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Agency

Salmonella in animals and feed in Great Britain

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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 strains 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 livestock species in Great Britain (England, Wales and Scotland) collected and collated by the Animal and Plant Health Agency (APHA) during 2023 and also provides data from previous years for comparative purposes.

The data in the first 12 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 feedingstuffs. The 13th chapter covers the antimicrobial susceptibility of *Salmonella* (England and Wales only).

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 feedingstuffs, 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. The UK domestic legislation, including assimilated EU law can be found at the following link https://www.legislation.gov.uk. 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.

In practice, reports of *Salmonella* isolations must be made to a Veterinary Investigation Officer at one of the Veterinary Investigation Centres (previously Regional Laboratories) of the APHA or to a Regional Veterinary Lead in Scotland. A culture of the organism must be provided to the relevant veterinary *Salmonella* reference laboratory in England, Wales and Scotland.

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 European Council Directive 2003/99/EC currently provides the statutory basis for monitoring of zoonoses and zoonotic agents in the EU. Member States are required to monitor certain zoonoses and to report to the Commission each year the trends and sources of those zoonotic infections. This Directive covers animals, feed, food and the relevance to human infection, as well as trends in antimicrobial resistance in *Salmonella*, *Campylobacter* and other indicator organisms.

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, the Control of *Salmonella* in Broiler Flocks Order 2009 came into force in England and Wales, and 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 implemented the requirement for a *Salmonella* National Control Programme in the broiler chicken sector.

In January 2010, the 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. 1190/2012 and implements the requirement for a *Salmonella* National Control Programme 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 an 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 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, whilst 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 feedingstuffs 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) replaced phenotypic serotyping as the primary method of characterisation of *Salmonella* isolates from submissions to APHA. In 2023 only poultry submissions subject to NCPs (chicken and turkeys) were routinely characterised by conventional serotyping methods in parallel to WGS.

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. Sequenced isolates were analysed using the APHA in-house in-silico *Salmonella* typing pipeline to confirm the serovar (APHA NextflowSerotypingPipeline v7.4; available at https://github.com/APHA-BAC/NextflowSerotypingPipeline).

This will have negligible impact on the presentation of results in this report other than the differentiation of monophasic *S.* Typhimurium variants. Whole genome sequencing has not yet been validated to differentiate between 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 described as monophasic *S.* Typhimurium.

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 cultures 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 culture (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).

Serotyping and phage typing of samples received from premises in England and Wales is carried out by the 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.

A new procedure for simplified presumptive identification of *Salmonella* Derby from certain known persistently infected turkey fattening farm sources was introduced in 2016 to reduce the cost of serotyping large numbers of such isolates. In this process, slide agglutination testing of such Group B isolates was used to identify *S.* Derby [4,5,12:f,g:((1,2)], and to exclude the possibility of *S.* Typhimurium [4,5,12:i:1,2] or *S*. Agona [4,5,12:f,g,s:1,2]. After confirmation, the isolates were reported as ‘presumptive *S*. Derby’ as full serotyping had not been carried out. Any non-Group B isolates, isolates which react with Hi or Hs antiserum or isolates for which definitive *S*. Derby related antigens could not be confirmed were subjected to full serotyping. The use of this procedure was discontinued for 2019 due to a fall in the number of *S*. Derby isolates received for serotyping.

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.

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*.

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.

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* whilst 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 formally 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 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).

Figures 1.1.2 to 1.1.7 show the most common *Salmonella* serovars isolated from the relevant livestock species in Great Britain in 2023 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. However, *S*. Infantis which was the third most frequently reported serovar in humans in 2023 was the second most commonly reported from dogs in 2023.

In 2023, a total of 10,070 isolations of *Salmonella* from humans were reported to UK Health Security Agency (UKHSA), Public Health Wales and Public Health Scotland. 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 and 2023 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 2023 (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 2023, the total number of *Salmonella* isolation reports from cattle, sheep, pigs and poultry increased by 4.9% compared with 2022 (3,630 isolations versus 3,461 isolations) and increased by 29.2% compared with 2021 (2,809 isolations) (Table 1.1). Trends were also variable across serovars, for example, reports of *Salmonella* 13,23:i:- and *S*. Kedougou were almost double that of 2022, reports of *S.* Agona increased by 50.0% and reports of *S*. Typhimurium increased by 31.8% compared to 2022. However, reports of *S*. Senftenberg were 60.3% less in 2023 compared to 2022 and reports of *S*. Enteritidis were 56.0% fewer in 2023 compared to 2022. Reports of *S*. Mbandaka fell by 53.4% in 2023 in comparison to 2022 and reports of *S*. Infantis down 34.7%.

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 Animal and Plant Health Agency (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 increased by 3.8% in 2023 compared with 2022. This increase was seen for cattle, pigs and other birds with the greatest increase being in cattle (19.9%). The number of submissions also increased by 53.5% for miscellaneous species. 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 4,462 isolations of *Salmonella* in livestock and dogs in 2023 which represents a decrease of 1.5% compared with 2022 (4,529 isolations). This comprised 4,319 isolations from species covered by the statutory reporting requirements of the Zoonoses Order 1989 (2,633 isolations from chickens, 689 isolations from dogs, 436 isolations from cattle, 258 isolations from pigs, 109 isolations from turkeys, 96 isolations from ducks, 98 isolations from sheep, 55 isolations from horses, 18 isolations from pigeons, 2 isolations each from partridges and pheasants, and one isolation each from a goat and a deer), plus 143 isolations from non-statutory species (for example, cats and reptiles, which are not reported in detail in this publication).

Relative to 2022, in 2023 there were more isolations from chickens (2,633 versus 2,404 isolations), pigs (258 versus 214 isolations), cattle (436 versus 430 isolations) and sheep (98 versus 94 isolations). In contrast, there were fewer isolations from turkeys (109 versus 188 isolations) and ducks (96 versus 121 isolations).

The surveillance data for 2023 shows that 33.2% of the isolations of *Salmonella* reported to APHA resulted from samples taken due to clinical disease in livestock. This is higher than during both 2022, where 20.2% of isolations were from clinical disease investigations, and 2021 where 28.1% 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 (93.9% and 89.0%, respectively) during 2023 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 2023, all of the *Salmonella* isolations from ducks resulted from voluntary surveillance.

Reports of *S*. Enteritidis in 2023 were less than half that in 2022 (11 versus 25 isolations), though were the same compared with 2021 (11 isolations). As in previous years, the majority of *S*. Enteritidis isolations in 2023 were reported from chickens (9 of 11 isolations), but there was also one isolation each from cattle and ducks. This is similar to 2022 when most isolations of *S*. Enteritidis came from chickens (23 of 25), with 2 isolations from sheep (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 rose by 38.9% in 2023 (257 isolations) relative to 2022 (185 isolations). There was an increase in the number of isolations from 2 sectors relative to the previous year. Isolations from cattle increased by over half (82 versus 58) and isolations from sheep increased (12 versus 8 in 2022). Isolations from turkeys increased from 1 in 2022 to 2 in

2023 (Figure 1.5). Isolations of *S*. Typhimurium in chickens increased by 16.7 % in 2023 compared to 2022 (21 versus 18 isolations). Isolations of *S*. Typhimurium in pigs increased by around a third 2023 compared to 2021 (139 versus 100 isolations). There was one isolation of *S.* Typhimurium from ducks in 2023, compared to no isolations in 2022. 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.

Total isolations of monophasic *Salmonella* Typhimurium increased by 5.1% in 2023 compared to 2022 (83 versus 79 isolations, Figure 1.6). There was a marked increase in isolations of monophasic *Salmonella* Typhimurium in cattle in 2023 compared to 2022 (14 versus 3 isolations) but a reduction in Chickens (6 versus 19 isolations).

Highlights

Cattle

Isolations of *Salmonella* from cattle in 2023 were 1.4% higher than during 2022 (436 versus 430 isolations) and 16.3% lower than during 2021 (521 isolations).

As in previous years, *S*. Dublin remained the most common serovar in cattle (252 isolations, 57.8% of total cattle isolations). The number of isolations of *S*. Dublin decreased by 4.9%, compared with 2022 and by 17.6%, compared with 2021.

The relative number of *Salmonella* Typhimurium isolations rose in 2023 and this serovar was the second most commonly isolated serovar from cattle (82 isolations, 18.8% of total cattle isolations) and *S*. Mbandaka was the third most commonly isolated (46 isolations, 10.6% of total cattle isolations). This is a change from 2022, 2021, 2020 and 2019 where *S*. Mbandaka was the second most commonly isolated serovar and *Salmonella* Typhimurium was the third most commonly isolated (Figure 2.2).

There were 82 isolations of *S.* Typhimurium from cattle in 2023, which is an increase of 41.4% compared with 2022. The most common phage types of *S*. Typhimurium reported from cattle during 2023 were DT105 (33 isolations, 40.2% of isolations), DT75 (28 isolations, 34.2% of isolations), DT104 (6 isolations, 7.3% of isolations) and DT193 (5 isolations, 6.1% of isolations each).

There were 14 isolations of Monophasic Typhimurium (3.2% of total cattle isolations) during 2023 compared with 3 isolations during 2022, and 15 isolations during 2021. The majority of isolations in 2023 were phage type DT193 (7 isolations), followed by UNTY (4 isolations) and NOPT, DT1 and DT191 (all one isolation each).

There was one isolation of *S.* Enteritidis (PT5) from cattle during 2023 compared with none in 2022.

Small ruminants

Isolations of *Salmonella* from sheep in 2023 were 4.3% higher than during 2022 (98 versus 94 isolations) and 32.0% fewer than during 2021 (144 isolations) (Table 3.1).

Salmonella enterica subspecies *diarizonae* serovar 61:k:1,5,(7) (and variants) remained the most common serovar isolated from sheep (65 isolations, 66.3% of total sheep isolations).

Salmonella Montevideo was the second most commonly isolated serovars from sheep in 2023, with 13 isolations (13.3% of total isolations). This was similar to 2022 where it was the third most commonly isolated serovar and the same as in 2019 and 2020.

Salmonella Typhimurium was the third most commonly isolated serovar from sheep in 2023 (12 isolations, 12.2% of total isolations), higher than the number of isolations recorded in 2022 (8 isolations, 8.5% of total sheep isolations). The phage types reported during 2023 were DT75 (5 isolations), DT105 (4 isolations) and U288 (one isolation). Two isolates could not be phage typed due to the presence of a natural phage infection (NOPT).

S. Dublin was the next most commonly isolated serovars from sheep in 2023, with 4 isolations (4.1% each of total isolations).

There was one isolation from goats in 2023 (*S. enterica* subspecies *diarizonae* 61:(k):1,5,(7)) compared to 2 isolations from goats in 2022 (both were *S. enterica* subspecies *diarizonae* 61:(k):1,5,(7)) and 2 isolations during 2021 (*S.* Dublin and *S. enterica* subspecies *diarizonae* 61:k:1,5).

Pigs

There were 258 *Salmonella* isolations from pigs in 2023 which was slightly higher compared to 2022 (214 isolations) and 2021 (223 isolations) (Table 4.1).

Salmonella Typhimurium and its monophasic variants (*Salmonella* 4,[5],12:i:-) were together responsible for 77.5% of all isolations from pigs in 2023 (200 isolations). This is similar to previous years. However, for the fourth time since 2014 (and the fourth year in a row), the number of *S*. Typhimurium isolations (139 isolations) exceeded isolations of both monophasic variations combined (61 isolations).

The most common phage type of *S*. Typhimurium isolated from pigs in 2023 was U308a (46 isolations, 33.1% of total *S*. Typhimurium isolations in pigs), followed by DT193 (31 isolations). Most typable isolations of both monophasic variants of *S*. Typhimurium from pigs in 2023 were phage type DT193 (43 isolations) but there were also single isolations of DT120, DT194 and U302.

Deer, horses and rabbits

There was one isolation of *Salmonella* (DT105) from deer during 2022, this compared to no isolations during 2022, 2021 and 2020 (Table 5.1).

There were no isolations of *Salmonella* from rabbits during 2023 compared to 2 isolations during 2022 (one isolation each of *S*. Fluntern and *S*. Newport). Prior to 2022 the last isolation of *Salmonella* from rabbits was in 2016 (*Salmonella* 21:g,t:-) (Table 5.2).

There were 55 isolations of *Salmonella* from horses during 2023, 8.3% lower than during 2022 (60 isolations) and 22.2% higher than during 2021 (45 isolations) (Table 5.3).

Salmonella Typhimurium was the most common serovar isolated from horses in 2023 (20 isolations, 36.4% of total horse isolations). This is similar to the number of isolations in 2022 and 2021 (18 and 15 respectively). The most common phage types of *S*. Typhimurium in 2023 was DT75 (5 isolations each, 25.0% of *S*. Typhimurium isolations each).

Salmonella Newport was the second most commonly reported serovar from horses during 2023 (7 isolations, 12.7% of total horse isolations), which was similar to 2022 (6 isolations) but presents a large increase compared to 2021 (one isolation).

There was one isolation of monophasic *S.* Typhimurium (DT193) in 2023 compared to 2 isolations in 2022 (both DT104), and with no isolations during 2021.

Chickens

Including both NCP and non-statutory surveillance data, there were 2,633 isolations of *Salmonella* from chickens in 2023. This is an increase of 9.5% compared with 2022 (2,404 isolations) and an increase of 57.5% compared with 2021 (1,671 isolations) (Table 6.1).

The most commonly reported serovars were:

- *Salmonella* 13,23:i:- (675 isolations, 25.6% of total chicken isolations)
- *S*. Montevideo (591 isolations, 22.4% of total chicken isolations)
- *S*. Kedougou (537 isolations, 20.4% of total chicken isolations)
- *S*. Mbandaka (305 isolations, 11.6% of total chicken isolations)
- *S*. Agona (200 isolations, 7.6% of total chicken isolations)

There were 9 isolations of *S*. Enteritidis in 2023 compared with 23 isolations during 2022 and 9 isolations during 2021. The most commonly reported phage type in 2023 was PT8 (7 isolations).

There were 21 isolations of *S*. Typhimurium compared with 18 isolations in 2022. The most commonly reported phage types were DT75 (6 isolations) and DT105 (6 isolations). There also were 6 isolations of monophasic strains of *S*. Typhimurium, including 5 isolations of *Salmonella* 4,5,12:i:- (all DT193). This was a third of the number of isolations in 2022 (18 isolations).

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 NCPs was well below the EU targets of 1% for breeders, 2% for layers and 1% for broilers (0.43% for breeders, 0.17% for layers and 0.04% for broilers).

Turkeys

Including both NCP and non-statutory surveillance data, there were 109 isolations of *Salmonella* from turkeys in 2023. This is a decrease of 42.0% compared with 2022 (188 isolations) and a decrease of 22.1% compared within 2021 (140 isolations) (Table 7.1).

During 2023 the most common serovar isolated from turkeys was *S.* Kedougou (43 isolations, 39.4% of total turkey isolations), the second most common serovar was *S.* Anatum (19 isolations, 17.4% of total turkey isolations) and the third most common was *S.* Orion var.15+ (11 isolations, 10.1% of total turkey isolations).

There were 2 isolations of *S*. Typhimurium during 2023 (all DT193), compared within one isolation during 2022 (DT99) and 3 isolations during 2021 (all U203). There was one isolation of monophasic *S.* Typhimurium 2023, compared with 2 isolations during 2022 and 9 isolations during 2021.

Information and data are given in Chapter 7 (Reports of *Salmonella* in turkeys) on the National Control Programmes (NCP) for *Salmonella* in turkeys. The NCP sampling prevalence of regulated serovars was 0.05% for turkey fatteners and 0.58% for turkey breeders. This is well below the EU target of 1% for each of these turkey production sectors.

Ducks and geese

There were 96 isolations of *Salmonella* from ducks in 2023. This is a 20.7% decrease compared with 2022 (121 isolations) and 12.7% decrease compared within 2021 (110 isolations) (Table 8.1).

The most commonly isolated serovars from ducks in 2023 were *S.* Indiana (52 isolations, 54.2% of total duck isolations), *S.* Kottbus (12 isolations, 12.5% of total duck isolations), *S.* Give (9 isolations, 9.4% of total duck isolations each), *S.* Lexington (8 isolations, 8.3% of total duck isolations), *S.* Hadar (6 isolations, 6.3% of total duck isolations each) and *S.* Orion var. 15^+ (5 isolations, 5.2% 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).

There was one isolations of *S*. Typhimurium (DT1) from ducks in 2023. This compared to no isolations during 2022 and 2021 when for the first time *S*. Typhimurium was not recorded from ducks in Great Britain since 2001. There was one isolation of *S*. Enteritidis (PT9) from ducks in 2023 compared with no isolations during 2022 and one isolation during 2021 (PT9b).

There were no isolations of *Salmonella* from geese in 2023, which was the same as in 2022 and 2021.

Other statutory birds (as specified in the Zoonoses Order)

There were 4 isolations of *Salmonella* from game birds in 2023, which is an increase from 2022 (1 isolation) but less than in 2021 (7 isolations). The isolations in 2023 were from pheasants (2 isolations) and partridges (2 isolations). Game birds include guinea fowl, partridges, pheasants and quail.

Compared with 2022 there was an increase in the number of isolations from pheasants (2 versus 1 isolations), and partridges (2 versus no isolations) in 2023 but in both years there were no isolations of *Salmonella* reported from quail or guinea fowl.

There were 18 *Salmonella* isolations from pigeons in 2022, which is similar to 2022 (17 isolations) and over double the number of reports in 2021 (8 isolations) (Table 9.4). All of the isolations were *S*. Typhimurium (13 isolations of DT2, 3 of DT99 and one each of DT105 and DT193).

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 689 isolations of *Salmonella* from dogs in 2023, a decrease of 19.6% compared to 2022 (857 isolations). The majority of these isolations (98.8%) were from reports of clinical disease.

The most common serovars reported were *S*. Typhimurium (90 isolations, 13.1% of total isolations from dogs), *S.* Infantis (79 isolations, 11.5% of isolations from dogs) and monophasic *S.* Typhimurium (42 isolations, 6.1% each of total isolations from dogs). All of these serovars are of public health importance.

The most common phage types of *S*. Typhimurium from dogs during 2023 were RDNC (22 isolations, 24.4% each of isolations), DT75 (16 isolations, 17.8% of isolations), DT193 (10 isolations, 11.1% of isolations) and DT2 (9 isolations, 10.0% of isolations). There were also 42 isolations of monophasic *S*. Typhimurium (78.6% of which were DT193).

There were 26 isolations of *S*. Enteritidis from dogs during 2023. The most common phage type was PT8 (5 isolations, 19.2% of isolations).

Wildlife

There were 9 isolations of *Salmonella* from wildlife during 2023. Of these, 4 isolations were from badgers (one isolation each of *S*. Agama, *S*. Anatum, *S*. Berta and *S*. Newport), 2 isolations of *S.* Enteritidis (PT11) from a hedgehog, one isolation of *Salmonella* Typhimurium (RDNC) from a red squirrel, and one isolation each of *S*. Typhimurium from a buzzard (DT2) and a gull (RDNC). This is higher than in 2022 where there were 2 isolations but lower than 2021 when there were 19 isolations of *Salmonella* from wildlife.

Feedingstuffs

There were 897 isolations of *Salmonella* from feedingstuffs during 2023, including 94 isolations from compound feeds (Tables 12.3 to 12.6) and 759 from feed ingredients or products associated with testing under Animal By-Products Regulations (ABPR). This is an increase of 12.0% compared with 2022 (801 isolations) and an increase of 7.4% compared with 2021 (835 isolations).

There were 265 isolations of regulated *Salmonella* serovars from animal feedingstuffs and related products during 2023. Regulated serovars are key serovars of public health importance targeted by the NCPs. This is 41.7% higher than in 2022 (187 isolations) and 113.7% higher than in 2021 (124 isolations). There were 132 isolations of *S*. Infantis, 70 isolations of *S.* Typhimurium, 29 isolations of monophasic *S.* Typhimurium, 19 isolations of *S.* Enteritidis, 14 isolations of *S.* Hadar and one isolation of *S*. Virchow.

There were 331 reports of *Salmonella* from raw meat pet food (Table 12.8b). This is lower than during 2022 (406 reports) and higher than 2021 (295 reports). The most common serovars reported during 2023 were *S*. Indiana (46 isolations), *S*. Derby (31 isolations) and *S*. Infantis (29 isolations). Overall there were 99 isolations of regulated serovars from raw meat pet food in 2023. This is an increase of 19.5% compared with 2022 (123 isolations) and a 39.0% increase in the number of isolations in 2021 (71 isolations).

The isolation rate of *Salmonella* from domestic processed animal protein in 2023 was 1.2%, which is twice the number in 2022 when it was 0.7%.

No batches of imported processed animal protein were tested during 2023, which is the same as during 2022 and 2021.

Antimicrobial resistance

Of the 5,513 *Salmonella* isolates examined during 2023, 73.3% were susceptible to all 16 antimicrobial compounds tested against. This is less than in 2022, when 75.7% of isolates were susceptible to all 16 antimicrobials.

A total of 317 cultures of *S*. Dublin from cattle were examined in 2023, of which 96.3% were susceptible to all the antimicrobials tested against. This is the same as in 2022 when 96.4% were susceptible to all antimicrobials tested against.

A total of 558 cultures of *S.* Typhimurium were examined in 2023, of which 55.0% were susceptible to all the antimicrobials tested against which is an increase from the 2022 (47.8%), and 2021 figures (44.3%).

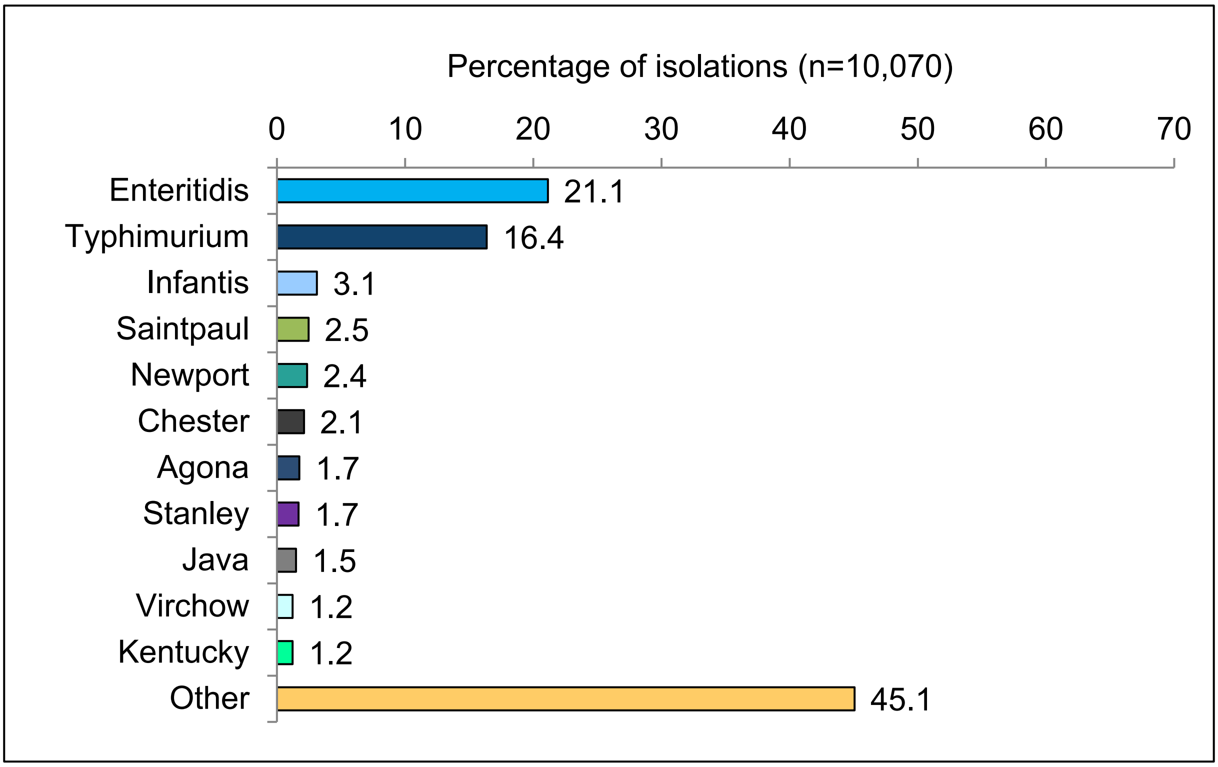
In total, 4,638 cultures of serovars other than *S*. Dublin or *S*. Typhimurium were tested in 2023 and 73.9% of these were sensitive to all the antimicrobials tested against. This is lower than in 2022 when 77.2% of cultures were fully sensitive.

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* cultures that were resistant to ciprofloxacin in 2023 was 0.8%. Cefotaxime, ceftazidime or ciprofloxacin resistance was not detected in *S*. Infantis from animals in 2023. Cefotaxime and ceftazidime resistance was 0.1% (8 isolates) in 2023 with 7 *Salmonella* isolates (including one *S.* Enteritidis) 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 Great Britain 2023

Figure 1.1.1: Isolations from people

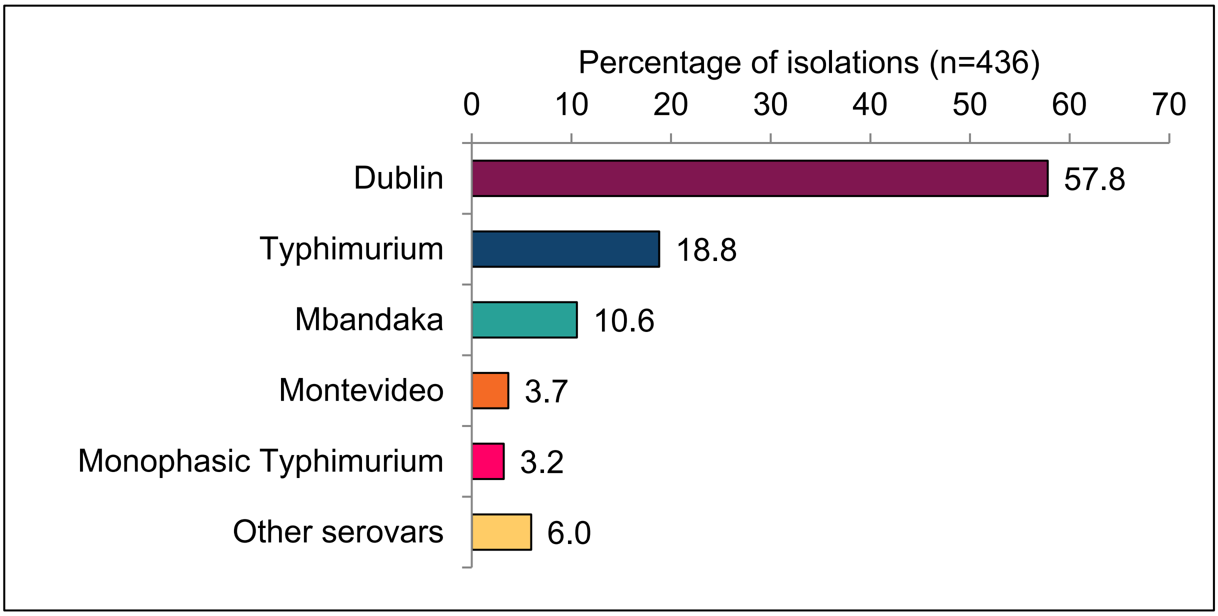


In 2023 the most commonly reported *Salmonella* serovar in people was *S.* Enteritidis, accounting for 21.1% of total isolations, followed by *S.* Typhimurium (16.4%), *S.* Infantis (3.1%) and *S.* Saintpaul (2.5%).

S. Typhimurium isolates in people include both monophasic and biphasic strains.

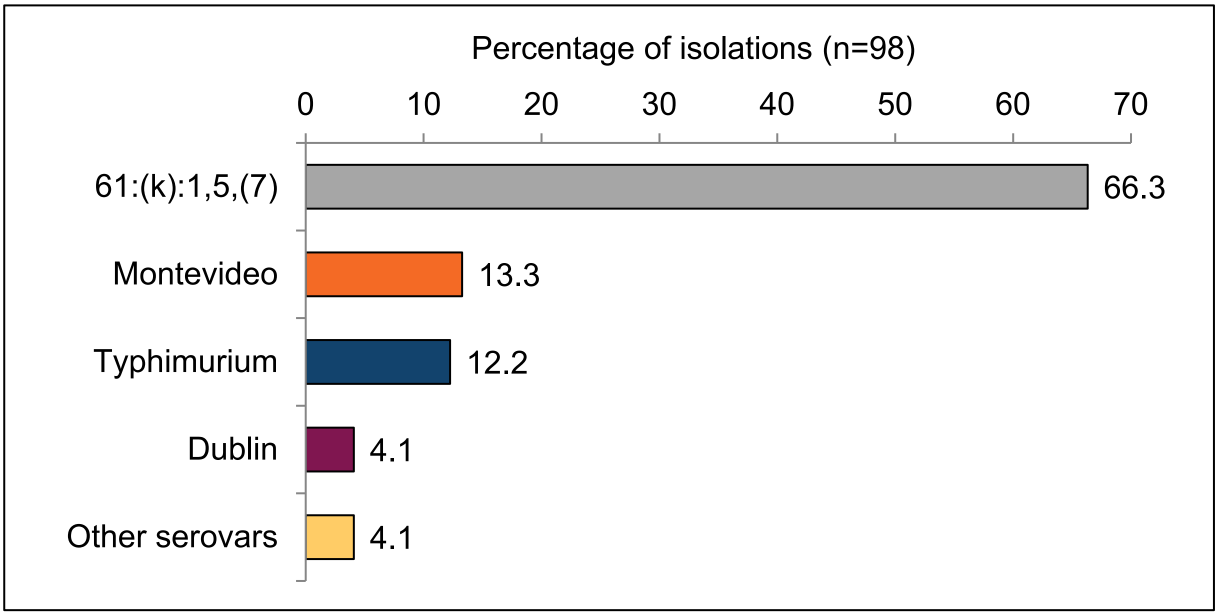
Data on human isolates was provided by UK Health Security Agency (UKHSA), Public Health Wales and Public Health Scotland. The UKHSA Second-Generation System (SGSS) is a live laboratory reporting system therefore numbers are subject to change and may not be directly comparable with data reported in previous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

Figure 1.1.2: Isolations from cattle



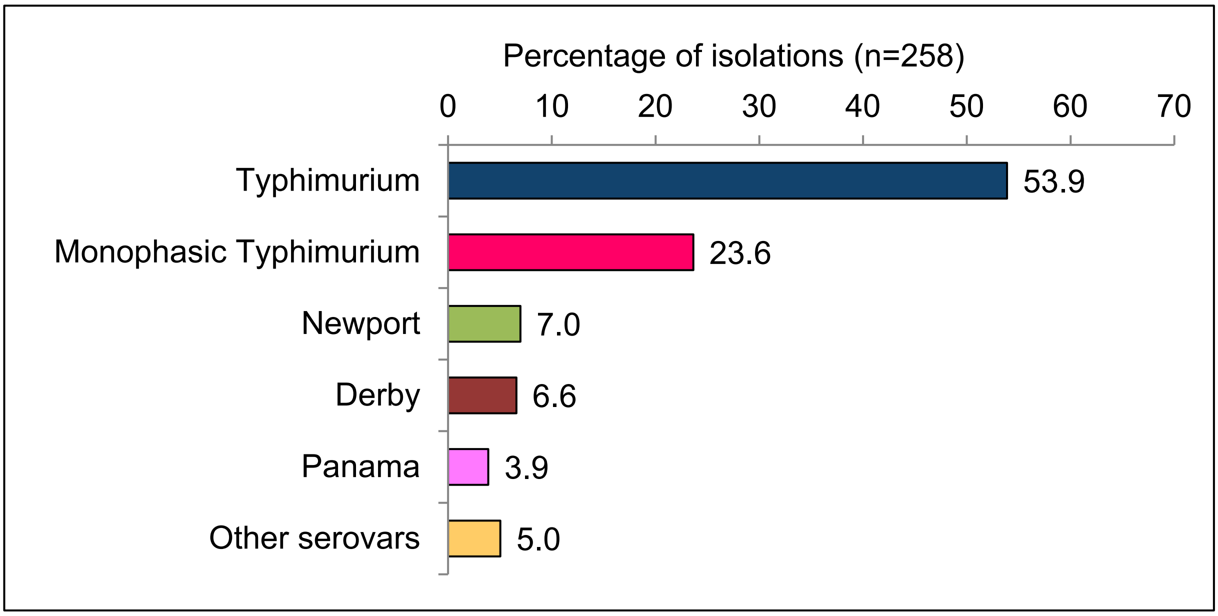
In 2023 the most common *Salmonella* serovar in cattle was *S.* Dublin (57.8% of total isolations), followed by *S.* Typhimurium (18.8%) and *S.* Mbandaka (10.6%).

Figure 1.1.3: Isolations from sheep



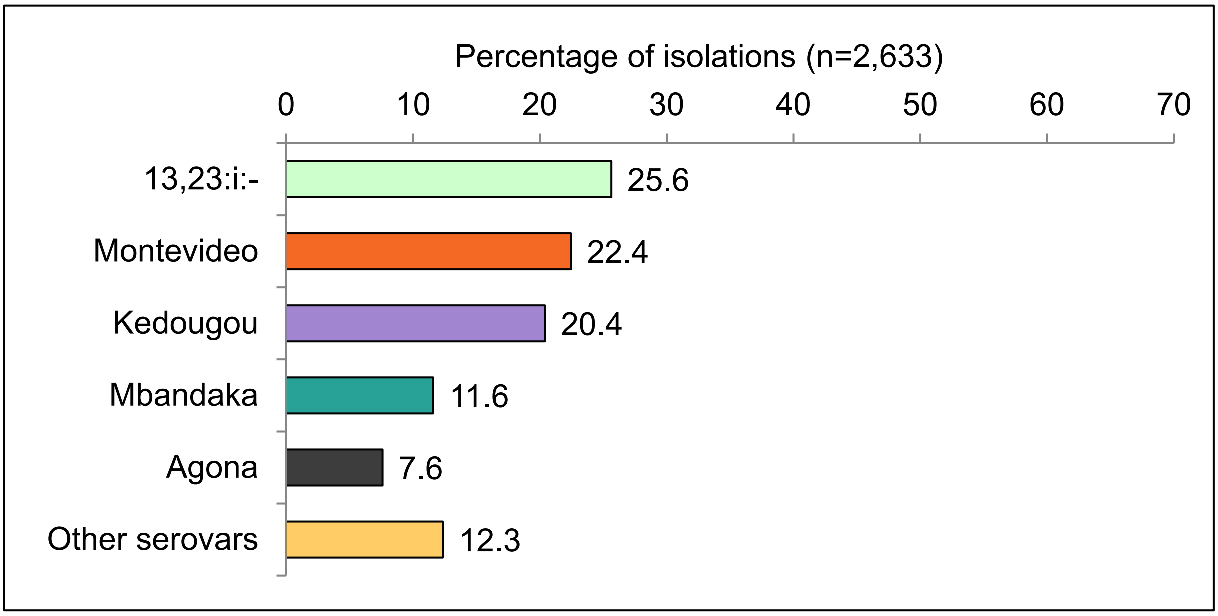
In 2023 the most common *Salmonella* serovar in sheep was *S.* 61:(k):1,5,(7) which includes enterica diarizonae and variants (66.3% of total isolations), followed by *S.* Montevideo (13.3%), *S*. Typhimurium (12.2%) and *S.* Dublin (4.1%).

Figure 1.1.4: Isolations from pigs



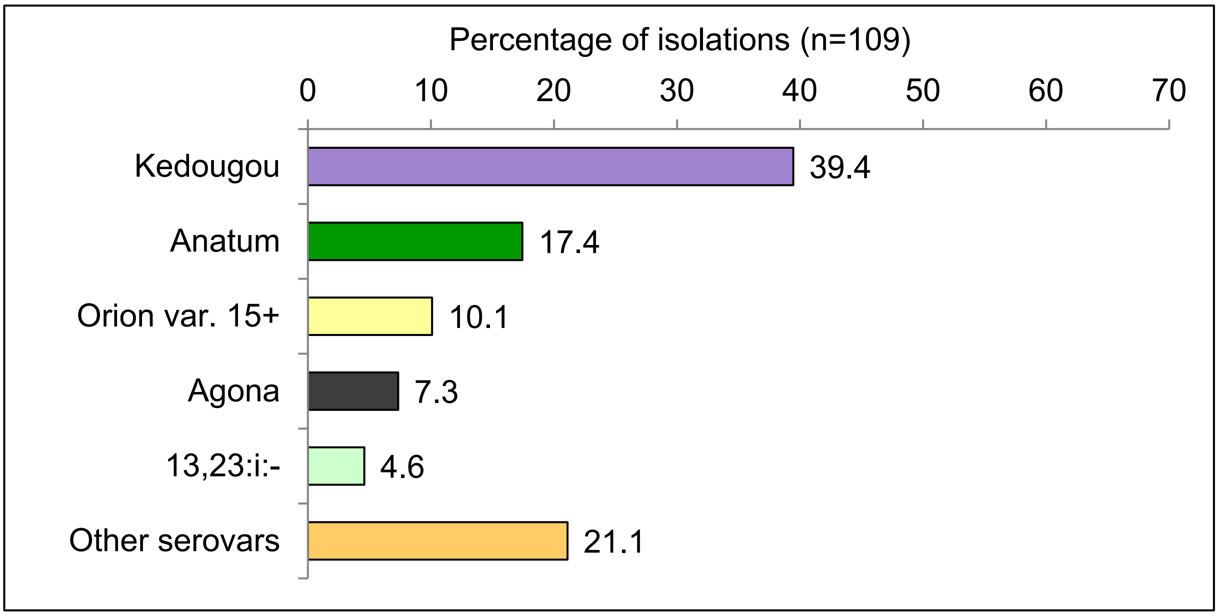
In 2023 the most common *Salmonella* serovar in pigs was *S.* Typhimurium (53.9% of total isolations), followed by monophasic *S*. Typhimurium (23.6%) and *S.* Newport (7.0%).

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



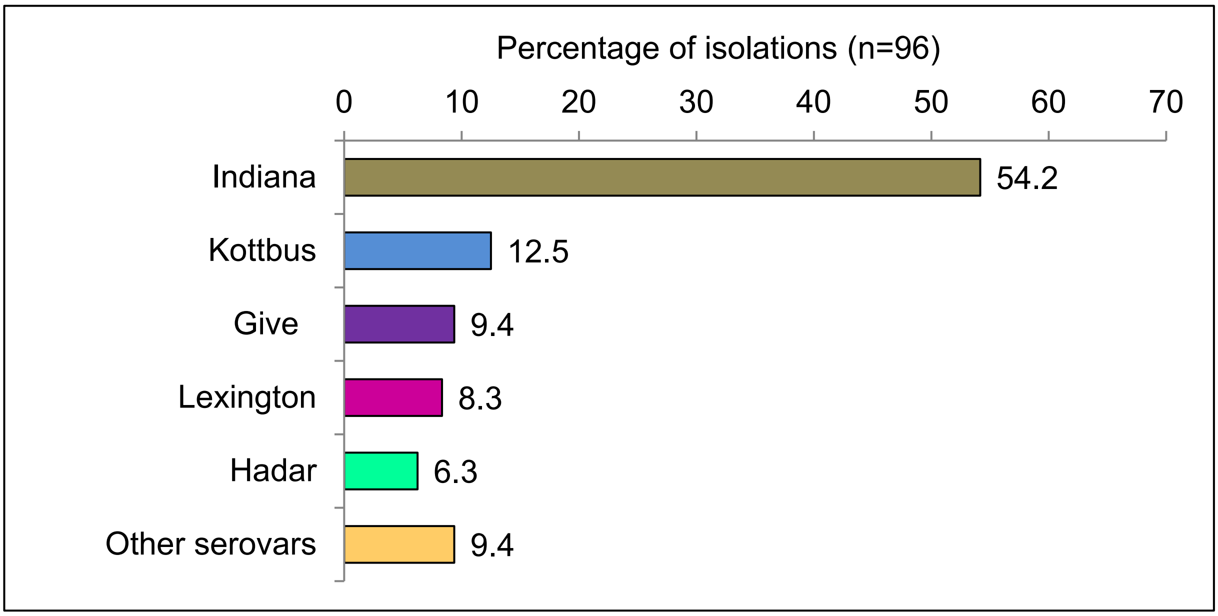
In 2023 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:- (25.6% of total isolations), followed by *S.* Montevideo (22.4%), *S.* Kedougou (20.4%) and *S*. Mbandaka (11.6%).

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



In 2023 the most common *Salmonella* serovar in turkeys was *S.* Kedougou (39.4% of total isolations), followed by *S*. Anatum 17.4%), *S.* Orion var. 15^+ (10.1%) and *S.* Agona (7.3%).

Figure 1.1.7: Isolations from ducks



In 2023 the most common *Salmonella* serovar in ducks was *S.* Indiana (54.2% of total isolations), followed by *S.* Kottbus (12.5%), *S.* Give (9.4%) and *S*. Lexington (8.3%).

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 2019 to 2023. Poultry includes chickens, turkeys and ducks.

The data includes statutory and non-statutory results.

***Salmonella* serovar**	**2019 isolations**	**2020 isolations**	**2021 isolations**	**2022 isolations**	**2023 isolations**
Africana	1	0	0	0	0
Agama	12	7	5	3	3
Agona	40	102	42	139	208
Ajiobo	0	0	2	0	1
Albany	2	0	0	0	0
Amsterdam	0	0	0	0	1
Anatum	12	52	42	70	25
Bardo	1	14	10	5	0
Bareilly	0	0	1	0	0
Berta	1	1	0	2	1
Bovismorbificans	20	43	30	18	3
Braenderup	0	1	2	2	5
Brandenburg	0	0	0	1	0
Bredeney	0	3	1	0	0
Cerro	0	0	0	0	1
Chester	0	1	0	0	3
Chomedey	0	0	0	0	1
Coeln	2	3	1	4	7
Corvallis	0	0	0	3	0
Cubana	0	0	0	0	1
Derby	183	39	49	40	35
Dublin	268	235	321	274	258
Durham	0	0	0	0	1
Eastbourne	4	0	0	0	0
Eboko	0	1	0	1	0
Enteritidis	50	34	11	25	11
Essen	0	0	1	0	0
Ferruch	0	0	2	0	0
Fresno	1	0	0	0	1
Gaminara	0	0	1	1	0
Give	11	9	6	3	14
Give var. 15⁺	57	36	23	23	5
Glostrup	0	1	0	0	0
Goldcoast	0	0	1	0	0

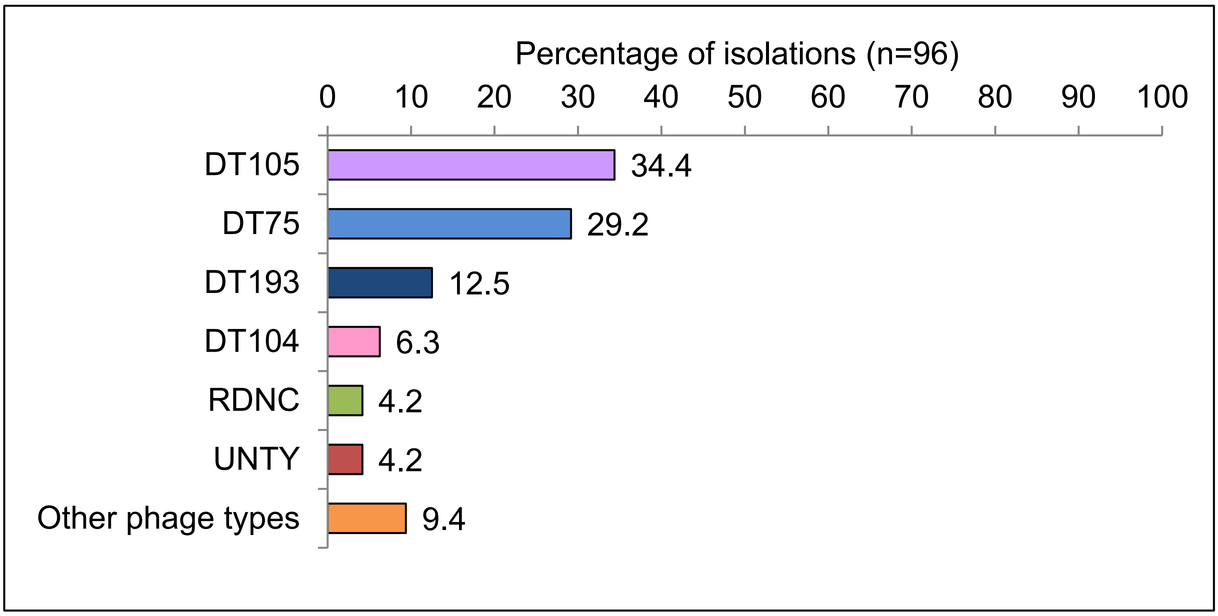
Salmonella serovar	2019 isolations	2020 isolations	2021 isolations	2022 isolations	2023 isolations
Hadar	39	21	1	17	6
Havana	1	1	2	6	0
Idikan	17	9	5	45	23
Indiana	101	65	44	40	57
Infantis	2	1	42	98	64
Isangi	0	0	3	0	0
Kedougou	409	499	235	310	583
Kentucky	1	1	0	4	1
Kingston	4	3	1	3	2
Kottbus	22	13	15	7	15
Lagos	1	0	0	0	0
Lexington	2	7	10	9	8
Liverpool	0	2	0	1	0
Livingstone	11	13	18	3	14
London	3	6	12	14	2
London var 15$^+$	0	0	0	1	0
Mbandaka	451	326	369	754	351
Menston	0	0	2	0	0
Minnesota	0	0	1	0	0
Mikiwasima	0	1	0	0	0
Molade	0	0	1	0	0
Monohapasic Typhimurium	101	95	100	79	83
Monschaui	4	2	0	0	0
Montevideo	203	270	454	491	621
Muenchen	1	8	4	9	5
Muenster	0	0	0	0	3
Newport	23	66	62	33	25
Nima	1	0	0	0	0
Nottingham	13	0	7	4	0
Odozi	0	0	4	0	0
Offa	1	0	0	0	0
Ohio	76	34	55	50	37
Orion	19	16	12	3	3
Orion var. 15$^+$	51	44	47	80	77
Oslo	15	6	3	0	4
Oxford	0	0	0	0	1
Panama	1	2	5	13	11
Paratyphi B var. Java	0	2	0	0	0
Poona	0	1	0	0	1
Ramatgan	0	1	0	0	0
Reading	2	3	3	4	2

Salmonella serovar	2019 isolations	2020 isolations	2021 isolations	2022 isolations	2023 isolations
Rissen	1	0	0	1	2
Saintpaul	0	1	0	0	0
Schwarzengrund	0	1	0	0	2
Senftenberg	120	111	84	63	25
Soerenga	0	0	0	0	0
Stanley	1	0	0	1	0
Stanleyville	0	1	0	1	0
Stourbridge	0	1	3	1	0
Takoradi	0	0	0	1	0
Tennessee	2	1	0	1	0
Typhimurium	124	159	200	195	257
Uganda	2	0	0	0	0
Wangata	0	0	0	0	1
Yoruba	0	0	0	0	2
13,23:i:-	436	716	279	343	663
61:k:1,5	5	11	40	4	12
61:k:1,5,7	10	4	2	17	60
61:-:1,5	11	18	32	0	0
61:-:1,5,7	37	17	0	50	3
untypable strains	52	100	68	59	17
rough strains	5	37	33	32	2
Total	**3,046**	**3,278**	**2,809**	**3,461**	**3,630**

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.

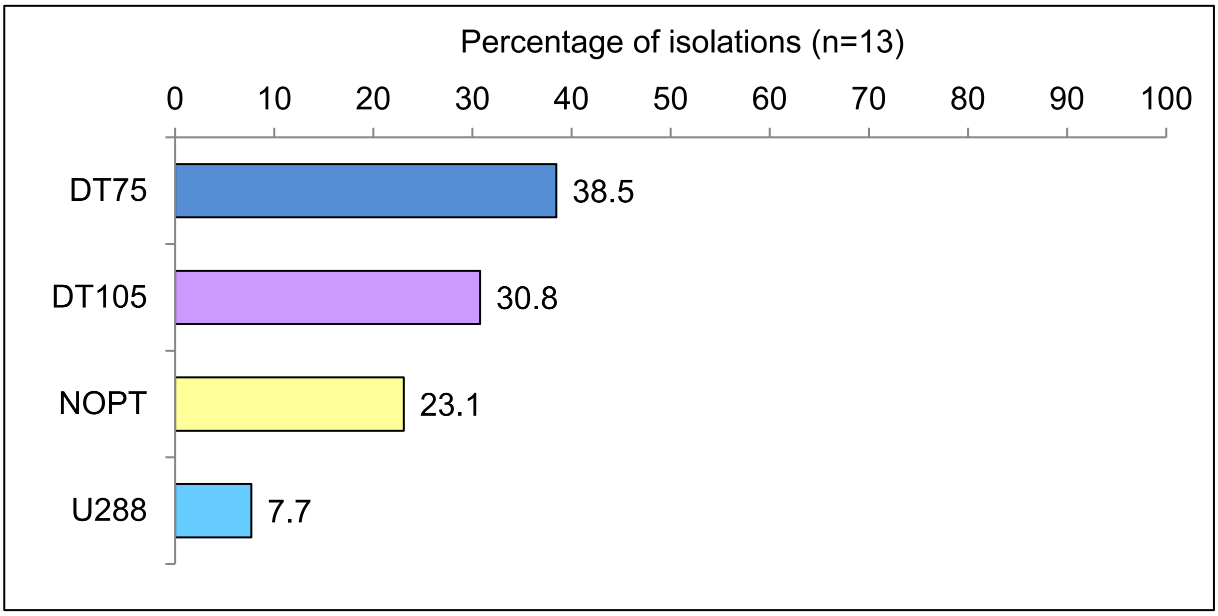
Figure 1.2: Isolations of the most common *S.* Typhimurium phage types (including monophasic strains) in livestock in 2023

Figure 1.2.1: Isolations from cattle



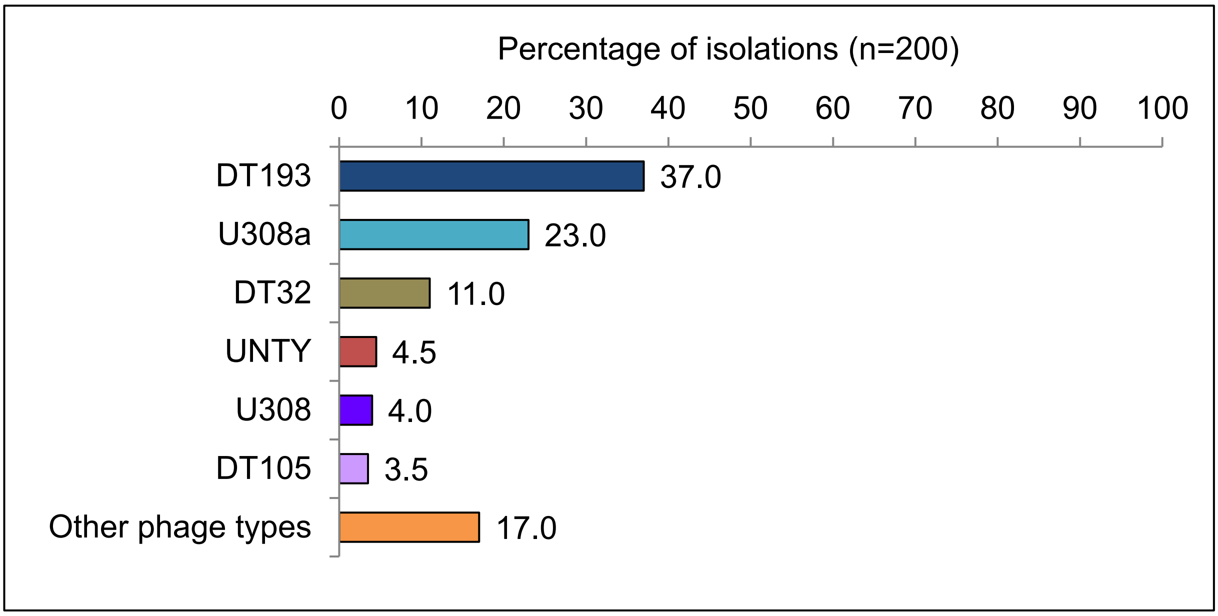
The most common *S.* Typhimurium phage type in cattle in 2023 was DT105 (34.4% of all cattle isolations), followed by DT75 (29.2%), DT193 (12.5%), DT104 (6.3%) and RDNC and UNTY (4.2% each).

