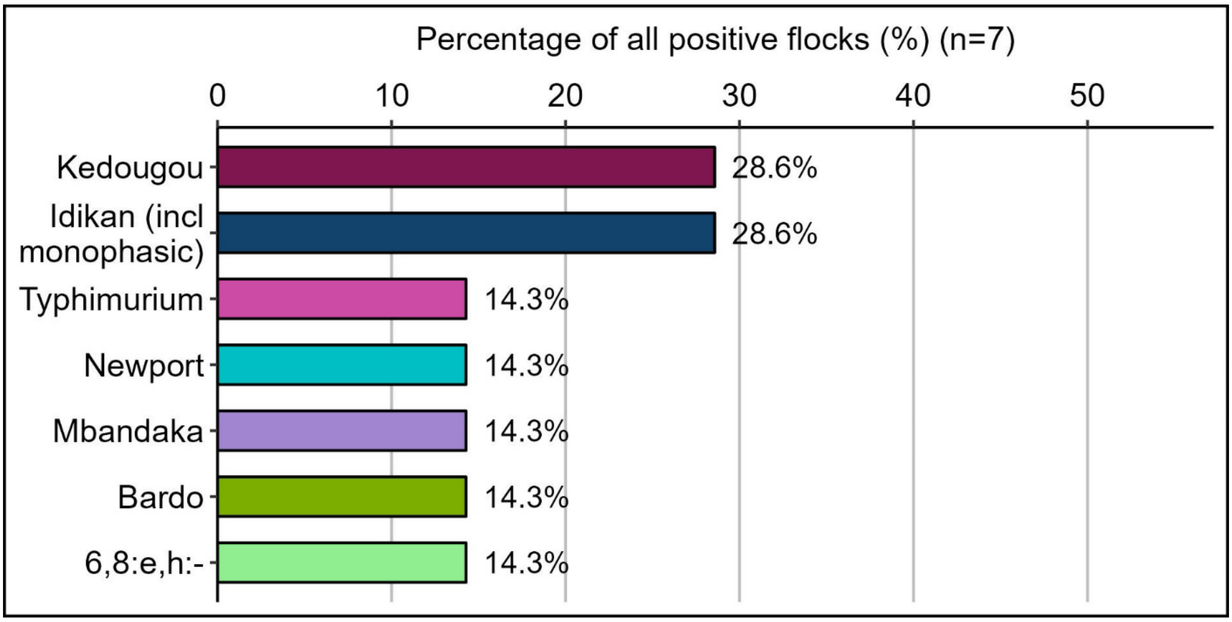
Some flocks tested positive for more than one serovar. Each flock was counted only once in the overall figure to calculate prevalence.

In 2020 one flock tested positive for *S*. Bardo, *S*. Newport and *S*. 6,8:e,h:-.

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

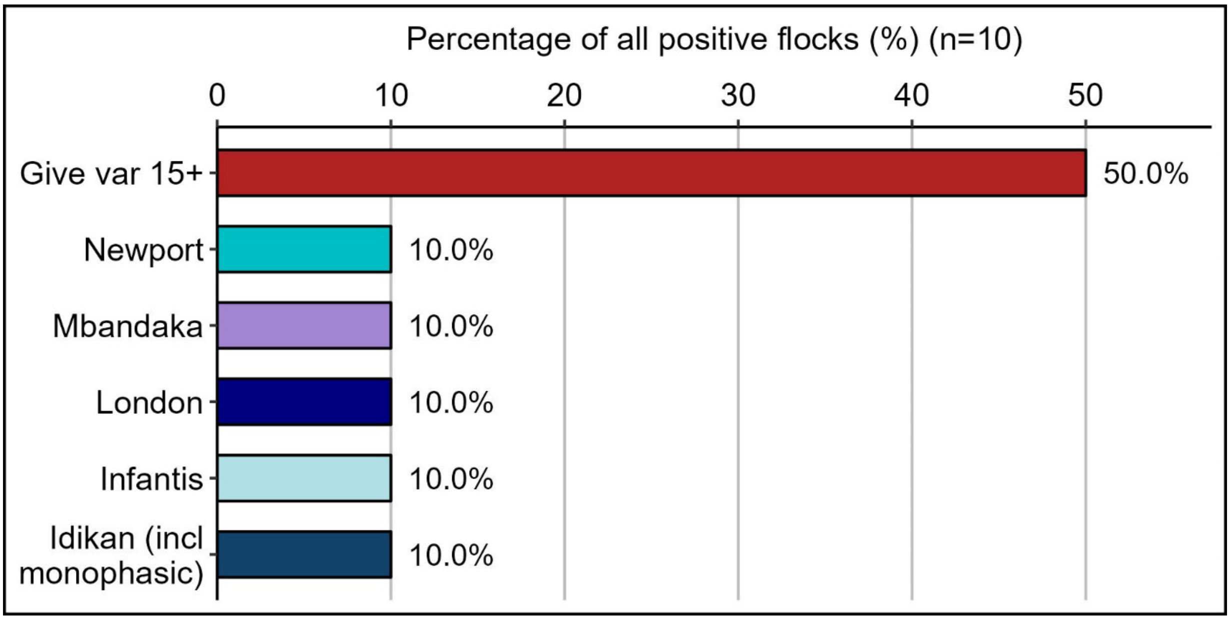
Figure 6.5: Serovars identified in adult chicken breeding flocks in Great Britain 2020 to 2024 reported from NCP testing

Figure 6.5.1: Isolations in adult breeding chickens in 2020



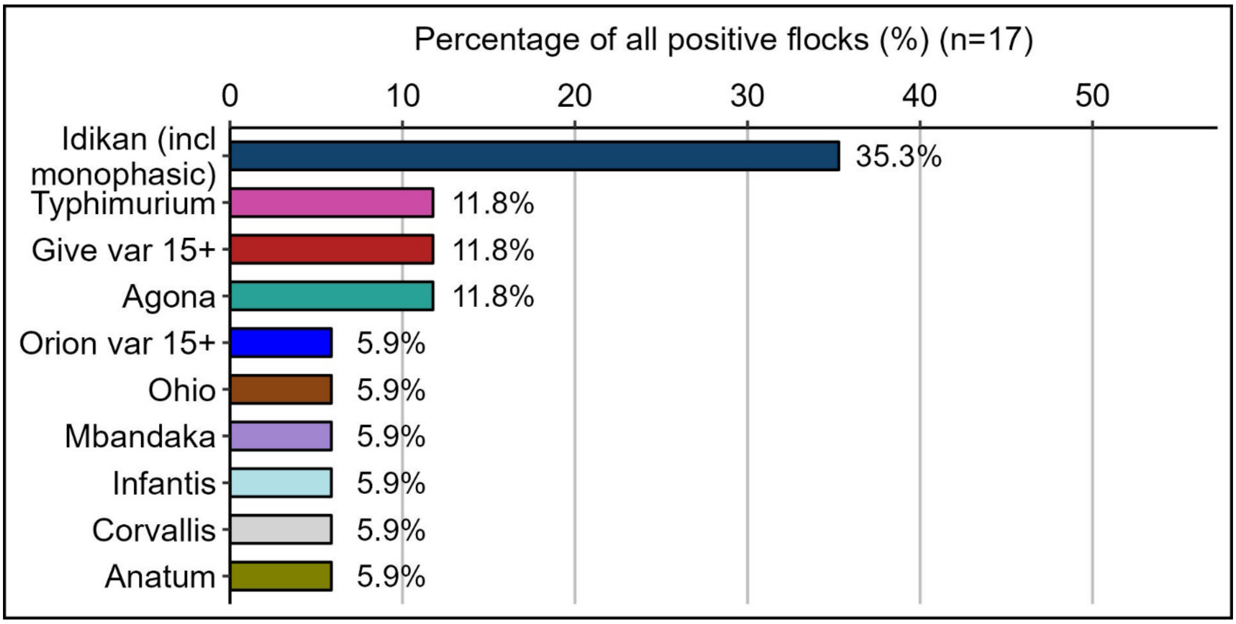
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding chickens in 2020. In 2020, the most common *Salmonella* serovars in all positive flocks were *S.* Kedougou and *S.* Idikan (including monophasic variants), each accounting for 28.6% of total positive breeding flocks. This was followed by *S.* Bardo, *S.* Mbandaka, *S.* Newport, *S*. Typhimurium and *Salmonella* 6,8:e,h:-, each accounting for 14.3% of total positive breeding flocks.

Figure 6.5.2: Isolations in adult breeding chickens in 2021



Horizontal bar graph showing the percentage of *Salmonella* isolations 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 isolations. Each of the other 5 serovars recorded, accounted for 10.0% of total isolations.

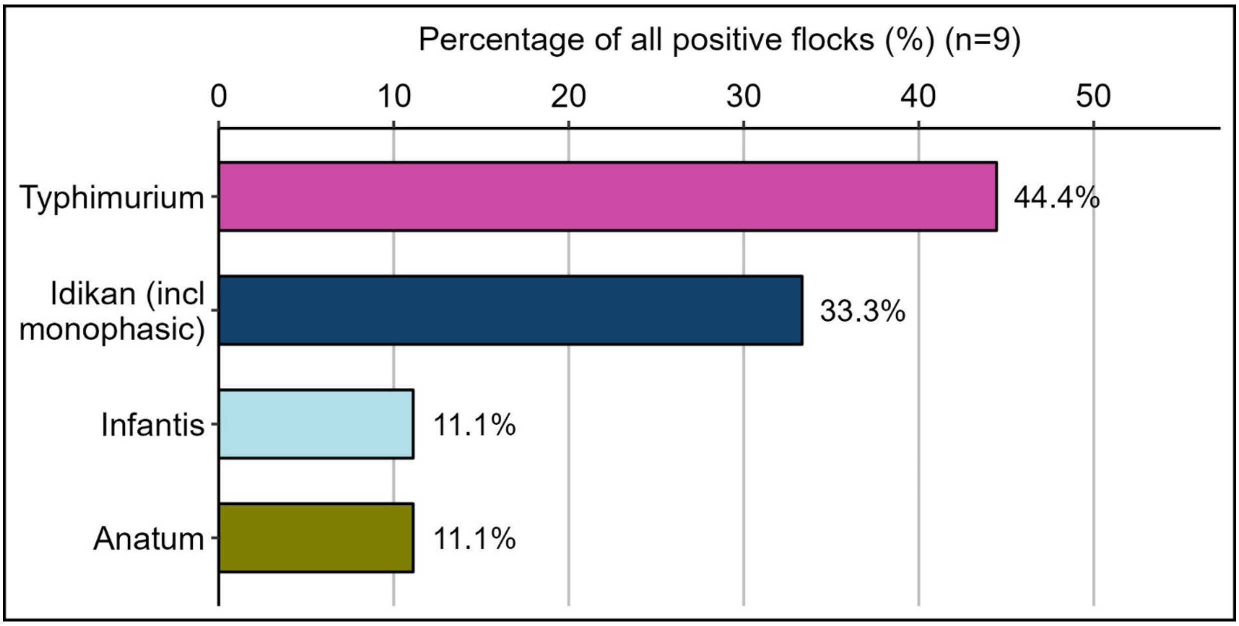
Figure 6.5.3: Isolations in adult breeding chickens in 2022



Horizontal bar graph showing the percentage of *Salmonella* isolations 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 29.4% 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 41.3%.

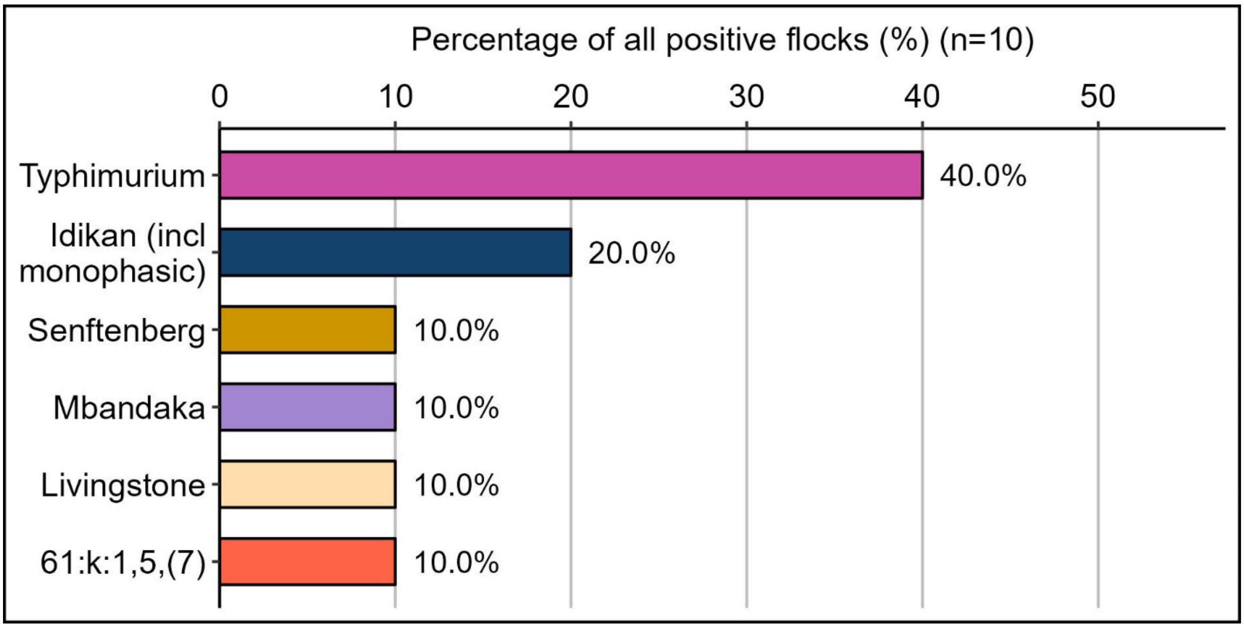
In 2022 one flock tested positive for 2 serovars plotted (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

Figure 6.5.4: Isolations in adult breeding chickens in 2023



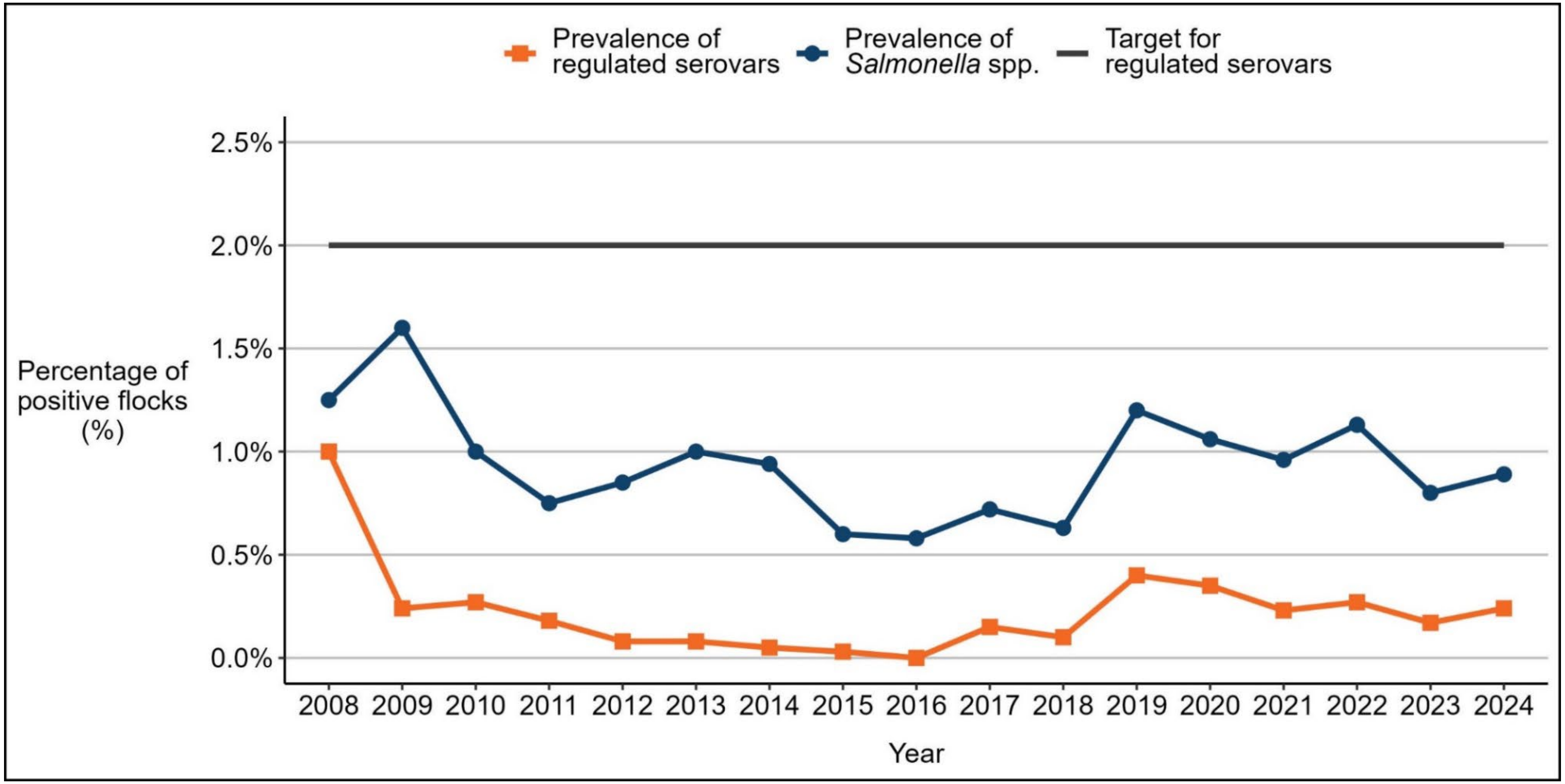
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding chickens in 2023. In 2023, the most common *Salmonella* serovar in all positive flocks was *S.* Typhimurium, accounting for 44.4% of total isolations, followed by *S.* Idikan (including monophasic variants) (33.3%),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

Figure 6.5.5: Isolations in adult breeding chickens in 2024



Horizontal bar graph showing the percentage of *Salmonella* isolations 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 isolations, 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 6.6: Prevalence of *Salmonella* in laying hen flocks tested under NCP in Great Britain 2008 to 2024



A line graph showing the prevalence of *Salmonella* in chicken laying flocks tested under the NCP from 2008 to 2024. 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 2020 to 2024

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Typhimurium	3	4	2	6	2	5	2	2	1	7
61:k:1,5,(7)	0	0	0	0	0	0	0	0	2	6
Newport	4	2	1	7	4	3	2	2	3	4
Enteritidis	1	11	4	3	2	5	1	3	4	2
Kedougou	5	1	0	0	6	1	0	0	4	2
Mbandaka	0	0	6	1	1	6	3	1	4	2
Agama	4	2	6	1	6	1	3	1	5	1
Anatum	5	1	6	1	0	0	0	0	5	1
Chester	0	0	0	0	0	0	0	0	5	1
Corvallis	0	0	0	0	0	0	0	0	5	1
Havana	0	0	6	1	0	0	0	0	5	1
Indiana	0	0	0	0	6	1	3	1	5	1
Kottbus	5	1	0	0	0	0	0	0	5	1
Montevideo	5	1	5	2	5	2	2	2	5	1
Oslo	5	1	6	1	0	0	0	0	5	1
Senftenberg	0	0	0	0	6	1	0	0	5	1
Agona	2	6	0	0	6	1	0	0	0	0
Amsterdam	0	0	0	0	0	0	3	1	0	0
Bardo	0	0	3	5	4	3	0	0	0	0
Bareilly	0	0	6	1	0	0	0	0	0	0
Bovismorbificans	4	2	4	3	0	0	0	0	0	0
Bredeney	5	1	0	0	0	0	0	0	0	0
Coeln	5	1	0	0	0	0	3	1	0	0

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Cubana	0	0	0	0	0	0	3	1	0	0
Derby	5	1	6	1	3	4	0	0	0	0
Dublin	0	0	0	0	3	4	3	1	0	0
Give	0	0	0	0	0	0	1	3	0	0
Idikan (incl. monophasic)	4	2	0	0	0	0	0	0	0	0
Infantis	0	0	6	1	4	3	1	3	0	0
Isangi	0	0	6	1	0	0	0	0	0	0
Kentucky	0	0	0	0	6	1	3	1	0	0
Kingston	5	1	0	0	0	0	3	1	0	0
Lexington	0	0	6	1	0	0	0	0	0	0
Liverpool	5	1	0	0	0	0	0	0	0	0
Livingstone	4	2	0	0	6	1	3	1	0	0
Molade	0	0	6	1	0	0	0	0	0	0
Monophasic Typhimurium	0	0	0	0	0	0	3	1	0	0
O rough:z_{38}:-	0	0	6	1	0	0	0	0	0	0
Odozi	0	0	5	2	0	0	0	0	0	0
Orion	0	0	0	0	0	0	3	1	0	0
Ramatgam	5	1	0	0	0	0	0	0	0	0
Reading	5	1	0	0	0	0	0	0	0	0
Schwarzengrund	5	1	0	0	0	0	0	0	0	0
Stanleyville	5	1	0	0	0	0	0	0	0	0
Stourbridge	0	0	6	1	6	1	0	0	0	0
Yoruba	0	0	0	0	0	0	3	1	0	0
4,12:b:-	0	0	0	0	0	0	3	1	0	0
6,7:-:enz$_{15}$	0	0	6	1	0	0	0	0	0	0

For details of laying flocks reported positive in 2014 to 2019, see the 2019 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
2020	1.06%	0.35%
2021	0.96%	0.23%
2022	1.13%	0.27%
2023	0.80%	0.17%
2024	0.89%	0.24%

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 2020 1 flock tested positive for both *S*. Enteritidis and *S*. Agama and 1 flock tested positive for *S*. Enteritidis, *S.* Typhimurium and *S*. Bovismorbificans.

In 2021 3 flocks tested positive for *S*. Newport and *S*. Bardo and 1 flock that tested positive for *S*. Derby and *S*. Oslo.

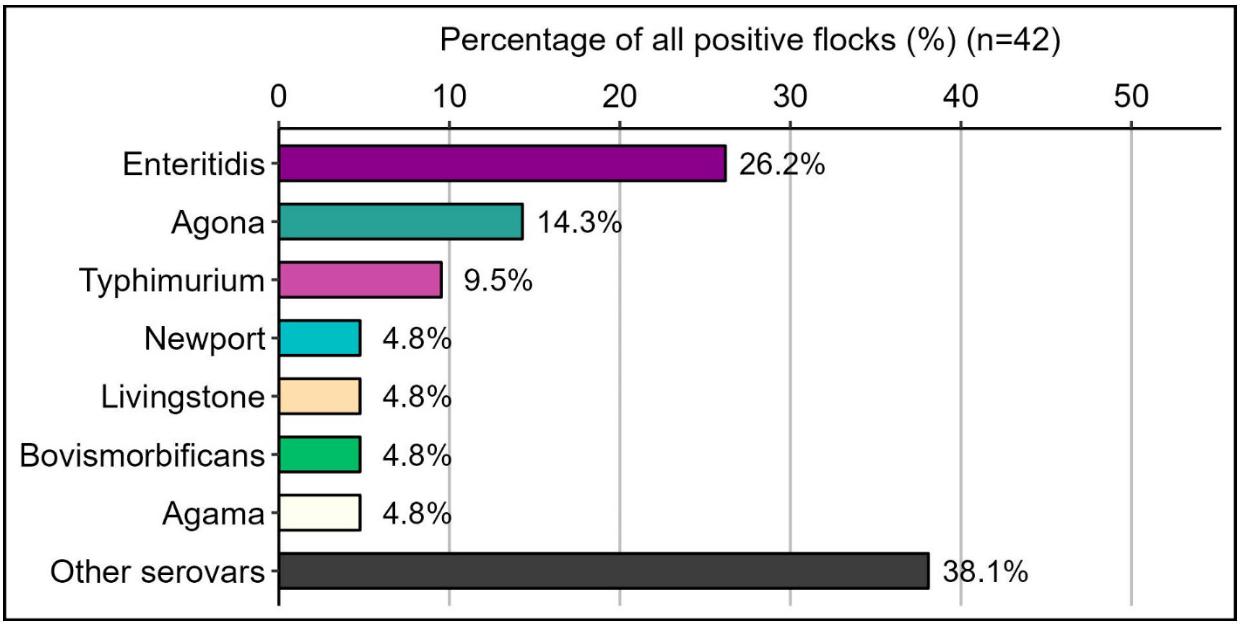
In 2022 1 flock tested positive for *S*. Bardo and *S*. Newport.

In 2023 no flocks tested positive for 2 different serovars.

In 2024 no flocks tested positive for 2 different serovars.

Figure 6.7: Serovars identified in adult laying hen flocks in Great Britain 2020 to 2024 reported from NCP testing

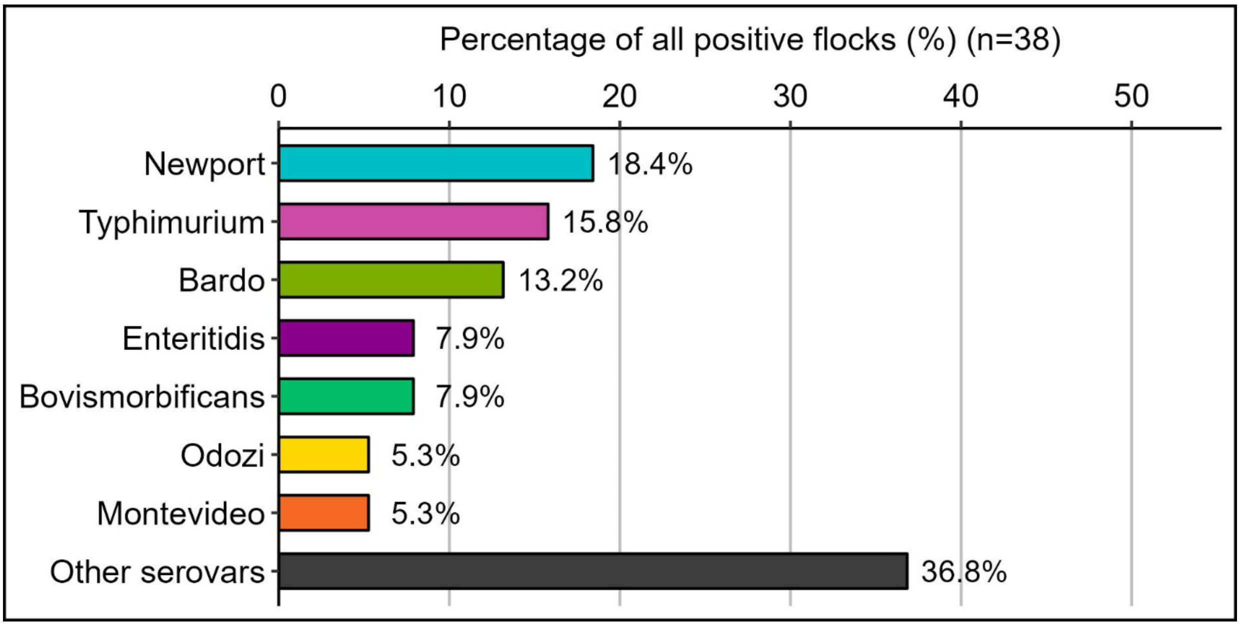
Figure 6.7.1: Isolations in adult laying chickens in 2020



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult laying chickens in 2020. In 2020 the most common *Salmonella* serovar in adult laying hen flocks was *S.* Enteritidis accounting for 26.2% of total isolations, followed by *S.* Agona (14.3%) and *S.* Typhimurium (9.5%).

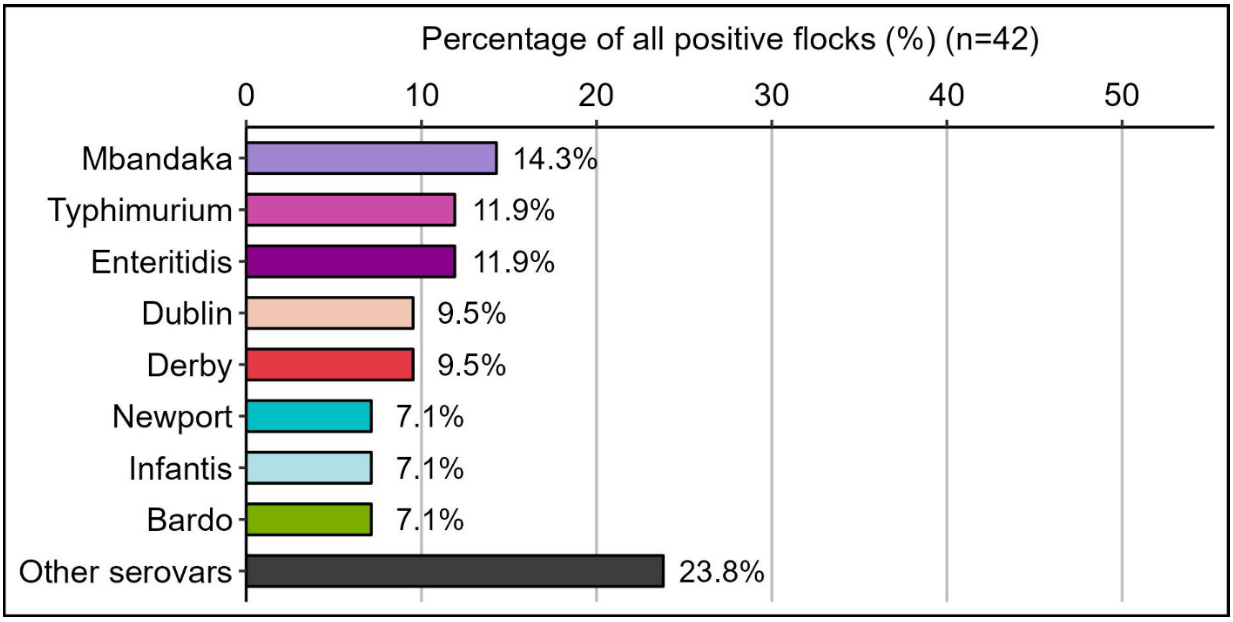
In 2020 4 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

Figure 6.7.2: Isolations in adult laying chickens in 2021



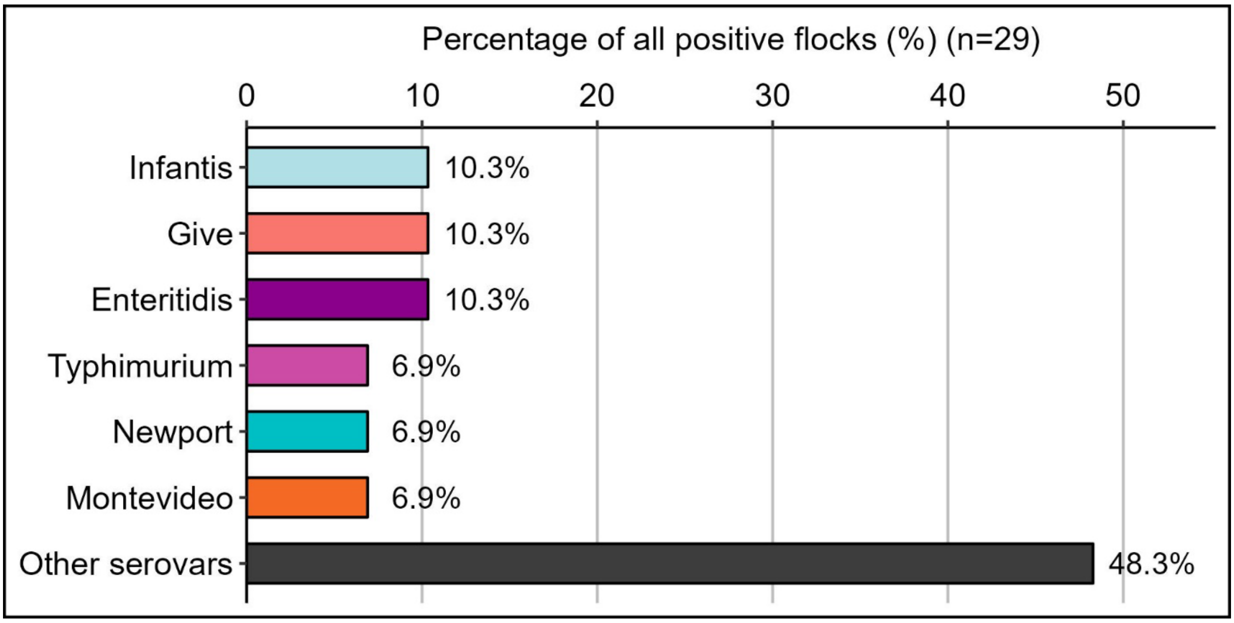
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult laying chickens in 2021. In 2021 the most common *Salmonella* serovar in adult laying hen flocks was S. Newport accounting for 18.4% of total positive flocks, followed by S. Typhimurium (15.8%) and S. Bardo (13.2%).

Figure 6.7.3: Isolations in adult laying chickens in 2022



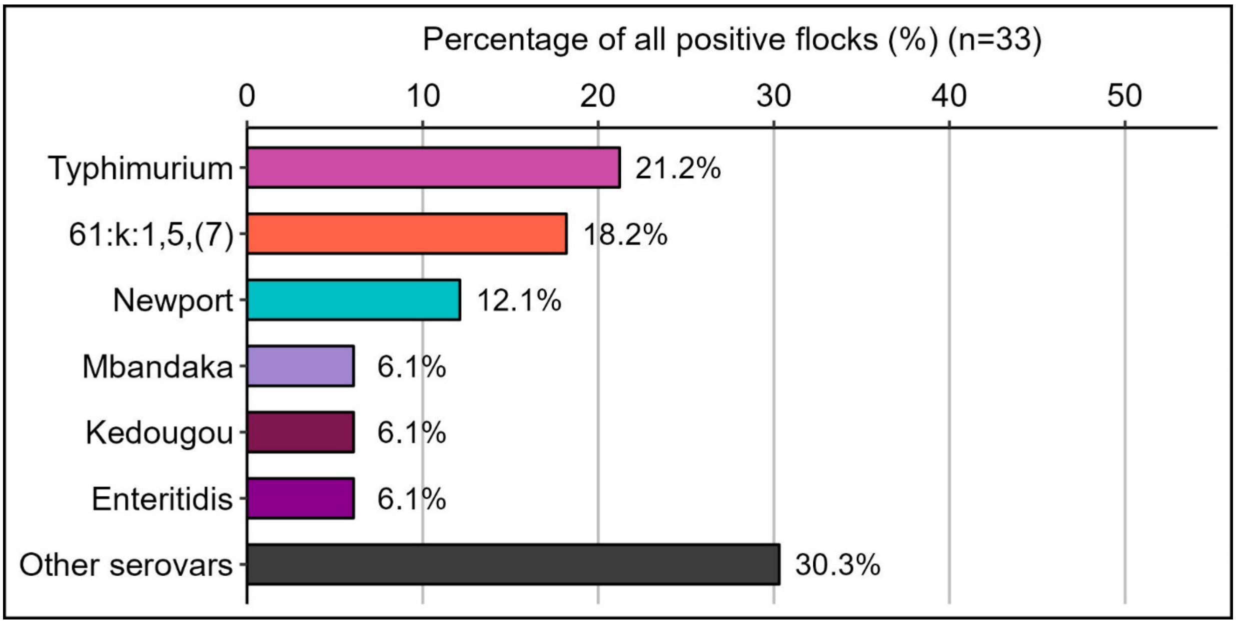
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult laying chickens in 2022. In 2022 the most common *Salmonella* serovar in adult laying hen flocks was S. Mbandaka accounting for 14.3% of total positive flocks, followed by S. Enteritidis (11.9%) and S. Typhimurium (11.9%).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

Figure 6.7.4: Isolations in adult laying chickens in 2023



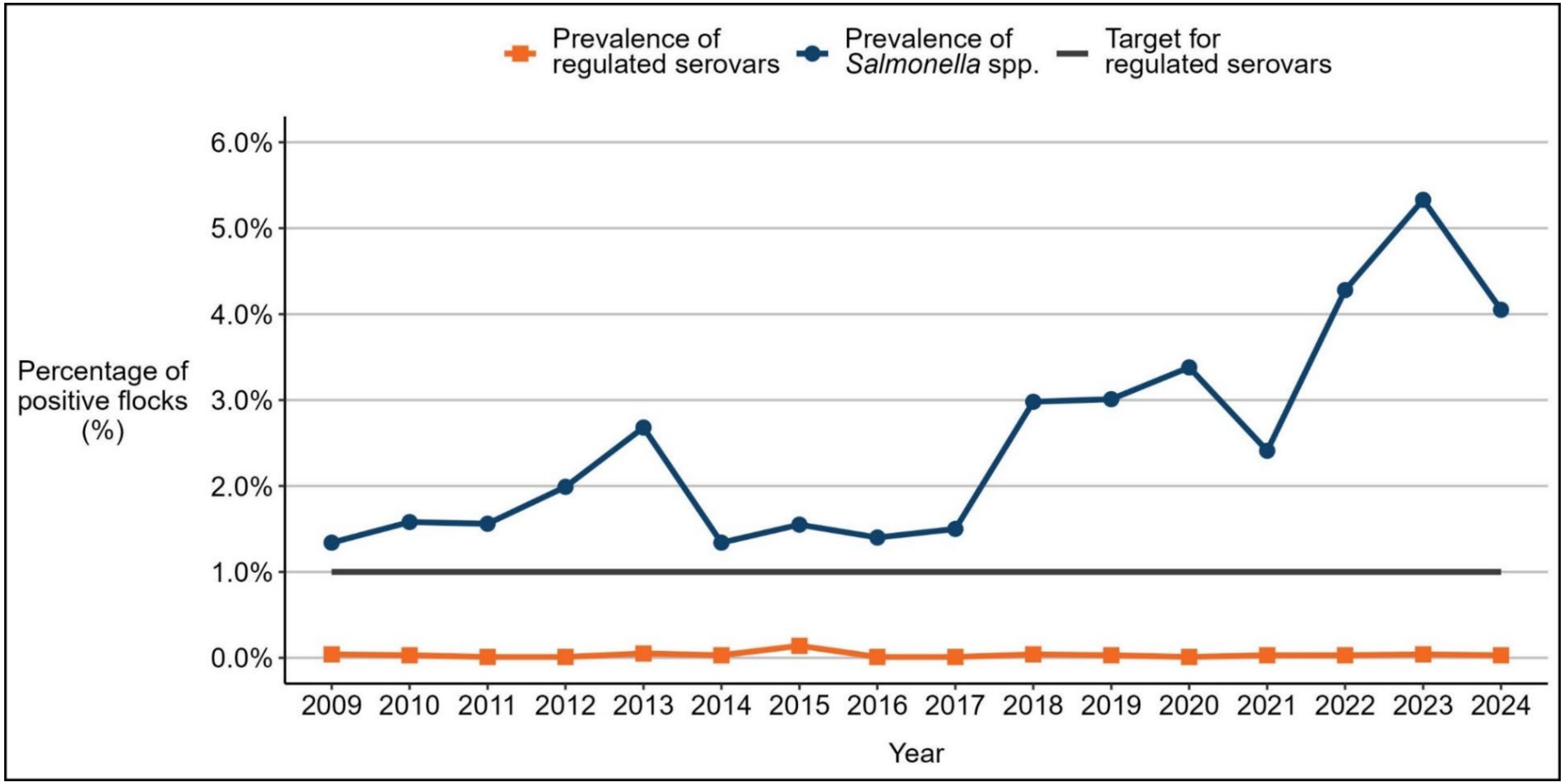
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult laying chickens in 2023. In 2023 the most common *Salmonella* serovars in adult laying hen flocks were *S.* Enteritidis, *S.* Give and *S.* Infantis, each accounting for 10.3% of total positive flocks, followed by *S.* Typhimurium, *S.* Montevideo and *S.* Newport at 6.9% each.

Figure 6.7.5: Isolations in adult laying chickens in 2024



Horizontal bar graph showing the percentage of *Salmonella* isolations 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 6.8: Prevalence of *Salmonella* in broiler chicken flocks tested under NCP in Great Britain 2009 to 2024



A line graph showing the prevalence of *Salmonella* in chicken broiler flocks tested under the NCP from 2009 to 2024. 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 2020 to 2024

The following table shows the number of broiler chicken flocks reported positive with each *Salmonella* serovar from 2020 to 2024 and the rank within that year. This data comes from NCP testing.

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Idikan (incl. monophasic)	1	601	2	257	3	341	1	607	1	628
Kedougou	2	339	4	192	4	232	3	421	2	342
Montevideo	3	245	1	330	2	409	2	545	3	285
Mbandaka	4	231	3	238	1	579	4	272	4	157
Agona	5	67	6	33	5	114	5	191	5	135
Orion var. 15^{+}	8	28	6	33	7	54	6	56	6	50
Ohio	7	33	5	54	8	43	8	35	7	41
Muenchen	13	6	13	4	13	9	14	5	8	23
Newport	11	10	15	2	14	7	17	2	9	20
Infantis	0	0	9	22	6	77	7	50	10	19
Kentucky	0	0	0	0	18	3	0	0	11	17
Anatum	14	5	14	3	20	1	15	4	12	9
Derby	16	3	10	7	14	7	10	14	12	9
Enteritidis	18	1	15	2	20	1	14	5	12	9
Senftenberg	6	53	8	23	11	18	9	17	13	8
Indiana	17	2	0	0	0	0	15	4	14	5
Typhimurium	18	1	13	4	17	4	12	7	14	5
Kottbus	18	1	0	0	20	1	0	0	15	3
Braenderup	18	1	15	2	19	2	14	5	16	2

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Livingstone	12	7	13	4	20	1	11	11	16	2
4,12:d:-	14	5	16	1	19	2	17	2	16	2
Berta	0	0	0	0	20	1	0	0	17	1
Bredeney	0	0	0	0	0	0	0	0	17	1
Chester	0	0	0	0	0	0	0	0	17	1
Coeln	18	1	0	0	17	4	16	3	17	1
Kingston	18	1	0	0	19	2	0	0	17	1
Nottingham	0	0	0	0	19	2	0	0	17	1
Oslo	18	1	16	1	0	0	18	1	17	1
Panama	0	0	16	1	20	1	0	0	17	1
Poona	18	1	0	0	0	0	0	0	17	1
6,7:-:enz$_{15}$	0	0	0	0	0	0	0	0	17	1
Agama	17	2	0	0	0	0	17	2	0	0
Ajioba	0	0	0	0	0	0	18	1	0	0
Bovismorbificans	10	14	13	4	0	0	18	1	0	0
Chomedey	0	0	0	0	0	0	18	1	0	0
Corvallis	0	0	0	0	20	1	0	0	0	0
Durham	0	0	0	0	0	0	18	1	0	0
Eboko	0	0	0	0	20	1	0	0	0	0
Ferruch	0	0	15	2	0	0	0	0	0	0
Frenso	0	0	0	0	0	0	18	1	0	0
Give	17	2	0	0	0	0	18	1	0	0
Give var 15^{+}	15	4	16	1	15	6	14	5	0	0
Goldcoast	0	0	16	1	0	0	0	0	0	0
Havana	18	1	16	1	16	1	0	0	0	0
Liverpool	0	0	0	0	20	1	0	0	0	0

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
London	0	0	0	0	19	2	0	0	0	0
Mikawasima	18	1	0	0	0	0	0	0	0	0
Orion	0	0	0	0	20	1	0	0	0	0
Oxford	0	0	0	0	0	0	18	1	0	0
O rough:l,v:1,7	18	1	0	0	0	0	0	0	0	0
Reading	0	0	16	1	0	0	0	0	0	0
Rissen	0	0	0	0	20	1	0	0	0	0
Stanley	0	0	0	0	20	1	0	0	0	0
Stourbridge	18	1	16	1	0	0	0	0	0	0
3,15:l,v: -	18	1	0	0	0	0	0	0	0	0
3,19: - : -	0	0	15	2	0	0	0	0	0	0
4,5,12:a:-	0	0	0	0	0	0	18	1	0	0
Monophasic Typhimurium	18	1	11	9	12	10	15	4	0	0
4,12:e,h:-	13	6	0	0	0	0	0	0	0	0
4,12:i,v:-	0	0	0	0	0	0	18	1	0	0
6,7:d:-	0	0	0	0	20	1	0	0	0	0
6,7:z_{10}:-	9	21	8	23	10	21	13	6	0	0
6,7:-:enz$_{15}$	17	2	0	0	0	0	0	0	0	0
6,7:-:-	0	0	0	0	15	6	0	0	0	0
6,8:d: -	0	0	0	0	20	1	0	0	0	0
13,22: -:1,6	18	1	0	0	0	0	0	0	0	0
13,23: - : -	18	1	0	0	0	0	0	0	0	0
47:z_4,z_{23}: -	0	0	0	0	20	1	0	0	0	0

For details of broiler chicken flocks reported positive in 2014 to 2019, see the 2019 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
2020	3.38%	0.01%
2021	2.41%	0.03%
2022	4.28%	0.03%
2023	5.33%	0.04%
2024	4.05%	0.03%

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 2020:

- 4 flocks tested positive for *S*. Mbandaka and *S*. 6,7:z10:-
- 4 flocks tested positive for *S*. Idikan (including monophasic variants)
- 3 flocks tested positive for *S*. Mbandaka and *S*. Kedougou
- 2 flocks tested positive for *S*. Orion var 15$^+$ and *S*. 13,23:i:-
- 2 flocks tested positive for *S*. Mbandaka and *S*. 6,7:-:enz15
- 2 flocks tested positive for *S*. Mbandaka and *S*. Montevideo
- 1 flock tested positive for *S*. Anatum and *S*. Senftenberg
- 1 flock tested positive for *S*. Mbandaka and *S*. Orion var. 15$^+$
- 1 flock tested positive for *S*. Senftenberg and *S*. Montevideo

- 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*. Livingstone and *S*. Idikan (including monophasic variants)
- 1 flock tested positive for *S*. Ohio and *S*. Mbandaka

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

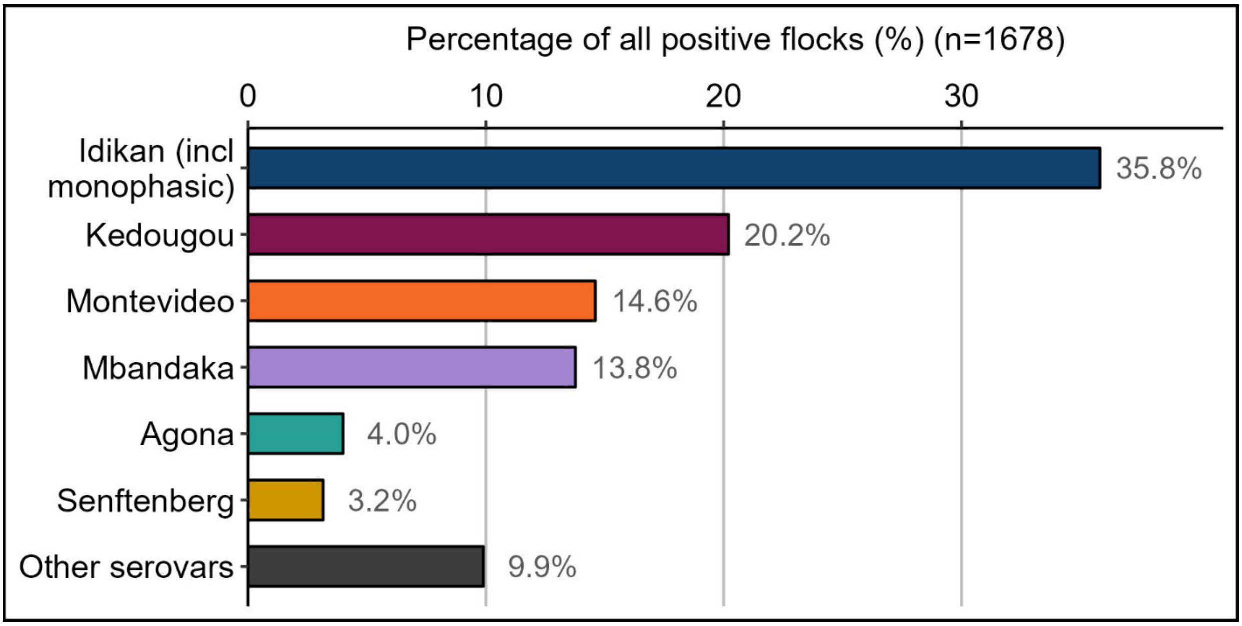
- 1 flock tested positive for *S*. Idikan (including monophasic variants) and *S*. Montevideo
- 1 flock tested positive for *S*. Idikan (including monophasic variants) and *S*. Orion var 15+
- 1 flock tested positive for *S*. Idikan (including monophasic variants) and *S*. Infantis,
- 1 flock tested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

Figure 6.9: Serovars identified in broiler chickens in Great Britain 2020 to 2024 reported from NCP testing

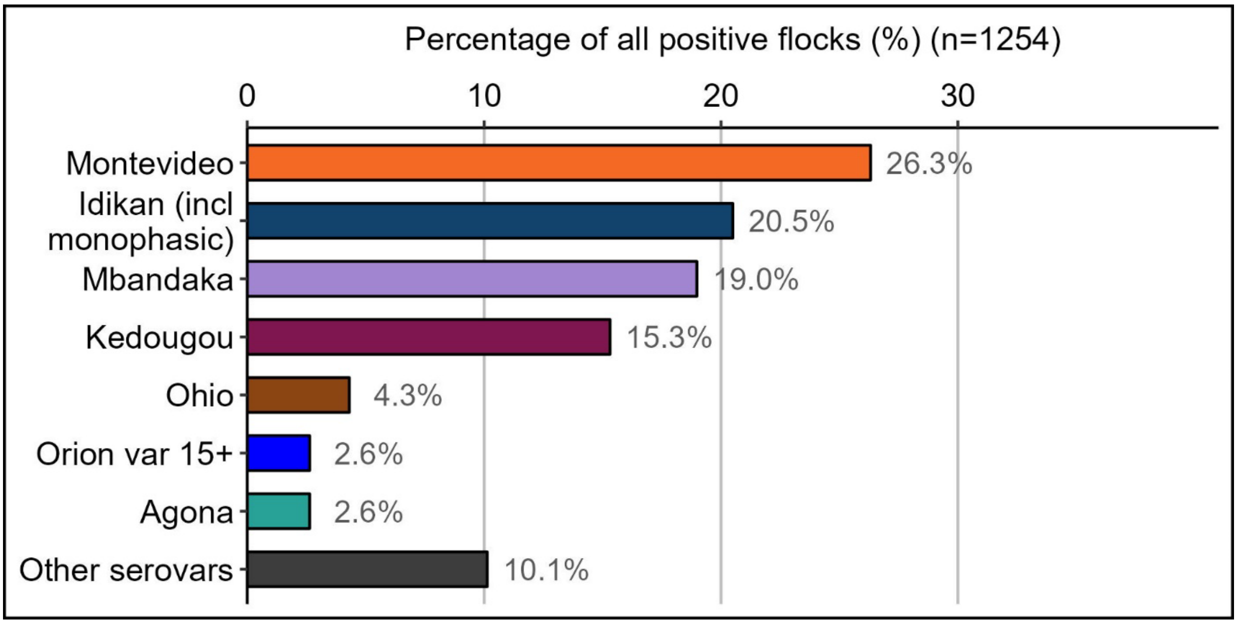
Figure 6.9.1: Isolations in broiler chickens in 2020



Horizontal bar graph showing the percentage of *Salmonella* isolations in broiler chickens in 2020. In 2020 the most common *Salmonella* serovar in broiler flocks was *S.* Idikan (including monophasic variants), accounting for 35.8% of total positive flocks, followed by *S*. Kedougou (20.2%), *S.* Montevideo (14.6%) and *S.* Mbandaka (13.8%).