Figure 1.2.2: Isolations from sheep



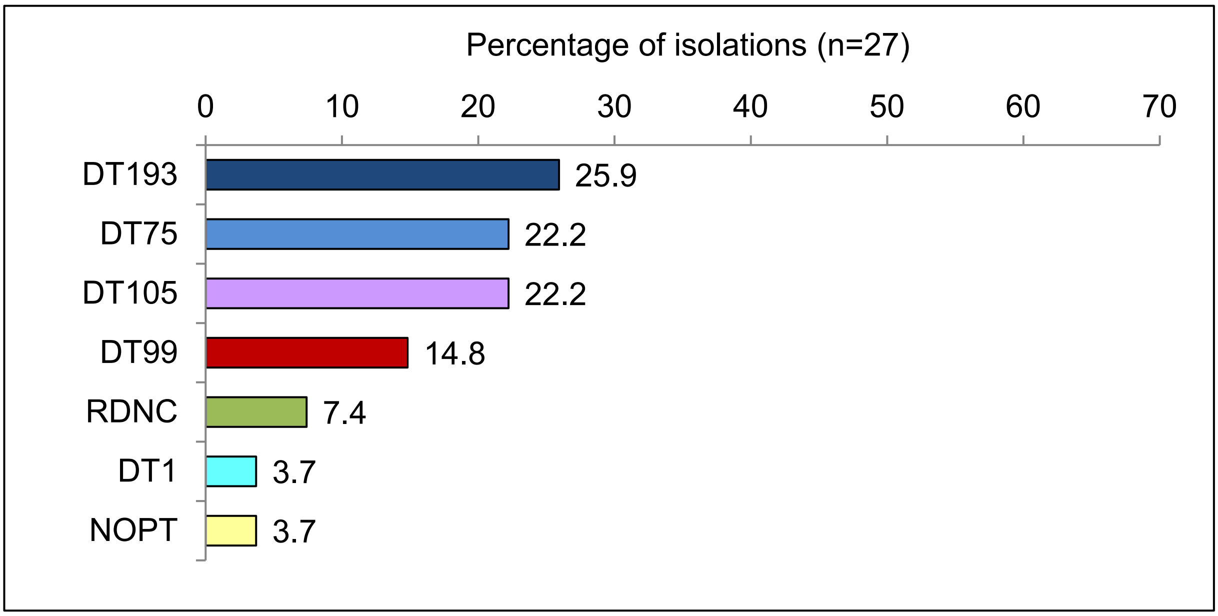
The most common *S.* Typhimurium phages type in sheep in 2023 were DT75 (38.5% of all sheep isolations), followed by DT105 (30.8%), NOPT (23.1%) and U288 (7.7%).

Figure 1.2.3: Isolations from pigs



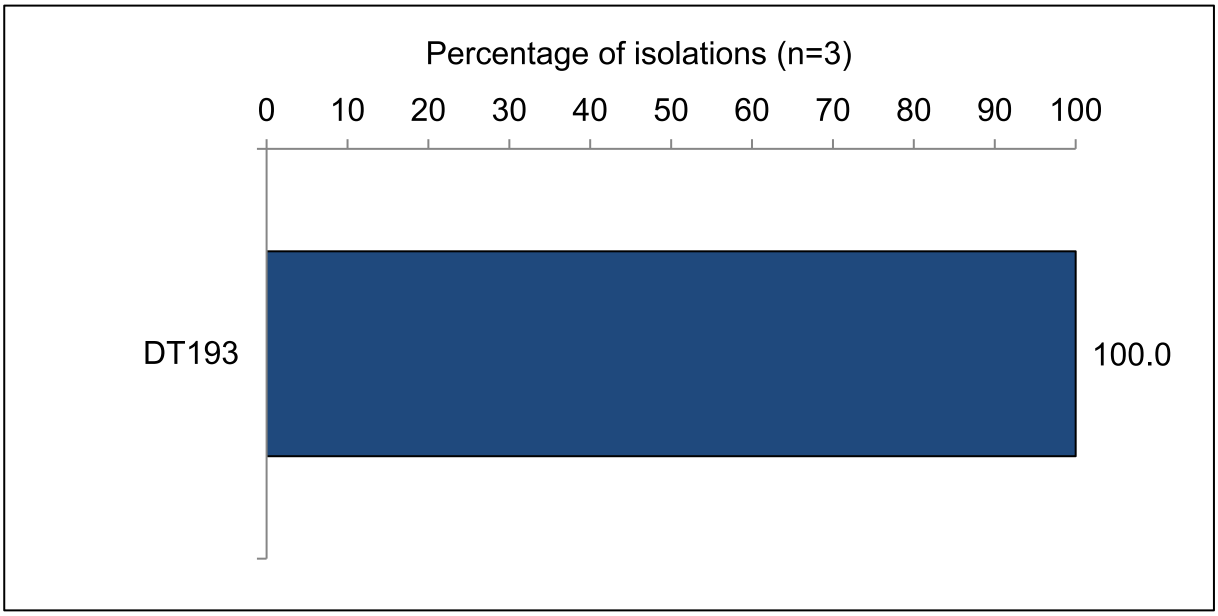
The most common *S.* Typhimurium phages type in pigs in 2023 was DT193 (37.0% of all pig isolations), followed by U308a (23.0%) and DT32 (11.0%).

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



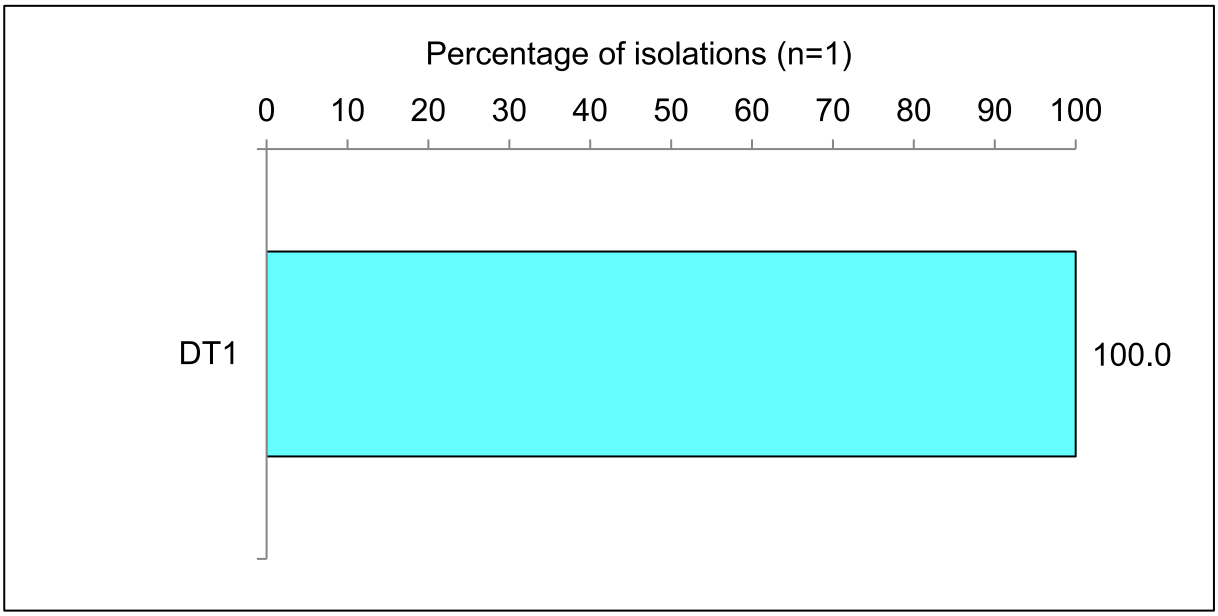
The most common *S.* Typhimurium phages type in chickens in 2023 was DT193 (25.9% of all chicken isolations), followed by DT75 and DT105 (22.2% each) and DT99 (14.8%).

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



The most common *S.* Typhimurium phages type in turkeys in 2023 was DT193 (100.0% of all turkey isolations).

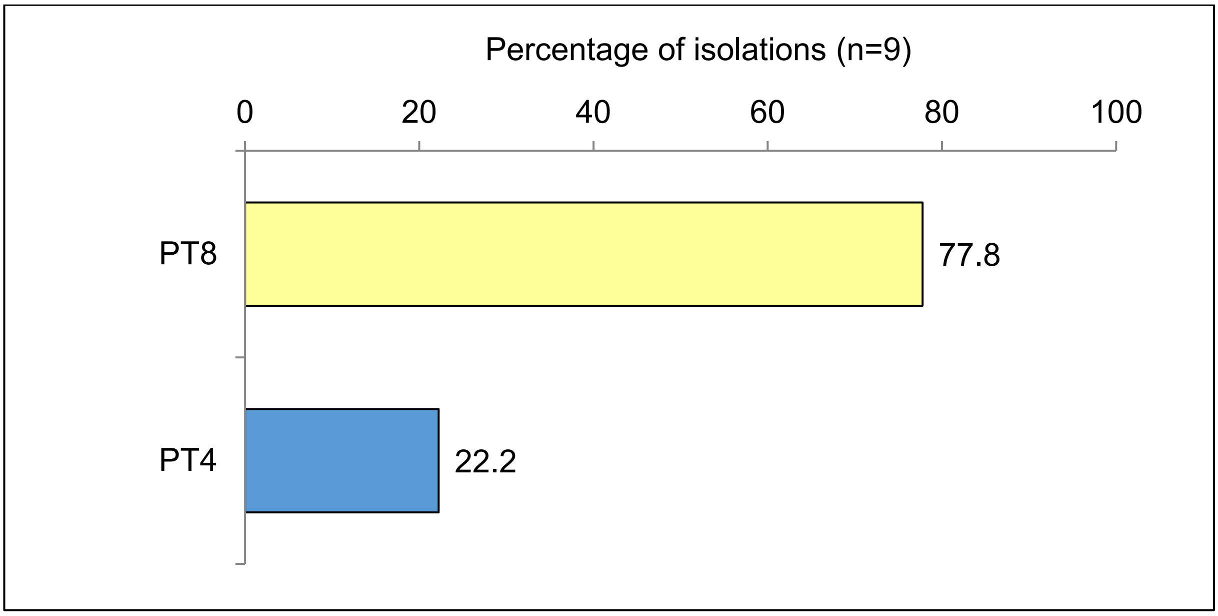
Figure 1.2.6: Isolations from ducks



The most common *S.* Typhimurium phages type in ducks in 2023 was DT1 (100.0% of all duck isolations).

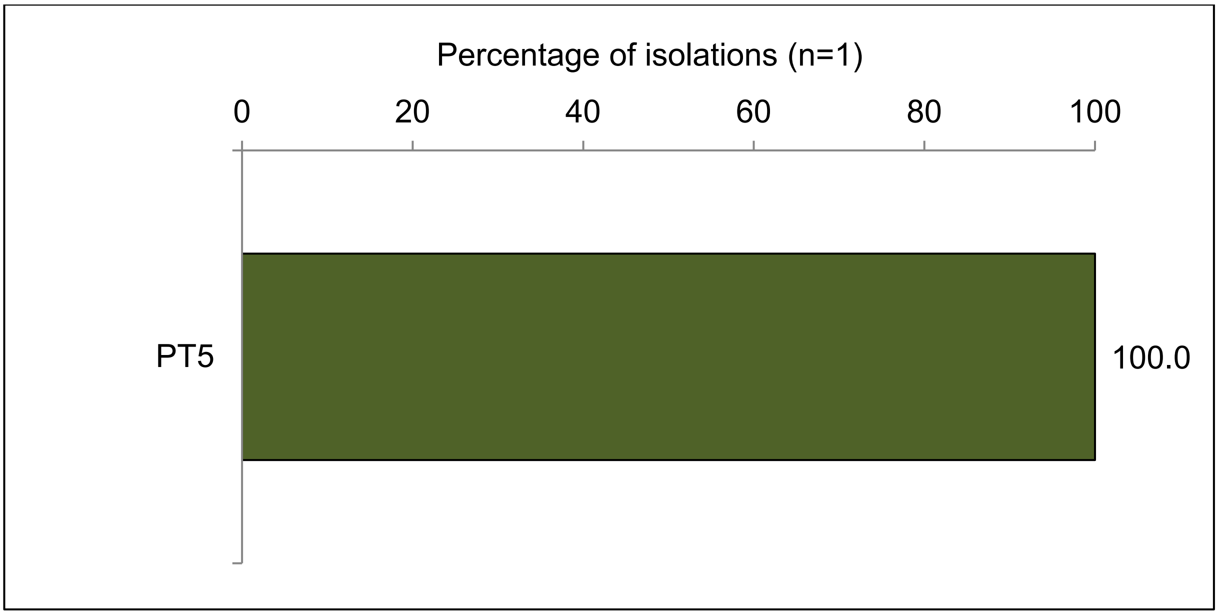
Figure 1.3: Isolations of the most common *S.* Enteritidis phage types in livestock in 2023

Figure 1.3.1 Isolations from chickens (statutory and non-statutory testing)



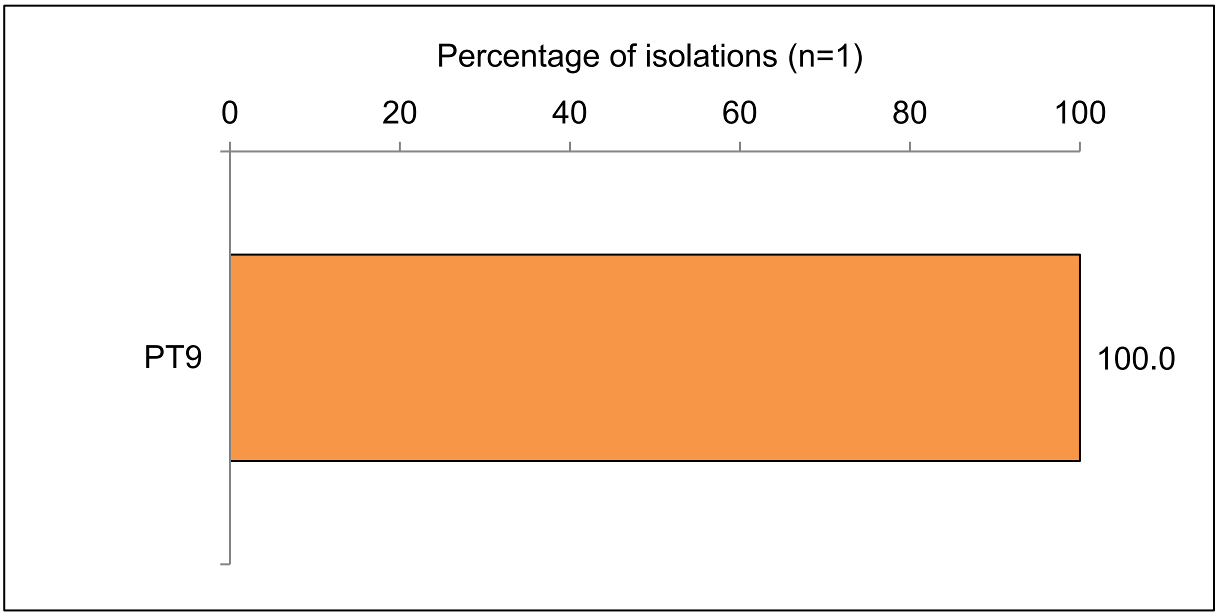
The most common *S*. Enteritidis phages types in chickens in 2023 were PT8 (77.8% of all chicken isolations) and PT4 (22.2% of isolations).

Figure 1.3.2 Isolations from cattle



The most common *S*. Enteritidis phages type in cattle in 2023 was PT5 (100.0% of all sheep isolations).

Figure 1.3.2 Isolations from ducks



The most common *S*. Enteritidis phages type in ducks in 2023 was PT9 (100.0% of all duck isolations).

There were no isolations of *S*. Enteritidis in pigs, sheep or turkeys in 2023.

Figure 1.4: Isolations of *S*. Enteritidis in livestock in Great Britain 2021 to 2023

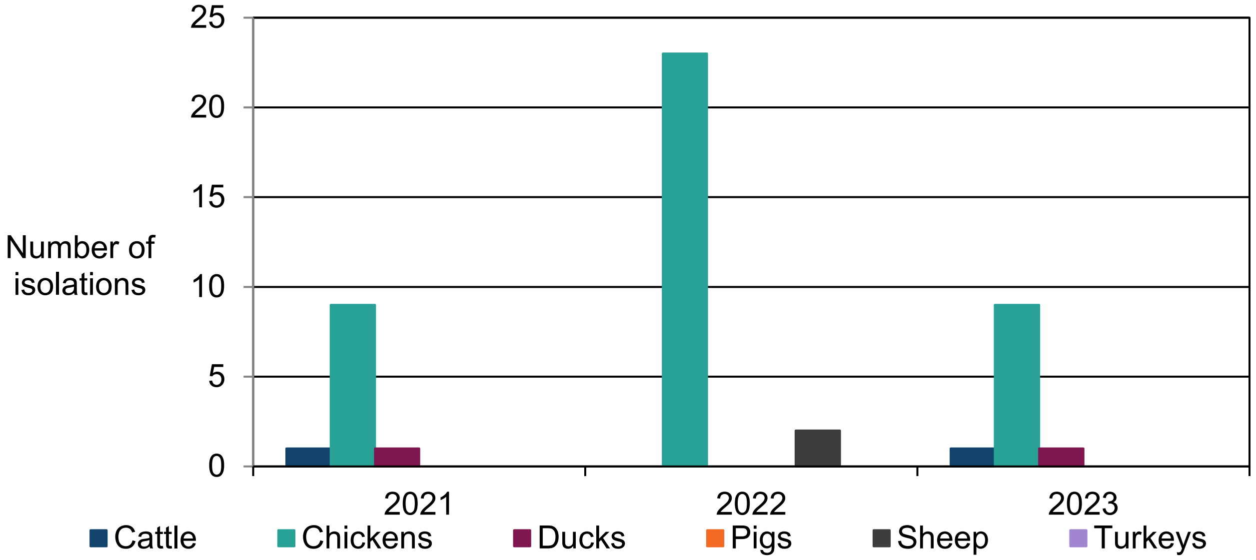


Figure 1.4 shows *Salmonella* Enteritidis was most commonly isolated from chickens during 2023, and in fewer numbers from cattle and ducks. This compares to chickens also being the most commonly isolated species in 2022 and 2021. *S*. Enteritidis was isolated from cattle and ducks in 2021, though not in 2022. *S*. Enteritidis was not isolated in pigs or turkeys in 2021, 2022 or 2023.

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

Figure 1.5: Isolations of *S*. Typhimurium in livestock in Great Britain 2021 to 2023

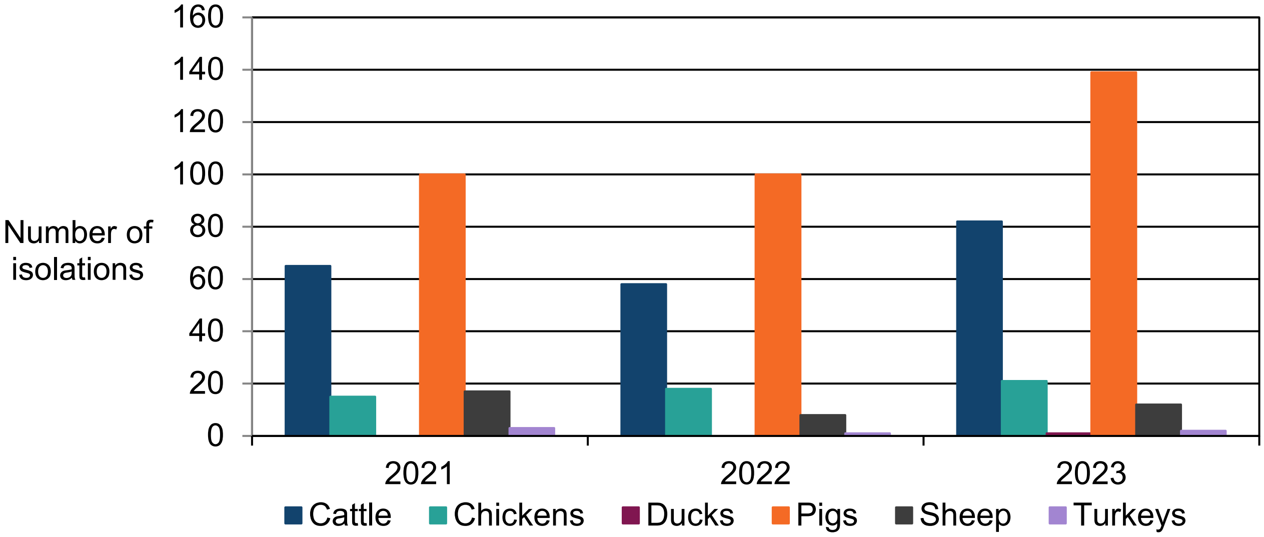


Figure 1.5 shows *Salmonella* Typhimurium was most commonly isolated from pigs amongst livestock species during 2023, and in lesser numbers from cattle, chickens, sheep and turkeys. This compares to pigs also being the most commonly isolated species in 2022 and 2021. *S*. Typhimurium was also isolated from cattle, chickens, ducks, sheep and turkeys in 2022.

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 2021 to 2023

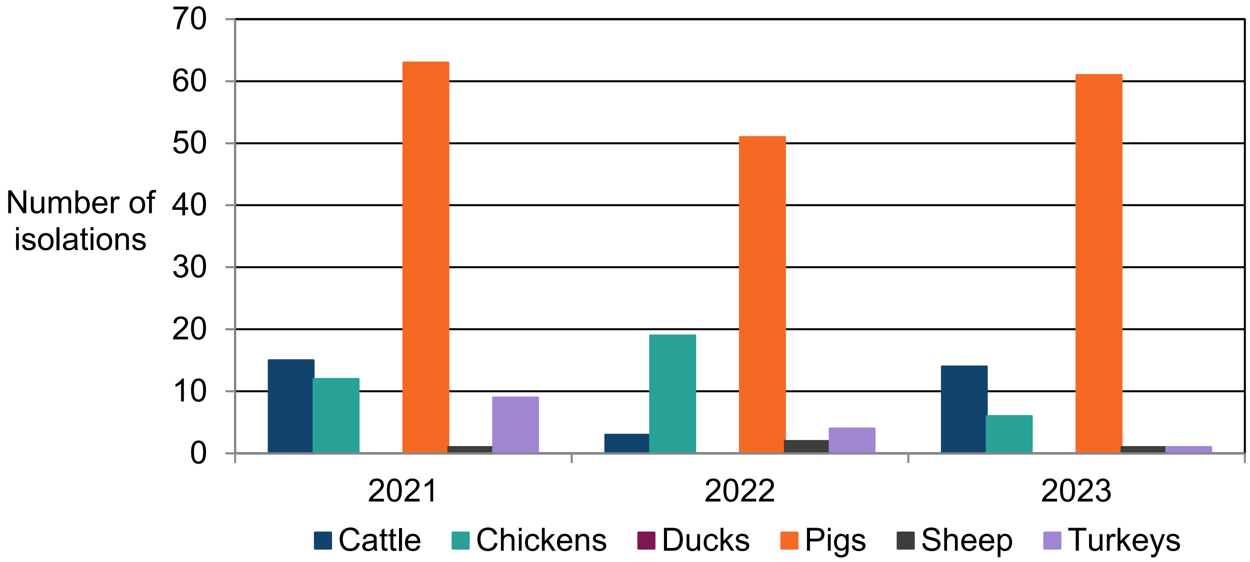


Figure 1.6 shows monophasic *S*. Typhimurium was most commonly isolated from pigs amongst livestock species during 2023, and in lesser numbers from cattle, chickens, sheep and turkeys. This compares to pigs also being the most commonly isolated species in 2022 and 2021. Monophasic *S*. Typhimurium was also isolated from cattle, chickens, sheep and turkeys in 2022 and 2021.

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

Chapter 2: Reports of *Salmonella* in cattle

The total number of cattle (including calves) on agricultural holdings in Great Britain was just over 7.88 million in June 2023 according to Defra figures, a decrease of 0.79% compared to June 2022. With the exception of 2022, there has been a gradual decline in the cattle population since 2016 (Figure 2.1). 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, 2021, 2022 and 2023 data with previous years.

On the Veterinary Investigation Diagnoses Analysis (VIDA) database there were 17,910 submissions recorded from cattle in 2023, which was an increase of 1.6% when compared with 2022 (17,624). There is no active monitoring for Salmonellae in bovines, with nearly all isolations being made 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 through the Cattle Dashboard | Tableau Public link.

There were 436 *Salmonella* isolations from cattle in 2023, an increase of 1.4% from 2022 when there were 430 isolations but 16.3% lower than during 2021 (521 isolations). The 3 most commonly reported 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). However, in 2023 for the first time since 2018, *S*. Typhimurium was the second most isolated serovar. The number of *S.* Dublin isolations, the most commonly reported serovar in cattle, fell by 4.9% from 265 isolations in 2022 to 252 isolations in 2023. The proportion of *S*. Dublin isolates as a proportion of total *Salmonella* isolated from cattle fell marginally from 61.6% in 2022 to 57.8% in 2023 (Figure 2.2). There was a marked increase of 41.4% in isolations of *S.* Typhimurium in 2023 compared to 2022 (82 versus 58 in 2022). This represents the highest number of isolations since before 2012. Isolations of *S.* Mbandaka fell by 22.0% in 2023 compared to 2022 from 59 to 46 isolations (Table 2.1).

Salmonella Dublin

The most common serovar isolated from cattle in Great Britain was *Salmonella* Dublin for the 25th successive year. There were 252 isolations of *Salmonella* Dublin, representing 57.8% of the total 436 *Salmonella* isolates from cattle.

As in previous years, the number of isolations peaked in the autumn (Figure 2.4). In 2023 the highest numbers were recorded in November with September and October also recording high incidences compared to the rest of the year. Alimentary tract disease was the most common presentation, with the majority of 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

Since the start of 2023 following the move to whole genome sequencing, the monophasic variants *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- are 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.

The second most common serovar isolated from cattle submissions was *S.* Typhimurium, with the number of isolations increasing by 41.4% to 82 isolations in 2023 from 58 in 2022. The proportion of *Salmonella* Typhimurium isolations also increased from 13.5% in 2022 to 18.8% in 2023.

Phage types identified in 2023 were consistent with those identified in 2022 when changes in phage types were noted compared with previous years (Table 2.2). The most common phage types in 2023 were DT105 (33 isolations), DT75 (28 isolations). DT105 was identified for the first time in cattle in 2021 (one isolation) and DT75 was identified for the first time in 2022 having previously never isolated from cattle in Great Britain. There was one isolation of *S.* Typhimurium DT1, last isolated in 2015 and one isolation of DT109 which has not been isolated from cattle previously. There were no isolations of *S.* Typhimurium UNTY in 2023, which is the same as in 2022, 2021 and 2020. This strain had been associated with sheep and human illness and concerted efforts by both APHA and UKHSA (formerly PHE) were made to investigate the transmission of this *Salmonella*.

There were 14 isolations of the monophasic *S.* Typhimurium in cattle in 2023, a marked increase compared to 2022 (3 isolations) but similar to years prior (15 isolations in 2021;17 isolations in 2020). The most common phage type in 2023 with 7 isolations was phage type DT193, followed by UNTY with 4 isolations (Table 2.3).

Salmonella Mbandaka

The third most common serovar in cattle was *S.* Mbandaka (46 isolations, 10.6% of total cattle isolations), with the number of isolations falling by 22.0% compared with 2022 (46 versus 59). This is the lowest number of isolations since 2018 when there were 35 isolations. The proportion of *S.* Mbandaka isolations also decreased compared with 2022 figures from13.7% to 10.6% in 2023.

Other serovars

The number of *Salmonella* Montevideo isolates, the fourth most commonly isolated serovar in cattle in 2023, fell from 18 isolations in 2022 to 16 in 2023 (Table 2.1, Figure 2.3).

For the first time since 2016, there was an isolation of *S*. Muenster in cattle in 2023. There was a single isolation of *S.* Enteritidis (PT5) in cattle in 2023, compared to no isolations in 2022 (Table 2.4). Other notable increases in isolations in 2023 included *Salmonella* 61:k:1,5,7 increasing from 2 isolations in 2022 to 8 isolations in 2023.

Reports of non-Great Britain origin

There was one report of *S*. Dublin (from a clinical disease investigation) in cattle imported from the Republic of Ireland and 2 reports of *S*. Montevideo (also associated with clinical disease) in cattle imported from Denmark. These reports are excluded from the tables and figures of this publication.

Figure 2.1: Cattle population and numbers of holdings with cattle in Great Britain 2013 to 2023

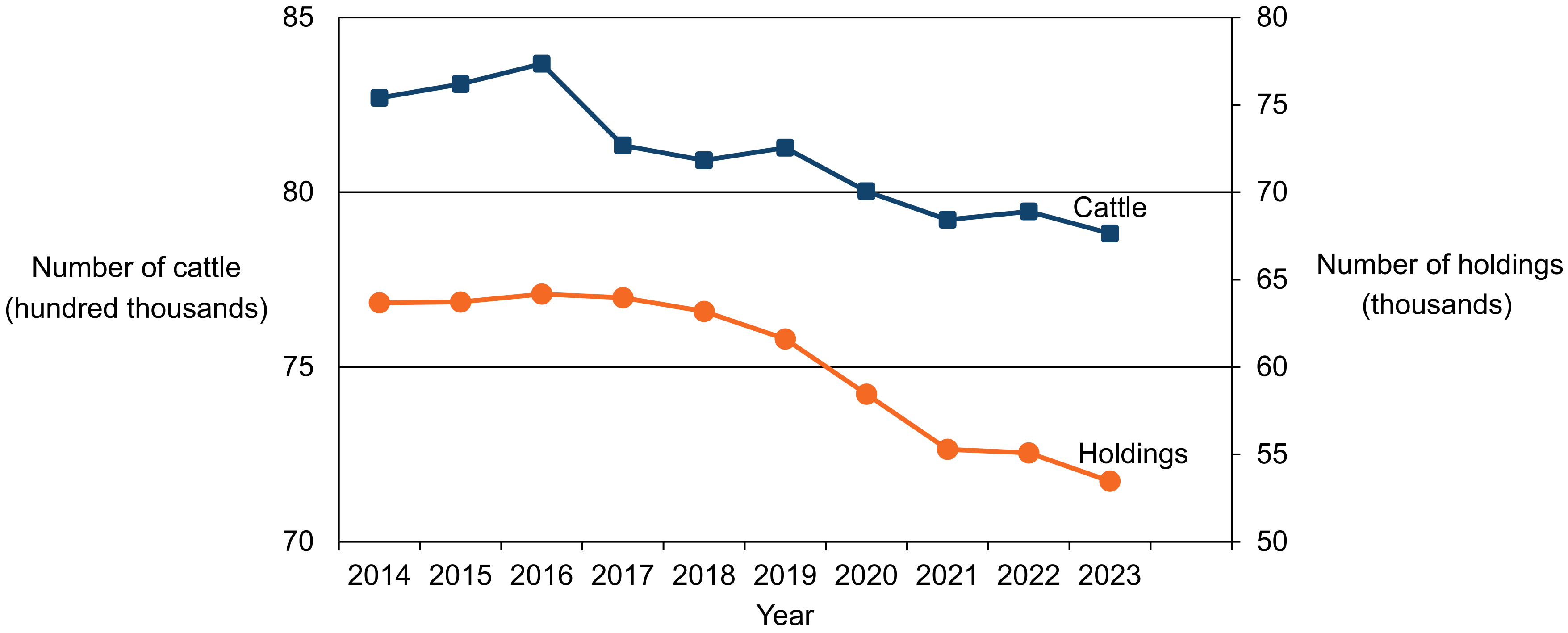


Figure 2.1 above shows a steady decline in the number of cattle holdings since 2013 and while the number of cattle has also declined there was an upturn in 2022 before declining again 2023.

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

Number of holdings in 2020 is estimated. Source: June 2023 Agricultural Census.

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

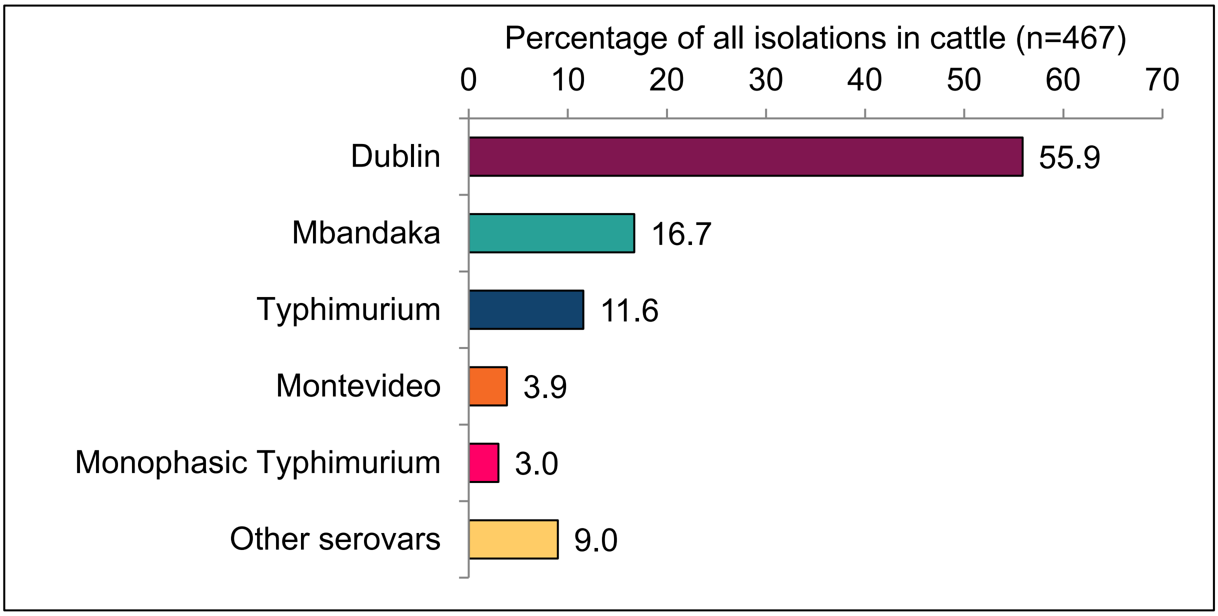
Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Agama	1	1	1	1	1	1	0	0	0	0
Anatum	2	2	2	2	5	4	1	1	1	1
Bardo	1	1	0	0	0	0	0	0	0	0
Berta	1	1	0	0	0	0	0	0	0	0
Bovismorbificans	0	0	1	1	0	0	0	0	0	0
Bredeney	0	0	2	2	1	1	0	0	0	0
Chester	0	0	1	1	0	0	0	0	1	1
Coeln	0	0	0	0	1	1	0	0	3	2
Derby	0	0	1	1	0	0	0	0	1	1
Dublin	261	223	225	199	306	253	265	219	252	217
Eboko	0	0	1	1	0	0	0	0	0	0
Enteritidis	1	0	2	2	1	1	0	0	1	1
Gaminara	0	0	0	0	1	1	1	1	0	0
Glostrup	0	0	1	1	0	0	0	0	0	0
Indiana	0	0	1	1	0	0	1	1	0	0
Infantis	2	1	0	0	0	0	0	0	1	1
Kingston	2	1	0	0	1	1	0	0	1	1
Kottbus	3	3	2	2	6	6	0	0	0	0
Lagos	1	1	0	0	0	0	0	0	0	0
London	0	0	1	1	0	0	0	0	0	0
Mbandaka	78	59	63	56	73	64	59	54	46	42
Menston	0	0	0	0	2	2	0	0	0	0
Monophasic Typhimurium	14	12	17	10	15	14	3	3	14	12
Montevideo	18	16	5	4	23	19	18	17	16	13
Muenster	0	0	0	0	0	0	0	0	1	1

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Newport	6	6	2	2	2	2	0	0	3	3
Nottingham	3	2	0	0	0	0	0	0	0	0
Oslo	4	3	1	1	1	1	0	0	3	2
Panama	0	0	0	0	0	0	1	1	1	1
Paratyphi B var. Java	0	0	2	2	0	0	0	0	0	0
Saintpaul	0	0	1	1	0	0	0	0	0	0
Typhimurium	54	34	45	35	65	46	58	48	82	73
Uganda	1	1	0	0	0	0	0	0	0	0
61:k:1,5,7	1	1	0	0	0	0	2	2	8	8
61:-:1,5,7	1	1	1	1	0	0	4	4	0	0
61:k:1,5	0	0	1	1	3	3	0	0	0	0
61:-:1,5	1	1	3	3	2	2	0	0	0	0
untypable strains	10	10	7	5	9	9	12	12	1	1
rough strains	1	1	1	1	3	3	5	5	0	0
Total	**467**	**381**	**390**	**337**	**521**	**434**	**430**	**368**	**436**	**378**

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

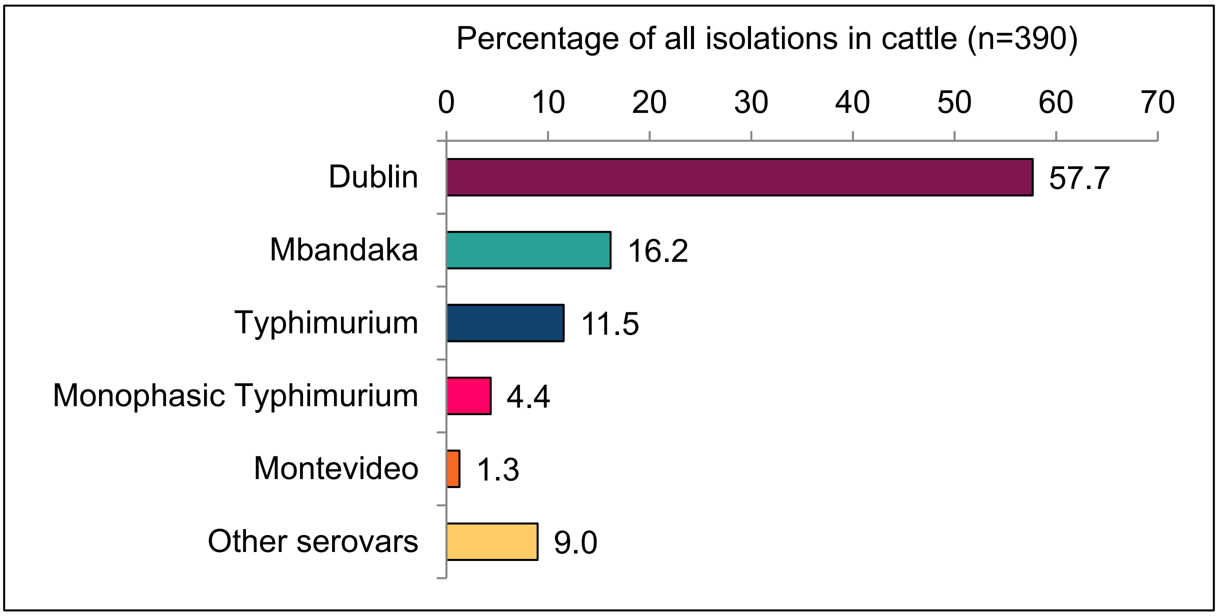
Figure 2.2: Isolations of the most common serovars in cattle in Great Britain 2019 to 2023

Figure 2.2.1: Isolations in 2019



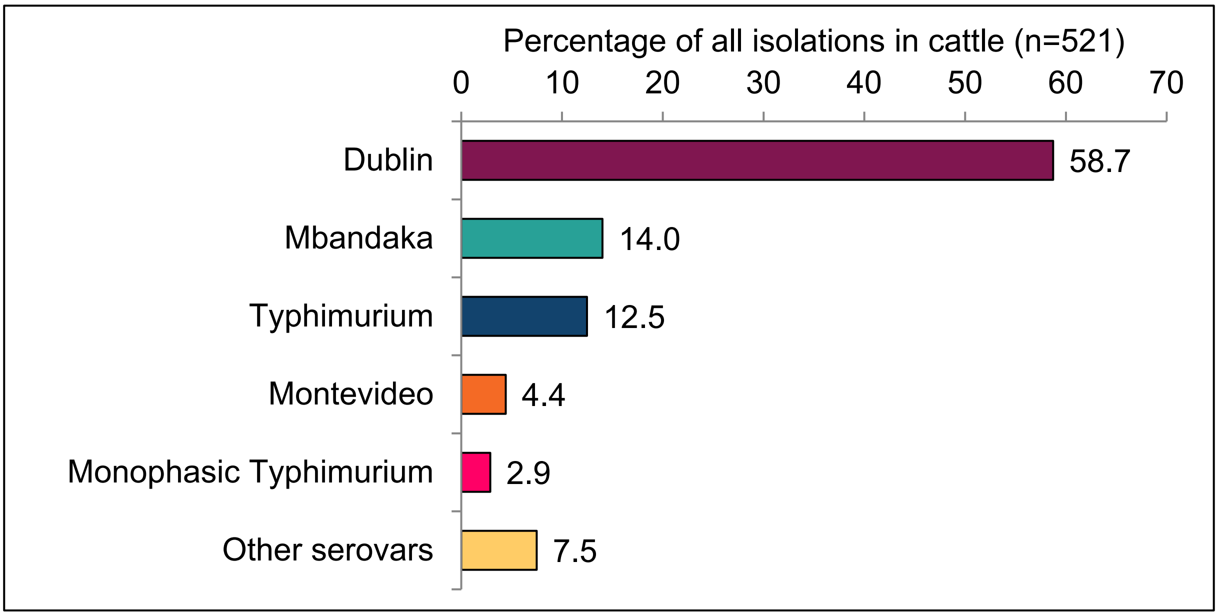
The most common serovar in cattle in 2019 was *S.* Dublin (55.9% of isolations), followed by *S.* Mbandaka (16.7% of isolations), *S.* Typhimurium (11.6% of isolations) and *S.* Montevideo (3.9% of isolations).

Figure 2.2.2: Isolations in 2020



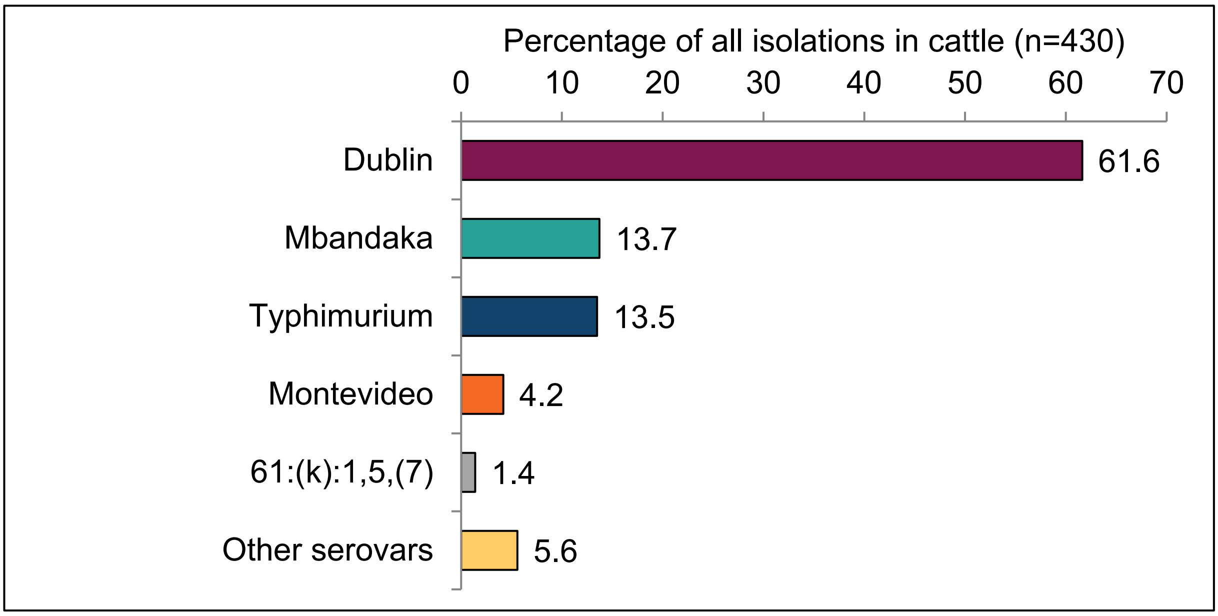
The most common serovar in cattle in 2020 was *S.* Dublin (57.7% of isolations), followed by *S.* Mbandaka (16.2% of isolations), *S.* Typhimurium (11.5% of isolations) and monophasic *S.* Typhimurium (4.4% of isolations).

Figure 2.2.3: Isolations in 2021



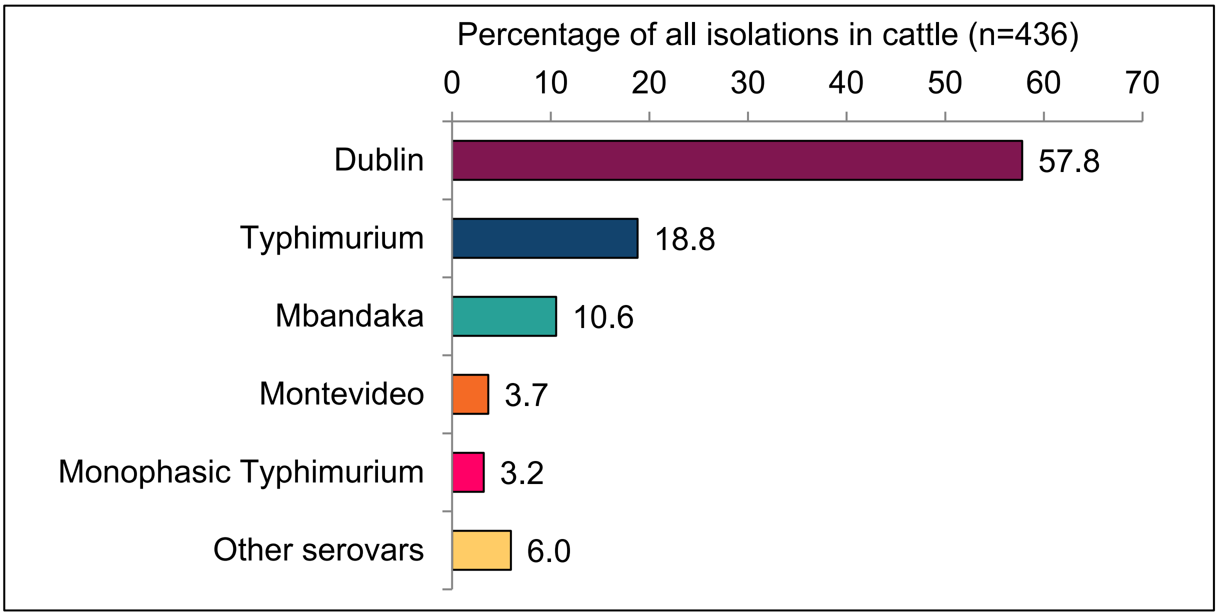
The most common serovar in cattle in 2021 was *S.* Dublin (58.7% of isolations), followed by *S.* Mbandaka (14.0% of isolations), *S*. Typhimurium (12.5% of isolations) and *S.* Montevideo (4.4% of isolations).

Figure 2.2.4: Isolations 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 2.2.5: Isolations 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) and *S.* Mbandaka (10.6%) and *S*. Montevideo (3.7% of isolations).

All isolates 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 2023 and their trends over time since 2019

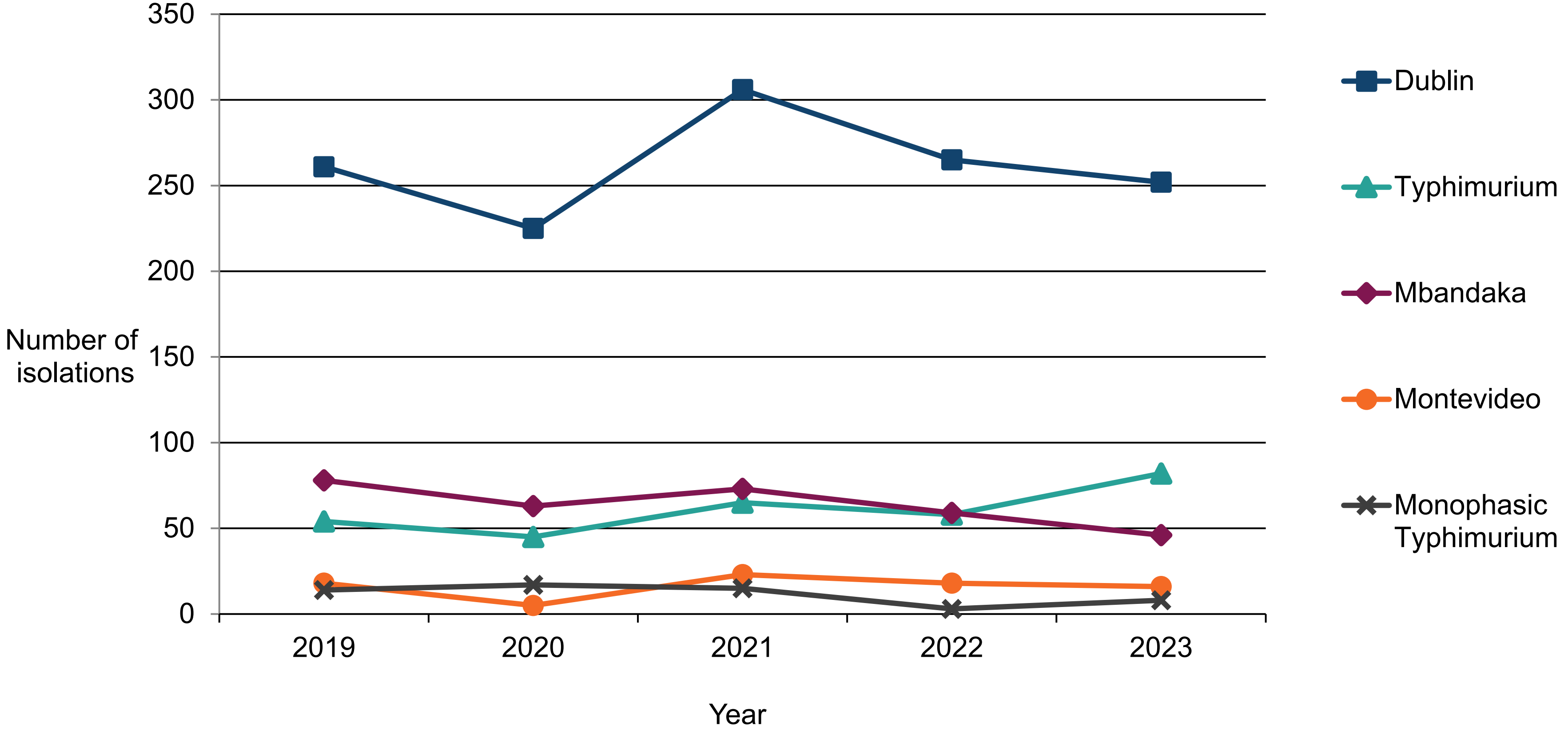


Figure 2.3 shows the most common serovar in cattle for all years was *S.* Dublin with above 225 isolations in all years. There was a dip in isolations in 2020 and following a peak in 2021 isolations have been decreasing since. The number of isolations of *S.* Mbandaka, *S.* Typhimurium, *S.* Montevideo and monophasic *S.* Typhimurium have shown less fluctuation and were consistently less than 100.
All isolates of 61:(k):1,5(7) are variants of *Salmonella* enterica subspecies diarizonae.

Figure 2.4: Seasonality of *Salmonella* Dublin in cattle in Great Britain 2019 to 2023

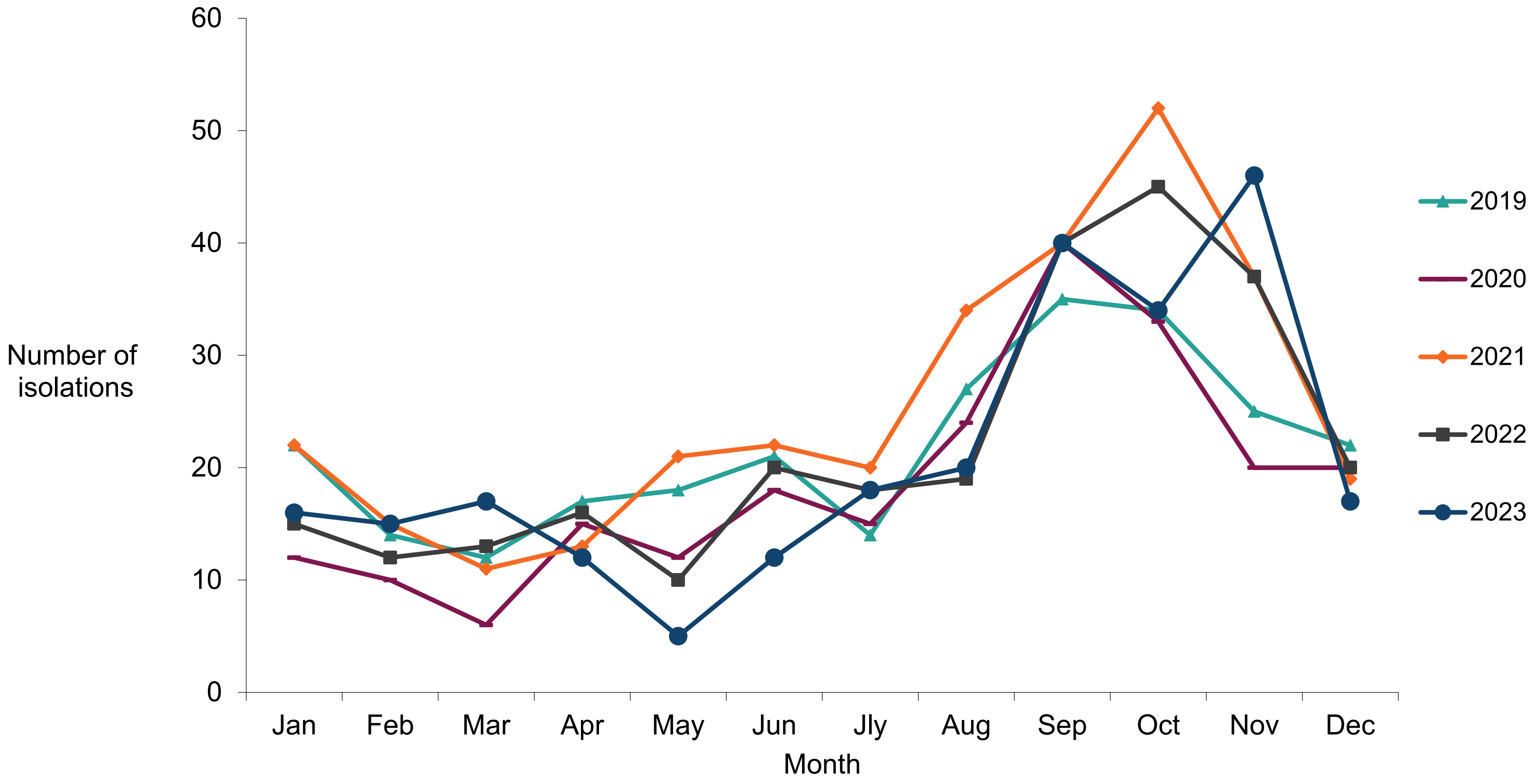


Figure 2.4 above shows a marked seasonality in *S.* Dublin in all years peaking in September-Novemeber, dropping to lower levels in January to June.

Figure 2.5: *S*. Dublin, *S*. Enteritidis, *S*. Typhimurium and monophasic *S.* Typhimurium as a proportion of all isolations in cattle in Great Britain 2003 to 2023

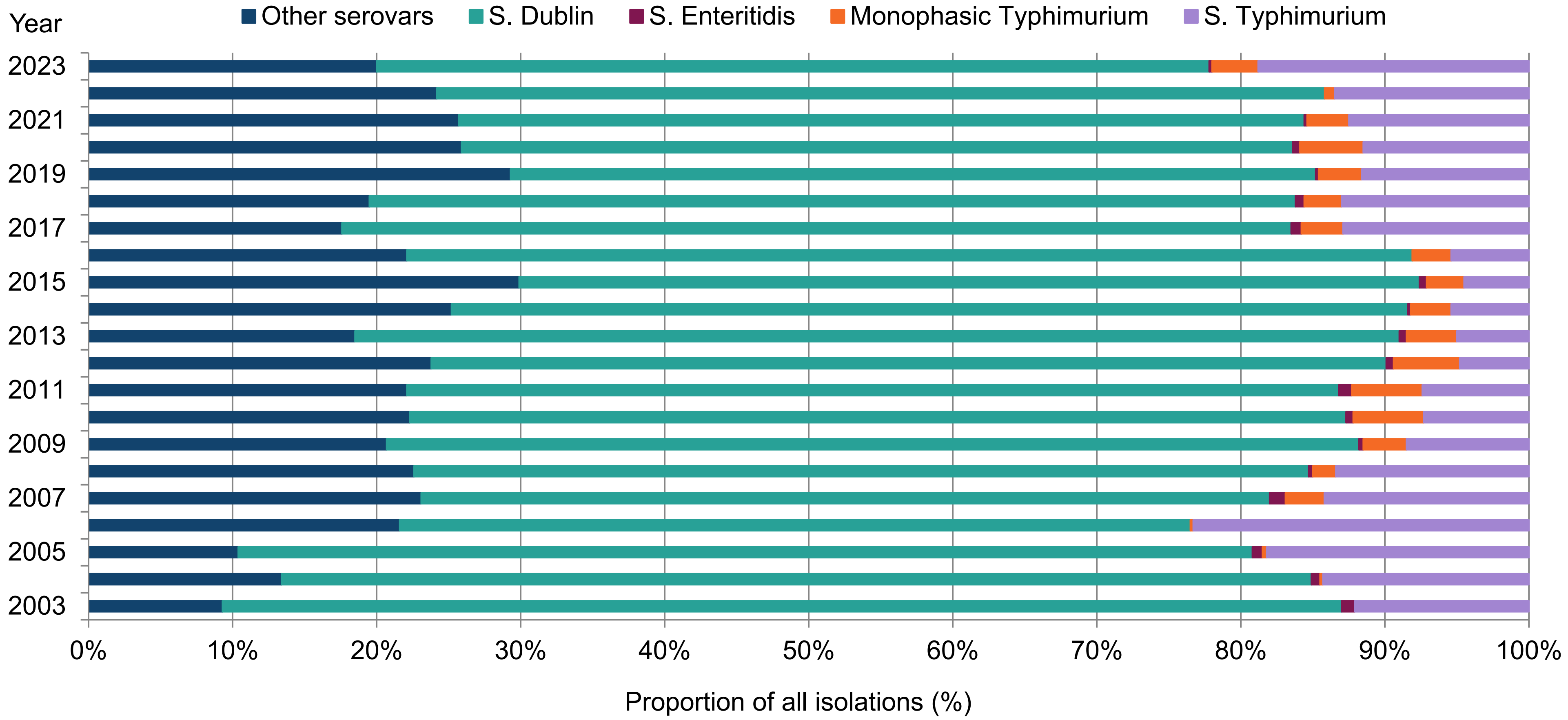


Figure 2.5 shows that as a proportion of all isolates in cattle in Great Britain between 2002 and 2023:

- *S.* Dublin accounted for the greatest proportion of isolates, but rates remained stable across the years at 50% to 80%
- *S.* Enteritidis was variable 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 18.8% in 2023
- 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	Other serovars	*S.* Dublin	*S.* Enteritidis	Monophasic *S.* Typhimurium	*S.* Typhimurium
2003	9.3%	77.7%	0.9%	0.0%	12.1%
2004	13.4%	71.5%	0.6%	0.2%	14.3%
2005	10.4%	70.4%	0.7%	0.3%	18.2%
2006	21.6%	54.9%	0.0%	0.2%	23.3%
2007	23.1%	58.9%	1.1%	2.7%	14.2%
2008	22.6%	62.1%	0.3%	1.6%	13.4%
2009	20.7%	67.5%	0.3%	3.0%	8.5%
2010	22.3%	65.0%	0.5%	4.9%	7.3%
2011	22.1%	64.7%	0.9%	4.9%	7.4%
2012	23.8%	66.3%	0.5%	4.6%	4.8%
2013	18.5%	72.5%	0.5%	3.5%	5.0%
2014	25.2%	66.4%	0.2%	2.8%	5.4%
2015	29.9%	62.5%	0.5%	2.6%	4.5%
2016	22.1%	69.8%	0.0%	2.7%	5.4%
2017	17.6%	65.9%	0.7%	2.9%	12.9%
2018	19.5%	64.3%	0.6%	2.6%	13.0%
2019	29.3%	55.9%	0.2%	3.0%	11.6%
2020	25.9%	57.7%	0.5%	4.4%	11.5%
2021	25.7%	58.7%	0.2%	2.9%	12.5%
2022	24.2%	61.6%	0.0%	0.7%	13.5%
2023	20.0%	57.8%	0.2%	3.2%	18.8%

Table 2.2: Isolations and incidents of *S.* Typhimurium in cattle on all premises in Great Britain

Phage type	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT1	0	0	0	0	0	0	0	0	1	1
DT2	2	2	1	1	6	4	2	2	1	1
DT9	0	0	1	1	0	0	0	0	0	0
DT11	0	0	0	0	1	1	0	0	0	0
DT12	0	0	0	0	0	0	0	0	0	0
DT19	0	0	0	0	0	0	0	0	0	0
DT36	0	0	0	0	1	1	0	0	0	0
DT41	0	0	0	0	0	0	0	0	0	0
DT41b	0	0	1	1	0	0	0	0	0	0
DT46	0	0	0	0	1	1	0	0	0	0
DT75	0	0	0	0	0	0	11	10	28	25
DT104	18	14	15	10	8	6	6	6	6	4
DT105	0	0	0	0	1	1	22	17	33	31
DT109	0	0	0	0	0	0	0	0	1	1
DT116	0	0	10	5	4	3	4	3	0	0
DT120	0	0	0	0	1	1	0	0	0	0
DT189	1	1	1	1	0	0	1	1	0	0
DT193	4	4	2	2	6	3	3	2	5	4
DT204b	1	1	1	1	0	0	0	0	0	0
U289	0	0	0	0	0	0	1	1	0	0
U300	0	0	0	0	2	2	0	0	0	0
U302	1	1	1	1	0	0	0	0	0	0
U308	0	0	1	1	14	11	0	0	0	0
NOPT	4	0	10	10	9	5	6	4	3	2

Phage type	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
RDNC	8	7	1	1	11	7	2	2	4	4
UNTY	15	4	0	0	0	0	0	0	0	0
Total	**54**	**34**	**45**	**35**	**65**	**46**	**58**	**48**	**82**	**73**

Figure 2.6: *Salmonella* Typhimurium DT104 and related strains as a proportion of all isolations of *S*. Typhimurium and in cattle in Great Britain 2003 to 2023

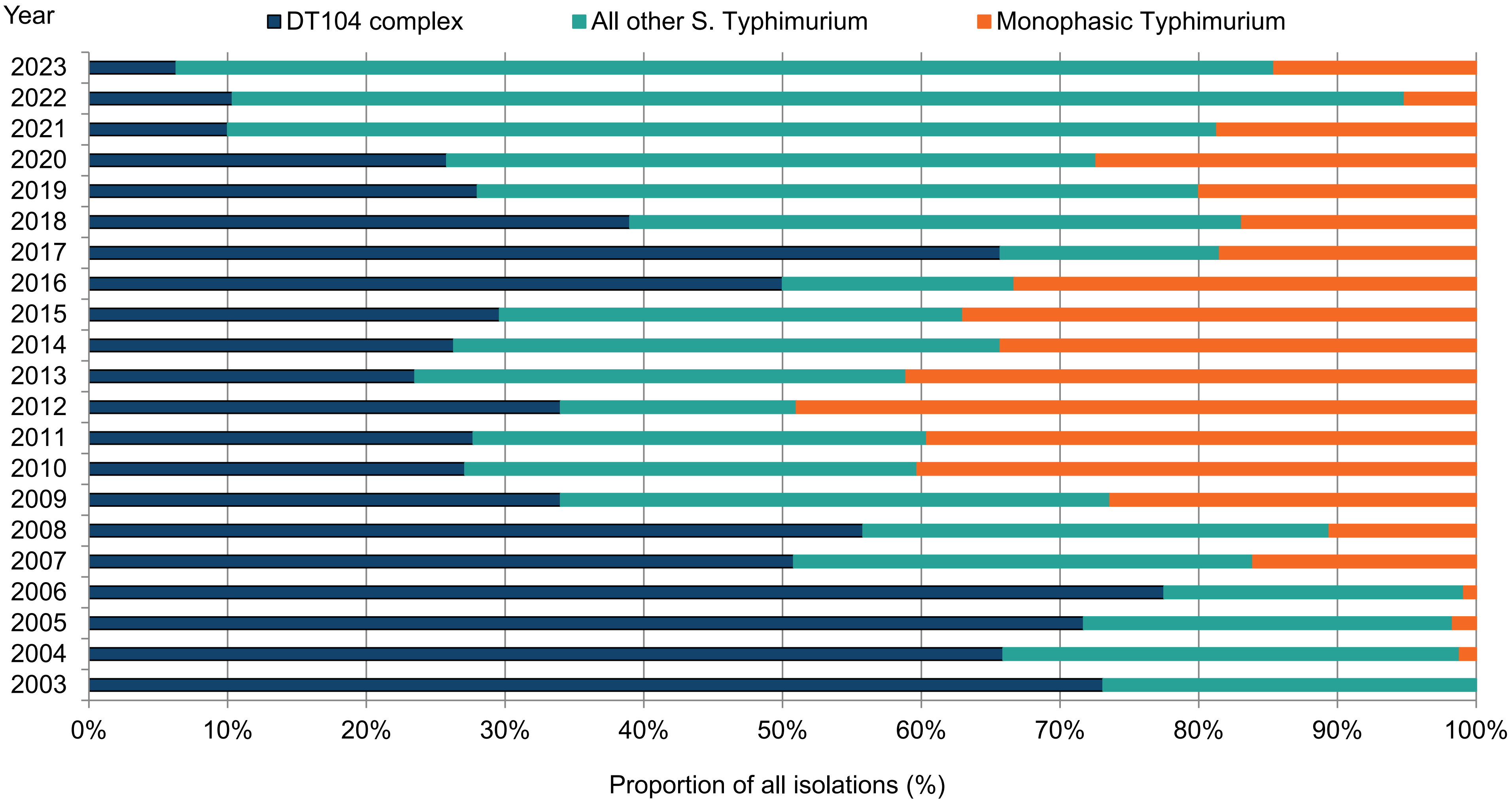


Figure 2.6 shows the proportion of all isolates of *S.* Typhimurium DT104 (and related strains), other *S.* Typhimurium strains and monophasic *S.* Typhimurium in cattle in Great Britain between 2003 and 2023:

- there was a fluctuating but overall decline in the proportion of DT104 complex (including DT104, DT104b, DT12 and U302) across the years with the lowest rates in 2021, 2022 and 2023 (approx. 10% of all isolates)
- all other *S.* Typhimurium showed an increase from 2017 onwards, with the highest proportion of 84.5% in 2022
- monophasic *S.* Typhimurium show wide ranging proportions, following a large increase in 2007

Figure 2.6: Table of data

Year	DT104 complex	All other *S.* Typhimurium	Monophasic *S.* Typhimurium
2003	73.1%	26.9%	0.0%
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%
2019	28.0%	52.0%	20.0%
2020	25.8%	46.8%	27.4%

Year	DT104 complex	All other *S.* Typhimurium	Monophasic *S.* Typhimurium
2021	10.0%	71.3%	18.7%
2022	9.8%	80.3%	4.9%
2023	6.3%	79.2%	14.6%

DT104 complex includes DT104, DT104b, DT12 and U302.

Table 2.3: Monophasic *S*. Typhimurium phage types in cattle in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT1	0	0	0	0	0	0	0	0	1	1
DT191	0	0	0	0	0	0	0	0	1	1
DT120	0	0	0	0	1	1	0	0	0	0
DT193	10	8	11	7	11	10	3	3	7	5
DT194	0	0	3	1	0	0	0	0	0	0
U311	0	0	2	1	0	0	0	0	0	0
NOPT	0	0	0	0	0	0	0	0	1	1
RDNC	0	0	0	0	1	1	0	0	0	0
UNTY	4	4	1	1	2	2	0	0	4	4
Total	**14**	**12**	**17**	**10**	**15**	**14**	**3**	**3**	**14**	**12**

Table 2.4: *S.* Enteritidis phage types in cattle in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
PT5	0	0	0	0	0	0	0	0	1	1
PT8	0	0	0	0	0	0	0	0	0	0
PT11	0	0	1	1	0	0	0	0	0	0
NOPT	1	0	1	1	1	1	0	0	0	0
Total	**1**	**0**	**2**	**2**	**1**	**1**	**0**	**0**	**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 2023, rising from 31.1 million animals in 2022 to 29.8 million animals in 2023 according to the June agricultural census (Figure 3.1). 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, 2021, 2022 and 2023 data with previous years.

There were 5,979 ovine diagnostic submissions recorded on the VIDA database in Great Britain in 2023 compared to 6,076 in 2022, a decrease of 1.6%. This continues the decreasing trend in submission numbers seen since 2016 (with the exception of 2020 when submissions increased). Surveillance data, including clinical signs, age and country information, associated with diagnoses of salmonellosis in sheep can be accessed through the Sheep Dashboard | Tableau Public link.

A total of 98 isolations of *Salmonella* were reported from sheep in 2023. This figure is comparable to 2022 (94 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 to be isolated from sheep in 2023 (Figure 3.2). It was isolated on 65 occasions, one of the highest recorded compared to previous years but well within the annual range of 37 to 109 isolations seen since 2008. *Salmonella* Montevideo (13 isolations), *S.* Typhimurium (12 isolations), and *S.* Dublin (4 isolations) were the next most commonly isolated serovars. Although the number of isolations of these 3 serovars fluctuates year on year, they regularly appear in the top 4 most commonly isolated serovars from sheep. *Salmonella* Montevideo and *S.* Typhimurium showed increased isolations compared to 2022, with *S.* Dublin slightly fewer isolations compared to 2022; however, isolation numbers were within the typical range seen for each serovar in previous 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 2023 there were 65 isolations, accounting for 66.3% of the total isolations obtained from sheep samples (Figure 3.2). This is comparable to the percentage contribution of this serovar in 2022 (69.1%), which was higher than the preceding 4 years. *Salmonella 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 pathogenicity 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 2023, diarrhoea and abortion were the most common presenting signs. Clinical signs recorded in other cases were sudden death and malaise. Concurrent diagnoses included parasitic gastroenteritis and meningitis or encephalitis.

Salmonella Montevideo

As in 2019 and 2021 *Salmonella* Montevideo was the second most commonly isolated serovar from sheep in 2023, with a total of 13 isolations accounting for 13.3% of all isolations from sheep (Figure 3.2). 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 Typhimurium and monophasic *Salmonella* Typhimurium

Since the start of 2023 following the move to whole genome sequencing, the monophasic variants *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- are 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.

Salmonella Typhimurium was the third most common serovar isolated from sheep in 2023, representing 12.2% of the total *Salmonella* isolations (Figure 3.2). Isolations were higher this year compared to 2022 (12 versus 8) but were still within the range seen for this serovar over the preceding 4 years (4 to 17 isolations). This year, the most common reasons for submission were wasting or sudden death. Cases were most commonly reported in adult animals, however post-weaned lambs and one neonatal lamb were also recorded.

Phage-typing was carried out on all 12 *S.* Typhimurium isolates from sheep in 2023 (Table 3.3). Phage-type DT75 predominated (5 isolates) with DT105 being the second most identified phage-type (4 isolates). There were no records of the previously reported predominant phage-types DT104 and U308 in 2023. One other *S.* Typhimurium phage-type was identified this year, U288 (one isolate) which was last reported from sheep in Great Britain in 2004. Two isolates were not phage typed (NOPT).

There was one isolation of monophasic *S.* Typhimurium in 2023 which was not phage typed (NOPT). This is comparable to other single monophasic variant isolations in 2019 and 2021 (both NOPT).

Salmonella Dublin

There were 4 isolations of *S.* Dublin in sheep in 2023, representing 4.1% of the total sheep *Salmonella* isolations (Figure 3.2) making it the fourth most common serovar. Although typically a cattle adapted strain, infection in sheep predominately causes abortion, diarrhoea and sudden deaths.

Other serovars

Other serovars reported in sheep as single isolations during 2023 included *S.* Infantis (last reported from sheep in GB in 2010) and *S.* Ohio (single reports in 2020 and 2022). *S.* Derby (also reported in 2021 and 2022) was also isolated, associated with abortion in an adult ewe.

There were no isolations of *Salmonella* Agama in 2023, differing from the previous 3 years when a single isolation was made each year. This serovar is typically associated with badgers.

Goats

The Great Britain goat population fell slightly in 2023 to 109,534, compared to 107,824 in 2021 (June 2023 Agricultural Census).

There were 444 diagnostic submissions from goats recorded on the VIDA database in 2023 compared to 502 in 2022, a decrease of 11.6%.

Salmonellae are seldom isolated from goats, in most years single or zero isolations are reported. There was one isolation of *Salmonella* in goats during 2023. This was *Salmonella enterica* subspecies *diarizonae* 61:k:1,5,(7) which has been isolated from goats in previous years.

Figure 3.1: Sheep population and number of holdings with sheep in Great Britain 2014 to 2023

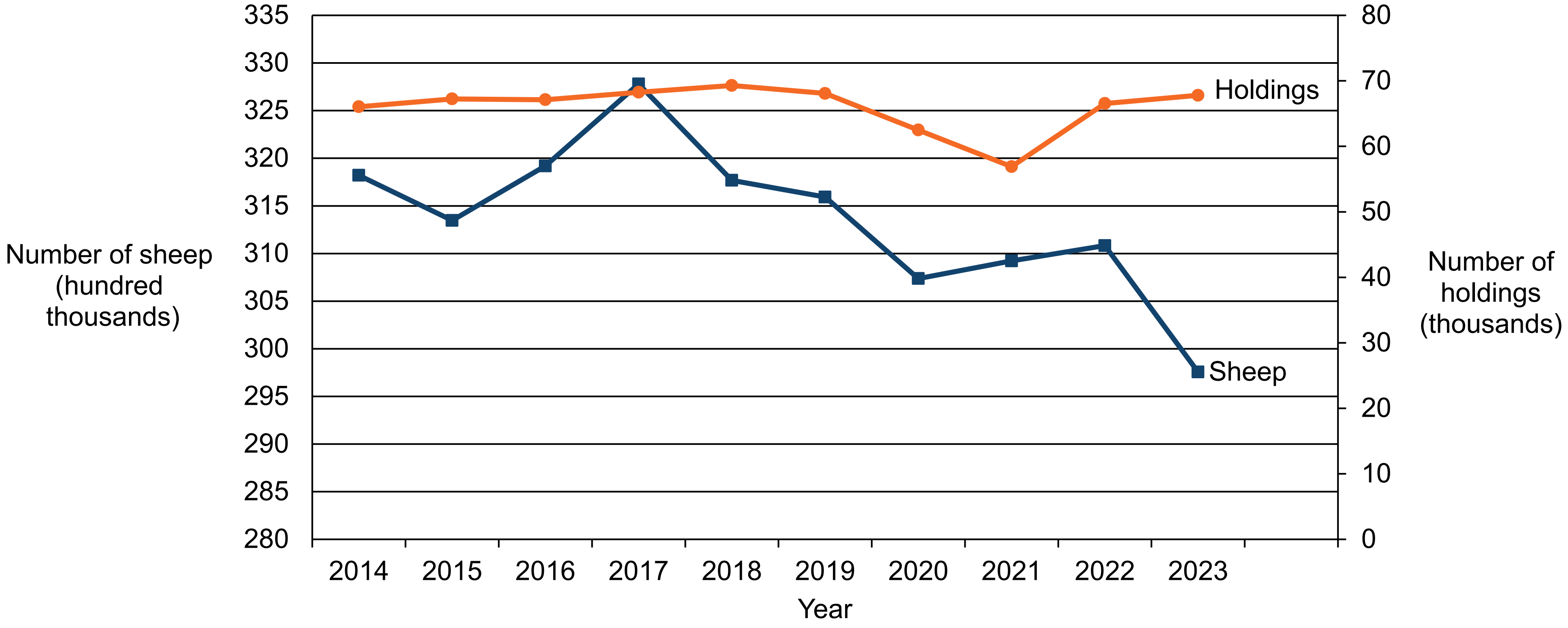


Figure 3.1 shows a relatively constant level of sheep holdings until 2019 when it starts to decline but with an upturn in 2022 and 2023 to 67,791 holdings in 2023. The number of sheep in Great Britain increased peaking in 2017 with approximately 32,600,000 after which it declined until 2020 before increasing again to approximately 31,000,000 until 2022. Numbers in 2023 declined sharply to approximately 29,800,000.

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

Number of holdings in 2020 is estimated. Source: June 2023 Agricultural Census

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

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Agama	4	4	1	1	1	1	1	1	0	0
Ajiobo	0	0	0	0	1	1	0	0	0	0
Anatum	0	0	0	0	1	1	0	0	0	0
Berta	0	0	1	1	0	0	0	0	0	0
Derby	0	0	0	0	1	1	1	1	1	1
Dublin	6	6	10	9	14	12	5	4	4	4
Enteritidis	0	0	0	0	0	0	2	2	0	0
Indiana	0	0	0	0	1	1	0	0	0	0
Infantis	0	0	0	0	0	0	0	0	1	1
Kingston	1	1	0	0	0	0	1	1	0	0
Mbandaka	1	1	0	0	1	1	0	0	0	0
Monophasic Typhimurium	1	1	0	0	1	1	2	2	1	1
Montevideo	16	13	3	3	28	18	5	5	13	10
Newport	1	1	1	1	0	0	0	0	0	0
Ohio	0	0	1	1	0	0	1	1	1	1
Stourbridge	0	0	0	0	1	1	0	0	0	0
Typhimurium	4	2	8	5	17	13	8	8	12	11
61:k:1,5	5	4	10	10	37	35	4	4	12	12
61:k:1,5,7	9	9	4	4	2	2	15	13	52	51
61:-:1,5	10	7	15	15	30	29	0	0	0	0
61:-:1,5,7	35	31	16	16	0	0	46	44	1	1

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
untypable strains	10	10	7	5	8	8	1	1	0	0
rough strains	0	0	0	0	0	0	2	2	0	0
Total	**103**	**90**	**77**	**71**	**144**	**125**	**94**	**89**	**98**	**93**

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

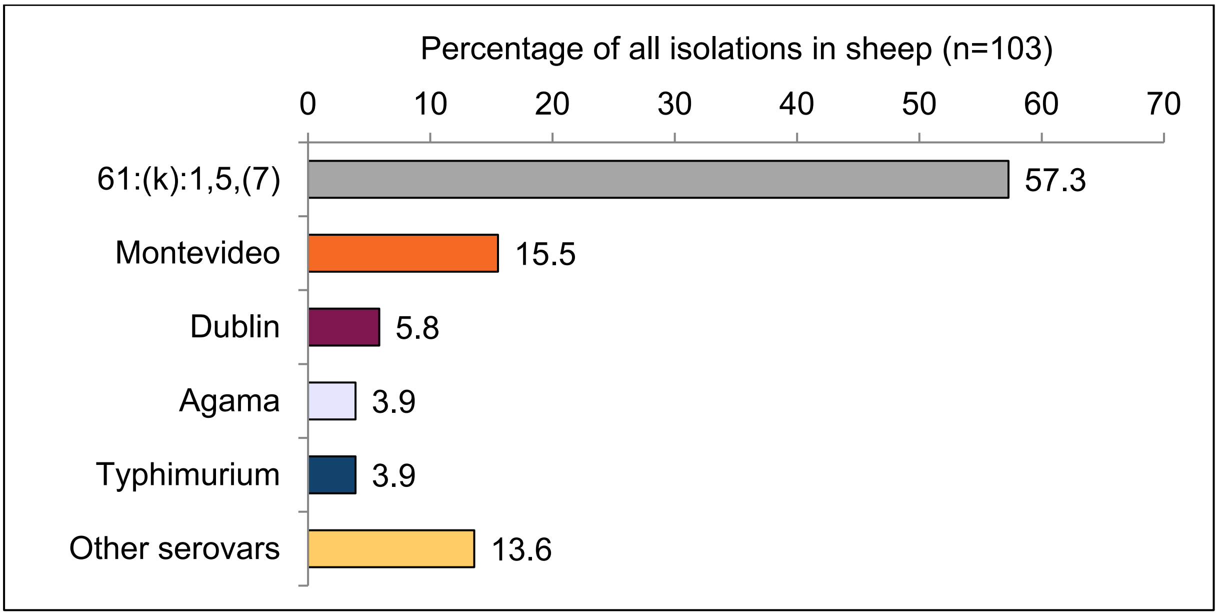
Table 3.2: Isolations and incidents of *Salmonella* in goats on all premises in Great Britain

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Dublin	0	0	1	1	1	1	0	0	0	0
61:k:1,5	0	0	0	0	1	1	1	1	0	0
61:k:1,5,7	0	0	0	0	0	0	0	0	1	1
61:-:1,5,7	0	0	0	0	0	0	1	1	0	0
untypable strains	1	1	0	0	0	0	0	0	0	0
Total	**1**	**1**	**1**	**1**	**2**	**2**	**2**	**2**	**1**	**1**

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

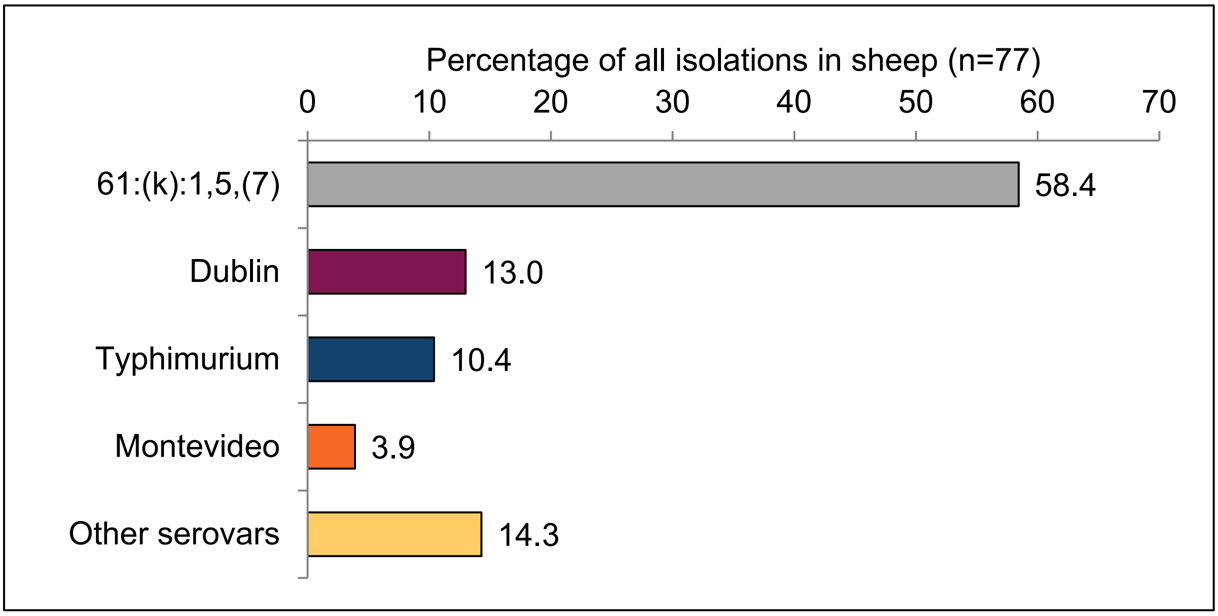
Figure 3.2: Isolations of the most common serovars in sheep in Great Britain 2019 to 2023

Figure 3.2.1: Isolations in 2019



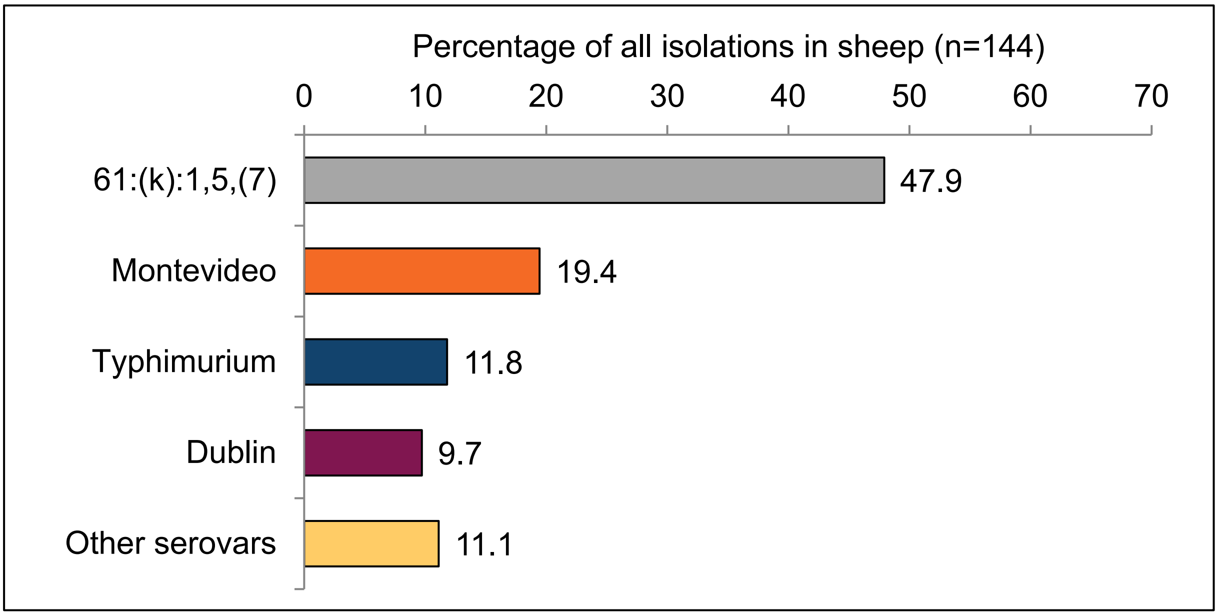
The most common serovar in sheep in 2019 was *Salmonella* 61:(k):1,5,(7) (57.3% of isolations), followed by *S*. Montevideo (15.5% of isolations), *S*. Dublin (5.8% of isolations) and *S*. Agama (3.9% of isolations).

Figure 3.2.2: Isolations in 2020



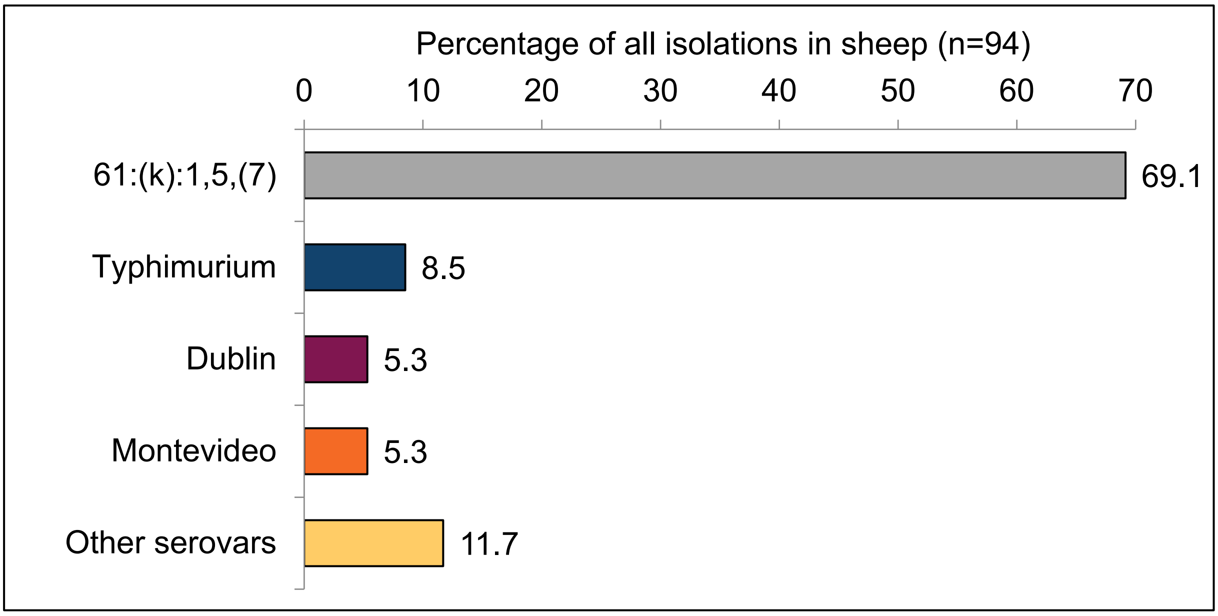
The most common serovar in sheep in 2020 was *Salmonella* 61:(k):1,5,(7) (58.4% of isolations), followed by *S*. Dublin (13.0% of isolations), *S*. Typhimurium (10.4% of isolations) and *S*. Montevideo (3.9% of isolations).

Figure 3.2.3: Isolations in 2021



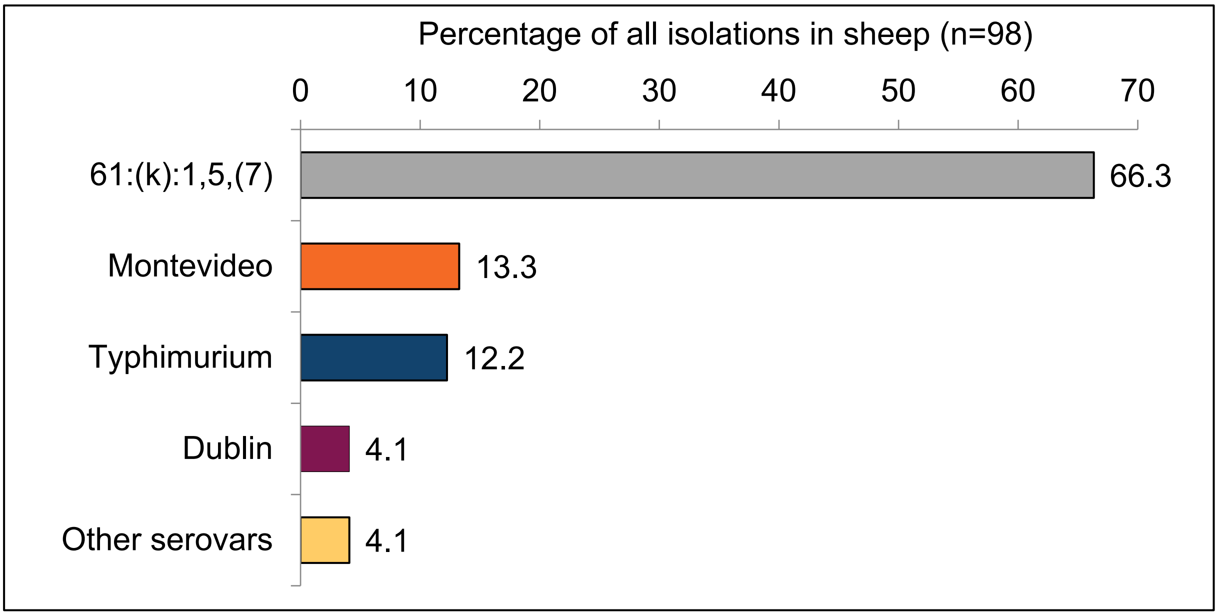
The most common serovar in sheep in 2021 was *Salmonella* 61:(k):1,5,(7) (47.9% of isolations), followed by *S*. Montevideo (19.4% of isolations), *S*. Typhimurium (11.8% of isolations) and *S*. Dublin (9.7% of isolations).

Figure 3.2.4: Isolations 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 (5.3% of isolations) and *S.* Montevideo (5.3% of isolations).

Figure 3.2.5: Isolations 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).

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

Figure 3.3 The 5 most common *Salmonella* serovars in sheep in Great Britain in 2023 and their trends over time since 2019

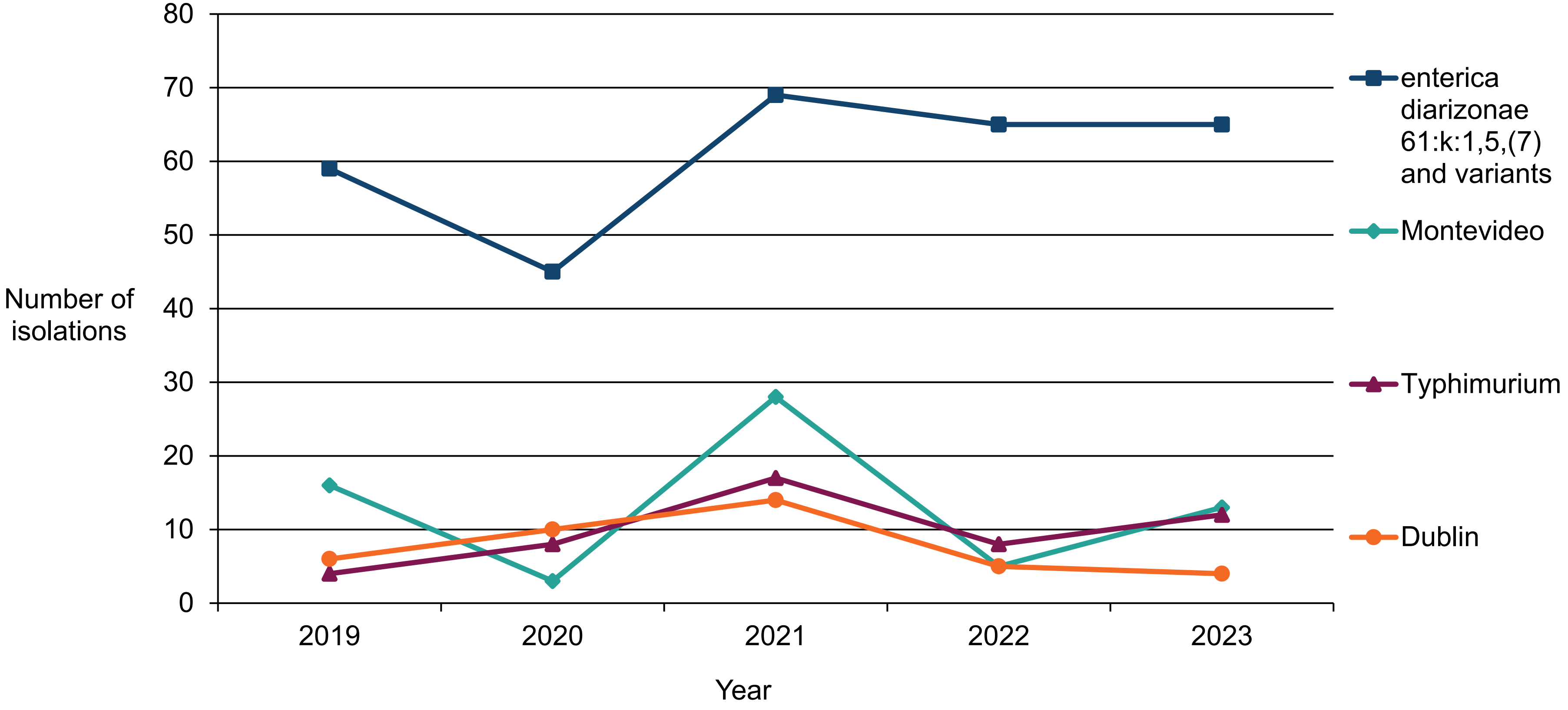


Figure 3.3 shows the most common serovar in sheep for all years was *S.* enterica diarizonae 61:k:1,5,(7) and its variants with 65 isolations in 2022 and 2023. There were increases in the isolations of the next 3 most common serovars in 2023 compared to 2022. *Salmonella* Montevideo was the second most common serovar isolated in 2023 with 13 isolations, followed by *S.* Typhimurium with 12 isolations and *S.* Dublin with 4 isolations in 2023.

Table 3.3: Isolations and incidents of *S.* Typhimurium in sheep on all premises in Great Britain

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT2	0	0	2	1	0	0	0	0	0	0
DT75	0	0	0	0	0	0	2	2	5	5
DT104	1	0	4	3	3	2	1	1	0	0
DT105	0	0	0	0	0	0	2	2	4	3
DT116	0	0	0	0	2	2	0	0	0	0
U288	0	0	0	0	0	0	0	0	1	1
U289	0	0	0	0	0	0	1	1	0	0
U300	0	0	0	0	1	1	0	0	0	0
U308	0	0	0	0	10	7	1	1	0	0
U320	2	1	0	0	0	0	0	0	0	0
NOPT	0	0	0	0	1	1	0	0	2	2
RDNC	0	0	2	1	0	0	1	1	0	0
UNTY	1	1	0	0	0	0	0	0	0	0
Total	**4**	**2**	**8**	**5**	**17**	**13**	**8**	**8**	**12**	**11**

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 2003 to 2023

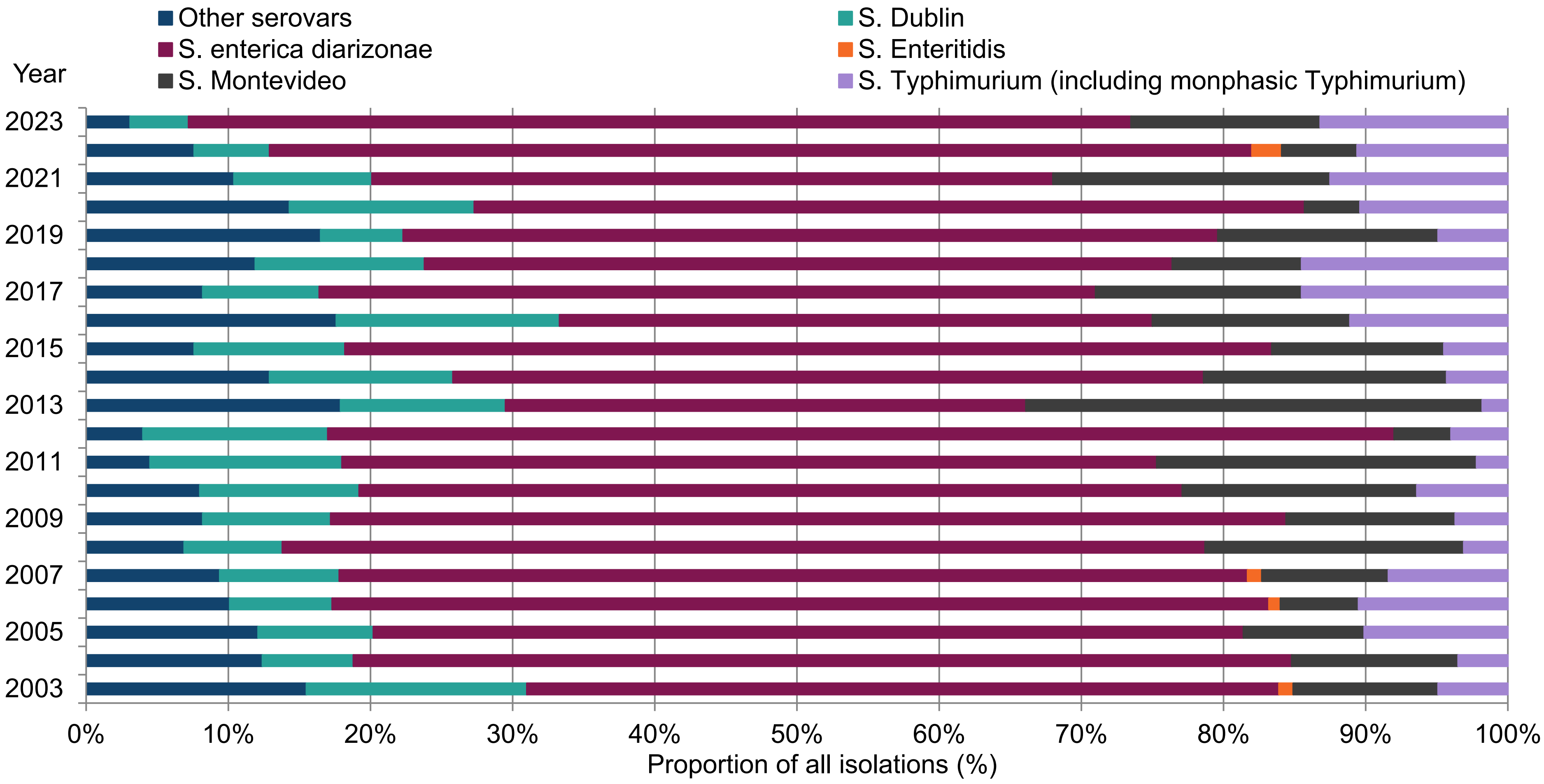


Figure 3.4 shows the proportion of all isolates of *S*. Dublin, *S*. enterica diarizonae, *S*. Enteritidis, *S*. Montevideo, *S*. Typhimurium and monophasic *S.* Typhimurium in sheep in Great Britain between 2003 and 2023:

- *S*. enterica diarizonae accounted for the greatest proportion of isolates but rates remained stable across the years at 36% to 75%
- *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 19.0% of isolations in 2002 but has since declined and made up 4.1% in 2023
- *S*. Typhimurium (including monophasic variants) increased as a proportion of the total until 2017 when it accounted for 14.5% but declined in 2022 to 10.6% which has risen to 13.2% in 2023
- *S.* Enteritidis was also more variable and was only isolated in 2003, 2006, 2007 and 2022
- other serovars have accounted for between 3.1% and 17.9% since with fluctuations year on year

Figure 3.4 table of data

Year	Other serovars	*S.* Dublin	*S. enterica diarizonae*	*S.* Enteritidis	*S.* Montevideo	*S.* Typhimurium (including monophasic Typhimurium)
2003	15.5%	15.5%	52.9%	1.0%	10.2%	4.9%
2004	12.4%	6.4%	66.0%	0.0%	11.7%	3.5%
2005	12.1%	8.1%	61.2%	0.0%	8.5%	10.1%
2006	10.1%	7.2%	65.9%	0.8%	5.5%	10.5%
2007	9.4%	8.4%	63.9%	1.0%	8.9%	8.4%
2008	6.9%	6.9%	64.9%	0.0%	18.2%	3.1%
2009	8.2%	9.0%	67.2%	0.0%	11.9%	3.7%
2010	8.0%	11.2%	57.9%	0.0%	16.5%	6.4%
2011	4.5%	13.5%	57.3%	0.0%	22.5%	2.2%
2012	4.0%	13.0%	75.0%	0.0%	4.0%	4.0%
2013	17.9%	11.6%	36.6%	0.0%	32.1%	1.8%

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

Chapter 4: Reports of *Salmonella* in pigs

Compared with 2022, there was a decrease of 10.7% in the total Great Britain pig herd in 2023 to just over 4 million animals according to the 2023 agricultural census (Figure 4.1).

There remains no current national scheme for monitoring *Salmonella* on pig farms in Great Britain 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, in which *Salmonella* may be the causal pathogen, or a secondary incidental finding. Where it is considered the cause of disease in APHA submissions, it is recorded as a salmonellosis diagnosis in the Veterinary Investigation Diagnoses Analysis (VIDA) database. Surveillance data, including clinical signs, pig age and country information, associated with diagnoses of salmonellosis in pigs can be accessed through the Great Britain disease surveillance dashboard.

There was an increase (16.9%) in the total number of pig submissions from Great Britain to APHA and SRUC during 2023 (3,818 submissions) compared to 2022 (3,267 submissions). Similarly, there was an increase (20.2%) in diagnostic pig submissions during 2023 (1,732 submissions) compared to 2022 (1,441 submissions).

There were 258 isolations of *Salmonella* from 238 *Salmonella* incidents in pigs in 2023. This is higher than in recent years 2019 to 2022 in which the number of isolations ranged from 167 to 223 and the number of incidents ranged from 156 to 206. The different serovars isolated, are detailed in Table 4.1 and Figure 4.2.

Salmonella Typhimurium and monophasic *S.* Typhimurium

Since the start of 2023 following the move to whole genome sequencing, the monophasic variants *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- are 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.

As in previous years, isolations of *S*. Typhimurium and its monophasic variants together accounted for the majority of isolations of *Salmonella* from pigs in 2023 (77.5% of all isolations from pigs, Figures 4.2, 4.3 and 4.4). This has reversed the downward trend in isolations in this category in 2021 (73.1%) and 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 2023 was *S*. Typhimurium (139 isolations). This is increased from 2022 (100 isolations) and is also higher than the 3 previous years 2019 to 2021 (Table 4.1).

Phage type U308a was the most commonly isolated phage type of *S*. Typhimurium in 2023, increasing since 2022 (46 versus 18 isolations) and having been first reported from surveillance in pigs in Great Britain in 2021. This was followed by DT193 (31 isolations) and DT32 (22 isolations). This contrasts with 2022 when the most common phage type was DT193 with U308a and DT32 as second and third most frequently identified respectively (Table 4.2). Two *S.* Typhimurium phage types identified in 2023, namely DT11 and DT20, have not been recorded previously in pigs in Great Britain.

The next most common *Salmonella* serovar isolated from pigs in 2023 was monophasic *S.* Typhimurium (61 isolations) which represents 23.7% of total pig isolations in 2023. Isolations of monophasic *S*. Typhimurium increased compared to 2022 (51 isolations), having been on a downward trend in recent years (Figure 4.2 and 4.3).

Of the monophasic *S.* Typhimurium isolations that could be phage typed in 2023, 93.5% (43 of 46) 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 3 non-DT193 phage types of monophasic *S*. Typhimurium isolations were DT120 (x1), DT194 (x1) and U302 (x1). Monophasic *S*. Typhimurium DT194 has never previously been isolated from pigs in GB.