In 2020 24 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

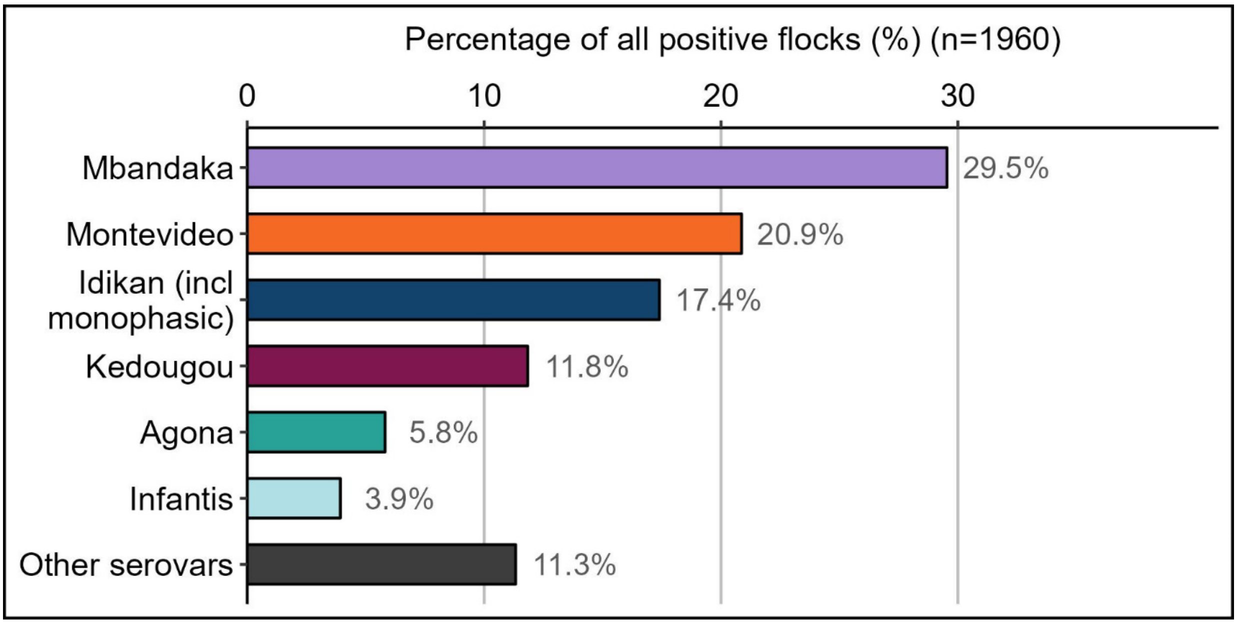
Figure 6.9.2: Isolations in broiler chickens in 2021



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

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

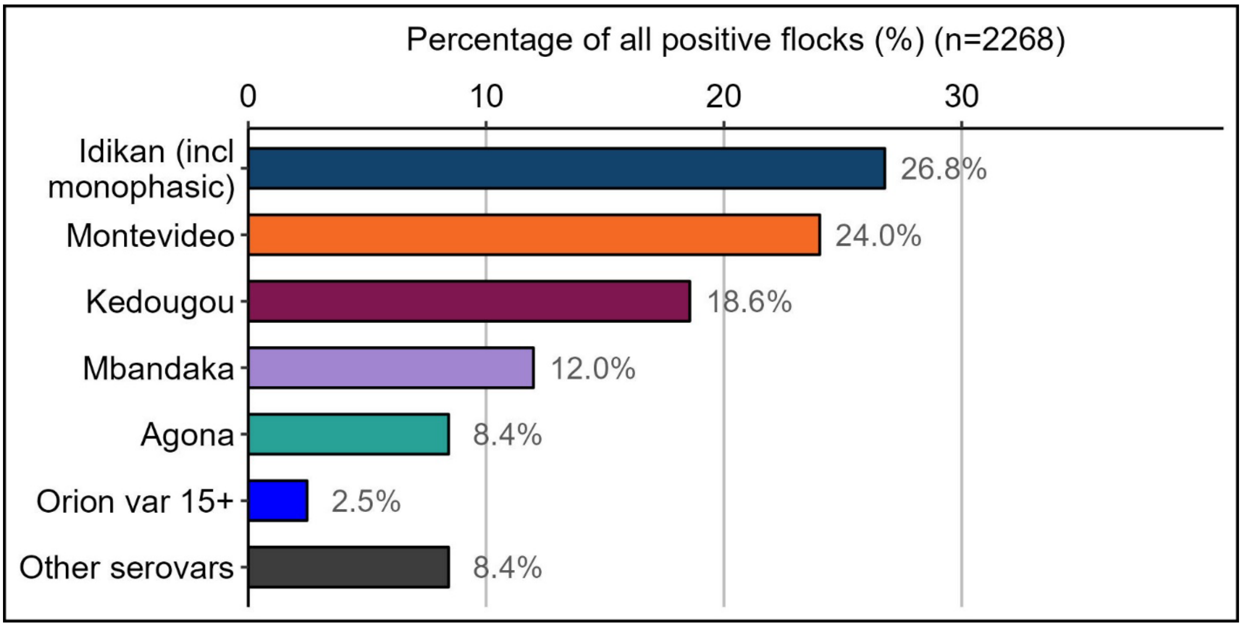
Figure 6.9.3: Isolations in broiler chickens in 2022



Horizontal bar graph showing the percentage of *Salmonella* isolations 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 (11.8%).

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

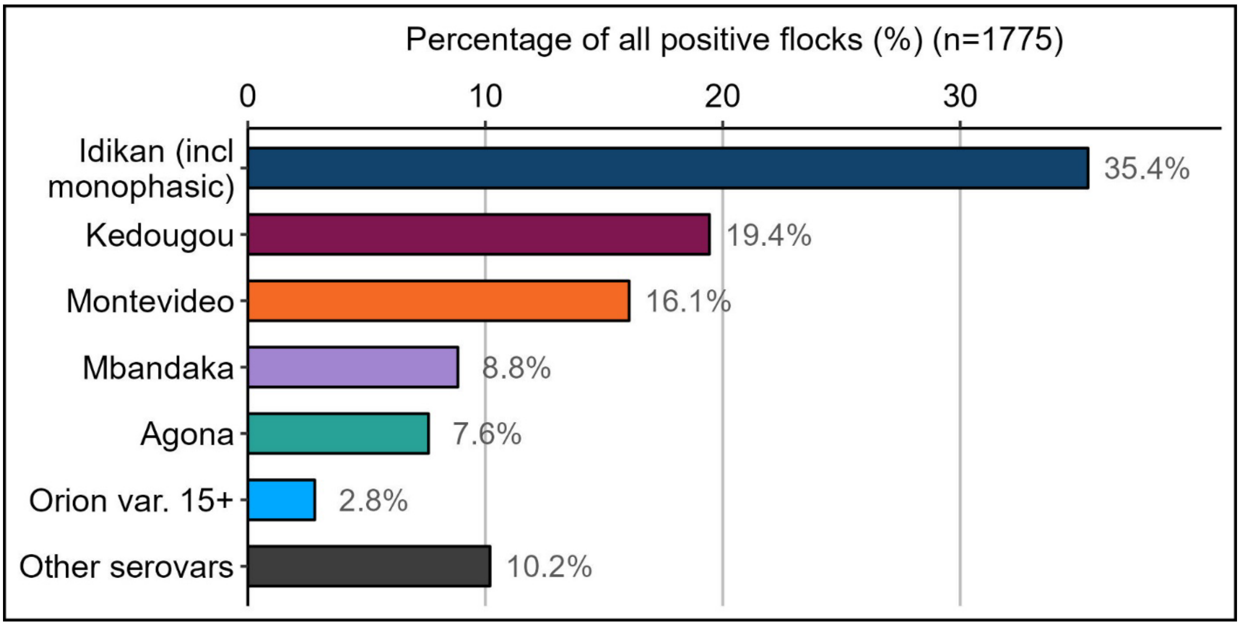
Figure 6.9.4: Isolations in broiler chickens in 2023



Horizontal bar graph showing the percentage of *Salmonella* isolations 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 (18.6%) and *S.* Mbandaka (12.0%).

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

Figure 6.9.5: Isolations in broiler chickens in 2024



Horizontal bar graph showing the percentage of *Salmonella* isolations 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.* Montevideo (16.1%), *S.* Mbandaka (8.8%), and *S.* Agona (7.6%).

In 2024, 6 flocks 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

During the early part of 2022 to 2024 there was significant disruption to the poultry industry due to national outbreaks of Avian Influenza affecting all industry sectors. This resulted in altered management and biosecurity measures. Although these factors did not impact NCP sampling by operators (the bulk of NCP sampling), the loss of flocks due to AI and the associated control measures including culling may have, and AI control measures are likely to have impacted non-statutory submission numbers. 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. This should therefore be borne in mind when comparing 2020 to 2024 data with previous years.

According to the June Agricultural Census, there were 3.17 million turkeys in Great Britain in 2024 compared with 2.48 million in 2023, 3.73 million in 2022 and 3.72 million in 2021.

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 over a 12 month period and fattening turkey farms with more than 500 birds are required to participate in *Salmonella* testing under the NCP. This is a mix of mostly testing undertaken by operators and some official NCP sampling of flocks, although some smaller turkey fattening farms meeting specific product marketing requirements may apply for 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 2 submissions from the same group of birds 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 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 counted as positive more than once if a flock is positive for more than one serovar, but under the NCP it is only counted once as a positive flock, although each isolate is included in the data published on isolations.

There were 277 turkey diagnostic and monitoring submissions made to APHA and SRUC laboratories in 2024. This compares to 264 in 2023, representing an increase of 4.9%. 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 total number of submissions submitted to private laboratories from turkeys, but just those that resulted in a positive test result for *Salmonella,* as these are reportable under the Zoonoses Order.

Total *Salmonella* isolations

A total of 108 *Salmonella* isolations were reported from turkeys in 2024 (Table 7.1), similar to 2023 (109 isolations) and the lowest number of isolations since the inception of the NCP in turkeys in 2010. Prior to 2022 there had been a decreasing trend in isolations since 2015.

In 2009, before the introduction of the NCP, only 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 isolations 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. There was an increase in isolations in 2022 (which was not associated with an increase in *S*. Derby isolations) and the number of isolations has subsequently decreased in 2023 and 2024.

The total number of isolations in 2024 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 99 (91.7%)
- voluntary surveillance: 9 (8.3%)

Thirteen different serovars of *Salmonella* were isolated in 2024, accounting for all of the isolations (no rough or untypeable strains). Table 7.1 shows the absolute number of isolations of each *Salmonella* serovar isolated from turkeys, from 2020 to 2024, and Figure 7.1 shows the relative percentages of the most common serovars.

Salmonella Kedougou (21 isolations, 19.4% of all isolations), a feed related serovar, was the joint most common serovar in 2024. This represents a 51.2% decrease in the number of isolations compared with 2023 (43 isolations). *S*. Kedougou has regularly featured among the 3 most common serovars isolated from turkeys since at least 2004 (Figure 7.1).

Similarly, with 21 isolations, *Salmonella* Anatum was the other joint most common serovar in 2024 having been the most frequently isolated serovar in 2022 (66 isolations) and 2021 (31 isolations). Isolations of this serovar had increased since 2019 (4 isolations), which is likely to be associated with contaminated feed.

There were 20 isolations (18.5% of all isolations) of *S.* Agona in 2024, which represents more than a 100% increase from 2023 (8 isolations, 7.3% of all isolations). In recent years there have often been less than 10 isolations of this serovar with the exception of 2022 (11 isolations). The proportion of isolations associated with this serovar have been increasing in recent years with 5.8% in 2022 and 7.3% in 2023 (Figure 7.1).

In 2024 there were 13 isolations of regulated serovars from turkey flocks. All isolations were of *S*. Typhimurium which is an 84.6% increase in this serovar compared to 2023. Seven isolations originated from 4 flocks on a single turkey fattener site as part of NCP sampling. The remaining 6 isolations (5 x statutory sampling, 1 x voluntary surveillance) were from 2 turkey fattener sites and 2 turkey breeder sites. This compares with 2 isolations in 2023 (from a turkey breeder site) and one isolation (from a turkey fattener site) 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). Phage types of *S*. Typhimurium isolated from turkeys between 2020 and 2024 are shown in Table 7.2. The isolations of *S*. Typhimurium reported in 2024 were DT75 (x9), DT193 (x1), DT99 (x1), DT104 (x1) and DT105 (x1). Phage type DT104 was last reported in turkeys in GB in 2011 and DT105 has never previously been reported from turkeys in Great Britain. These phage types have previously been isolated from chicken flocks.

There were 9 isolations of *S*. Indiana from 6 turkey fattener flocks in 2024. This serovar was last detected in 2019, with one flock testing positive. Prior to this, *S*. Indiana was isolated intermittently as part of the turkey NCP and is more often associated with farmed ducks.

Isolations of *S*. Senftenberg in recent years have represented a large proportion of total isolations, among the top 3 most common serovars. In 2023, only 3 isolations were recorded, a decrease of 88.5% compared to 2022 (26 isolations). Isolations in 2024 were consistent with this decrease with 4 isolations of *S.* Senftenberg. There has been no consistent trend in isolations in recent years with the number of isolations and relative contributions to overall isolations fluctuating (Figure 7.1). *Salmonella* Senftenberg is often a hatchery associated serovar that is also able to colonise feed mills.

Historically *Salmonella* Derby has been associated with high numbers of isolations from turkeys in GB, 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. In 2024 this serovar represented only 2.8% of all isolations (3 isolations) compared with 1.8% in 2023 and 6.4% in 2022 (Figure 7.1). 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. This decreasing trend in isolations continued in 2023 and 2024 with no reported isolations of *S*. Newport.

There were no isolations of monophasic strains of *S.* Typhimurium (*S.* 4,12:i:- and *S.* 4,5, 12:i:-) in 2024 which is the first time that these two strains have 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 2024, consistent with 2023, 2022 and 2021. This serovar was last isolated from turkey flocks in 2017.

Notably, *S*. Ago (one isolation from statutory testing) and *S.* Javiana (one isolation from statutory testing) have never previously been reported from turkeys in Great Britain. *S.* Oslo (2 isolations from voluntary sampling) was last reported in turkeys in GB in 2008.

There were no reported cases of *Salmonella* from turkeys imported into Great Britain in 2024.

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 legislation 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 2024

One adult turkey breeding flock tested positive for *Salmonella* in 2024. This is consistent with the 1 positive flock in 2023 and a reduction from 2022 (4 positive flocks) and 2021 (2 positive flocks) and an 85.7% reduction compared with 2020 (7 positive flocks) (Table 7.4).

A total of 149 adult turkey breeding flocks were in production in Great Britain in 2024 and were included in the NCP. Therefore, the estimated GB prevalence for regulated serovars was 0.67% (1 of 149). National prevalence figures were all below the national targets of 1% of flocks positive for *S.* Enteritidis and/or *S.* Typhimurium (including monophasic strains). The estimated GB prevalence for all *Salmonella* serovars in 2024 was 0.67% (1 of 149), an increase from 0.58% in 2023 but lower than in 2022, 2021 and 2020 (1.97%, 0.83% 2.62%, respectively). Figure 7.3 shows the change in prevalence of turkey breeder flocks in GB 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.

One adult turkey breeding flock tested positive for a regulated serovar in 2024*, Salmonella* Typhimurium (DT104). This is the second time a regulated serovar has been identified in adult turkey breeder flocks since 2019 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 adult breeder turkey flocks in the NCP was in 2018 when 6 positive flocks (all under the same ownership) tested positive for *S*. Typhimurium 4,5,12:i:-. This is the second year that *S*. Typhimurium has been isolated from adult turkey breeder flocks (first in 2023).

No adult turkey breeding flocks tested positive for non-regulated serovars in 2024 (Table 7.4). Since the NCP started for breeding turkeys in 2010, this is the second time that no non-regulated serovars have been detected in breeding turkey flocks, the first being in 2023.

The estimated prevalence for regulated *Salmonella* serovars in adult breeding flocks in England in 2024 was 0.7% (1/143), 0.0% (0/5) in Wales and 0.0% (0/1) in Scotland. This is well below the target of 1% of flocks testing positive for a regulated serovar in each administration.

For comparison, the serovars identified in the adult turkey breeder NCP between 2020 and 2024 are shown in Table 7.4. Figure 7.4 shows the relative percentages of the serovars in the turkey breeder NCP from 2020 to 2024.

No immature turkey breeding flocks were positive for *Salmonella* spp. via NCP sampling in 2024 but one immature flock was positive for *Salmonella* Typhimurium (DT99) via voluntary sampling. Flocks are classified as immature when birds are under 20 weeks old on the date of sampling. Immature flocks are not counted in prevalence estimates or national targets. This is more than in 2023, when no immature flocks tested positive and compared to 6 positive flocks in 2022 and 7 flocks in 2021.

Positive flocks identified in the NCP for fattening turkeys in 2024

In total, 68 fattening turkey flocks (on 37 different holdings) were positive for *Salmonella* in 2024. This is similar to 2023 (70 positive flocks on 34 different holdings) and a 29.9% decrease from 2022 (97 flocks) (Table 7.5). Figure 7.6 illustrates the most common serovars isolated from fattening flocks from 2020 to 2024.

In 2024, 7 flocks, on 3 sites, tested positive for a regulated serovar compared to one flock in 2023 and 2 flocks in 2022. All 7 flocks tested positive for *S*. Typhimurium. Six were DT75 and the other was DT193. All 3 sites were epidemiologically linked. *S*. Typhimurium was last detected in fattening turkeys in 2021 where 3 flocks tested positive, a decrease from the previous detection of 4 positive flocks in 2018. The proportion of positive flocks represented by this serovar was 10.3% in 2024, an increase from 3.2% in 2021.
A total of 2,191 turkey fattening flocks were in production in Great Britain in 2024 and were included in the NCP. Therefore, the estimated GB prevalence for regulated *Salmonella* serovars was 0.32% (7 of 2,191), with all 3 national prevalence estimates below the targets of a maximum of 1% of flocks positive for regulated serovars (Figure 7.5). The estimated prevalence for regulated *Salmonella* serovars in adult fattening flocks in England in 2024 was 0.32% (7/2,155), 0.0% (0/35) in Wales and 0.0% (0/1) in Scotland. This was higher than in 2023 (0.05%), 2022 (0.10%), 2020 and 2019 (0.0% in both years). The estimated GB prevalence of all *Salmonella* spp. in 2024 was 3.1% (68 of 2,191). Figure 7.5 shows the change in prevalence of turkey fattening flocks in GB testing positive for *Salmonella* since 2015. Estimated prevalence of all *Salmonella* serovars in 2024 was lower than in previous years but similar to that in 2023 and a marked reduction compared to a peak of 17.4% in 2016.

A total of 61 fattening turkey flocks tested positive for *Salmonella* serovars other than *S.* Enteritidis and *S.* Typhimurium (including monophasic strains). The serovars identified in turkey fattening flocks in the NCP between 2020 and 2024 are shown in Table 7.5. The relative percentages of the most common serovars from turkey fattening flocks each year from 2020 to 2024 are shown in Figure 7.6.

The most common serovar isolated in 2024 was *S.* Anatum (27.9% of isolations), with 19 flocks testing positive for this serovar. This is a 5.6% increase from 18 flocks testing positive for this serovar in 2023 and compares to 40 flocks in 2022 and 31 flocks in 2021. Isolations remain higher than pre-2020 (4 flocks in 2019, 2 flocks in 2018) and the years 2015 to 2017 when no flocks tested positive for *S*. Anatum. Increased isolations of this serovar are considered likely to be associated with contaminated feed.

The second most common serovar isolated in 2024 was *S.* Kedougou, with 15 flocks testing positive. This was a 53.1% decrease from 32 flocks testing positive in 2023 and 21 flocks testing positive for this serovar in 2022. The proportion of flocks testing positive for this serovar in 2024 was 22.1%, almost half that in 2023 (42.1%) but comparable to 2022 (21.7%). Like *S.* Anatum, *S.* Kedougou is often associated with feedmill contamination.

S. Idikan (including monophasic variants) was isolated from 4 flocks in 2024, all phenotypically confirmed as *S.* 13,23:i:-, compared to 5 flocks in 2023. *Salmonella* 13,23:i:- is a monophasic variant of *S.* Idikan associated with contaminated feed mills and can be persistent in the hatchery and farm environment.

Other notable increases in the number of flocks associated with serovars in 2024 compared to 2023 include *S.* Agona (11 versus 4) and *S.* Indiana (6 versus 0).

Two flocks tested positive for *S.* Orion var 15+ in 2024, a decrease from 6 positive flocks in 2023. This serovar was not detected between 2014 and 2019. In 2020 one flock tested positive followed by 4 in 2021 and 3 in 2022. The proportion of positive flocks with this serovar was 2.9% in 2024, a decrease from 7.9% in 2023

The number of flocks testing positive for *S.* Derby continued to decrease from 19 in 2021, 7 in 2022, 2 in 2023 and 2 in 2024. This follows dramatic decreases from 259 flocks in 2018 to 105 flocks in 2019, and 19 flocks in 2020. The proportion of positive samples represented by this serovar peaked in 2018 at 87.5% but decreased to 2.9% in 2024. This is the fifth year in a row since the NCP began in 2010 that *S*. Derby was not the most common serovar isolated. This reduction follows successful control of *S.* Derby in adult turkey breeding flocks and hatcheries and gradual resolution of persistent contamination of some fattening farms.

Salmonella Senftenberg, a known hatchery contaminant, was not isolated in 2024, a decrease from 1 flock in 2023 and 5 flocks in 2022. The number of flocks testing positive for this serovar generally has declined in recent years following a peak in isolation in 2019 when 21 flocks tested positive.

One flock tested positive for *Salmonella* Ago and one flock tested positive for *S*. Javiana in 2024. These were the first instances of these serovars in turkeys or chickens in Great Britain since the inception of the NCP in 2010

Antimicrobial susceptibility in turkeys

A total of 91 *Salmonella* isolates from turkeys were tested against a panel of 16 antimicrobials in 2024. Susceptibility increased notably to 53.8%, compared to 30.3% in 2023 (n=76), but different serovars have significantly different resistance phenotypes. The observed rise in susceptibility was largely driven by changes in serovar distribution between the 2 years. In 2024, a greater proportion of isolates belonged to serovars that exhibited higher susceptibility (such as *S*. Agona, *S*. Typhimurium, and *S*. Indiana), while the prevalence of serovars consistently associated with lower susceptibility (e.g., *S*. Kedougou, *S*. Anatum) remained unchanged. Only one isolate (*S.* Orion var. 15+ [Binza]) was classified as multidrug-resistant (MDR; resistant to 4 or more antimicrobials) in 2024, consistent with the single MDR isolate *(S.* Kedougou) in 2023.

The most commonly resistant serovars were *S.* Kedougou (n=17) and *S.* Anatum (n=14). Tetracycline resistance decreased from 44.7% in 2023 to 19.8% in 2024, mainly due to a reduction in tetracycline resistant S. Kedougou. Resistance to nalidixic acid also declined slightly to 4.4% (from 7.9%), with all 4 resistant isolates belonging to the serovar *S*. Senftenberg and showing resistance to nalidixic acid alone. Resistance to sulphonamides remained among the most frequently detected (23.2%), alongside streptomycin (19.8%), tetracycline (19.8%), and ampicillin (19.8%).

None of the *Salmonella* isolates from turkeys exhibited resistance to third generation cephalosporins or fluoroquinolones, which are classified as “highest priority critically important antibiotics” (HP-CIAs).

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

Salmonella serovar	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
Agama	1	1	2	2	0	1	0	0	0	0
Ago	0	0	0	0	0	0	0	0	1	1
Agona	2	2	4	7	7	11	4	8	11	20
Anatum	38	42	31	31	40	66	18	19	19	21
Berta	0	0	0	0	0	1	0	1	0	0
Bovismorbificans	0	0	2	2	0	1	0	0	0	0
Brandenburg	0	0	0	0	1	1	0	0	0	0
Chester	0	0	0	0	0	0	1	1	0	0
Derby	20	22	19	22	7	12	2	2	2	3
Dublin	0	0	0	0	0	0	0	1	0	0
Give	0	0	0	0	0	2	1	1	0	0
Give var. 15+	0	0	1	1	0	0	0	0	0	0
Idikan (incl monophasic)	6	15	2	4	2	2	5	5	4	5
Indiana	0	0	0	0	0	0	0	0	6	9
Javiana	0	0	0	0	0	0	0	0	1	2
Kedougou	33	68	9	16	21	30	32	43	15	21
Kingston	1	1	0	0	0	0	0	0	0	0
Kottbus	0	0	0	0	0	0	2	3	0	0
Livingstone	0	2	0	0	0	0	0	0	0	2
London	0	0	1	6	3	5	0	0	0	0
Mbandaka	1	2	1	1	0	0	0	0	0	0
Monophasic Typhimurium	0	0	9	9	2	4	1	1	0	0

Salmonella serovar	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
Montevideo	0	0	0	0	3	8	0	1	0	0
Newport	1	2	2	3	1	1	0	0	0	0
Orion	0	0	0	0	0	0	1	1	0	0
Orion var. 15+	1	2	4	5	3	5	6	11	2	5
Oslo	0	0	0	0	0	0	0	0	0	2
Schwarzengrund	0	0	0	0	0	0	1	2	0	0
Senftenberg	9	15	3	20	9	26	1	3	0	4
Typhimurium	0	2	3	3	0	1	1	2	8	13
untypable strains	12	15	4	6	3	4	0	3	0	0
rough strains	4	5	1	2	2	7	1	1	0	0
Total	**124**	**196**	**96**	**140**	**101**	**188**	**71**	**109**	**69**	**108**

In 2020 5 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 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.

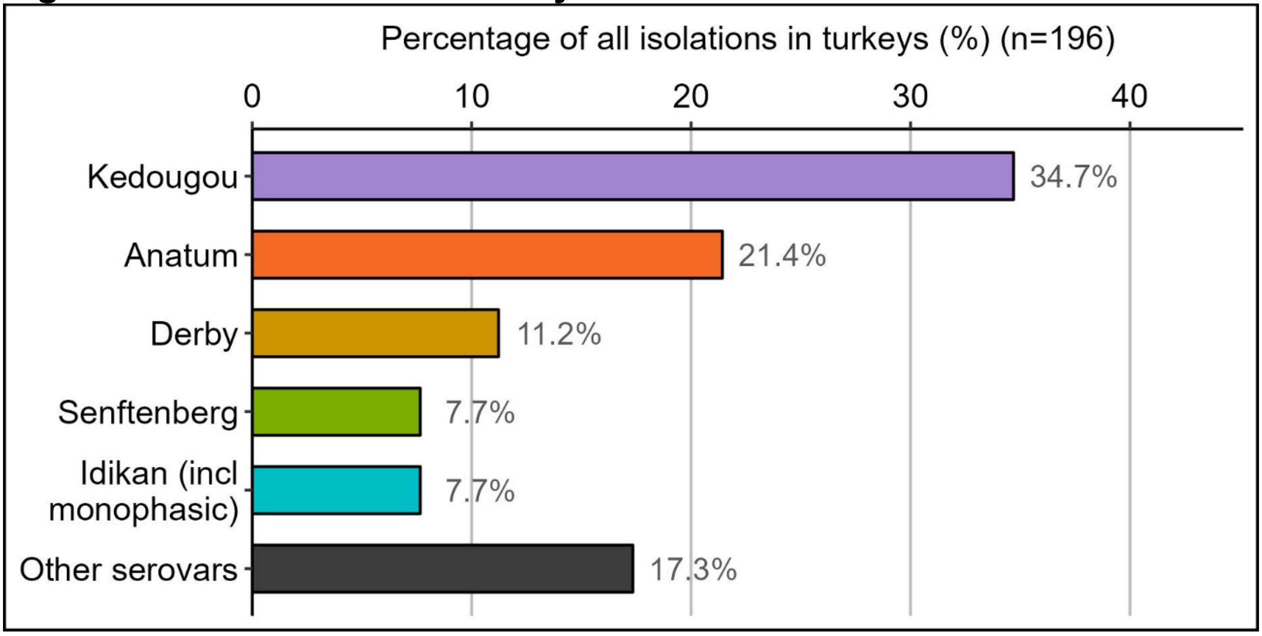
In 2022 3 flocks tested positive for 2 different *Salmonella* serovars. These are included in the table under both serovars but only once in the overall total.

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 no flocks tested positive for 2 different *Salmonella* serovars.

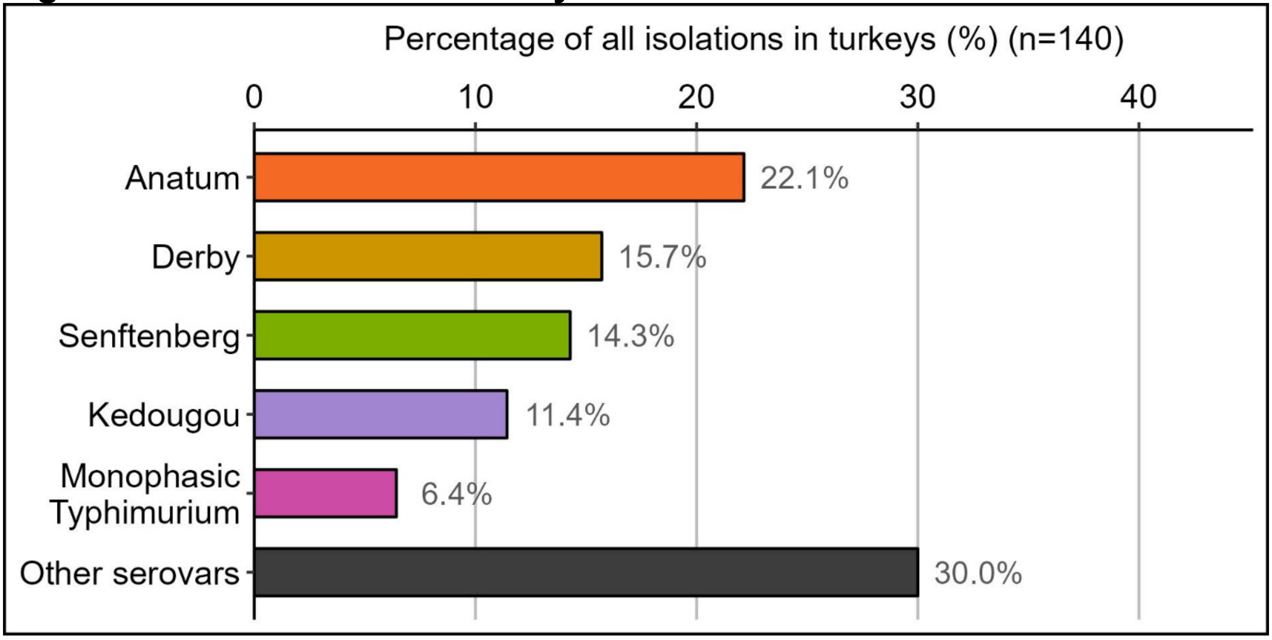
Figure 7.1: The most common serovars in turkeys by number of isolations in Great Britain 2020 to 2024 (statutory and non-statutory testing)

Figure 7.1.1: Isolations in turkeys in 2020



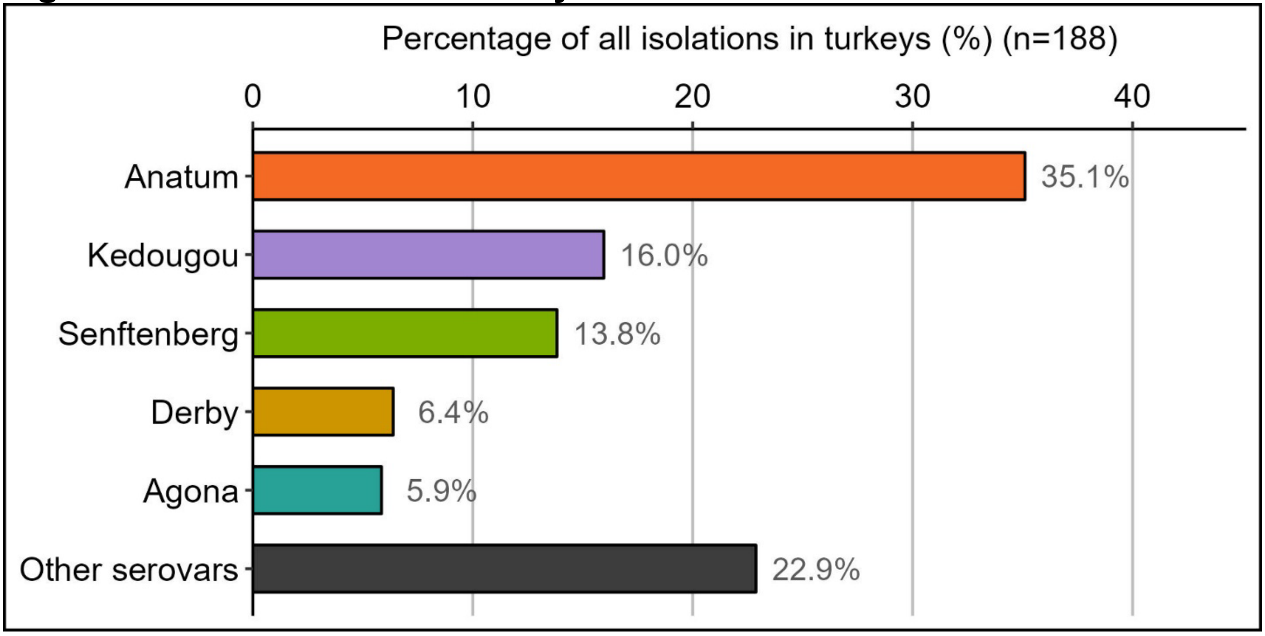
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in turkeys in 2020. The most common *Salmonella* serovar in turkeys in 2020 was *S.* Kedougou, accounting for 34.7% of total isolations, followed by *S.* Anatum (21.4%), *S.* Derby (11.2%), *S.* Senftenberg (7.7%) and *S.* Idikan (incl monophasic variants) (7.7%).

Figure 7.1.2: Isolations in turkeys in 2021



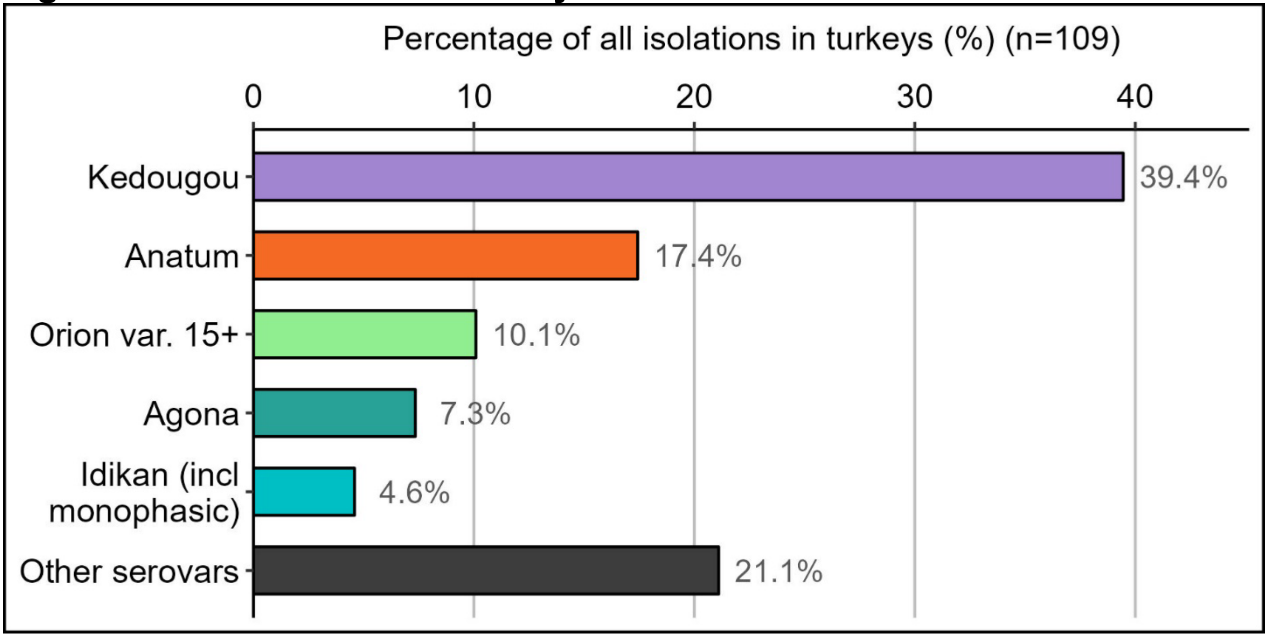
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in turkeys in 2021. The most common *Salmonella* serovar in turkeys in 2021 was *S.* Anatum, accounting for 22.1% of total isolations, followed by *S*. Derby (15.7%), *S.* Senftenberg (14.3%) and *S.* Kedougou (11.4%).

Figure 7.1.3: Isolations in turkeys in 2022



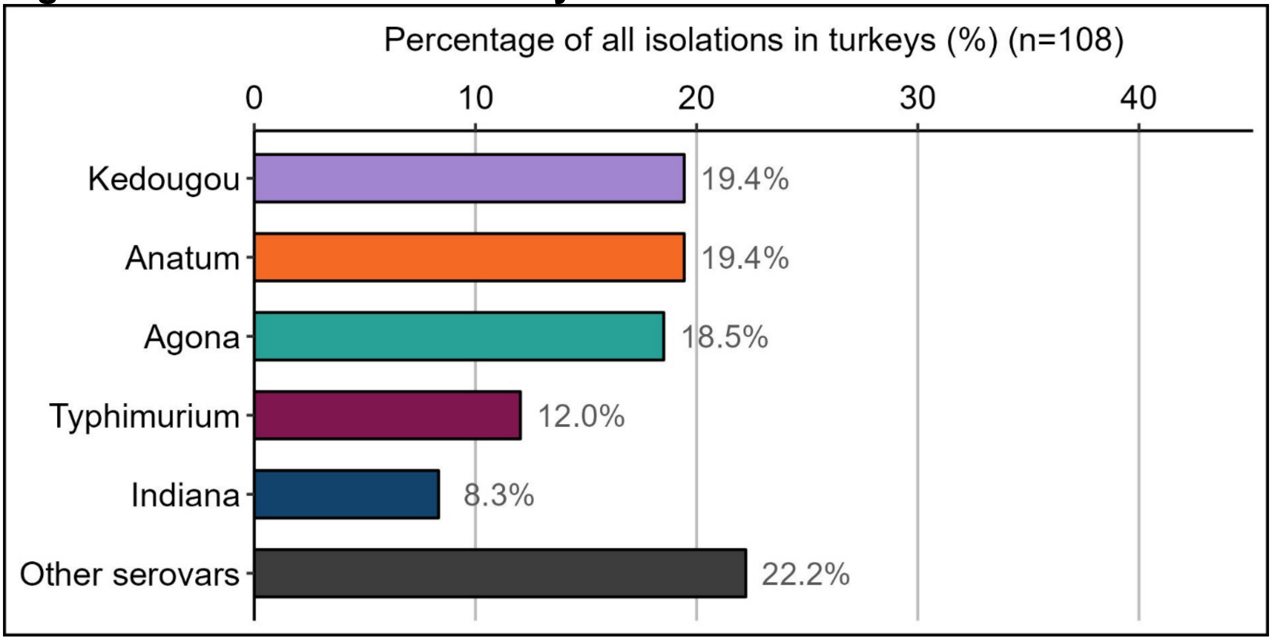
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in turkeys in 2022. The most common *Salmonella* serovar in turkeys in 2022 was *S.* Anatum, accounting for 35.1% of total isolations, followed by *S*. Kedougou (16.0%), *S.* Senftenberg (13.8%) and *S.* Derby (6.4%).