Other serovars

Other frequently isolated serovars from pigs in 2023 were *S*. Newport (18 isolations) and *S*. Derby (17 isolations), with similar numbers of isolations to 2022 (Table 4.1 and Figure 4.2). *S*. Panama was also frequently isolated (10 isolations), with isolations of this serovar increasing since 2019.

Twelve different serovars were identified in 2023 (Table 4.1). Two serovars, *S*. Cerro and *S*. Chester, were detected in 2023 which have never previously been identified in pigs in Great Britain. Of interest, there were 2 isolations of *S.* Rissen which was last detected in pigs in GB in 2018.

There were no isolations of *S*. Enteritidis in 2023, which was last isolated on one occasion in pigs in 2019 (phage type 11) (Tables 4.1 and 4.3).

Figure 4.1: Pig population and number of holdings with pigs in Great Britain 2014 to 2023

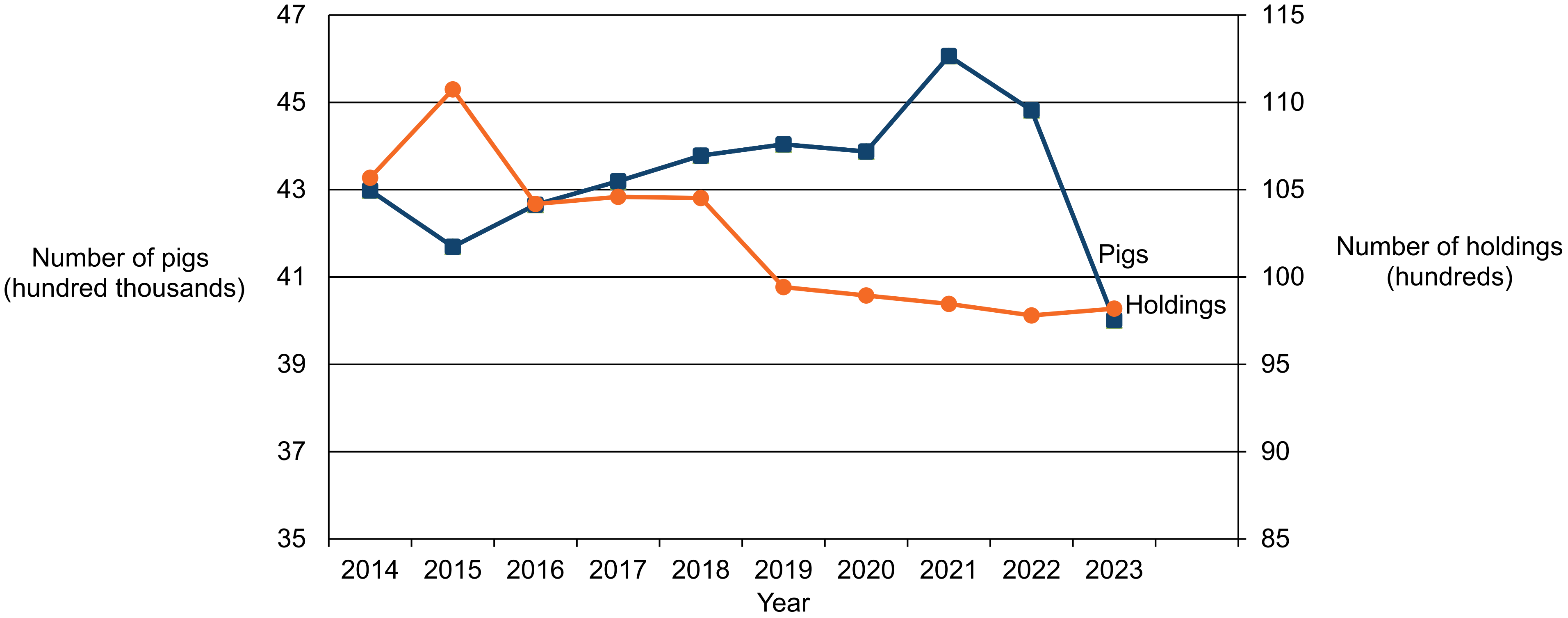


Figure 4.1 above shows a variable number of pig holdings until 2019 when it starts to slowly decline until 2022 before increasing slightly to around 9800. The number of pigs in Great Britain increased until 2021 after which there was a decline in 2022 before decreasing sharply in 2023 to just over 4 million (4,000,980). Data is sourced from the June 2021 and 2022 Agricultural Census.

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

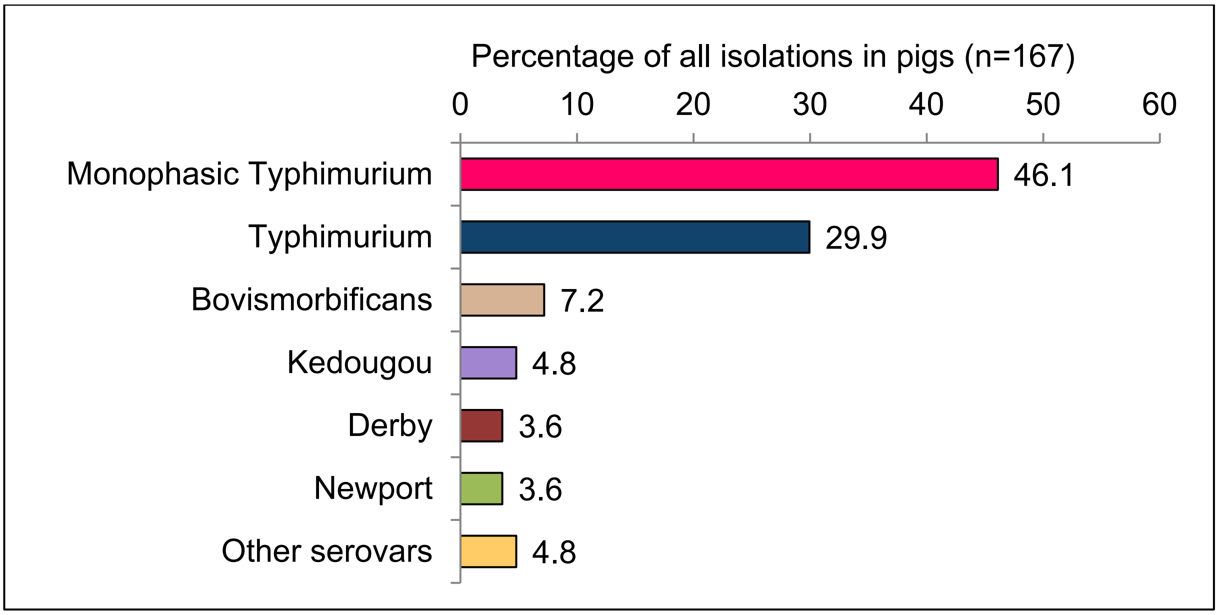
The number of holdings in 2020 is estimated.

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

Salmonella **serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Bardo	0	0	1	1	0	0	0	0	0	0
Bovismorbificans	12	10	5	5	7	6	2	2	2	2
Cerro	0	0	0	0	0	0	0	0	1	1
Chester	0	0	0	0	0	0	0	0	1	1
Derby	6	5	12	11	17	16	15	13	17	16
Dublin	0	0	0	0	1	1	0	0	0	0
Enteritidis	1	1	0	0	0	0	0	0	0	0
Indiana	0	0	1	1	2	1	0	0	0	0
Kedougou	8	8	1	1	1	1	3	2	3	3
Livingstone	1	1	0	0	1	1	0	0	0	0
London	1	1	5	5	5	5	7	6	2	2
London var 15⁺	0	0	0	0	0	0	1	1	0	0
Monophasic Typhimurium	77	72	65	62	63	57	51	44	61	59
Newport	6	6	7	7	19	18	20	19	18	16
Panama	1	1	2	2	4	4	10	9	10	10
Reading	1	1	2	2	2	2	3	3	2	2
Rissen	0	0	0	0	0	0	0	0	2	2
Typhimurium	50	47	83	76	100	93	100	97	139	124
Uganda	1	1	0	0	0	0	0	0	0	0
rough strains	0	0	3	3	1	1	0	0	0	0
untypable strains	2	2	2	2	0	0	2	2	0	0
Total	**167**	**156**	**189**	**178**	**223**	**206**	**214**	**198**	**258**	**238**

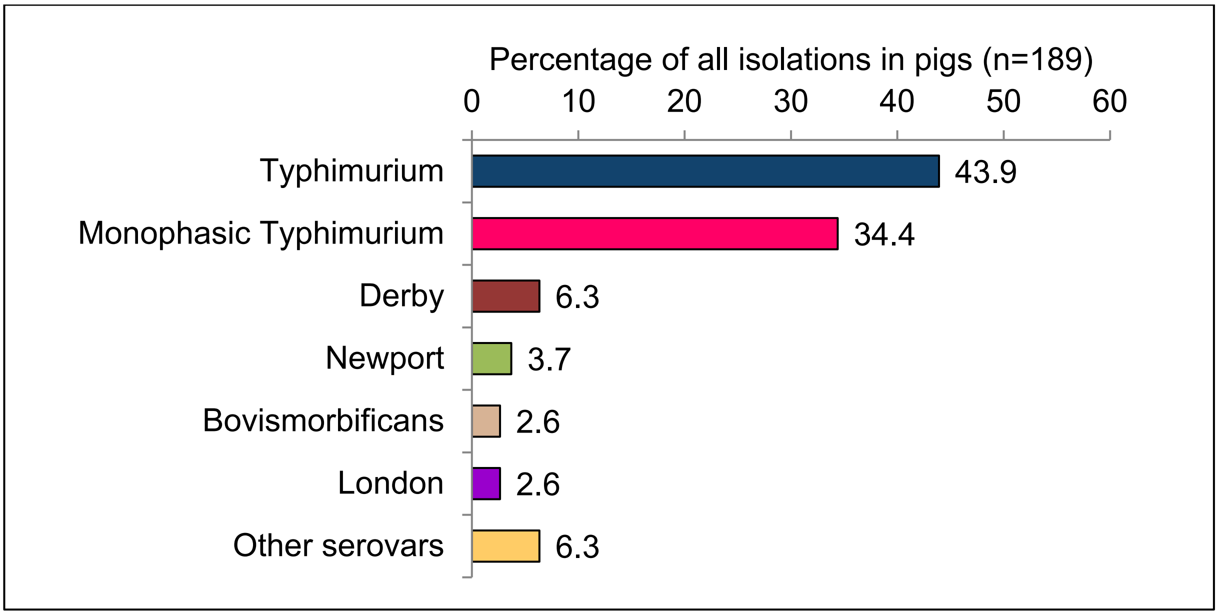
Figure 4.2: Isolations of the most common serovars in pigs in Great Britain 2019 to 2023

Figure 4.2.1: Isolations in 2019



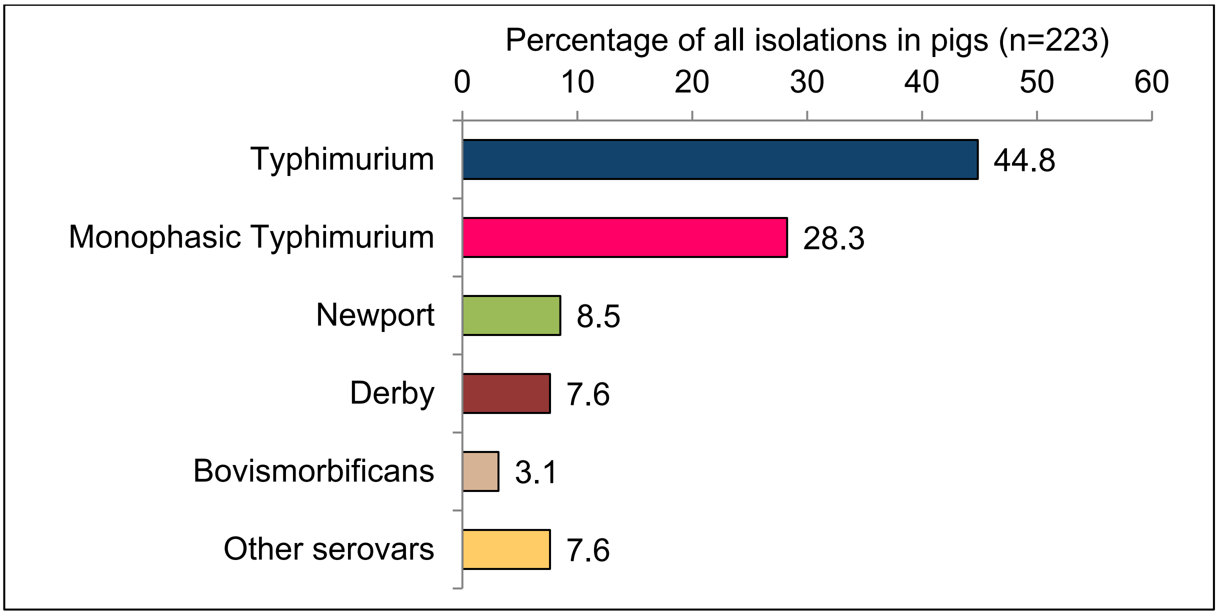
The most common serovar in pigs in 2019 was monophasic *Salmonella* Typhimurium (46.1% of isolations), followed by *S.* Typhimurium (29.9% of isolations) and *S.* Bovismorbificans (7.2% of isolations).

Figure 4.2.2: Isolations in 2020



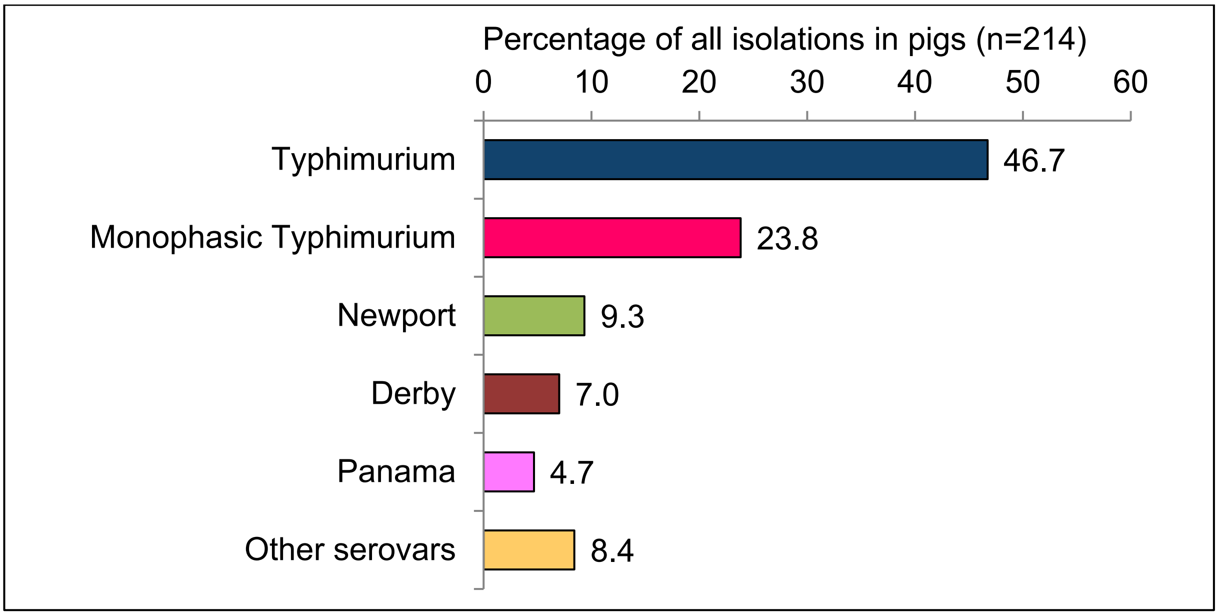
The most common serovar in pigs in 2020 was *S.* Typhimurium (43.9% of isolations), followed by monophasic *Salmonella* Typhimurium (34.4% of isolations) and *S.* Derby (6.3% of isolations).

Figure 4.2.3: Isolations in 2021



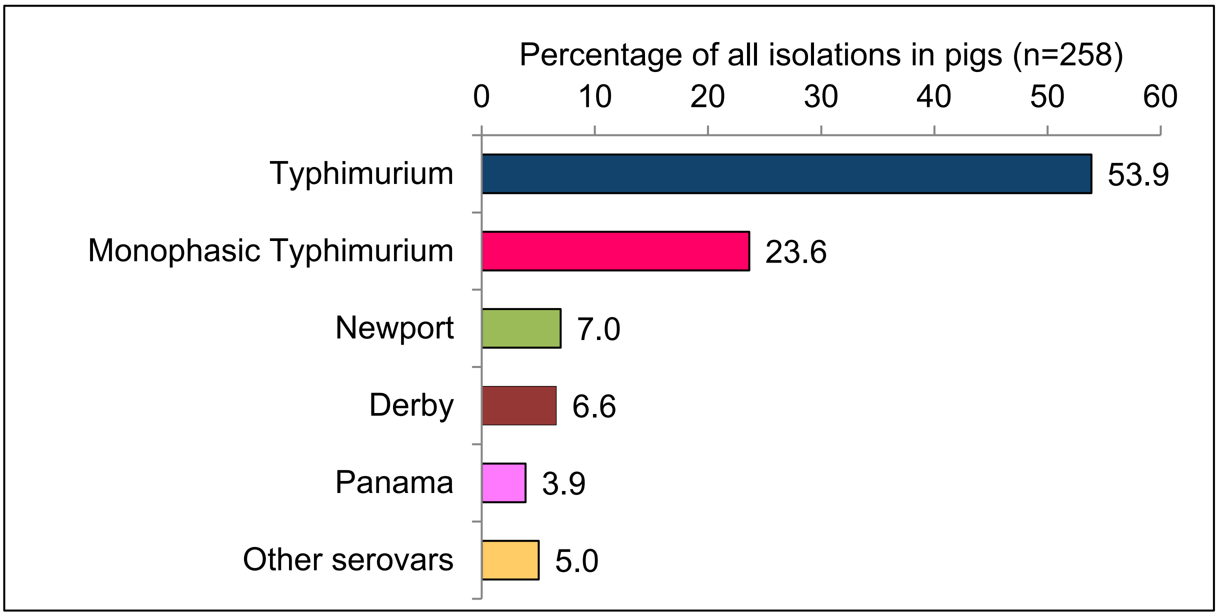
The most common serovar in pigs in 2021 was *S.* Typhimurium (44.8% of isolations), followed by monophasic *Salmonella* Typhimurium (28.3% of isolations) and *S.* Newport (8.5% of isolations).

Figure 4.2.4: Isolations 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 4.2.5: Isolations in 2023



The most common serovar in pigs in 2023 was *S.* Typhimurium (53.9% of isolations), followed by monophasic *S.* Typhimurium (23.6% of isolations) and *S.* Newport (7.0% of isolations).

Figure 4.3: The 5 most common *Salmonella* serovars in pigs in Great Britain in 2023 and their trends over time since 2019

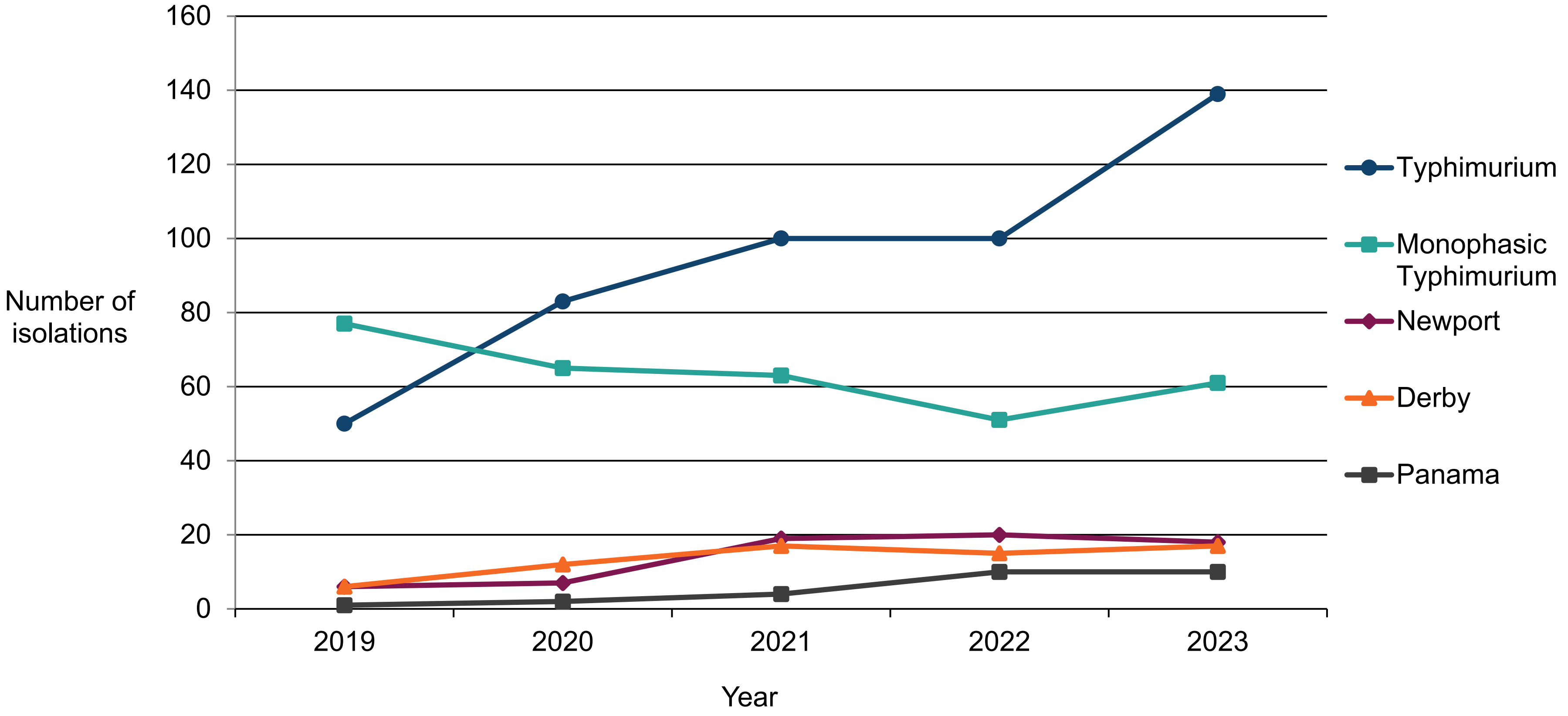


Figure 4.3 shows the most common serovars in pigs for all years was *S.* Typhimurium peaking at 1390 isolations in 2023. The number of isolations of the monophasic *S.* Typhimurium (4,12:i:- and 4,5,12:i:-) decreased until 2022 but increased to 61 isolations in 2023, isolations of *S.* Newport and *S.* Derby were similar to 2022 at below 30 isolations in 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 2003 to 2023

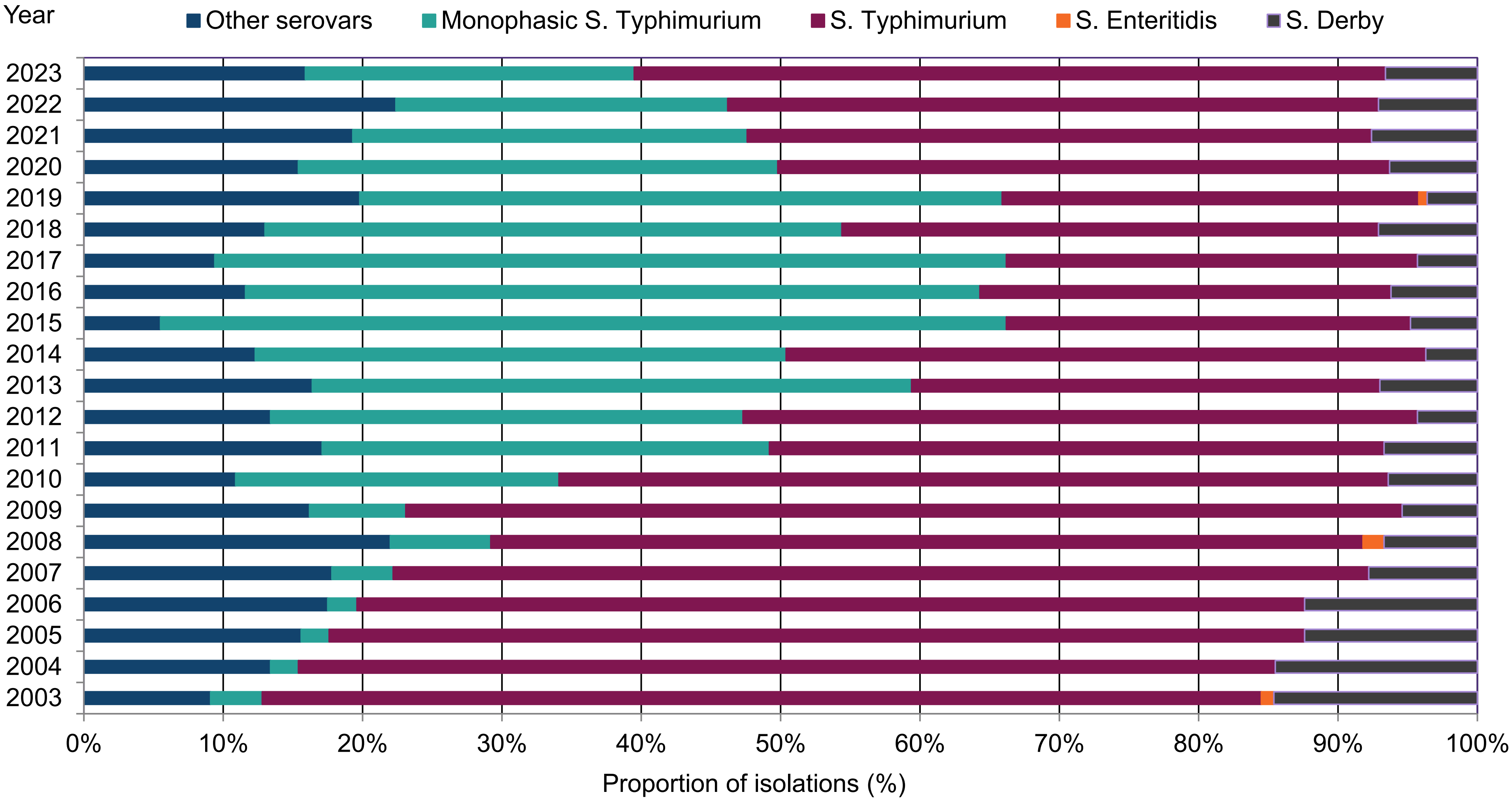


Figure 4.4 shows that as a proportion of all isolates in pigs in Great Britain between 2003 and 2023:

- *S.* Typhimurium accounted for the greatest proportion of isolates 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 23.6% in 2023
- Isolations of *S.* Derby decreased as a proportion of the total from a high of 14.6% in 2003 to 7.1% in 2023
- With the exception of 2003, 2008 and 2019 *S.* Enteritidis has not been isolated from pigs.
- Other serovars have accounted for between 1.4% and 22.4% since 2002 with fluctuations year on year

Figure 4.4: Table of data

Year	Other serovars	Monophasic *S.* Typhimurium	*S.* Typhimurium	*S.* Enteritidis	*S.* Derby
2003	9.1%	3.7%	71.7%	0.9%	14.6%
2004	13.4%	2.0%	70.1%	0.0%	14.5%
2005	15.6%	2.0%	70.0%	0.0%	12.4%
2006	17.5%	2.1%	68.0%	0.0%	12.4%
2007	17.8%	4.4%	70.0%	0.0%	7.8%
2008	22.0%	7.2%	62.6%	1.5%	6.7%
2009	16.2%	6.9%	71.5%	0.0%	5.4%
2010	10.9%	23.2%	59.5%	0.0%	6.4%
2011	17.1%	32.1%	44.1%	0.0%	6.7%
2012	13.4%	33.9%	48.4%	0.0%	4.3%
2013	16.4%	43.0%	33.6%	0.0%	7.0%
2014	12.3%	38.1%	45.9%	0.0%	3.7%
2015	5.5%	60.7%	29.0%	0.0%	4.8%
2016	11.6%	52.7%	29.5%	0.0%	6.2%
2017	9.4%	56.8%	29.5%	0.0%	4.3%
2018	13.0%	41.4%	38.5%	0.0%	7.1%
2019	19.8%	46.1%	29.9%	0.6%	3.6%
2020	15.4%	34.4%	43.9%	0.0%	6.3%
2021	19.3%	28.3%	44.8%	0.0%	7.6%
2022	22.4%	23.8%	46.7%	0.0%	7.1%
2023	15.9%	23.7%	53.9%	0.0%	6.6%

Table 4.2: Isolations and incidents of *S*. Typhimurium in pigs on all premises in Great Britain

Phage Types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT4	0	0	5	5	5	4	6	6	2	2
DT8	0	0	0	0	1	1	0	0	0	0
DT9	0	0	0	0	2	2	4	3	0	0
DT20	0	0	0	0	0	0	0	0	3	3
DT11	0	0	0	0	0	0	0	0	1	1
DT32	2	2	0	0	2	2	16	16	22	16
DT52	0	0	0	0	1	1	1	1	0	0
DT104	1	1	4	4	0	0	1	1	5	5
DT105	0	0	0	0	0	0	2	2	7	6
DT118	0	0	0	0	0	0	1	1	0	0
DT120	0	0	0	0	1	1	2	2	5	5
DT181	0	0	0	0	0	0	1	1	3	3
DT193	17	17	26	26	27	27	27	25	31	30
DT204b	0	0	1	1	0	0	0	0	0	0
U288	22	21	36	33	36	35	6	6	4	4
U302	4	4	1	1	0	0	0	0	0	0
U308	0	0	1	1	8	6	3	3	8	8
U308a	0	0	0	0	7	7	18	18	46	39
U323	0	0	1	1	0	0	0	0	0	0
NOPT	2	0	2	0	2	1	0	0	0	0
RDNC	1	1	5	3	8	6	12	12	2	2
UNTY	1	1	1	1	0	0	0	0	0	0
Total	**50**	**47**	**83**	**76**	**100**	**93**	**100**	**97**	**139**	**124**

Table 4.3: Monophasic *S.* Typhimurium phage types in pigs in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT120	2	2	0	0	3	2	1	1	1	1
DT193	68	64	56	53	48	44	45	39	43	42
DT194	0	0	0	0	0	0	0	0	1	1
DT208	0	0	0	0	1	1	0	0	0	0
U302	1	1	0	0	0	0	0	0	1	1
U311	0	0	0	0	1	1	1	1	0	0
NOPT	1	0	3	3	2	2	0	0	4	3
RDNC	0	0	2	2	2	2	0	0	2	2
UNTY	5	5	4	4	5	4	4	3	9	9
Total	**77**	**72**	**65**	**62**	**62**	**56**	**51**	**44**	**61**	**59**

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

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

Where *Salmonella* is isolated, in APHA submissions, 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.

Since the start of 2023 following the move to whole genome sequencing, the monophasic variants *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- are 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.

Deer

There was one *Salmonella* isolation, *Salmonella* Typhimurium (DT105) from deer during 2023 compared with no isolations during 2020, 2021 or 2022. Prior to that there were 2 isolations in 2019 (*S*. Montevideo and monophasic *S.* Typhimurium). The serovar reported in 2023 was a single isolation of *S*. Typhimurium DT105. APHA received 115 diagnostic submissions from deer in 2023.

Horses

The number of horses recorded as being kept in Great Britain at the June 2023 Agricultural Census was 209,058, which is a decrease of 1.5% compared to 2022 (212,211 animals). Of note the 2022 census data published in the 2022 report differs slightly due to the need to base figures on an estimation at the time of publication.

There were 55 isolations of *Salmonella* from horses during 2023, 54 isolations were from clinical disease investigations and one isolation resulted from voluntary surveillance. This represents an 8.3% decrease compared to the total number of isolations recorded from horses during 2022 (60 isolations) and 22.2% more than in 2021 (45 isolations). As companion animals, horses are a potential source of infection to their keepers, the zoonotic implications of salmonellosis in horses must be considered.

The most commonly isolated serovars from horses during 2023 were *S*. Typhimurium (20 isolations, 36.4% of total horse isolations), *S*. Newport (7 isolations, 12.7% of total horse isolations), *S.* Concord (6 isolations, 10.9% of total horse isolations), *S*. Bovismorbificans (3 isolations, 5.5% of total horse isolations), *S.* Infantis (3 isolations, 5.5% of total horse isolations) and *S.* Kingston (3 isolations, 5.5% of total horse isolations). Similarly, during 2022 the most common serovars were *S*. Typhimurium (18 isolations, 30.0% of total horse isolations), followed by *S*. Newport (6 isolations, 10.0% of total horse isolations) and *S*. Agama, *S*. Bovismorbificans, *S*. Enteritidis and *S*. Oslo (4 isolations each, 6.7% of total horse isolations each).

The number of *S.* Typhimurium isolations during 2023 was slightly higher than that reported in 2022 (20 versus 18 isolations) and 2021 (15 isolations). There was one isolation of monophasic *S.* Typhimurium (DT193) in 2023, compared to 2 isolations of monophasic *S.* Typhimurium (both DT104) in 2022, and no isolations in 2021 (Table 5.5).

The 20 isolations of *S*. Typhimurium reported from horses during 2023 comprised 7 different phage types (excluding RDNC) (Table 5.4). The most common phage type was DT75 (5 isolations). This phage type has not been previously identified by APHA in horses in Great Britain and the isolations originated from 5 different incidents. Three incidents stated diarrhoea as the main clinical sign, no information was available for the other 2 incidents. There were 2 isolations each of DT1, DT2 and DT99 and one isolation each of DT104, DT105 and DT193.

There was one isolation of *S*. Enteritidis (PT8) in 2023, a quarter of that seen in 2022 when there were 4 isolations (PT9a x2, PT8 x1 and PT13a x1). The isolation resulted from clinical disease investigation with diarrhoea being the main clinical sign. *S*. Enteritidis PT8 is often associated with feed and poultry.

There were 2 isolations each of *S.* Anatum and *S.* Oslo in 2023 and single isolations each of *S*. Birkenhead, *S*. Braenderup, *S*. Coeln, *S*. Kottbus, *S*. Paratyphi B var. Java and *S*. Sanga, all resulting from clinical disease investigations. Neither *S.* Birkenhead nor *S.* Sanga have been reported in horses previously in Great Britain.

Notably, there were 3 isolations of *S*. Infantis in 2023 which has not been reported in horses since 2017.

There were 6 isolations of *S.* Concord in 2023 compared to no isolations in 2022 and a single isolation in 2021.

There was one isolation of *S*. Fulica in 2023 from a horse imported from the Netherlands. The isolation resulted from clinical disease investigation, though information on clinical signs were not available. This isolation is not reported in the tables and figures of this report.

Rabbits

APHA received 10 diagnostic rabbit submissions in 2023. Of these there were no isolations of *Salmonella*. The last isolations from rabbits were in 2021 (one isolation each of *S.* Fluntern and *S.* Newport). 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

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Monophasic Typhimurium	1	1	0	0	0	0	0	0	0	0
Montevideo	1	1	0	0	0	0	0	0	0	0
Typhimurium	0	0	0	0	0	0	0	0	1	1
Total	**2**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**1**

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

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Fluntern	0	0	0	0	0	0	1	1	0	0
Newport	0	0	0	0	0	0	1	1	0	0
Total	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**2**	**0**	**0**

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

Salmonella **serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Agama	1	1	4	4	0	0	4	4	0	0
Agona	0	0	0	0	1	1	0	0	0	0
Anatum	0	0	2	2	0	0	1	1	2	2
Birkenhead	0	0	0	0	0	0	0	0	1	1
Bovismorbificans	19	11	0	0	16	10	4	4	3	3
Braenderup	0	0	0	0	0	0	1	1	1	1
Coeln	2	2	0	0	0	0	2	2	1	1
Concord	0	0	0	0	1	1	0	0	6	5
Dublin	1	1	0	0	1	1	2	2	0	0
Durham	0	0	0	0	0	0	1	1	0	0
Eboko	0	0	0	0	0	0	3	3	0	0
Enteritidis	5	5	1	1	2	2	4	4	1	1
Hessarek	1	1	0	0	0	0	0	0	0	0
Infantis	0	0	0	0	0	0	0	0	3	2
Javiana	0	0	1	1	0	0	0	0	0	0
Kingston	5	4	3	3	2	2	3	2	3	3
Kottbus	0	0	1	1	1	1	3	3	1	1
Mbandaka	3	2	0	0	0	0	0	0	0	0
Mokola	0	0	1	1	0	0	0	0	0	0
Monophasic Typhimurium	18	8	3	1	0	0	2	1	1	1
Montevideo	0	0	0	0	1	1	0	0	0	0
Newport	12	8	7	6	1	1	6	6	7	7
Oslo	23	7	1	1	1	1	4	4	2	1
Paratyphi B var. Java	0	0	1	1	1	1	0	0	1	1

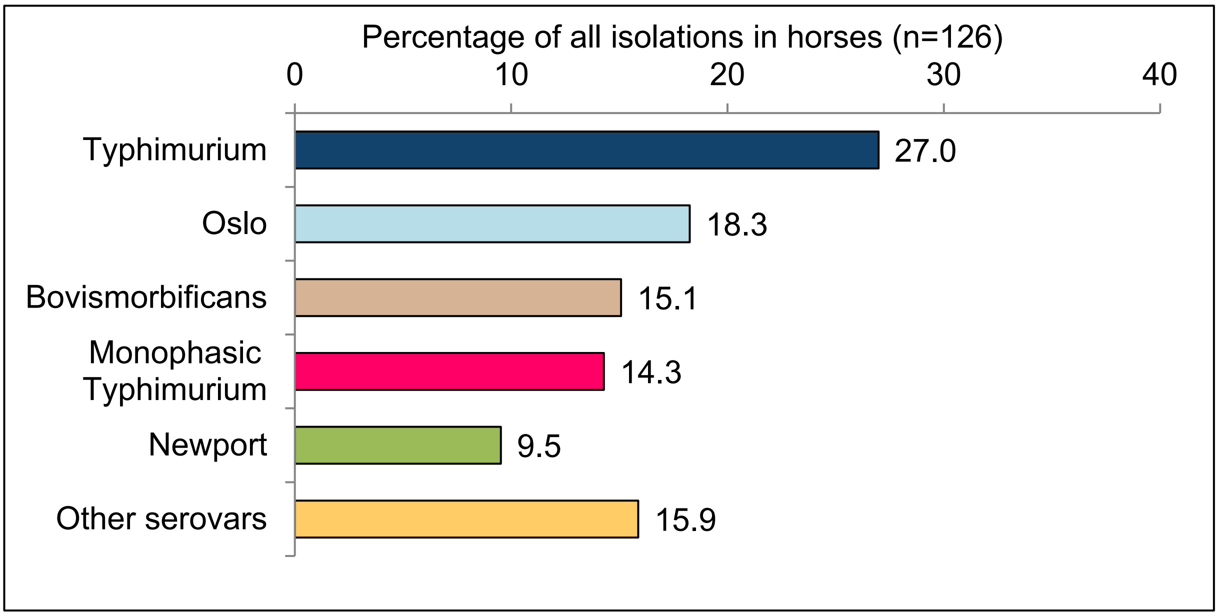
Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Sanga	0	0	0	0	0	0	0	0	1	1
Stanleyville	0	0	0	0	1	1	0	0	0	0
Typhimurium	34	23	16	15	15	12	18	17	20	20
untypable strains	2	2	0	0	1	1	2	2	1	1
Total	**126**	**75**	**41**	**37**	**45**	**36**	**60**	**57**	**55**	**52**

Table 5.4: Isolations and incidents of *S*. Typhimurium in horses on all premises in Great Britain

Phage Types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT1	2	1	1	1	5	5	2	2	2	2
DT2	0	0	0	0	2	2	0	0	2	2
DT8	3	3	0	0	0	0	2	1	0	0
DT29	0	0	0	0	1	1	0	0	0	0
DT32	0	0	0	0	0	0	1	1	0	0
DT40	4	2	0	0	0	0	0	0	0	0
DT41	3	3	0	0	0	0	0	0	0	0
DT75	0	0	0	0	0	0	0	0	5	5
DT99	0	0	0	0	0	0	0	0	2	2
DT104	3	3	0	0	0	0	1	1	1	1
DT105	0	0	0	0	0	0	3	3	1	1
DT109	0	0	0	0	0	0	2	2	0	0
DT116	0	0	5	4	0	0	2	2	0	0
DT135	1	1	0	0	0	0	0	0	0	0
DT193	4	2	2	2	0	0	2	2	1	1
U188	2	2	0	0	0	0	0	0	0	0
U302	6	3	0	0	1	1	0	0	0	0
U320	0	0	1	1	0	0	0	0	0	0
RDNC	5	2	7	7	6	3	3	3	6	6
UNTY	1	1	0	0	0	0	0	0	0	0
Total	**34**	**23**	**16**	**15**	**15**	**12**	**18**	**17**	**20**	**20**

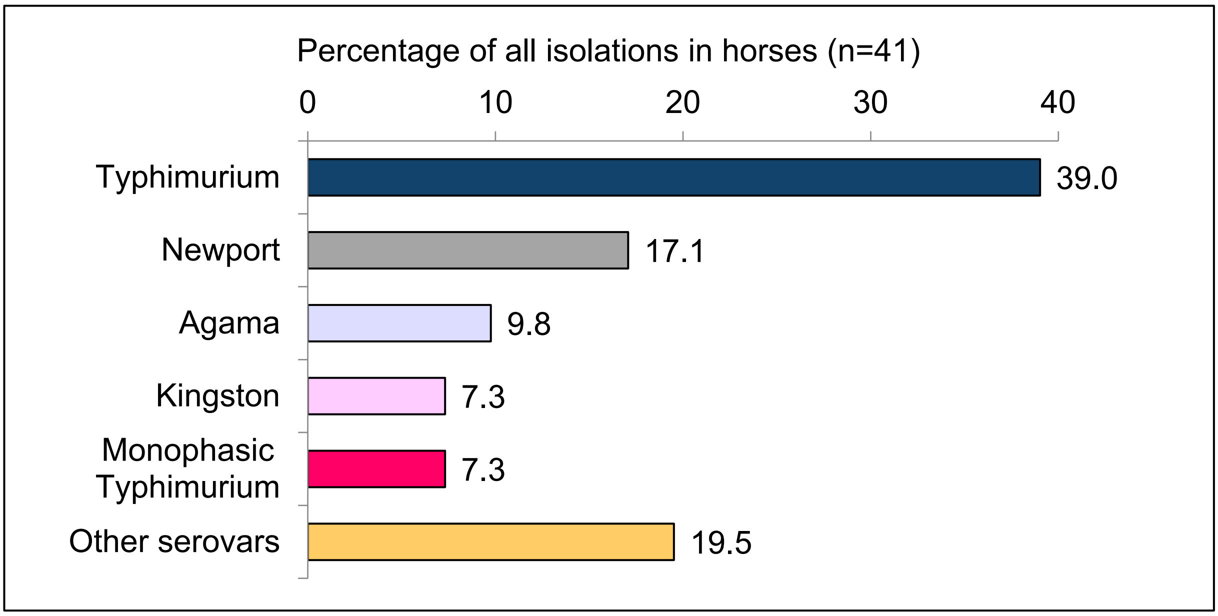
Figure 5.1: Isolations of the most common serovars in horses in Great Britain 2019 to 2023

Figure 5.1.1: Isolations in 2019



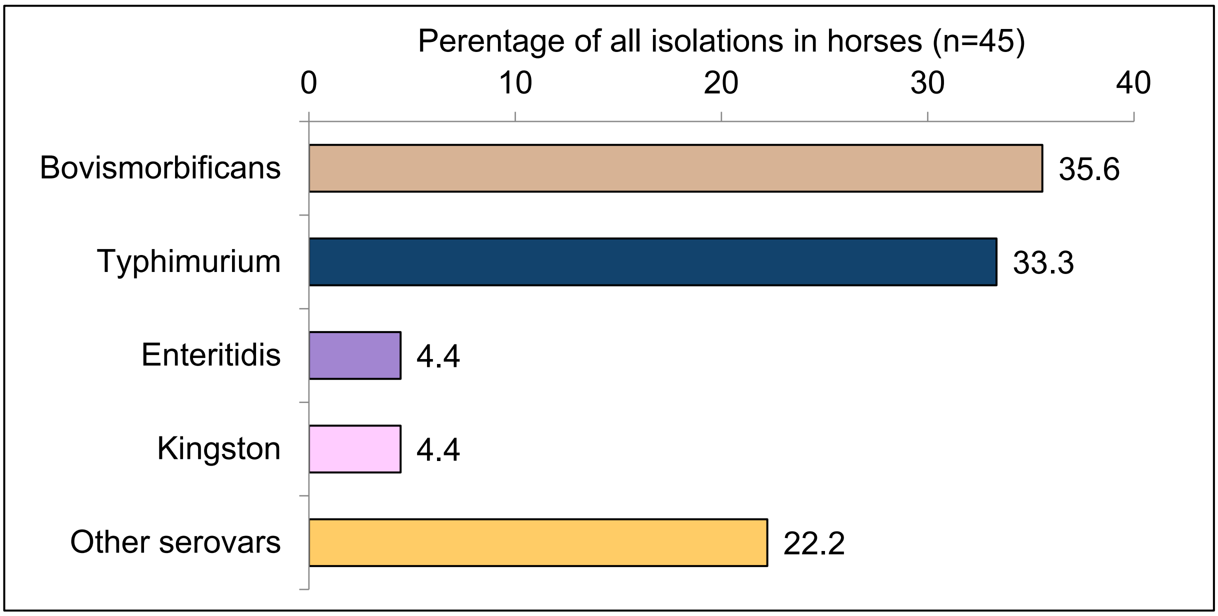
The most common serovar in horses in 2019 was *S.* Typhimurium (27.0% of isolations), followed by *S*. Oslo (18.3% of isolations), *S.* Bovismorbificans (15.1% of isolations), monophasic *S.* Typhimurium (14.2% of isolations) and *S*. Newport (9.5% of isolations).

Figure 5.1.2: Isolations in 2020



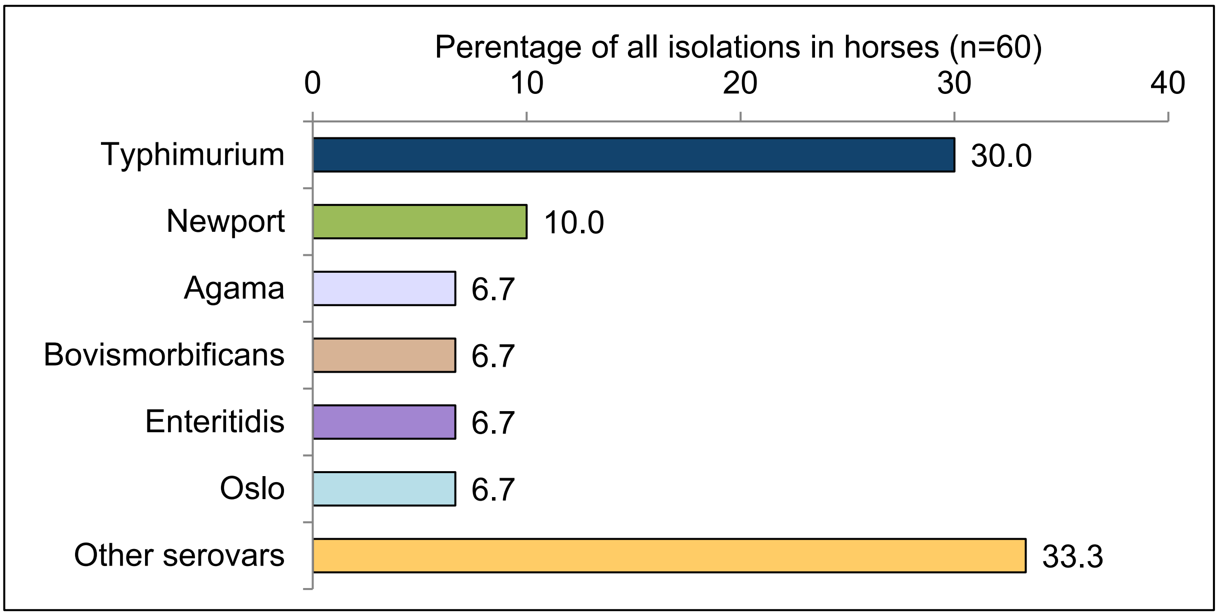
The most common serovar in horses in 2020 was *S.* Typhimurium (39.0% of isolations), followed by *S*. Newport (17.1% of isolations), *S.* Agama (9.8% of isolations) and *S*. Kingston and monophasic *Salmonella* Typhimurium (7.3% of isolations each).

Figure 5.1.3: Isolations in 2021



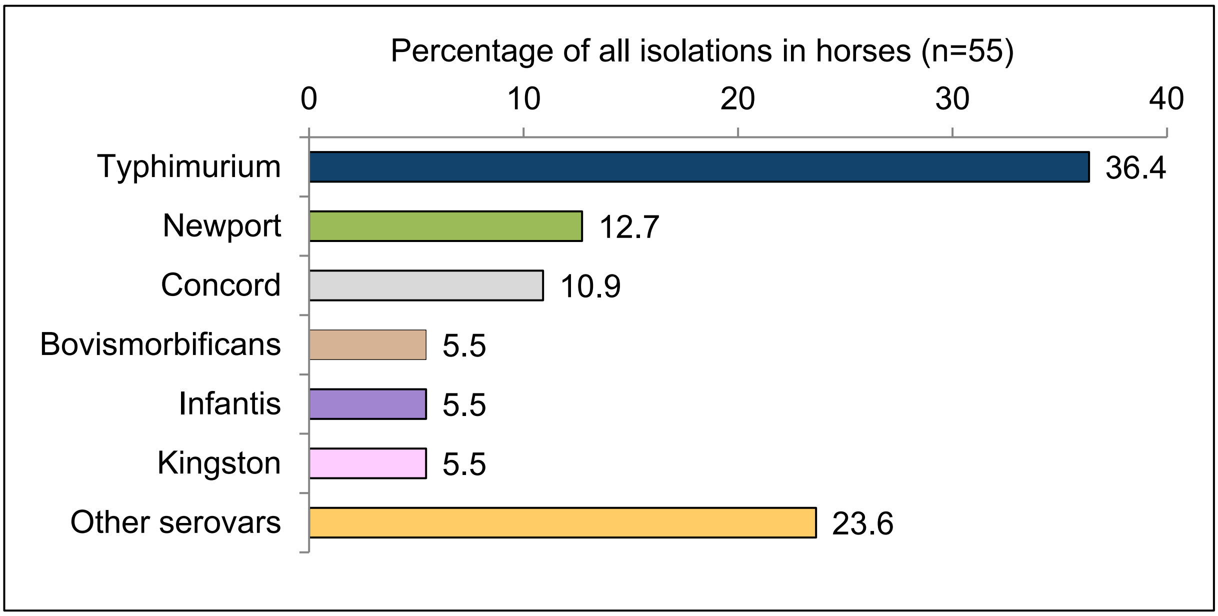
The most common serovar in horses in 2021 was *S.* Bovismorbificans (35.6% of isolations), followed by *S*. Typhimurium (33.3% of isolations), *S.* Enteritidis and *S*. Kingston (4.4% of isolations each).

Figure 5.1.4: Isolations 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 5.1.5: Isolations 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) and *S.* Bovismorbificans, *S.* Infantis and *S.* Kingston (5.5% of isolations each).

Figure 5.2: The 6 most common *Salmonella* serovars in horses in Great Britain in 2022 and their trends over time since 2018

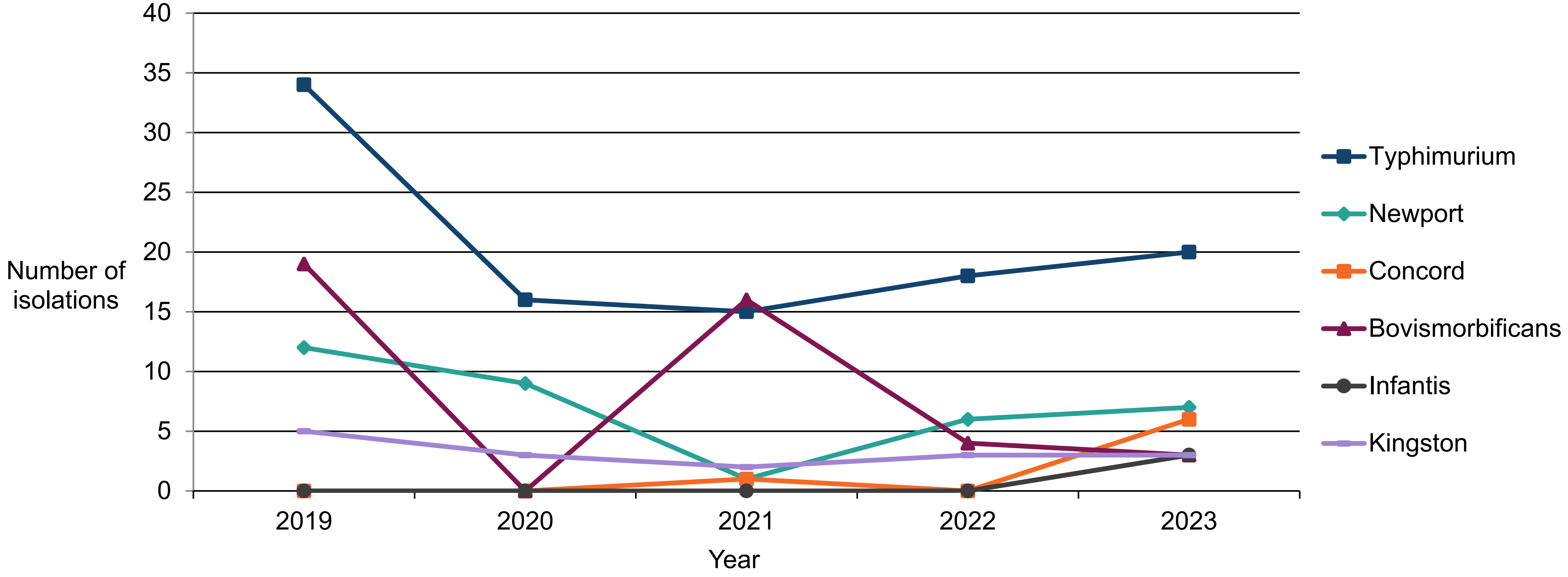


Figure 5.2 shows that *S*. Typhimurium remains the top serovar in horses with 20 isolations in 2023, remaining relatively stable since 2020. *S*. Newport, the second most common serovar in 2023, has decreased from 12 isolations in 2019 to 7 in 2023. There has been an increase in *S.* Concord from very low levels or none in previous years to 6 in 2023. *S*. Kingston has remained fairly stable with less than 5 isolations across all years while *S.* Bovismorbificans has fluctuated. *S*. Infantis which was isolated for the first time in horses this year. These 3 made up joint fourth most common serovar in horses with 3 isolations each in 2023.

Figure 5.3: *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and monophasic *S*. Typhimurium as a proportion of all isolations in horses in Great Britain 2003 to 2023

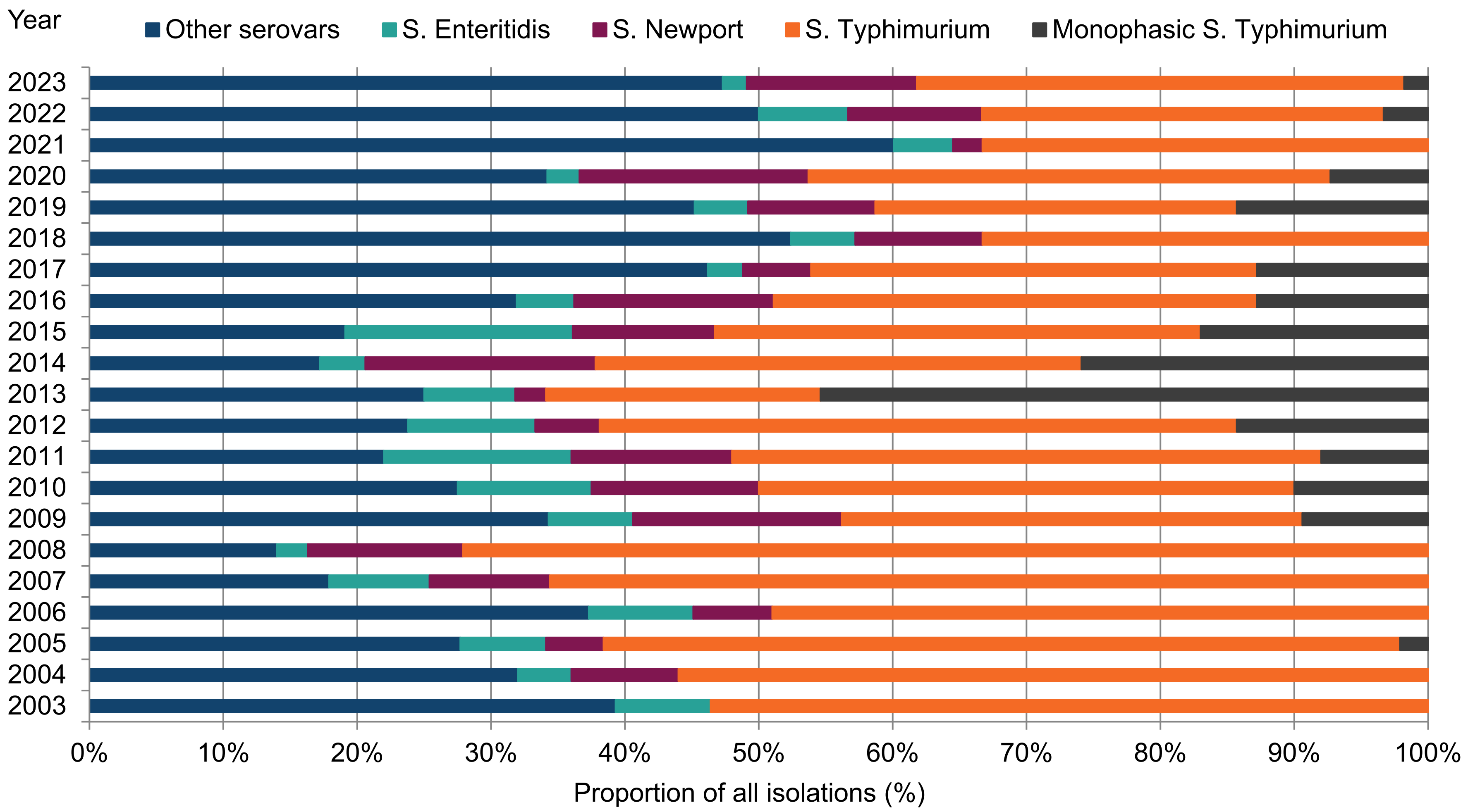


Figure 5.3 shows the proportion of all isolates of *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and monophasic *S*. Typhimurium in horses in Great Britain between 2002 and 2023:

- *S*. Typhimurium accounted for the greatest proportion of isolates and has remained relatively stable since 2014
- Monophasic *S*. Typhimurium as a proportion of all isolates peaked in 2013 at 45.40% but has since returned to lower levels at 1.8% in 2023
- *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.
- other serovars have accounted for between 14.0% and 60.1% since with fluctuations year on year but an overall increase in the proportion of isolations in horses.

Figure 5.3: Table of data

Year	Other serovars	*S.* Enteritidis	*S.* Newport	*S.* Typhimurium	Monophasic *S.* Typhimurium
2003	39.3%	7.1%	0.0%	53.6%	0.0%
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%
2014	17.2%	3.4%	17.2%	36.3%	25.9%
2015	19.1%	17.0%	10.6%	36.3%	17.0%

Year	**Other serovars**	***S.* Enteritidis**	***S.* Newport**	***S.* Typhimurium**	**Monophasic *S.* Typhimurium**
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%

Table 5.5: Isolations and incidents of monophasic *S*. Typhimurium in horses on all premises in Great Britain

Phage type	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT104	0	0	0	0	0	0	2	1	0	0
DT193	18	8	3	1	0	0	0	0	1	1
Total	**18**	**8**	**3**	**1**	**0**	**0**	**2**	**1**	**1**	**1**

Table 5.6: Isolations and incidents of *S*. Enteritidis in horses on all premises in Great Britain

Phage type	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
PT8	0	0	1	1	0	0	1	1	1	1
PT9A	0	0	0	0	0	0	2	2	0	0
PT11	1	1	0	0	0	0	0	0	0	0
PT13a	3	3	0	0	1	1	1	1	0	0
PT21	1	1	0	0	0	0	0	0	0	0
NOPT	0	0	0	0	1	1	0	0	0	0
Total	**5**	**5**	**1**	**1**	**2**	**2**	**4**	**4**	**1**	**1**

Chapter 6: Reports of *Salmonella* in chickens

During the early part of 2023 there was significant disruption to the poultry industry due to a national outbreak of Avian Influenza affecting all industry sectors. This resulted in altered management and biosecurity measures and is likely to have impacted on 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, 2021, 2022 and 2023 data with previous years.

According to the June Agricultural Census, the total number of chickens held in Great Britain was 144.8 million birds in 2023, comprising approximately 44.2 million breeding and laying hens, and 100.6 million broiler chickens (Figure 6.1). This compares to 153.5 million chickens in 2022, a decrease of 5.7%.

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 and turkey flocks. The *Salmonella* serovars considered to be of particular public health significance under 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.

Since the start of 2023 following the move to whole genome sequencing, the monophasic variants *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- are 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.

There was a total of 5,210 chicken diagnostic and monitoring submissions received by APHA and SRUC laboratories and partner post mortem providers in 2023, a decrease of 3.8% compared to 5,414 in 2022. However, APHA does not have information on the number of non-statutory submissions submitted to private laboratories that do not result in a positive culture of *Salmonella,* as the negative results are not reportable under the Zoonoses Order.

There were 2,633 isolations of *Salmonella* from chickens in 2023 (Table 6.1) an increase of 9.5% compared with 2022 (2,404 isolations) and the highest number of isolations since before 2009. *Salmonella* isolations from chickens increased substantially between 2018-2020 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 2023 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 2,509 (95.3%)
- voluntary surveillance: 120 (4.6%)
- clinical disease: 4 (0.2%)

The percentage of *Salmonella* isolations reported through statutory surveillance in 2023 was more than in 2022 when 92.9% of total chicken isolations arose from statutory surveillance.

Forty-one different *Salmonella* serovars were isolated in 2023, accounting for 2,619 of the 2,633 isolations. Fourteen isolations involved un-typable *Salmonella* isolates (including one rough strain). Table 6.1 shows the *Salmonella* serovars isolated from chickens between 2019 and 2023. Figure 6.2 shows the relative percentages of the most common serovars isolated from chickens between 2019 and 2023.

The 4 most common serovars isolated from chickens in 2023 is consistent with 2018 to 2022, however the relative contribution of each serovar varied (Figure 6.3). The increase in isolations from 2022 to 2023 is largely the result of increases in isolations of the 3 most common serovars *S.* 13,23:i:-, *S*. Montevideo and *S.* Kedougou.

Consistent with 2018 to 2020, *Salmonella* 13,23:i:- was the most frequently isolated serovar in 2023 (675 isolations) accounting for 25.6% of all chicken isolations, almost a 2-fold increase compared to 2022 (343 isolations). Isolations of *S.* 13,23:i:- peaked in 2020 with 716 isolations representing 32.2% of all *Salmonella* isolations but in recent years isolations of this serovar had decreased both in real and relative terms. There is increasing evidence that *Salmonella* 13,23:i:- strains represent a monophasic variant of *S.* Idikan with a mutation that prevents expression of the phase 2 flagella antigens. This serovar is associated with contaminated feed mills and can also become established and persistent in hatcheries and on poultry farms (Gosling *et al.,* 2022).

With 591 isolations, *S*. Montevideo was the second most common serovar isolated in 2023 accounting for 22.4% of all chicken isolations. This serovar was also the second most frequently isolated serovar in 2022 (460 isolations, 19.1% of all chicken isolations, Figure 6.2). Isolations of this serovar have been increasing year-on-year since 2015 (when there were 31 isolations) with a steep rise in 2021 when there was a 53.8% increase compared with 2020 (262 isolations). The 28.5% increase in 2023 compared to 2022 is a continuation of this trend (Figure 6.3).

Salmonella Kedougou accounted for 537 isolations in 2023 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). The almost 2-fold increase in the number of isolations in 2023 compared to 2022 (277 isolations) is also reflected in the relative proportion associated with this serovar increasing from 11.5% in 2022 to 20.4% in 2023. Isolations of *S*. Kedougou almost halved in 2021 compared to 2020 (430 isolations), prior to which there had been a steadily increasing occurrence in its isolation.

Isolations of *Salmonella* Mbandaka in 2023 (305 isolations, 11.6% of all chicken isolations) have markedly reduced from 2022 when it was the most frequently isolated serovar (695 isolations, 28.9% of all chicken isolations) having increased by over 2-fold compared to 2021 (294 isolations). Isolations of *S*. Mbandaka, which can be feed related serovar associated with soya products, had been generally increasing since 2010 peaking in 2018 (472 isolations, 25.7% of all chicken 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, when it was associated with 17.6% of all chicken isolations (Figure 6.3), and 2022 when isolations were at their highest since before 2009.

Isolations of *S*. Agona from chickens increased by 56.3% in 2023 (200 isolations) compared to 2022 (128 isolations). This is the highest number of isolations of this serovar ever reported, though the rate of increase was higher in 2022 compared to 2021 (34 isolations). 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 2023 compared with 2022 included *S.* Braenderup (5 versus 2 isolations), *S.* Livingstone (14 versus 3 isolations), *S.* Give (4 versus 0 isolations).

There were 9 isolations of *S.* Enteritidis in 2023 representing more than a 2-fold decrease compared to 2022 (23 isolations) when isolations were at a 3-year high. Isolations in 2023 were associated with 8 flocks (3 of which were from the layer sector) on 5 holdings, compared with 6 flocks in 2022. There was similar diversity of phage types of *S.* Enteritidis isolated in 2023 compared to 2022 with 7 of the 9 isolations in 2023 belonging to PT8 (Table 6.4), also the most common phage type in 2022, 2020 and 2019. The remaining phage types isolated in 2023 were associated with PT4 which is frequently reported from chickens in Great Britain.

There were 21 *S.* Typhimurium isolations from chickens in 2023 originating from 13 flocks, accounting for 0.80% of all *Salmonella* isolations consistent with recent years (0.75% of all *Salmonella* isolations in 2022 (18 isolations), 0.90% of all *Salmonella* isolations in 2021 (15 isolations)). There was increased variability in phage types in 2023 (7 phage types) compared with 2022 (4 phage types) (Table 6.2). The most common phage types in 2023 were DT75 (6 isolations), first isolated from chickens in 2022 and DT105 (6 isolations) originating from 4 flocks (3 broiler flocks) on 4 different holdings, which has not previously been reported from chickens in Great Britain. Three further isolates did not conform to any phage reaction pattern in the current typing scheme (RDNC or NOPT). Many of these RDNC strains are likely to be associated with wild birds.

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 2023, there were 6 isolations of monophasic *S.* Typhimurium compared with 19 isolations in 2022. All isolations were phage type DT193 (Table 6.3). This has been the only phage type isolated since 2020. The cases of monophasic *S.* Typhimurium are considered 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 marked increases across all chicken sectors in 2022 (98 isolations compared with 42 isolations in 2021 and one isolation in 2020). Isolations in 2023 decreased by 36.7% to 62 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 in mainland Europe. There have been associated human outbreaks of *S*. Infantis in recent years

Following a sharp rise in the number of isolations of *S.* Idikan (45 isolations) in 2022 isolations of this serovar decreased in 2023 to levels consistent with the years previous (6 isolations).

Other notable trends include decreases in isolations of *S.* Kentucky, *S*. Newport, *S*. Senftenberg from chickens in 2023 compared to 2022. There were 4 isolations of *S.* Newport, a reduction of 66.7% on the number in 2022 (12 isolations) and sees the number of isolations return to similar levels to those pre-2020. During 2020, 52 isolations of *S.* Newport were reported associated with an ongoing outbreak investigation in the layer sector. *Salmonella* Senftenberg isolations from chickens have been highly variable in recent years. The recent trend in decreasing isolations of this serovar continued in 2023 with 22 isolations compared to 37 isolations in 2022 and 96 isolations in 2020. Isolations of *Salmonella* Senftenberg peaked in 2017 (238 isolations) and are often related to hatchery contamination.

In 2023 the following serovars were isolated from chickens in Great Britain for the first time: *S.* Chomedey (one isolation) and *S.* Oxford (one isolation). Other unusual serovars included *S*. Ajiobo (last reported from chickens in 2018), *S*. Durham (last reported from chickens in 2016), *S.* Muenster (last reported from chickens in 2016), *S.* Wangata (last reported from chickens in 2002) and *S.* Yoruba (last reported from chickens in 2007).

There were no reported isolations of *Salmonella* from chickens imported into Great Britain in 2023 compared to one report in 2022.

National Control Programme for *Salmonella* in chickens

The Regulation (EC) No 2160/2003 of the European Parliament and of the Council of 17 November 2003 on the control of salmonella and other specified food-borne zoonotic agents, which came into force on 21 December 2003, aims to reduce the prevalence of certain zoonotic infections at the primary production level, by requiring the implementation of species-specific *Salmonella* National Control Programmes (NCPs). There are 3 *Salmonella* NCPs for chickens (*Gallus gallus*) in Great Britain for breeding flocks, laying flocks and broiler flocks*.*

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

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

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

The NCP for *Salmonella* in breeding flocks includes all holdings with 250 or more birds*.* The NCP in Great Britain is enforced by separate, equivalent Control of *Salmonella* in Poultry Orders (CSPO) in England, Scotland and Wales. The assimilated target for reduction is only concerned with regulated serovars in adult breeding 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 breeding flocks identified in the NCP in 2023

In 2023, 9 adult breeding flocks, on 6 separate holdings, tested positive for *Salmonella* spp. under the statutory testing programme. This is a 47.06% reduction compared to 2022 (17 positive flocks) but more consistent with previous years, 2021 (10 positive flocks) and 2020 (7 positive flocks). Since 2013, there has been a generally increasing trend in the proportion of adult breeding flocks testing positive for *Salmonella*, though the proportion has fluctuated in more recent years (Figure 6.4).

Five adult breeding flocks tested positive for a regulated *Salmonella* serovar in 2023 (Table 6.5). *Salmonella* Typhimurium DT99 was identified in 3 broiler parent breeding flocks (one via routine annual official sampling and 2 via operator sampling) originating from 2 premises, one layer parent flock tested positive for *Salmonella* Typhimurium DT105 (via operator sampling) and *S*. Infantis was identified in a layer parent breeding flock (via official sampling). Having first been isolated in 2021, this is the third year that *S*. Infantis has been isolated from a chicken breeder flock since the inception of the NCP but the first time it has been isolated from breeder layer flocks. The number of flocks testing positive for *Salmonella* Typhimurium has increased in recent years from 2 flocks in 2022 to 4 flocks in 2023. Prior to this, *S*. Typhimurium was last identified in one breeder flock as part of the NCP in 2020, from a broiler grandparent breeding flock. *Salmonella* Enteritidis has never been detected in breeding chickens as part of the NCP.

Four adult breeding flocks, on 2 separate holdings, were positive for non-regulated *Salmonella* serovars. This included 3 broiler parent flocks on the same holding which tested positive for *Salmonella* 13,23:i:- via operator samples, fewer than in 2022 (5 flocks). In most cases, this serovar is a monophasic variant of *S*. Idikan and 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 2019 (7 positive flocks). The small number of positive flocks in 2023 continues a decreasing trend in occurrence of this serovar in breeding flocks in recent years.

Salmonella Anatum was isolated from a layer breeding flock via operator sampling which was isolated from breeder flocks in 2022 (one flock) but prior to this was last isolated as part of the NCP in 2007. This serovar has most often been isolated from production layers or broiler flocks in previous years but was not isolated from any production layer flocks in the NCP in 2023. *Salmonella* Anatum is often associated with wild birds.

No immature (in-rear) breeding flocks tested positive for *Salmonella* spp. during 2023 consistent with 2022 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 2019 and 2023 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. However, it is noteworthy that the number of flocks testing positive for *Salmonella* Typhimurium has increased in the last 2 years (4 flocks in 2023). In addition, *Salmonella* Anatum has been isolated in 2022 and 2023 having not been isolated in preceding years from breeding flocks and *S.* 13,23:i:- has been identified every year since 2013 (and always in broiler breeder flocks).

In Great Britain, a total of 1,159 adult breeding flocks on 254 premises were registered in 2023, and a total of 1,090 flocks were subject to *Salmonella* testing via routine annual official sampling visits. In 2023 there was a shortfall of approximately 6% in the number of flocks subject to annual official sampling, which is less than in 2022 when there was a shortfall of approximately 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 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 GB, tested within the NCP was 0.78% (9 of 1,159) in 2023 (Table 6.5, Figure 6.4).

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. 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 NCP is 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 2023

During 2023, a total of 29 adult laying hen flocks, originating from 25 separate holdings, tested positive for *Salmonella* under the statutory testing programme. This is 56.7% lower than the number of flocks testing positive in 2008 when the NCP was first implemented (67 positive flocks), and a decrease of 31.0% compared to 2022 (42 positive flocks) (Table 6.6) and is the lowest number of positive flocks in the NCP for 3 years (Figure 6.6).

A total of 6 adult flocks, from 4 separate holdings, tested positive for regulated *Salmonella* serovars during 2023, less than in 2022 (10 positive flocks from 8 holdings) and 2021 (9 positive flocks from 9 separate holdings) and 2020 (14 flocks) and continues a 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).

Three adult flocks from one holding tested positive for *S.* Enteritidis via operator sampling (PT4 (x2) and PT8 (x1)) in 2023. This is a decrease compared to 2022 (5 positive flocks on 4 holdings), and a large reduction compared to 2020 (11 flocks from 4 holdings) and 2019 (14 flocks from 5 holdings), when the highest number of flocks tested positive for *S*. Enteritidis since the implementation of the NCP in 2008 (49 positive flocks). 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 BEIC on some premises that were linked via egg packing centres. In contrast, no positive flocks were identified via risk-based enhanced sampling during 2022, and no more than 2 flocks tested positive on a given holding.

Two adult flocks, from 2 separate holdings, tested positive for *S.* Typhimurium (DT99 (x1), DT1 (x1)) in 2023. This is a decrease from 5 flocks in 2022 and continues 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.

One adult flock of laying hens was positive for *Salmonella* 4,12:i:- (DT193) in 2023. This is the first time a laying flock has tested positive for this monophasic strain of *S*. Typhimurium since 2015. No flocks tested positive for *S.* 4,5,12:i:- in 2023, the last isolations of this serovar was in 2019 when one flock tested positive. This continues a generally low prevalence of these monophasic strains of *S*. Typhimurium in adult laying flocks.

A comparison of the serovars identified in adult laying flocks in the NCP between 2019 and 2023 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, 17 different non-regulated serovars were identified from adult laying chickens in 2023, from 23 flocks on 21 separate holdings. No flocks tested positive for 2 different non-regulated serovars. The most common serovars were *S*. Give, which was isolated from 3 flocks on 2 different holdings, and *S*. Infantis, which was isolated from 3 flocks on 3 different holdings. *S*. Give was the most common non-regulated serovar in 2023 but this serovar has not been isolated from adult laying flocks since 2013 in the NCP. This serovar is more often associated with in-rear (immature) flocks. Isolations of *S*. Infantis have increased in recent years in layer flocks but also more dramatically in chicken broiler flocks.

Isolations of several serovars regularly isolated in adult flocks as part of the NCP declined in 2023. *Salmonella* Mbandaka was identified in one flock in 2023 compared with 6 flocks in 2022, which is consistent with the years prior to 2022. *Salmonella* Derby was not identified in any flocks in 2023, compared to 4 flocks in 2022. The last time no flocks tested positive for *S.* Derby as part of the layer NCP was in 2018. *S.* Bardo was isolated from 5 flocks in 2021 and 3 flocks in 2022 having never previously been identified from adult flocks as part of the NCP. No adult flocks tested positive for this serovar in 2023. Furthermore, no adult flocks tested positive for the partially typeable serovar *Salmonella* 13,23:i:- in 2023; 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 2023, 3 different serovars were isolated from adult laying flocks in the NCP for the first time. These were *S*. Amsterdam, *S*. Muenster and *S*. Poona (although this serovar was isolated from an immature flock in 2008). *Salmonella* Coeln is rarely isolated from chicken layer flocks with 3 other isolations in the NCP since its inception in 2008. *S.* Cubana, isolated from an adult laying flock, is also a rare serovar in the NCP, last isolated from adult chicken flocks in 2016 which was the first time it had been isolated from laying flocks.

A total of 3 in-rear (immature) flocks from 3 separate holdings were positive for *Salmonella* in 2023 in Great Britain. This is the same as in 2022 (3 positive flocks) 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.

The 3 *Salmonella* positive in-rear (immature) flocks in 2023 included isolations of *S.* Yoruba and *S*. 4,12:b:- , both of which have never been isolated from in-rear (immature) flocks as part of the NCP. One further flock tested positive for *S.* Kentucky which was last isolated from an in-rear (immature) flock in 2020. *S*. Kentucky is more frequently isolated from adult flocks, last identified in 2022. *Salmonella* Senftenberg is most often associated with in-rear (immature) flocks but there were no isolations in 2023.

No in-rear layer flocks tested positive for regulated serovars in 2023. 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 2023 as the denominator population, the estimated prevalence of *Salmonella* spp. in laying flocks was 0.80% (29 of 3,372) in 2023. This compares to an increased prevalence of 1.13% (42 of 3,721) in 2022 although prior to this there had been a decreasing trend in flocks testing positive since 2019 (0.96% in 2021, 1.06% in 2020, 1.20% in 2019) (Figure 6.6). The estimated prevalence of regulated *Salmonella* serovars in 2023 in adult laying flocks has also decreased compared to 2022 with 0.17% flocks testing positive versus 0.27% (10 of 3,721) in 2022. This figure remains well below the target of 2.00% and is the lowest since 2018 (0.1%).

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 target 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 target is 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 NCP for *Salmonella* in broiler flocks includes all commercial broiler holdings with 2,000 or more birds. The NCP is 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 2023

During 2023, a total of 2,268 broiler flocks from 511 separate holdings tested positive for *Salmonella* under NCP testing with an estimated prevalence of 5.33%, the highest prevalence since the inception of the NCP. This represents an increase of 15.7% relative to 2022 (1,960 flocks). The increase in 2023 continues a generally increasing trend (with exception of 2021) in positive flocks since 2017 (Table 6.7 and Figure 6.8). The increase in 2023 compared with 2022 is attributable to increases in the number of flocks positive for a limited number of different serovars, including *Salmonella* 13,23:i:- (602 versus 301 flocks), *S.* Montevideo (545 versus 409 flocks), and *S.* Kedougou (421 versus 232 flocks).

Sixteen broiler flocks, on 11 separate holdings, tested positive for regulated serovars in 2023 which is consistent with years 2021 and 2022 (15 flocks) 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 2023 relative to 2022 the proportion of each regulated serovars varied.

Seven broiler flocks from 6 separate holdings tested positive for *S.* Typhimurium (DT105 (x3), DT75 (x2), and RDNC (x2)) in 2023 compared to 4 flocks from 4 holdings in 2022 (Table 6.7). This is the second consecutive year that DT75 has been isolated from broiler flocks as part of the NCP having been isolated for the first time in 2022.

Flocks testing positive for *S.* Enteritidis increased in 2023, with 5 positive flocks compared to one flock in 2022 and 2 flocks in 2021. All flocks in 2023 were positive for a single phage type PT8 (x5). These 5 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.

Four flocks, from one holding, tested positive for monophasic *S*. Typhimurium 4,5,12:i:- (all DT193) in 2023, compared to 10 flocks from 6 holdings in 2022 and 6 flocks (from a single holding) testing positive for this serovar in 2021, and none in 2020. No broiler flocks tested positive for monophasic *S*. Typhimurium 4,12:i:- in 2023 or 2022, which compares with 3 positive flocks in 2021 and is in keeping with the generally low numbers of broiler flocks that are positive for this serovar each year.

A comparison of the serovars identified in broiler flocks in the NCP between 2019 and 2023 is shown in Table 6.7 and Figure 6.9. Data for years prior to this are available in the *Salmonella* in Livestock Production reports from the relevant year. There were 2,252 broiler flocks positive for non-regulated *Salmonella* serovars in 2023, including 15 flocks that tested positive for more than one non-regulated serovar. The 4 most common serovars isolated from broiler chickens in 2023 was consistent across all years since 2019.

The occurrence of *Salmonella* 13,23:i:- increased between 2018 and 2020, before a marked reduction in 2021. Since then isolations have risen again, and in 2023, it was the most frequently isolated serovar with 602 flocks compared to 301 flocks in 2022 and 252 in 2021. This serovar is associated with some hatcheries and feed mills and has been commonly observed in broiler flocks since 2013, previous to which it was only isolated from a single flock in 2009. In 2023, *S.* 13,23:i:- was identified on 176 premises, of which 89 (50.6%) were repeatedly positive for the same serovar in subsequent flocks. Repeated occurrence of *S.* 13,23:i:-, defined as at least one positive flock placed on the premises in a particular month, were observed on individual premises. Of the 176 premises which had at least one flock positive for *S*. 13,23:i:-, 16.5% (29 of 176) had 2 occurrences of *S*. 13,23:i:-, whilst 17.6% (31 of 176), 7.4% (13 of 176), 5.1% (9 of 176), 1.7% (3 of 176), and 1.1% (2 of 176) had 3, 4, 5, 6 and 7 occurrences of this serovar in 2023, respectively. The maximum number of repeat isolations of *S*. 13,23:i:- in 2023 was 8 (1 of 176; 0.6%).

Consistent with 2022, *Salmonella* Montevideo was the second most frequently reported serovar from broiler flocks in 2023 (545 flocks). Reports of the serovar have steadily risen in recent years from 69 flocks in 2018, 144 in 2019, 245 in 2020, 330 flocks in 2021, and 409 flocks in 2022. *S.* Montevideo was identified on 167 premises in 2023, of which 80 (47.9%) were repeatedly positive for the same serovar in subsequent flocks. Up to 8 occurrences of *S.* Montevideo were observed on one premises, with 11.4% (19 of 167), 9.0% (15 of 167), 4.8% (8 of 167) and 0.6% (1 of 167) of premises having 3, 4, 5 and 6 occurrences respectively.

The occurrence of *S*. Kedougou has increased by 81.0% in 2023 and is the third most frequently reported serovar (421 flocks) compared to 232 in 2022, and 192 in 2021. *S*. Kedougou is associated with feed mill environments and can be found in ingredients such as oilseed meals. In 2023, *S.* Kedougou was identified on 99 premises, of which 55 (55.6%) were repeatedly positive for the same serovar in subsequent flocks.

Salmonella Mbandaka observed a 53% decrease in occurrence, from 579 reports in 2022, when it was the most frequently isolated serovar, to 272 in 2023. *S*. Mbandaka is typically a feed-related serovar, often associated with soya products, and, like the other common serovars found in broilers, can colonise the pellet cooling systems in feed mills and equipment in hatcheries, as well as persist on farms between flocks.

Other notable increases in the number of broiler flocks testing positive in 2023 compared to 2022 include: *S*. Derby (14 versus 7 flocks), *S*. Agona (191 versus 114 flocks). *Salmonella* Agona is usually associated with feed contamination.

Notable decreases in the number of flocks testing positive in 2023 compared to 2022 include *S*. Infantis (50 versus 75 flocks) and *S*. Idikan (5 versus 40 flocks). *Salmonella* Infantis is an unusual serovar in 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 Ajiobo, *S.* Chomedey and *S*. Oxford were new serovars isolated in 2023 that have never previously reported from broiler flocks from NCP samples.

An estimated 42,562 broiler flocks were tested in Great Britain according to the requirements of the *Salmonella* NCP during 2023. Using this as the denominator population, the estimated prevalence of *Salmonella*-positive broiler flocks was 5.33% (2,268 of 42,562). This is an increase compared to recent years (4.28% in 2022, 2.41% in 2021 and 3.38% in 2020) and is the highest since the inception of the NCP in 2009 (Table 6.7, Figure 6.8).

The estimated prevalence of regulated *Salmonella* serovars in broiler flocks in Great Britain during 2023 was 0.04% (16 of 42,562). This is slightly higher than in 2022 and 2021 (0.03%) (Table 6.7, Figure 6.8). The prevalence of regulated *Salmonella* serovars in broiler chickens in 2023 was well below the legislative target of 1% and is consistent with the ongoing maintenance of a low prevalence of regulated serovars in this sector.

Figure 6.1: Chicken population in Great Britain 2014 to 2023

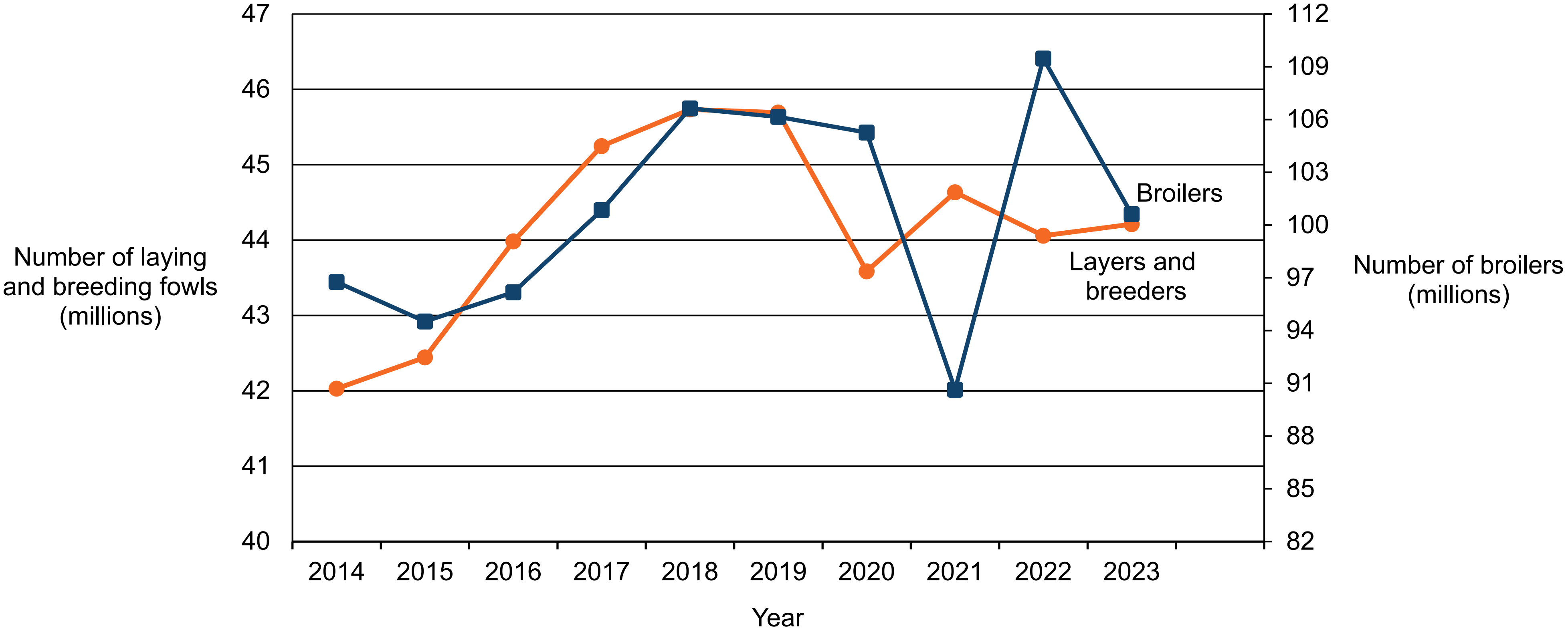


Figure 6.1 shows that the number of broiler, laying and breeding fowl in Great Britain increased steadily from 2013 to 2018 peaking at just over 106 million broilers and 45 million laying and breeding fowl in 2018. After this the has been a slight decline in the number of layers to between 44 and 45 million birds for the last 3 years while the number of broilers increased sharply to 109 million in 2022 but has dropped to just over 100 million in 2023. 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	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
Africana	1	1	0	0	0	0	0	0	0	0
Agama	7	7	4	4	1	1	1	1	3	3
Agona	29	31	73	101	33	34	117	128	191	200
Ajiobo	0	0	0	0	0	0	0	0	1	1
Amsterdam	0	0	0	0	0	0	0	0	1	1
Anatum	5	5	6	8	4	5	2	3	5	5
Bareilly	0	0	0	0	1	1	0	0	0	0
Bardo	0	0	1	13	5	10	3	5	0	0
Berta	0	0	0	0	0	0	1	1	0	0
Bovismorbificans	0	0	16	21	7	21	0	0	1	1
Braenderup	0	0	1	1	2	2	2	2	5	5
Bredeney	0	0	1	1	0	0	0	0	0	0
Chomedey	0	0	0	0	0	0	0	0	1	1
Coeln	1	1	2	3	0	0	4	4	4	4
Corvallis	0	0	0	0	0	0	2	3	0	0
Cubana	0	0	0	0	0	0	0	0	1	1
Derby	30	44	4	4	8	9	11	12	14	14
Dublin	1	1	0	0	0	0	4	4	1	1
Durham	0	0	0	0	0	0	0	0	1	1
Eastbourne	3	3	0	0	0	0	0	0	0	0
Eboko	0	0	0	0	0	0	1	1	0	0
Enteritidis	16	48	12	31	5	9	6	23	8	9
Essen	0	0	0	0	0	1	0	0	0	0

Salmonella serovar	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
Ferruch	0	0	0	0	2	2	0	0	0	0
Fresno	0	1	0	0	0	0	0	0	1	1
Give	0	0	2	3	0	0	0	0	4	4
Give var. 15^{+}	4	4	4	4	6	16	8	8	5	5
Goldcoast	0	0	0	0	1	1	0	0	0	0
Havana	1	1	1	1	2	2	5	6	0	0
Idikan	16	17	5	8	5	5	41	45	5	6
Indiana	7	7	2	3	0	0	1	1	5	5
Infantis	0	0	0	1	24	42	81	98	54	62
Isangi	0	0	0	0	1	3	0	0	0	0
Kedougou	335	357	342	430	192	217	233	277	421	537
Kentucky	1	1	0	1	0	0	4	4	1	1
Kingston	1	1	2	2	0	0	2	2	1	1
Kottbus	2	4	2	5	0	0	1	1	0	0
Lexington	0	0	0	0	1	1	0	0	0	0
Liverpool	0	0	1	2	0	0	1	1	0	0
Livingstone	7	10	9	11	4	17	2	3	12	14
London	2	2	0	0	1	1	2	2	0	0
Mbandaka	335	367	232	261	240	294	586	695	273	305
Mikawasima	0	0	1	1	0	0	0	0	0	0
Minnesota	0	0	0	0	0	1	0	0	0	0
Molade	0	0	0	0	1	1	0	0	0	0
Montevideo	146	169	246	262	332	403	411	460	547	591
Monophasic Typhimurium	6	7	1	13	9	12	10	19	5	6
Muenchen	1	1	6	8	4	4	9	9	5	5
Muenster	0	0	0	0	0	0	0	0	1	2

Salmonella serovar	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
Newport	5	5	13	52	10	37	10	12	4	4
Nima	1	1	0	0	0	0	0	0	0	0
Nottingham	4	9	0	0	0	7	2	4	0	0
Odozi	0	0	0	0	2	4	0	0	0	0
Offa	1	1	0	0	0	0	0	0	0	0
Ohio	71	75	33	33	54	55	44	49	35	36
Orion	3	4	0	0	0	0	1	1	0	0
Orion var. 15^{+}	12	14	28	30	33	34	55	60	57	61
Oslo	2	2	2	2	2	2	0	0	1	1
Oxford	0	0	0	0	0	0	0	0	1	1
Panama	0	0	0	0	1	1	1	2	0	0
Poona	0	0	1	1	0	0	0	0	1	1
Ramatgan	0	0	1	1	0	0	0	0	0	0
Reading	1	1	1	1	1	1	0	1	0	0
Rissen	1	1	0	0	0	0	1	1	0	0
Schwarzengrund	0	0	1	1	0	0	0	0	0	0
Senftenberg	33	72	53	96	29	63	19	37	17	22
Stanley	1	1	0	0	0	0	1	1	0	0
Stanleyville	0	0	1	1	0	0	0	1	0	0
Stourbridge	0	0	1	1	2	2	1	1	0	0
Takoradi	0	0	0	0	0	0	0	1	0	0
Tennessee	2	2	0	1	0	0	0	1	0	0
Typhimurium	11	14	6	19	10	15	11	18	13	21
Wangata	0	0	0	0	0	0	0	0	0	1
Yoruba	0	0	0	0	0	0	0	0	1	2
13,23:i:-	426	436	600	716	253	279	306	343	605	675
61:-:1,5,7	1	1	0	0	0	0	0	0	1	2

Salmonella serovar	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
untypable strains	16	19	38	37	27	28	32	35	11	13
rough strains	1	1	1	26	1	27	0	18	0	1
Total	**1,533**	**1,749**	**1,727**	**2,221**	**1,302**	**1,671**	**2,019**	**2,404**	**2,309**	**2,633**

16 flocks were positive for more than one serovar in 2019.

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

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

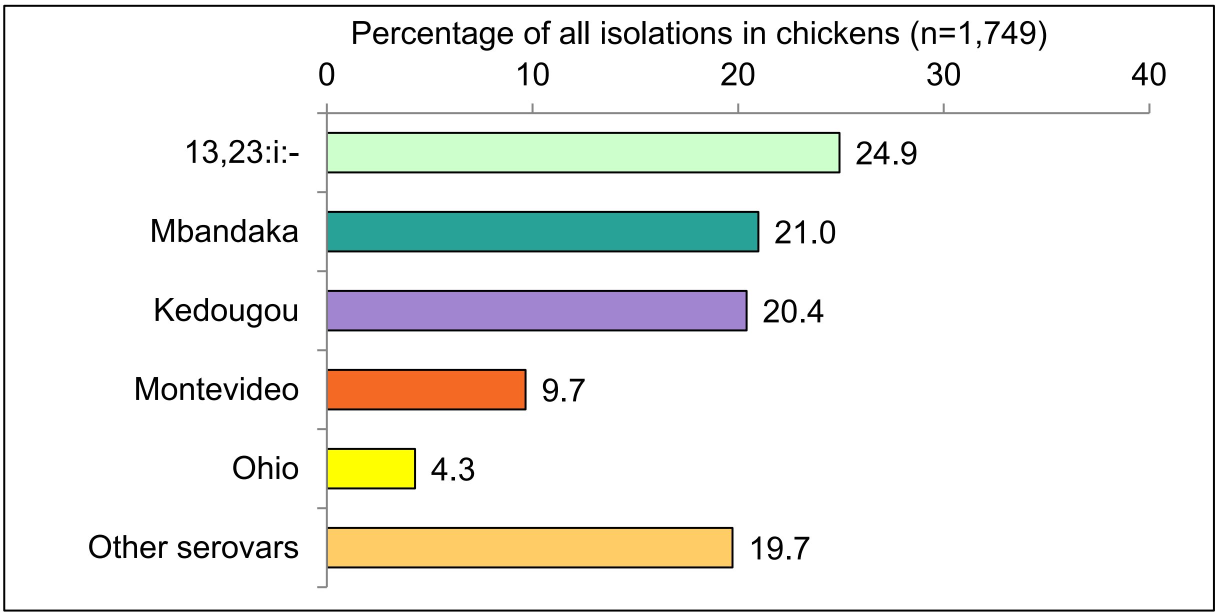
16 flocks were positive for more than one serovar in 2022.

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

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

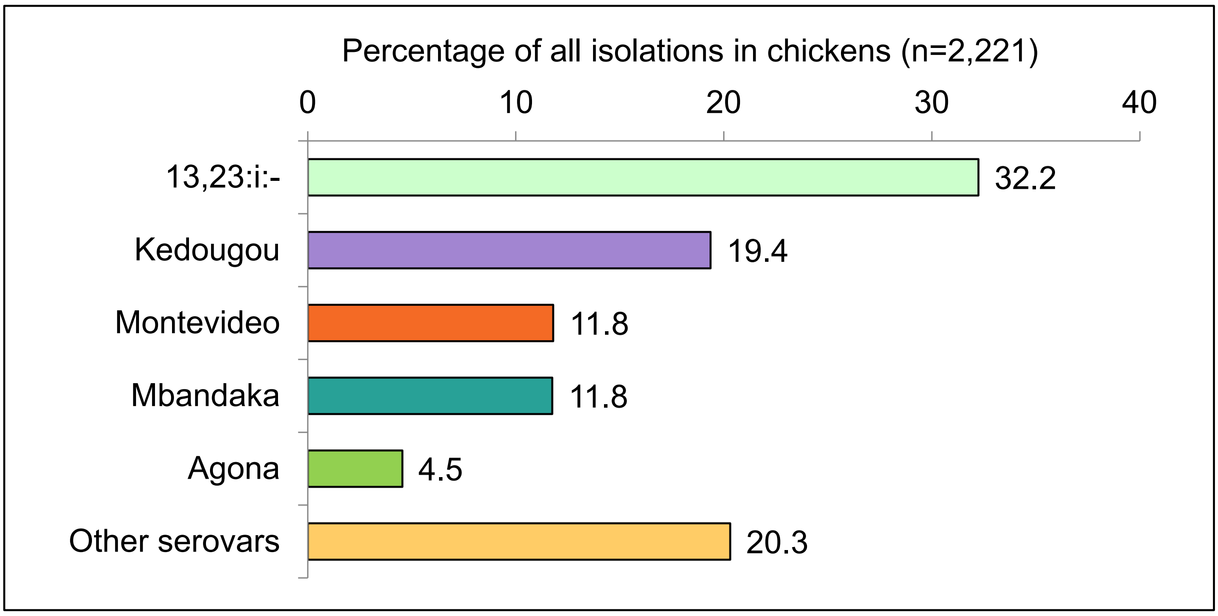
Figure 6.2: Isolations of the most common serovars in chickens in Great Britain 2019 to 2023 (statutory and non-statutory testing)

Figure 6.2.1: Isolations in 2019



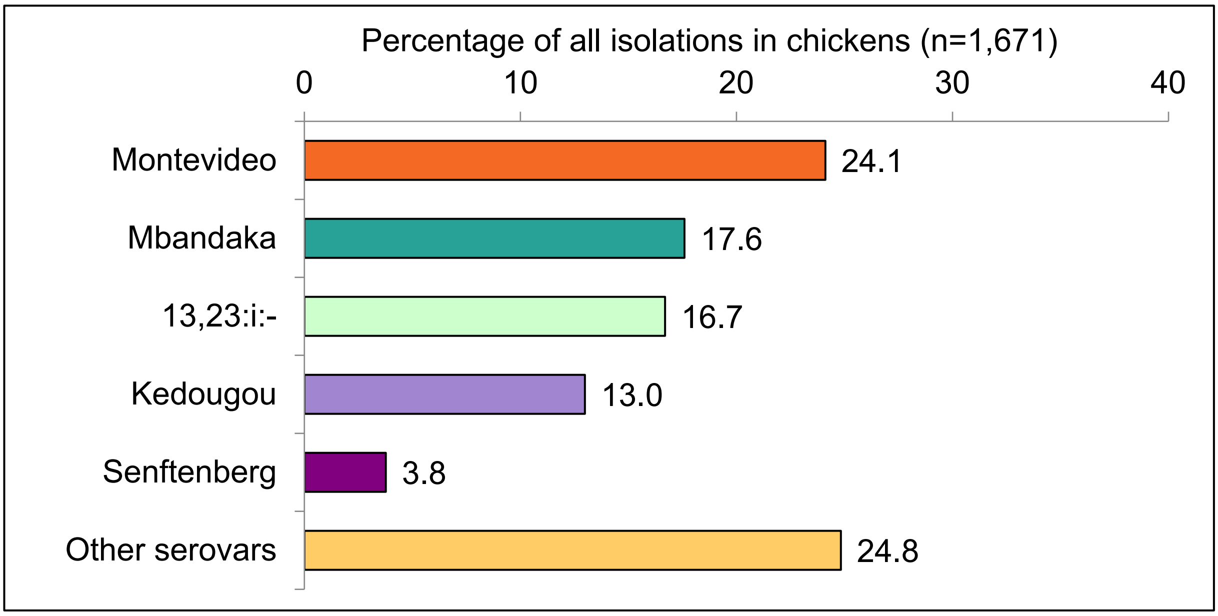
In 2019 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:-, accounting for 24.9% of total isolations, followed by *S.* Mbandaka (21.0%), *S.* Kedougou (20.4%) and *S.* Montevideo (9.7%).

Figure 6.2.2: Isolations in 2020



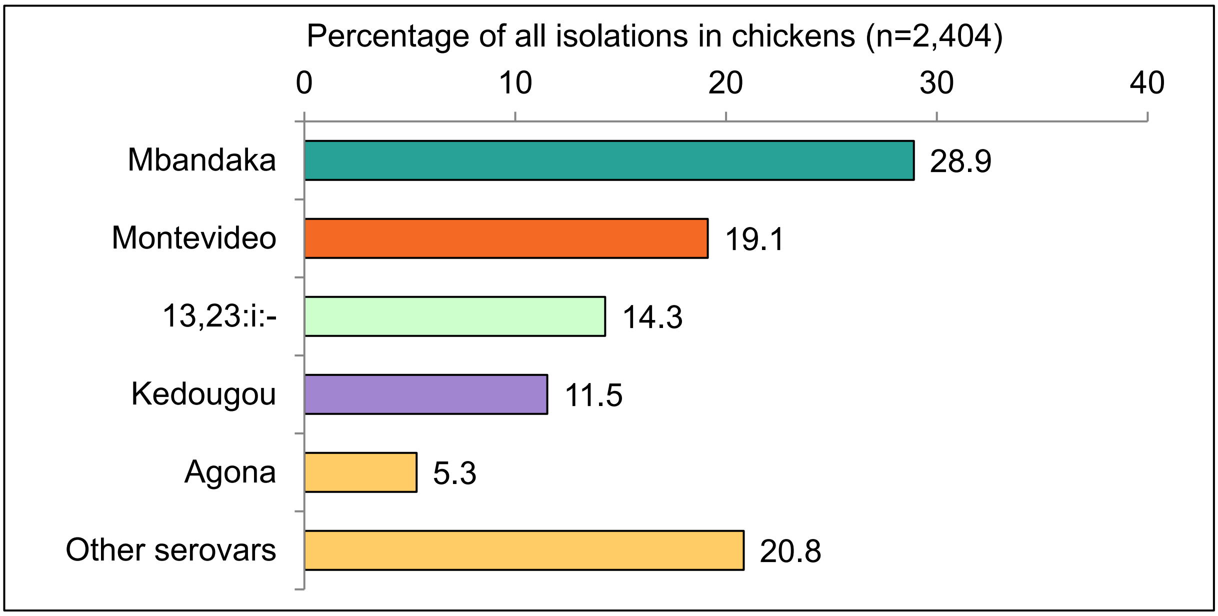
In 2020 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:-, accounting for 32.2% of total isolations, followed by *S.* Kedougou (19.4%), *S.* Montevideo (11.8%) and *S.* Mbandaka (11.8%).

Figure 6.2.3: Isolations in 2021



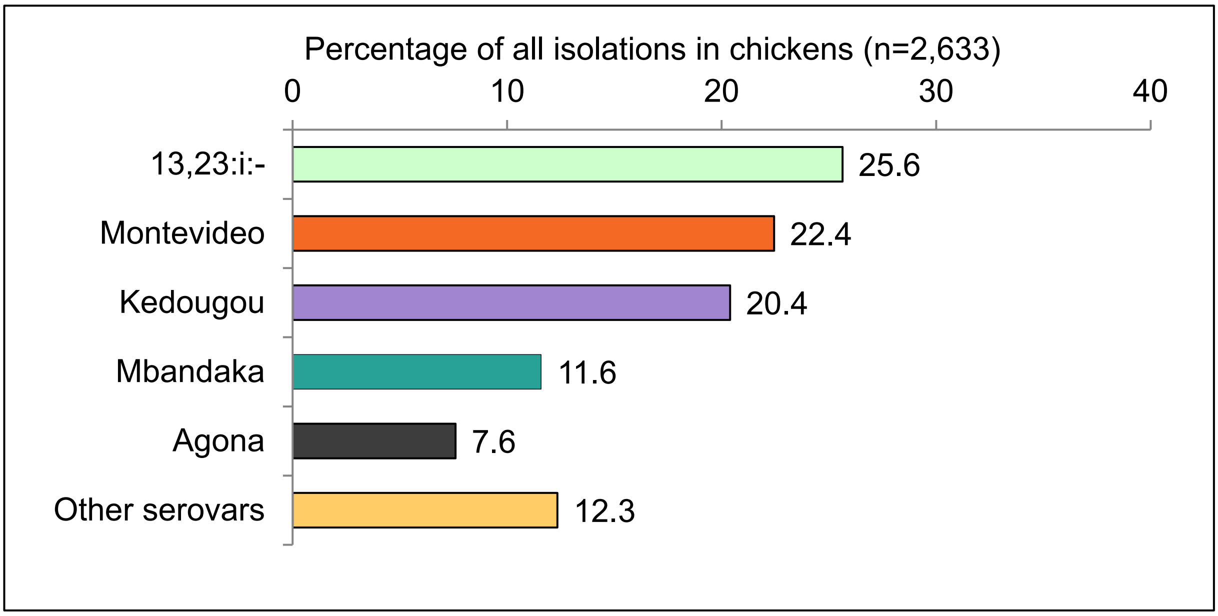
In 2021 the most common *Salmonella* serovar in chickens was *S.* Montevideo accounting for 24.1% of total isolations, followed by *S.* Mbandaka (17.6%), *S*. 13,23:i:- (16.7%) and *S.* Kedougou (13.0%).