Figure 7.1.4: Isolations in turkeys in 2023



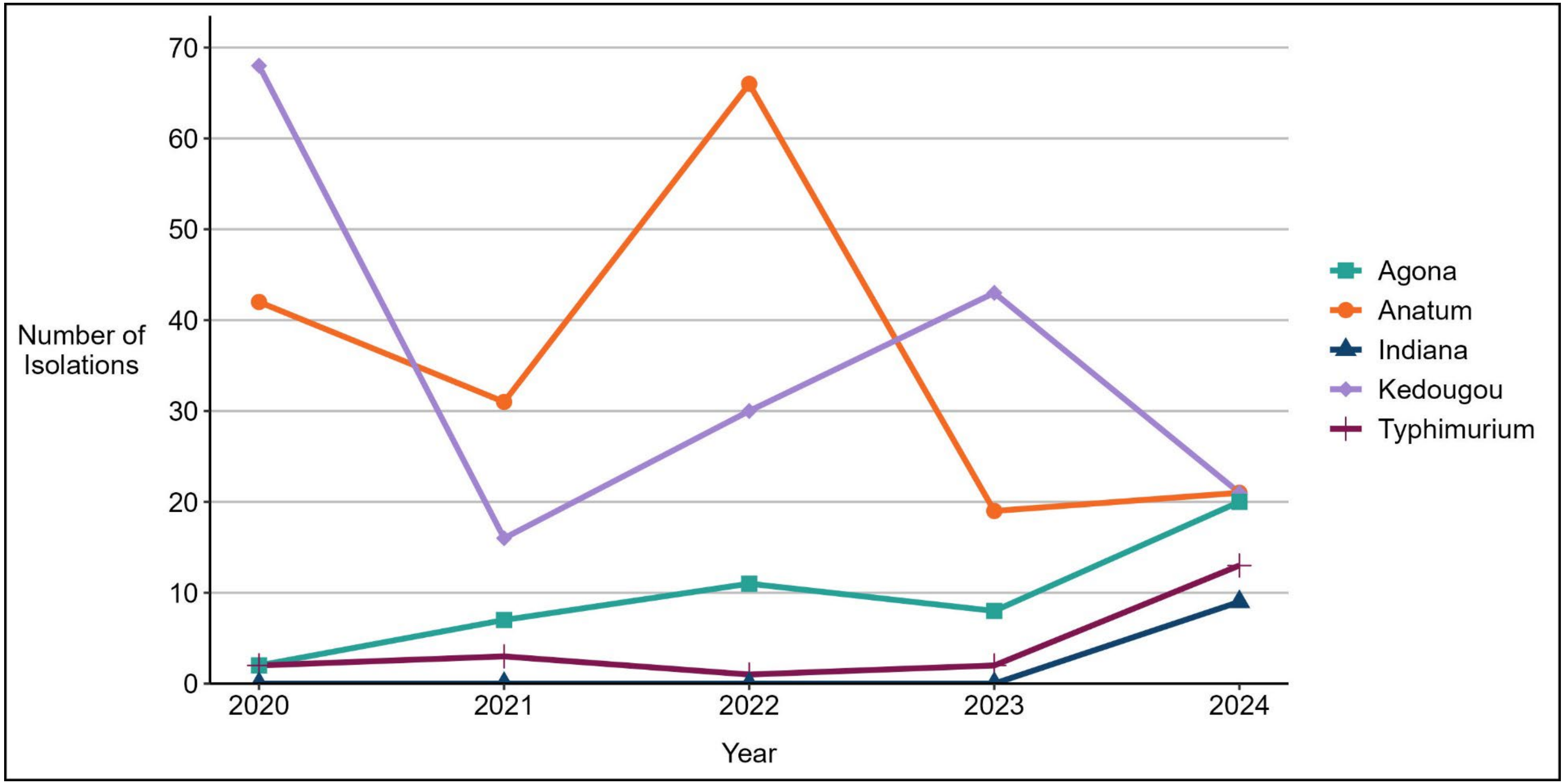
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in turkeys in 2023. The most common *Salmonella* serovar in turkeys in 2023 was *S.* Kedougou, accounting for 39.4% of total isolations, followed by *S*. Anatum (17.4%), *S.* Orion var 15$^+$ (10.1%) and *S.* Agona (7.3%).

Figure 7.1.5: Isolations in turkeys in 2024



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

Figure 7.2: The 5 most common *Salmonella* serovars in turkeys in Great Britain in 2024 and their trends over time since 2020



A line graph showing the 5 most common serovars in turkeys from 2020 to 2024. The figure shows that *S.* Kedougou and *S.* Anatum are the most common serovars in turkeys in 2024. The number of isolations of *S.* Kedougou has been variable with a high in 2020 of 68 isolations, dropping to 16 isolations in 2021 and then rising steadily to 43 in 2023 before decreasing in 2024 to 21 isolations. *S.* Anatum isolations have also been variable with 42 isolations in 2020, dropping to 31 in 2021 before doubling in 2022 to 66 isolations, but decreased considerably in 2023 to 19 isolations and 21 isolations in 2024. The other 3 serovars, *S.* Agona, *S.* Indiana, and *S.* Typhimurium have remained low and stable over the last 5 years, rarely exceeding 11 isolations. The number of isolations of each of these serovars increased between 2023 and 2024: *S.* Agona from 8 to 20 isolations, *S.* Indiana from 0 to 9 isolations, and *S.* Typhimurium from 2 to 13 isolations.

Table 7.2: *S.* Typhimurium phage types in turkeys in Great Britain 2020 to 2024

Phage type	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
DT9	0	1	0	0	0	0	0	0	0	0
DT75	0	0	0	0	0	0	0	0	6	9
DT99	0	0	0	0	0	1	0	0	0	1
DT104	0	0	0	0	0	0	0	0	1	1
DT105	0	0	0	0	0	0	0	0	0	1
DT193	0	0	0	0	0	0	1	2	1	1
U302	0	0	3	3	0	0	0	0	0	0
RDNC	0	1	0	0	0	0	0	0	0	0
Total	**0**	**2**	**3**	**3**	**0**	**1**	**1**	**2**	**8**	**13**

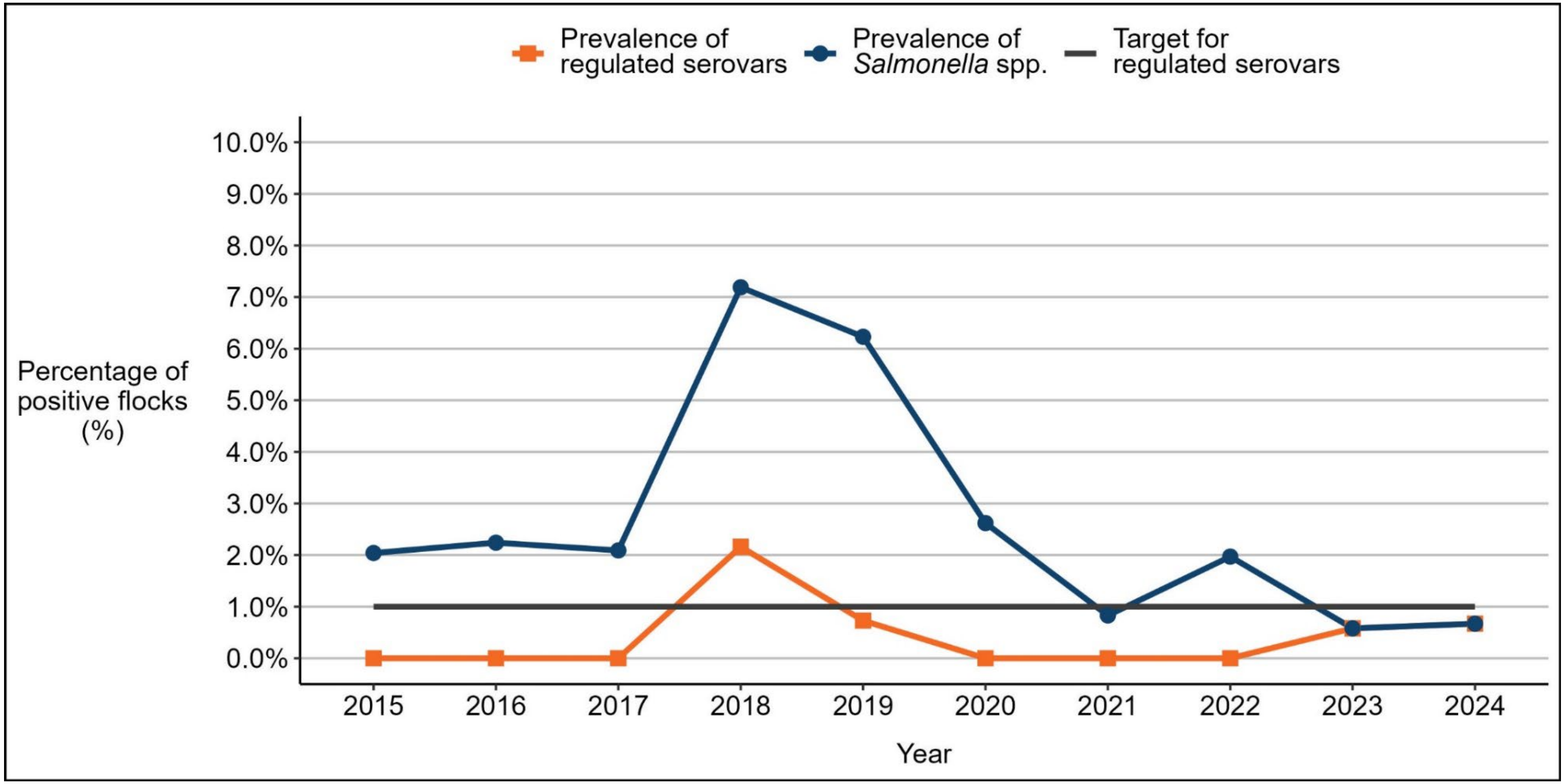
Flocks from statutory testing, isolations from both statutory and non-statutory testing.

Table 7.3: Monophasic *Salmonella* phage types in turkeys in Great Britain 2020 to 2024

Phage type	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations	2024 flocks	2024 isolations
DT193	0	0	8	8	2	3	1	1	0	0
UNTY	0	0	1	1	0	1	0	0	0	0
Total	**0**	**0**	**9**	**9**	**2**	**4**	**1**	**1**	**0**	**0**

Flocks from statutory testing, isolations from both statutory and non-statutory testing.

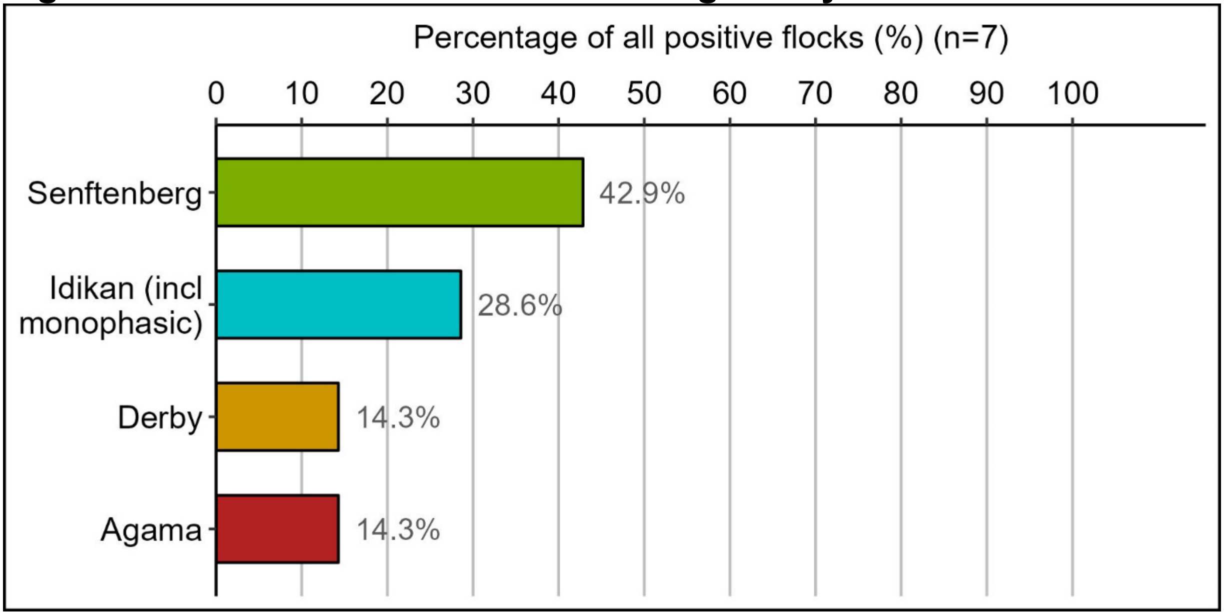
Figure 7.3: Prevalence of *Salmonella* in adult turkey breeding flocks tested under NCP in Great Britain 2015 to 2024



A line graph showing the prevalence of *Salmonella* in adult turkey breeding flocks tested under the NCP from 2015 to 2024. 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 0.67% in 2024. The prevalence of regulated serovars remains low at 0.67% 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.

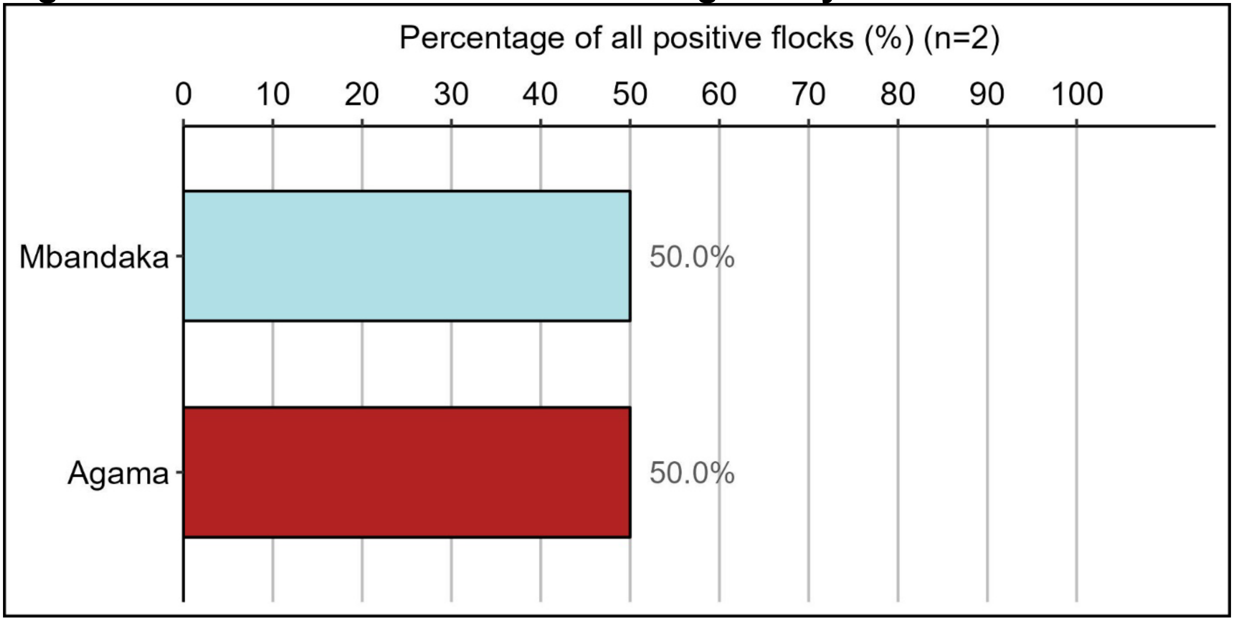
Figure 7.4: The most common serovars identified in adult turkey breeding flocks in Great Britain 2020 to 2024 reported from NCP testing

Figure 7.4.1: Isolations in adult breeding turkeys in 2020



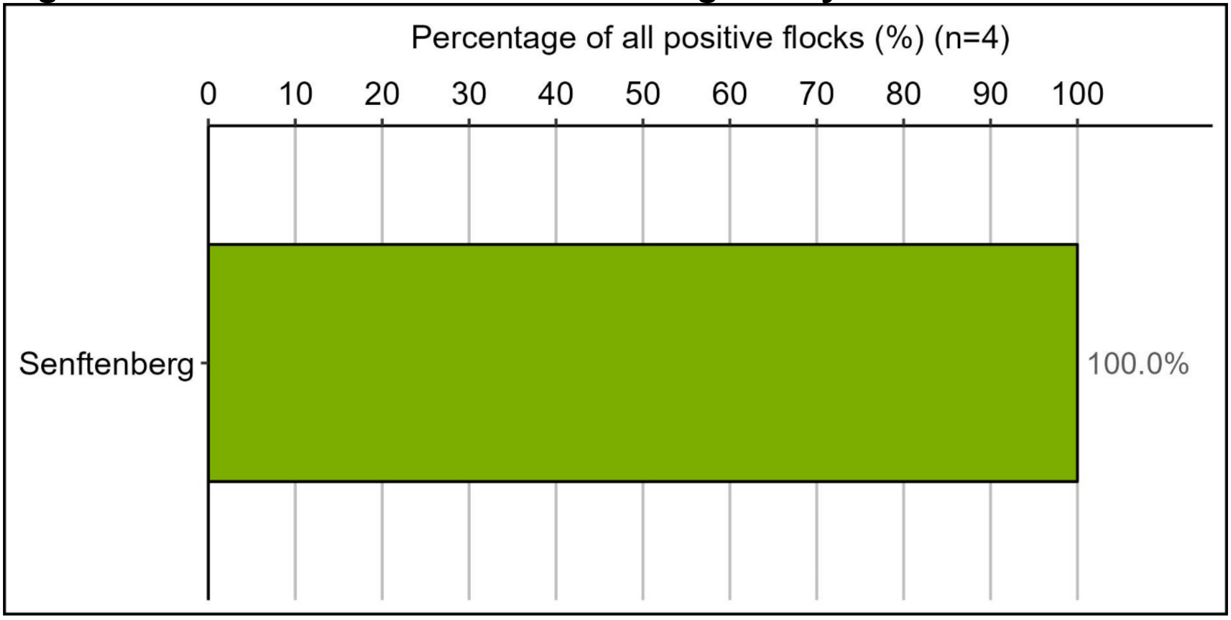
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding turkeys in 2020. In 2020 the most common *Salmonella* serovar in fattening turkey flocks in 2020 was *S.* Senftenberg, accounting for 42.9% of total isolations, followed by *S*. Idikan (incl monophasic) (28.6%), *S.* Agama (14.3%) and *S*. Derby (14.3%).

Figure 7.4.2: Isolations in adult breeding turkeys in 2021



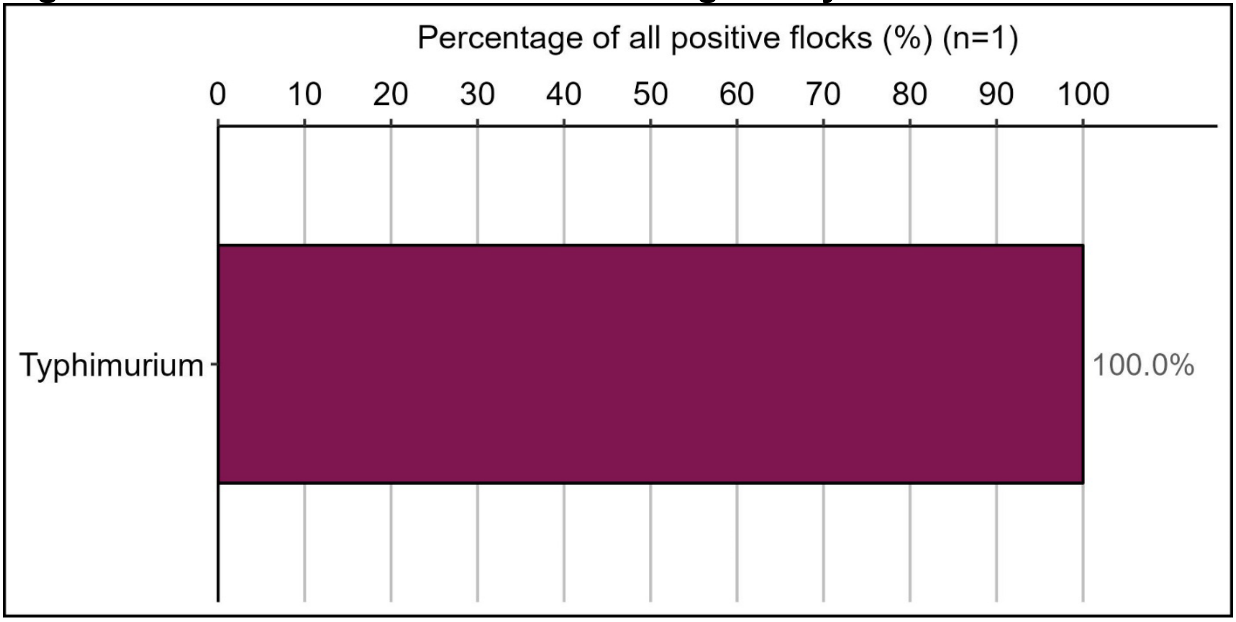
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding turkeys in 2021. In 2021 the most common *Salmonella* serovars in breeding turkey flocks in 2021 were *S*. Agama and *S.* Mbandaka, each accounting for 50.0% of total isolations.

Figure 7.4.3: Isolations in adult breeding turkeys in 2022



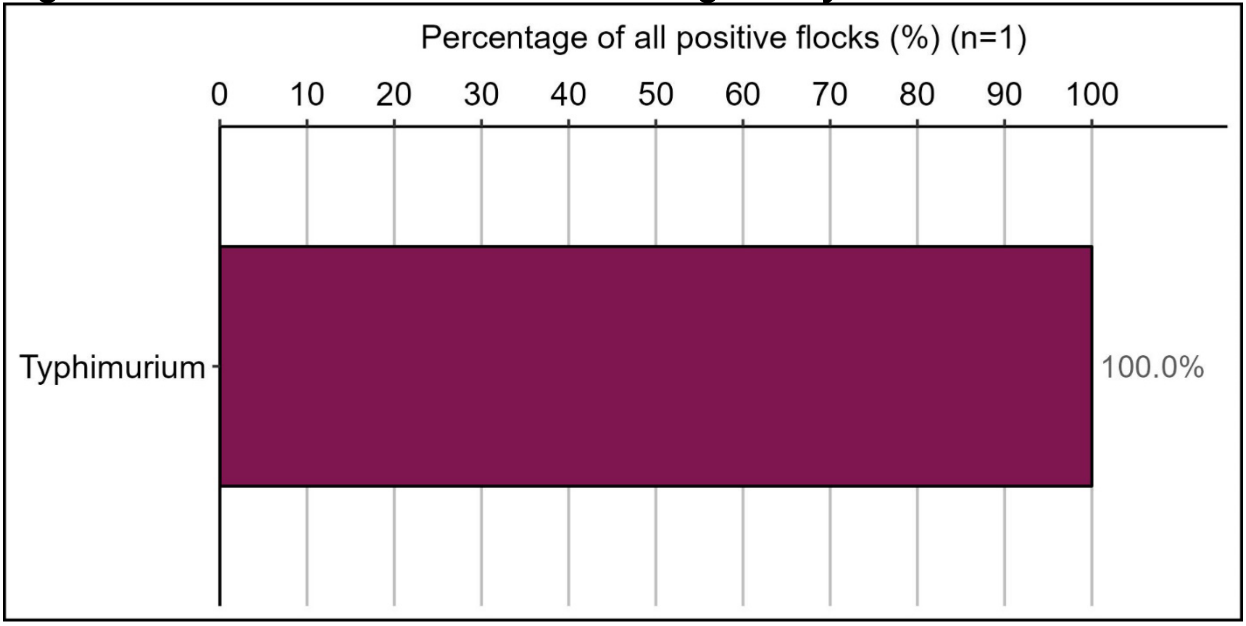
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding turkeys in 2022. In 2022 the only *Salmonella* serovar in breeding turkey flocks was *S*. Senftenberg accounting for 100% of all isolations.

Figure 7.4.4: Isolations in adult breeding turkeys in 2023



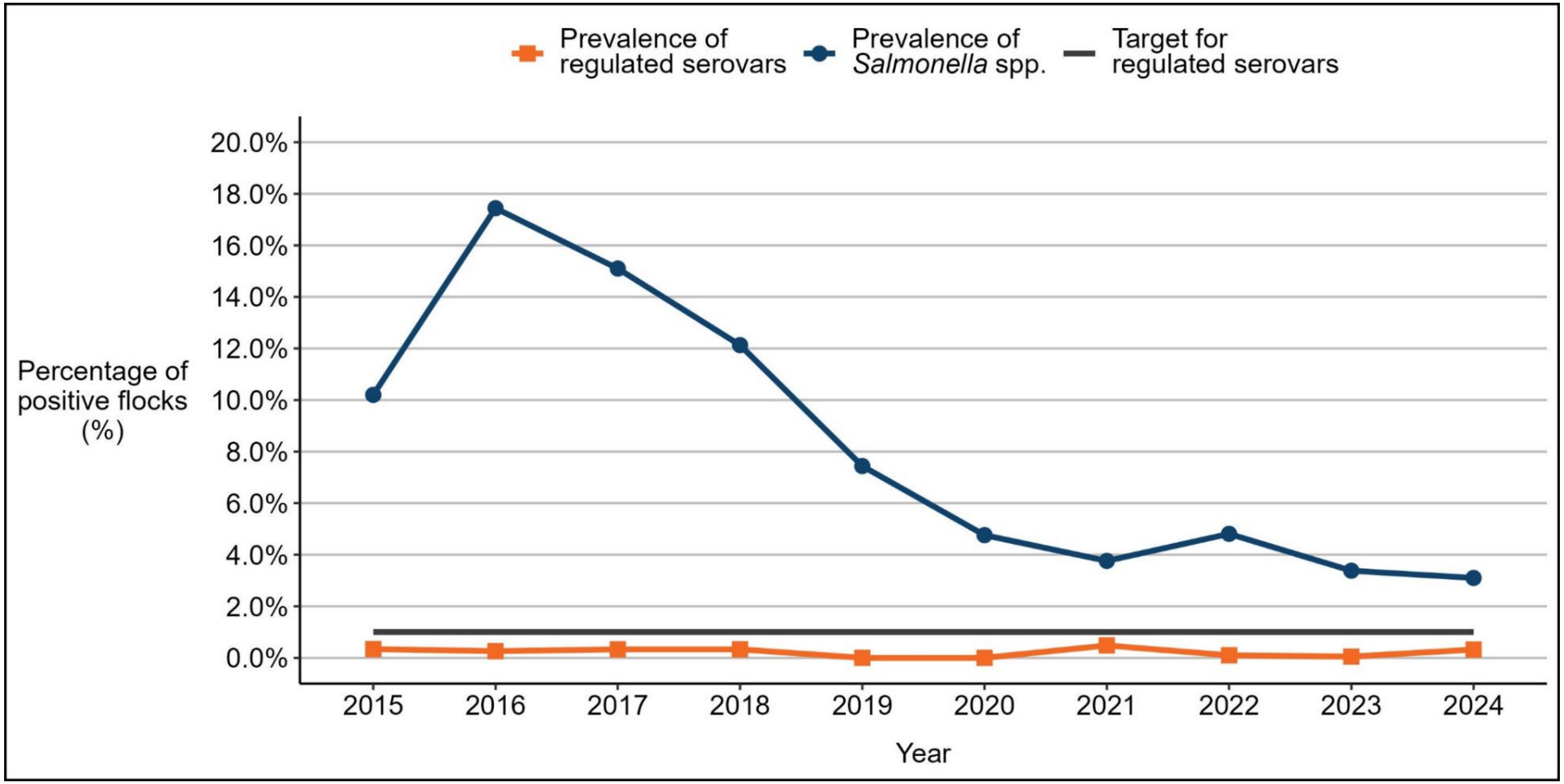
Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding turkeys in 2023. In 2023 the only *Salmonella* serovar isolated in breeding turkey flocks was *S*. Typhimurium, accounting for 100% of all isolations.

Figure 7.4.5: Isolations in adult breeding turkeys in 2024



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult breeding turkeys in 2024. In 2024 the only *Salmonella* serovar isolated in adult breeding turkey flocks was *S*. Typhimurium, accounting for 100% of all isolations.

Figure 7.5: Prevalence of *Salmonella* in turkey fattening flocks tested under NCP in Great Britain 2015 to 2024



A line graph showing the prevalence of *Salmonella* in adult turkey fattening flocks tested under the NCP from 2015 to 2024. 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 3.1% in 2024.The prevalence of regulated serovars remains very low and below 1% prevalence across all years.

Table 7.4: Turkey breeding flocks in Great Britain (number of adult flocks reported positive for each *Salmonella* serovar, NCP testing 2020 to 2024)

The following table shows the number of turkey breeding flocks reported positive with each *Salmonella* serovar from 2020 to 2024 and the rank within that year. This data comes from NCP testing.

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Typhimurium	0	0	0	0	0	0	1	1	1	1
Agama	3	1	1	1	0	0	0	0	0	0
Derby	3	1	0	0	0	0	0	0	0	0
Idikan (incl monophasic)	2	2	0	0	0	0	0	0	0	0
Mbandaka	0	0	2	1	0	0	0	0	0	0
Monophasic Typhimurium	0	0	0	0	0	0	0	0	0	0
Senftenberg	1	3	0	0	1	4	0	0	0	0

For details of turkey breeding flocks reported positive in 2014 to 2019, see the 2019 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
2020	2.62%	0.00%
2021	0.83%	0.00%
2022	1.97%	0.00%

Year	Prevalence of all serovars	Prevalence of regulated serovars
2023	0.58%	0.58%
2024	0.67%	0.67%

Table 7.5: Turkey fattening flocks in Great Britain (number of flocks reported positive for each *Salmonella* serovar, NCP testing 2020 to 2024)

The following table shows the number of turkey fattening flocks reported positive with each *Salmonella* serovar from 2020 to 2024 and the rank within that year. This data comes from NCP testing.

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
Anatum	1	38	1	31	1	40	2	18	1	19
Kedougou	2	33	3	9	2	21	1	32	2	15
Agona	7	2	5	4	3	7	5	4	3	11
Typhimurium	0	0	6	3	0	0	0	0	4	7
Indiana	0	0	0	0	0	0	0	0	5	6
Idikan (incl monophasic)	6	4	7	2	6	2	4	5	6	4
Derby	3	19	2	19	3	7	6	2	7	2
Orion var. 15+	8	1	5	4	5	3	3	6	7	2
Ago	0	0	0	0	0	0	0	0	8	1
Javiana	0	0	0	0	0	0	0	0	8	1
Agama	0	0	8	1	0	0	0	0	0	0
Bovismorbificans	0	0	7	2	0	0	0	0	0	0
Brandenburg	0	0	0	0	6	1	0	0	0	0
Chester	0	0	0	0	0	0	7	1	0	0
Give	0	0	0	0	0	0	7	1	0	0
Give var. 15+	0	0	8	1	0	0	0	0	0	0
Kingston	8	1	0	0	0	0	0	0	0	0
Kottbus	0	0	0	0	0	0	6	2	0	0

Salmonella serovar	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023	Rank 2024	Flocks 2024
London	0	0	8	1	5	3	0	0	0	0
Mbandaka	8	1	0	0	0	0	0	0	0	0
Monophasic Typhimurium	0	0	12	9	12	2	7	1	0	0
Montevideo	0	0	0	0	5	3	0	0	0	0
Newport	8	1	7	2	6	1	0	0	0	0
O rough:e,h:1,6	8	1	0	0	0	0	0	0	0	0
O rough:f,g:-	7	2	0	0	0	0	0	0	0	0
Orion	0	0	0	0	0	0	7	1	0	0
Schwarzengrund	0	0	0	0	0	0	7	1	0	0
Senftenberg	5	6	6	3	4	5	7	1	0	0
3,10:e,h:-	4	11	6	3	6	3	0	0	0	0
3,19:rough:-	8	1	8	1	6	1	7	1	0	0
6,8:e,h:-	8	1	8	1	0	1	0	0	0	0

For details of turkey fattening flocks reported positive in 2014 to 2019, see the 2019 edition of *Salmonella* in livestock production in Great Britain.

Prevalence of all serovars and regulated serovars in fattening turkey flocks

Year	Prevalence of all serovars	Prevalence of regulated serovars
2020	4.76%	0.00%
2021	3.76%	0.48%
2022	4.81%	0.10%
2023	3.38%	0.05%
2024	3.10%	0.32%

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 2020:

- 4 flocks tested positive for *S*. Anatum and *Salmonella* 3,10:e,h:-
- 1 flock tested positive for *S*. Derby and *S*. O rough:f,g:-

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

In 2023:

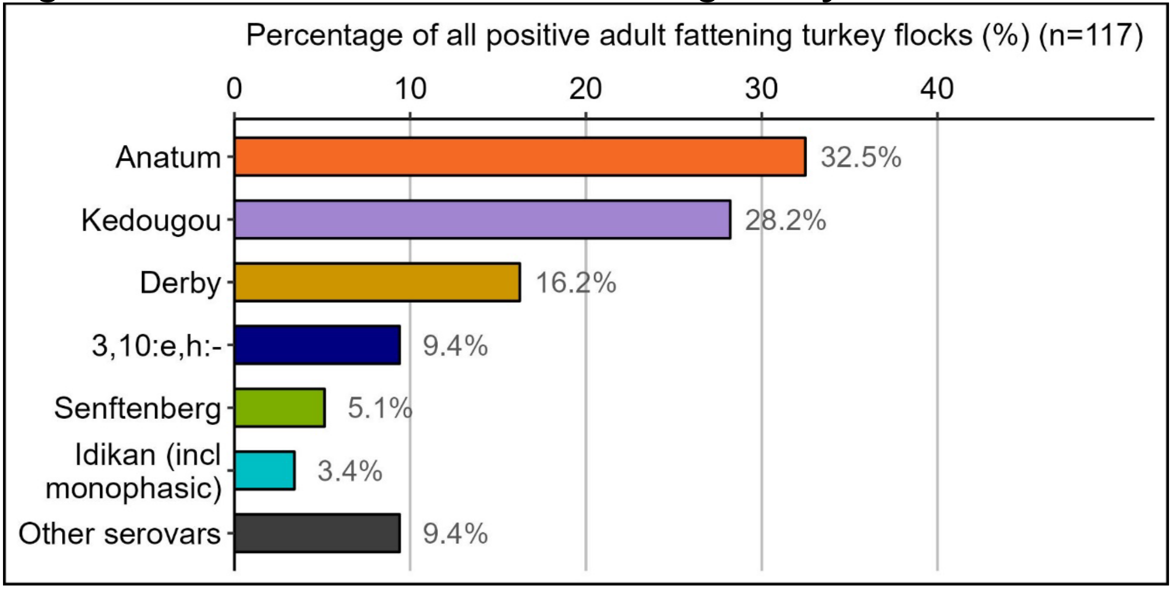
- 4 flocks tested positive for both *S*. Kedougou and *S*. 13,23:i:-
- 1 flock tested positive for both *S*. Kedougou and *S*. Anatum
- 1 flock tested positive for both *S.* Orion and *S.* Orion var 15+

In 2024:

- 0 flocks tested positive for more than one serovar.

Figure 7.6: The most common serovars identified in turkey fattening flocks in Great Britain 2020 to 2024 reported from NCP testing

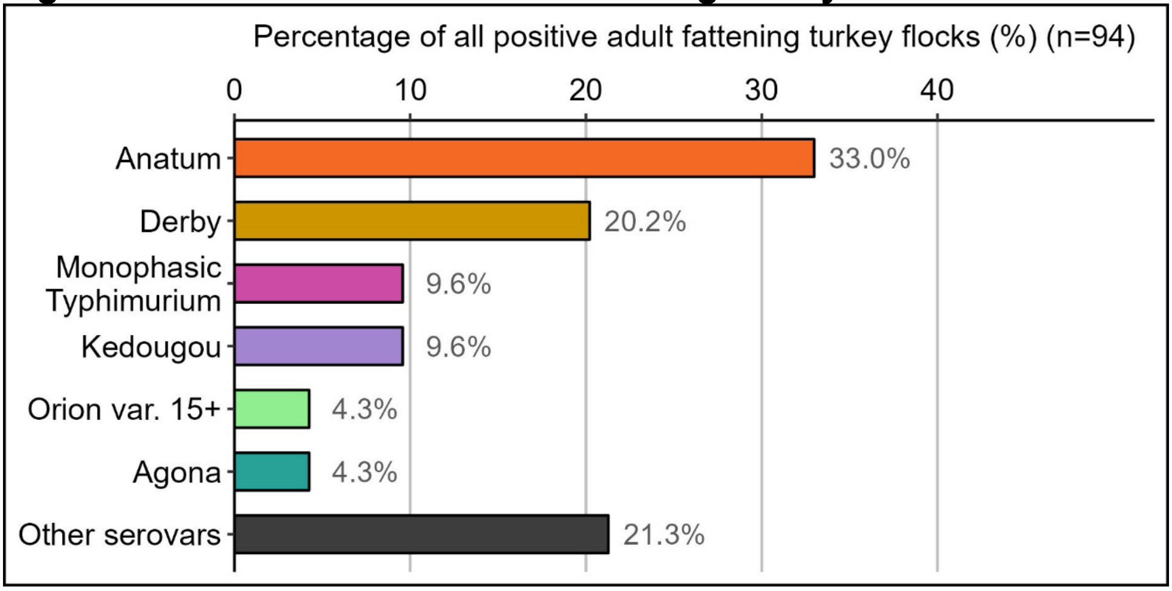
Figure 7.6.1: Isolations in adult fattening turkeys in 2020



Horizontal bar graph showing the percentage of *Salmonella* isolations in adult fattening turkeys in 2020. In 2020 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Anatum, accounting for 32.5% of total isolations, followed by *S.* Kedougou (28.2%), *S*. Derby (16.2%) and *S.* 3,10:e,h:- (9.4%).

In 2020 5 flocks were positive for 2 serovars (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

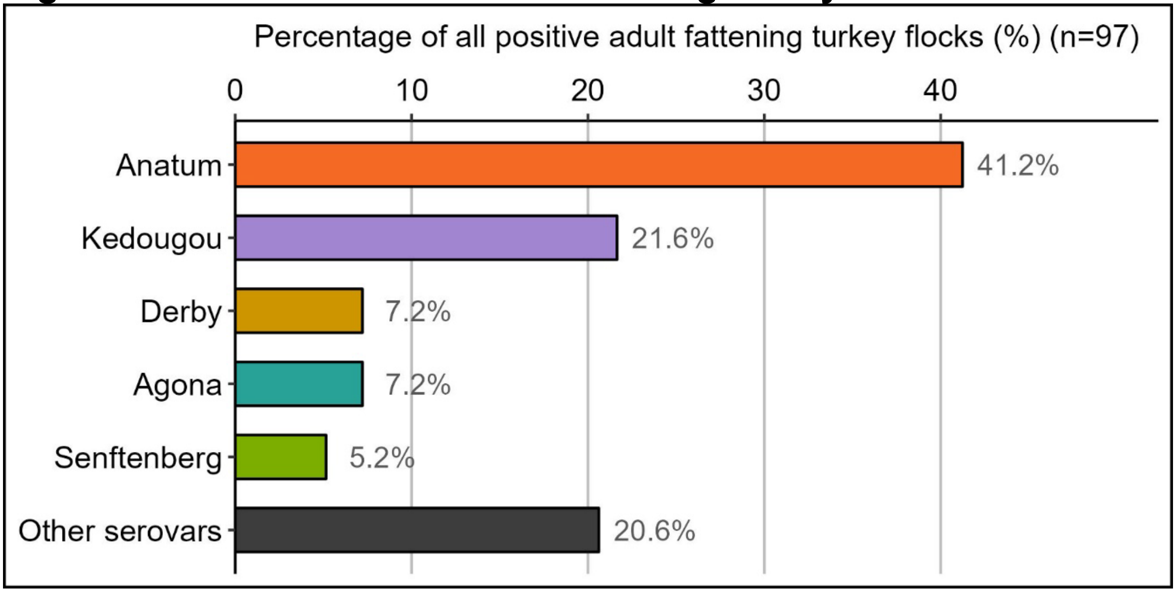
Figure 7.6.2: Isolations in adult fattening turkeys in 2021



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 (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%.

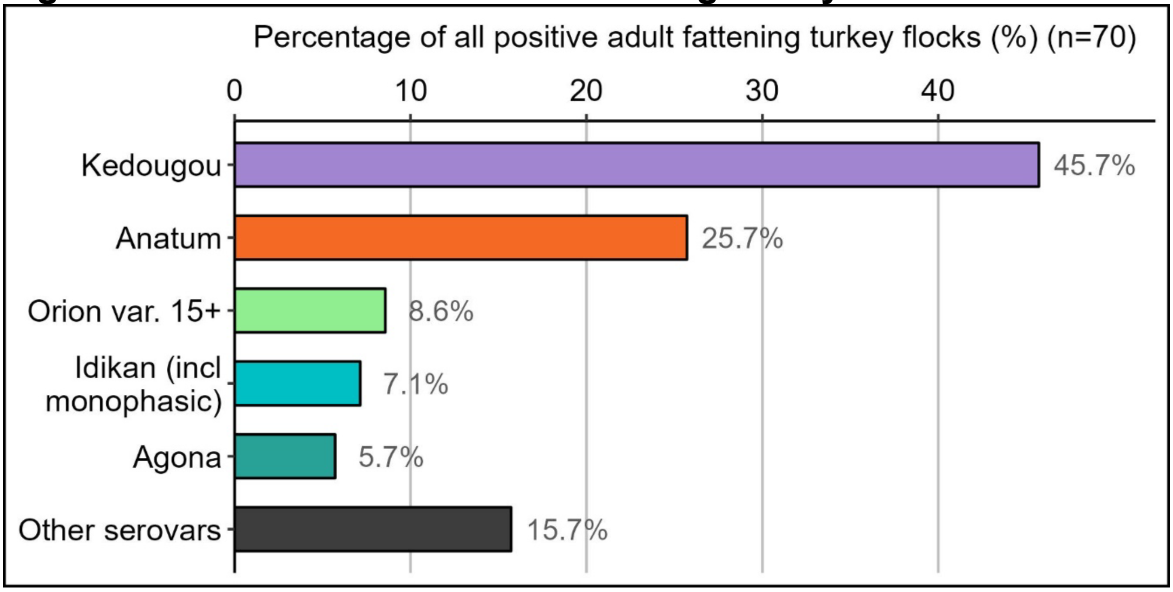
Figure 7.6.3: Isolations in adult fattening turkeys in 2022



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 (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%.

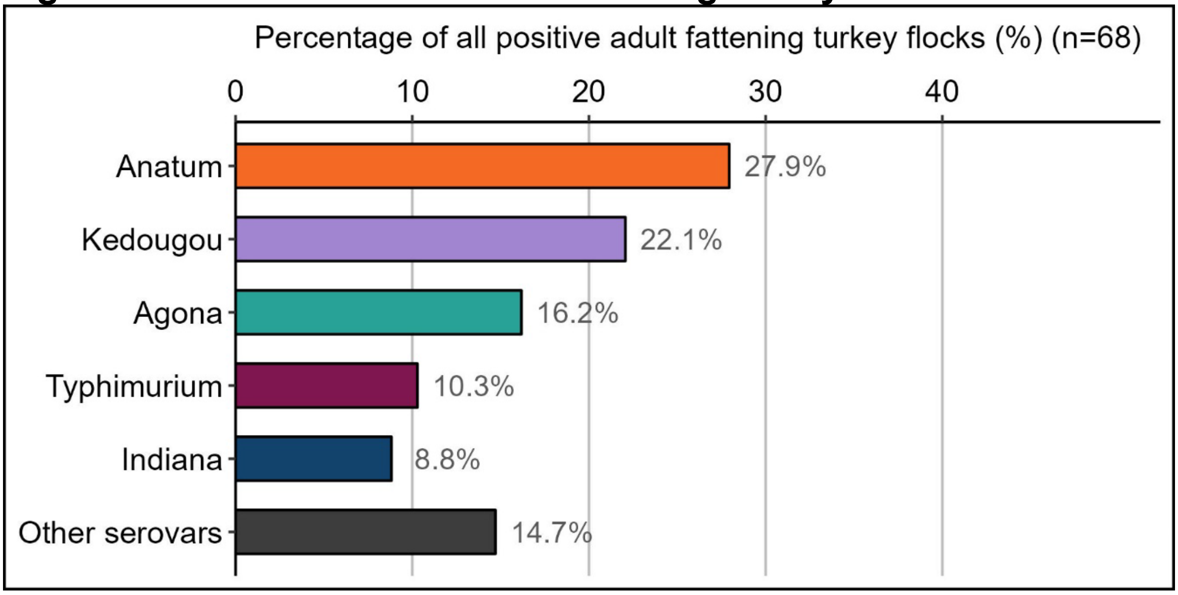
Figure 7.6.4: Isolations in adult fattening turkeys in 2023



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, accounting for 45.7% of total isolations, followed by *S*. Anatum (25.7%), *S*. Orion var 15$^+$ (8.6%) and *S*. Idikan (incl monophasic) (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 7.6.5: Isolations 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%).

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

Between 2020 and 2023 there was a reduction in non-statutory surveillance and clinical diagnostic submissions in many livestock species as a consequence of both the Covid-19 pandemic and associated lockdown measures and then large Avian Influenza outbreaks and the associated control measures placed on the poultry industry. This should therefore be borne in mind when comparing data between years.

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 2024 there were 92 diagnostic submissions from ducks recorded on the VIDA database in Great Britain compared to 107 in 2023. The VIDA database records both farmed and wild ducks.

During 2024 there were 196 isolations of *Salmonella* from ducks in Great Britain, which is over double that seen in 2023 (96 isolations) and a 62.0% increase compared to 2022 (121 isolations) (Table 8.1). This upturn was influenced by an increase in voluntary surveillance testing carried out by the duck industry, resulting in a higher number of isolations in 2024. Surveillance in this sector can fluctuate depending on external factors.

The most common serovars isolated from ducks during 2024 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). Together these serovars accounted for 95.4% of all *Salmonella* isolations from ducks (Figure 8.1). In contrast, during 2023 the most common serovars were *S.* Indiana (52 isolations, 54.2% of duck isolations), *S.* Kottbus (12 isolations, 12.5% of duck isolations), *S*. Give (9 isolations, 9.4% of duck isolations), *S*. Lexington (8 isolations, 8.3% of duck isolations) and *S*. Hadar (6 isolations, 6.3% of duck isolations).

Salmonella Indiana remained the most commonly reported serovar from ducks during 2024 (147 isolations). This serovar accounted for a higher proportion of total isolations from ducks in 2024 (75.0%) compared to 2023 (54.2%) (Figure 8.1 and Figure 8.3).

The second most commonly reported serovar in 2024 was *S.* Newport, with 20 isolations, accounting for 10.2% of duck isolations. Isolations of this serovar have been low in recent years with no isolations in 2022 or 2023, one isolation in 2021 and 2 isolations in 2020.

There were 12 isolations of *S.* Kottbus from ducks in 2024, the same as in 2023. *S.* Kottbus isolations accounted for 6.1% of total isolations from ducks in 2024 and was the third most common serovar. *Salmonella* Kottbus has been isolated from ducks every year since 2013, and until 2023 there had been a generally declining trend in the number of isolations since 2018 (Table 8.1).

There were 5 isolations of *S*. Give from ducks in 2024, a decrease compared to 2023 (9 isolations) which represented the highest number of isolations since 2019 but was still lower than in the period 2014 to 2018 when there were greater than 20 isolations.