Figure 6.2.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in chickens was *S.* Mbandaka accounting for 28.9% of total isolations, followed by *S.* Montevideo (19.1%), *S*. 13,23:i:- (14.3%) and *S.* Kedougou (11.5%).

Figure 6.2.5: Isolations in 2023



In 2023 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:- accounting for 25.6% of total isolations, followed by *S.* Montevideo (22.4%), *S*. Kedougou (20.4%) and *S.* Mbandaka (11.6%).

Figure 6.3: The 5 most common *Salmonella* serovars in chickens in Great Britain in 2023 and their trends over time since 2019

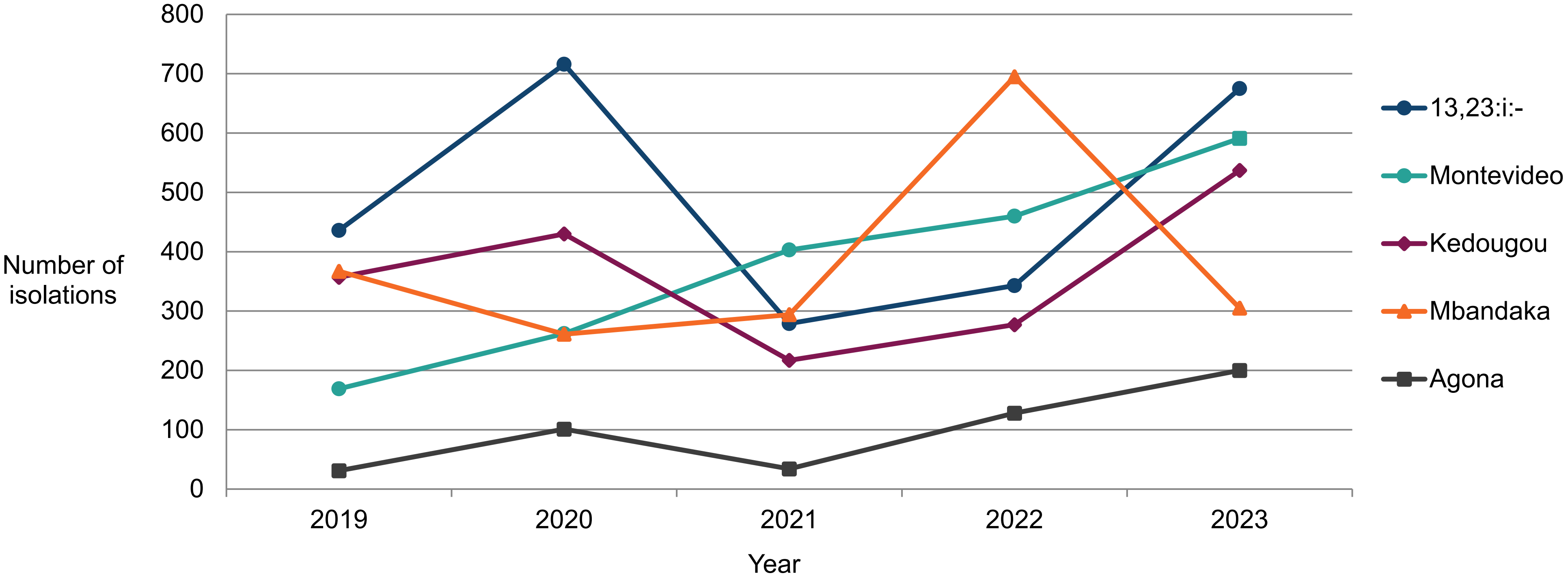


Figure 6.3 shows that in 2019 and 2020 *S.* 13,23:i:- was the most common serovar isolated from chickens and while it fell to third most common in 2022 (343 isolations) it has increased in 2023 to 675 isolations. *S.* Mbandaka, which has typically been second or third most common dropped to fourth most frequently isolated serovar in 2023 with 305 isolations. *S.* Kedougou isolations fluctuate and it was third most common in 2023 (537 isolations).*S.* Montevideo has steadily increased over time to be the second most common in 2023 (591 isolations) and *S.* Agona remains the fifth most commonly isolated with 200 isolations in 2023.

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

Phage types	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
DT1	0	0	0	0	1	2	1	2	1	1
DT2	1	1	3	9	3	4	0	0	0	0
DT13	0	1	0	0	0	0	0	0	0	0
DT35	1	1	0	0	0	0	0	0	0	0
DT36	1	1	0	0	0	0	0	0	0	0
DT75	0	0	0	0	0	0	5	8	2	6
DT99	4	4	0	0	0	0	1	1	4	4
DT104	0	0	0	0	2	2	0	0	0	0
DT105	0	0	0	0	0	0	0	0	4	6
DT116	0	0	0	0	0	1	0	0	0	0
DT193	1	2	2	6	1	1	0	0	0	1
U308	0	0	0	2	0	0	0	0	0	0
U320	0	0	0	0	1	1	0	0	0	0
NOPT	0	0	0	0	0	0	0	0	0	1
RDNC	3	4	1	2	4	4	4	7	2	2
Total	**11**	**14**	**6**	**19**	**10**	**15**	**11**	**18**	**13**	**21**

In 2021 one flock tested positive for U320, DT193 and RDNC in 2021 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 2019 to 2023

Phage types	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
DT120	0	0	0	0	0	0	0	1	0	0
DT193	4	5	1	12	9	12	10	18	5	6
NOPT	0	0	0	0	0	0	0	0	0	0
RDNC	0	0	0	1	0	0	0	0	0	0
UNTY	2	2	0	0	0	0	0	0	0	0
Total	**6**	**7**	**1**	**13**	**9**	**12**	**10**	**19**	**5**	**6**

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 types	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
PT2	1	1	0	0	0	0	0	0	0	0
PT4	0	1	0	2	3	3	0	0	2	2
PT7	0	0	0	0	0	0	0	0	0	0
PT8	12	35	9	22	0	2	3	19	6	7
PT8a	0	0	0	0	1	1	0	0	0	0
PT9b	0	0	0	0	0	1	0	0	0	0
PT11	0	0	0	0	0	0	1	1	0	0
PT11b	1	1	0	0	0	0	0	0	0	0
PT13	1	1	3	5	0	0	0	0	0	0
PT13a	2	8	0	0	0	1	0	0	0	0
PT14b	0	0	0	0	0	0	1	1	0	0
PT20	0	0	0	0	1	1	1	1	0	0
PT62	0	0	0	0	0	0	0	0	0	0
NOPT	0	0	0	0	0	0	0	1	0	0
UNTY	0	1	1	2	0	0	0	0	0	0
Total	**16**	**48**	**12**	**31**	**5**	**9**	**6**	**23**	**8**	**9**

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

In 2019 one flock tested positive for both PT11b and PT13a but is included only once in the total.

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 2023

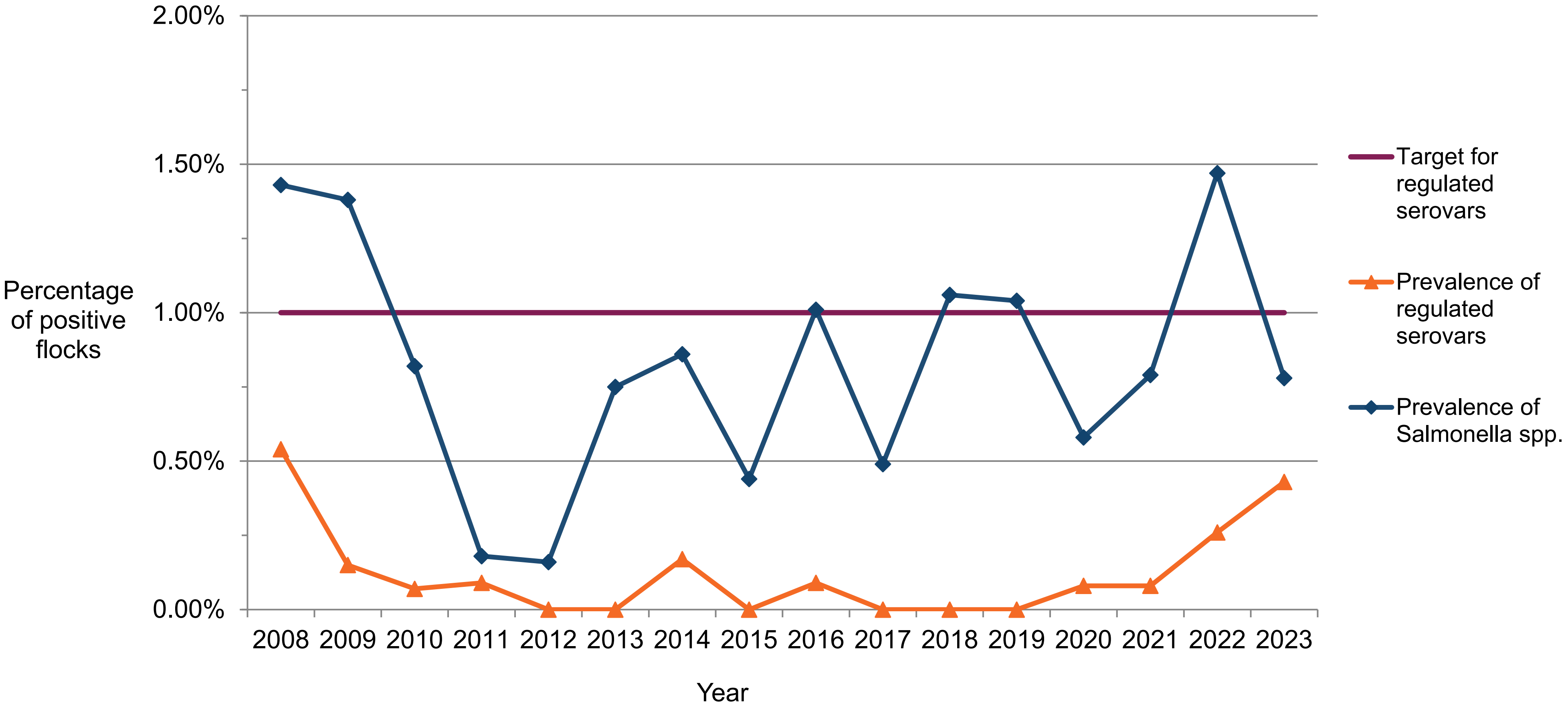


Figure 6.4 shows a variable prevalence of *Salmonella spp.* in breeding chicken flocks of between 0.16% and 1.47% but a more constant, lower prevalence of regulated serovars of between 0.0% and 0.54% which does not exceed the target of 1% prevalence.

Table 6.5: Chicken breeding flocks in Great Britain. Number of flocks reported positive with each *Salmonella* serovar, NCP testing 2019 to 2023

The following table shows the number of chicken breeding flocks reported positive with each *Salmonella* serovar from 2019 to 2023 and serovar rank in that year.

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Typhimurium	0	0	2	1	0	0	2	2	1	4
13,23:i:-	1	7	1	2	2	1	1	5	2	3
Anatum	0	0	0	0	0	0	3	1	3	1
Infantis	0	0	0	0	2	1	3	1	3	1
Agona	0	0	0	0	0	0	2	2	0	0
Bardo	0	0	2	1	0	0	0	0	0	0
Corvallis	0	0	0	0	0	0	3	1	0	0
Give var. 15^{+}	0	0	0	0	1	5	2	2	0	0
Idikan	0	0	0	0	0	0	3	1	0	0
Kedougou	0	0	1	2	0	0	0	0	0	0
Kottbus	3	1	0	0	0	0	0	0	0	0
London	0	0	0	0	2	1	0	0	0	0
Mbandaka	0	0	2	1	2	1	3	1	0	0
Newport	0	0	2	1	2	1	0	0	0	0
Nottingham	3	1	0	0	0	0	0	0	0	0
O rough:g,m,t:-	0	0	0	0	0	0	0	0	0	0
Ohio	2	2	0	0	0	0	3	1	0	0
Orion var. 15^{+}	0	0	0	0	0	0	3	1	0	0
3,19:z_{27}:-	3	1	0	0	0	0	0	0	0	0
6,7:-:enz$_{15}$	3	1	0	0	0	0	0	0	0	0

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
6,8:e,h:-	0	0	2	1	0	0	0	0	0	0

For details of chicken breeding flocks reported positive in 2010 to 2018, see the 2018 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
2019	1.04%	0.00%
2020	0.58%	0.08%
2021	0.79%	0.08%
2022	1.47%	0.26%
2023	0.78%	0.43%

Flocks testing positive for more than one serovar

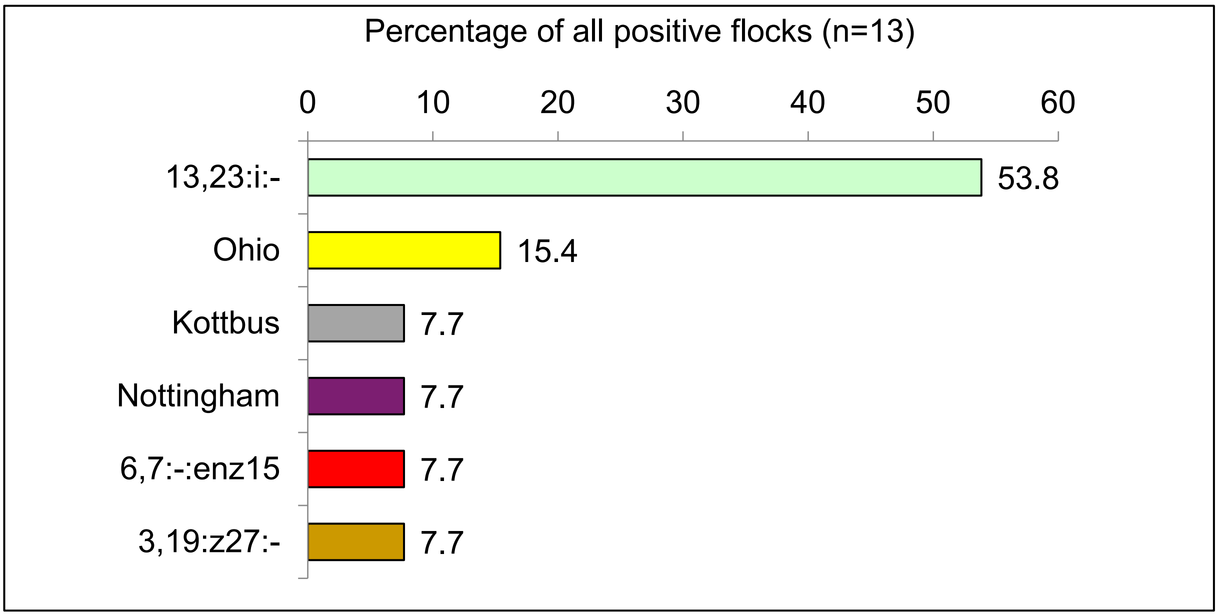
Some flocks tested positive for more than one serovar. Each flock was counted only once in the overall figure to calculate prevalence.

In 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^+.

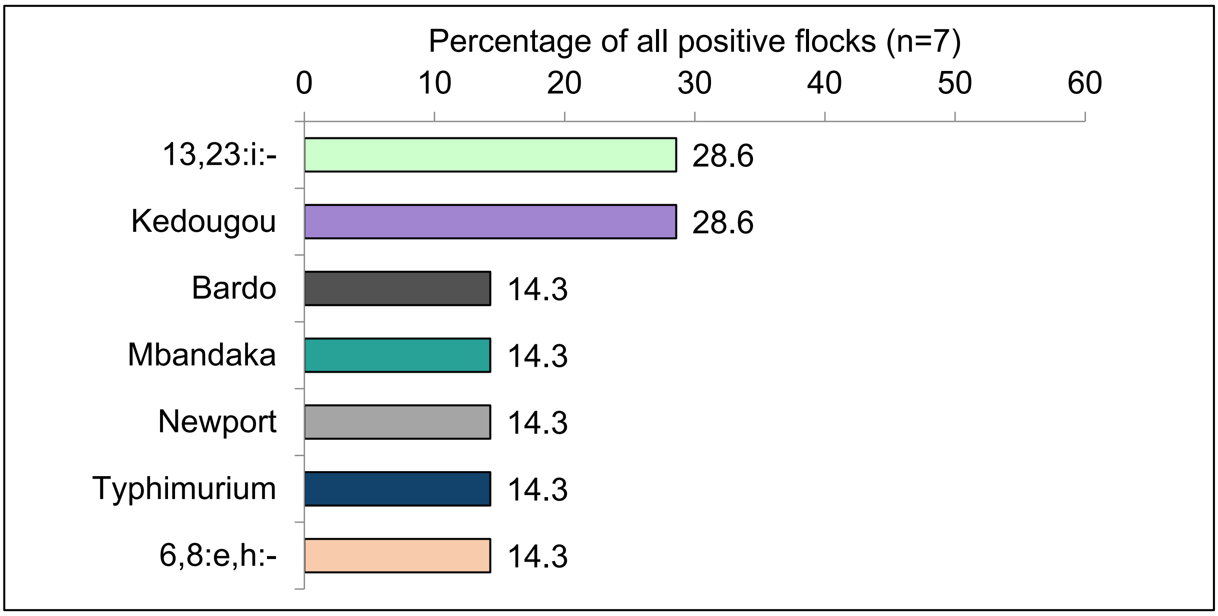
Figure 6.5: Serovars identified in adult chicken breeding flocks in Great Britain 2019 to 2023 reported from NCP testing

Figure 6.5.1: Isolations in 2019



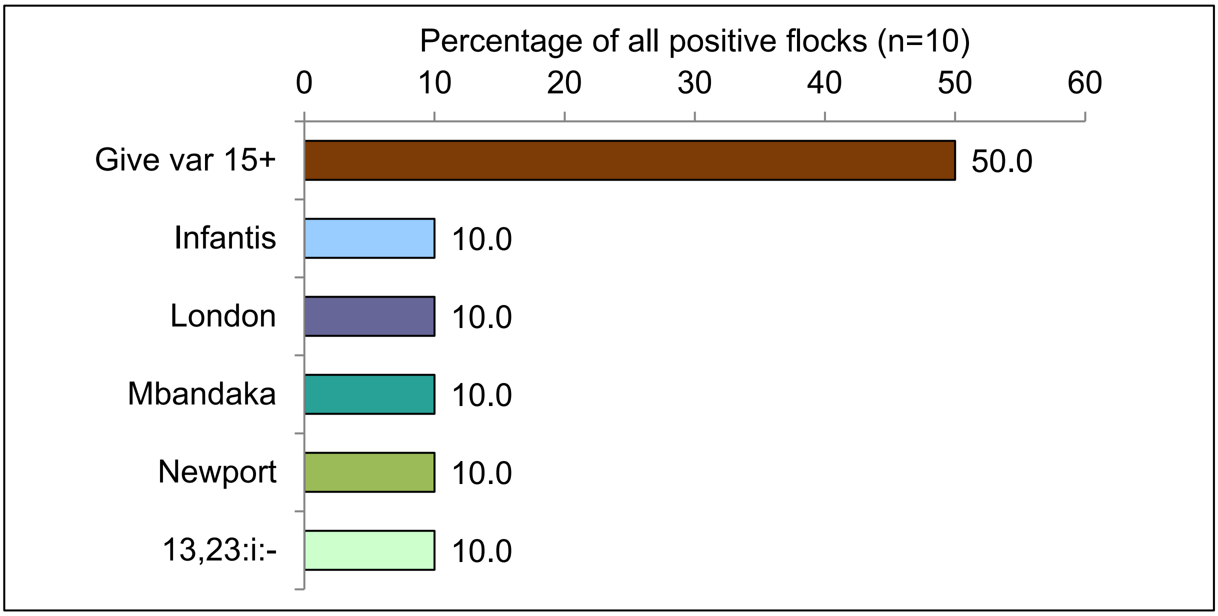
In 2019 the most common *Salmonella* serovar in all positive flocks was *S.* 13,23:i:- accounting for 53.8% of total isolations, followed by *S.* Ohio (15.4%). All other Serovars made up the remaining 30.8%

Figure 6.5.2: Isolations in 2020



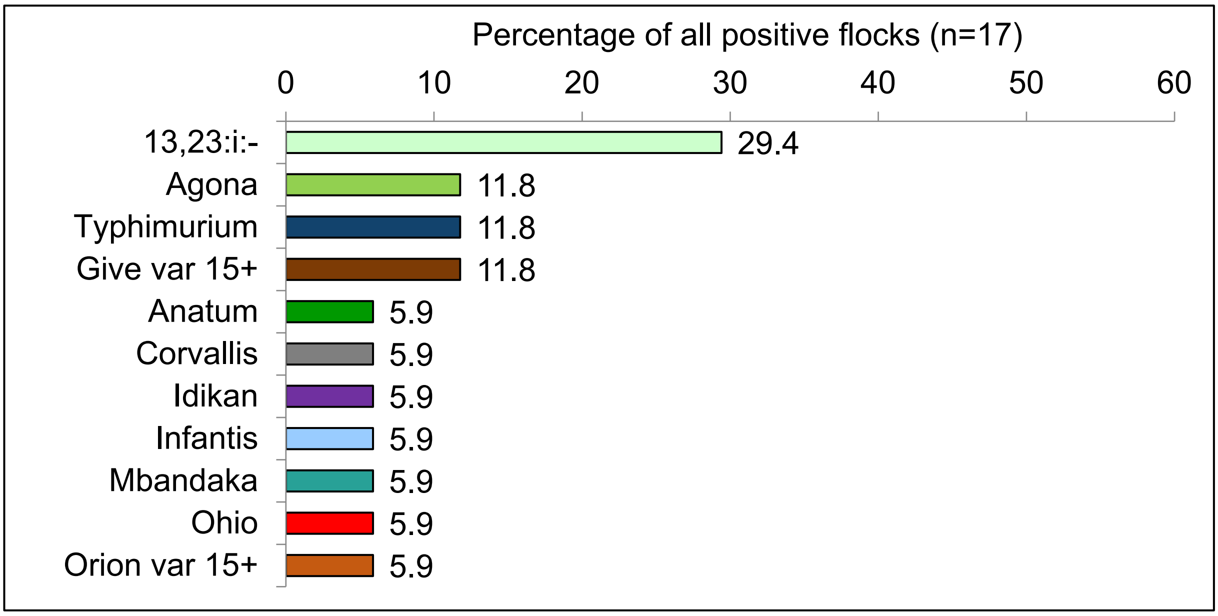
In 2019 the most common *Salmonella* serovars in all positive flocks was *S.* 13,23:i:- and *S.* Kedougou both accounting for 28.6% of total isolations each. All other Serovars made up the remaining 71.5%

Figure 6.5.3: Isolations in 2021



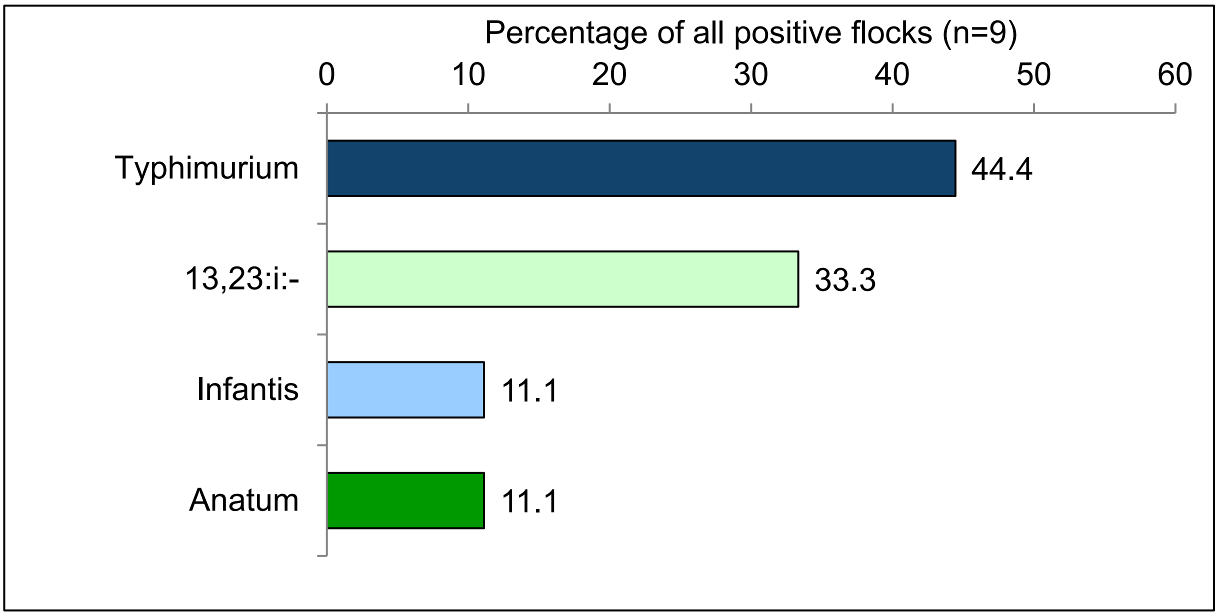
In 2021 the most common *Salmonella* serovar in all positive flocks was *S*. Give var. 15^+ accounting for 50.0% of total isolations. Each of the other 5 serovars recorded, accounted for 10% of total isolations.

Figure 6.5.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in all positive flocks was *S.* 13,23:i:- accounting for 29.4% of total isolations, followed by *S. Agona* (11.8%), *S.* Typhimurium (11.8%) and Give var. 15^+ (11.8%). All other Serovars made up the remaining 41.3%

Figure 6.5.5: Isolations 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.* 13,23:i:- (33.3%), *S*. Infantis (11.1%) and *S.* Anatum (11.1%).

In 2021 and 2022 1 flock tested positive for 2 serovars (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

Figure 6.6: Prevalence of *Salmonella* in laying hen flocks tested under NCP in Great Britain 2008 to 2023

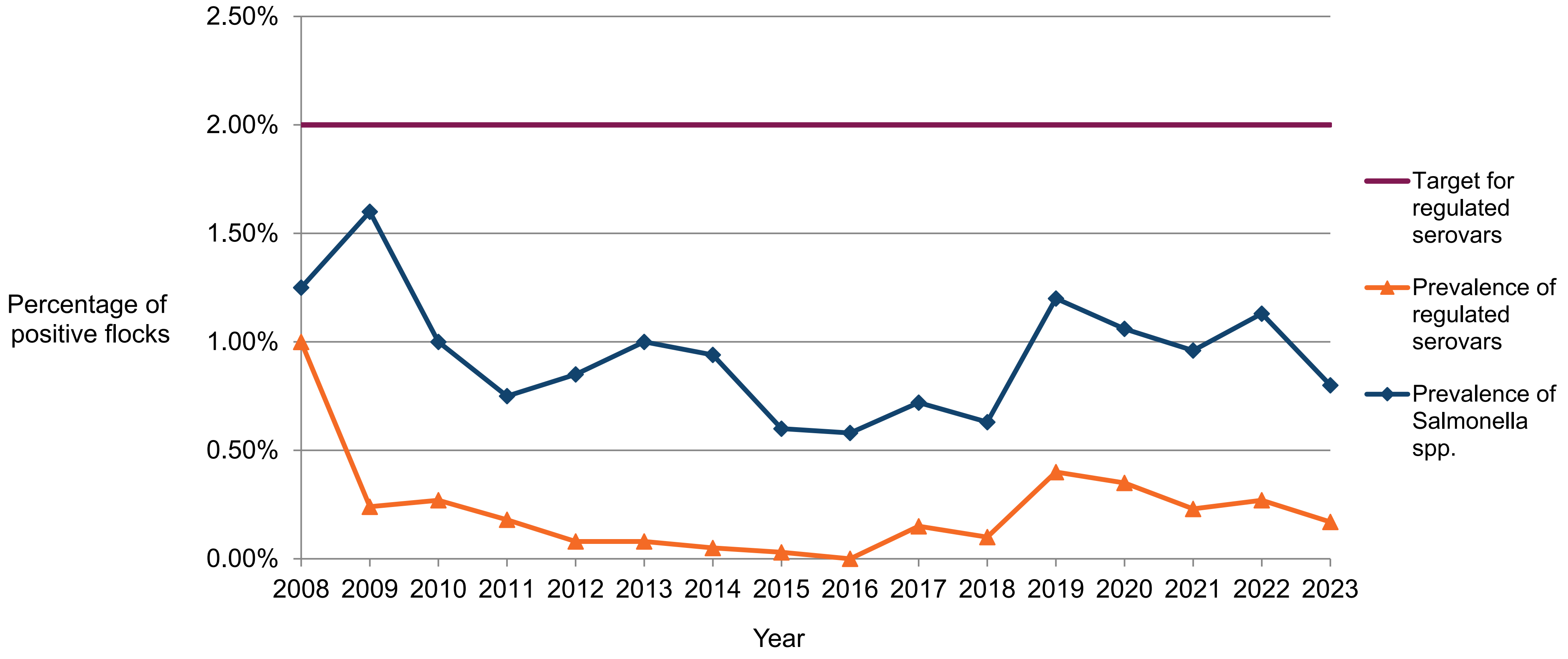


Figure 6.6 shows a variable prevalence of *Salmonella spp.* in laying hen flocks of between 0.58% and 1.60% and a similar but lower prevalence of regulated serovars of between 0.0% and 1.0% which does not exceed the target of 2% prevalence across all years.

Table 6.6: Laying hen flocks in Great Britain. Number of flocks reported positive with each *Salmonella* serovar, NCP testing 2019 to 2023

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Enteritidis	1	14	1	11	4	3	2	5	1	3
Give	0	0	0	0	0	0	0	0	1	3
Infantis	0	0	0	0	6	1	4	3	1	3
Typhimurium	5	1	3	4	2	6	2	5	2	2
Montevideo	4	2	5	1	5	2	5	2	2	2
Newport	3	3	4	2	1	7	4	3	2	2
Monophasic Typhimurium	5	1	0	0	0	0	0	0	3	1
Agama	2	4	4	2	6	1	6	1	3	1
Amsterdam	0	0	0	0	0	0	0	0	3	1
Coeln	0	0	5	1	0	0	0	0	3	1
Cubana	0	0	0	0	0	0	0	0	3	1
Dublin	5	1	0	0	0	0	3	4	3	1
Indiana	0	0	0	0	0	0	6	1	3	1
Kentucky	0	0	0	0	0	0	6	1	3	1
Kingston	0	0	5	1	0	0	0	0	3	1
Livingstone	0	0	4	2	0	0	6	1	3	1
Mbandaka	5	1	0	0	6	1	1	6	3	1
Orion	0	0	0	0	0	0	0	0	3	1
Yoruba	0	0	0	0	0	0	0	0	3	1
4,12:b:-	0	0	0	0	0	0	0	0	3	1
Africana	5	1	0	0	0	0	0	0	0	0
Agona	0	0	2	6	0	0	6	1	0	0
Anatum	4	2	5	1	6	1	0	0	0	0

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Bardo	0	0	0	0	3	5	4	3	0	0
Bareilly	0	0	0	0	6	1	0	0	0	0
Bovismorbificans	0	0	4	2	4	3	0	0	0	0
Bredeney	0	0	5	1	0	0	0	0	0	0
Budapest	0	0	0	0	0	0	0	0	0	0
Derby	5	1	5	1	6	1	3	4	0	0
Havana	0	0	0	0	6	1	0	0	0	0
Idikan	5	1	5	1	0	0	0	0	0	0
Isangi	0	0	0	0	6	1	0	0	0	0
Kedougou	2	4	5	1	0	0	6	1	0	0
Kottbus	5	1	5	1	0	0	0	0	0	0
Lexington	0	0	0	0	6	1	0	0	0	0
Liverpool	0	0	5	1	0	0	0	0	0	0
London	5	1	0	0	0	0	0	0	0	0
Molade	0	0	0	0	6	1	0	0	0	0
Nima	5	1	0	0	0	0	0	0	0	0
Nottingham	4	2	0	0	0	0	0	0	0	0
O rough:z_{38}:-	0	0	0	0	6	1	0	0	0	0
O rough:g,m:-	0	0	0	0	0	0	0	0	0	0
Odozi	0	0	0	0	5	2	0	0	0	0
Oslo	0	0	5	1	6	1	0	0	0	0
Ramatgam	0	0	5	1	0	0	0	0	0	0
Reading	5	1	5	1	0	0	0	0	0	0
Rissen	5	1	0	0	0	0	0	0	0	0
Schwarzengrund	0	0	5	1	0	0	0	0	0	0
Senftenberg	5	1	0	0	0	0	6	1	0	0
Soerenga	0	0	0	0	0	0	0	0	0	0

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Stanleyville	0	0	5	1	0	0	0	0	0	0
Stourbridge	0	0	0	0	6	1	6	1	0	0
Tennessee	4	2	0	0	0	0	0	0	0	0
13,23:i:-	5	1	5	1	0	0	0	0	0	0
4,5,12:b:-	5	1	0	0	0	0	0	0	0	0
6,7:-:enz15	0	0	0	0	6	1	0	0	0	0

For details of laying hen flocks reported positive in 2013 to 2018, see the 2018 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
2019	1.20%	0.40%
2020	1.06%	0.35%
2021	0.96%	0.23%
2022	1.13%	0.27%
2023	0.80%	0.17%

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 2018 1 flock tested positive for both *S*. Enteritidis and *S*. O rough:g,m:-.

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.

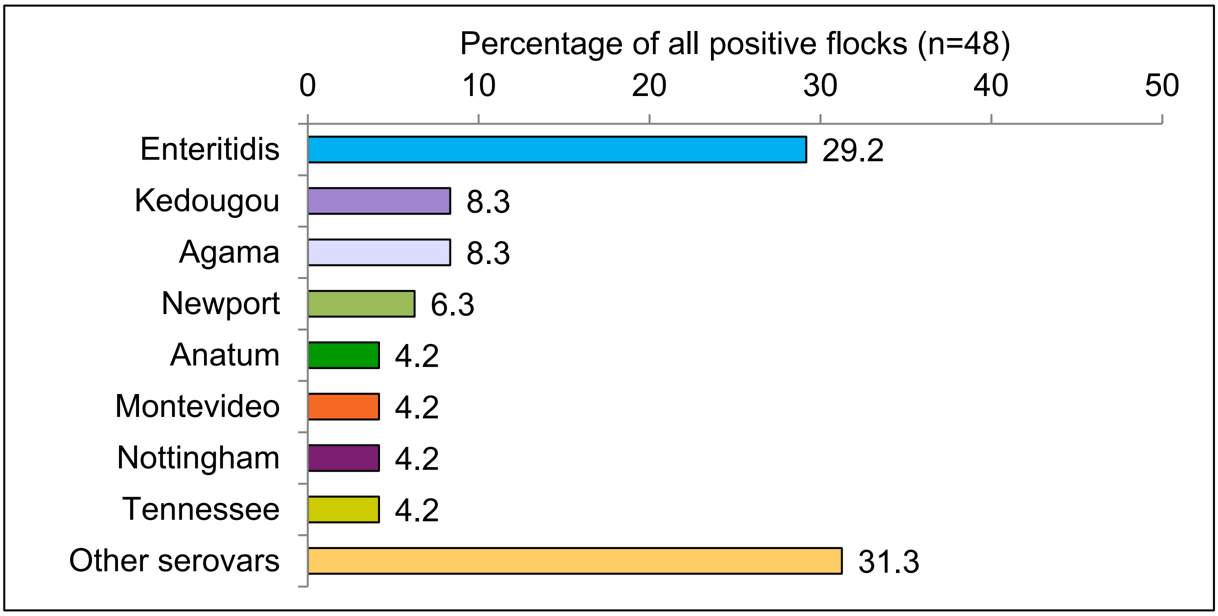
In 2021 3 flocks tested positive for *S*. Newport and *S*. Bardo and 1 flock that tested positive for *S*. Derby and *S*. Oslo.

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

In 2023 no flocks tested positive for 2 different serovars.

Figure 6.7: Serovars identified in adult laying hen flocks in Great Britain 2019 to 2023 reported from NCP testing

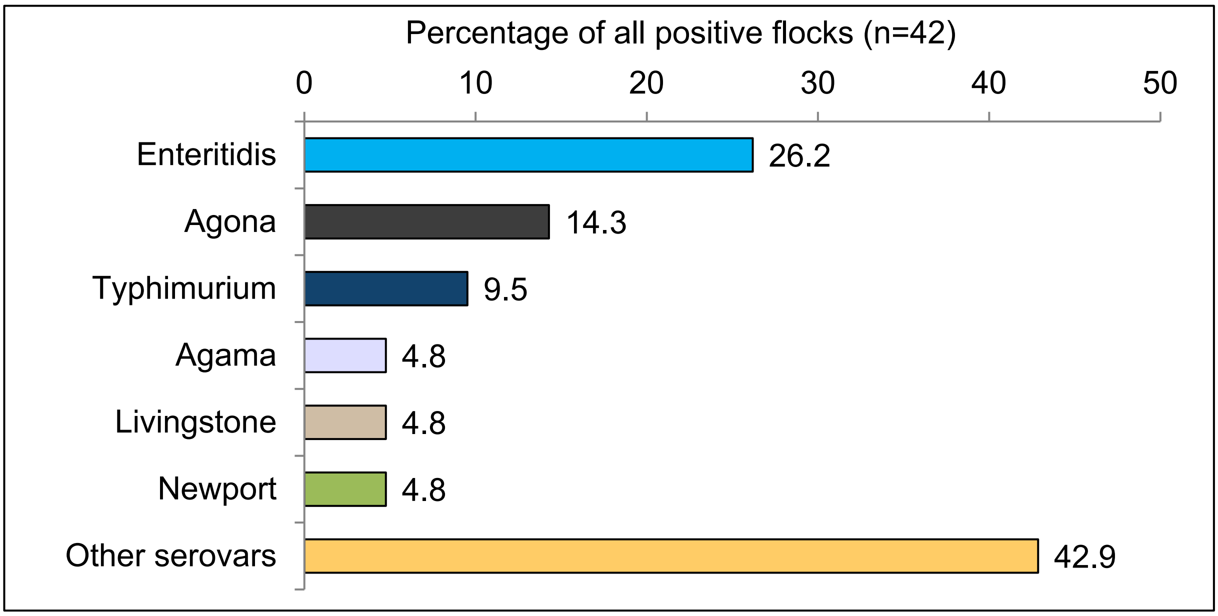
Figure 6.7.1: Isolations in 2019



In 2019 the most common *Salmonella* serovar in adult laying hen flocks was *S.* Enteritidis accounting for 29.2% of total isolations, followed by *S.* Kedougou (8.3%), *S. Agama* (8.3%) and *S.* Newport (6.3%).

In 2019 1 flock was positive for 2 serovars and 1 flock positive for 3 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%

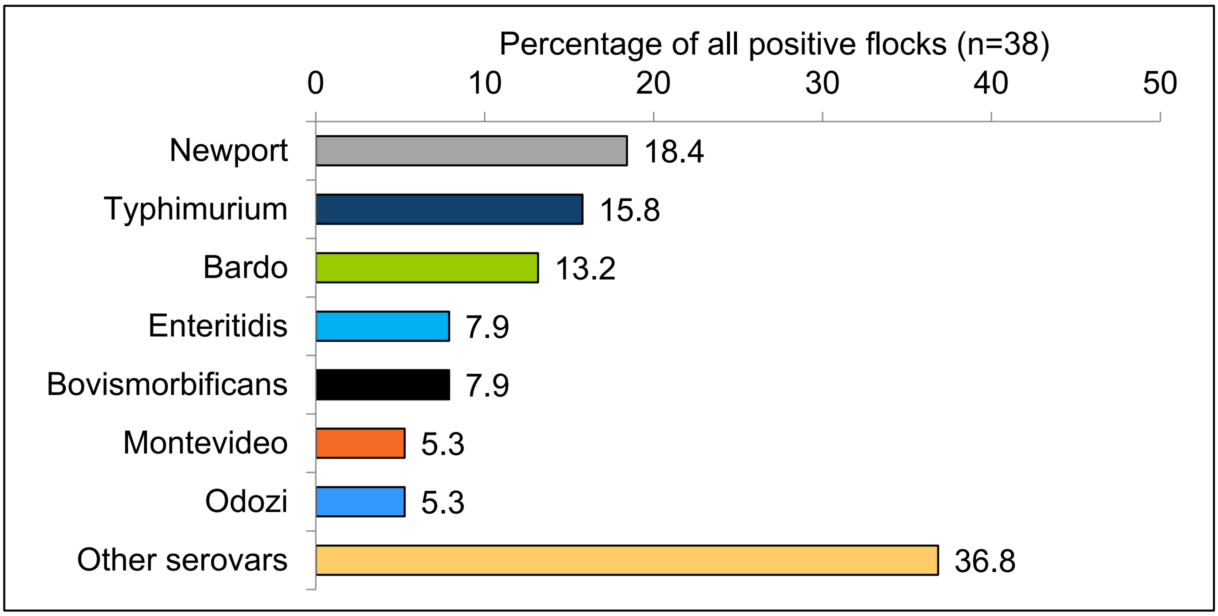
Figure 6.7.2: Isolations in 2020



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%).

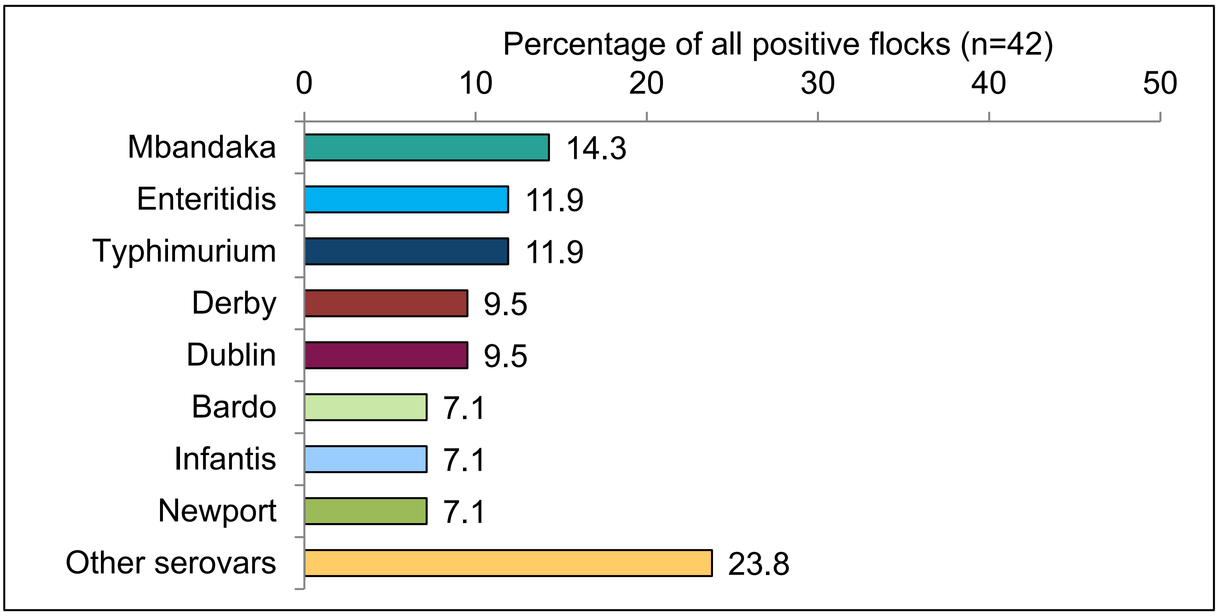
In 2020 4 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%

Figure 6.7.3: Isolations in 2021



In 2021 the most common *Salmonella* serovar in adult laying hen flocks was *S.* Newport accounting for 18.4% of total isolations, followed by *S.* Typhimurium (15.8%) and *S. B*ardo (13.2%).

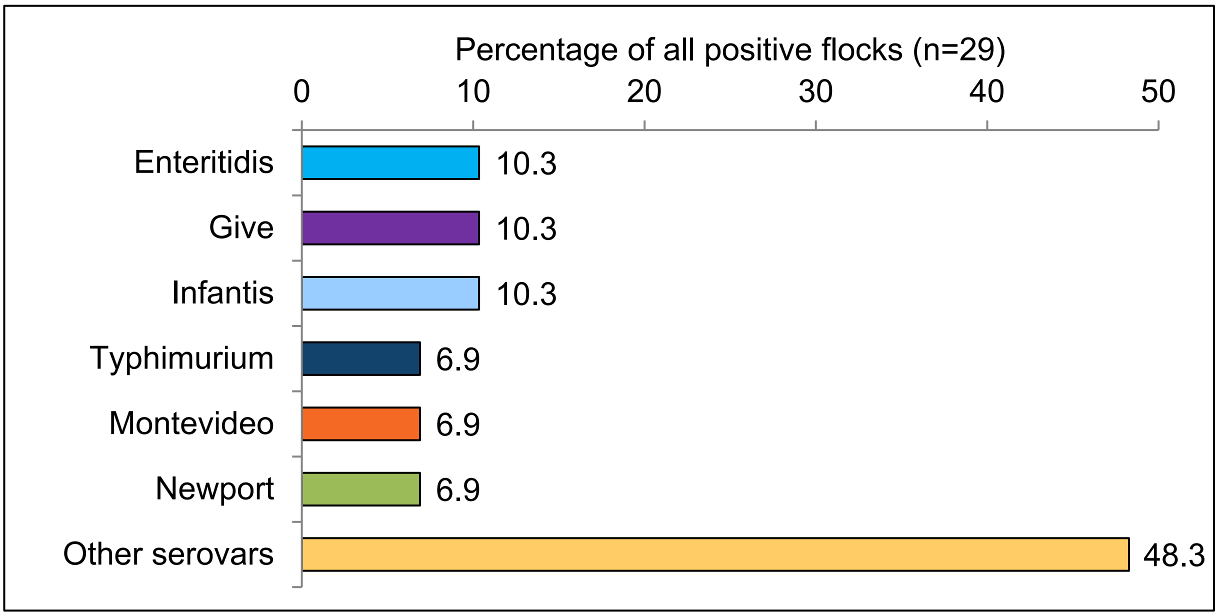
Figure 6.7.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in adult laying hen flocks was *S.* Mbandaka accounting for 14.3% of total isolations, 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 6.7.5: Isolations in 2023



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

Figure 6.8: Prevalence of *Salmonella* in broiler chicken flocks tested under NCP in Great Britain 2009 to 2023

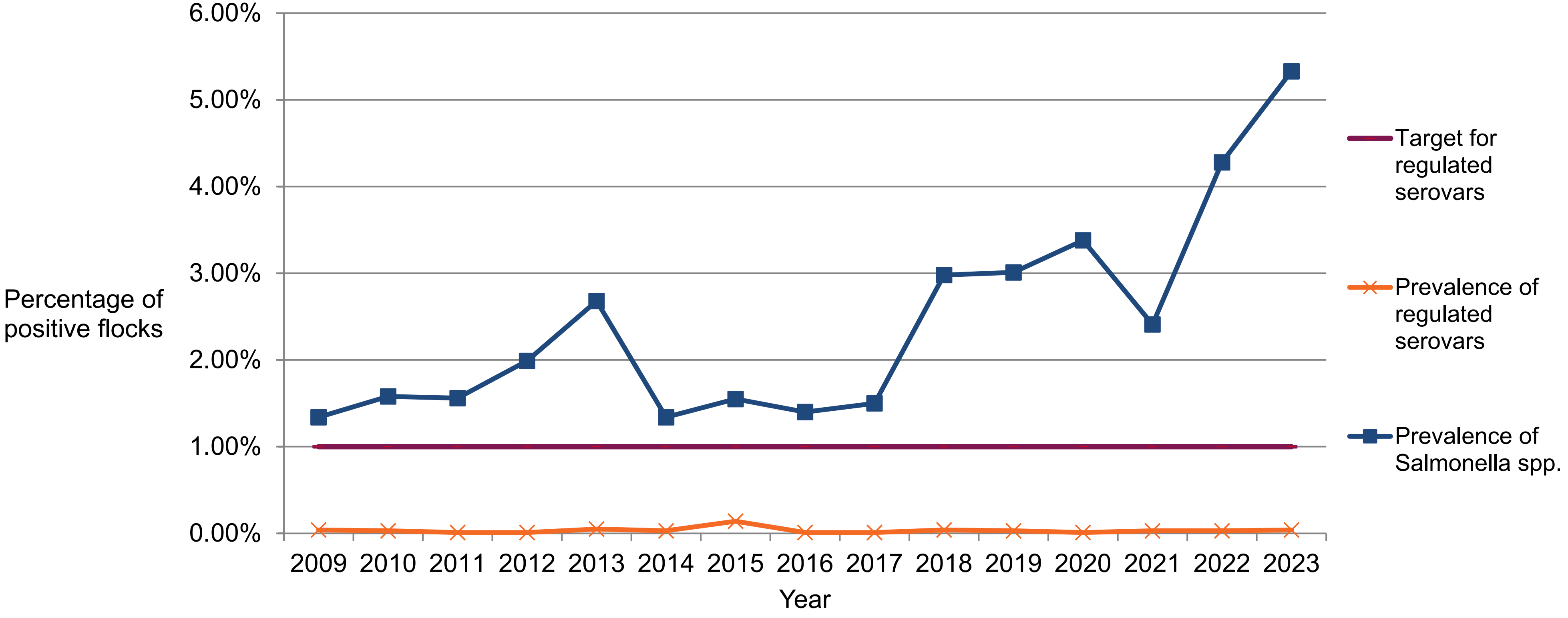


Figure 6.8 shows a variable prevalence of *Salmonella spp.* in broiler chicken flocks rising from 1.34% in 2009 to 5.33% in 2023 but a more constant, lower prevalence of regulated serovars of between 0.01% and 0.14% which does not exceed the target of 1% prevalence.

Table 6.7: Broiler chicken flocks in Great Britain. Number of flocks positive for each *Salmonella* serovar, NCP testing 2018 to 2023

The following table shows the number of broiler chicken flocks reported positive with each *Salmonella* serovar from 2018 to 2023 and the rank within that year. This data comes from NCP testing.

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
13,23:i:-	1	418	1	597	6	252	3	301	1	602
Montevideo	4	144	3	245	1	330	2	409	2	545
Kedougou	3	331	2	339	4	192	4	232	3	421
Mbandaka	2	334	4	231	3	238	1	579	4	272
Agona	7	29	5	67	6	33	5	114	5	191
Orion var. 15^{+}	9	12	8	28	6	33	7	54	6	56
Infantis	0	0	0	0	9	22	6	77	7	50
Ohio	5	69	7	33	5	54	8	43	8	35
Senftenberg	6	32	6	53	8	23	11	18	9	17
Derby	7	29	16	3	10	7	14	7	10	14
Livingstone	11	7	12	7	13	4	20	1	11	11
Typhimurium	10	10	18	1	13	4	17	4	12	7
6,7:z_{10}:-	13	3	9	21	8	23	10	21	13	6
Braenderup	0	0	18	1	15	2	19	2	14	5
Enteritidis	14	2	18	1	15	2	20	1	14	5
Give var 15+	12	4	15	4	16	1	15	6	14	5
Idikan	8	15	15	4	12	5	9	40	14	5
Muenchen	15	1	13	6	13	4	13	9	14	5
4,5,12:i:-	14	2	0	0	11	6	12	10	15	4
Anatum	13	3	14	5	14	3	20	1	15	4
Indiana	11	7	17	2	0	0	0	0	15	4
Coeln	15	1	18	1	0	0	17	4	16	3

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
4,12:d:-	11	7	14	5	16	1	19	2	17	2
Agama	13	3	17	2	0	0	0	0	17	2
Newport	14	2	11	10	15	2	14	7	17	2
Ajioba	0	0	0	0	0	0	0	0	18	1
Bovismorbificans	0	0	10	14	13	4	0	0	18	1
Chomedey	0	0	0	0	0	0	0	0	18	1
Durham	0	0	0	0	0	0	0	0	18	1
Frenso	0	0	0	0	0	0	0	0	18	1
Give	0	0	17	2	0	0	0	0	18	1
Oslo	14	2	18	1	16	1	0	0	18	1
Oxford	0	0	0	0	0	0	0	0	18	1
4,12:i,v:-	0	0	0	0	0	0	0	0	18	1
4,5,12:a:-	0	0	0	0	0	0	0	0	18	1
6,7:-:-	0	0	0	0	0	0	15	6	0	0
Havana	15	1	18	1	16	1	16	1	0	0
Kentucky	15	1	0	0	0	0	18	3	0	0
Kingston	15	1	18	1	0	0	19	2	0	0
London	15	1	0	0	0	0	19	2	0	0
Nottingham	15	1	0	0	0	0	19	2	0	0
47:z4,z23: -	0	0	0	0	0	0	20	1	0	0
6,7:d:-	0	0	0	0	0	0	20	1	0	0
6,8:d: -	0	0	0	0	0	0	20	1	0	0
Berta	0	0	0	0	0	0	20	1	0	0
Corvallis	0	0	0	0	0	0	20	1	0	0
Eboko	0	0	0	0	0	0	20	1	0	0
Kotbus	0	0	18	1	0	0	20	1	0	0
Liverpool	0	0	0	0	0	0	20	1	0	0
Orion	13	3	0	0	0	0	20	1	0	0
Panama	0	0	0	0	16	1	20	1	0	0

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Rissen	0	0	0	0	0	0	20	1	0	0
Stanley	15	1	0	0	0	0	20	1	0	0
13,22: -:1,6	0	0	18	1	0	0	0	0	0	0
13,23: - : -	0	0	18	1	0	0	0	0	0	0
13,23: -:l,w	14	2	0	0	0	0	0	0	0	0
28: - : -	15	1	0	0	0	0	0	0	0	0
3,10:e,h: -	15	1	0	0	0	0	0	0	0	0
3,15:l,v: -	0	0	18	1	0	0	0	0	0	0
3,19: - : -	0	0	0	0	15	2	0	0	0	0
4,12:e,h:-	0	0	13	6	0	0	0	0	0	0
4,12:i:-	13	3	18	1	14	3	0	0	0	0
6,7:-:enz15	0	0	17	2	0	0	0	0	0	0
61:-:1,5,7	15	1	0	0	0	0	0	0	0	0
Eastbourne	13	3	0	0	0	0	0	0	0	0
Ferruch	0	0	0	0	15	2	0	0	0	0
Goldcoast	0	0	0	0	16	1	0	0	0	0
Isangi	0	0	0	0	0	0	0	0	0	0
Mikawasima	0	0	18	1	0	0	0	0	0	0
O rough:l,v:1,7	0	0	18	1	0	0	0	0	0	0
O rough:z10:e,n,z15	15	1	0	0	0	0	0	0	0	0
Offa	15	1	0	0	0	0	0	0	0	0
Poona	0	0	18	1	0	0	0	0	0	0
Reading	0	0	0	0	16	1	0	0	0	0
Stourbridge	0	0	18	1	16	1	0	0	0	0

For details of broiler chicken flocks reported positive in 2013 to 2018, see the 2018 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
2019	3.01%	0.03%
2020	3.38%	0.01%
2021	2.41%	0.03%
2022	4.28%	0.03%
2023	5.33%	0.04%

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 2019:

- 3 flocks tested positive for both *S*. Kedougou and *S*. Ohio
- 3 flocks tested positive for both *S*. 13,23:i:- and *S*. Kedougou
- 2 flocks tested positive for both *S*. Mbandaka and *S*. Montevideo
- 2 flocks tested positive for both *S*. Anatum and *S*. Derby
- 1 flock tested positive for both *S*. 13,23:i:- and *S*. Agona
- 1 flock tested positive for both *S*. 13,23:i:- and *S*. Mbandaka
- 1 flock tested positive for both *S*. Orion var. 15^+ and *S*. Orion
- 1 flock tested positive for both *S*. 4,12:d:- and *S*. Montevideo
- 1 flock tested positive for both *S*. 4,12:i:- and *S*. Kedougou

- 1 flock tested positive for *S*. Typhimurium, *S*. 13.23:i:- and *S*. Nottingham

In 2020:

- 4 flocks tested positive for *S*. Mbandaka and *S*. 6,7:z10:-
- 4 flocks tested positive for *S*. Idikan and *S*. 13,23:i:-
- 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*. 13,23:i:- and *S*. Mbandaka
- 1 flock tested positive for *S*. 13,23:i:- and *S*. Agona
- 1 flock tested positive for *S*. Livingstone and *S*. 13,23:i:-
- 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*. 13,23:i:-
- 1 flock tested positive for both *S*. Mbandaka and *S*. Montevideo
- 1 flock tested positive for both *S*. 13,23:i:- and *S*. Orion var. 15^+
- 1 flock tested positive for both *S*. Kedougou and *S*. Mbandaka
- 1 flock tested positive for both *S*. 13,23:i:- 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

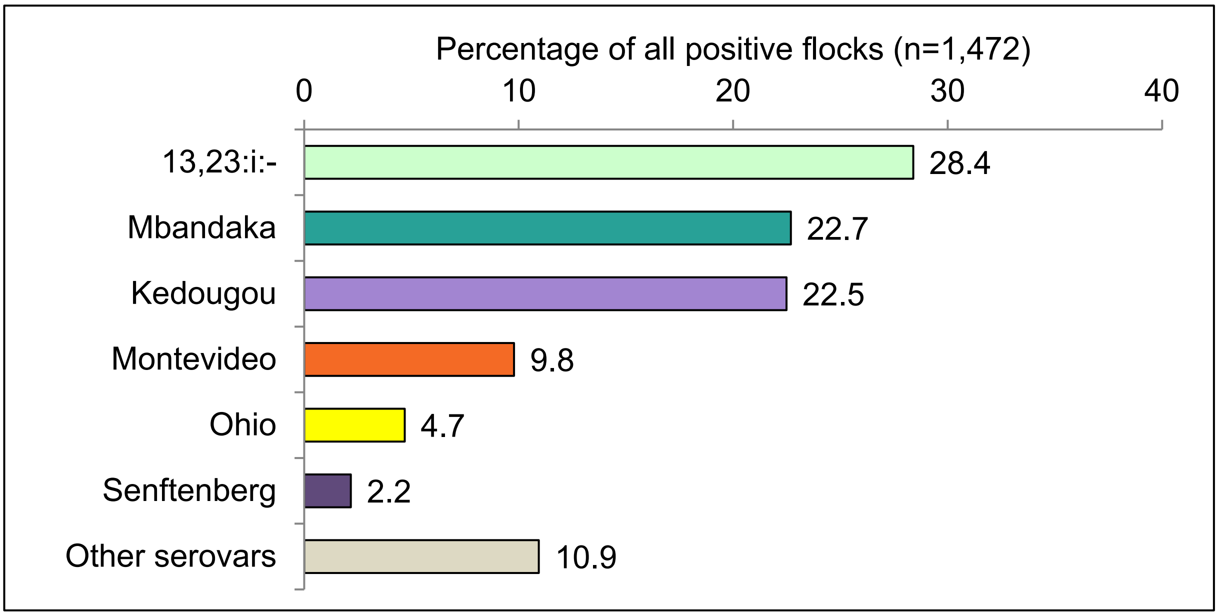
- 2 flocks tested positive for *S*. 13,23:i:- and *S*. Infantis
- 2 flocks tested positive for *S*. 13,23:i:- and *S*. Idikan
- 1 flock tested positive for the following combinations of multiple serovars: *S*. Mbandaka and *S*. Kedougou, *S*. Montevideo and *S*. Kedougou, *S*. Agona and *S*. Orion var. 15^{+}, *S*. Mbandaka and *S*. 6,7:d:-, *S*. Agona and *S*. Kedougou, *S*. 13,23:i:- and *S*. Montevideo x1, *S*. 6,7:-:- and *S*. Ohio

In 2023:

- 4 flocks tested positive for *S*. 13,23:i:- and *S*. Agona.
- 2 flocks tested positive for *S*. 13,23:i:- and *S*. Kedougou
- 2 flocks tested positive for *S*. Infantis and *S*. Kedougou
- 1 flock tested positive for *S*. 13,23:i:- and *S*. Muenchen
- 1 flock tested positive for *S*. 13,23:i:- and *S*. Montevideo
- 1 flock tested positive for *S*. 13,23:i:- and *S*. Orion var 15+
- 1 flock tested positive for *S*. 13,23:i:- 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.* 13,23:i:- and *S.* Agona in Official (routine annual) sampling
- 1 flock tested positive for *S.* Kedougou in both operator and official (replacement flocks) sampling

Figure 6.9: Serovars identified in broiler chickens in Great Britain 2019 to 2023 reported from NCP testing

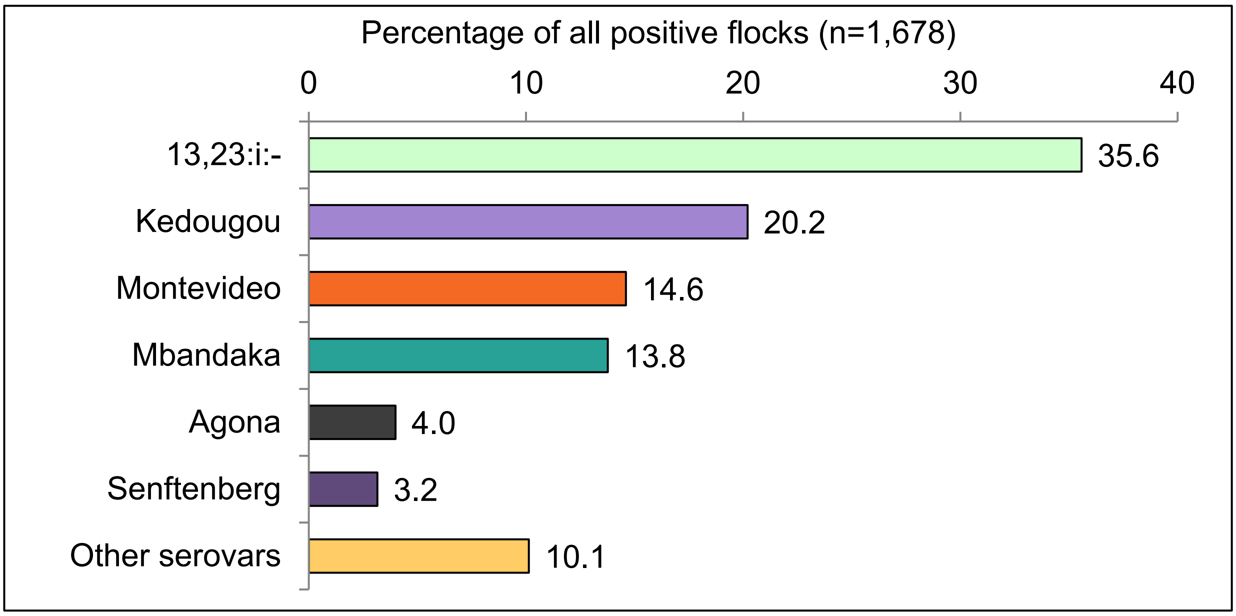
Figure 6.9.1: Isolations in 2019



In 2019 the most common *Salmonella* serovar in broiler flocks was *S.* 13,23:i:- accounting for 28.4% of total isolations, followed by *S.* Mbandaka (22.7%), *S.* Kedougou (22.5%) and *S.* Montevideo (9.8%).

In 2019 15 flocks were positive for 2 serovars and one flock positive for 3 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

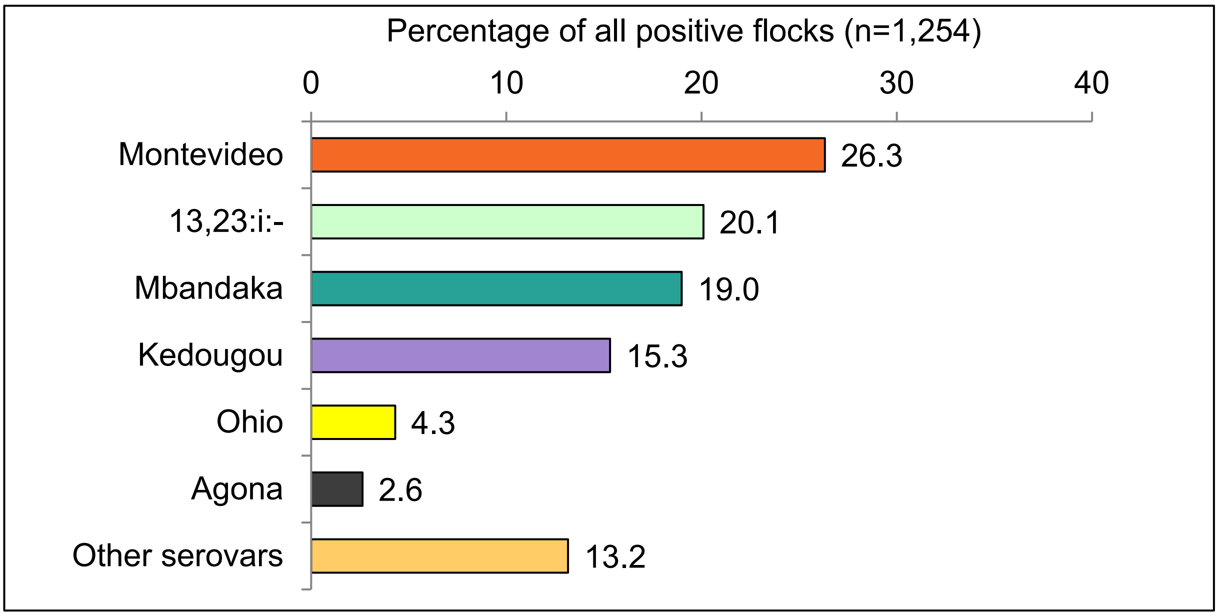
Figure 6.9.2: Isolations in 2020



In 2020 the most common *Salmonella* serovar in broiler flocks was *S.* 13,23:i:- accounting for 35.6% of total isolations, 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%.

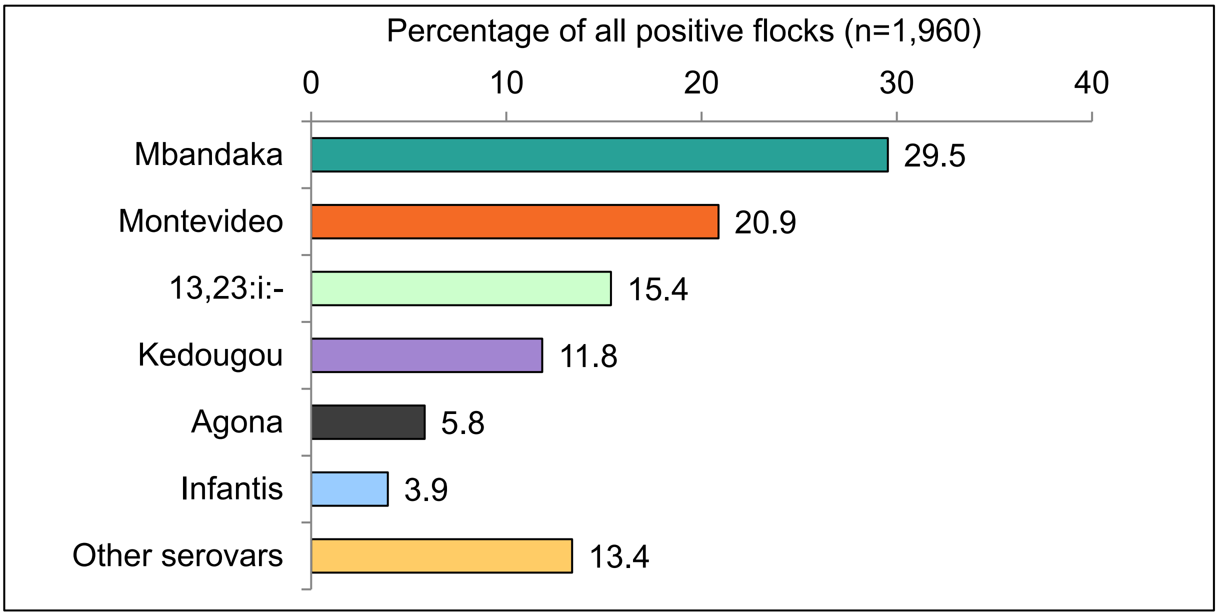
Figure 6.9.3: Isolations in 2021



In 2021 the most common *Salmonella* serovar in broiler flocks was *S.* Montevideo accounting for 35.6% of total isolations, followed by *S.* 13,23:i:- (20.1%), *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%.

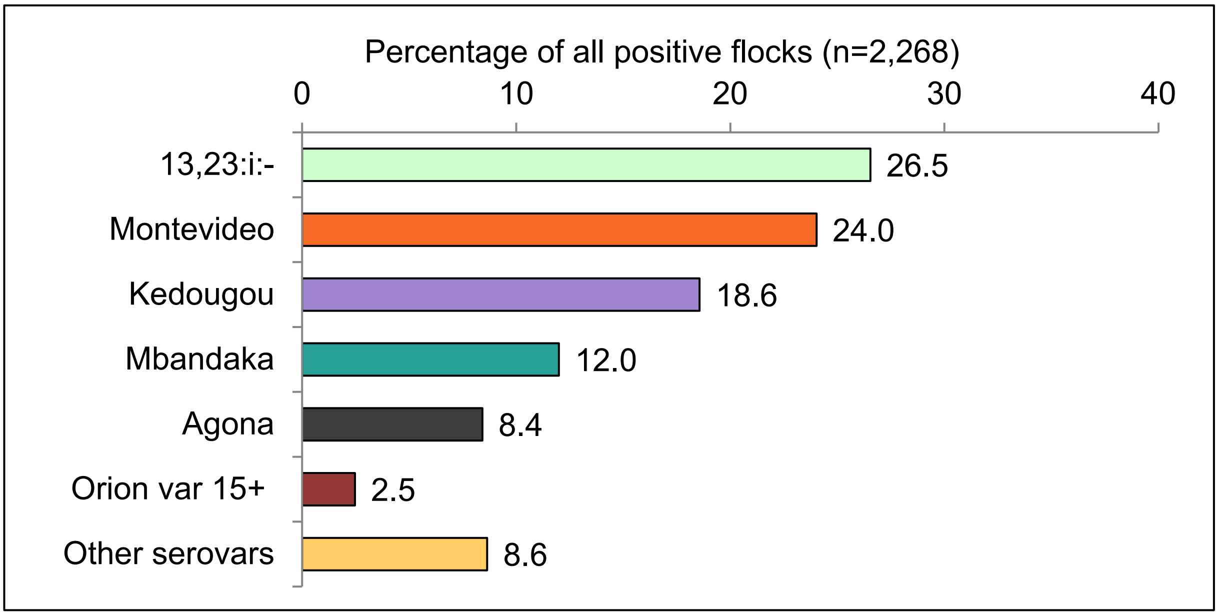
Figure 6.9.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in broiler flocks was *S.* Mbandaka accounting for 29.5% of total isolations, followed by *S*. Montevideo (20.9%), *S.* 13,23:i:- *(*15.4%) 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 6.9.5: Isolations in 2023



In 2023 the most common *Salmonella* serovar in broiler flocks was *S.* 13,23:i:- accounting for 26.5% of total isolations, 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%

Chapter 7: Reports of *Salmonella* in turkeys

During the early part of 2023 there was significant disruption to the poultry industry due to a national outbreak of Avian Influenza affecting all industry sectors. This resulted in altered management and biosecurity measures and is 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, 2021, 2022 and 2023 data with previous years.

According to the June Agricultural Census, there were 2.48 million turkeys in Great Britain in 2023 compared with 3.73 million in 2022, 3.72 million in 2021 and 3.65 million in 2020.

In January 2010, the National Control Programme (NCP) to control *Salmonella* in turkeys was implemented across the European Union. Breeding turkey farms with more than 250 adult birds on the holding at any time in a 12 month period and fattening turkey farms with more than 500 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 can be granted an exemption from operator testing. Since 2010, *Salmonella* reports from turkeys have largely originated from samples taken under the NCP, so data cannot be compared with previous years.

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

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

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

There were 264 turkey diagnostic and monitoring submissions made to APHA and SRUC laboratories in 2023. This compares to 283 in 2022, representing a decrease of 6.7%. In comparison, during 2009, before the introduction of the NCP for *Salmonella* in turkeys, the number of submissions was lower (240 submissions). However, APHA does not have information on the number of non-statutory submissions submitted to private laboratories that do not result in a positive culture of *Salmonella,* as these are not reportable under the Zoonoses Order.

A total of 109 *Salmonella* isolations were reported from turkeys in 2023 (Table 7.1), which represents a 42.0% decrease compared to 2022 (188 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 isolation of *S.* Derby. Subsequently the overall number of isolations from turkeys has declined each year up to 2021 (Table 7.1), which is primarily attributable to a decrease in *S.* Derby isolations. The increase in isolations in 2022, was not associated with an increase in *S*. Derby isolations.

The total number of isolations in 2023 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 101 (92.7%)
- voluntary surveillance: 7 (6.4%)
- investigations of clinical disease: 1 (0.9%)

Seventeen different serovars of *Salmonella* were isolated in 2023, accounting for 105 of the 109 isolations. The remaining 4 isolations included un-typable and rough *Salmonella* strains. Table 7.1 shows the absolute number of isolations of each *Salmonella* serovar isolated from turkeys, from 2019 to 2023, and Figure 7.1 shows the relative percentages of the most common serovars.

Salmonella Kedougou (43 isolations, 39.4% of all isolations), a feed related serovar, was the most common serovar in 2023. This represents a 43.3% increase in the number of isolations compared with 2022 (30 isolations). *S*. Kedougou has regularly featured among the 3 most common serovars isolated from turkeys since at least 2004 (Figure 7.1).

Salmonella Anatum (19 isolations, 17.4% of all isolations) was the second most frequently isolated serovar in 2023 having been the most frequently isolated serovar in 2022 (66 isolations) and 2021(31 isolations). Isolations of this serovar had increased dramatically since 2019 (4 isolations), which is likely to be associated with contaminated feed (Figure 7.1).

There were 11 isolations (10.1% of all isolations) of *S.* Orion var. 15^{+} in 2023, which represents more than a 50% increase from 2022 (5 isolations, 2.7% of all isolations). There has been an increasing number of isolations of this serovar in recent years since

2017 when no isolations of this serovar were recorded. A similar trend of increasing isolations of *S.* Orion var. 15^{+} has also been observed in chicken flocks in recent years.

Isolations of *S*. Senftenberg in recent years have represented a large proportion of total isolations, amongst the top 3 most common serovars. In 2023, only 3 isolations were recorded, a decrease of more than 88% compared to 2022 (26 isolations). 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 feedmills.

Historically *Salmonella* Derby has been associated with high numbers of isolations from turkeys in GB, representing the most common serovar isolated from turkeys from 2007-2019. Isolations of *S*. Derby peaked in 2016 with 501 isolations, subsequently isolations have been generally decreasing and in 2023 this serovar represented only 1.8% of all isolations (2 isolations) compared with 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 2022, with just one isolation of this serovar and in 2023 there were no isolations of *S*. Newport.

In 2023 there were 3 isolations of regulated serovars from turkey flocks with 2 isolations of *S*. Typhimurium (from a single turkey breeder site as part of NCP sampling and voluntary surveillance) compared to one isolation (from a turkey fattener site) in 2022. The prevalence of *S.* Typhimurium has 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 2019 and 2023 are shown in Table 7.2. The isolation of *S*. Typhimurium reported in 2023 was DT193 which has not been reported from turkeys in Great Britain since 2018.

The remaining isolation of regulated serovars originated from one turkey fattening holding, a single isolation of monophasic strain of *S.* Typhimurium 4,12:i:- (DT193). This is a reduction on recent years and compares with 3 isolations and 9 isolations of monophasic strains of *S.* Typhimurium from turkeys in 2022 and 2021 respectively (Tables 7.3 and 7.4). These strains are typically associated with pigs and were first reported from turkeys in 2011.

There were no isolations of *S*. Enteritidis in turkeys in 2023, consistent with 2022 and 2021. This serovar was last isolated from turkey flocks in 2017.

Notably, *S*. Chester (1 isolation from statutory official sampling in a fattening flock) has never previously been reported from turkeys, or other poultry in Great Britain. *S*. Dublin (1 isolation from a diagnostic sample), *S.* Orion (1 isolation from statutory operator sampling of fattening flocks) and *S*. Schwarzengrund (2 isolations from statutory operator sampling of fattening flocks) have all been isolated from turkeys for the first time in 2023.

There were no reported cases of *Salmonella* from turkeys imported into Great Britain in 2022.

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

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

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

The NCP is implemented via the Control of *Salmonella* in Turkey Flocks Order 2009 (CSTO) which came into force in England on the 1 January 2010.

Positive flocks identified in the NCP for breeding turkeys 2023

One adult turkey breeding flock tested positive for *Salmonella* in 2023. This has decreased from 4 positive flocks in 2022, and 2 positive flocks in 2021 and an 85.7% reduction compared with 2020 (7 positive flocks) (Table 7.5).

One turkey breeding flock tested positive for the regulated serovar, *Salmonella* Typhimurium (DT193) in 2023, the first time this serovar has been isolated from turkey breeder flocks. This is also the first time a regulated serovar has been identified in 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 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:-.

No adult turkey breeding flocks tested positive for *S.* Senftenberg in 2023, which has been the most frequently isolated serovar across the last 10 years and identified in 7 of the last 11 years (Table 7.5).

No immature breeding flocks tested positive for *Salmonella* in 2023 compared with 6 positive flocks in 2022 and 7 in 2021.

For comparison, the serovars identified in the adult turkey breeder NCP between 2019 and 2023 are shown in Table 7.5. Figure 7.5 shows the relative percentages of the serovars in the turkey breeder NCP from 2019 to 2023.

A total of 173 adult turkey breeding flocks were in production in Great Britain in 2023 and were included in the NCP. Therefore, the estimated prevalence for regulated serovars was 0.58% (1 of 173) which is below the target of a maximum of 1% of flocks testing positive. This figure is consistent with 2021 and 2020 (0.0%) and a decrease compared to 2019 (0.73%). The estimated prevalence for all serovars in 2023 was 0.58% (1 of 173), an increase from 0.83% in 2021 (2 flocks) but a decrease from 2.62% (7 flocks) in 2020. Figure 7.3 shows the change in prevalence of turkey breeder flocks testing positive for *Salmonella* serovars since 2013. 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.

Positive flocks identified in the NCP for fattening turkeys in 2023

In total, 70 fattening turkey flocks (on 34 different holdings) were positive for *Salmonella* in 2023. This represents a 27.8% decrease from 2022 (97 positive flocks on 46 different holdings) when there was a small increase in flocks testing positive for *Salmonella* which interrupted a year-on-year decreasing trend in the proportion of flocks testing positive from 2016-2021 (Table 7.5, Figure 7.4). Figure 7.6 illustrates the most common serovars isolated from fattening flocks from 2019-2023.

In 2023, one flock tested positive for regulated serovars compared to 2 flocks in 2022 both years having a notable reduction in the number of flocks testing positive from 12 flocks in 2021. One turkey fattening flock tested positive for monophasic *S.* Typhimurium strain 4,12:i:- DT193 (via operator sampling). This serovar was isolated from turkey flocks in 2022 (1 flock) and 2021 (1 flock). No turkey fattening flocks tested positive for either *S.* Enteritidis or *S.* Typhimurium in 2023, consistent with 2022, 2020 and 2019 and compares with 3 flocks positive for *S.* Typhimurium in 2021. *Salmonella* Enteritidis has not been isolated from turkey fattening flocks since 2017.

A total of 69 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 2019 and 2023 are shown in Table 7.5. The relative percentages of the most common serovars from turkey fattening flocks each year from 2019 to 2023 are shown in Figure 7.6.

Salmonella Kedougou was the most common serovar, isolated from 32 turkey fattening flocks in 2023. This represents a 51.4% increase in the number of flocks testing positive for this serovar compared with 2022 (21 flocks) when it was the most frequently isolated serovar in turkey fattening flocks.

In recent years *S.* Anatum has been the most common serovar isolated from turkey fattening flocks (2020 to 2022) but in 2023 there was a 55.0% reduction in the number of flocks testing positive for this serovar (18 flocks versus 40 flocks in 2022). 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. Contaminated feed is a likely source of infection in these flocks.

Six turkey fattener flocks tested positive for *S.* Orion var 15+ in 2023. This serovar was not detected between 2014 and 2019 but isolations have been generally increasing since. In 2020 one flock tested positive followed by 4 in 2021 and 3 in 2022. The proportion of positive flocks with this serovar was 7.9% in 2023.

Five flocks tested positive for *S.* 13,23:i:- in 2023 and the proportion of positive flocks represented by this serovar was 6.6%. This is the first time this serovar has been detected in turkey fattener flocks since the NCP began in 2010. *S.* 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.

The number of flocks testing positive for *S.* Derby continued to decrease from 19 in 2021, 7 in 2022 and 2 in 2023. 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 now decreased to 2.6% in 2023. This is the fourth 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 isolated from one flock in 2023, a decrease from 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. Subsequently fewer flocks have tested positive with 6 flocks in 2020 and 3 flocks in 2021.

One flock tested positive for *Salmonella* Chester and which is the first time this serovar has been isolated from turkeys or chickens in Great Britain since the inception of the NCP in 2010. *Salmonella* Orion (one isolation from one flock) and *S.* Schwarzengrund (2 isolations from the same flock) were all isolated for the first time in turkey fattening flocks in 2023 with this been the first time this serovar has been detected in turkey fattener flocks since the NCP began in 2010.

A total of 2,072 turkey fattening flocks were in production in Great Britain in 2023 and were included in the NCP. Therefore, the estimated prevalence for regulated *Salmonella* serovars was 0.05% (1 of 2,072), which is well below the target of a maximum of 1% of flocks positive for regulated serovars (Figure 7.4). The estimated prevalence of all *Salmonella* spp. In 2023 was 3.4% (70 of 2,072).

Figure 7.4 shows the change in prevalence of turkey fattening flocks testing positive for *Salmonella* since 2013. Estimated prevalence of regulated serovars in 2023 (0.05%) was lower than in 2022 (0.1%), 2020 and 2019 (0.0% in both years). Estimated prevalence of all *Salmonella* serovars in 2023 (3.4%) was lower than in 2022 (4.8%) and similar to that in 2021 (3.8%), and a marked reduction compared to a peak of 17.44% in 2016.

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	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
Agama	0	0	1	1	2	2	0	1	0	0
Agona	5	9	2	2	4	7	7	11	4	8
Albany	1	2	0	0	0	0	0	0	0	0
Anatum	4	4	38	42	31	31	40	66	18	19
Berta	0	0	0	0	0	0	0	1	0	1
Bovismorbificans	0	0	0	0	2	2	0	1	0	0
Brandenburg	0	0	0	0	0	0	1	1	0	0
Chester	0	0	0	0	0	0	0	0	1	1
Coeln	0	1	0	0	0	0	0	0	0	0
Derby	105	132	20	22	19	22	7	12	2	2
Dublin	0	0	0	0	0	0	0	0	0	1
Eastbourne	1	1	0	0	0	0	0	0	0	0
Give	0	0	0	0	0	0	0	2	1	1
Give var. 15$^+$	0	0	0	0	1	1	0	0	0	0
Idikan	0	0	0	1	0	0	0	0	0	0
Indiana	1	1	0	0	0	0	0	0	0	0
Kedougou	28	44	33	68	9	16	21	30	32	43
Kingston	0	0	1	1	0	0	0	0	0	0
Kottbus	4	4	0	0	0	0	0	0	2	3
Livingstone	0	0	0	2	0	0	0	0	0	0
London	0	0	0	0	1	6	3	5	0	0
Mbandaka	0	5	1	2	1	1	0	0	0	0
Monophasic Typhimurium	2	2	0	0	9	9	2	4	1	1

Salmonella serovar	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
Montevideo	0	0	0	0	0	0	3	8	0	1
Newport	1	5	1	2	2	3	1	1	0	0
Nottingham	1	1	0	0	0	0	0	0	0	0
Ohio	0	1	0	0	0	0	0	0	0	0
Orion	0	0	0	0	0	0	0	0	1	1
Orion var. 15^{+}	0	1	1	2	4	5	3	5	6	11
Schwarzengrund	0	0	0	0	0	0	0	0	1	2
Senftenberg	36	48	9	15	3	20	9	26	1	3
Typhimurium	0	0	0	2	3	3	0	1	1	2
13,23:i:-	3	3	9	14	4	4	2	2	4	5
untypable strains	1	1	10	15	2	6	3	4	1	3
rough strains	0	1	3	5	1	2	2	7	1	1
Total	**190**	**267**	**124**	**196**	**96**	**140**	**101**	**188**	**77**	**109**

In 2019 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 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.

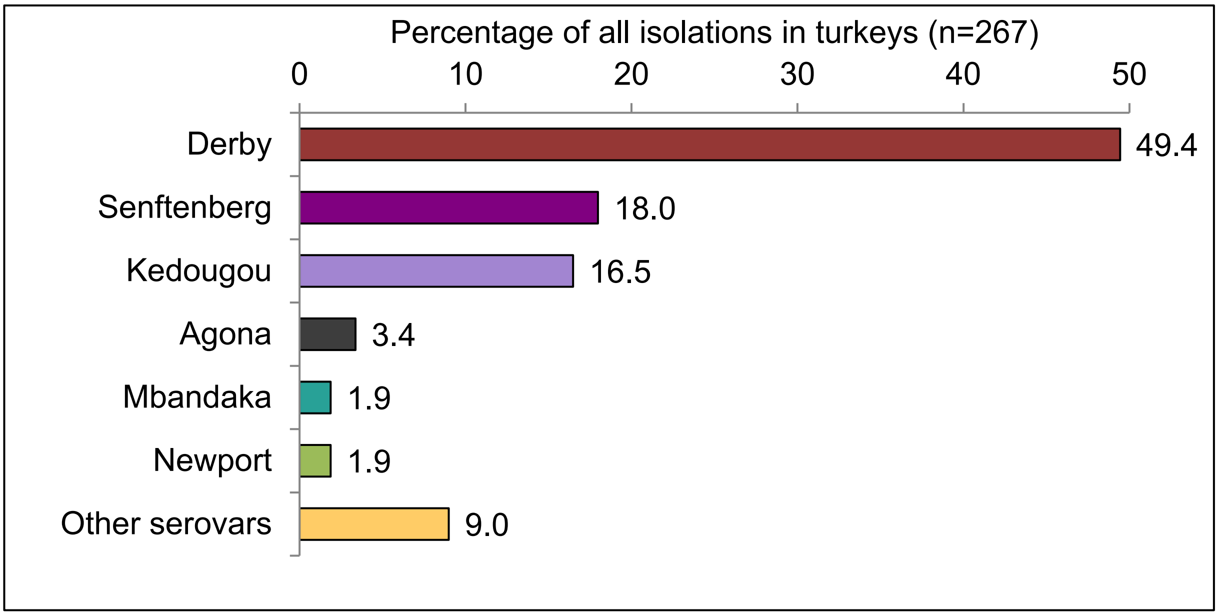
In 2021 2 flocks tested positive for 2 different *Salmonella* serovars. These are included in the table under both serovars but only once in the overall total.

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.

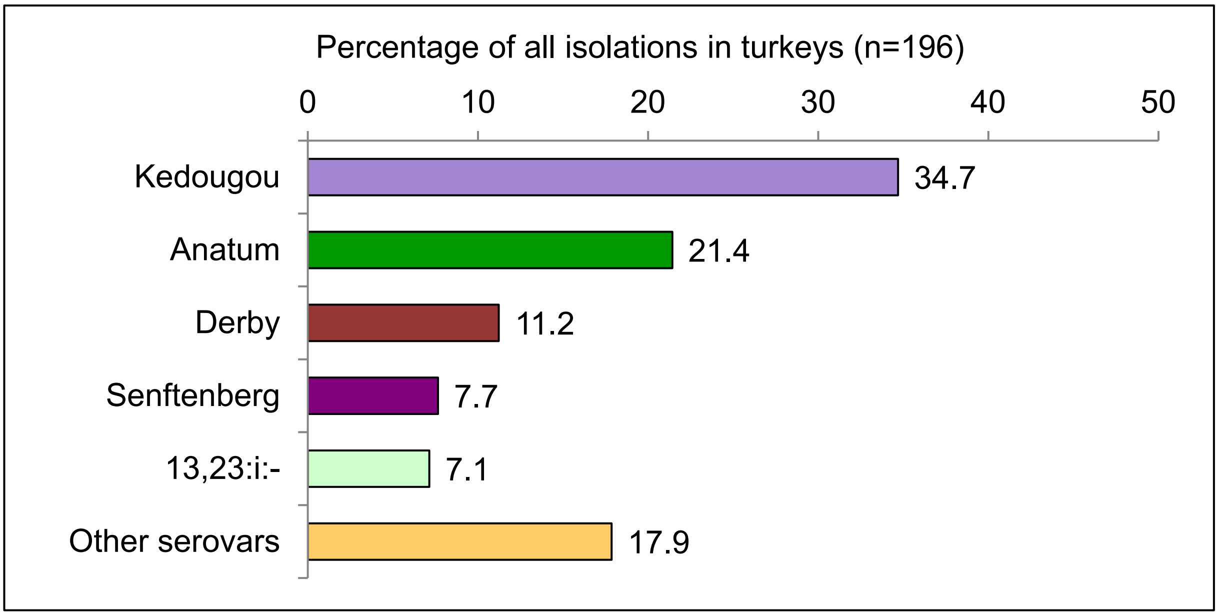
Figure 7.1: The most common serovars in turkeys by number of isolations in Great Britain 2019 to 2023 (statutory and non-statutory testing)

Figure 7.1.1: Isolations in 2019



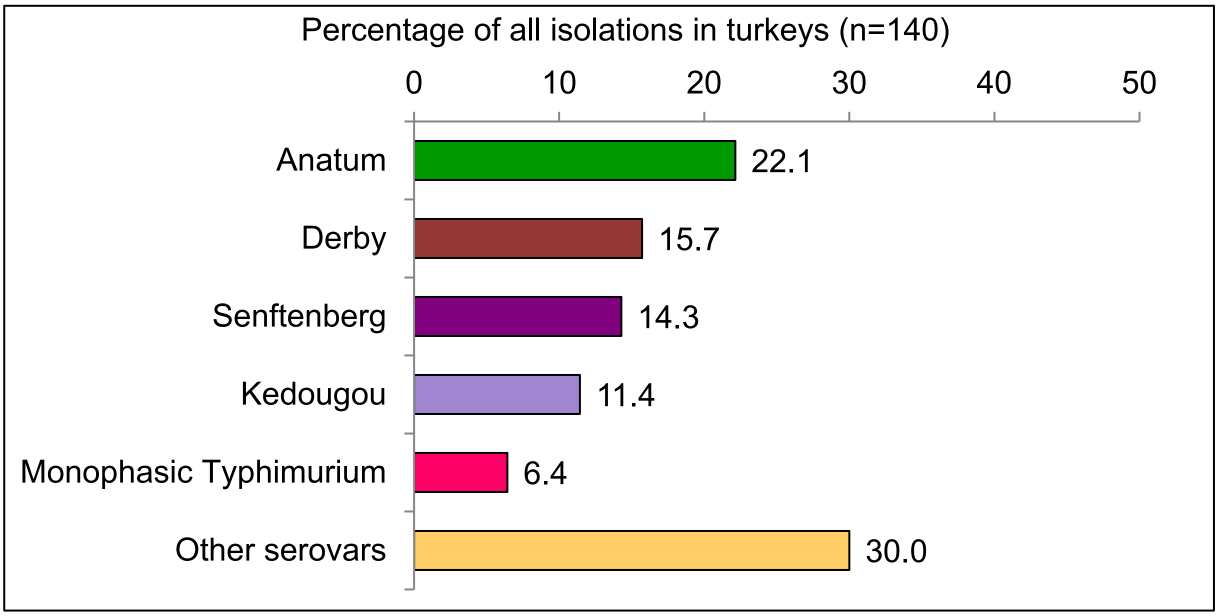
In 2019 the most common *Salmonella* serovar in turkeys was *S.* Derby, accounting for 49.4% of total isolations, followed by *S.* Senftenberg (18.0%), *S.* Kedougou (16.5%) and *S.* Agona (3.4%).

Figure 7.1.2: Isolations in 2020



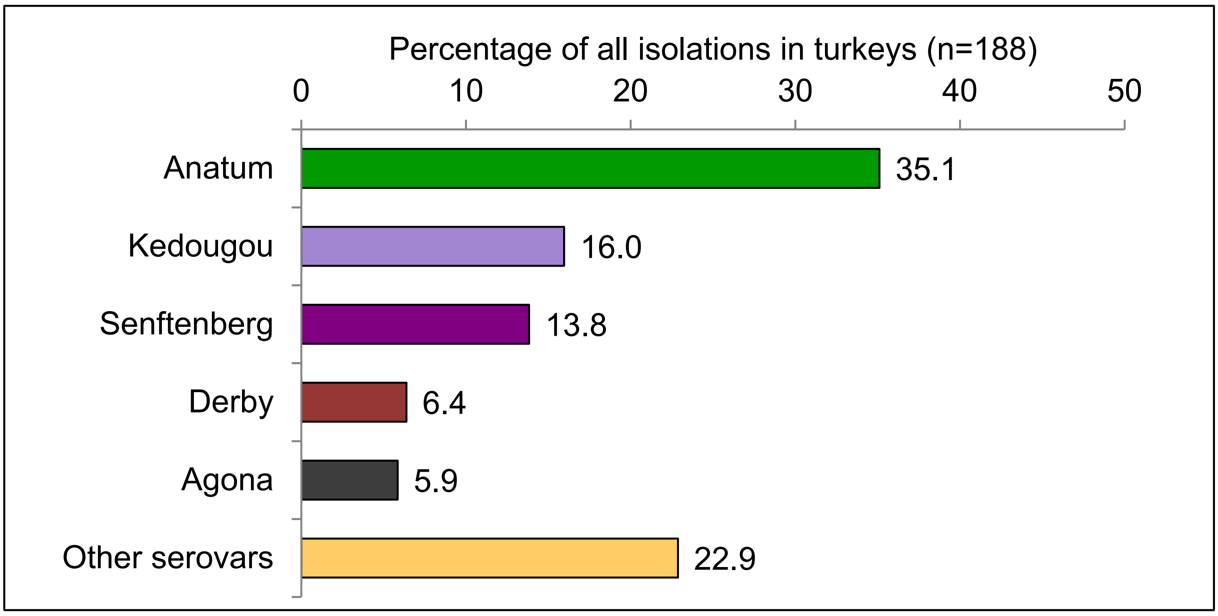
In 2020 the most common *Salmonella* serovar in turkeys was *S.* Kedougou, accounting for 34.7% of total isolations, followed by *S*. Anatum (21.4%), *S.* Derby (11.2%) and *S.* Senftenberg (7.7%).

Figure 7.1.3: Isolations in 2021



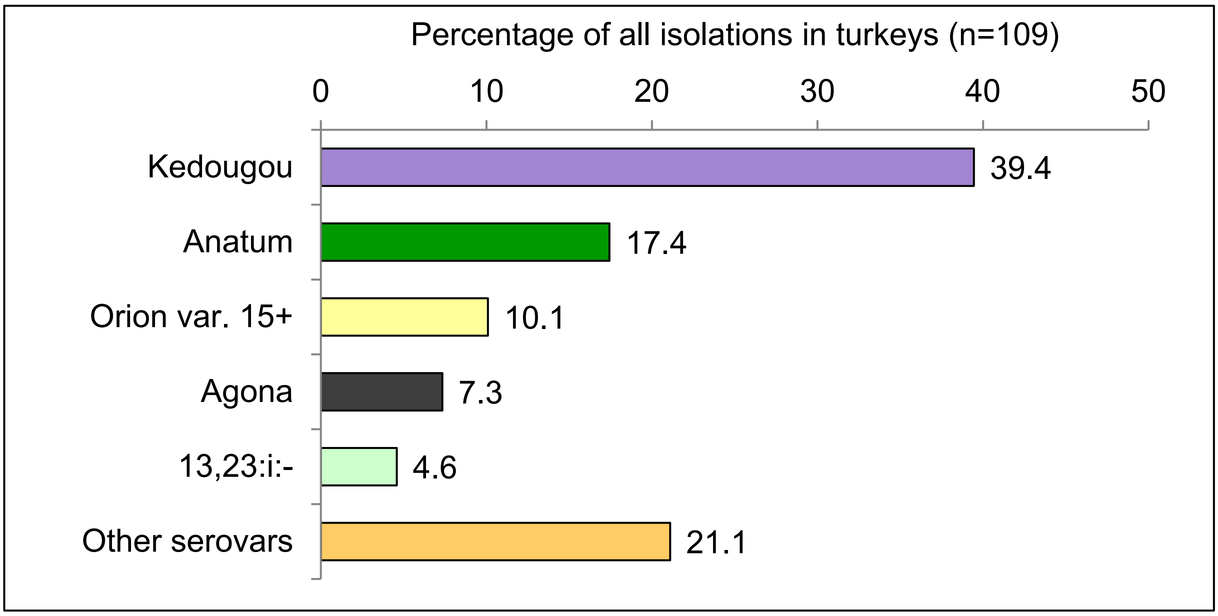
In 2021 the most common *Salmonella* serovar in turkeys was *S.* Anatum, accounting for 22.1% of total isolations, followed by *S*. Derby (15.7%), *S.* Senftenberg (14.3%) and *S.* Kedougou (11.4%).

Figure 7.1.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in turkeys 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 7.1.5: Isolations in 2023



In 2023 the most common *Salmonella* serovar in turkeys 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 7.2: The 5 most common *Salmonella* serovars in turkeys in Great Britain in 2022 and their trends over time since 2019

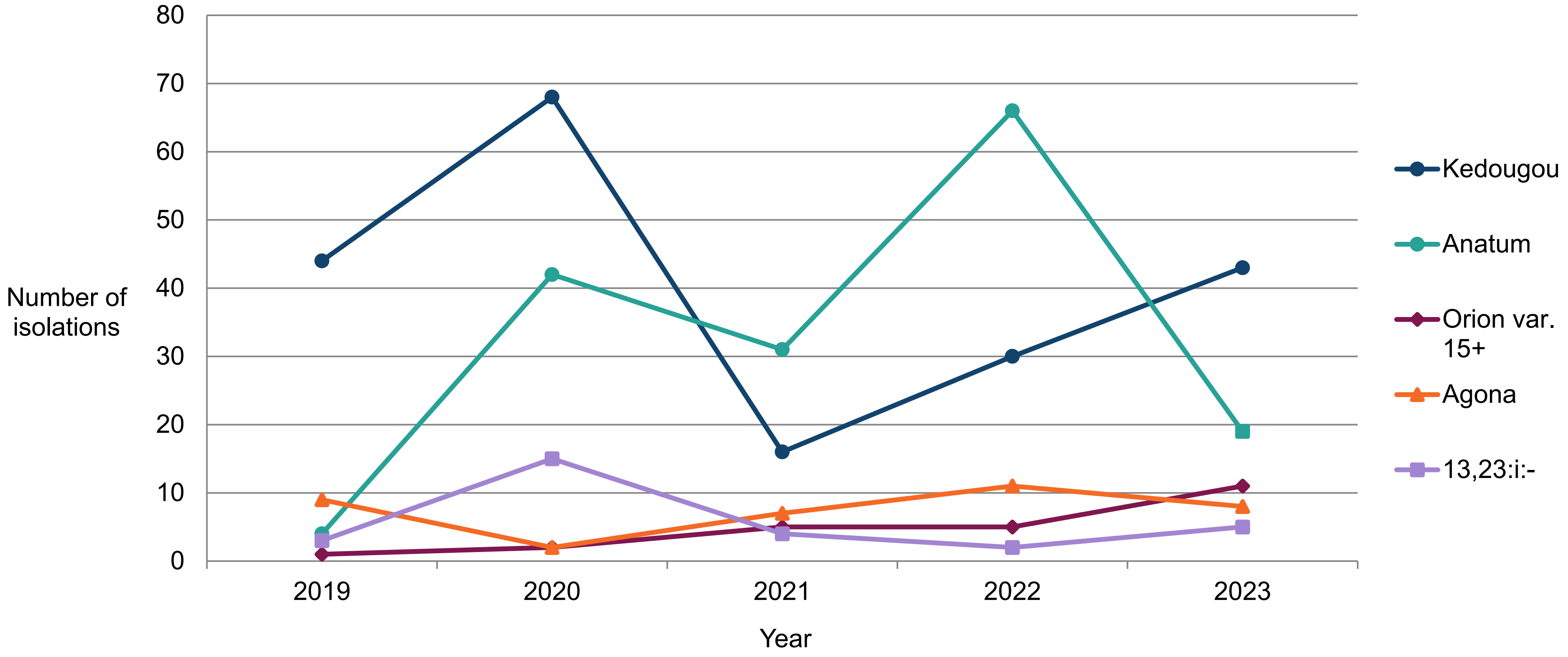


Figure 7.2 shows that the numbers of the most common serovar in turkeys in 2023, *S.* Kedougou has been variable with a high in 2020 (68 isolations), dropping to 16 isolations in 2021 and then rising steadily to 43 in 2023. *S.* Anatum rose from 3 isolations in 2019 to 66 in 2022 and has dropped considerably in 2023 to 19 isolations. The other 3 serovars, *S.* Orion var 15$^+$, *S.* Agona and *S.* 13,23:I:- (monophasic Idikan) have remained low and stable over the last 5 years, rarely exceeding 11 isolations.