There were 3 isolations of *Salmonella* Give var. 15^+ in 2024, an increase compared to no isolations in 2023. There has been a general decline in isolations since 2017 (70 isolations) however, *S*. Give var.15^+ was the joint third most common serovar to be isolated from ducks in 2022.

There were 2 isolations of *S.* Orion during 2024 (1.0% of duck isolations) the same as in 2023 (2.1% of duck isolations) and 2022 (1.7% of duck isolations) but much lower than the 12 isolations in 2021 when it was the second most commonly isolated serovar in ducks (10.9% of isolations). This represents an 83.3% decrease compared to 2021 and the lowest number of *S*. Orion isolations in ducks since 2011 (2 isolations).

There were 2 isolations of *S.* Hadar during 2024, a decrease compared to 2023 (6 isolations) and 2022 (17 isolations), when it was the second most common serovar isolated from ducks. In general, there has been a declining trend in the number of *S*. Hadar isolations since 2018 (44 isolations) with the exception of 2020 (21 isolations) and 2022 (17 isolations).

There was one *S.* Lexington isolation during 2024, a decrease compared to 2023 (8 isolations), 2021 and 2022 (9 isolations each) and 2020 (7 isolations). There was one isolation of *S.* Orion var. 15^+ during 2024, a decrease compared to 2023 (5 isolations) and 2022 (15 isolations).

There were no isolations of *S*. Enteritidis (Table 8.4) from ducks in 2024, compared to one in 2023 (PT9), none in 2022 and one isolation each in 2020 and 2021 (both PT9b). There were no isolations of *S*. Typhimurium (Table 8.3) from ducks during 2024, a decrease compared to 2023 when there was one isolation (DT1) but the same as 2021 and 2022 when there were no isolations from ducks. 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 duck assurance scheme in 2010. There were no isolations of Monophasic *S*. Typhimurium in ducks during 2024, consistent with 2020 to 2023.

Antimicrobial susceptibility in ducks

A total of 194 *Salmonella* isolates from ducks were tested against a panel of 16 antimicrobials in 2024. The proportion of fully susceptible isolates rose from 84.3% in 2023 (n=89) to 96.9% in 2024, maintaining the trend of low resistance in this species.

Only 6 isolates (5 *S.* Indiana, one *S.* Kottbus) displayed resistance, each to a single antimicrobial: ampicillin (n=2), apramycin (n=1), chloramphenicol (n=2), and neomycin (n=1).

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

Geese

There was one isolation of *Salmonella* from geese in 2024 of *S*. Typhimurium DT193. This compares to no isolations between 2021 and 2023 and 2 isolations during 2020. 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 2024 there were 119 diagnostic submissions from geese recorded on the VIDA database in Great Britain compared to 163 in 2023. The VIDA database records both farmed and wild geese.

One *Salmonella* isolate from geese was tested against a panel of 16 antimicrobials in 2024. The isolate was fully susceptible to all the antimicrobials.

Table 8.1: Isolations and incidents of *Salmonella* in ducks on all premises in Great Britain 2020 to 2024

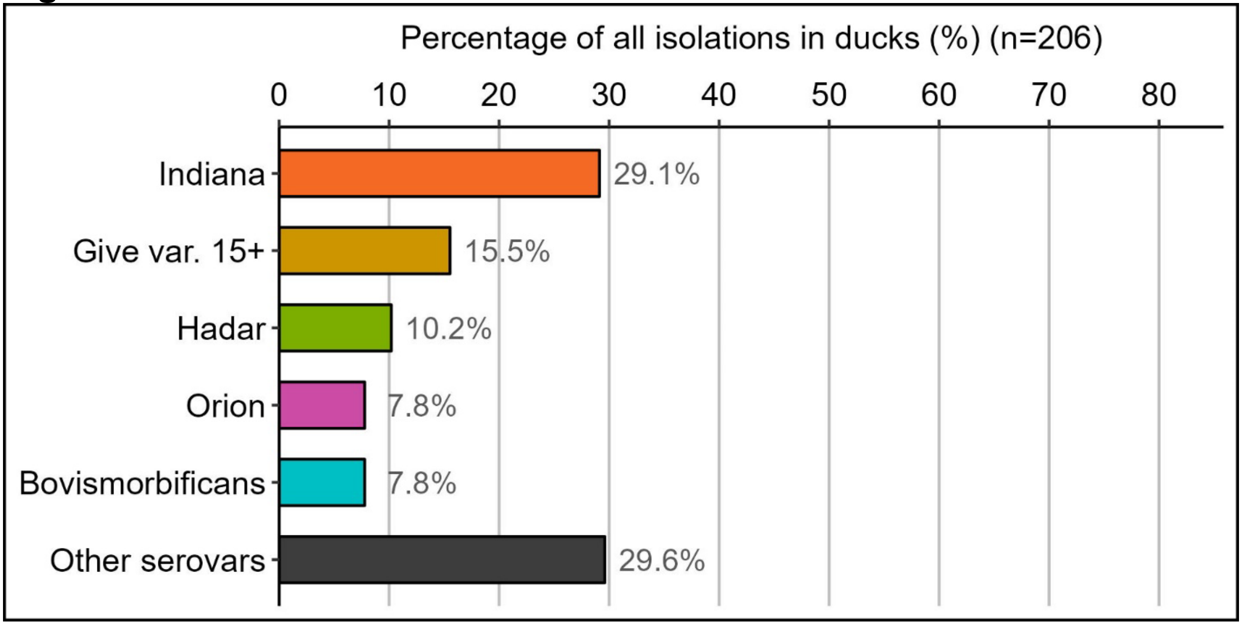
Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Agona	0	0	1	1	0	0	0	0	0	0
Bovismorbificans	16	8	0	0	15	3	0	0	0	0
Enteritidis	1	1	1	1	0	0	1	1	0	0
Give	6	6	6	5	1	1	9	9	5	5
Give var. 15$^+$	32	21	6	5	15	13	0	0	3	1
Hadar	21	20	1	1	17	10	6	5	2	2
Indiana	60	53	41	33	38	28	52	28	147	100
Kedougou	0	0	1	1	0	0	0	0	2	2
Kingston	0	0	0	0	0	0	0	0	1	1
Kottbus	6	5	9	9	6	5	12	10	12	10
Lexington	7	5	9	7	9	8	8	6	1	1
Monschaui	2	2	0	0	0	0	0	0	0	0
Newport	2	2	1	1	0	0	0	0	20	16
Orion	16	15	12	11	2	2	2	2	2	1
Orion var. 15$^+$	12	12	8	6	15	8	5	2	1	1
Oslo	3	2	0	0	0	0	0	0	0	0
Senftenberg	0	0	1	0	0	0	0	0	0	0
Typhimurium	2	2	0	0	0	0	1	1	0	0
untypable strains	18	18	13	13	3	3	0	0	0	0
rough strains	2	2	0	0	0	0	0	0	0	0
Total	**206**	**174**	**110**	**94**	**121**	**81**	**96**	**64**	**196**	**140**

Table 8.2: Isolations and incidents of *Salmonella* in geese on all premises in Great Britain 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Beaudesert	1	1	0	0	0	0	0	0	0	0
Typhimurium	1	1	0	0	0	0	0	0	1	1
Total	**2**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**1**

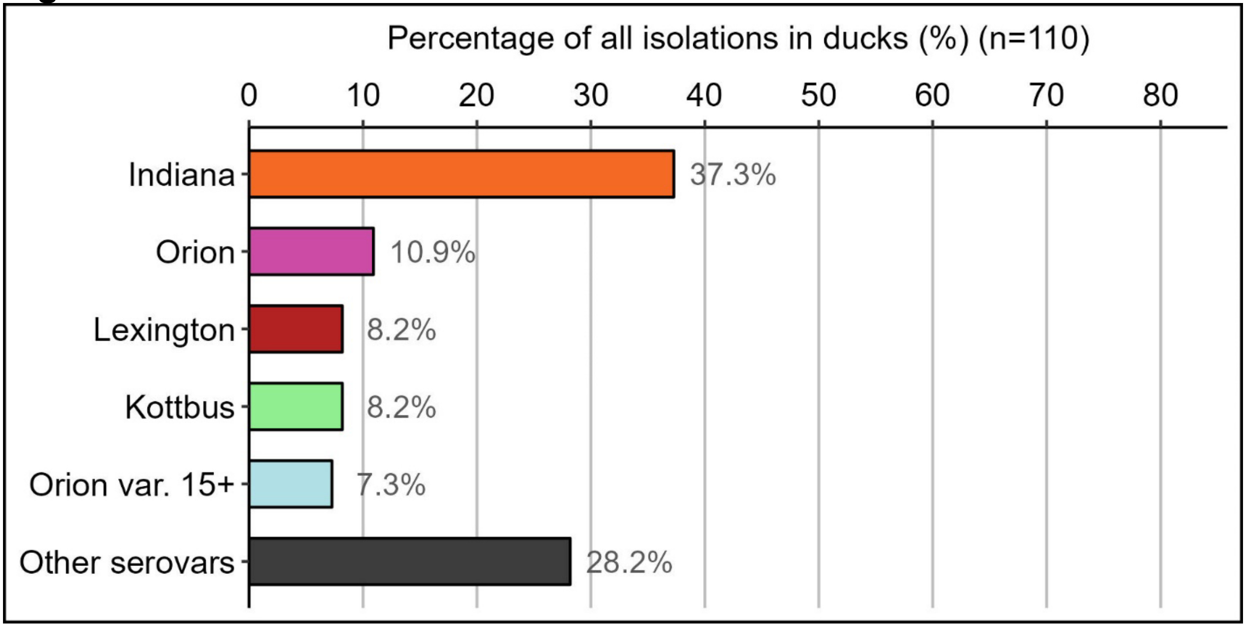
Figure 8.1: Isolations of the most common serovars in ducks in Great Britain 2020 to 2024

Figure 8.1.1: Isolations in ducks in 2020



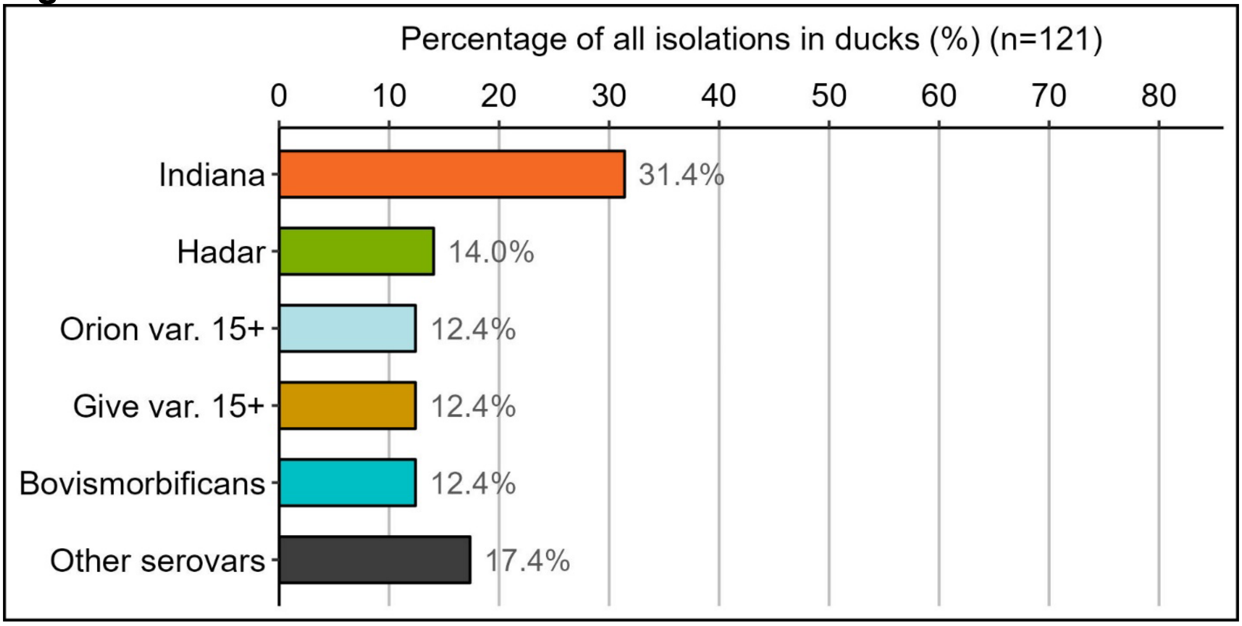
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in ducks in 2020. The most common *Salmonella* serovar in ducks in 2020 was *S.* Indiana, accounting for 29.1% of total isolations, followed by *S*. Give var. 15^+ (15.5%), *S.* Hadar (10.2%) and *S.* Bovismorbificans and *S*. Orion (7.8% each).

Figure 8.1.2: Isolations in ducks in 2021



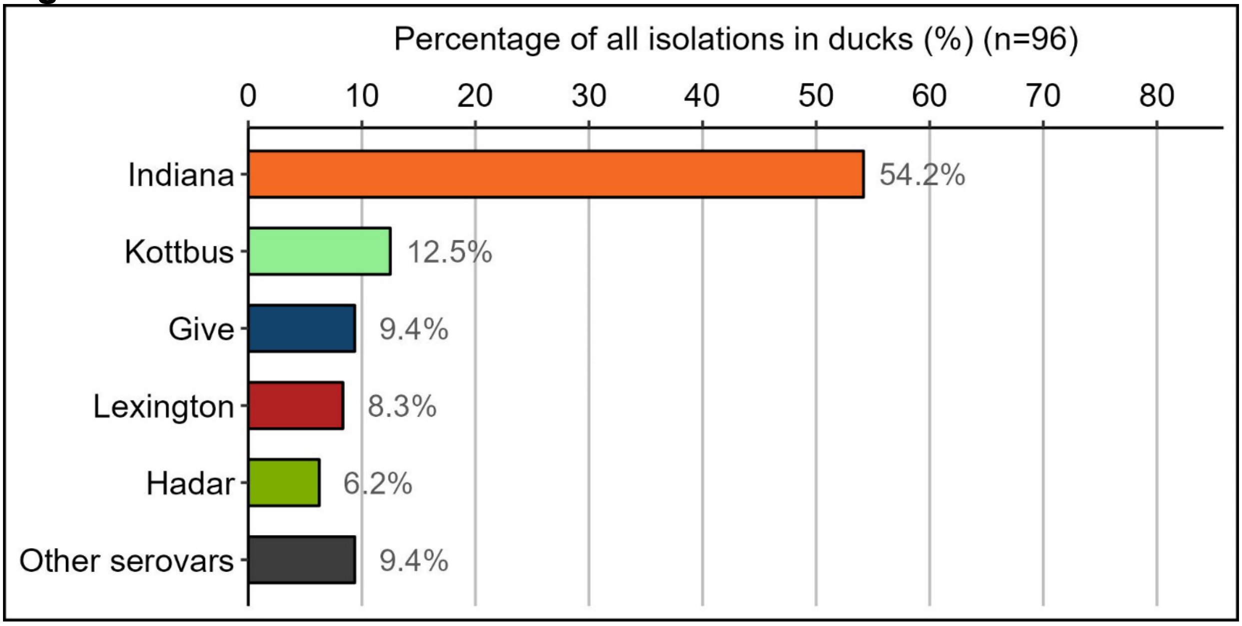
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in ducks in 2021. The most common *Salmonella* serovar in ducks in 2021 was *S.* Indiana, accounting for 37.3% of total isolations, followed by *S*. Orion (10.9%), *S.* Kottbus and *S.* Lexington (8.2% each) and *S*. Orion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

Figure 8.1.3: Isolations in ducks in 2022



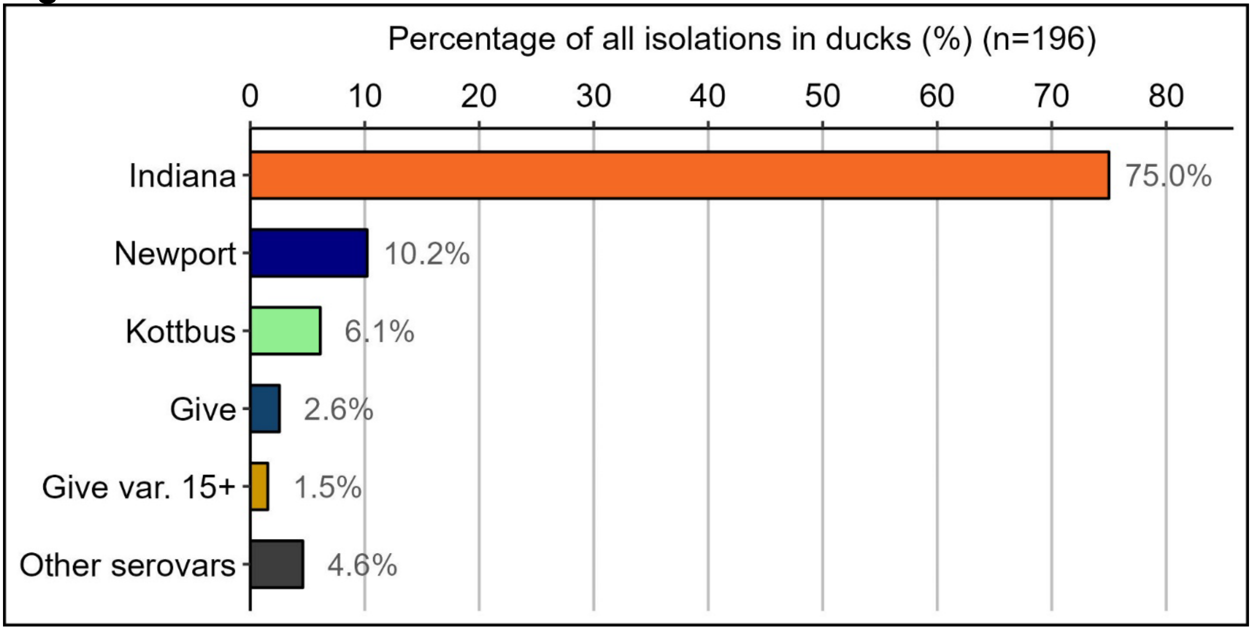
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in ducks in 2022. The most common *Salmonella* serovar in ducks in 2022 was *S.* Indiana, accounting for 31.4% of total isolations, followed by *S*. Hadar (14.0%), *S.* Bovismorbificans, *S.* Give var. 15⁺ and *S.* Orion var.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

Figure 8.1.4: Isolations in ducks in 2023



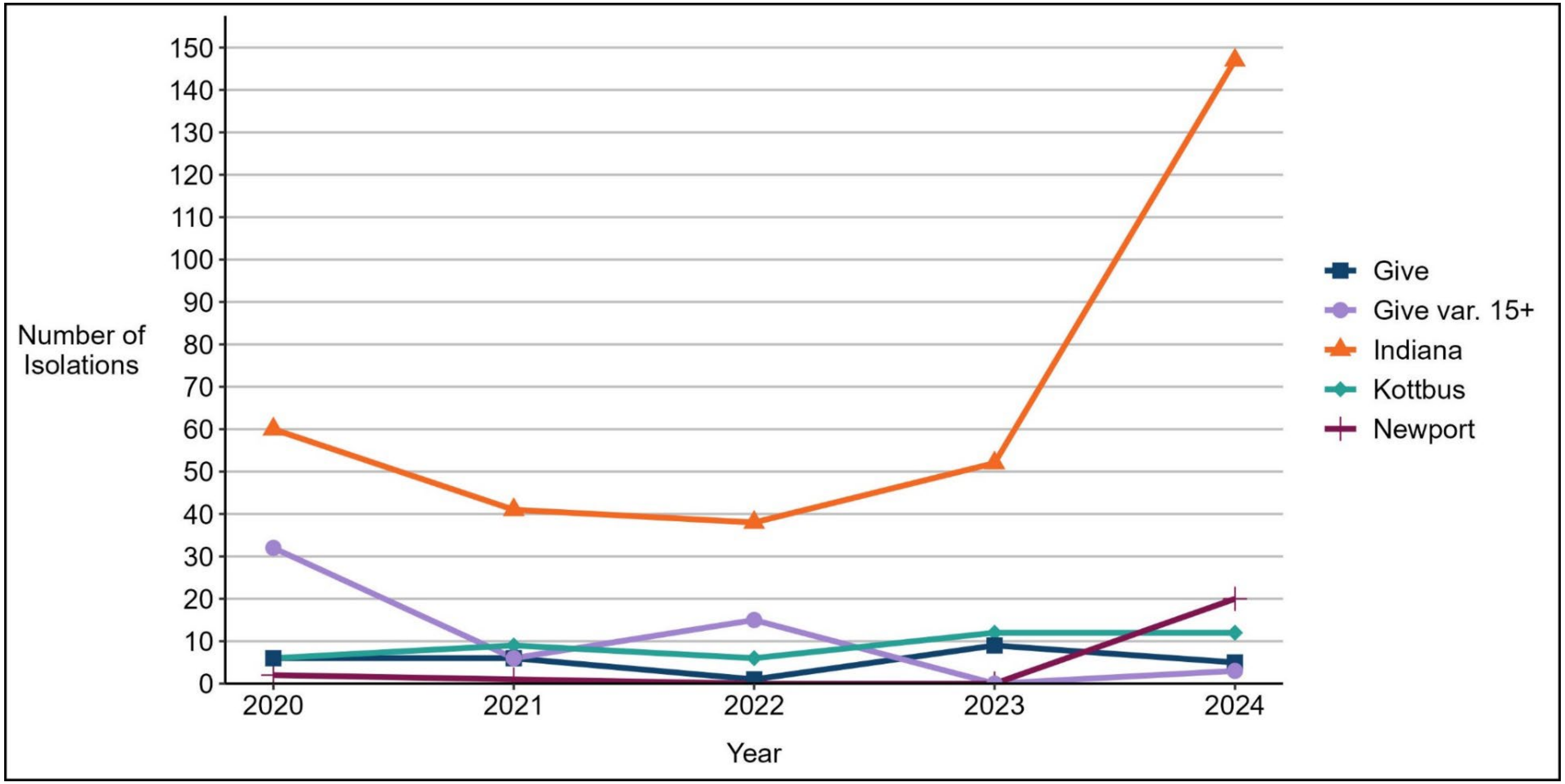
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in ducks in 2023. The most common *Salmonella* serovar in ducks in 2023 was *S.* Indiana, accounting for 54.2% of total isolations, followed by *S*. Kottbus (12.5%), *S.* Give (9.4%), *S.* Lexington (8.3%) and *S*. Hadar (6.2%).

Figure 8.1.5: Isolations in ducks in 2024



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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 8.2: The 5 most common *Salmonella* serovars in ducks in Great Britain in 2024 and their trends over time since 2020



A line graph showing the 5 most common serovars in ducks from 2020 to 2024. The figure shows that *S.* Indiana remains the most common serovar isolated from ducks with a marked increase from 52 isolations in 2023 to 147 in 2024. *S*. Newport was the second most common serovar in 2024 and isolations increased to 20 in 2024, compared to years 2020 to 2023 when isolations ranged from 0 to 2. *S*.

Kottbus has remained stable in recent years, 12 isolations in 2023 and 2024 and was the third most common serovar in 2024. *S.* Give has remained relatively stable from 6 isolations in 2020 to 5 isolations in 2024. *S.* Give var. 15^+ was the least common of the 5 in 2024 and isolations have declined since 2020 from 32 isolations to 3 isolations in 2024.

Figure 8.3: *S.* Enteritidis, *S.* Indiana, *S.* Typhimurium, Monophasic *S.* Typhimurium and other serovars as a percentage of all isolations in ducks in Great Britain 2004 to 2024

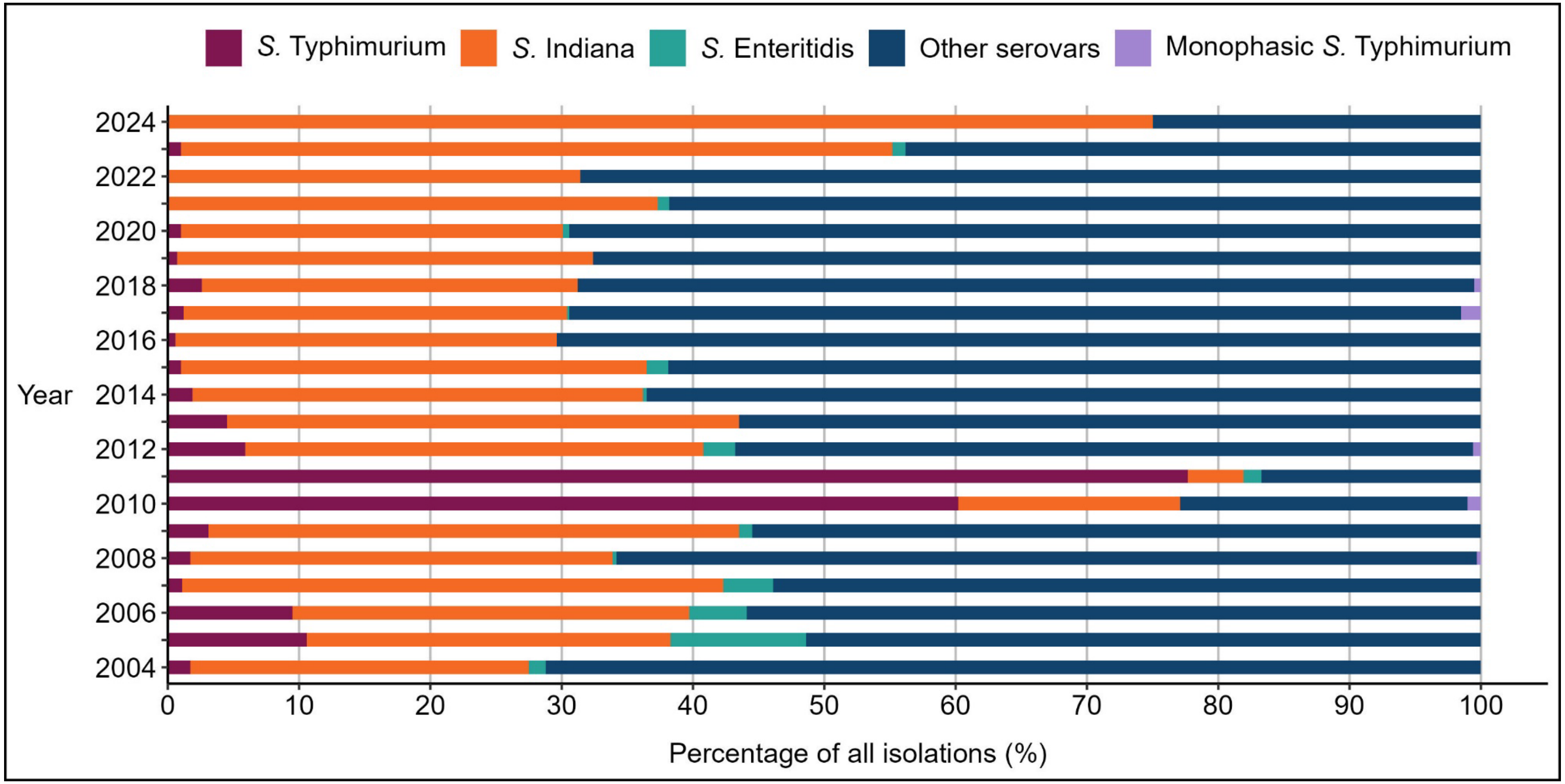


Figure 8.3 shows that *S.* Indiana accounts for the highest proportion of single serovar isolations in all years except 2010 and 2011, exceeding 25.0% every year since 2012. *S.* Typhimurium has accounted for less than 11.0% of all duck isolations every year except for

2010 and 2011 when it was 60.2% and 77.7% respectively. Monophasic *S.* Typhimurium and *S.* Enteritidis are typically very low, the highest being 1.5% in 2017 and 10.3% in 2005 respectively.

Figure 8.3: Table of data

Year	Other serovars	Monophasic *S.* Typhimurium	*S.* Typhimurium	*S.* Indiana	*S.* Enteritidis
2004	71.2%	0.0%	1.7%	25.8%	1.3%
2005	51.4%	0.0%	10.6%	27.7%	10.3%
2006	55.9%	0.0%	9.5%	30.2%	4.4%
2007	53.9%	0.0%	1.1%	41.2%	3.8%
2008	65.5%	0.3%	1.7%	32.2%	0.3%
2009	55.5%	0.0%	3.1%	40.4%	1.0%
2010	21.9%	1.0%	60.2%	16.9%	0.0%
2011	16.7%	0.0%	77.7%	4.2%	1.4%
2012	56.2%	0.6%	5.9%	34.9%	2.4%
2013	56.5%	0.0%	4.5%	39.0%	0.0%
2014	63.5%	0.0%	1.9%	34.3%	0.3%
2015	61.9%	0.0%	1.0%	35.5%	1.6%
2016	70.4%	0.0%	0.6%	29.0%	0.0%
2017	67.9%	1.5%	1.2%	29.2%	0.2%
2018	68.3%	0.5%	2.6%	28.6%	0.0%
2019	67.6%	0.0%	0.7%	31.7%	0.0%
2020	69.4%	0.0%	1.0%	29.1%	0.5%
2021	61.8%	0.0%	0.0%	37.3%	0.9%
2022	68.6%	0.0%	0.0%	31.4%	0.0%
2023	43.8%	0.0%	1.0%	54.2%	1.0%
2024	25.0%	0.0%	0.0%	75.0%	0.0%

Table 8.3: *S*. Typhimurium phage types in ducks and geese in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT1	0	0	0	0	0	0	1	1	0	0
DT9	2	2	0	0	0	0	0	0	0	0
DT193	1	1	0	0	0	0	0	0	1	1
Total	**3**	**3**	**0**	**0**	**0**	**0**	**1**	**1**	**1**	**1**

Two isolations and incidents in this table were reported from geese. These were one isolation and incident of phage type DT193 in 2020, and one isolation and incident of DT193 in 2024. The further 3 isolations and incidents in the table were reported from ducks.

Table 8.4: *S*. Enteritidis phage types in ducks and geese in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
PT9	0	0	0	0	0	0	1	1	0	0
PT9b	1	1	1	1	0	0	0	0	0	0
Total	**1**	**1**	**1**	**1**	**0**	**0**	**1**	**1**	**0**	**0**

All isolations and incidents in this table were reported from ducks. There were no isolations or incidents of *S*. Enteritidis from geese between 2020 and 2024.

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 22 isolations of *Salmonella* were reported from these species during 2024 which is comparable to 2023 (22 isolations) and an increase compared to 2022 (18 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 decreased by 11.0% to 161 submissions in 2024, compared to 181 submissions in 2023. As in previous years, the greatest number of submissions were from pheasants, though there was a decrease of 18.1% compared with 2023 (95 versus 116 submissions). During 2024 there were also 26 submissions from partridges which was an increase of 52.9% compared to 2023 (17 submissions) and 20 submissions from grouse, which was a decrease of 47.4% compared with 2023 (38 submissions).

Eight quail submissions were received during 2024, compared to only 2 submissions in 2023. Two guinea fowl submissions were received in 2024 whereas none were received in 2023. A further 10 submissions in 2024 were from birds reported as “other game” which is slightly higher than in 2023 (8 submissions).

There is no statutory *Salmonella* monitoring of game birds in Great Britain and the majority of submissions in 2024 were for diagnostic purposes (78.9%), which is more than during 2023 (65.7%). In 2024 there were no *Salmonella* isolations in game birds, compared to 4 isolations in 2023 and one isolation in 2022. In recent years there has been a decreasing trend in the number of *Salmonella* isolations from game birds, across all species.

Pheasants

There were no isolations of *Salmonella* from pheasants in 2024, in comparison to 2023 when there were 2 isolations (*S*. Sentfenberg and *S*. Typhimurium NOPT) and 2022 when there was one isolation (*S*. Dublin) (Table 9.1).

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

Partridges

There were no isolations of *Salmonella* in partridges in 2024, a change from 2023 when there were 2 isolations, though the same as in 2021 and 2022 when there were also no isolations. Prior to this there were 5 *Salmonella* isolations from partridges in Great Britain in 2020 (Table 9.2).

Quail

There were no isolations of *Salmonella* from quail in 2024. 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 2024. The last time *Salmonella* was isolated from guinea fowl was in 2015 when there was one isolation.

Pigeons

There were 106 VIDA submissions from pigeons to APHA and SRUC in 2024 which is a 55.9% increase compared to 2023 (68 submissions) and a 24.7% increase compared to 2022 (85 submissions).

There were 22 *Salmonella* isolations from pigeons in 2024, which is slightly higher than that in 2022 and 2023 (17 and 18 isolations, respectively) (Table 9.3). Six of these isolations were from clinical disease investigations with chicks dying in the nest being the presenting sign for one isolation and no available presenting signs for the other isolations. The other 16 isolations were from voluntary surveillance submissions. Most isolations in 2024 were *S*. Typhimurium (21 isolations), which is consistently the most commonly isolated serovar from pigeons. Among these, 16 isolations were phage type DT2, 2 were DT99, 2 were NOPT and one was UNTY (Table 9.7). DT2 and DT99 are considered to be pigeon adapted strains of *S.* Typhimurium and regularly isolated from pigeons in GB. The only other serovar isolated from pigeons in 2024 was *S*. Braenderup (1 isolation).

Table 9.1: Isolations and incidents of *Salmonella* in pheasants on all premises in Great Britain 2020 to 2024

***Salmonella* serovar**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**	**2024 isolations**	**2024 incidents**
Dublin	0	0	0	0	1	1	0	0	0	0
Monophasic Typhimurium	0	0	1	1	0	0	0	0	0	0
Montevideo	1	1	0	0	0	0	0	0	0	0
Orion	1	1	1	1	0	0	0	0	0	0
Senftenberg	3	2	4	3	0	0	1	1	0	0
Typhimurium	1	0	1	1	0	0	1	1	0	0
Total	**6**	**4**	**7**	**6**	**1**	**1**	**2**	**2**	**0**	**0**

Table 9.2: Isolations and incidents of *Salmonella* in partridges on all premises in Great Britain 2020 to 2024

***Salmonella* serovar**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**	**2024 isolations**	**2024 incidents**
Monophasic Typhimurium	3	1	0	0	0	0	0	0	0	0
Senftenberg	2	2	0	0	0	0	1	1	0	0
Typhimurium	0	0	0	0	0	0	1	1	0	0
Total	**5**	**3**	**0**	**0**	**0**	**0**	**2**	**2**	**0**	**0**

Table 9.3: Isolations and incidents of *Salmonella* in pigeons on all premises in Great Britain 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Braenderup	0	0	0	0	0	0	0	0	1	1
Enteritidis	0	0	1	1	0	0	0	0	0	0
Kedougou	1	1	0	0	0	0	0	0	0	0
Orion	1	1	0	0	0	0	0	0	0	0
Typhimurium	13	13	6	6	17	17	18	18	21	20
untypable strains	2	2	1	1	0	0	0	0	0	0
Total	**17**	**17**	**8**	**8**	**17**	**17**	**18**	**18**	**22**	**21**

Table 9.4: *S*. Typhimurium phage types in pheasants in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT193	1	0	0	0	0	0	0	0	0	0
NOPT	0	0	1	1	0	0	1	1	0	0
Total	**1**	**0**	**1**	**1**	**0**	**0**	**1**	**1**	**0**	**0**

Table 9.5: *S*. Typhimurium phage types in partridges in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT11	0	0	0	0	0	0	1	1	0	0
Total	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**1**	**0**	**0**

Table 9.7: *S.* Typhimurium phage types in pigeons in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT2	9	9	6	6	13	13	13	13	16	15
DT99	0	0	0	0	4	4	3	3	2	2
DT105	0	0	0	0	0	0	1	1	0	0
DT193	2	2	0	0	0	0	1	1	0	0
NOPT	0	0	0	0	0	0	0	0	2	2
RDNC	1	1	0	0	0	0	0	0	0	0
UNTY	1	1	0	0	0	0	0	0	1	1
Total	**13**	**13**	**6**	**6**	**17**	**17**	**18**	**18**	**21**	**20**

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 2024 annual summary therefore represents the third 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 2024, the UK dog population was estimated to be around 13.5 million, with 36% of UK households owning one or more dogs. 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 482 *Salmonella* isolations from dogs in 2024 (Table 10.1). This is a decrease of 30.0% compared to 2023 (689 isolations), and a decrease of 43.8% compared to 2022 (857 isolations). In total, 62 different serovars were reported (excluding untypable and rough strains), which is slightly lower than 2023 (79 serovars) and 2022 (70 serovars). The majority of isolations (475 isolations, 98.5%) arose from clinical investigations with the remainder for other submission reasons (7 isolations, 1.5%).

The most commonly reported serovar from dogs in 2024 was *S*. Typhimurium (77 isolations, 16.0% of all isolations). *S*. Typhimurium has been the most commonly reported serovar for the past 4 years though for years prior to *Salmonella* in dogs being made reportable, the number of isolations was much lower (90 isolations in 2023, 116 isolations in 2022, 97 isolations in 2021, 11 isolations in 2020). The second most commonly reported serovar was *S*. Infantis (39 isolations, 8.1% of all isolations). Other commonly reported serovars were *S.* Newport (30 isolations), *S.* Anatum (27 isolations), *S.* Indiana (21 isolations), monophasic *S.* Typhimurium (19 isolations), *S.* Derby (19 isolations), *S.* Enteritidis (17 isolations), *S.* Dublin (17 isolations) and *S.* Kentucky (17 isolations) (Table 10.1, Figure 10.1.5).

Salmonella Typhimurium and monophasic *Salmonella* Typhimurium

There were 77 isolations of *S*. Typhimurium during 2024 comprising 16 different phage types. The most common phage types were DT105 (15 isolations, 19.5% of all *S*. Typhimurium in dogs), RDNC (15 isolations, 19.5% of all *S*. Typhimurium in dogs), DT75 (13 isolations, 16.9% of all *S*. Typhimurium in dogs), and DT2 (10 isolations, 13% of all *S*. Typhimurium in dogs) (Table 10.2). This is compared to 2023 when the most common phage types were RDNC (22 isolations, 24.4% of all *S*. Typhimurium in dogs), DT75 (16 isolations, 17.7% of all *S*. Typhimurium in dogs), DT193 (10 isolations, 11.1% of all *S*. Typhimurium in dogs), and DT2 (9 isolations, 10% of all *S*. Typhimurium in dogs). One *S*. Typhimurium phage type was reported for the first time in dogs from Great Britain during 2024 (DT20).

There were 19 isolations of monophasic *S*. Typhimurium reported from dogs during 2024 comprising 3 different phage types. The most common phage type was DT193 (15 isolations, 78.9% of all monophasic *S.* Typhimurium in dogs) (Table 10.4).

Other notable serovars

The number of *Salmonella* Infantis isolations from dogs was 39 in 2024, down from 79 isolations in 2023, 109 isolations in 2022 and 51 isolations in 2021, but higher than years prior to *Salmonella* in dogs being made reportable (3 isolations in 2020) (Table 10.1 and Figure 10.2). *Salmonella* Enteritidis was isolated 17 times from dogs in 2024, which is a decrease from 2023 (26 isolations). The most common phage types of *S*. Enteritidis were PT8 and PT11 (Table 10.3).

Serovars not previously reported

Several isolations in 2024 had never previously been reported in dogs from Great Britain. These isolated serovars included *S.* Brancaster (2 isolations), *S.* Chailey (1 isolation), *S.* Fresno (1 isolation), *S.* Leeuwarden (1 isolation), and *S.* Singapore (1 isolation).

Public health significance

The change to make *Salmonella* in dogs reportable was made to improve the protection of public health. In 2024, *Salmonella* isolations in dogs accounted for 13.3% of *Salmonella* isolations from all animals. The most common serovars isolated included those which are important causes of human disease, including *S*. Enteritidis, *S*. Typhimurium and *S*. Newport, which were the 3 most commonly reported serovars isolated from people in England in 2024 (see Chapter 1).

Notably, while dogs and cats may become clinically ill when infected (Morley et al., 2006), they are often asymptomatically infected and can shed these bacteria (Finley et al., 2007). Therefore, while the vast majority of dog isolations this year arose from clinical investigations (98.5%), it is likely that the true burden of infection in this companion animal population is greater than what is captured in this report. Close contact with dogs may therefore represent an important source of human *Salmonella* infection via infected animals shedding the pathogen into the shared environment.

Moreover, companion animal feed, in particular raw meat pet food, is known to harbour pathogens including *Salmonella. Salmonella* continues to be isolated from raw meat pet food (RMPF) with 290 isolations in 2024 (see Chapter 12, Table 12.8b). Consistent with 2023, *S.* Infantis (38 isolations) and *S.* Typhimurium (28 isolations) were among the top 4 serovars isolated from RMPF in 2024, and overall, nearly one third 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.

Antimicrobial susceptibility in dogs

A total of 509 *Salmonella* isolates from dogs were tested against a panel of 16 antimicrobials in 2024. Susceptibility levels remained stable at 83.5%. The proportion of multidrug-resistant isolates (MDR; resistant to 4 or more antimicrobials), declined significantly from 8.3% in 2023 (n= 757) to 5.1% in 2024.

Resistance occurred across several serovars, most frequently monophasic *S.* Typhimurium (n=18), *S.* Typhimurium (n=14), *S.* Infantis (n=8), and *S.* Kentucky (n=8). The resistance profile remained broadly unchanged, with streptomycin (8.4%), tetracycline (7.5%), sulphonamides (7.3%), ampicillin (5.7%) most commonly involved. A noteworthy reduction was detected for ampicillin resistance from 9.8% in 2023 to 5.7% in 2024.

Thirteen isolates were resistant to ciprofloxacin, including 7 MDR *S.* Infantis and 2 MDR *S.* Typhimurium. All 13 isolates were also resistant to nalidixic acid. Two MDR *S.* Kentucky isolates from the same dog, and one MDR *S.* Goldcoast from another dog, exhibited resistance to cefotaxime and ceftazidime. Two *S.* Kentucky MDR isolates displayed resistance to ceftazidime, cefotaxime, ciprofloxacin, and to additional compounds including gentamicin, neomycin, and streptomycin.

Table 10.1: Isolations and incidents of *Salmonella* in dogs on all premises in Great Britain 2020 to 2024

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Aarhus	0	0	3	3	0	0	0	0	0	0
Abony	0	0	0	0	1	1	0	0	1	1
Adelaide	0	0	0	0	0	0	2	2	3	3
Agama	2	2	14	14	11	11	13	13	9	9
Agona	1	1	16	16	27	27	15	15	15	15
Ajiobo	0	0	4	4	2	2	1	1	1	1
Altona	0	0	0	0	1	1	0	0	0	0
Amersfoort	0	0	1	1	0	0	0	0	0	0
Anatum	1	1	20	20	22	22	32	32	27	27
Ank	0	0	0	0	0	0	4	4	1	1
Apeyeme	0	0	0	0	0	0	1	1	0	0
Ball	0	0	0	0	1	1	0	0	0	0
Bardo	0	0	0	0	1	1	0	0	0	0
Bareilly	0	0	1	1	1	1	1	1	0	0
Berta	0	0	2	2	1	1	3	3	3	3
Bonn	0	0	1	1	0	0	3	3	0	0
Bovismorbificans	1	1	25	25	9	9	12	12	6	6
Brancaster	0	0	0	0	0	0	0	0	2	2
Brandenburg	3	3	11	11	10	10	4	4	2	2
Bredeney	0	0	3	3	10	10	2	2	1	1
Budapest	0	0	0	0	1	1	0	0	0	0
Cannstatt	0	0	0	0	1	1	0	0	0	0

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Cerro	3	3	2	2	5	5	0	0	5	5
Chailey	0	0	0	0	0	0	0	0	1	1
Chester	0	0	0	0	0	0	1	1	0	0
Coeln	0	0	3	3	11	11	3	3	3	3
Concord	0	0	2	2	1	1	1	1	2	2
Corvallis	0	0	0	0	0	0	1	1	0	0
Cotham	0	0	0	0	0	0	1	1	0	0
Cubana	0	0	1	1	0	0	0	0	0	0
Derby	2	2	26	26	55	55	37	36	19	19
Dublin	5	5	61	61	55	54	35	35	17	17
Durham	1	1	1	1	1	1	0	0	0	0
Ealing	0	0	3	3	8	8	1	1	0	0
Eboko	0	0	1	1	0	0	1	1	0	0
Enteritidis	2	2	26	26	15	15	26	26	17	17
Fluntern	0	0	0	0	1	1	0	0	0	0
Fresno	0	0	0	0	0	0	0	0	1	1
Fulica	0	0	0	0	1	1	1	1	2	2
Give	2	2	4	4	0	0	6	6	4	4
Give var 15+	0	0	0	0	3	3	0	0	0	0
Goelzau	0	0	0	0	0	0	1	1	0	0
Goldcoast	0	0	9	9	2	2	3	3	1	1
Gueuletapee	0	0	0	0	1	1	1	1	0	0
Hadar	0	0	8	8	5	5	2	2	2	2
Haifa	0	0	0	0	2	2	0	0	0	0
Havana	0	0	1	1	3	3	3	3	1	1
Hessarek	0	0	2	2	1	1	3	3	1	1

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Hvittingfoss	0	0	0	0	0	0	1	1	0	0
Idikan (incl monophasic)	0	0	0	0	0	0	4	4	0	0
Indiana	2	2	13	13	20	20	7	7	21	20
Infantis	3	3	51	51	109	107	79	78	39	38
Isangi	0	0	1	1	2	2	0	0	0	0
Javiana	0	0	2	2	1	1	1	1	2	2
Kapemba	0	0	0	0	1	1	1	1	0	0
Kedougou	0	0	8	8	1	1	9	9	2	2
Kentucky	0	0	0	0	8	8	4	4	17	15
Kingston	0	0	4	4	1	1	2	2	1	1
Kisarawe	0	0	0	0	20	20	0	0	0	0
Kottbus	2	2	11	11	0	0	12	12	13	12
Larochelle	1	1	0	0	0	0	0	0	0	0
Leeuwarden	0	0	0	0	0	0	0	0	1	1
Litchfield	0	0	0	0	1	1	0	0	0	0
Liverpool	0	0	0	0	1	1	0	0	1	1
Livingstone	0	0	12	12	14	14	19	19	12	12
Lome	0	0	0	0	0	0	1	1	0	0
Lomita	0	0	1	1	0	0	0	0	0	0
London	0	0	7	7	13	13	5	5	8	8
Matopeni	0	0	1	1	0	0	0	0	0	0
Mbandaka	1	1	7	7	11	11	30	30	7	7
Meleagridis	0	0	1	1	0	0	0	0	1	1
Miami	0	0	1	1	0	0	0	0	0	0
Mikawasima	0	0	0	0	0	0	1	1	0	0

Salmonella serovar	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
Mishmarhaemek	0	0	0	0	0	0	1	1	0	0
Molade	0	0	0	0	0	0	1	1	0	0
Monophasic Typhimurium	10	10	71	71	64	64	42	42	19	19
Montevideo	1	1	17	17	27	26	35	35	10	9
Muenchen	0	0	0	0	2	2	1	1	3	3
Muenster	0	0	2	2	2	2	9	9	8	8
Nagoya	0	0	0	0	0	0	1	1	0	0
Newport	4	4	43	43	52	52	25	25	30	29
Ohio	0	0	3	3	0	0	1	1	1	1
Oranienburg	0	0	1	1	4	4	4	4	0	0
Orion	0	0	3	3	1	1	3	3	0	0
Orion var 15+	0	0	0	0	0	0	1	1	0	0
Oslo	2	2	6	6	10	10	7	7	7	7
Panama	0	0	5	5	9	9	4	4	1	1
Paratyphi B var. Java	0	0	11	11	9	9	1	1	0	0
Pomona	0	0	1	1	0	0	0	0	0	0
Poona	0	0	0	0	0	0	1	1	1	1
Putten	0	0	1	1	0	0	0	0	0	0
Reading	0	0	1	1	1	1	0	0	2	2
Rissen	0	0	10	9	6	6	3	3	1	1
Saintpaul	0	0	0	0	1	1	1	1	0	0
Saphra	0	0	1	1	0	0	0	0	0	0
Schwarzengrund	0	0	2	2	1	1	1	1	1	1
Senftenberg	1	1	3	3	0	0	0	0	4	4

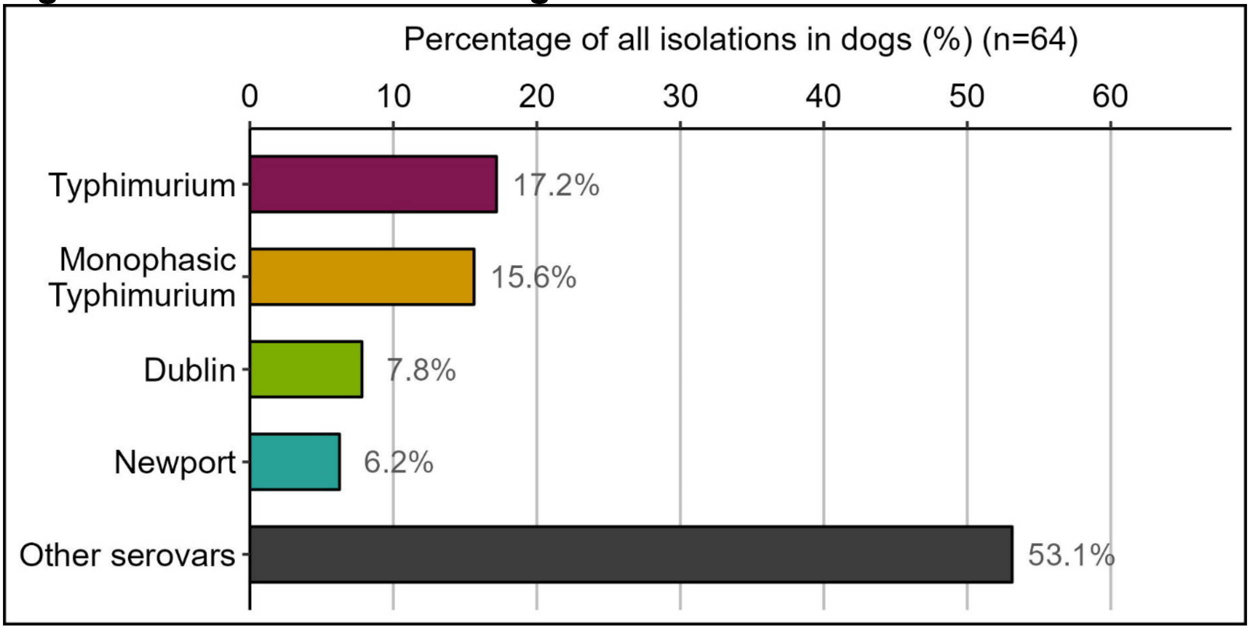
***Salmonella* serovar**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**	**2024 isolations**	**2024 incidents**
Singapore	0	0	0	0	0	0	0	0	1	1
Soerenga	0	0	3	3	1	1	0	0	0	0
Stanley	1	1	1	1	10	10	4	4	0	0
Stanleyville	0	0	4	4	0	0	1	1	12	12
Stendal	0	0	0	0	1	1	0	0	0	0
Stourbridge	0	0	2	2	0	0	1	1	1	1
Szentes	0	0	0	0	0	0	1	1	0	0
Tennessee	0	0	1	1	1	1	0	0	2	2
Thompson	0	0	1	1	0	0	22	20	10	10
Typhimurium	11	10	97	87	116	116	90	90	77	77
Uganda	2	2	7	7	3	3	1	1	1	1
Utah	0	0	0	0	0	0	1	1	0	0
Virchow	0	0	7	7	3	3	1	1	0	0
Wangata	0	0	1	1	0	0	0	0	0	0
Yoruba	0	0	0	0	0	0	3	3	0	0
4,5,12:b:-	0	0	5	5	2	2	1	1	2	2
6,7:-:-	0	0	17	17	23	23	1	1	0	0
6,8:-:-	0	0	3	3	0	0	2	2	2	2
61:k:1,5,(7)	0	0	0	0	8	7	3	3	1	1
untypable strains	0	0	22	22	19	19	18	18	13	12
rough strains	0	0	8	8	8	8	1	1	0	0
Total	**64**	**63**	**731**	**720**	**857**	**852**	**689**	**685**	**482**	**474**

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.

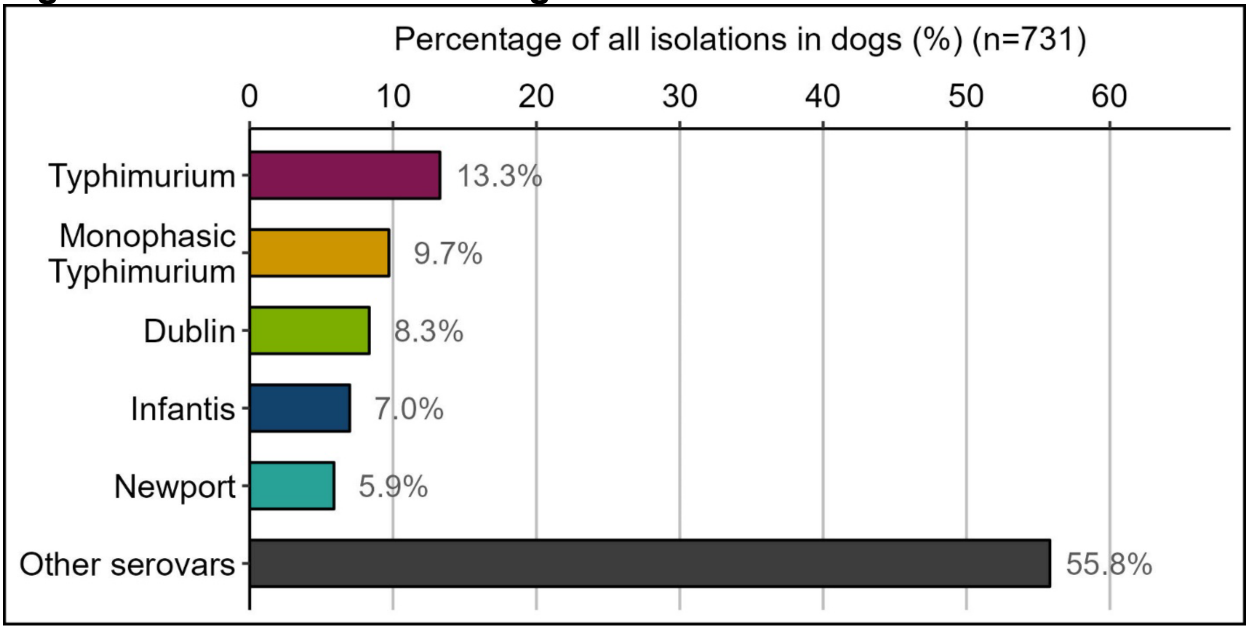
Figure 10.1: Isolations of the most common serovars in dogs in Great Britain 2020 to 2024

Figure 10.1.1: Isolations in dogs in 2020



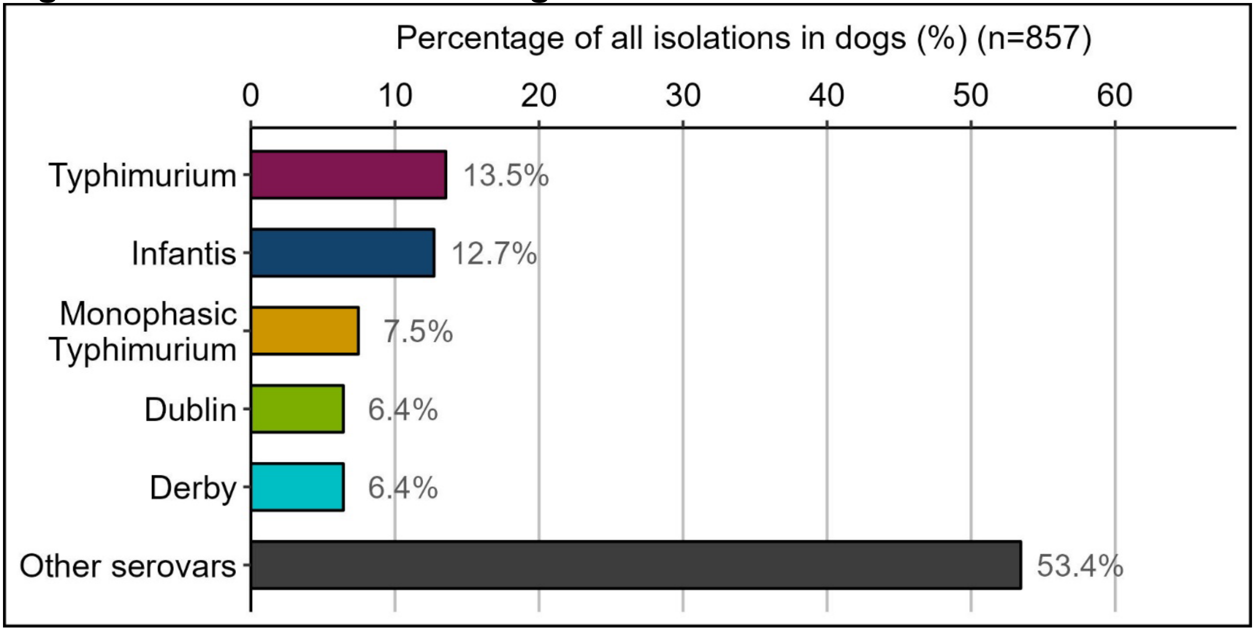
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in dogs in 2020. The most common *Salmonella* serovar in dogs in 2020 was *S.* Typhimurium, accounting for 17.2% of total isolations, followed by monophasic *S*. Typhimurium (15.6%), *S.* Dublin (7.8%) and *S*. Newport (6.3%).

Figure 10.1.2: Isolations in dogs in 2021



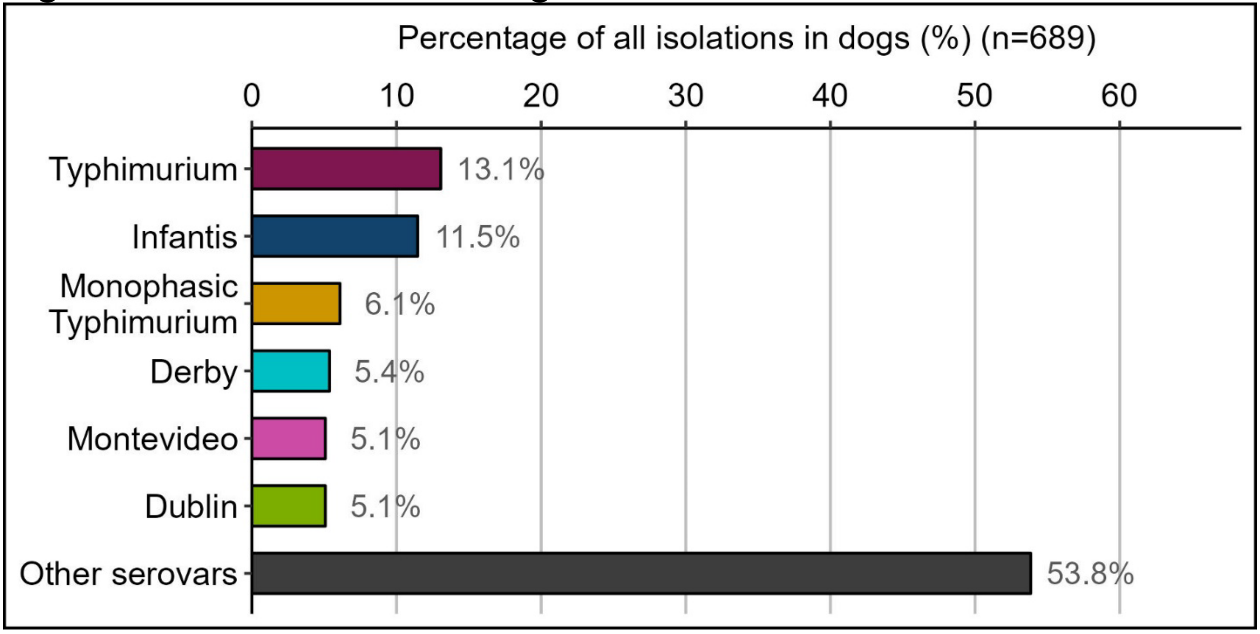
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in dogs in 2021. The most common *Salmonella* serovar in dogs in 2021 was *S*. Typhimurium, accounting for 13.3% of total isolations, followed by monophasic *S.* Typhimurium (9.7%), *S*. Dublin (8.3%) and *S*. Infantis (7.0%).

Figure 10.1.3: Isolations in dogs in 2022



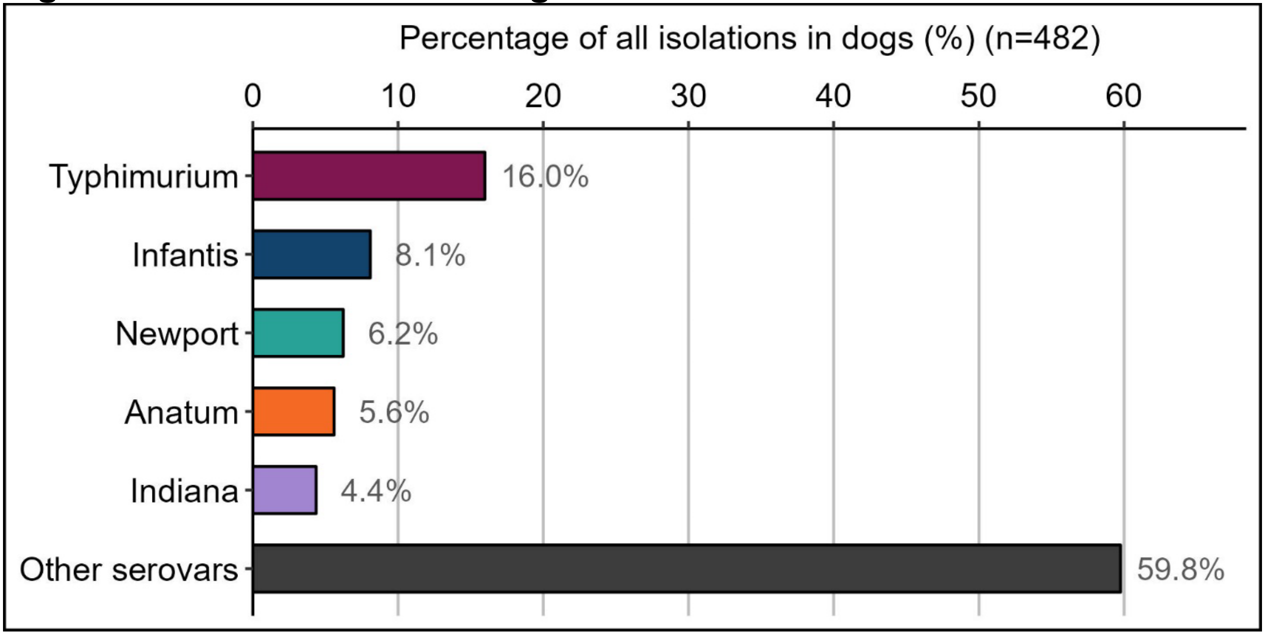
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in dogs in 2022. The most common *Salmonella* serovar in dogs in 2022 was *S*. Typhimurium, accounting for 13.5% of total isolations, followed by *S*. Infantis (12.7%), monophasic *S*. Typhimurium (7.5%), *S*. Derby (6.4%)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

Figure 10.1.4: Isolations in dogs in 2023



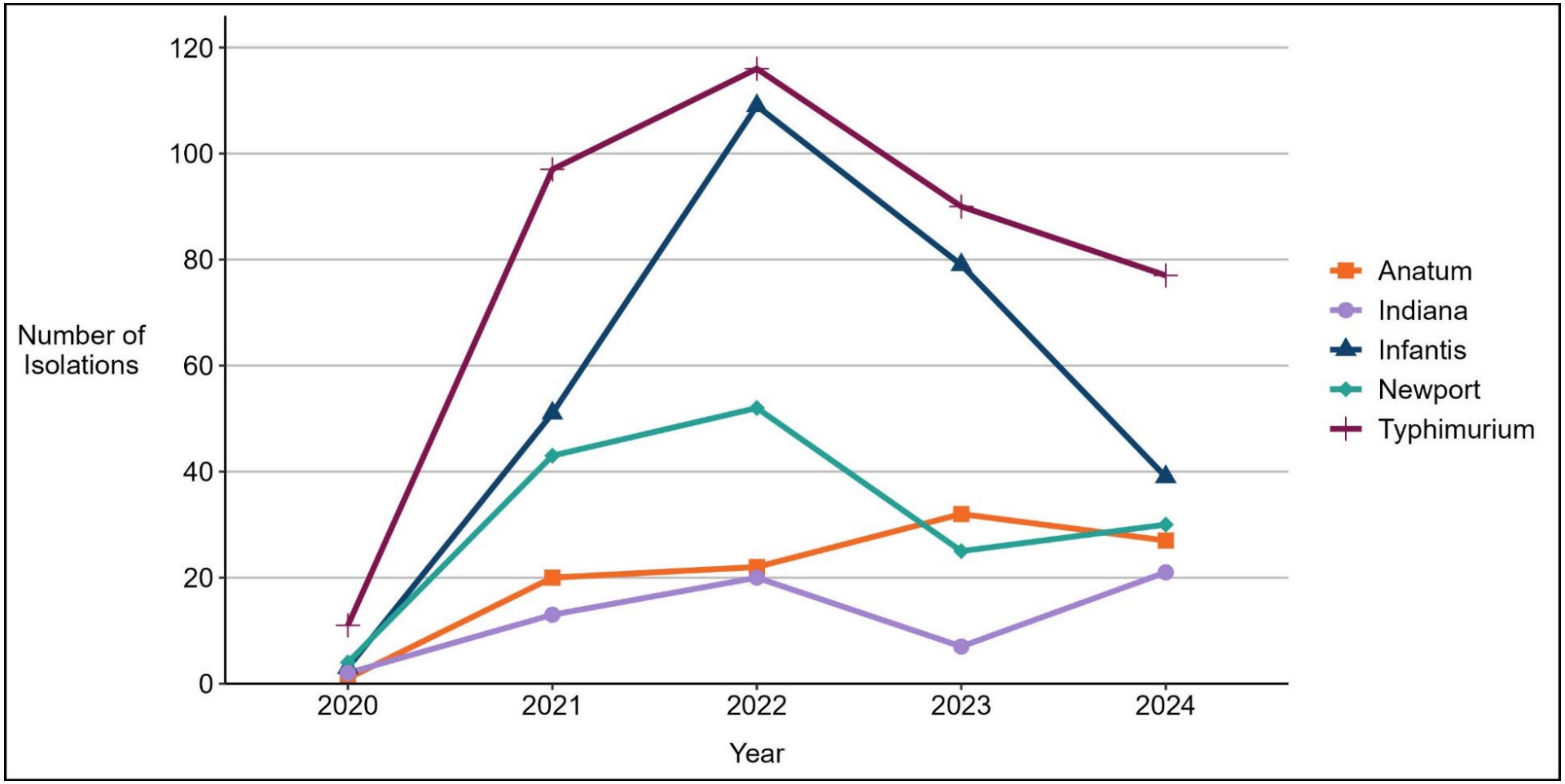
Horizontal bar graph showing the percentage of the top *Salmonella* isolations in dogs in 2023. The most common *Salmonella* serovar in dogs in 2023 was *S*. Typhimurium, accounting for 13.1% of total isolations, followed by *S*. Infantis (11.5%), monophasic *S*. Typhimurium (6.1%), *S*. Derby (5.4%),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

Figure 10.1.5: Isolations in dogs in 2024



Horizontal bar graph showing the percentage of the top *Salmonella* isolations 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 10.2: The 5 most common *Salmonella* serovars in dogs in Great Britain in 2024 and their trends over time since 2020



A line graph showing the 5 most common serovars in dogs from 2020 to 2024. The figure shows a very low number of isolations for all serovars before 2021 when reporting of *Salmonella* in dogs became statutory. All of the 5 most common serovars have increased significantly since then with *S.* Typhimurium still being the most common in 2024 (77 isolations), followed by *S*. Infantis (39 isolations), *S.* Newport (30 isolations), *S*. Anatum (27 isolations) and *S*. Indiana (21 isolations).

Table 10.2: *S*. Typhimurium phage types in dogs in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT1	0	0	2	2	9	9	6	6	3	3
DT2	3	3	14	10	8	8	9	9	10	10
DT2a	0	0	1	1	0	0	0	0	0	0
DT3	0	0	1	1	0	0	0	0	0	0
DT4	0	0	0	0	1	1	0	0	0	0
DT5	0	0	0	0	1	1	0	0	1	1
DT8	0	0	3	3	1	1	0	0	3	3
DT9	0	0	1	1	0	0	1	1	3	3
DT11	0	0	1	1	0	0	0	0	0	0
DT20	0	0	0	0	0	0	0	0	1	1
DT21	0	0	0	0	0	0	1	1	0	0
DT41	0	0	1	1	0	0	0	0	0	0
DT42	0	0	0	0	1	1	0	0	0	0
DT56	0	0	1	1	0	0	0	0	1	1
DT75	0	0	0	0	6	6	16	16	13	13
DT99	0	0	1	1	3	3	3	3	0	0
DT101	0	0	1	1	0	0	0	0	0	0
DT104	1	1	18	18	26	26	6	6	2	2
DT104b	0	0	0	0	0	0	1	1	0	0
DT105	1	1	5	5	11	11	8	8	15	15
DT106	0	0	0	0	1	1	0	0	0	0
DT115	1	1	0	0	0	0	0	0	0	0
DT116	0	0	2	2	1	1	5	5	1	1
DT120	0	0	0	0	2	2	1	1	0	0

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT189	2	1	1	1	1	1	0	0	0	0
DT193	0	0	13	13	15	15	10	10	1	1
DT194	0	0	0	0	1	1	0	0	0	0
U208	0	0	0	0	1	1	0	0	0	0
U288	0	0	1	1	0	0	0	0	0	0
U289	0	0	1	1	0	0	0	0	0	0
U308	1	1	4	4	0	0	0	0	2	2
U308a	0	0	1	1	0	0	0	0	0	0
U311	0	0	2	2	1	1	0	0	0	0
NOPT	0	0	1	0	0	0	0	0	5	5
RDNC	1	1	19	14	26	26	22	22	15	15
UNTY	1	1	2	2	0	0	1	1	1	1
Total	**11**	**10**	**97**	**87**	**116**	**116**	**90**	**90**	**77**	**77**

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.

Table 10.3: *S*. Enteritidis phage types in dogs in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
PT1	0	0	0	0	0	0	0	0	1	1
PT2	0	0	1	1	0	0	1	1	0	0
PT3	0	0	2	2	1	1	0	0	0	0
PT4	0	0	0	0	1	1	1	1	0	0
PT4b	0	0	0	0	1	1	0	0	1	1
PT8	0	0	2	2	6	6	5	5	2	2
PT9	0	0	0	0	1	1	3	3	1	1
PT9a	0	0	0	0	2	2	3	3	1	1
PT11	1	1	6	6	0	0	1	1	2	2
PT11b	0	0	0	0	1	1	2	2	0	0
PT13a	0	0	1	1	0	0	1	1	1	1
PT14b	0	0	0	0	0	0	1	1	1	1
PT21	0	0	1	1	0	0	3	3	1	1
PT28	0	0	1	1	0	0	0	0	0	0
PT31	1	1	0	0	0	0	0	0	0	0
PT33	0	0	0	0	1	1	0	0	0	0
PT35	0	0	0	0	0	0	1	1	0	0
NOPT	0	0	2	2	1	1	2	2	6	6
RDNC	0	0	6	6	0	0	2	2	0	0
UNTY	0	0	4	4	0	0	0	0	0	0
Total	**2**	**2**	**26**	**26**	**15**	**15**	**26**	**26**	**17**	**17**

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.

Table 10.4: Monophasic *S.* Typhimurium phage types in dogs in Great Britain 2020 to 2024

Phage type	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents	2024 isolations	2024 incidents
DT35	0	0	0	0	1	1	0	0	0	0
DT104	0	0	0	0	0	0	1	1	0	0
DT120	0	0	1	1	1	1	1	1	0	0
DT193	8	8	52	52	50	50	33	33	15	15
DT194	1	1	0	0	0	0	0	0	0	0
U308a	0	0	0	0	0	0	1	1	0	0
U311	0	0	4	4	6	6	0	0	0	0
NOPT	0	0	2	2	0	0	0	0	3	3
RDNC	1	1	3	3	4	4	2	2	1	1
UNTY	0	0	9	9	2	2	4	4	0	0
Total	**10**	**10**	**71**	**71**	**64**	**64**	**42**	**42**	**19**	**19**

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.

Chapter 11: Reports of *Salmonella* in wildlife

There is no routine monitoring of *Salmonella* in wild birds or wild mammals. Therefore, isolates usually originate from clinical cases, submitted to APHA for postmortem examination or laboratory testing, or occasionally from small-scale surveys. However, *Salmonella* is not necessarily the primary cause of disease when identified in wild animals. *Salmonella* is voluntarily reportable for most species of wildlife unless the species is covered by the Zoonoses Order.

Garden Wildlife Health (GWH), our partners in the Great Britain Wildlife Health Partnership (GBWHP), carry out the majority of disease surveillance in garden birds and hedgehogs and report *Salmonella* isolations separately. The GWH is a collaborative project between Zoological Society of London (ZSL), the British Trust for Ornithology (BTO), Froglife and the Royal Society for the Protection of Birds (RSPB), and it is part funded by Defra, Welsh Government and the Animal and Plant Health Agency (APHA) Diseases of Wildlife Scheme (DoWS).

Wild mammals

Hedgehogs

Salmonella isolates of *S*. Enteritidis phage types PT11 (4 submissions from lung samples), PT9a (1 submission of intestinal contents) and one isolate that was not phage typed (1 submission from a rectal swab), were reported in 6 European hedgehogs (*Erinaceus europaeus*). One hedgehog was found emaciated and dehydrated prior to death and postmortem findings were generally unremarkable, with *S*. Enteritidis being diagnosed from a rectal swab. *S*. Enteritidis PT9a was isolated from intestinal contents from a rescued hedgehog that had diarrhoea. Unfortunately, additional information regarding clinical findings or pathology are unavailable for lung samples from the other 4 hedgehogs. *Salmonella* infection has been described in free-living hedgehogs from Great Britain and continental Europe, including with *S*. Enteritidis PT9a and PT11 (Krawczyk et al., 2015; Nauerby et al., 2000). *S*. Enteritidis PT11 is reported to be the most common *Salmonella* spp. isolated from hedgehogs and is widespread in hedgehogs in England (Keymer et al., 1991) and is likely to be endemic (Robinson and Routh 1999).

European badger

One European badger cub (*Meles meles*) had 2 *Salmonella* serotypes isolated from liver samples: *S.* 4,5,12:b:- and *S.* Eboko. From postmortem examination, it was not possible to establish a cause of death beyond starvation and flea infestation. A wide range of *Salmonella* spp. are known to be commonly present in badgers in the UK (Wilson et al., 2003; O’Hagan et.al, 2021).

Red fox

A collapsed red fox (*Vulpes vulpes*) was euthanased and submitted to the Wildlife Network for Disease Surveillance for postmortem examination. The renal lymph nodes were enlarged and multifocal creamy abscess like lesions were seen in both kidneys. *S.* Typhimurium DT2 was the cause of disease. Infection of red foxes with *S*. Typhimurium has been described as the result of ingestion of *Salmonella* infected, sick or dead small passerine birds during winter (Handeland et al, 2008).

Marine mammals

There were 2 reports of *Salmonella* species in marine mammals. The post mortem of a pre weaned grey seal (*Halichoerus grypus*) pup with neurological signs revealed gingival disease, yellow joint fluid and an orange liver. *S.* Typhimurium DT75 was isolated from brain and blood swabs, and it was suspected that salmonellosis had caused septicaemia despite the lack of histological evidence. *S.* Typhimurium infection of free-ranging and stranded grey seals is recognised in UK waters and may occur via microbial marine pollution from wastewater, as the same strain was identified from a human clinical case (Baily and others, 2016). A postmortem examination was conducted on an adult common harbour porpoise (*Phocoena phocoena*) and *S.* 4,12:a:- was isolated. Severe fibrinonecrotising peritonitis and extensive severe enteritis were the main postmortem diagnoses. Since 1990, *Salmonella* 4,12:a:- has been identified from harbour porpoise carcases stranded in England, Wales and Scotland (Foster et al., 1999; Valderrama Vasquez et al., 2008).

Wild birds

S. Typhimurium was diagnosed in 2 herring gulls (*Larus argentatus*) and one black-headed gull (*Chroicocephalus ridibundus*). *S.* Typhimurium DT193 was isolated from a lung swab of an immature herring gull that had died due to a combination of air sacculitis and pneumonia. A liver swab from an adult Herring gull isolated *S.* Typhimurium RDNC. Septicaemia due to *S.* Typhimurium was the likely cause of death of the adult black-headed gull. A wide range of *Salmonella* serotypes are carried by herring gulls that are also found in humans (including *S.* Typhimurium), and gulls may ingest these serotypes when feeding at untreated sewage outfalls on the coast (Butterfield et al., 1983).

Table 11.1: Isolations of *Salmonella* in wild mammals in Great Britain 2020 to 2024

Species	Serovar and phage type	2020	2021	2022	2023	2024
Badger	Agama	0	1	0	1	0
Badger	Anatum	0	0	0	1	0
Badger	Berta	0	0	0	1	0
Badger	Eboko	0	0	0	0	1
Badger	Newport	0	1	0	1	0
Badger	4,5,12:b:-	0	0	0	0	1
Fox	Typhimurium DT2	0	0	0	0	1
Hedgehog	Enteritidis PT9a	0	0	0	0	1
Hedgehog	Enteritidis PT11	1	10	1	2	4
Hedgehog	Enteritidis PT20	0	1	0	0	0
Hedgehog	Enteritidis NOPT	0	0	0	0	1
Porpoise	4,12:-:-	0	0	1	0	0
Porpoise	4,12:a:-	0	0	0	0	1
Seal	Typhimurium DT75	0	0	0	0	1
Squirrel	Typhimurium RDNC	0	0	0	1	0
Total	Not applicable	**1**	**13**	**2**	**7**	**11**

Table 11.2: Isolations of *Salmonella* in wild birds in Great Britain 2020 to 2024

Species	Serovar and phage type	2020	2021	2022	2023	2024
Buzzard	Typhimurium DT2	0	0	0	1	0
Egret	Typhimurium DT2	1	0	0	0	0
Finch	Typhimurium DT193	0	2	0	0	0
Gull	Typhimurium DT193	0	0	0	0	1
Gull	Typhimurium NOPT	0	0	0	0	1
Gull	Typhimurium RDNC	0	0	0	1	1
Heron	Typhimurium DT193	0	1	0	0	0
Mixed species	Typhimurium NOPT	0	1	0	0	0
Swan	Typhimurium DT1	0	1	0	0	0
Swan	Typhimurium U308	0	1	0	0	0
Total	Not applicable	**1**	**6**	**0**	**2**	**3**

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 795 isolations of *Salmonella* from animal feeding stuffs and products associated with the Animal By-Products Regulations (ABPR) in 2024 (Table 12.7), including 69 isolations from compound feeds (Tables 12.3 to 12.6), 55 from feed ingredients (Table 12.8a) and 671 from other products associated with testing under ABPR (Table 12.8b). Total isolations decreased by 11.4% compared with 2023 (897 isolations) but increased by 13.2% compared with 2022 (702 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 28.3% in 2024 compared with 2023 (190 isolations versus 265 isolations) and increased by 1.6% compared with 2022 (187 isolations) (Table 12.1). In 2024, these comprised 84 isolations of *S.* Infantis, 57 isolations of *S.* Typhimurium, 28 isolations of *S.* Enteritidis, 20 isolations of monophasic *S.* Typhimurium, and one isolation 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. Details of these isolations are given in Table 12.6.

There were no isolations of *Salmonella* from compound ruminant feed during 2024, a decrease from 2023 (8 isolations) and 2022 (7 isolations).

There were no isolations of *Salmonella* from compound pig feed during 2024, which continues the declining trend from 14 isolations in 2022 and 1 in 2023.

There were 16 isolations from compound poultry feed during 2024, a 77.8% increase compared to 2023 (9 isolations) and a 6.7% increase compared to 2022 (15 isolations) (Table 12.5). Thirteen different serovars were reported, with the 3 most commonly isolated *Salmonella* Falkensee, *S.* Idikan (including monophasic variants *S.* 13,23:i:-), and *S.* Poona (2 isolations each, each accounting for 12.5% 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 2024 is shown in Figure 12.6. *S.* Idikan (including monophasic variants *S.* 13,23:i:-) was the most commonly isolated *Salmonella* serovar in broiler chicken flocks in 2024, accounting for 35.3% of total broiler flocks. This serovar was also isolated from chicken breeders and in previous years has 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 was one isolation of *S.* Poona in poultry in 2024 (in a broiler flock) and no isolations of *S.* Falkensee. There is a more direct relationship between feed contaminants and poultry isolates than for other livestock species, for which breeding animals and animal movements are 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 2024, there was a total of 55 *Salmonella* isolations arising from 10 different feeding stuff ingredient types (Table 12.8a). This is an increase of 25.0% compared to 2023 (44 isolations). *Salmonella* was most commonly isolated from rapeseed (16 isolations), followed by oilseeds (11 isolations) and soya (10 isolations), fishmeal (8 isolations), wheat (3 isolations), maize and soya bean meal (2 isolations each), and feather meal, guar protein and unspecified plant material (1 isolation each).

There were 16 isolations from rapeseed in 2024, a 300% increase compared to 2023 (4 isolations) but a 54.3% reduction compared to 2022 (35 isolations). There were 11 isolations from oilseeds in 2024, a 450% increase compared to 2023 (2 isolations). In 2024, there were 8 isolations in fishmeal compared to 2 in 2023 and 1 in 2022. There were reductions in *Salmonella* isolations from feed additives (0 in 2024 compared to 6 in 2023), maize (2 in 2024 compared to 4 in 2023), mixed vegetables (0 in 2024 compared to 6 in 2023), soya (10 in 2024 compared to 12 in 2023). In 2024, there was an increase in *Salmonella* isolations in soya bean meal compared to 2023 (2 versus 0), but a 93.3% reduction compared to 2022 (30 isolations).

The most commonly isolated serovars from feeding stuff ingredients during 2024 were *S.* Rissen (12 isolations), *S.* Typhimurium (7 isolations), *S.* Montevideo (6 isolations), and *S.* Mbandaka and *S.* Senftenberg (4 isolations each). During 2024, *S.* Rissen was isolated from rapeseed (7 isolations), oilseeds (4 isolations), and soya (1 isolation). In contrast, in 2023 there was a single isolation of *S.* Rissen from oilseeds, and 26 isolations in 2022 (23 of which were from rapeseed) (Table 12.8a). During 2024, *S.* Typhimurium was isolated from maize, rapeseed and soya (2 isolations each) and wheat (1 isolation), similar to in

2023 when *S.* Typhimurium was isolated from soya (5 isolations), rapeseed (1 isolation) and maize (4 isolations). All 6 isolations of *S.* Montevideo were from fishmeal, compared to 2023 where 2 isolations were from fishmeal and 1 isolation was from mixed vegetables. Isolations of *S.* Derby decreased from 6 isolations in 2023 to 0 isolations in 2024 (Table 12.8a).

Isolations from products associated with ABPR

During 2024, there were 671 *Salmonella* isolations arising from 17 different product types plus feedmill environments tested under ABPR in Great Britain (Table 12.8b). This is 11.6% lower than the number of isolations in 2023 (759 isolations) but 16.3% higher than that of 2022 (577 isolations). The highest number of isolations was from raw meat pet food (290 isolations), followed by samples from feedmill environments (267 isolations), digestate (35 isolations) and dog chews (16 isolations).

Compared with 2023, there was a decrease in the number of *Salmonella* isolates from feedmill environments (267 versus 289 isolations), while the number of isolations from digestate increased by one isolation from 2023 (35 vs 34 isolations). There were fewer isolations of *Salmonella* from raw meat pet food in 2024 compared to 2023 (290 versus 331 isolations) (Table 12.8b).

The most commonly isolated serovars from products tested under the ABPR were *S.* Ohio (111 isolations), *S.* Kedougou (100 isolations), *S.* Infantis (77 isolations), and *S.* Typhimurium (47 isolations). The majority of *S.* Ohio isolations were from samples collected from feedmill environments (100 isolations) and are likely to indicate resident contamination within some mills. Likewise, 92.0% of *S.* Kedougou isolations (92 isolations) were from feedmill environments. *S.* Infantis isolations were from a variety of sources including 38 isolations (49.4%) from raw pet food and 22 isolations (28.6%) from digestate (Table 12.8b). *S.* Typhimurium isolations were primarily from raw meat pet food (59.6%) and feedmill environments (21.3%).

Isolations from raw meat pet food

During 2024 there were 290 reports of *Salmonella* from raw meat pet food (Table 12.8b and Figure 12.7). This is lower than during 2023 (331 reports) and 2022 (406 reports). The most common serovars isolated from raw meat pet food during 2024 were *S.* Infantis (38 isolations), *S.* Indiana (36 isolations), and *S.* Typhimurium (28 isolations) (Figure 12.7.1). In comparison, *S.* Typhimurium, *S.* Infantis, and *S.* Newport were the 3 most commonly isolated serovars in dogs in 2024 (Figure 12.7.2 and Chapter 10).

There were 95 isolations of regulated serovars from raw meat pet food in 2024 (Table 12.2) which was 4.0% lower than in 2023 (99 isolations) and 22.8% lower than in 2022

(123 isolations). Regulated serovars comprise *S*. Enteritidis, *S*. Hadar, *S*. Infantis, monophasic *S*. Typhimurium, *S*. Typhimurium and *S*. Virchow. These included 38 isolations of *S.* Infantis, 28 isolations of *S.* Typhimurium, 17 isolations of monophasic *S.* Typhimurium, and 12 isolations of *S.* Enteritidis (Table 12.2, Figure 12.2.3). There were no isolations of *S*. Hadar in raw meat pet food in 2024, the first year this serovar has not been isolated since 2018.

Regulated serovars originating from raw meat pet food during 2024 accounted for 50.0% of total regulated serovars isolated from all feeding stuffs and products associated with the ABPR (Table 12.2). This is a higher proportion than during 2023 (37.4%) but a lower proportion than during 2022 (65.8% of total regulated serovars).

Testing of processed animal protein

A total of 459 batches of domestically produced processed animal protein were tested during 2024. This is a 42.1% increase compared with 2023 (323 batches) and a 52.5% increase compared with 2022 (301 batches) (Table 12.9 and Figure 12.8). Eight batches tested positive for *Salmonella* in 2024 (1.74%), which is double the number in 2023 (4 positive batches; 1.24%) and 4 times that of 2022 (2 positive batches; 0.66%).

Seven different serovars were isolated in 2024 including *S.* Typhimurium (one isolation each of DT105 and DT193), *S.* Anatum (one isolation), *S.* Cerro (one isolation), *S.* Livingstone (one isolation), *S.* Nottingham (one isolation), *S.* Senftenberg (one isolation), and *S.* Tennessee (one isolation) (Table 12.10).

No batches of imported animal protein were tested during 2024, which is the same as during both 2023 and 2022.The last batches of imported animal protein testing positive for *Salmonella* were reported during 2009.

Antimicrobial susceptibility in feeds

A total of 994 *Salmonella* isolates from feed were tested against a panel of 16 antimicrobials in 2024. Overall, 65.9% were fully susceptible, while 5.7% were classified as multidrug resistant (MDR; resistant to 4 or more antimicrobials).

The serovars with the greatest number of resistant isolates were *S.* Ohio (n=108), *S.* Kedougou (n=76), *S.* Infantis (n=38), and *S.* Indiana (n=33). However, MDR cases were mostly linked to *S.* Infantis (n=24) and monophasic *S.* Typhimurium (n=15). Resistance trends remained stable compared to 2023, with patterns often involving resistance to sulphonamides (24.4%), tetracycline (22.3%), and streptomycin (12.5%).

Nalidixic acid resistance was observed in 90 of isolates, of which 12 were also resistant to ciprofloxacin (10 S. Infantis and 2 S. Kottbus). Overall, 13 isolates were resistant to ciprofloxacin in 2024. Ten isolates were resistant to both ciprofloxacin and streptomycin, and 4 to ciprofloxacin, neomycin, and streptomycin. One MDR *S.* Typhimurium isolate showed resistance to ciprofloxacin, ceftazidime, cefotaxime, and 7 additional antimicrobials, including neomycin, gentamicin, and streptomycin.

Table 12.1: Regulated *Salmonella* serovars in animal feeding stuffs in Great Britain 2022 to 2024

Salmonella serovar	2022 Finished feed	2022 Vegetable material	2022 Misc.	2023 Finished feed	2023 Vegetable material	2023 Misc.	2024 Finished feed	2024 Vegetable material	2024 Misc.
Enteritidis PT3	0	0	0	0	0	1	0	0	1
Enteritidis PT4	0	1	0	1	0	0	0	0	1
Enteritidis PT5	0	0	0	0	0	1	0	0	0
Enteritidis PT6	0	0	0	0	0	2	0	0	0
Enteritidis PT6a	0	0	0	0	0	0	0	0	1
Enteritidis PT8	1	0	1	0	0	1	0	0	7
Enteritidis PT9	0	0	0	0	0	1	0	0	0
Enteritidis PT9b	0	0	0	0	0	1	0	0	1
Enteritidis PT11b	0	0	0	0	0	2	0	0	0
Enteritidis PT13	0	0	0	0	0	0	0	0	2
Enteritidis PT13a	0	0	0	0	0	3	0	0	4
Enteritidis PT21	0	0	1	0	0	3	0	0	0
Enteritidis PT22	0	0	0	0	0	1	0	0	0
Enteritidis PT34	0	0	0	0	0	0	0	0	2
Enteritidis PT35	0	0	0	0	0	0	0	0	1
Enteritidis NOPT	0	0	0	0	0	1	0	0	6
Enteritidis RDNC	1	0	1	0	0	1	0	0	2
Hadar	0	0	1	1	0	13	0	0	0
Infantis	11	0	50	10	1	121	5	2	77

Salmonella serovar	2022 Finished feed	2022 Vegetable material	2022 Misc.	2023 Finished feed	2023 Vegetable material	2023 Misc.	2024 Finished feed	2024 Vegetable material	2024 Misc.
Monophasic Typhimurium DT59	0	0	0	0	0	1	0	0	0
Monophasic Typhimurium DT104	0	0	3	0	0	0	0	0	0
Monophasic Typhimurium DT120	0	0	1	0	0	3	0	0	0
Monophasic Typhimurium DT193	8	0	42	2	1	20	0	0	16
Monophasic Typhimurium DT208	0	0	1	0	0	0	0	0	0
Monophasic Typhimurium U311	0	0	1	0	0	0	0	0	1
Monophasic Typhimurium U323	0	0	0	0	0	0	0	0	2
Monophasic Typhimurium NOPT	0	0	0	0	0	1	0	0	1
Monophasic Typhimurium UNTY	0	0	7	0	0	1	0	0	0
Typhimurium DT1	0	0	0	0	1	2	0	0	0
Typhimurium DT2	1	3	5	1	4	13	1	6	13
Typhimurium DT4	0	0	0	0	0	1	0	0	0
Typhimurium DT8	0	0	2	0	0	1	0	0	0
Typhimurium DT9	0	0	3	0	0	1	0	0	0
Typhimurium DT11	0	0	0	0	0	0	0	0	1

Salmonella serovar	2022 Finished feed	2022 Vegetable material	2022 Misc.	2023 Finished feed	2023 Vegetable material	2023 Misc.	2024 Finished feed	2024 Vegetable material	2024 Misc.
Typhimurium DT30	0	0	0	0	0	0	0	0	1
Typhimurium DT32	0	0	0	0	0	1	0	0	0
Typhimurium DT75	0	0	3	0	0	2	0	0	12
Typhimurium DT99	0	4	3	4	5	6	1	0	1
Typhimurium DT104	0	1	3	0	0	0	0	0	2
Typhimurium DT105	1	0	5	0	0	4	0	0	3
Typhimurium DT116	0	0	0	0	0	2	0	0	1
Typhimurium DT120	0	0	2	0	0	1	0	0	0
Typhimurium DT130	0	0	0	0	0	1	0	0	0
Typhimurium DT193	0	0	3	0	0	4	0	1	3
Typhimurium U308	0	0	0	0	0	0	0	0	1
Typhimurium U310	0	0	0	0	0	1	0	0	0
Typhimurium U311	0	0	3	0	0	0	0	0	0
Typhimurium U322	0	0	0	0	0	4	0	0	0
Typhimurium NOPT	0	0	2	0	0	3	0	0	6
Typhimurium RDNC	1	0	8	0	0	7	0	0	3
Typhimurium UNTY	0	0	0	0	0	1	1	0	0
Virchow	0	0	3	0	0	1	0	0	1
Total	**24**	**9**	**154**	**19**	**12**	**234**	**8**	**9**	**173**

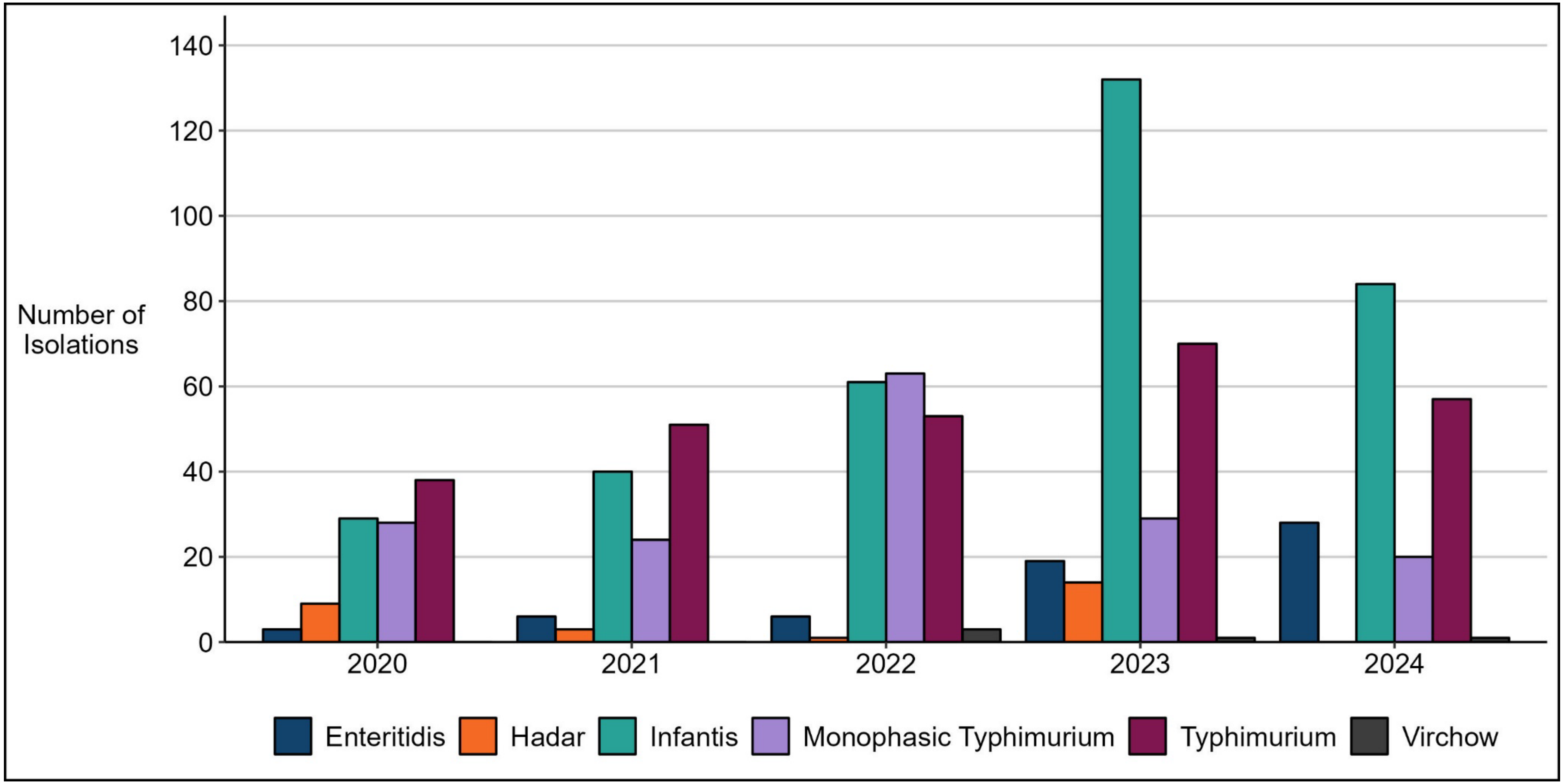
Miscellaneous includes pet food (raw).

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, 2024

Salmonella serovar	Feeding stuff	N
Enteritidis PT3	Pet food (raw)	1
Enteritidis PT4	Feeder mice	1
Enteritidis PT6a	Feeder mice	1
Enteritidis PT8	Feedmill environmental	7
Enteritidis PT9b	Pet food (raw)	1
Enteritidis PT13	Pet food (raw)	2
Enteritidis PT13a	Pet food (raw)	4
Enteritidis PT34	Pet food (raw)	2
Enteritidis PT35	Feeder mice	1
Enteritidis NOPT	Feedmill environmental	4
Enteritidis NOPT	Pet food (raw)	2
Enteritidis RDNC	Feeder mice	2
Infantis	Aeration tank	1
Infantis	Centrate liquor	2
Infantis	Compost	2
Infantis	Compound dog feed	3
Infantis	Compound feed (species unknown)	2
Infantis	Digestate	22
Infantis	Environmental	1
Infantis	Feedmill environmental	8
Infantis	Oilseeds	1
Infantis	Pasteurised liquor	1
Infantis	Pet food (raw)	38
Infantis	Process water tank	2
Infantis	Soya bean meal	1
Monophasic Typhimurium DT193	Bloodmeal	1
Monophasic Typhimurium DT193	Feedmill environmental	1
Monophasic Typhimurium DT193	Feeder mice	1
Monophasic Typhimurium DT193	Pet food (raw)	13
Monophasic Typhimurium U311	Pet food (raw)	1
Monophasic Typhimurium U323	Pet food (raw)	2
Monophasic Typhimurium NOPT	Pet food (raw)	1
Typhimurium DT2	Compound feed (species unknown)	1

Salmonella serovar	Feeding stuff	N
Typhimurium DT2	Environmental	4
Typhimurium DT2	Feedmill environmental	7
Typhimurium DT2	Maize	2
Typhimurium DT2	Pet food (raw)	2
Typhimurium DT2	Rapeseed	2
Typhimurium DT2	Soya	1
Typhimurium DT2	Wheat	1
Typhimurium DT11	Pet food (raw)	1
Typhimurium DT30	Pet food (raw)	1
Typhimurium DT75	Feedmill environmental	1
Typhimurium DT75	Pet food (raw)	11
Typhimurium DT99	Compound feed (species unknown)	1
Typhimurium DT99	Pet food (raw)	1
Typhimurium DT104	Dog chews	2
Typhimurium DT105	Digestate	1
Typhimurium DT105	Pet food (raw)	2
Typhimurium DT116	Pet food (raw)	1
Typhimurium DT193	Compost	1
Typhimurium DT193	Pet food (raw)	2
Typhimurium DT193	Soya	1
Typhimurium U308	Pet food (raw)	1
Typhimurium NOPT	Environmental	1
Typhimurium NOPT	Feedmill environmental	2
Typhimurium NOPT	Pet food (raw)	3
Typhimurium RDNC	Pet food (raw)	3
Typhimurium UNTY	Compound feed (species unknown)	1
Virchow	Feedmill environmental	1
Total	Not applicable	**190**

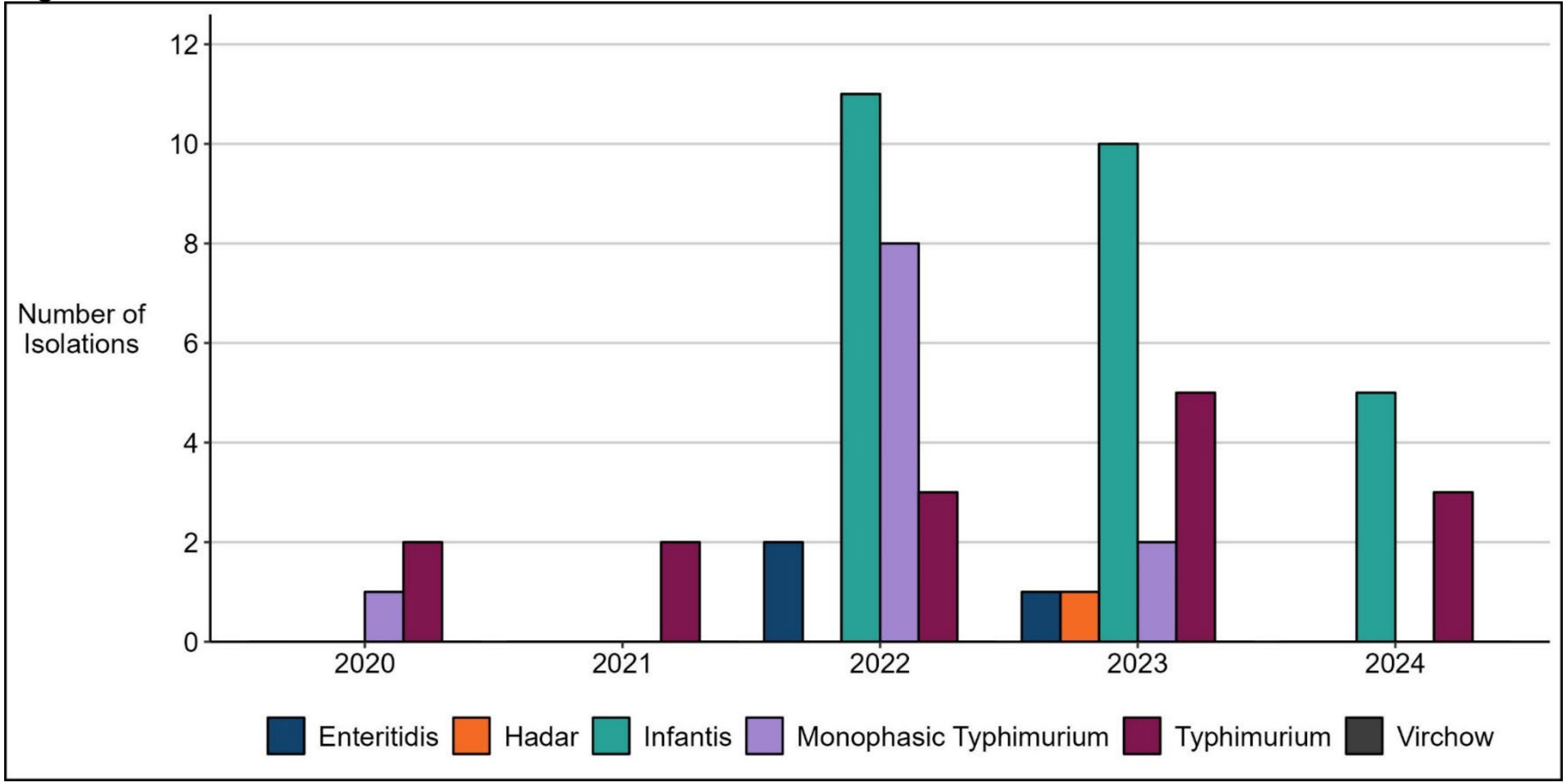
Figure 12.1: Number of isolations of regulated *Salmonella* serovars in animal feeding stuffs and products associated with the ABPR, 2020 to 2024



A vertical cluster bar graph showing the number of isolations of regulated *Salmonella* serovars in animal feeding stuffs and products associated with the ABPR from 2020 to 2024. Figure 12.1 shows the number of isolations of monophasic *S*. Typhimurium and *S.* Virchow have decreased since 2022. Isolations of *S.* Infantis have increased since 2020 from 29 isolations to 132 in 2023 but dropped to 84 in 2024. *S*. Enteritidis isolations have increased since 2020 from 3 to 28 in 2024. There were no *S.* Hadar isolations during 2024, compared to 14 isolations in 2023. Isolations of *S.* Virchow have remained very low in all years.

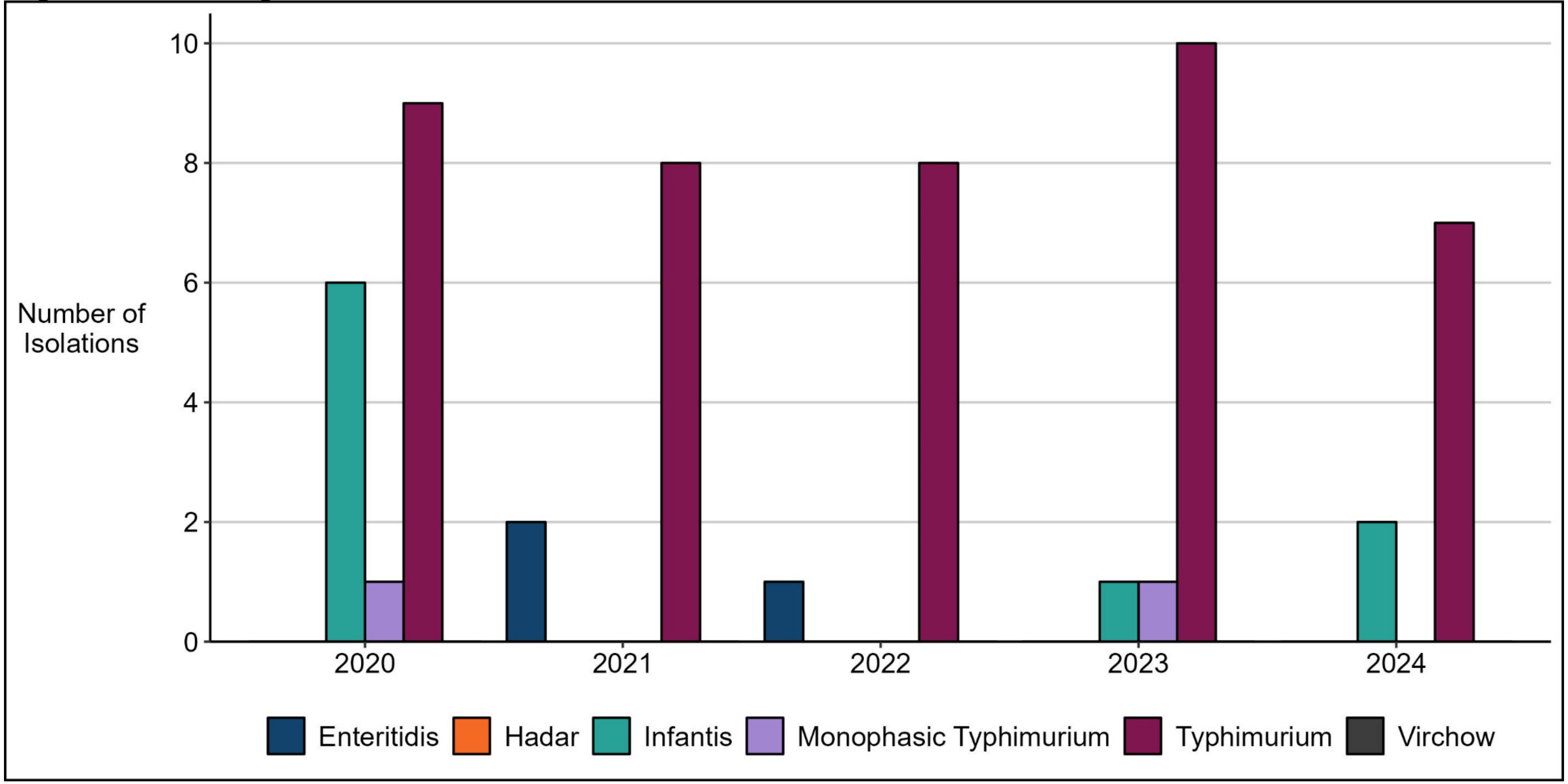
Figure 12.2: Number of isolations of regulated *Salmonella* serovars in animal feeding stuffs and products associated with the ABPR, 2020 to 2024 by type of feeding stuff

Figure 12.2.1 Finished feed



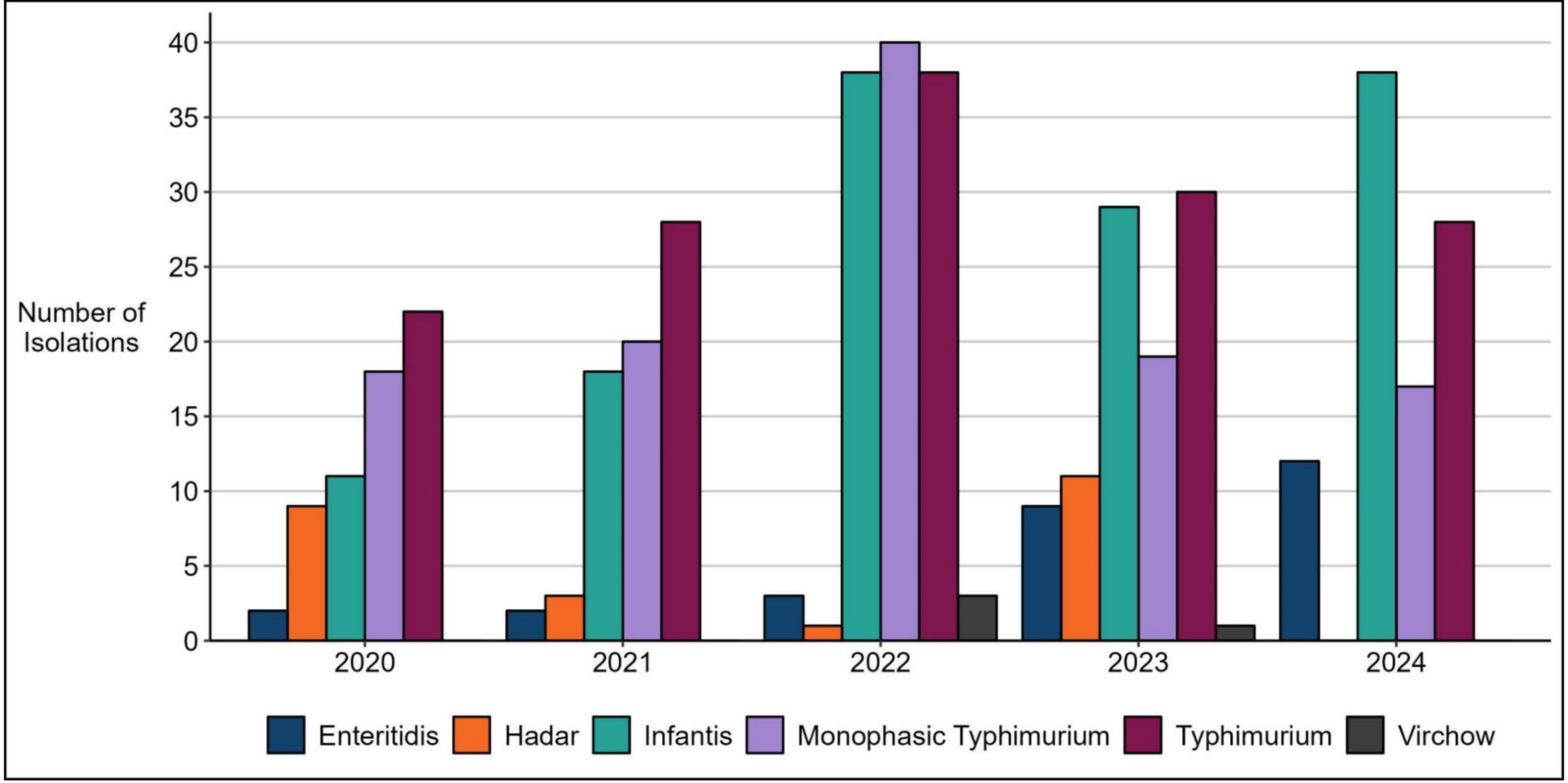
A vertical cluster bar graph showing the number of isolations of regulated *Salmonella* serovars in finished feed from 2020 to 2024. There were 8 isolations of regulated serovars from finished feed during 2024, down from 19 isolations in 2023. There were no isolations of monophasic *S.* Typhimurium in 2024, after a steady rise from 2 in 2020 to a peak of 8 in 2022 and back to 2 isolations in 2023. The number of isolations of the regulated serovar *S*. Typhimurium from finished feed increased between 2019 and 2023, however isolations decreased to 3 isolations during 2024 from a peak of 5 isolations in 2023. Isolations of *S.* Infantis decreased to 5 isolations in 2024 from a peak of 11 isolations in 2022. There were no isolations of *S*. Enteritidis in 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



A vertical cluster bar graph showing the number of isolations of regulated *Salmonella* serovars in vegetable material from 2020 to 2024. *S.* Infantis was isolated from vegetable material in 2020 (6 isolations), 2023 (1 isolation), and 2024 (2 isolations). *S*. Enteritidis has not been isolated from vegetable material since 2022. *S.* Typhimurium has remained stable and was isolated 7 times in 2024, a decrease from a peak of 10 isolations in 2023. Neither *S*. Hadar nor *S.* Virchow have been isolated in vegetable material between 2020 and 2024. There were no isolations of monophasic *S.* Typhimurium in 2024, compared to one isolation in 2023 and 2020.

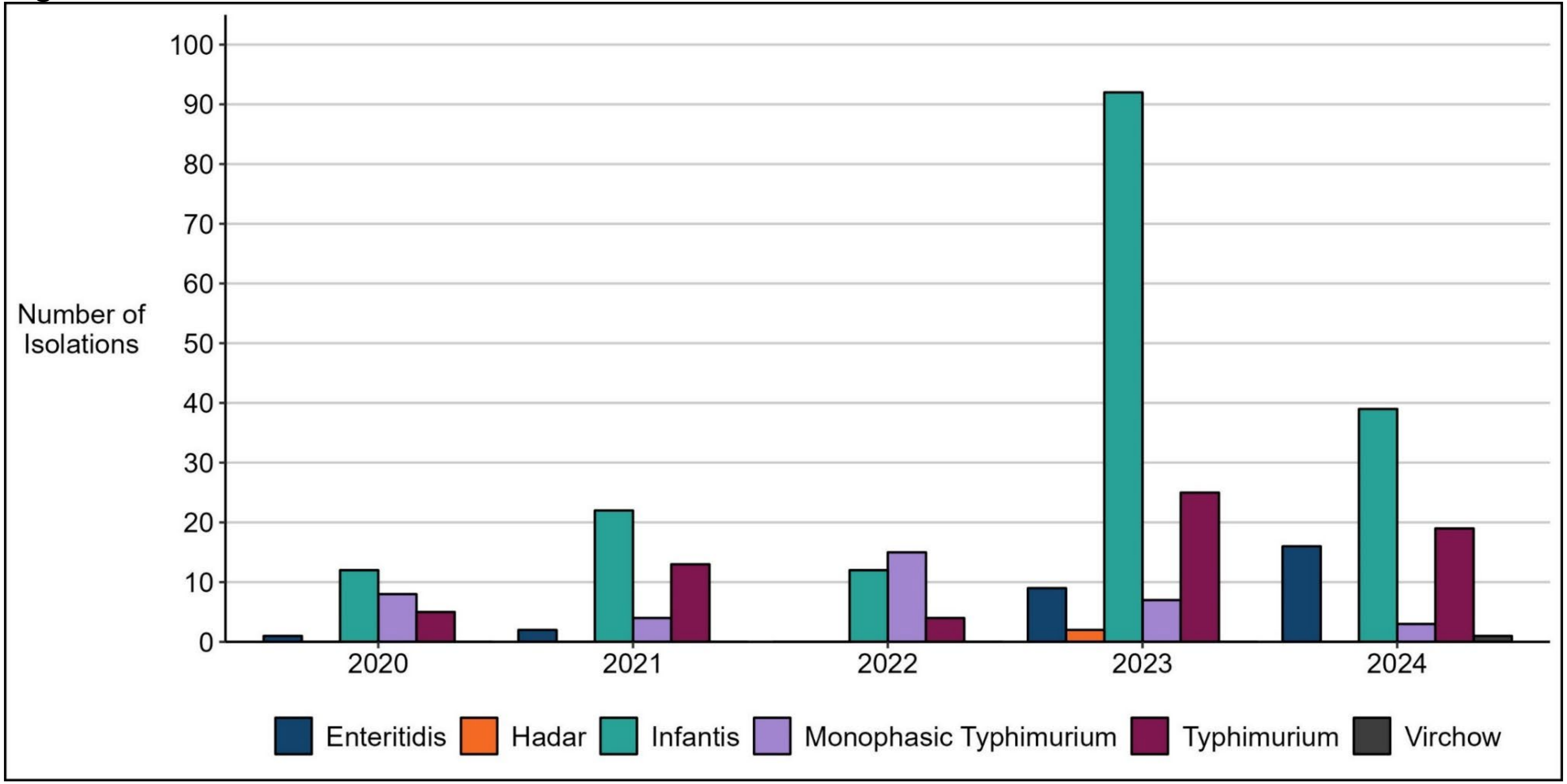
Figure 12.2.3 Pet food (raw)



A vertical cluster bar graph showing the number of isolations of regulated *Salmonella* serovars in pet food (raw) from 2020 to 2024. *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 3 rose steadily and peaked in 2022 but dropped in 2023. There was a further small reduction in isolations of monophasic *S.* Typhimurium and *S.* Typhimurium in 2024 however isolations of *S.* Infantis increased to 38, the same as

2022. *S.* Virchow is infrequently isolated from raw pet food, only being isolated in 2022 and 2023. There were no isolations of *S.* Hadar during 2024. Isolations of *S.* Enteritidis were steady at less than 5 between 2020 and 2022 but increased to 9 in 2023, and to 12 in 2024.

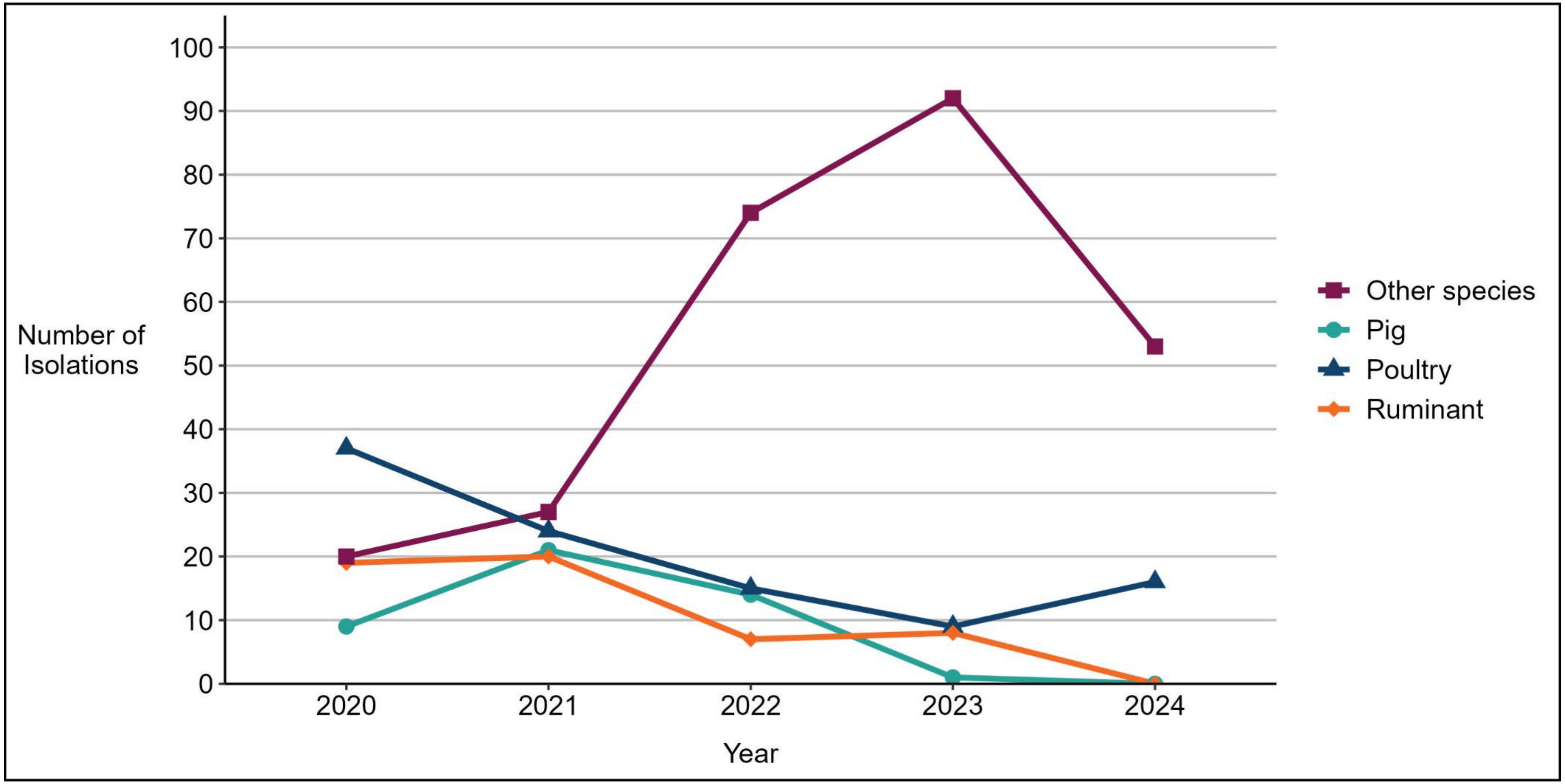
Figure 12.2.4 Miscellaneous



A vertical cluster bar graph showing the number of isolations of regulated *Salmonella* serovars in miscellaneous from 2020 to 2024. The number of isolations of *S*. Enteritidis in miscellaneous feedstuffs (not including raw pet food) 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. Isolations of *S.* Infantis increased from 12 in 2020 to 92 in 2023 but decreased to 39 isolations in 2024. *S.* Typhimurium isolations increased between 2022 and 2023 (25 versus 4 in 2022) but decreased in 2024 to 19 isolations. There was one isolation of *S.* Virchow in 2024, the first isolation of this serovar between 2020 and 2024. Isolations of monophasic *S.* Typhimurium have halved since 2023, from 7 to 3 in 2024.

Figure 12.3: Number of isolations of *Salmonella* in compound animal feeding stuffs, 2020 to 2024



A line graph showing the 5 most common serovars in compound animals feeding stuffs from 2020 to 2024. 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 each in 2024. 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. There were 53 isolations in compound feed from other species or un-specified species in 2024, a decline from 2023 (92 isolations).

Table 12.3: Serovars of *Salmonella* isolated from compound ruminant feed in Great Britain in 2024, compared with the previous 2 years

***Salmonella* serovar**	**Isolations 2022**	**Isolations 2023**	**Isolations 2024**
3,19:rough:-	0	0	0
4,12:d:-	0	0	0
Aarhus	0	0	0
Agama	0	0	0
Agona	2	0	0
Budapest	0	0	0
Derby	1	0	0
Emek	0	0	0
Kedougou	1	0	0
Kentucky	2	0	0
Korlebu	0	0	0
London	0	0	0
Mbandaka	0	0	0
Molade	0	1	0
Newport	0	0	0
Poona	0	0	0
Rissen	0	0	0
Senftenberg	0	0	0
Tennessee	1	7	0
Typhimurium DT193	0	0	0
Total	**7**	**8**	**0**

Table 12.4: Serovars of *Salmonella* isolated from compound pig feed in Great Britain in 2024, compared with the previous 2 years

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
4,5,12:i:-	1	0	0
6,7:-:-	0	0	0
Agona	0	0	0
California	0	0	0
Derby	2	1	0
Enteritidis	1	0	0
Hindmarsh	1	0	0
Kedougou	3	0	0
Odozi	0	0	0
Ohio	1	0	0
Panama	0	0	0
Rissen	5	0	0
Senftenberg	0	0	0
Tennessee	0	0	0
Total	**14**	**1**	**0**

Figure 12.4: Isolations of the most common serovars in compound ruminant feed in Great Britain in 2024

Figure 12.4.1: Isolations from compound ruminant feed

There were no isolations of compound ruminant feed in 2024.

Figure 12.5: Isolations of the most common serovars in compound pig feed in Great Britain in 2024

Figure 12.5.1: Isolations from compound pig feed

There were no isolations of *Salmonella* in compound pig feed in 2024.

Table 12.5: Serovars of *Salmonella* isolated from compound poultry feed in Great Britain in 2024, compared with the previous 2 years

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
4,12:b:-	0	1	0
6,7:-:enz15	1	0	0
Agama	2	0	1
Agona	1	0	1
Amager	0	0	1
Cubana	0	1	0
Derby	1	0	0
Enteritidis	1	0	0
Falkensee	0	0	2
Idikan (incl. monophasic)	1	0	2
Infantis	1	0	0
Kedougou	2	0	0
Kentucky	0	0	1
Kingston	0	0	1
Mbandaka	0	0	1
Newport	1	0	1
Ohio	0	0	1
Poona	0	0	2
Rissen	0	0	1
Senftenberg	0	1	0
Soerenga	2	0	0
Typhimurium	1	5	0
Utah	1	1	0
Yoruba	0	0	1
Total	**15**	**9**	**16**

Table 12.6: Serovars of *Salmonella* isolated from compound feed for other species feed in Great Britain in 2024, compared with the previous 2 years

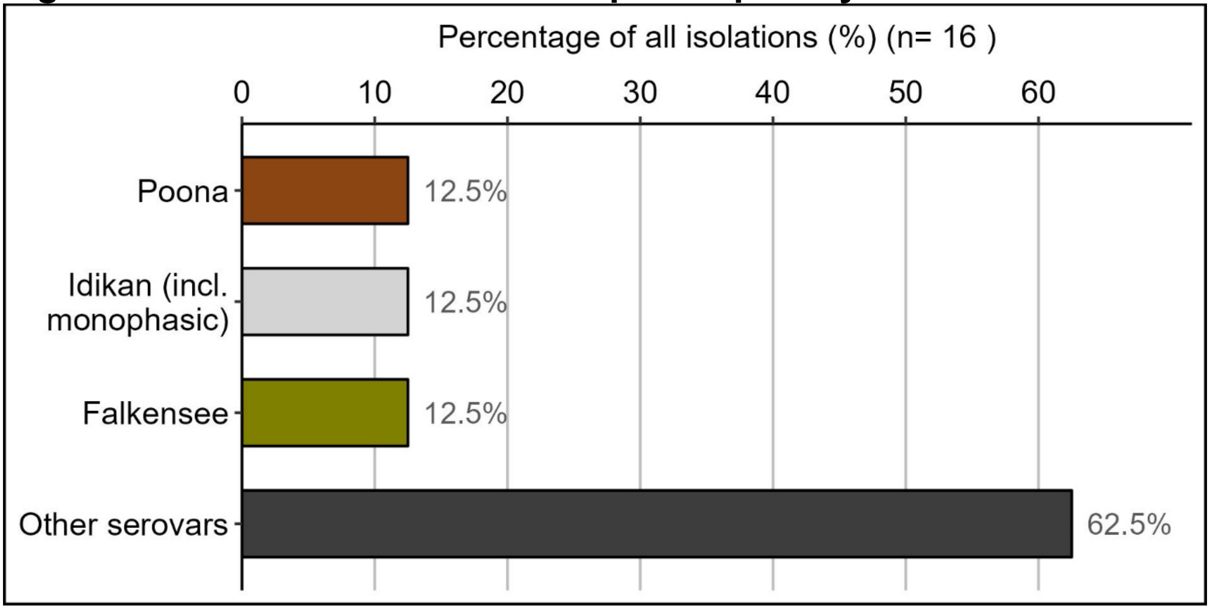
Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
13,23:i:-	0	2	0
3,10:-:1,5	0	1	0
4,12:d:-	0	0	0
4,12:z:-	0	0	0
42:z:1,5	0	0	0
6,7:-:-	7	0	0
6,7:r:-	1	0	0
61:-:-	0	0	0
Aarhus	0	0	0
Aba	1	0	0
Agama	0	0	0
Agona	1	1	4
Anatum	1	0	0
Bovismorbificans	2	0	1
Brancaster	1	0	0
Cerro	1	0	0
Coeln	1	0	1
Cubana	0	0	1
Derby	5	9	6
Duisburg	0	1	0
Enteritidis PT4	0	1	0
Give	0	1	1
Hadar	0	1	0
Havana	0	1	0
Ibadan	1	0	0
Idikan (incl. monophasic)	1	0	1
Indiana	0	4	0
Infantis	10	10	5
Isangi	1	0	1
Kedougou	5	2	2
Kentucky	1	1	0
Kingston	1	0	0
Lexington	0	1	0

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
Liverpool	0	0	1
Livingstone	1	0	0
London	0	1	0
Mbandaka	3	0	2
Molade	1	0	0
Monophasic Typhimurium	7	2	0
Mons	0	0	0
Montevideo	3	4	1
Morbihan	0	1	0
Muenster	0	1	0
Newport	2	3	2
Nottingham	1	1	0
O rough:g,p:-	1	0	0
Ohio	0	6	0
Panama	2	0	1
Poona	0	1	0
Putten	0	2	0
Riggil	0	0	1
Rissen	4	0	10
Senftenberg	0	13	3
Soerenga	0	3	0
Takoradi	1	0	0
Taksony	0	0	0
Tennessee	3	1	0
Thompson	2	0	1
Typhimurium	2	0	0
Typhimurium DT2	0	0	1
Typhimurium DT99	0	0	1
Typhimurium UNTY	0	0	1
Uganda	0	0	5
Worthington	0	1	0
Total	**74**	**76**	**53**

Other species in 2024 were: dogs (7 isolations) and unspecified (46 isolations).

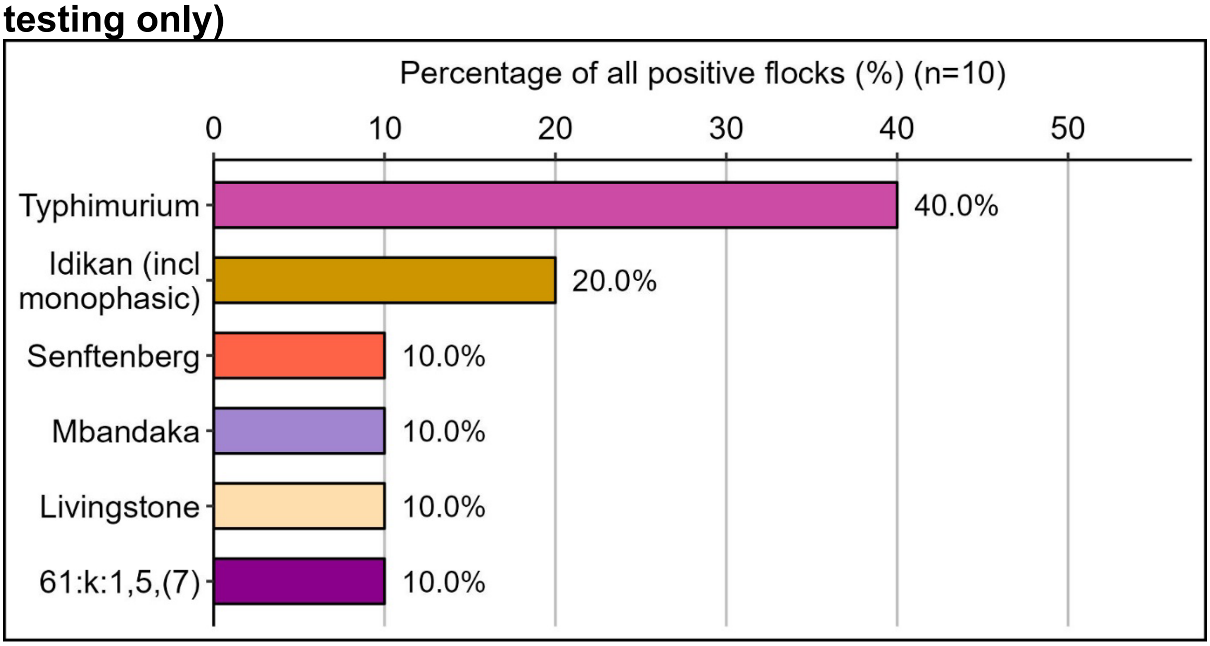
Figure 12.6: Isolations of the most common serovars in compound poultry feed and positive flocks of chickens and turkeys from NCP testing in Great Britain in 2024

Figure 12.6.1: Isolations from compound poultry feed



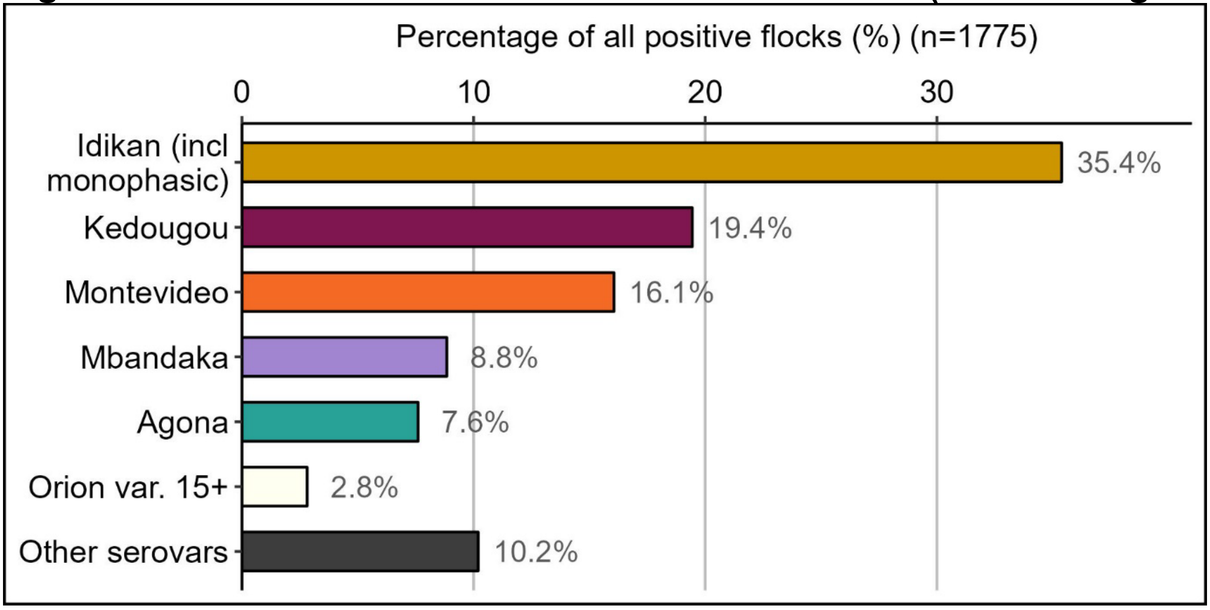
A horizontal bar graph showing the most common serovars in compound poultry feed in 2024. The 3 most commonly isolated serovars from compound poultry feed in 2024 were *S.* Falkensee, *S.* Idikan (including monophasic variants), and *S.* Poona (2 isolations each, each representing 12.5% of total isolations).

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



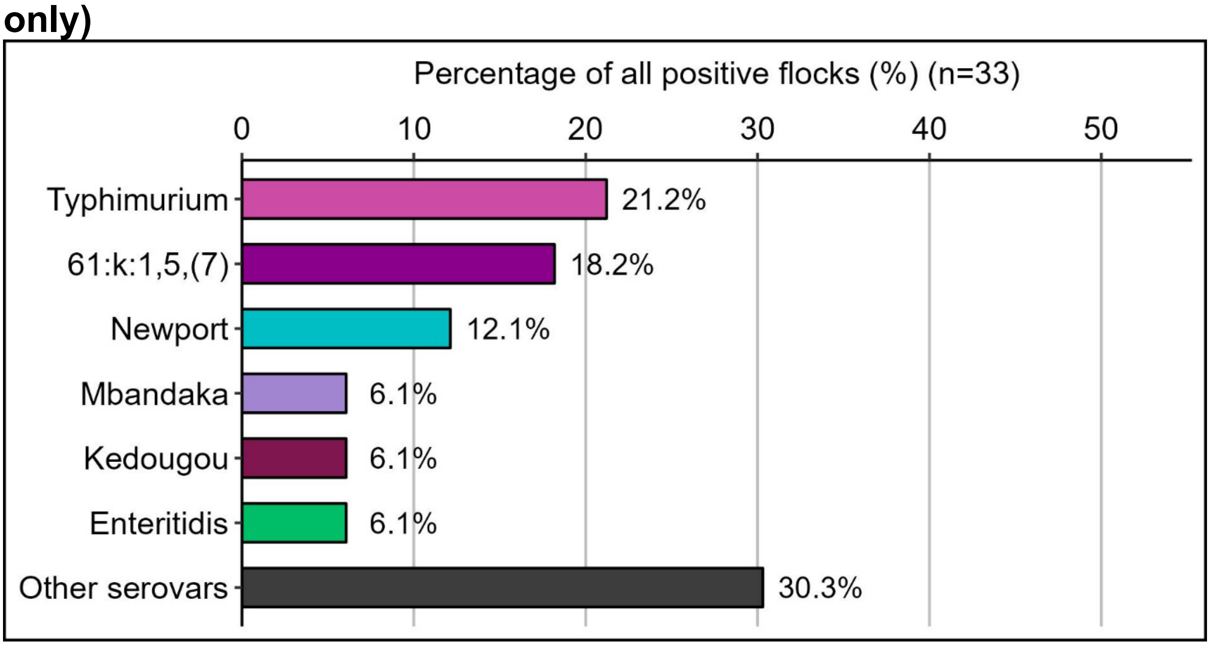
Horizontal bar graph showing the percentage of *Salmonella* isolations in breeder chickens in 2024. The most common *Salmonella* serovar in (adult) breeder chicken flocks in 2024 was *S.* Typhimurium, isolated from for 40.0% of total flocks, followed by *S.* Idikan (including monophasic variants) (20.0%),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

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



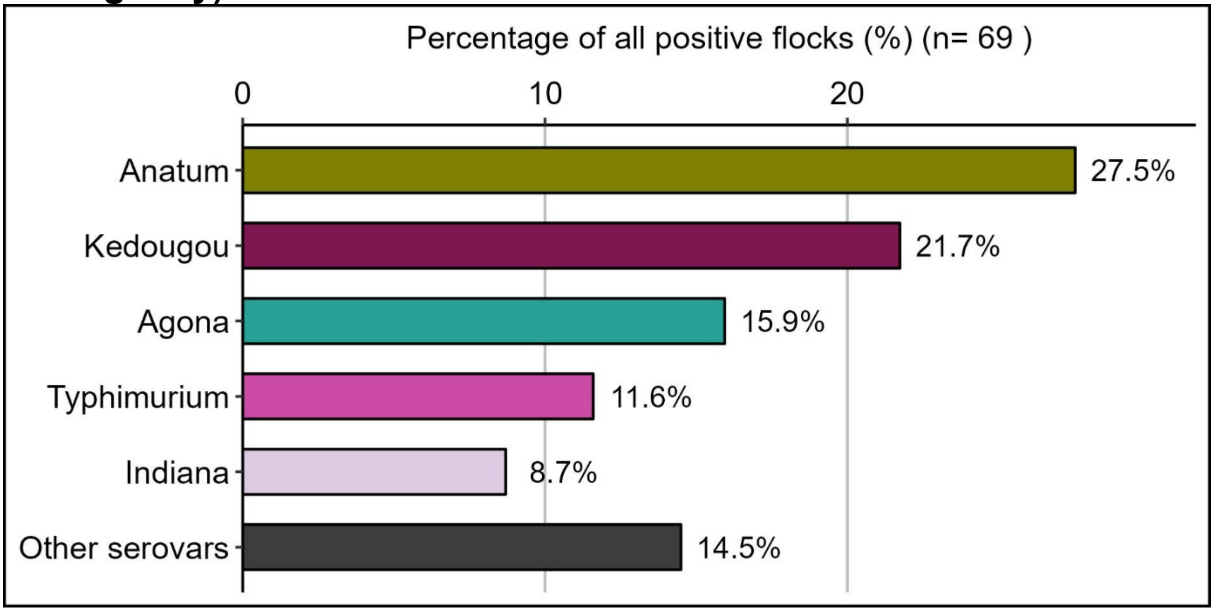
Horizontal bar graph showing the percentage of *Salmonella* isolations in broiler chickens in 2024. The most common *Salmonella* serovar in broiler chicken flocks in 2024 was *S.* Idikan (including its monophasic variants), accounting for 35.3% of total flocks, followed by *S.* Montevideo (16.0%), *S.* Mbandaka (8.8%), *S.* Agona (7.6%), and *S.* Orion var 15+ (2.8%).

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



Horizontal bar graph showing the percentage of *Salmonella* isolations in layer chickens in 2024. The most common serovar in adult chicken layer flocks in 2024 was *S.* Typhimurium (21.2% of total flocks), followed by *Salmonella* 61:k:1,5,(7) (18.2%) and *S.* Newport (12.1%). *S.* Mbandaka, *S.* Kedougou, and *S.* Enteritidis each isolated from 6.1% of *Salmonella* positive adult chicken layer flocks.

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



Horizontal bar graph showing the percentage of *Salmonella* isolations in breeder and fattener turkeys in 2024. The most common *Salmonella* serovar in 2024 in breeder and fattening turkey flocks was *S.* Anatum, accounting for 27.5% of total flocks, followed by *S.* Kedougou (21.7%).

Table 12.7: *Salmonella* serovars reported from animal feeding stuff ingredients and products associated with the ABPR in Great Britain, 2022 to 2024

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
Aba	1	0	0
Agama	1	4	9
Agona	13	13	29
Ajiobo	1	0	0
Amager	0	0	1
Amsterdam	0	0	1
Anatum	9	10	12
Banana	1	0	0
Bareilly	1	0	0
Bere	1	0	0
Bonn	2	1	0
Bovismorbificans	6	4	2
Brandenburg	2	1	1
Bredeney	0	2	1
Carmel	1	0	0
Cerro	6	5	2
Coeln	0	1	2
Corvallis	0	0	1
Cubana	6	1	2
Derby	37	57	27
Dublin	4	5	12
Duisburg	1	1	0
Ealing	3	0	4
Eastbourne	0	1	0
Enteritidis	4	19	28
Falkensee	0	0	2
Fresno	2	2	0
Give	7	13	3
Give var 15+ (Newbrunswick)	10	1	0
Goldcoast	3	0	1
Hadar	1	14	0
Havana	3	3	7
Heidelberg	0	1	0

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
Idikan (incl. monophasic)	4	3	10
Indiana	49	53	37
Infantis	61	132	84
Isangi	0	2	13
Kaapstad	0	0	1
Kassel	0	0	1
Kedougou	57	94	103
Kentucky	2	6	7
Kiambu	0	1	0
Kingston	2	1	1
Kottbus	17	12	14
Lexington	8	2	1
Litchfield	0	3	0
Liverpool	3	0	1
Livingstone	9	9	3
London	10	3	3
Mbandaka	21	13	30
Meleagridis	0	1	0
Miami	0	1	0
Molade	0	1	4
Monophasic Typhimurium	55	29	20
Montevideo	10	26	19
Morbihan	0	1	0
Morehead	0	1	0
Muenchen	0	1	1
Muenster	5	6	3
Nagoya	0	1	0
Neunkirchen	0	1	0
Newport	20	32	14
Nottingham	0	19	3
Ohio	22	82	114
Oranienburg	1	1	0
Orion	6	2	0
Orion var 15$^+$	1	1	0
O rough:z_{10}:enz$_{15}$	2	0	0
O rough:z_{29}:-	1	0	0
Oslo	1	1	1

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
Ouakam	1	0	0
Panama	15	5	2
Paratyphi B var. Java	2	5	0
Poona	0	1	2
Putten	0	2	0
Reading	1	2	1
Richmond	0	0	1
Riggil	0	0	1
Rissen	35	8	29
Rublislaw	2	0	0
Saintpaul	1	0	3
Schwarzengrund	2	1	1
Senftenberg	15	41	19
Senftenberg (z_{27})	1	0	0
Soerenga	1	3	0
Stanley	1	2	1
Stanleyville	0	1	2
Szentes	1	0	1
Telaviv	0	0	1
Tennessee	11	12	2
Teshie	1	0	0
Tsevie	1	0	0
Thompson	0	1	2
Typhimurium	50	70	57
Uganda	1	3	8
Umbilo	0	0	1
Utah	0	1	0
Virchow	3	1	1
Wilhelmsberg	1	2	0
Worthington	0	1	0
Yoruba	0	0	2
Zehlendorf	0	0	1
3,10:z_{10}:-	1	0	0
3,10:-:-	0	0	1
3,10:-:1,5	0	1	0
3,15:rough:-	1	0	0
3,19:z_{27}:-	4	0	0

Salmonella serovar	Isolations 2022	Isolations 2023	Isolations 2024
3,19:-:-	1	0	0
4,12:b:-	0	3	0
4,12:z:-	2	0	0
4,12:rough:-	1	0	0
6,7:b:-	1	0	0
6,7:enz$_{15}$	6	0	0
6,7:-:-	10	0	0
6,8:e,h:-	3	0	0
13,23:i:-	5	15	0
17:b:-	0	1	0
38:l,v,z$_{13}$:-	1	0	0
41:z$_{4}$,z$_{24}$:-	1	0	0
42:b:e,n,x,z15	0	1	0
47:z4,z23:-	0	1	0
48:z4,z23:-	0	0	2
61:i:z53	0	0	3
61:k:1,5,7	9	12	16
61:-:1,5,7	17	1	0
Total	**702**	**897**	**795**

Table 12.8a: Serovars of *Salmonella* in feeding stuff ingredients in Great Britain, 2022 to 2024

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Barley	Bovismorbificans	1	0	0
Barley	Kottbus	1	0	0
Barley	Panama	1	0	0
Barley	Rissen	1	0	0
Biscuit	Typhimurium DT193	1	0	0
Broken rice	Typhimurium DT2	1	0	0
Buckwheat	Enteritidis PT4	1	0	0
Cocoa	41:z_4,z_{24}:-	1	0	0
Feather meal	Tennessee	0	0	1
Feed additive	Derby	0	4	0
Feed additive	Infantis	0	1	0
Feed additive	Nottingham	0	1	0
Feeder mice	Montevideo	1	0	0
Fishmeal	Livingstone	0	0	1
Fishmeal	Montevideo	0	2	6
Fishmeal	Schwarzengrund	1	0	0
Fishmeal	Tennessee	0	0	1
Ginger root	Teshie	1	0	0
Guar protein	Cubana	0	0	1
Guar protein	Senftenberg	1	0	0
Liquorice root	Anatum	1	0	0
Liquorice root	Montevideo	1	0	0
Liquorice root	Tennessee	1	0	0
Maize	Typhimurium DT2	0	3	2
Maize	Typhimurium DT99	1	1	0
Malt	Agama	0	3	0
Malt	Anatum	3	0	0
Malt	Infantis	2	0	0
Minerals	Derby	1	0	0
Minerals	Hadar	0	1	0
Minerals	Kedougou	1	0	0
Minerals	Tennessee	1	0	0
Mixed cereals	Anatum	1	0	0
Mixed ingredients	Lexington	1	0	0

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Mixed oil seeds	Banana	1	0	0
Mixed oil seeds	Cubana	1	0	0
Mixed oil seeds	Livingstone	1	0	0
Mixed oil seeds	Rissen	2	0	0
Mixed oil seeds	Senftenberg	4	0	0
Mixed oil seeds	Soerenga	1	0	0
Mixed oil seeds	Typhimurium DT99	1	0	0
Mixed vegetables	Derby	1	2	0
Mixed vegetables	Indiana	0	2	0
Mixed vegetables	Newport	1	0	0
Mixed vegetables	Monophasic Typhimurium DT193	0	1	0
Mixed vegetables	Montevideo	0	1	0
Mixed vegetables	Panama	1	0	0
Oats	Typhimurium DT104	1	0	0
Oilseeds	Agama	0	0	2
Oilseeds	Agona	0	0	1
Oilseeds	Infantis	0	1	1
Oilseeds	Kentucky	0	0	1
Oilseeds	Ohio	0	0	1
Oilseeds	Rissen	0	1	4
Oilseeds	Senftenberg	0	0	1
Palm kernel	Senftenberg	0	1	0
Plant material	Anatum	0	0	1
Protein blend	Derby	1	0	0
Protein blend	London	1	0	0
Protein blend	4,12:i:- DT104	1	0	0
Rapeseed	Agona	0	1	1
Rapeseed	Ealing	1	0	3
Rapeseed	Idikan	1	0	0
Rapeseed	Kedougou	0	1	1
Rapeseed	Kentucky	0	0	1
Rapeseed	Kingston	1	0	0
Rapeseed	Mbandaka	0	0	1
Rapeseed	Rissen	23	0	7
Rapeseed	Senftenberg	1	0	0
Rapeseed	Tennessee	5	1	0

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Rapeseed	Typhimurium DT2	1	1	2
Rapeseed	Typhimurium DT99	1	0	0
Rapeseed	6,7:-:-	1	0	0
Separated fibre	Agona	0	1	0
Soya	Agona	0	1	0
Soya	Fresno	0	1	0
Soya	Havana	0	1	0
Soya	Lexington	0	0	1
Soya	Livingstone	0	1	0
Soya	Mbandaka	0	1	2
Soya	Rissen	0	0	1
Soya	Senftenberg	0	1	3
Soya	Tennessee	0	1	0
Soya	Typhimurium DT1	0	1	0
Soya	Typhimurium DT2	0	0	1
Soya	Typhimurium DT99	0	4	0
Soya	Typhimurium DT193	0	0	1
Soya	Yoruba	0	0	1
Soya bean meal	Anatum	1	0	0
Soya bean meal	Bareilly	1	0	0
Soya bean meal	Bere	1	0	0
Soya bean meal	Carmel	1	0	0
Soya bean meal	Cerro	2	0	0
Soya bean meal	Cubana	4	0	0
Soya bean meal	Duisburg	1	0	0
Soya bean meal	Fresno	2	0	0
Soya bean meal	Havana	1	0	0
Soya bean meal	Infantis	0	0	1
Soya bean meal	Kedougou	1	0	0
Soya bean meal	Kentucky	1	0	0
Soya bean meal	Livingstone	2	0	0
Soya bean meal	Mbandaka	1	0	1
Soya bean meal	Ohio	1	0	0
Soya bean meal	Tennessee	1	0	0
Soya bean meal	Typhimurium DT2	1	0	0
Soya bean meal	Typhimurium DT99	1	0	0

Feeding stuff	***Salmonella* serovar**	**Isolations 2022**	**Isolations 2023**	**Isolations 2024**
Soya bean meal	Uganda	1	0	0
Soya bean meal	3,15:rough:-	1	0	0
Soya bean meal	3,19:-:-	1	0	0
Soya bean meal	3,19:z_{27}:-	3	0	0
Soya bean meal	6,7:b:-	1	0	0
Sunflower	Liverpool	1	0	0
Sunflower	Tennessee	1	0	0
Wheat	Agona	2	0	0
Wheat	Idikan (incl. monophasic)	0	0	1
Wheat	Kedougou	0	1	0
Wheat	Kingston	0	1	0
Wheat	Ohio	0	0	1
Wheat	Typhimurium DT1	0	0	0
Wheat	Typhimurium DT2	0	0	1
Wheat	Typhimurium DT193	0	0	0
Wheat	Typhimurium U308	0	0	0
Yucca	Mbandaka	1	0	0
Total	Not applicable	**114**	**44**	**55**

Table 12.8b: Serovars of *Salmonella* in other products associated with the ABPR in Great Britain, 2022 to 2024

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Aeration tank	Infantis	0	4	1
Beef concentrate	Isangi	0	1	0
Biogas	Infantis	0	1	0
Biogas	Typhimurium DT75	0	1	0
Blood products	Cerro	2	0	0
Blood products	Derby	7	0	0
Blood products	Monophasic Typhimurium	0	0	1
Blood products	Panama	6	0	0
Blood products	Rissen	2	0	0
Blood products	4,12:i:- DT193	2	0	0
Blood products	4,5,12:i:- DT193	6	0	0
Blood products	4,5,12:i:- UNTY	1	0	0
Centrate liquor	Infantis	0	13	2
Compost	Aba	1	0	0
Compost	Anatum	0	0	1
Compost	Infantis	0	2	2
Compost	Kentucky	0	0	1
Compost	London	1	0	0
Compost	Muenster	0	0	1
Compost	Newport	0	0	2
Compost	Senftenburg	1	0	0
Compost	Tennessee	1	0	0
Compost	Typhimurium DT193	0	0	1
Compost	13,23:i:-	0	1	0
Digestate	Agona	0	1	5
Digestate	Anatum	0	0	1
Digestate	Bovismorbificans	0	1	0
Digestate	Derby	0	0	1
Digestate	Eastbourne	0	1	0
Digestate	Infantis	0	22	22
Digestate	Kentucky	0	1	0
Digestate	Livingstone	0	2	0

Feeding stuff	***Salmonella* serovar**	**Isolations 2022**	**Isolations 2023**	**Isolations 2024**
Digestate	Monophasic Typhimurium DT193	2	1	0
Digestate	Muenster	0	0	1
Digestate	Newport	1	1	0
Digestate	Nottingham	0	0	1
Digestate	Ohio	0	2	1
Digestate	Oslo	0	1	0
Digestate	Saintpaul	0	0	1
Digestate	Schwarzengrund	0	0	1
Digestate	Typhimurium DT105	0	0	1
Digestate	Typhimurium DT116	0	0	0
Digestate	Typhimurium DT130	0	1	0
Digestate	61:k:1,5,7	1	0	0
Digestate liquor	Infantis	0	18	0
Dog treat	Agona	0	0	1
Dog treat	Anatum	0	0	3
Dog treat	Derby	0	1	1
Dog treat	Infantis	0	1	0
Dog treat	Kentucky	0	0	1
Dog treat	Montevideo	0	1	1
Dog treat	Newport	0	0	1
Dog treat	Nottingham	0	1	0
Dog treat	Sentenberg	0	0	2
Dog treat	Telaviv	0	0	1
Dog treat	Typhimurium DT104	0	0	2
Dog treat	Uganda	0	0	2
Dog treat	Umbilo	0	0	1
Effluent tank	13,23:i:-	0	1	0
Environmental	61:k:1,5,7	0	0	1
Environmental	Indiana	0	0	1
Environmental	Infantis	0	0	1
Environmental	Kedougou	0	0	1
Environmental	Kottbus	0	0	1
Environmental	Newport	0	0	2
Environmental	Typhimurium	0	0	5
Feeder mice	Enteritidis	0	0	5

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Feeder mice	Monophasic Typhimurium	0	0	1
Feedmill environment	Agama	1	0	6
Feedmill environment	Agona	2	1	3
Feedmill environment	Ajiobo	1	0	0
Feedmill environment	Anatum	2	0	3
Feedmill environment	Bonn	0	1	0
Feedmill environment	Cerro	1	3	1
Feedmill environment	Cubana	1	0	0
Feedmill environment	Derby	1	5	1
Feedmill environment	Ealing	1	0	1
Feedmill environment	Enteritidis PT5	0	1	0
Feedmill environment	Enteritidis PT6	0	2	0
Feedmill environment	Enteritidis PT8	0	0	7
Feedmill environment	Enteritidis PT9	0	1	0
Feedmill environment	Enteritidis PT11b	0	1	0
Feedmill environment	Enteritidis NOPT	0	1	4
Feedmill environment	Enteritidis RDNC	0	1	0
Feedmill environment	Give	0	1	0
Feedmill environment	Hadar	0	1	0
Feedmill environment	Heidelberg	0	1	0
Feedmill environment	Idikan (Incl. monophasic)	2	3	1
Feedmill environment	Infantis	8	20	8
Feedmill environment	Kassel	0	0	1
Feedmill environment	Kedougou	50	82	92
Feedmill environment	Kentucky	1	4	0
Feedmill environment	Kiambu	0	1	0
Feedmill environment	Kottbus	1	1	0
Feedmill environment	Liverpool	1	0	0
Feedmill environment	Livingstone	1	1	0
Feedmill environment	Mbandaka	9	3	0
Feedmill environment	Molade	0	0	4
Feedmill environment	Monophasic Typhimurium DT193	1	3	1
Feedmill environment	Monophasic Typhimurium NOPT	0	1	0

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Feedmill environment	Monophasic Typhimurium UNTY	0	1	0
Feedmill environment	Montevideo	0	7	0
Feedmill environment	Morehead	0	1	0
Feedmill environment	Nagoya	0	1	0
Feedmill environment	Neunkirchen	0	1	0
Feedmill environment	Newport	1	4	0
Feedmill environment	Nottingham	0	16	2
Feedmill environment	Ohio	20	68	110
Feedmill environment	Oranienburg	1	1	0
Feedmill environment	Oslo	1	0	1
Feedmill environment	Ouakam	1	0	0
Feedmill environment	Paratyphi var. java	1	1	0
Feedmill environment	Rissen	3	2	5
Feedmill environment	Saintpaul	0	0	1
Feedmill environment	Senftenberg	2	9	0
Feedmill environment	Senftenberg (z_{27})	1	0	0
Feedmill environment	Stanley	0	0	1
Feedmill environment	Stanleyville	0	1	1
Feedmill environment	Szentes	1	0	0
Feedmill environment	Tennessee	0	1	0
Feedmill environment	Typhimurium DT2	0	4	7
Feedmill environment	Typhimurium DT75	0	0	1
Feedmill environment	Typhimurium DT99	2	4	0
Feedmill environment	Typhimurium DT105	0	2	0
Feedmill environment	Typhimurium U322	0	4	0
Feedmill environment	Typhimurium NOPT	0	1	2
Feedmill environment	Typhimurium RDNC	1	4	0
Feedmill environment	Typhimurium UNTY	0	1	0
Feedmill environment	Uganda	0	3	1
Feedmill environment	Virchow	0	0	1
Feedmill environment	Williamsberg	0	1	0
Feedmill environment	Zehlendorf	0	0	1
Feedmill environment	3,19:z_{27}:-	1	0	0
Feedmill environment	6,7:enz$_{15}$	2	0	0
Feedmill environment	6,7:-:-	4	1	0
Feedmill environment	13,23:i:-	5	8	0

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Feedmill environment	61:k:1,5,7	0	1	0
Feedmill environment	61:-:1,5,7	1	0	0
Feedmill environment	42:b:e,n,x,z15	0	1	0
Feedmill environment	47:z4,z23:-	0	1	0
Fertilizer - tea fungal additive	Anatum	0	1	0
Landfill	Derby	0	1	0
Liquid waste	Derby	0	0	1
Meat and bone	Derby	0	1	0
Meat and tallow	4,5,12:i:- DT193	2	0	0
Meat and tallow	Infantis	2	0	0
Other raw materials	Agona	0	0	1
Other raw materials	Derby	0	0	1
Other raw materials	Isangi	0	0	12
Other raw materials	Senftenberg	0	0	1
PAP	Cerro	0	0	1
Pasteurised liquor	Infantis	0	4	1
Pet food (raw)	Agama	0	1	0
Pet food (raw)	Agona	9	7	11
Pet food (raw)	Amsterdam	0	0	1
Pet food (raw)	Anatum	1	8	3
Pet food (raw)	Bonn	2	0	0
Pet food (raw)	Bovismorbificans	5	2	1
Pet food (raw)	Brandenburg	2	1	1
Pet food (raw)	Bredeney	0	1	1
Pet food (raw)	Cerro	1	0	0
Pet food (raw)	Coeln	0	0	1
Pet food (raw)	Derby	26	31	16
Pet food (raw)	Dublin	4	5	12
Pet food (raw)	Ealing	1	0	0
Pet food (raw)	Enteritidis	0	0	1
Pet food (raw)	Enteritidis PT3a	0	1	0
Pet food (raw)	Enteritidis PT8	1	1	0
Pet food (raw)	Enteritidis PT9a	0	1	0
Pet food (raw)	Enteritidis PT9b	0	0	1
Pet food (raw)	Enteritidis PT11b	0	1	0
Pet food (raw)	Enteritidis PT13	0	0	2

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Pet food (raw)	Enteritidis PT13a	0	2	4
Pet food (raw)	Enteritidis PT21	1	2	0
Pet food (raw)	Enteritidis PT22	0	1	0
Pet food (raw)	Enteritidis PT34	0	0	2
Pet food (raw)	Enteritidis NOPT	0	0	2
Pet food (raw)	Enteritidis RDNC	1	0	0
Pet food (raw)	Give	7	10	2
Pet food (raw)	Give var 15^+ (Newbrunswick)	10	1	0
Pet food (raw)	Goldcoast	3	0	1
Pet food (raw)	Hadar	1	11	0
Pet food (raw)	Havana	2	1	1
Pet food (raw)	Idikan (incl. monophasic)	1	0	5
Pet food (raw)	Indiana	49	46	36
Pet food (raw)	Infantis	38	29	38
Pet food (raw)	Isangi	0	1	0
Pet food (raw)	Kaapstad	0	0	1
Pet food (raw)	Kedougou	5	2	7
Pet food (raw)	Kentucky	0	0	2
Pet food (raw)	Kingston	1	0	0
Pet food (raw)	Kottbus	15	11	13
Pet food (raw)	Lexington	7	1	0
Pet food (raw)	Litchfield	0	3	0
Pet food (raw)	Liverpool	1	0	0
Pet food (raw)	Livingstone	5	3	2
Pet food (raw)	London	8	2	3
Pet food (raw)	Mbandaka	10	8	23
Pet food (raw)	Meleagridis	0	1	0
Pet food (raw)	Miami	0	1	0
Pet food (raw)	Monophasic Typhimurium DT104	2	0	0
Pet food (raw)	Monophasic Typhimurium DT120	1	3	0
Pet food (raw)	Monophasic Typhimurium DT193	29	16	13
Pet food (raw)	Monophasic Typhimurium U208	1	0	0

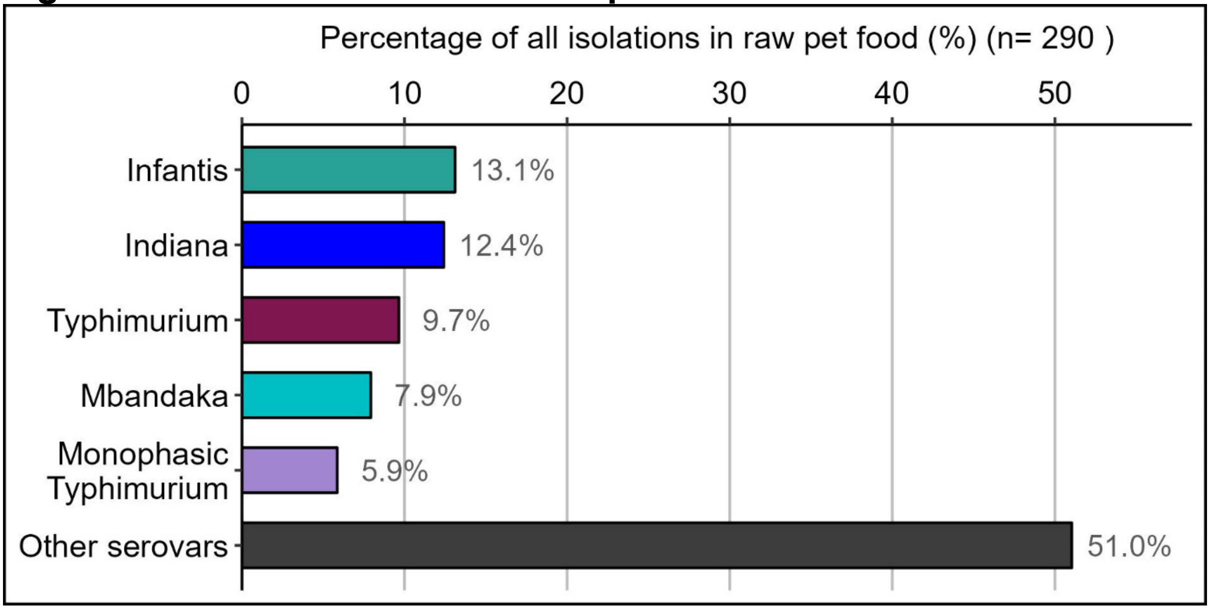
Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Pet food (raw)	Monophasic Typhimurium U311	1	0	1
Pet food (raw)	Monophasic Typhimurium U323	0	0	2
Pet food (raw)	Monophasic Typhimurium NOPT	0	0	1
Pet food (raw)	Monophasic Typhimurium UNTY	6	0	0
Pet food (raw)	Montevideo	8	8	10
Pet food (raw)	Muenchen	0	1	0
Pet food (raw)	Muenster	5	5	1
Pet food (raw)	Newport	17	22	6
Pet food (raw)	Ohio	1	0	0
Pet food (raw)	Orion	6	2	0
Pet food (raw)	Orion var. 15^{+}	1	1	0
Pet food (raw)	O rough:z_{10}:enz_{15}	2	0	0
Pet food (raw)	Panama	7	4	1
Pet food (raw)	Paratyphi var. Java	1	3	0
Pet food (raw)	Reading	1	2	0
Pet food (raw)	Rissen	4	4	1
Pet food (raw)	Rubislaw	2	0	0
Pet food (raw)	Saintpaul	1	0	1
Pet food (raw)	Schwarzengrund	1	0	0
Pet food (raw)	Senftenberg	6	13	9
Pet food (raw)	Stanley	1	2	0
Pet food (raw)	Szentes	0	0	1
Pet food (raw)	Tennessee	1	0	0
Pet food (raw)	Thompson	0	0	1
Pet food (raw)	Tsevie	1	0	0
Pet food (raw)	Typhimurium DT1	0	2	0
Pet food (raw)	Typhimurium DT2	5	8	2
Pet food (raw)	Typhimurium DT4	0	1	0
Pet food (raw)	Typhimurium DT8	2	1	0
Pet food (raw)	Typhimurium DT9	3	1	0
Pet food (raw)	Typhimurium DT11	0	0	1
Pet food (raw)	Typhimurium DT30	0	0	1
Pet food (raw)	Typhimurium DT32	0	1	0

Feeding stuff	*Salmonella* serovar	Isolations 2022	Isolations 2023	Isolations 2024
Pet food (raw)	Typhimurium DT75	3	1	11
Pet food (raw)	Typhimurium DT99	1	2	1
Pet food (raw)	Typhimurium DT104	3	0	0
Pet food (raw)	Typhimurium DT105	5	1	2
Pet food (raw)	Typhimurium DT116	0	2	1
Pet food (raw)	Typhimurium DT120	2	1	0
Pet food (raw)	Typhimurium DT193	2	3	2
Pet food (raw)	Typhimurium U308	0	0	1
Pet food (raw)	Typhimurium U311	3	1	0
Pet food (raw)	Typhimurium NOPT	2	2	3
Pet food (raw)	Typhimurium RDNC	7	3	3
Pet food (raw)	Virchow	3	1	0
Pet food (raw)	Wilhelmsberg	1	1	0
Pet food (raw)	3,10:-:-	0	0	1
Pet food (raw)	3,10:z_{10}:-	1	0	0
Pet food (raw)	4,12:b:-	0	2	0
Pet food (raw)	4,12:rough	1	0	0
Pet food (raw)	4,12:z:-	2	0	0
Pet food (raw)	6,7:-:enz_{15}	4	0	0
Pet food (raw)	6,7:-:-	5	0	0
Pet food (raw)	6,8:e,h:-	3	0	0
Pet food (raw)	13,23:i:-	0	3	0
Pet food (raw)	38:l,v,z_{13}:-	1	0	0
Pet food (raw)	48:z4,z23:-	0	0	2
Pet food (raw)	61:-:1,5,7	16	1	0
Pet food (raw)	61:i:z53	0	0	3
Pet food (raw)	61:k:1,5,7	8	11	15
Process water tank	Infantis	0	5	2
Raw meat	Bovismorbificans	0	1	0
Raw meat	Enteritidis	0	1	0
Raw meat	Indiana	0	1	0
Raw meat	Livingstone	0	2	0
Raw meat	Mbandaka	0	1	0
Raw meat	Monophasic Typhimurium DT59	0	1	0
Raw meat	Montevideo	0	1	0
Raw meat	Newport	0	2	0

Feeding stuff	***Salmonella* serovar**	**Isolations 2022**	**Isolations 2023**	**Isolations 2024**
Raw meat	Paratyphi b variant Java	0	1	0
Raw meat	Schwarzengrund	0	1	0
Slurry	Agona	0	0	1
Slurry	Corvallis	0	0	1
Slurry	Havana	0	0	6
Slurry	Montevideo	0	0	1
Slurry	Reading	0	0	1
Slurry	Richmond	0	0	1
Slurry	Stanleyville	0	0	1
Unspecified	Anatum	0	1	0
Unspecified	Bredeney	0	1	0
Unspecified	Cerro	0	2	0
Unspecified	Coeln	0	1	0
Unspecified	Derby	0	2	0
Unspecified	Enteritidis PT21	0	1	0
Unspecified	Fresno	0	1	0
Unspecified	Give	0	1	0
Unspecified	Infantis	0	1	0
Unspecified	Kedougou	0	6	0
Unspecified	Montevideo	0	2	0
Unspecified	Ohio	0	6	0
Unspecified	Panama	0	1	0
Unspecified	Rissen	0	1	0
Unspecified	Senftenberg	0	3	0
Unspecified	Tennessee	0	1	0
Unspecified	Thompson	0	1	0
Unspecified	Typhimurium DT2	0	1	0
Unspecified	Typhimurium DT015	0	1	0
Unspecified	Typhimurium DT193	0	1	0
Windrow	Muenchen	0	0	1
Total	Not applicable	**577**	**759**	**671**

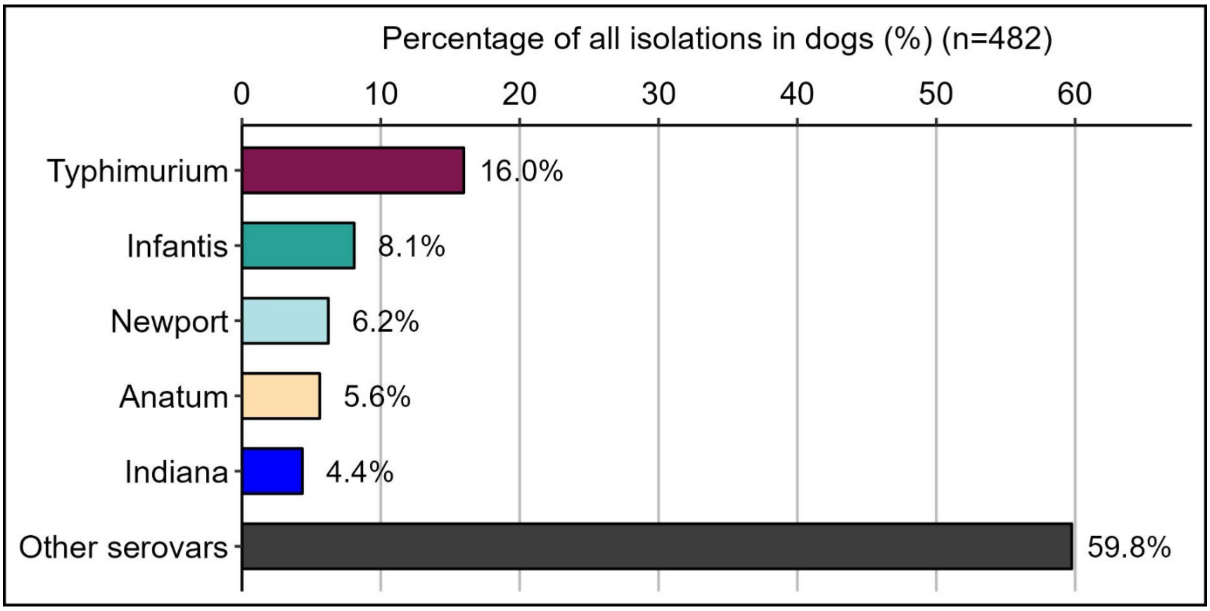
Figure 12.7: Isolations of the most common serovars in raw pet food and dogs in Great Britain in 2024

Figure 12.7.1: Isolations from raw pet food



A horizontal bar graph showing the most common serovars in compound poultry feed in 2024. The most common *Salmonella* serovar in raw pet food in 2024 was *S.* Infantis, accounting for 13.1% of total isolations, followed by *S.* Indiana (12.4%), *S.* Typhimurium (9.7%), *S.* Mbandaka (7.9%), and monophasic *S.* Typhimurium (5.9%). Other serovars accounted for 51.0% of total *Salmonella* isolations from raw pet food.

Figure 12.7.2: Isolations from dogs



A horizontal bar graph showing the most common serovars 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.* Indiana (4.4%). Other serovars accounted for 59.7% 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, 2022 to 2024

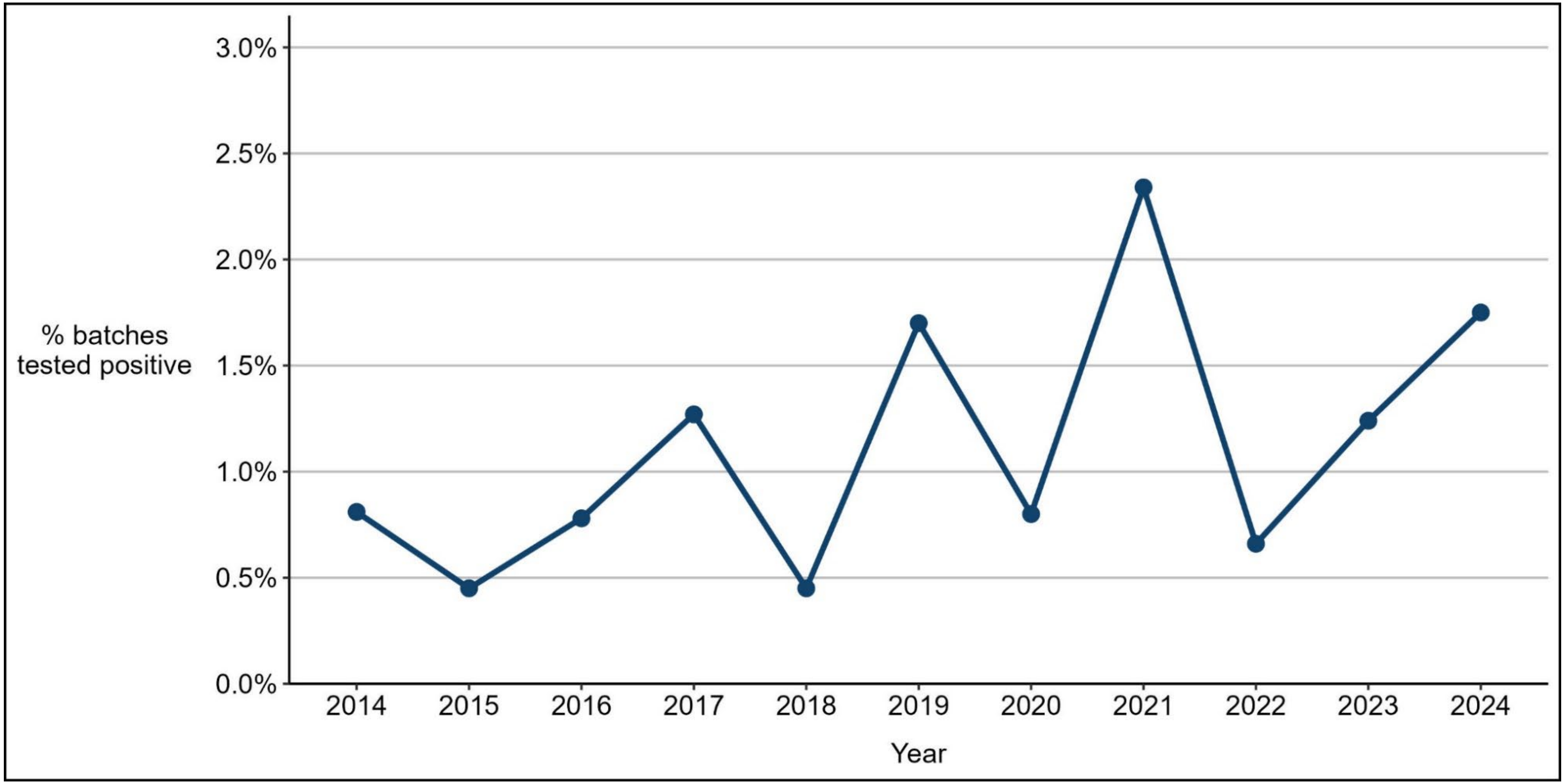
Sample Type	2022 Batches	2022 number +ve	2022 % +ve	2023 Batches	2023 number +ve	2023 % +ve	2024 Batches	2024 number +ve	2024 % +ve
Blood meal	0	0	0	2	0	0	5	0	0.00
Feather meal	1	0	0	9	0	0	12	1	8.33
Greaves	1	0	0	0	0	0	0	0	0.00
Meat and bone meal	3	0	0	2	0	0	0	0	0.00
Poultry offal meal	0	0	0	7	0	0	10	1	10.00
Other fish meal	1	0	0	0	0	0	3	0	0.00
White fish meal	14	0	0	15	0	0	11	0	0.00
Others	281	2	0.71	288	4	1.39	418	6	1.44
Total	**301**	**2**	**0.66**	**323**	**4**	**1.24**	**459**	**8**	**1.74**

This table excludes the results of private testing.

Table 12.10: Animal By-Products (Enforcement) Regulations, 2013. Serovars isolated during 2022 to 2024 from official and private testing of domestic protein and other products associated with the regulations in Great Britain

Serovar	Isolations 2022	Isolations 2023	Isolations 2024
Anatum	0	0	1
Cerro	0	0	1
Derby	1	0	0
Gueuletapee	0	1	0
Infantis	0	1	0
Livingstone	0	0	1
Nottingham	0	0	1
Senftenberg	0	0	1
Tennessee	1	0	1
Typhimurium DT75	0	1	0
Typhimurium DT105	0	1	1
Typhimurium DT193	0	0	1
Total	**2**	**4**	**8**

Figure 12.8: *Salmonella* contamination rate for domestic processed animal protein (batches tested) in Great Britain, 2014 to 2024



A line graph showing the *Salmonella* contamination rate for domestic processed animal protein from 2014 to 2024. The figure shows the proportion of positive batches for domestic processed animal protein had fluctuated year on year with an overall increase in positivity. 2021 saw the highest proportion of contaminated batches (2.34%) but fell in 2022 to 0.66% of batches. before increasing again in 2023 (1.24%) and 2024 (1.74%).

For data prior to 2013, see *Salmonella* in livestock production in Great Britain 2014

Chapter 13: Antimicrobial susceptibility in *Salmonella*

Salmonella isolates received for serotyping 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 which have been recovered under the *Salmonella* National Control Programmes which apply to chickens and turkeys. These isolates are derived from premises located throughout Great Britain.

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 changed for ciprofloxacin from the historical APHA veterinary breakpoint of resistant ≤ 13mm used in previous years, to the BSAC breakpoint of resistant or intermediate ≤ 19mm (this breakpoint was that recommended by BSAC on 1 January 2007). Longer term trends in ciprofloxacin resistance should therefore be interpreted taking into account 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 2023 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	25	TM	15
Chloramphenicol	30	C	20
Amikacin	30	AK	18
Amoxicillin and clavulanic acid	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 from each incident has usually been tested unless there has been a reason for enhanced surveillance identified. 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 numbers 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 December 2024, the APHA discontinued phage typing as a supplementary test for the characterization of *S.* Typhimurium and *S.* Enteritidis. Therefore, phage type information could not be obtained for approximately 50 isolates collected in late 2024 and is not included in this report.

Salmonella Dublin

A total of 246 *Salmonella* Dublin isolates underwent antimicrobial susceptibility testing in 2024. Overall, 225 isolates (91.5%) were susceptible to all 16 antimicrobials tested.

As in previous years, most *S.* Dublin isolates originated from cattle (203, 82.5%). Among these, 183 isolates (90.2%) were fully susceptible. This represents a statistically significant decrease in susceptibility among cattle isolates compared to 96.4% in 2022 and 96.3% in 2023 (Table 13.2). While antimicrobial resistance remained generally low, resistance to both neomycin and furazolidone increased to 2.5% in 2024 after being undetected in the previous 2 years. Resistance to streptomycin also rose from 1.9% in 2023 to 4.9% in 2024. Resistance to apramycin, which was detected for the first time after several years in 2023, was not identified in any of the *S*. Dublin isolates tested in 2024. All non-susceptible isolates (n=21) showed resistance to only one antimicrobial in the panel, except for one isolate that exhibited resistance to both furazolidone and streptomycin.

S. Dublin isolates from species other than cattle were recovered from dogs (n=17), sheep (n=10), feed (n=9), environmental sources (n=5), one goat, and one pig. Of these 43 isolates, 97.7% were fully susceptible. The only resistant isolate, recovered from an environmental sample, showed resistance to furazolidone.

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. However, the decline observed in 2024 marks a renewed decrease in susceptibility following the brief recovery of the previous 2 years. Despite this, the majority of *S.* Dublin isolates remains susceptible.

Salmonella Typhimurium

In 2024, 569 isolates of *Salmonella* Typhimurium were tested for antimicrobial susceptibility. The most frequent definitive or undefined phage types subjected to susceptibility testing at APHA are given in Table 13.3. The percentage of the 8 most common definitive and undefined phage types of *S.* Typhimurium sensitive to all 16 antimicrobial agents in 2024 is given in Figure 13.1.

As shown in Table 13.4, the proportion of *S*. Typhimurium isolates that were susceptible to all tested antimicrobials remained relatively stable between 2023 and 2024, with rates of 55.0% and 54.3%, respectively. This trend aligns with the increase observed after the drop in susceptibility in 2020, which was recorded at 39.9%.

Over half of all *S.* Typhimurium tested in 2024 originated from pigs, feed, and dogs. Among pig isolates (n=214), only 0.9% were susceptible, while 91.1% tested multidrug resistant (MDR: resistant to 4 or more antimicrobials). In contrast, 86.5% of isolates from feed (n=89) and 83.1% from dogs (n=83) were susceptible. These contrasting resistance patterns reflect differences in the phage types associated with each source.

DT193 and DT32 *S.* Typhimurium isolates from pigs accounted for 15.6% and 12.5% of the total *S.* Typhimurium isolates (n=569), respectively. Of 89 DT193 isolates, 2.2% were fully susceptible, while 93.5% were MDR. None of the 71 DT32 isolates from pigs were fully susceptible, and 95.8% were MDR.

Among 60 *S.* Typhimurium isolates from cattle, 88.3% were fully susceptible. DT105, which has increased in cattle in recent years, was the most frequently resistant phage type, typically exhibiting the SSuT resistance pattern. Of the 21 DT105 isolates from cattle, 71.4% were fully susceptible.

The *S.* Typhimurium phage types DT104, its variants DT104b, and U302 are preferentially selected for susceptibility testing because of the importance of the pentavalent resistance pattern AmCSSuT. These have comprised more than a quarter of tested isolates in some years of the last decade. However, no *S.* Typhimurium U302 strains have been observed since 2022. DT104 strains and their variants showed a general decline from 2007 to 2014 and, following a brief resurgence from 2015 to 2017, levels have been decreasing steadily since 2019 (Table 13.4). In 2024, the lowest recorded level was observed for DT104 strains (3.2%), and no DT104b isolates were detected.

Of the 18 DT104 *S.* Typhimurium isolates tested in 2024, 6 were from pigs, 6 from feed, 2 from dogs, one from a chicken, one from a turkey, one from a non statutory species and one from an environmental sample. The AmCSSuT resistance pattern was detected in 55.6% of DT104 isolates. In all 6 isolates from pigs, the pattern included additional resistance to neomycin and the sulphamethoxazole and trimethoprim combination. The pattern was also present alongside nalidixic acid resistance in one isolate from feed. Nalidixic acid resistance in DT104 has historically been observed in livestock species, while in 2024 it was only detected in the 6 DT104 isolates from feed (Table 13.5).

Resistance to the sulphamethoxazole and trimethoprim combination across all definitive phage types increased to 36.4% in 2024. This was largely driven by isolates from pigs (Table 13.6). Among pig isolates, resistance to this combination included 95.5% of all DT193 isolates (n=89), 98.6% of all DT32 isolates (n=71), and all U308a isolates (n=12). Phage type U288, once an important contributor to resistance in pigs, was not detected in 2024 following a decline since 2022 (Table 13.7).

Apramycin resistance in *S.* Typhimurium increased to 11.1% in 2024, with all resistant isolates originating from pigs (Table 13.4). Though lower than in 2012 (20.4%), the last 3 years have shown a consistent rise. Neomycin resistance also rose to 17.4% in 2024, with isolates detected in pigs (n=94), feed (n=2), one chicken, and one pigeon. Among pig isolates (n=214), 29.4% showed a resistance pattern including apramycin, neomycin, and the sulphamethoxazole and trimethoprim combination, contributing to the increasing trend. In contrast, resistance to tetracycline, streptomycin, and nalidixic acid continued to decline (Table 13.4).

Twelve *S.* Typhimurium isolates were resistant to nalidixic acid in 2024: 6 from feed, 4 from dogs, and 2 from pigs. Two of the isolates from dogs (RDNC) were also resistant to ciprofloxacin. A third ciprofloxacin resistant *S*. Typhimurium isolate (RDNC) detected in 2024 originated from feed and was MDR, displaying also resistance to cefotaxime and ceftazidime.

MDR was detected in a range of phage types, including DT104 (from dogs, feed, pigs, a non statutory species, and an environmental sample), DT105 (from pigs and a chicken), DT116, DT120, DT181, DT193, DT32, DT4, DT75 (all from pigs), and RDNC isolates (from pigs, feed, and a non statutory species). Of 26 phage types detected, 8 (DT11, DT20, DT30, DT36, DT5, DT56, DT8, and DT9) were exclusively composed of fully susceptible isolates.

Monophasic *Salmonella* Typhimurium serovars

A total of 140 isolates of monophasic *S.* Typhimurium were tested in 2024. Most were from pigs (65.7%), dogs (14.3%), and feed (13.6%). Only 4.3% of isolates tested in 2024 were fully susceptible, while 79.3% were MDR. The proportion of susceptible isolates and MDR levels were similar to those observed in 2023.

The AmSuT resistance pattern was found in 75.7% of isolates, mostly associated with phage types DT193 and UNTY. This pattern was frequently accompanied by resistance to neomycin, gentamicin, and apramycin, and occasionally by resistance to the sulphamethoxazole and trimethoprim combination and chloramphenicol. Resistance was identified in 20.0% of isolates for apramycin, 22.9% for neomycin, and 20.7% for gentamicin. Seventeen isolates (12.1%) were resistant to all 3 of these aminoglycosides and all originated from pigs.

Nalidixic acid resistance was observed in one monophasic *S.* Typhimurium isolate (DT120) from cattle, that was also resistant to tetracycline.

Serovars other than *Salmonella* Dublin and *Salmonella* Typhimurium

Of the 3,890 *Salmonella* isolates tested in 2024, excluding *S.* Dublin and *S.* Typhimurium, 74.9% were susceptible to all antimicrobials in the test panel (Table 13.8). This represents a stable trend compared to 2023 but remains lower than the level observed in 2022 (77.2%). Susceptibility remained stable at 82.4% also for *S.* Enteritidis isolates (n=108) in comparison to 2023 (74.2%, n=66). Twelve *S.* Enteritidis isolates from chickens (n=5), feed (n=5), a dog (n=1) and the environment (n=1) were MDR.

Resistance to nalidixic acid was identified in 149 isolates (3.8%) of serovars other than *S.* Dublin and *S.* Typhimurium. The majority of these originated from feed (n=84) and belonged to serovars S. Infantis (n= 36) and S. Indiana (n=32). Other main sources of nalidixic acid resistant isolates were chickens (n=26) and dogs (n=20). Among the 19 non-susceptible *S.* Enteritidis isolates, 16 showed resistance to nalidixic acid. These included 6 isolates from feed (phage types PT35, PT4, PT6a, PT9b, and 2 RDNC), 5 from chickens (all PT30), 3 from dogs (1 PT1 and 2 untyped), and 2 from environmental samples (1 PT30 and 1 RDNC).

Ciprofloxacin resistance was detected in 32 isolates. This included 12 isolates from feed (10 *S.* Infantis and 2 *S.* Kottbus), 11 from dogs (7 *S.* Infantis, 2 *S.* Kentucky, one *S.* Newport, and 1 *S.* Rissen), 7 from chickens (4 *S.* Infantis, 2 *S.* Idikan, and one *S.* Agona), one *S.* Infantis from the environment, and one isolate of serovar *S.* 48:Z52:Z from a non statutory species.

Four isolates were resistant to both cefotaxime and ceftazidime. These included 3 isolates from dogs (2 *S.* Kentucky and one *S.* Goldcoast) and one *S.* Agona isolate from a chicken sample.

MDR was observed in 126 isolates (3.2%). These included 12 *S.* Enteritidis (5 from chickens, 5 from feed, one from a dog, one from the environment), 41 *S.* Infantis (24 from feed, 8 from dogs, 5 from chickens, 4 from the environment), and 15 *S.* Kedougou (6 from chickens, 5 from the environment, 3 from pigs, one from feed).

Of the 174 *S.* Infantis isolates tested, 67.8% were fully susceptible, while 23.6% were MDR. The main sources of *S.* Infantis isolates were feed (n=101), dogs (n=40), and chickens (n= 20). Of the isolates from feed, 77 were susceptible and 24 were MDR. In dogs, 32 isolates were susceptible and 8 were MDR. Among *S.* Infantis isolates from chickens, 14 were susceptible and 5 were MDR.

Individual antimicrobials

Of the 4,705 *Salmonella* isolates tested in 2024, 73.3% were susceptible to all the antimicrobials tested (Table 13.9). This is in line with the levels recorded in 2023 (73.3% of 5,513 isolates), although a slight decrease in susceptibility in comparison to 2022 (75.7% of 5,562 isolates).

Overall, resistance to most antibiotics in the testing panel remained stable between 2023 and 2024. Ampicillin resistance was 10.9% in 2024 and unchanged across most sources of isolates. However, a significant decrease was detected in cattle, with ampicillin resistance dropping from 4.5% in 2023 (21 of 471 isolates) to 0.58% in 2024 (2 of 346).

Considering all *Salmonella* serovars tested in 2024, a modest decline was detected for resistance to the sulphamethoxazole and trimethoprim combination, which decreased from 12.3% in 2023 to 11.6% in 2024. Resistance to apramycin (2.2%), streptomycin (12.2%), and gentamicin (2.6%) remained similar to the levels observed in 2023, while neomycin-resistant isolates increased from 3.0% to 5.1%. Despite no detection in the previous year, amikacin resistance was observed in 13 isolates in 2024. *Salmonella* isolates from pigs (n=404), contributed most to the overall figures of resistance to aminoglycosides, with 56.9% of pig isolates showing resistance to streptomycin, 34.4% to neomycin, 29.0% to gentamicin, 25.7% to apramycin, and 3.0% to amikacin. Sixty-two 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. Twelve *S.* Typhimurium isolates from pigs showed resistance to neomycin, gentamycin and amikacin.

In 2024, 3.4% of isolates were resistant to nalidixic acid, in line with results from the previous year. Overall, 55.9 % of isolates resistant to nalidixic acid (n=161) originated from feed, mostly involving the serovars *S*. Indiana (32 of 33 isolates) and *S*. Infantis (36 of 38). In turkeys 4 isolates resistant to nalidixic acid belonged to the serovar *S.* Senftenberg, with all 4 isolates showing resistance only to this antibiotic. In chickens, all *S.* Senftenberg isolates were fully susceptible, while nalidixic acid resistance was detected in *S.* Idikan (6 of 334), *S.* Enteritidis (5 of 15), *S.* Infantis (5 of 20), *S.* 13,23:I:- (4 of 118), *S.* Kedougou (3 of 220), *S.* Montevideo (1 of 301), *S.* Agona (1 of 110) and *S.* Newport (1 of 26).

Resistance to ciprofloxacin remained stable (0.7%) in 2024 and it was observed in 13 isolates from feed (10 *S.* Infantis, 2 *S.* Kottbus, and one *S.* Typhimurium), 13 from dogs (7 *S.* Infantis, 2 *S.* Kentucky, 2 *S.* Typhimurium, one *S.* Rissen, one *S.* Newport), 7 from chickens (4 *S.* Infantis, 2 *S.* Idikan and one *S.* Agona), one *S.* Infantis from an environmental sample and one *S.* 48:Z52:Z from a non statutory species.

Resistance to cefotaxime and ceftazidime remained stable in 2024 (0.1%) and it was detected in 3 dog isolates (2 *S.* Kentucky from the same dog and one *S.* Goldcoast from a different dog), one *S.* Typhimurium isolate from raw pet food and one *S.* Agona from a poultry sample. All isolates were MDR, with 4 showing a resistance pattern that involved 10 or more antimicrobials, including the 2 *S.* Kentucky isolates (both showing the same resistance pattern), the *S.* Typhimurium isolate and the *S.* Agona isolate.

Public health considerations

Antimicrobial susceptibility patterns have been useful in conjunction with *Salmonella* serovar and (where appropriate) phage type data to investigate the epidemiology of

Salmonella infections. However, genome sequencing has replaced phenotypic methods of *Salmonella* typing for human isolates and is the primary method of characterisation for APHA isolates. As such genomic analysis is used for outbreak detection and investigation and when comparing isolates from animal and human sources. Ongoing liaison takes place between the Agencies concerned in relation to the strains detected and their antimicrobial resistance patterns.

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 2024, MDR isolates (n=453) were mostly from pigs, accounting for 66.7% of the total. None of the MDR isolates from pigs showed resistance to ciprofloxacin or third generation cephalosporins. In contrast, although feed, chickens, and dogs contributed fewer MDR isolates overall (12.6%, 9.3%, and 5.7%, respectively) they included strains resistant to critically important antimicrobials. Of the 26 MDR isolates from these 3 sources, 21 belonged to the serovar *S.* Infantis.

Ciprofloxacin resistance was identified in 0.7% of all isolates (n=4,705), including 13 from feed, 13 from dogs, 7 from chickens, one from an environmental sample, and one from a reptile. All 35 ciprofloxacin resistant isolates detected in 2024 were also resistant to nalidixic acid.

Resistance to cefotaxime and ceftazidime remained stable in 2024 (0.1%). It was detected in 3 dog isolates: 2 *S.* Kentucky producing extended-spectrum beta-lactamase (ESBL) from the same dog, and one *S.* Goldcoast producing AmpC beta-lactamase from another dog. In addition, one ESBL-producing *S.* Typhimurium isolate was recovered from raw pet food, and one *S.* Agona isolate carrying the IMP-1 metallo-beta-lactamase gene was detected from a chicken sample. All 5 isolates were MDR, and all except the *S.* Goldcoast isolate also showed resistance to ciprofloxacin.

APHA offers an advisory visit 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.

***S.* Agona isolate**

In 2024, a single *Salmonella* Agona isolate resistant to carbapenems was recovered from a poultry sample as part of the National Control Programme (NCP) for *Salmonella*. Whole genome sequencing showed that the isolate possessed the carbapenem resistance gene *bla*$_{\text{IMP-1}}$*.* This was the first detection of a carbapenem-resistant *Salmonella* from UK livestock. Carbapenems are highest priority critically important antibiotics (HPCIAs) and are considered “last resort” antibiotics used to treat multi-drug resistant infections in people; the use of carbapenems is prohibited in food-producing animals. APHA undertook detailed epidemiological investigations and worked with the farm to implement on-farm *Salmonella* control measures, including enhanced monitoring, cleaning and disinfection and biosecurity protocols. APHA also carried out extensive on-farm sampling and no further *Salmonella* Agona, or resistance to carbapenems in other Enterobacterales, were detected. APHA is undertaking further genetic characterisation of the isolate. The source of the carbapenem-resistant *S.* Agona was not definitively determined. The incident is considered to reflect an incursion of a carbapenem-resistant / MDR *S.* Agona into UK livestock, rather than the emergence of this resistance in UK livestock. Ongoing surveillance and horizon scanning for AMR continue at the APHA, in close collaboration with the FSA, VMD, and UKHSA.

In 2024, 179 *S.* Agona isolates were tested against a panel of 16 antimicrobials and 88.3% were tested as fully susceptible. Out of the 21 antibiotic-resistant isolates identified, 15 were resistant to only one compound, while 2 were classified as multi-drug resistant (MDR), meaning they were resistant to 4 or more antibiotics. In addition to the MDR isolate discussed above, a second MDR *S.* Agona isolate was identified from a feed sample, which did not exhibit resistance to HPCIAs.

Focusing specifically on the *S.* Agona isolates obtained from chickens in 2024, 87.3% were fully susceptible. Besides the one MDR isolate previously discussed, the remaining 13 antibiotic-resistant isolates from chickens did not show any resistance to HPCIA and were primarily resistant to just one antibiotic.

Table 13.2: *Salmonella* Dublin in cattle: antimicrobial susceptibility monitoring 2014 to 2024

The table below shows the percentage of *S.* Dublin isolates from cattle resistant to each of the antimicrobials from 2014 to 2024. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
AM	0.7%	1.7%	0.4%	0.0%	0.0%	0.0%	1.2%	1.1%	0.0%	0.4%	0.0%
C	0.0%	0.4%	0.4%	0.0%	0.3%	0.4%	2.3%	1.1%	0.4%	0.0%	0.5%
NA	0.0%	2.2%	1.2%	0.0%	2.2%	0.0%	1.6%	0.7%	0.0%	0.4%	0.0%
S	2.4%	0.4%	1.6%	0.0%	0.3%	0.4%	0.8%	0.7%	3.2%	1.9%	4.9%
APR	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%	0.0%
CN	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
N	0.3%	2.2%	0.0%	0.0%	0.3%	0.0%	5.1%	2.6%	0.0%	0.0%	2.5%
FR	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%	2.5%
SU	0.7%	0.0%	0.0%	0.0%	0.3%	0.4%	0.8%	0.4%	0.8%	0.0%	0.0%
TM	0.7%	0.0%	0.0%	0.0%	0.0%	0.7%	0.8%	0.4%	0.4%	0.0%	0.0%
T	1.1%	0.4%	0.4%	0.0%	0.3%	0.4%	3.9%	6.0%	0.0%	0.0%	0.0%
Susceptible to all 16 antimicrobials	96.5%	94.2%	96.3%	100.0%	96.2%	99.6%	88.9%	88.3%	96.4%	96.3%	90.2%
Total isolates tested	**286**	**226**	**245**	**272**	**320**	**269**	**256**	**267**	**250**	**270**	**203**

Table 13.3: Number of isolates of *S*. Typhimurium of the most frequent phage types subjected to susceptibility testing at APHA 2014 to 2024

Phage type	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
UNTY	0	0	0	0	43	19	0	3	0	2	3
RDNC	0	0	0	0	201	24	53	88	70	52	41
U310	18	0	0	0	0	0	0	0	0	1	0
U308	7	0	0	0	0	0	5	51	0	10	9
U308a	0	0	0	0	0	0	0	0	25	67	12
U302	13	27	13	9	39	18	0	6	0	0	0
U288	28	24	30	26	40	27	58	48	0	6	0
DT193	21	19	13	19	34	38	65	69	60	65	109
DT120	0	0	0	0	0	0	0	2	0	8	1
DT116	0	0	0	0	0	0	22	16	0	7	8
DT104	19	12	40	59	47	45	52	60	58	27	18
DT99	0	0	0	7	0	0	0	1	22	31	7
DT73	0	0	0	0	0	14	0	0	0	0	0
DT41	0	0	0	4	0	0	0	1	0	0	0
DT40	13	7	0	5	0	0	0	0	0	0	0
DT12	0	0	5	2	28	0	0	0	0	0	0
DT9	17	0	0	0	0	0	5	3	0	3	3
DT8	0	7	5	2	0	0	0	7	0	1	3
DT4	0	0	0	0	0	0	5	0	0	4	4
DT2	17	25	24	19	13	13	39	42	41	60	63
DT1	9	9	8	4	0	0	0	15	0	18	9
DT105	0	0	0	0	0	0	0	0	51	76	48
DT75	0	0	0	0	0	0	0	0	42	70	104

Phage type	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
DT32	0	0	0	0	0	0	0	0	19	26	71
Total	162	130	138	156	445	198	304	412	388	534	513

Table 13.4: *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2014 to 2024

The table below shows the percentage of *S.* Typhimurium isolates that were resistant to each of the antimicrobials over the last 11 years. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
AM	43.3%	46.7%	60.2%	58.3%	30.1%	46.1%	50.0%	43.0%	39.7%	36.6%	38.7%
C	36.6%	46.0%	57.8%	53.5%	29.9%	44.1%	45.2%	37.0%	32.4%	31.2%	35.7%
NA	0.9%	1.2%	0.0%	1.6%	0.4%	0.0%	3.0%	8.8%	4.4%	2.9%	2.1%
S	39.7%	51.5%	63.9%	57.1%	40.7%	40.2%	49.7%	34.3%	37.2%	31.4%	30.4%
APR	0.9%	0.0%	2.4%	0.0%	1.8%	0.8%	0.9%	1.5%	4.4%	6.8%	11.1%
N	0.0%	2.4%	0.6%	0.0%	1.8%	0.8%	7.8%	9.9%	7.3%	12.5%	17.4%
FR	0.0%	0.0%	0.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
SU	43.8%	48.5%	66.3%	62.6%	44.0%	46.1%	58.4%	47.1%	43.9%	40.3%	42.7%
TM	35.7%	32.1%	28.9%	19.8%	15.7%	24.0%	33.7%	25.3%	22.9%	30.5%	36.4%
T	49.1%	46.7%	61.4%	54.5%	36.3%	42.1%	50.6%	39.0%	36.4%	30.3%	29.2%
Susceptible to all 16 antimicrobials	44.2%	41.8%	30.1%	34.2%	54.4%	49.2%	39.9%	44.3%	47.8%	55.0%	54.3%
Total isolates tested	**224**	**165**	**166**	**187**	**504**	**254**	**340**	**467**	**494**	**558**	**569**

The number of total isolates tested that were DT104 and its variants was:

- 33 (14.7%) in 2014
- 39 (23.6%) in 2015 (no DT104b)
- 52 (31.3%) in 2016 (no DT104b)
- 67 (35.8%) in 2017 (no DT104b)
- 47 (17.0%) in 2018 (no DT104b)
- 67 (26.4%) in 2019
- 54 (16.1%) in 2020 (no DT104b)
- 66 (14.1%) in 2021 (no DT104b)
- 58 (11.7%) in 2022 (no DT104b)
- 28 (5.0%) in 2023 (including 1 fully susceptible DT104b)
- 18 (3.2%) in 2024 of these strains were DT104 and its variants (no DT104b)

Table 13.5: Nalidixic acid resistance in *Salmonella* Typhimurium DT104 from domestic livestock in 2013 to 2024

The following table outlines the number of isolates tested in different species of livestock between 2013 and 2024 and the percentages of these that were resistant to nalidixic acid.

Year	Cattle (%)	Sheep (%)	Pigs (%)	Chickens (%)	Turkeys (%)	Ducks (%)
2013	9 (33.3)	0 (0.0)	1 (0.0)	8 (0.0)	0 (0.0)	0 (0.0)
2014	10 (0.0)	0 (0.0)	1 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2015	5 (0.0)	0 (0.0)	1 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2016	11 (0.0)	7 (0.0)	2 (0.0)	5 (0.0)	0 (0.0)	0 (0.0)
2017	34 (5.9)	16 (0.0)	1 (0.0)	1 (0.0)	0 (0.0)	0 (0.0)
2018	20 (0.0)	12 (0.0)	1 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2019	21 (0.0)	1 (0.0)	1 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2020	24 (0.0)	4 (0.0)	5 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2021	9 (0.0)	3 (0.0)	0 (0.0)	4 (0.0)	0 (0.0)	0 (0.0)
2022	8 (0.0)	1 (0.0)	1 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
2023	7 (42.9)	0 (0.0)	5 (20.0)	4 (100.0)	0 (0.0)	0 (0.0)
2024	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)

Table 13.6: Sulphamethoxazole and trimethoprim combination resistance in *Salmonella* Typhimurium (all phage types) from domestic livestock in 2013 to 2024

The following table outlines the number of *S.* Typhimurium isolates tested in different species of livestock between 2013 and 2024 and the percentages of these that were resistant to sulphamethoxazole and trimethoprim combination.

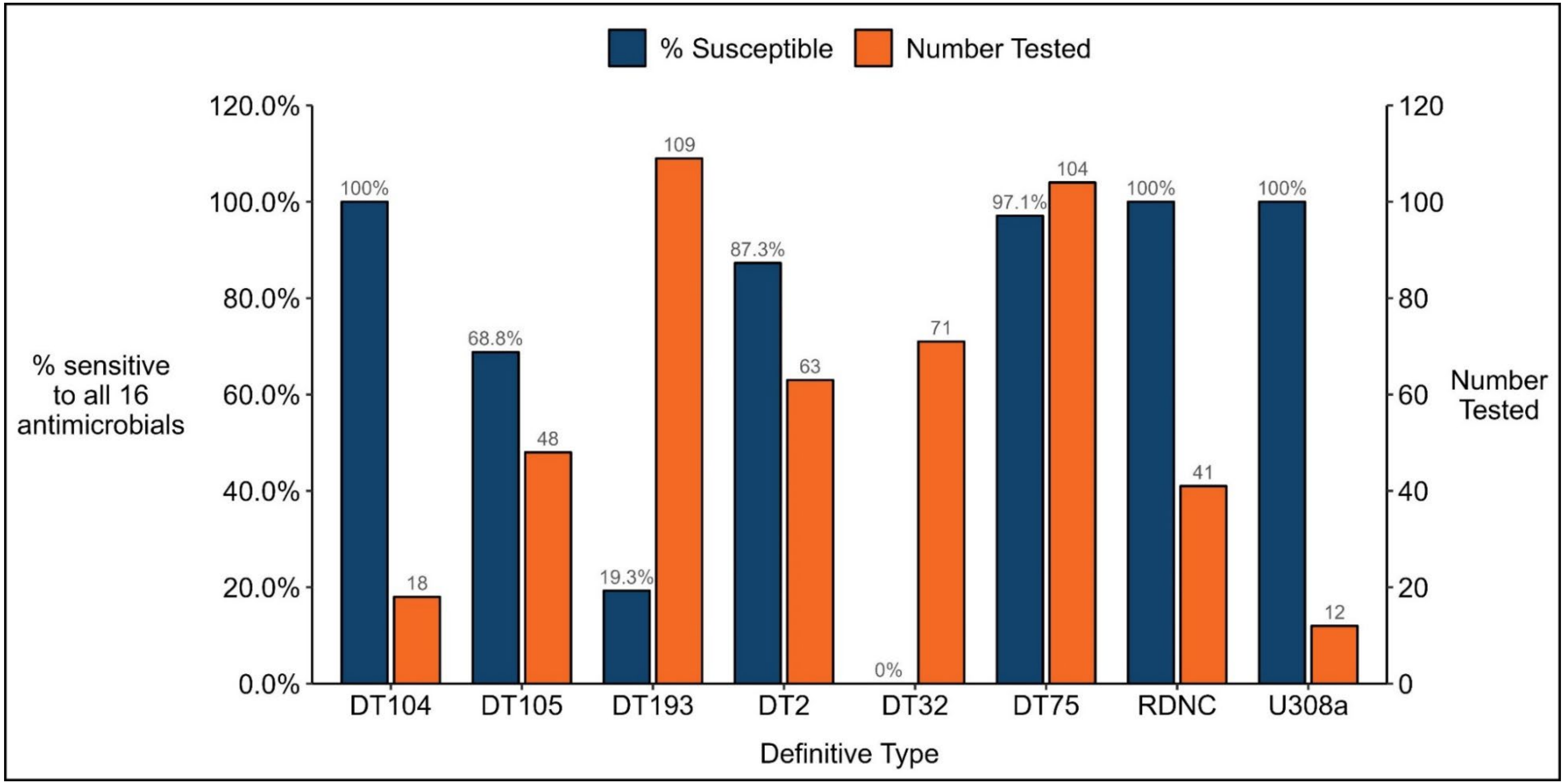
Year	Cattle (%)	Sheep (%)	Pigs (%)	Chickens (%)	Turkeys (%)	Ducks (%)
2013	24 (12.5)	0 (0.0)	71 (93.0)	12 (8.3)	0 (0.0)	3 (0.0)
2014	26 (11.5)	0 (0.0)	102 (66.7)	1 (0.0)	1 (0.0)	6 (0.0)
2015	9 (0.0)	0 (0.0)	52 (92.3)	6 (0.0)	0 (0.0)	2 (0.0)
2016	23 (8.7)	12 (0.0)	47 (87.2)	8 (0.0)	0 (0.0)	1 (0.0)
2017	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 (1.67)	8 (0.0)	214 (95.33)	18 (0.0)	13 (0.0)	0 (0.0)

Table 13.7: Trends in sulphamethoxazole and trimethoprim combination resistance in certain types of *Salmonella* Typhimurium from pigs over the period 2013 to 2024

The following table outlines the number *S.* Typhimurium DT193, DT208 and U288 isolates tested in different species of livestock between 2013 and 2024 and the percentages of these that were resistant to sulphamethoxazole and trimethoprim combination.

Year	Definitive phage type DT193 (%)	Definitive phage type DT208 (%)	Undefined phage type U288 (%)
2013	22 (91.0)	0 (0.0)	21 (100.0)
2014	13 (100.0)	0 (0.0)	28 (96.4)
2015	9 (100.0)	0 (0.0)	23 (95.7)
2016	7 (100.0)	0 (0.0)	29 (96.6)
2017	19 (47.4)	0 (0.0)	26 (88.5)
2018	34 (67.6)	0 (0.0)	40 (97.5)
2019	17 (100.0)	0 (0.0)	27 (100.0)
2020	65 (46.1)	2 (50.0)	58 (84.5)
2021	28 (89.3)	0 (0.0)	46 (89.1)
2022	28 (82.1)	0 (0.0)	5 (100.0)
2023	39 (84.6)	0 (0.0)	5 (100.0)
2024	89 (95.5)	0 (0.0)	0 (0.0)

Figure 13.1: Percentage of the 8 most common definitive and undefined phage types of *Salmonella* Typhimurium susceptible to all 16 antimicrobial agents in 2024



A vertical bar graph showing the percentage of the top 8 phage types of *Salmonella* Typhimurium susceptible to all 16 antimicrobials in 2024. The figure shows that the highest rates of isolates sensitive to all 16 antimicrobials were in found in DT104 (100.0%), U308a (100.0%) and RDNC (100.0%). 0.0% of DT32 isolates were fully susceptible.

Table 13.8: *Salmonella* other than *Salmonella* Dublin and *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2013 to 2024

The following table outlines the number *Salmonella* isolates other than *S.* Dublin and *S.* Typhimurium tested between 2013 and 2024 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	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
AM	12.3	12.7	13.3	11.1	10.3	7.7	7.4	10.3	11.2	9.8	7.3	7.5
C	1.7	1.8	2.4	2.6	2.0	1.5	2.1	2.4	2.6	1.9	2.4	2.3
NA	5.7	4.0	5.5	2.6	5.8	1.4	2.7	3.3	5.5	3.9	3.4	3.8
S	19.2	18.8	22.6	16.0	13.1	11.7	15.0	11.4	13.4	10.2	9.8	10.1
APR	1.4	1.6	2.9	2.0	1.6	0.8	1.3	1.2	2.4	1.2	1.2	1.1
N	3.4	2.0	3.2	2.2	2.0	1.8	2.6	3.0	5.2	2.3	2.1	3.5
FR	3.1	2.1	1.9	1.4	1.6	1.2	1.6	1.0	2.0	0.8	1.0	1.5
SU	26.5	20.9	26.4	23.7	19.0	15.7	20.2	19.8	16.2	13.3	17.8	16.5
TM	12.2	7.5	10.4	10.4	6.2	5.3	10.2	11.7	6.4	6.7	10.9	8.7
T	28.0	20.0	25.5	22.9	19.6	14.9	20.2	19.3	18.5	11.8	14.6	12.8
Percentage susceptible to all 16 antimicrobials	61.2	68.2	60.2	68.9	71.2	77.7	71.9	69.5	68.5	77.2	73.9	74.9
No of isolates	2328	1837	2198	1986	5652	3589	4010	3617	3665	4735	4638	3890

Table 13.9: All *Salmonella*: antimicrobial susceptibility 2024 and resistances to individual antimicrobials

The tables below show the percentage of isolates resistant to each antimicrobial in 2024 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	0.6 %	0.0 %	77.2 %	3.2 %	19.8 %	1.0 %	14.4 %	10.9 %
AMC	0.0 %	0.0 %	0.0 %	0.1 %	0.0 %	0.0 %	0.0 %	0.1 %
CAZ	0.0 %	0.0 %	0.0 %	0.1 %	0.0 %	0.0 %	0.0 %	0.1 %
CTX	0.0 %	0.0 %	0.0 %	0.1 %	0.0 %	0.0 %	0.0 %	0.1 %
C	0.6 %	0.0 %	58.4 %	1.1 %	0.0 %	1.0 %	9.7 %	6.2 %
NA	0.3 %	0.0 %	0.5 %	1.7 %	4.4 %	0.0 %	1.2 %	3.4 %
CIP	0.0 %	0.0 %	0.0 %	0.5 %	0.0 %	0.0 %	0.3 %	0.7 %
S	6.1 %	2.3 %	56.9 %	5.6 %	19.8 %	0.0 %	13.5 %	12.2 %
APR	0.0 %	0.0 %	25.7 %	0.0 %	0.0 %	0.5 %	4.0 %	2.2 %
CN	0.0 %	0.0 %	29.0 %	0.3 %	0.0 %	0.0 %	4.6 %	2.6 %
N	1.7 %	1.1 %	34.4 %	3.5 %	0.0 %	0.5 %	7.6 %	5.1 %
FR	1.5 %	0.0 %	0.0 %	0.4 %	0.0 %	0.0 %	0.4 %	1.3 %
SU	2.6 %	0.0 %	76.7 %	15.5 %	23.1 %	0.0 %	21.8 %	18.8 %
TM	0.9 %	0.0 %	62.4 %	11.7 %	6.6 %	0.0 %	16.6 %	11.6 %
T	3.2 %	1.1 %	59.7 %	6.8 %	19.8 %	0.0 %	14.2 %	14.1 %

Antimicrobial	Cattle	Sheep	Pigs	Chickens	Turkeys	Ducks	Total livestock	TOTAL (livestock and non-livestock)
Percentage susceptible to all 16 antimicrobials	89.6%	95.5%	17.3%	78.6%	53.8%	96.9%	71.7%	73.3%
No of isolates	346	88	404	1523	91	194	2646	4705

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	3.4 %	5.7 %	3.9 %	0.0 %	8.2 %	3.9 %	6.4 %	10.9 %
AMC	0.0 %	0.2 %	0.0 %	0.0 %	0.3 %	0.0 %	0.2 %	0.1 %
CAZ	0.0 %	0.6 %	0.0 %	0.0 %	0.1 %	0.0 %	0.2 %	0.1 %
CTX	0.0 %	0.6 %	0.0 %	0.0 %	0.1 %	0.0 %	0.2 %	0.1 %
C	0.0 %	2.2 %	3.1 %	0.0 %	1.3 %	2.7 %	1.8 %	6.2 %
NA	8.5 %	4.7 %	1.6 %	0.0 %	9.1 %	2.1 %	6.2 %	3.4 %
CIP	0.0 %	2.6 %	0.8 %	0.0 %	1.3 %	0.3 %	1.4 %	0.7 %
S	10.2 %	8.4 %	20.9 %	16.2 %	12.5 %	3.6 %	10.6 %	12.2 %
APR	0.0 %	0.0 %	0.0 %	0.0 %	0.0 %	0.0 %	0.0 %	2.2 %
CN	0.0 %	0.4 %	0.0 %	0.0 %	0.1 %	0.0 %	0.2 %	2.6 %
N	1.7 %	1.4 %	0.0 %	2.7 %	2.2 %	2.7 %	1.9 %	5.1 %
FR	0.0 %	1.6 %	2.3 %	0.0 %	3.6 %	1.5 %	2.5 %	1.3 %
SU	5.1 %	7.3 %	3.9 %	0.0 %	24.4 %	5.7 %	14.9 %	18.8 %
TM	1.7 %	2.0 %	1.6 %	0.0 %	8.6 %	3.0 %	5.3 %	11.6 %
T	10.2 %	7.5 %	6.2 %	0.0 %	22.3 %	4.5 %	14.0 %	14.1 %

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	78.0%	83.5%	74.4%	83.8%	65.9%	89.7%	75.3%	73.3%
No of isolates	59	509	129	37	994	331	2059	4705

Other non-avian species included Alpaca, badger, cat, cheetah, deer, fox, goat, hedgehog, leopard, lion, lizard, mouse, other mammal, porpoise, primate, reptile/amphibian, seal, snake, turtle, wildcat and wolf. Other avian species included budgerigar, goose, gull, other birds, parrot, pigeon, rhea and toucan

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 multilocus 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

Salmonella serovar	Sequence Type (ST)	2024 isolations
4,5,12:-:-	34	2
4,5,12:a:-	1063	1
6,7:z10:-	413	2
Anatum	64	1
Coeln	1995	2
Dublin	10	214
Dublin	No ST data	1
Enteritidis	11	1
Indiana	17	3
London	No ST data	1
Mbandaka	413	44
Mbandaka	5078	1
Monophasic Typhimurium	34	3
Montevideo	138	24
Newport	45	2
Newport	166	1
Orion	639	1
Typhimurium	19	62
Total	not applicable	**366**

Table A2: Sequence types of *Salmonella* isolations in sheep in 2024

Salmonella serovar	Sequence Type	2024 isolations
Agama	2223	1
Dublin	10	12
Dublin	8819	2
Montevideo	195	14
Typhimurium	19	6
Monophasic Typhimurium	34	1
61:k:1,5,(7)	432	65
Total	not applicable	**101**

Table A3: Sequence types of *Salmonella* isolations in goats in 2024

Salmonella serovar	Sequence Type	2024 isolations
Dublin	10	1
61:k:1,5,(7)	432	1
Total	not applicable	**2**

Table A4: Sequence types of *Salmonella* isolations in pigs in 2024

Salmonella serovar	Sequence Type	2024 isolations
Bovismorbificans	142	7
Bovismorbificans	377	1
Derby	39	1
Derby	40	7
Derby	682	25
Dublin	10	1
Hessarek	5723	1
Kedougou	1543	5
London	2124	1
Monophasic Typhimurium	19	1
Monophasic Typhimurium	34	69
Newport	166	20
Panama	48	7
Reading	1628	2
Reading	No ST data	5
Rissen	469	1
Typhimurium	19	156
4,5,12:-:-	34	1
Total	not applicable	**311**

Table A5: Sequence types of *Salmonella* isolations in horses in 2024

Salmonella serovar	Sequence Type	2024 isolations
Agama	2223	1
Agama	885	1
Anatum	64	1
Blockley	52	1
Bonn	2636	1
Bovismorbificans	377	1
Concord	3937	1
Eastbourne	93	1
Enteritidis	11	1
Enteritidis	183	1
Enteritidis	5492	1
Enteritidis	6086	1
Enteritidis	8943	2
Enteritidis	10467	2
Fulica	1063	2
Kingston	2005	1
Monophasic Typhimurium	34	1
Newport	45	4
Newport	614	1
Oslo	1370	3
Stanleyville	97	1
Typhimurium	19	21
Typhimurium	34	1
Typhimurium	568	2
Total	not applicable	**53**

Table A6: Sequence types of *Salmonella* isolations in deer in 2024

Salmonella serovar	Sequence Type	2024 isolations
Monophasic Typhimurium	34	1
Typhimurium	19	1
Total	not applicable	**2**

Table A7: Sequence types of *Salmonella* isolations in rabbits in 2024

There were no *Salmonella* isolations in rabbits in 2024.

Table A8: Sequence types of *Salmonella* isolations in chickens in 2024

Salmonella serovar	Sequence Type	2024 isolations
Agama	885	1
Agona	13	136
Anatum	64	10
Berta	435	1
Braenderup	22	2
Bredeney	897	1
Chester	411	1
Chester	1954	1
Coeln	2015	1
Corvallis	1541	1
Derby	40	1
Derby	71	8
Enteritidis	11	7
Enteritidis	6086	1
Enteritidis	8943	1
Enteritidis	10467	3
Havana	1524	1
Idikan (incl monophasic variants)	1891	679
Indiana	17	7
Infantis	32	20
Kedougou	1543	381
Kedougou	No ST data	1
Kentucky	314	18
Kingston	2005	1
Kottbus	212	4
Livingstone	457	4
Livingstone	638	2
Mbandaka	413	168
Montevideo	138	1
Montevideo	316	307
Monophasic Typhimurium	34	1
Muenchen	82	27
Newport	45	5
Newport	166	7
Newport	614	14
Nottingham	1640	1
Ohio	329	44
Orion var 15+ (Binza)	639	50
Oslo	1370	2
Panama	48	1

Salmonella serovar	Sequence Type	2024 isolations
Poona	812	1
Senftenberg	14	9
Senftenberg	185	1
Typhimurium	19	17
4,12:d:-	279	2
6,7:-:enz15	413	1
61:k:1,5,(7)	432	8
Total	not applicable	**1,961**

Table A9: Sequence types of Salmonella isolations in turkeys in 2024

Salmonella serovar	Sequence Type	2024 isolations
Ago	2565	1
Agona	13	20
Anatum	64	21
Derby	71	3
Indiana	17	9
Javiana	24	2
Kedougou	1543	21
Livingstone	457	2
Orion var 15+ (Binza)	639	5
Oslo	1370	2
Senftenberg	14	4
Typhimurium	19	13
Idikan (incl monophasic variants)	1891	5
Total	not applicable	**108**

Table A10: Sequence types of *Salmonella* isolations in ducks in 2024

Salmonella serovar	Sequence Type	2024 isolations
Give	524	5
Give var 15+ (Newbrunswick)	524	3
Hadar	33	2
Indiana	17	146
Indiana	no result	1
Kedougou	1543	2
Kingston	2005	1
Kottbus	582	12
Lexington	247	1
Newport	614	20
Orion	639	2
Orion var 15+ (Binza)	639	1
Total	not applicable	**196**

Table A11: Sequence types of *Salmonella* isolations in geese in 2024

Salmonella serovar	Sequence Type	2024 isolations
Typhimurium	19	1
Total	not applicable	**1**

Table A12: Sequence types of *Salmonella* isolations in pigeons in 2024

Salmonella serovar	Sequence Type	2024 isolations
Braenderup	22	1
Typhimurium	19	3
Typhimurium	128	15
Typhimurium	8937	3
Total	not applicable	**22**

Table A13: Sequence types of *Salmonella* isolations in dogs in 2024

Salmonella serovar	Sequence Type	2024 isolations
Abony	1583	1
Adelaide	4024	3
Agama	885	6
Agama	2223	2
Agama	2267	1
Agona	13	15
Ajiobo	2017	1
Anatum	64	27
Ank	8073	1
Berta	435	3

Salmonella serovar	Sequence Type	2024 isolations
Bovismorbificans	142	5
Bovismorbificans	377	1
Brancaster	9048	2
Brandenburg	65	2
Bredeney	897	1
Cerro	367	1
Cerro	1593	4
Chailey	582	1
Coeln	1995	1
Coeln	2015	2
Concord	3937	2
Derby	39	1
Derby	40	3
Derby	71	7
Derby	682	8
Dublin	10	16
Dublin	8819	1
Enteritidis	11	4
Enteritidis	183	7
Enteritidis	6086	1
Enteritidis	8943	1
Enteritidis	10467	4
Fresno	649	1
Fulica	1063	2
Give	516	1
Give	524	3
Goldcoast	358	1
Hadar	33	2
Havana	588	1
Hessarek	5723	1
Indiana	17	21
Infantis	32	39
Javiana	24	2
Kedougou	1543	2
Kentucky	198	2
Kentucky	314	15
Kingston	2005	1
Kottbus	212	9
Kottbus	582	4
Leeuwarden	No ST data	1
Liverpool	1959	1
Livingstone	543	1

Salmonella serovar	Sequence Type	2024 isolations
Livingstone	1941	11
London	155	4
London	No ST data	4
Mbandaka	413	5
Mbandaka	5078	1
Mbandaka	No ST data	1
Meleagridis	463	1
Monophasic Typhimurium	34	19
Montevideo	195	4
Montevideo	316	6
Muenchen	82	3
Muenster	321	8
Newport	45	11
Newport	118	1
Newport	164	1
Newport	166	11
Newport	614	6
Ohio	329	1
Oslo	1370	7
Panama	48	1
Poona	812	1
Reading	93	1
Reading	1628	1
Rissen	11431	1
Schwarzengrund	96	1
Senftenberg	14	3
Senftenberg	210	1
Singapore	5213	1
Stanleyville	97	12
Stourbridge	736	1
Tennessee	2538	1
Tennessee	3288	1
Thompson	26	10
Typhimurium	19	60
Typhimurium	36	2
Typhimurium	313	13
Typhimurium	568	2
Uganda	684	1
21:g,f,t:-	6970	5
4,12:b:-	53	1
4,12:b:-	679	1

Salmonella serovar	Sequence Type	2024 isolations
4,12:d:-	279	1
4,12:z:-	No ST data	1
4,5,12:b:-	679	2
4,[5],12,[27]:b:e,n,x	53	1
48:z4,z23:-	2811	1
6,8:-:-	8767	2
61:k:1,5,7	432	1
9,12:l,v:-	20	1
untypeable	N/A	1
Total	not applicable	**482**

Table A14: Sequence types of *Salmonella* isolations in wildlife in 2024

Salmonella serovar	Sequence Type	2024 isolations
4,12:a:-	416	1
4,5,12:b:-	679	1
Eboko	5470	1
Enteritidis	183	6
Typhimurium	19	4
Typhimurium	313	1
Total	not applicable	**14**

Table A15: Sequence types of *Salmonella* isolations in feeds in 2024

Salmonella serovar	Sequence Type	2024 isolations
Agama	885	9
Agona	13	29
Amager	293	1
Amsterdam	2090	1
Anatum	64	12
Bovismorbificans	142	2
Brandenburg	65	1
Bredeney	306	1
Cerro	1593	2
Coeln	1995	2
Corvallis	1541	1
Cubana	286	1
Cubana	7940	1
Derby	39	1
Derby	40	9
Derby	71	8
Derby	682	8

***Salmonella* serovar**	**Sequence Type**	**2024 isolations**
Derby	No ST data	1
Dublin	10	12
Ealing	2013	4
Enteritidis	11	8
Enteritidis	6086	5
Enteritidis	10467	15
Falkensee	3093	2
Give	524	3
Goldcoast	358	1
Havana	1526	7
Idikan (incl monophasic variants)	1891	10
Indiana	17	37
Infantis	32	84
Isangi	216	12
Isangi	1994	1
Kaapstad	4605	1
Kassel	6849	1
Kedougou	1543	103
Kentucky	314	7
Kingston	2005	1
Kottbus	212	2
Kottbus	582	12
Lexington	247	1
Liverpool	1959	1
Livingstone	457	1
Livingstone	543	1
Livingstone	1941	1
London	155	1
London	2124	1
London	No ST data	1
Mbandaka	413	26
Mbandaka	5078	3
Mbandaka	9414	1
Molade	544	4
Monophasic Typhimurium	34	20
Montevideo	138	6
Montevideo	195	3
Montevideo	316	9
Montevideo	12723	1

Salmonella serovar	Sequence Type	2024 isolations
Muenchen	112	1
Muenster	321	3
Newport	45	4
Newport	164	1
Newport	166	7
Newport	614	2
Nottingham	1640	3
Ohio	329	114
Oslo	1370	1
Panama	48	2
Poona	308	2
Reading	1628	1
Richmond	909	1
Riggil	No ST data	1
Rissen	469	27
Rissen	11431	2
Saintpaul	49	1
Saintpaul	2059	1
Saintpaul	No ST data	1
Schwarzengrund	96	1
Senftenberg	14	3
Senftenberg	185	7
Senftenberg	210	9
Stanley	29	1
Stanleyville	97	1
Stanleyville	1986	1
Szentes	427	1
Telaviv	1068	1
Tennessee	319	1
Tennessee	5018	1
Thompson	26	2
Typhimurium	19	53
Typhimurium	34	1
Typhimurium	513	1
Typhimurium	8937	2
Uganda	684	8
Umbilo	2014	1
Virchow	303	1
Yoruba	1316	2

Salmonella serovar	Sequence Type	2024 isolations
Zehlendorf	No ST data	1
3,10:-:-	No ST data	1
48:z4,z23:-	2811	2
61:i:z53	4303	3
61:k:1,5,(7)	432	16
Total	Not applicable	**795**

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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 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
Apramicin	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.

Some of the *Salmonella* serovars are recorded and reported in APHA under the old nomenclature. The nomenclature for these serovars under the original Kauffmann-White scheme is clarified in the table below.

APHA serovar	White-Kauffmann-Le Minor serovar
Pullorum	Gallinarum (biovar Pullorum)
Java	Paratyphi B var. Java
Newington	Anatum var. 15^+

The *Salmonella* serovars *S*. Binza and *S*. Thomasville, which were previously recorded by the APHA under their old nomenclature, are now recorded using the White-Kauffmann-Le Minor notation as *Salmonella* Orion var. 15^+ and *Salmonella* Orion var. 15^+ 34^+ respectively. This change was implemented during 2008.

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 distance to laboratories.

TA 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/phage type 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 DT104.

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 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

Date created

31 March 2025 data retrieval from FarmFile/*Salmonella* database

Identifier

Salmonella Annual Surveillance Report 2024, Version 1

Quality

See Section A

Publisher

Salmonella Surveillance team, DES, APHA Weybridge, New Haw, Addlestone, Surrey, KT15 3NB

Source

FarmFile/*Salmonella* database.

Title

Salmonella surveillance in animals and feed in Great Britain 2024

Additional report metadata elements and definitions

Coverage spatial

Salmonella reports made in Great Britain

Date. Issued

19 September 2025

Date. Updating frequency

Annually

Format medium

Word document

Language

English

Mandate authorising statutes

Data collected under:

- Zoonoses Order 1989
- CSPO 2007
- CSBO 2009
- CSTO 2009
- ABPR 2013
- IPAPO 1981

Rights. copyright

Crown copyright

Subject. Category

Zoonoses, Animal Health

Subject. Keywords

Salmonella, Livestock

Subject. programme

Bacterial Diseases and Food Safety

Subject. project

Surveillance of *Salmonella* in animals (FZ2000)

Monitoring of Antimicrobial Resistance in Bacteria from Animals and their Environment (OM0190)

Microbiological monitoring of Animal By Products, laboratory inspection scheme and Quality Assurance sample supply (ABPR and IPAPO) (FZ2000)

Status

Approved by:

Francesca Martelli

(Francesca.Martelli@apha.gov.uk)

Version 1

Type

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

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