Table 7.2: *S.* Typhimurium phage types in turkeys in Great Britain 2019 to 2023

Phage types	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
DT9	0	0	0	1	0	0	0	0	0	0
DT99	0	0	0	0	0	0	0	1	0	0
DT193	0	0	0	0	0	0	0	0	1	2
U302	0	0	0	0	3	3	0	0	0	0
RDNC	0	0	0	1	0	0	0	0	0	0
Total	**0**	**0**	**0**	**2**	**3**	**3**	**0**	**1**	**1**	**2**

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

Table 7.3: Monophasic *Salmonella* phage types in turkeys in Great Britain 2019 to 2023

Phage types	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations	2023 flocks	2023 isolations
DT193	2	2	0	0	8	8	2	3	1	1
NOPT	0	0	0	0	0	0	0	0	0	0
UNTY	0	0	0	0	1	1	0	0	0	0
Total	**2**	**2**	**0**	**0**	**9**	**9**	**2**	**3**	**1**	**1**

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

Figure 7.3: Prevalence of *Salmonella* in turkey breeder flocks tested under NCP in Great Britain 2014 to 2023

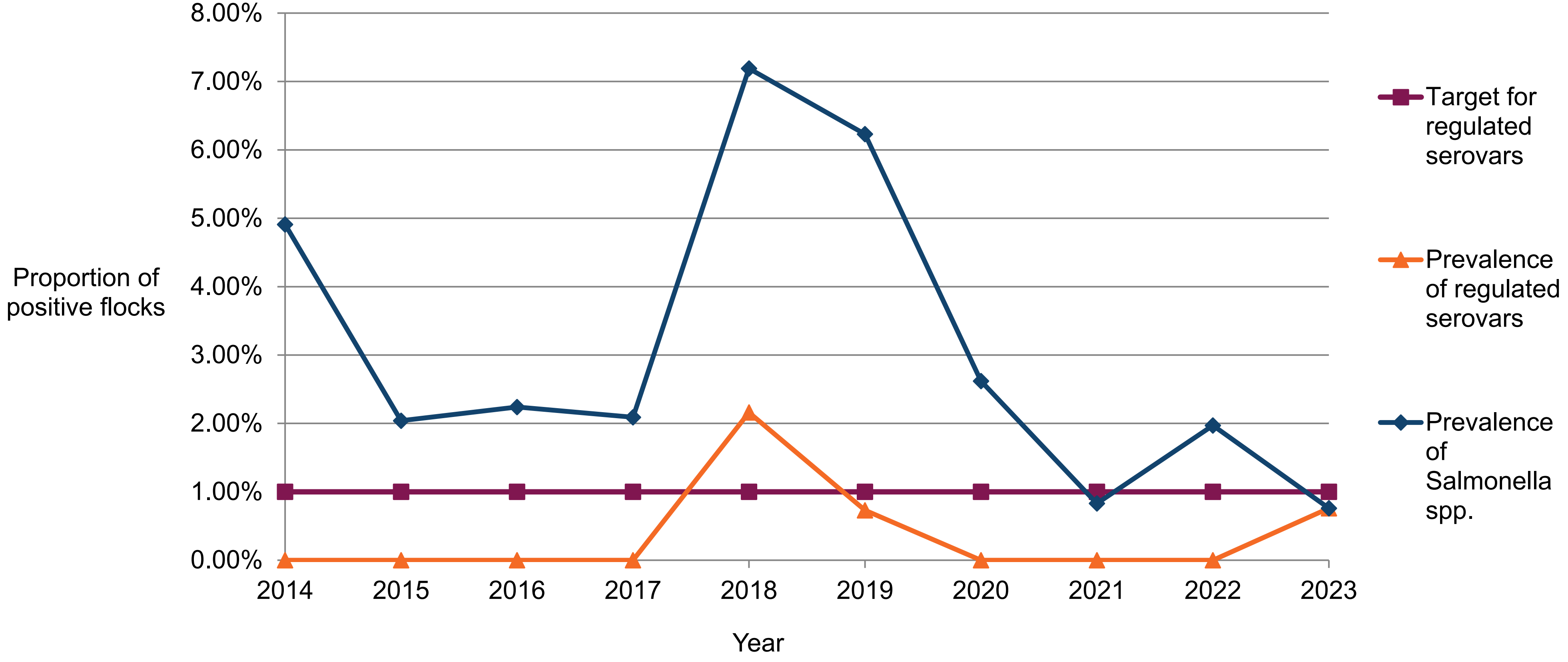


Figure 7.3 shows a peak in the prevalence of *Salmonella spp.* In breeding turkey flocks of 7.19% in 2018 but a subsequent decline thereafter to 0.76% in 2023.The prevalence of regulated serovars remains low at 0.76% despite a small peak in 2018 to 2.16% which was above the target of 1% prevalence. The 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: Prevalence of *Salmonella* in turkey fattening flocks tested under NCP in Great Britain 2014 to 2023

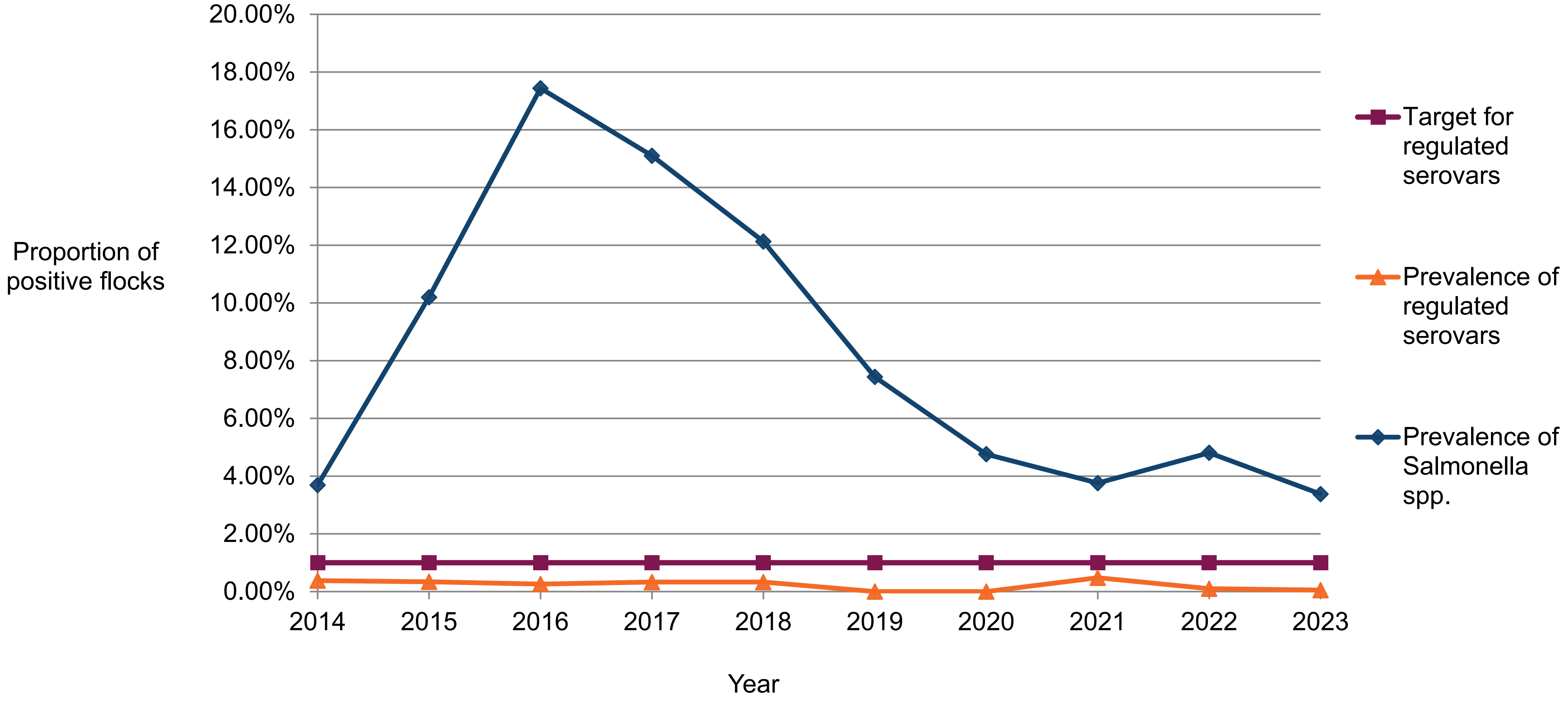


Figure 7.4 shows a peak in the prevalence of *Salmonella spp.* In fattening turkey flocks of 17.4% in 2016 but a subsequent decline thereafter to 3.38% in 2023.The prevalence of regulated serovars remains very low and below the target of 1% prevalence across all years.

Table 7.4: Turkey breeding flocks in Great Britain (number of adult flocks reported positive for each *Salmonella* serovar, NCP testing 2019 to 2023)

The following table shows the number of turkey breeding flocks reported positive with each *Salmonella* serovar from 2019 to 2023 and the rank within that year. This data comes from NCP testing.

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Typhimurium	0	0	0	0	0	0	0	0	1	1
Senftenberg	1	15	1	3	0	0	1	4	0	0
13,23:i:-	0	0	2	2	0	0	0	0	0	0
Monophasic Typhimurium	2	2	0	0	0	0	0	0	0	0
Agama	0	0	3	1	1	1	0	0	0	0
Derby	0	0	3	1	0	0	0	0	0	0
Mbandaka	0	0	0	0	2	1	0	0	0	0

In 2016 *S.* Derby included 1 presumptive *S.* Derby flock.

For details of turkey breeding flocks reported positive in 2013 to 2018, see the 2018 edition of *Salmonella* in livestock production in Great Britain.

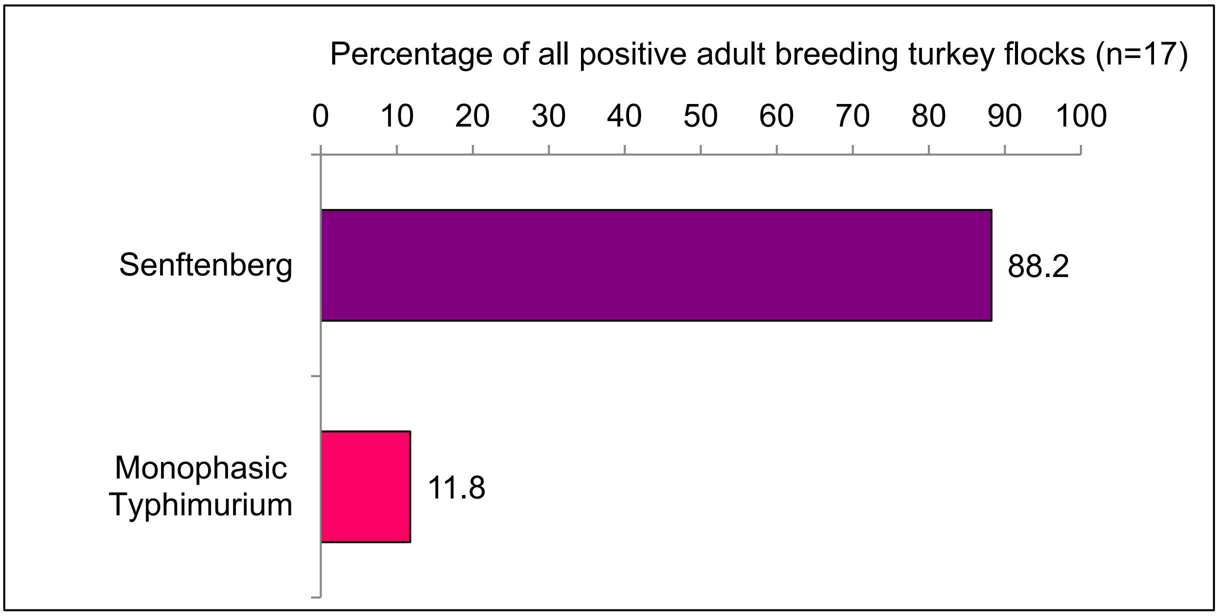
Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2019	6.23%	0.73%
2020	2.62%	0.00%

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

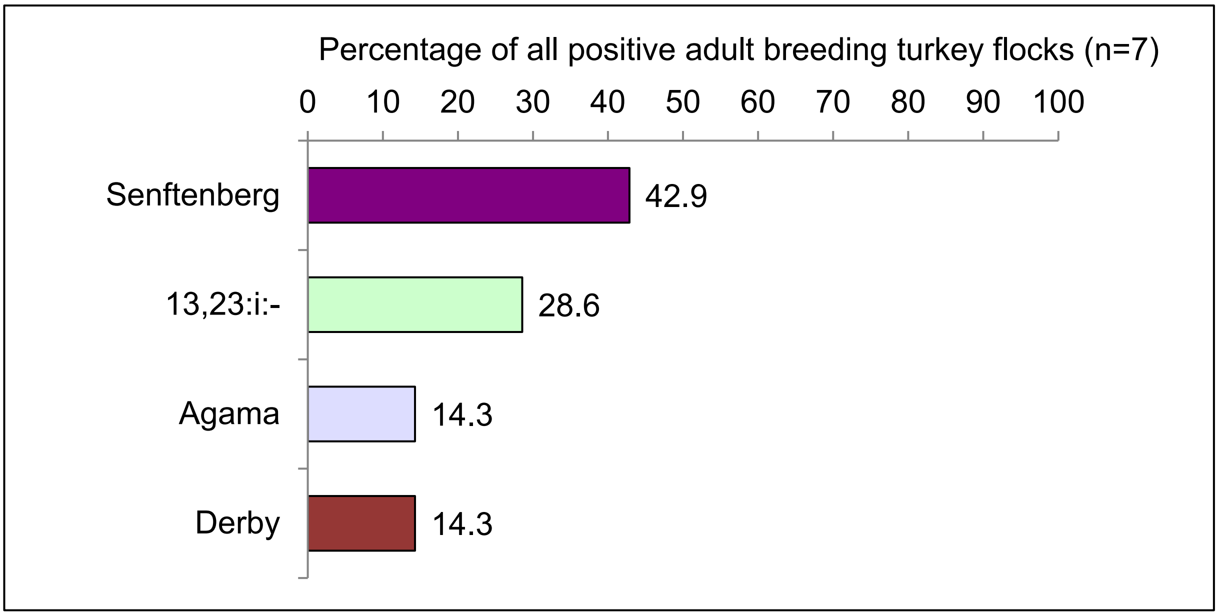
Figure 7.5: The most common serovars identified in adult turkey breeding flocks in Great Britain 2018 to 2022 reported from NCP testing

Figure 7.5.1: Isolations in 2019



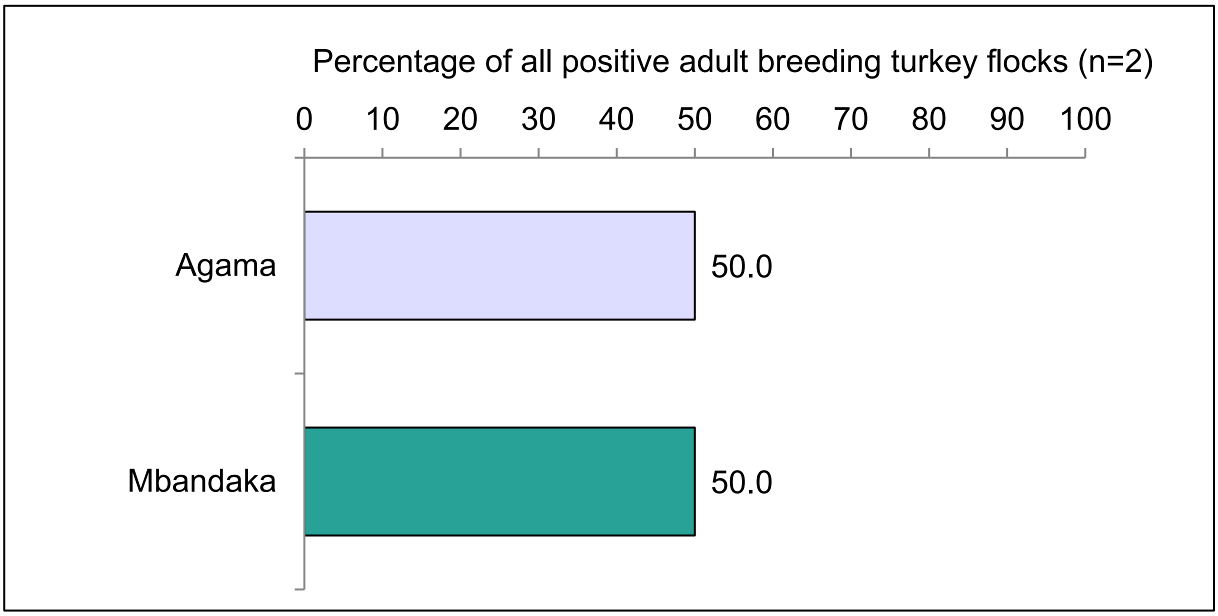
In 2019 the most common *Salmonella* serovar in breeding turkey flocks was *S*. Senftenberg accounting for 88.2% of isolations followed by *S*. 4,5,12:i:- which accounted for the remaining 11.8%.

Figure 7.5.2: Isolations in 2020



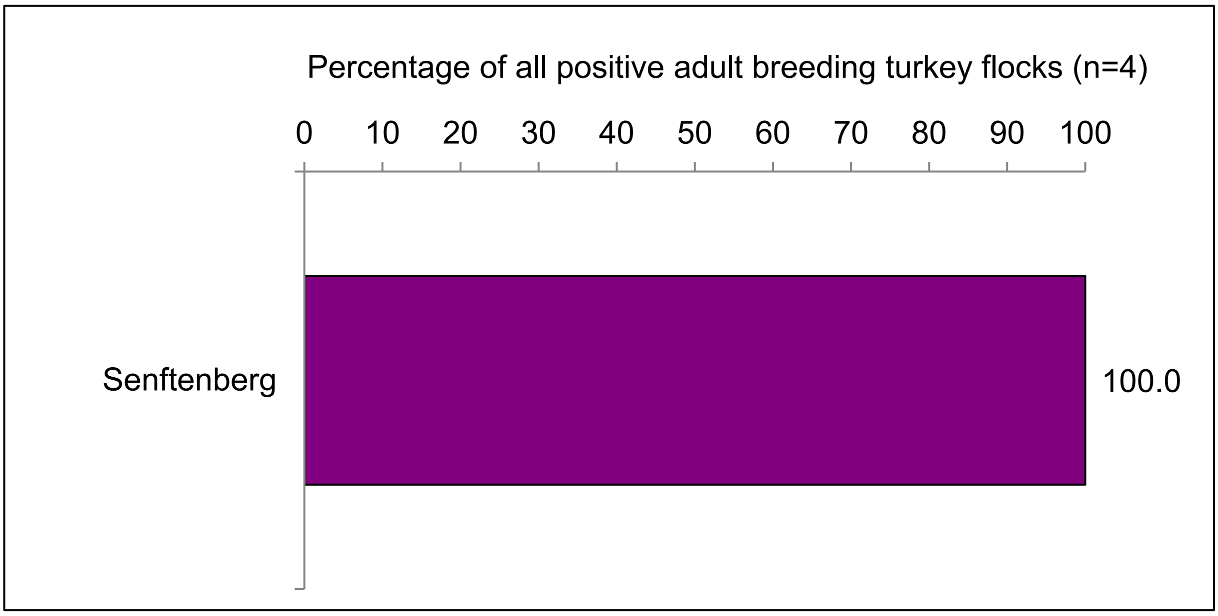
In 2020 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Senftenberg, accounting for 42.9% of total isolations, followed by *S*. 13,23:i:- (28.6%), *S.* Agama (14.3%) and *S*. Derby (14.3%).

Figure 7.5.3: Isolations in 2021



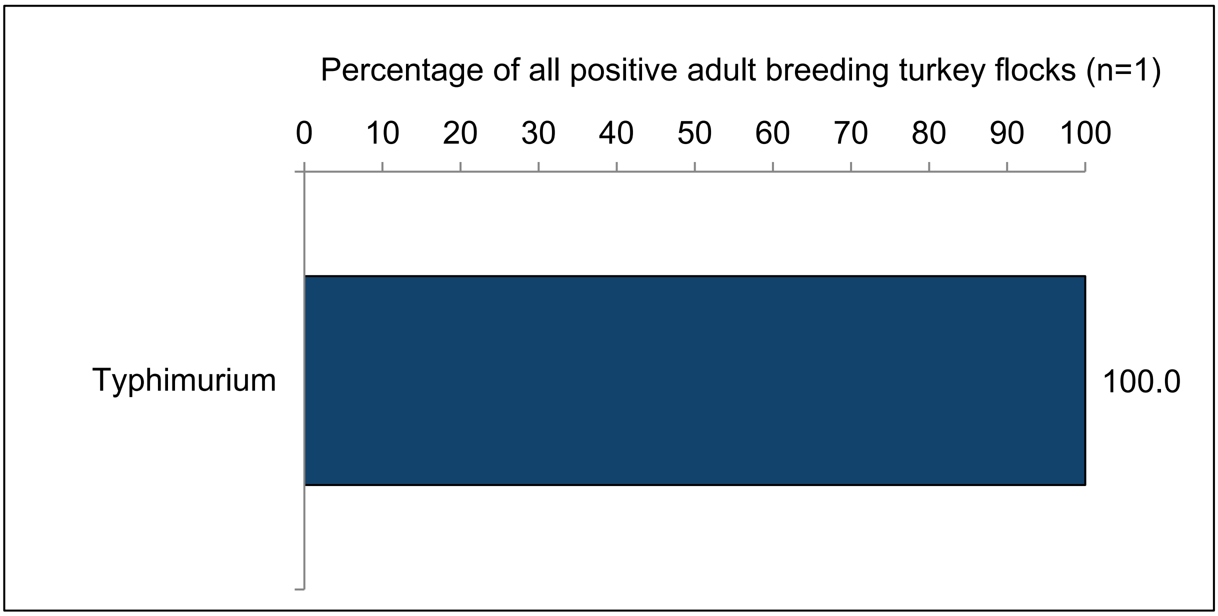
In 2021 the most common *Salmonella* serovar in breeding turkey flocks was *S*. Agama accounting for 50.0% of isolations followed by *S.* Mbandaka which accounted for the other 50.0% of isolations.

Figure 7.5.4: Isolations in 2022



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

Figure 7.5.5: Isolations in 2023



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

Table 7.5: Turkey fattening flocks in Great Britain (number of flocks reported positive for each *Salmonella* serovar, NCP testing 2019 to 2023)

The following table shows the number of turkey fattening flocks reported positive with each *Salmonella* serovar from 2019 to 2023 and the rank within that year. This data comes from NCP testing.

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Kedougou	2	28	2	33	3	9	2	21	1	32
Anatum	5	4	1	38	1	31	1	40	2	18
Orion var. 15$^+$	0	0	8	1	5	4	5	3	3	6
13,23:i:-	6	3	6	4	7	2	6	2	4	5
Agona	4	5	7	2	5	4	3	7	5	4
Derby	1	105	3	19	2	19	3	7	6	2
Kottbus	5	4	0	0	0	0	0	0	6	2
3,19:rough:-	0	0	8	1	0	0	6	2	7	1
Chester	0	0	0	0	0	0	0	0	7	1
Give	0	0	0	0	0	0	0	0	7	1
Monophasic Typhimurium	0	0	0	0	12	9	12	2	7	1
Orion	0	0	0	0	0	0	0	0	7	1
Schwarzengrund	0	0	0	0	0	0	0	0	7	1
Senftenberg	3	21	5	6	6	3	4	5	7	1
3,10:e,h:-	7	1	4	11	6	3	6	3	0	0
6,8:e,h:-	0	0	8	1	8	1	0	0	0	0
Agama	0	0	0	0	8	1	0	0	0	0
Albany	7	1	0	0	0	0	0	0	0	0
Bovismorbificans	0	0	0	0	7	2	0	0	0	0

Serovar	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022	Rank 2023	Flocks 2023
Brandenburg	0	0	0	0	0	0	6	1	0	0
Eastbourne	7	1	0	0	0	0	0	0	0	0
Give var. 15⁺	0	0	0	0	8	1	0	0	0	0
Indiana	7	1	0	0	0	0	0	0	0	0
Kingston	0	0	8	1	0	0	0	0	0	0
Kottbus	5	4	0	0	0	0	0	0	0	0
London	0	0	0	0	8	1	5	3	0	0
Mbandaka	0	0	8	1	0	0	0	0	0	0
Montevideo	0	0	0	0	0	0	5	3	0	0
Newport	7	1	8	1	7	2	6	1	0	0
Nottingham	7	1	0	0	0	0	0	0	0	0
O rough:e,g:1,6	0	0	8	1	0	0	0	0	0	0
O rough:f,g:-	0	0	7	2	0	0	0	0	0	0
Typhimurium	0	0	0	0	6	3	0	0	0	0

In 2018 *S*. Derby isolations include 172 presumptive *S*. Derby flocks.

For details of turkey fattening flocks reported positive in 2013 to 2018, see the 2018 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
2019	7.44%	0.00%

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%

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 2019:

- 2 flocks tested positive for both *S*. Agona and *S*. Derby
- 1 flock tested positive for both *S*. Derby and *S*. Kedougou

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:

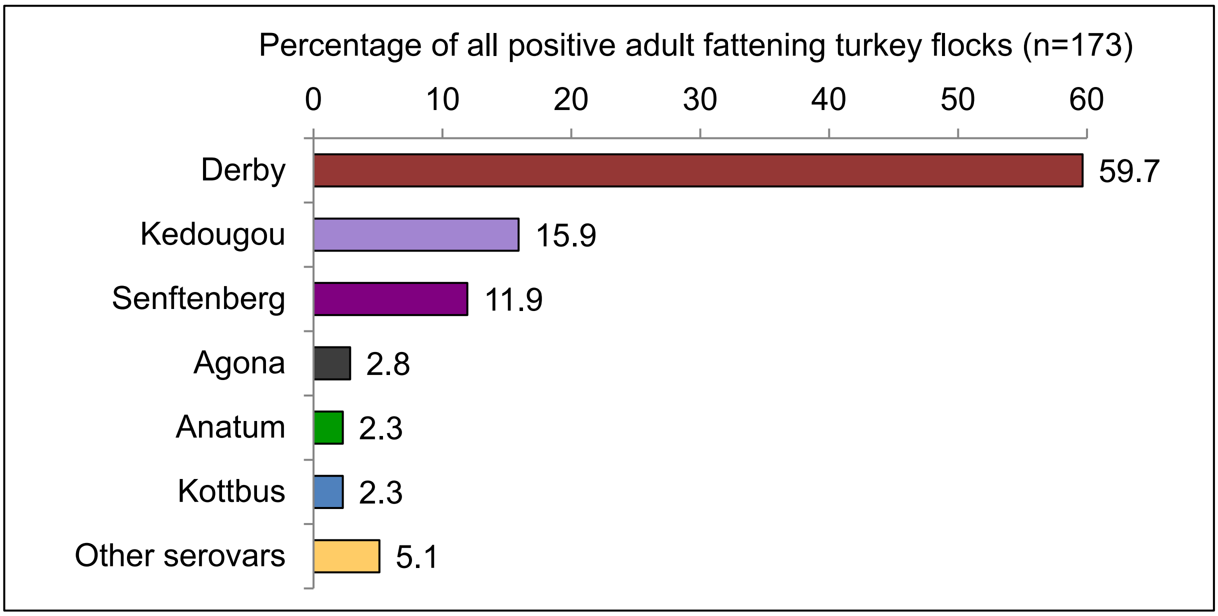
- 2 flocks tested positive for both *Salmonella* 3,10:e,h:- and *S*. Anatum
- 1 flock tested positive for both *Salmonella* 3,10:e,h:- and *S*. Kedougou

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+

Figure 7.6: The most common serovars identified in turkey fattening flocks in Great Britain 2019 to 2023 reported from NCP testing

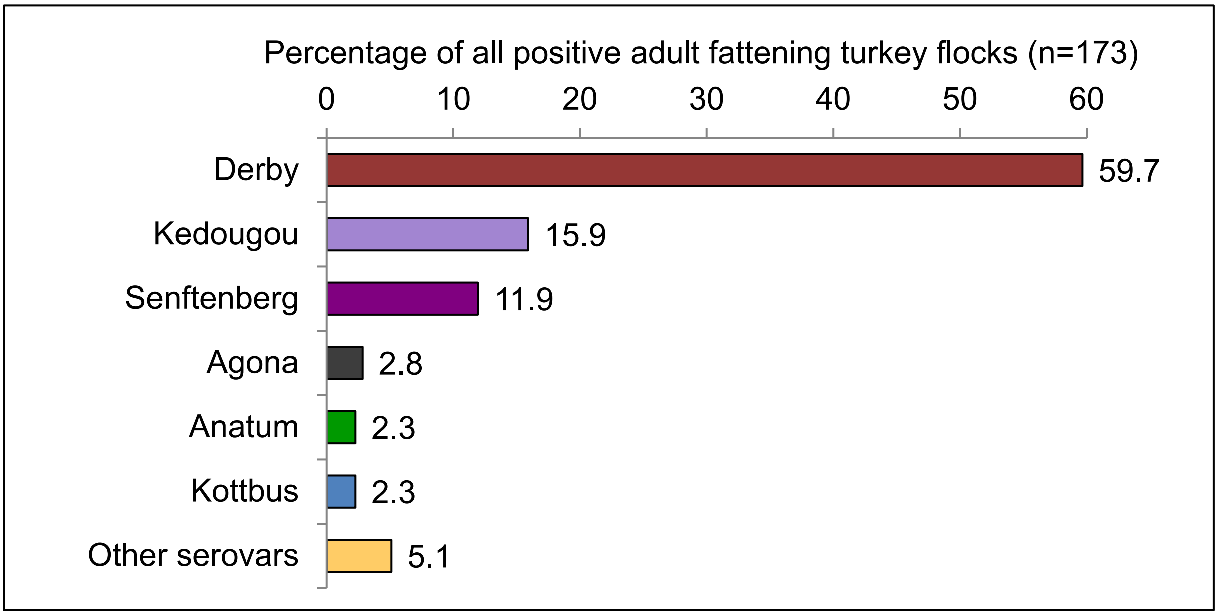
Figure 7.6.1: Isolations in 2019



In 2019 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Derby, accounting for 59.7% of total isolations, followed by *S*. Kedougou (15.9%), *S*. Senftenberg (11.9%) and *S.* Agona (2.8%).

In 2019 3 flocks were positive for 2 serovars (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

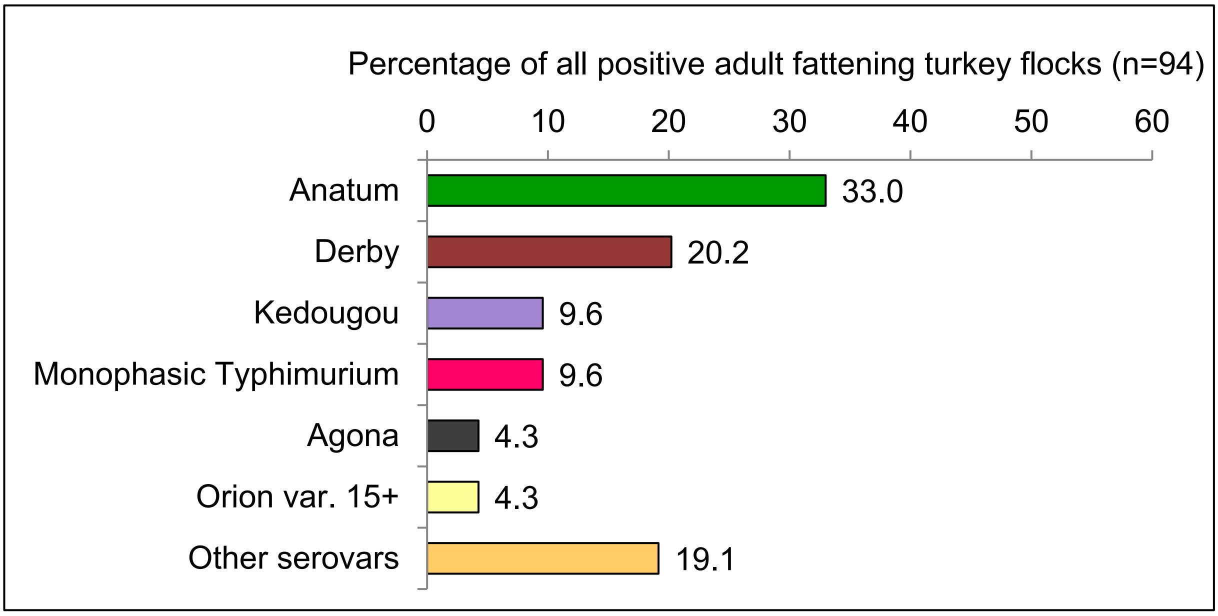
Figure 7.6.2: Isolations in 2020



In 2020 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Anatum, accounting for 31.1% of total isolations, followed by *S.* Kedougou (27.0%), *S*. Derby (15.6%) and *S.* 3,10:e,h:- (9.0%).

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

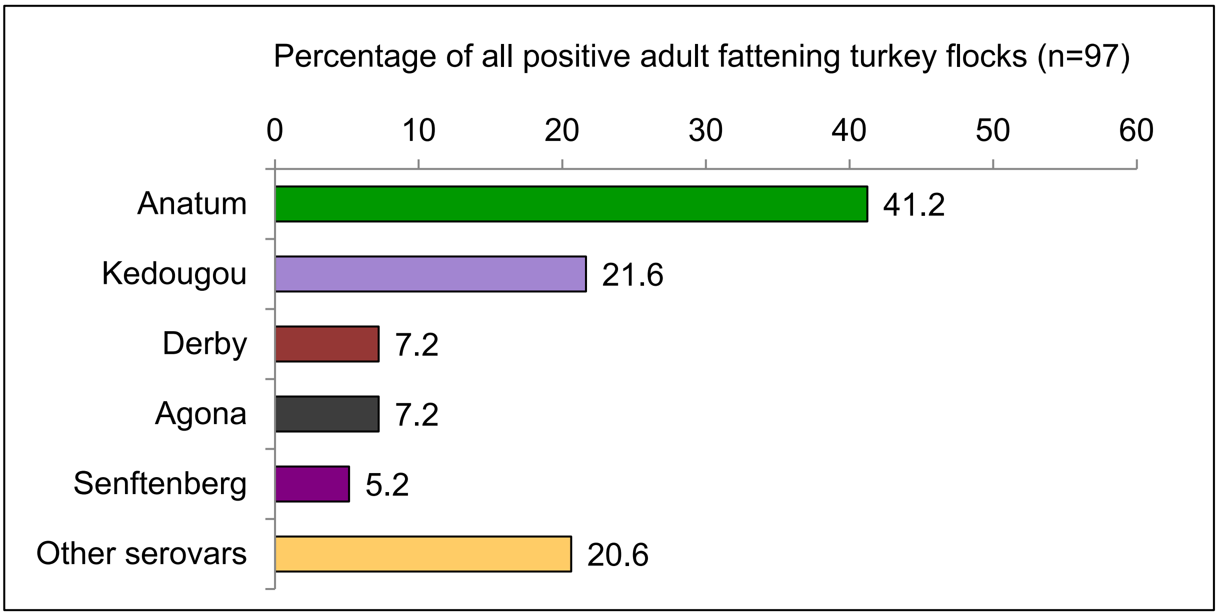
Figure 7.6.3: Isolations in 2021



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%.

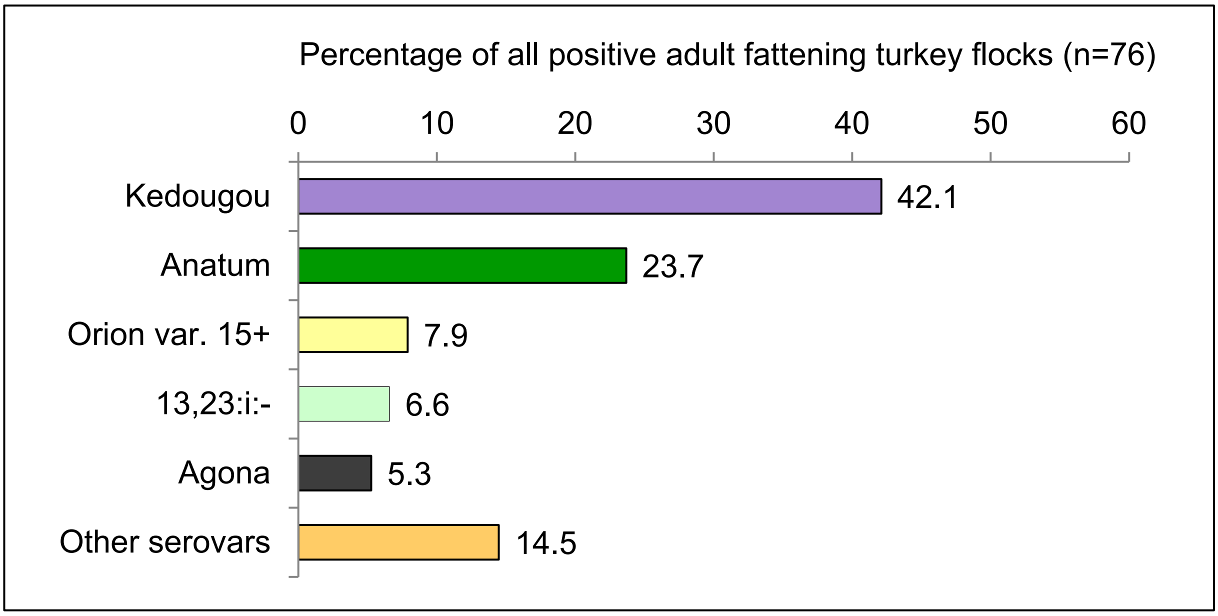
Figure 7.6.4: Isolations in 2022



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 7.6.5: Isolations in 2023



In 2023 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Kedougou, accounting for 42.1% of total isolations, followed by *S*. Anatum (23.7%), *S*. Orion var 15^+ (7.9%) and *S*. 13,23:i:- (6.6%).

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

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 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 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

During 2023 there were 96 isolations of *Salmonella* from ducks in Great Britain, which is 20.7% less than in 2022 (121 isolations) and 12.7% fewer than in 2021 (110 isolations) (Table 8.1). There had been increased voluntary surveillance activity within the duck industry up to 2019, but more recently there has been a general reduction.

The most common serovars isolated from ducks during 2023 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), *S*. Hadar (6 isolations, 6.3% of duck isolations) and Orion var. 15^+ (5 isolations, 5.2% of duck isolations). Together these serovars accounted for 95.8% of all *Salmonella* isolations from ducks (Figure 8.1). In contrast, during 2022 the most common serovars were *S.* Indiana (38 isolations; 31.4% of duck isolations), *S.* Hadar (17 isolations; 14.0% of duck isolations), *S*. Bovismorbificans (15 isolations; 12.4% of duck isolations), *S*. Give var.15^+ (15 isolations; 12.4% of duck isolations), *S*. Orion var 15^+ (15 isolations; 12.4% of duck isolations), *S*. Lexington (9 isolations; 7.4% of duck isolations), and *S*. Kottbus (6 isolations; 5.0% of duck isolations).

Salmonella Indiana remained the most commonly reported serovar from ducks during 2023 (52 isolations). This is the first year since 2018 that the number of *S*. Indiana isolations has increased. This serovar accounted for a higher proportion of total isolations from ducks in 2023 (54.2%) compared to 2022 (31.4%) (Figure 8.1 and Figure 8.3).

There were 12 isolations of *S*. Kottbus during 2023, the second most common serovar isolated from ducks, compared to 6 isolations in 2022. *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 9 isolations of *S.* Give from ducks in 2023, an increase compared to 2022 (1 isolation). *S.* Give isolations accounted for 9.4% of total isolations from ducks in 2023 and was the third most common serovar. Until 2023 the number of *S.* Give isolations had been decreasing (11 isolations in 2019 and 6 isolations in both 2020 and 2021).

There were 8 *S.* Lexington isolations during 2023, similar to the number in 2022 (9 isolations), an increase on 2020 (7 isolations) and the largest number of *S*. Lexington isolations from ducks since 2017 (26 isolations). *Salmonella* Lexington was the fourth most commonly isolated serovar in 2023 accounting for a larger proportion of total isolations from ducks in 2023 (8.3% of isolations), 2022 (7.4% of isolations) and 2021 (8.2% of isolations) compared to 2020 (3.4% of isolations).

There were 6 isolations of *S.* Hadar during 2023, a decrease compared to 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 were 5 isolations of *S*. Orion var. 15^{+} from ducks in 2023, a decrease compared to 2022 (15 isolations) which representing the highest number of isolations since 2019 but still lower than in the period 2014 to 2018 when there were greater than 20 isolations.

There were 2 isolations of *S.* Orion during 2023 (2.1% of duck isolations) the same as in 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 no isolations of *Salmonella* Give var.15^{+} in 2023, a decrease compared to 2022 (15 isolations). 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 no isolations of *S*. Bovismorbificans in 2023 compared to 15 isolations in 2022 and no isolations during 2021. In 2022 this serovar was associated with 12.4% of isolations in ducks (Figure 8.1) which is the highest proportion since before 2009.

There was one isolation of *S*. Enteritidis (PT9, Table 8.4) from ducks in 2023 compared to none in 2022 but the same as in 2021 and 2020. There was one isolation of *S*. Typhimurium (DT1, Table 8.3) from ducks during 2023, an increase compared to the previous 3 years where 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 ducks during 2023, consistent with 2019 to 2022.

Geese

There were no isolations of *Salmonella* from geese in 2023. This is consistent with 2022 and 2021 and compares to 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 2023 there 163 diagnostic submissions from Geese were recorded on the VIDA database in Great Britain compared to 289 in 2022.

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

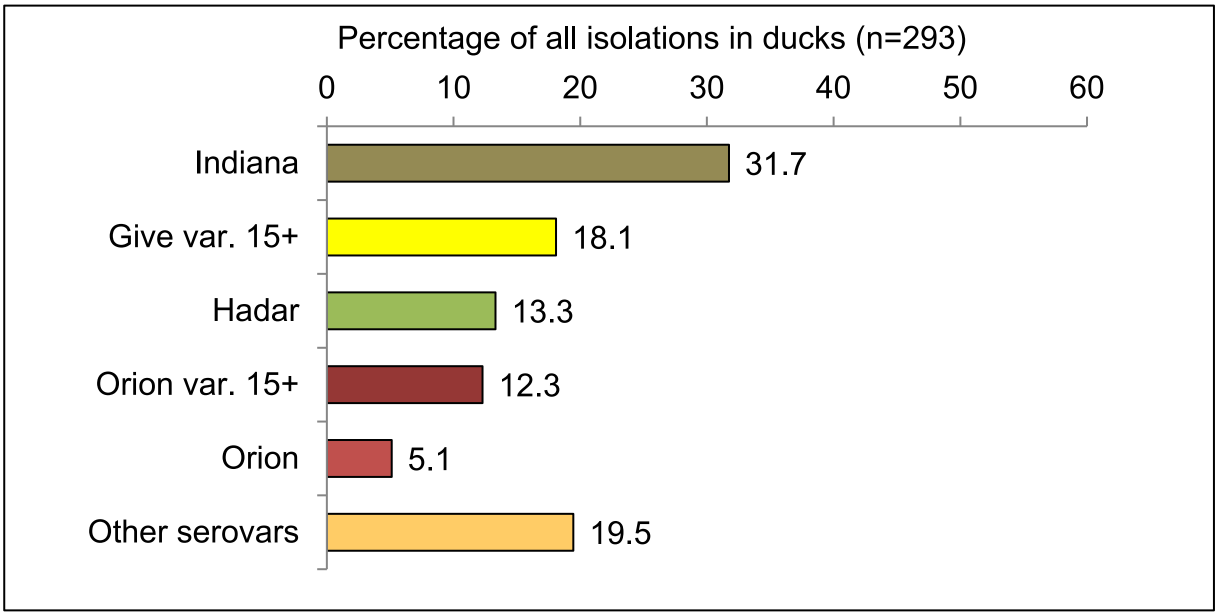
Salmonella **serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Agona	0	0	0	0	1	1	0	0	0	0
Anatum	1	1	0	0	0	0	0	0	0	0
Bovismorbificans	8	5	16	8	0	0	15	3	0	0
Derby	1	1	0	0	0	0	0	0	0	0
Enteritidis	0	0	1	1	1	1	0	0	1	1
Give	11	9	6	6	6	5	1	1	9	9
Give var. 15$^+$	53	41	32	21	6	5	15	13	0	0
Hadar	39	36	21	20	1	1	17	10	6	5
Indiana	93	79	60	53	41	33	38	28	52	28
Kedougou	0	0	0	0	1	1	0	0	0	0
Kottbus	11	9	6	5	9	9	6	5	12	10
Lexington	2	2	7	5	9	7	9	8	8	6
Monschaui	4	4	2	2	0	0	0	0	0	0
Newport	0	0	2	2	1	1	0	0	0	0
Orion	15	13	16	15	12	11	2	2	2	2
Orion var. 15$^+$	36	32	12	12	8	6	15	8	5	2
Oslo	9	8	3	2	0	0	0	0	0	0
Senftenberg	0	0	0	0	1	0	0	0	0	0
Typhimurium	2	2	2	2	0	0	0	0	1	1
untypable strains	6	5	18	18	13	13	3	3	0	0
rough strains	2	2	2	2	0	0	0	0	0	0
Total	**293**	**249**	**206**	**174**	**110**	**94**	**121**	**81**	**96**	**64**

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

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Beaudesert	0	0	1	1	0	0	0	0	0	0
Typhimurium	0	0	1	1	0	0	0	0	0	0
Total	**0**	**0**	**2**	**2**	**0**	**0**	**0**	**0**	**0**	**0**

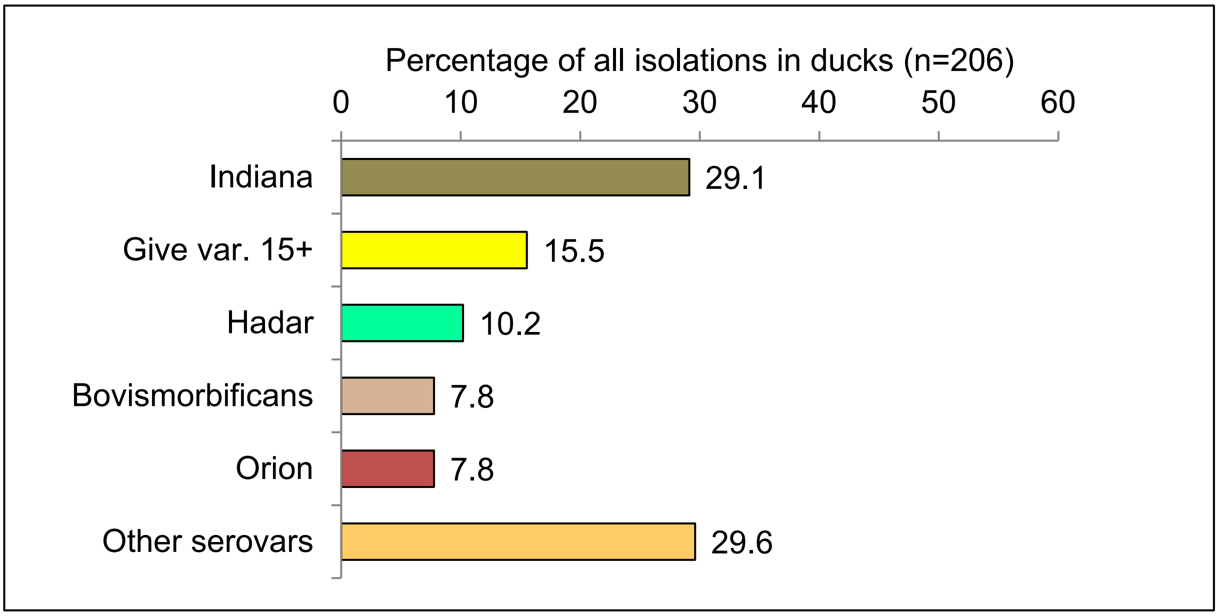
Figure 8.1: Isolations of the most common serovars in ducks in Great Britain 2019 to 2023

Figure 8.1.1: Isolations in 2019



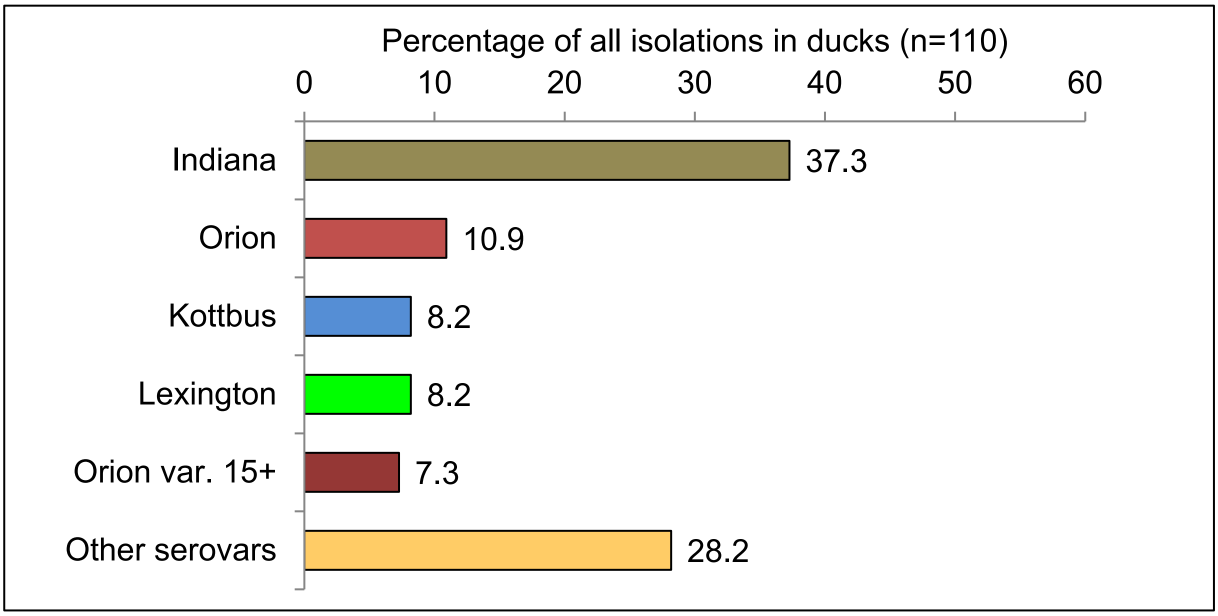
In 2019 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 31.7% of total isolations, followed by *S.* Give var. 15^+ (18.1%), *S.* Hadar (13.3%) and *S.* Orion var. 15^+ (12.3%).

Figure 8.1.2: Isolations in 2020



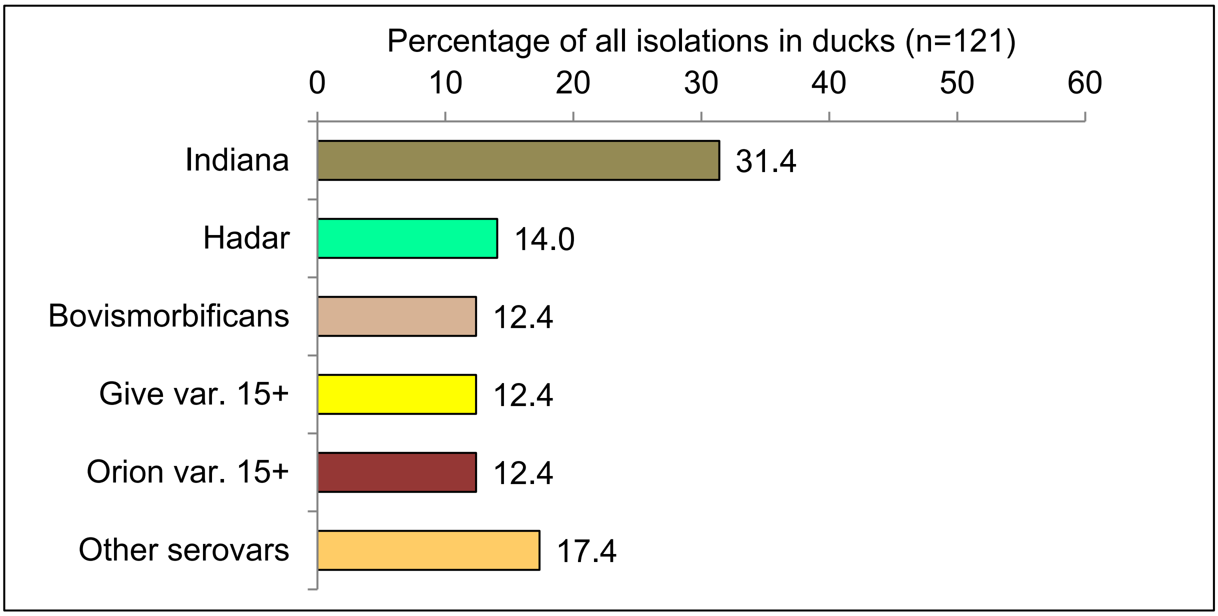
In 2020 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 29.1% of total isolations, followed by *S*. Give var. 15^{+} (15.5%), *S.* Hadar (10.2%) and *S.* Bovismorbificans (7.8%).

Figure 8.1.3: Isolations in 2021



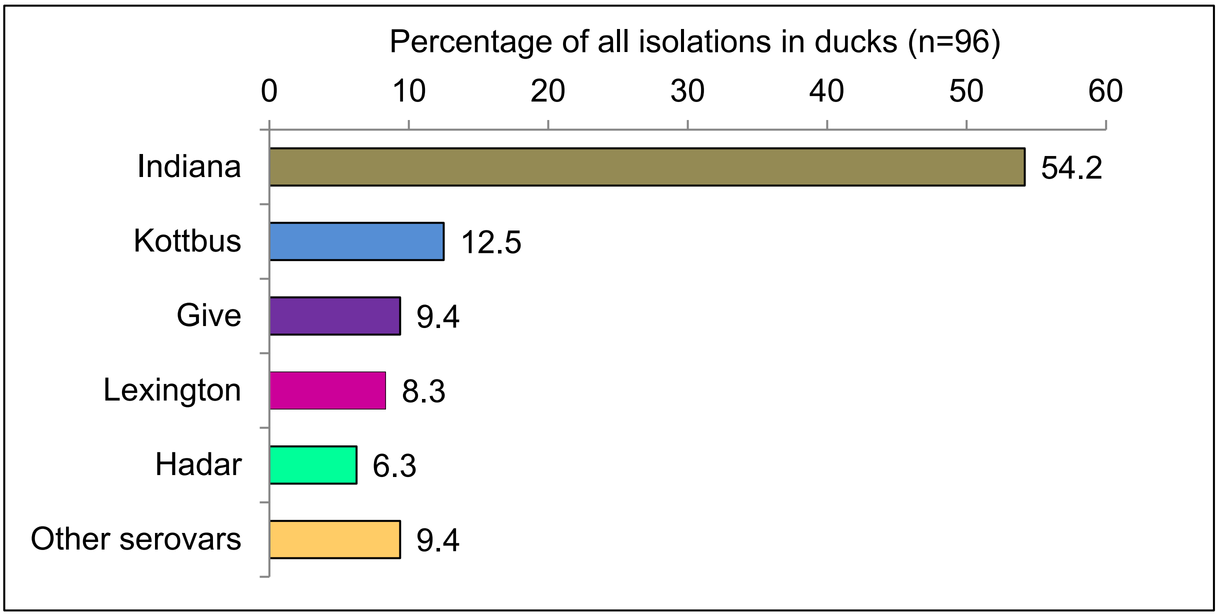
In 2021 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 37.3% of total isolations, followed by *S*. Orion (10.9%), *S.* Kottbus (8.2%) and *S.* Lexington (8.2%).

Figure 8.1.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in ducks 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 8.1.5: Isolations in 2023



In 2023 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 54.2% of total isolations, followed by *S*. Kottbus (12.5%), *S.* Give (9.4%) and *S.* Lexington (8.3%).

Figure 8.2: The 5 most common *Salmonella* serovars in ducks in Great Britain in 2023 and their trends over time since 2019

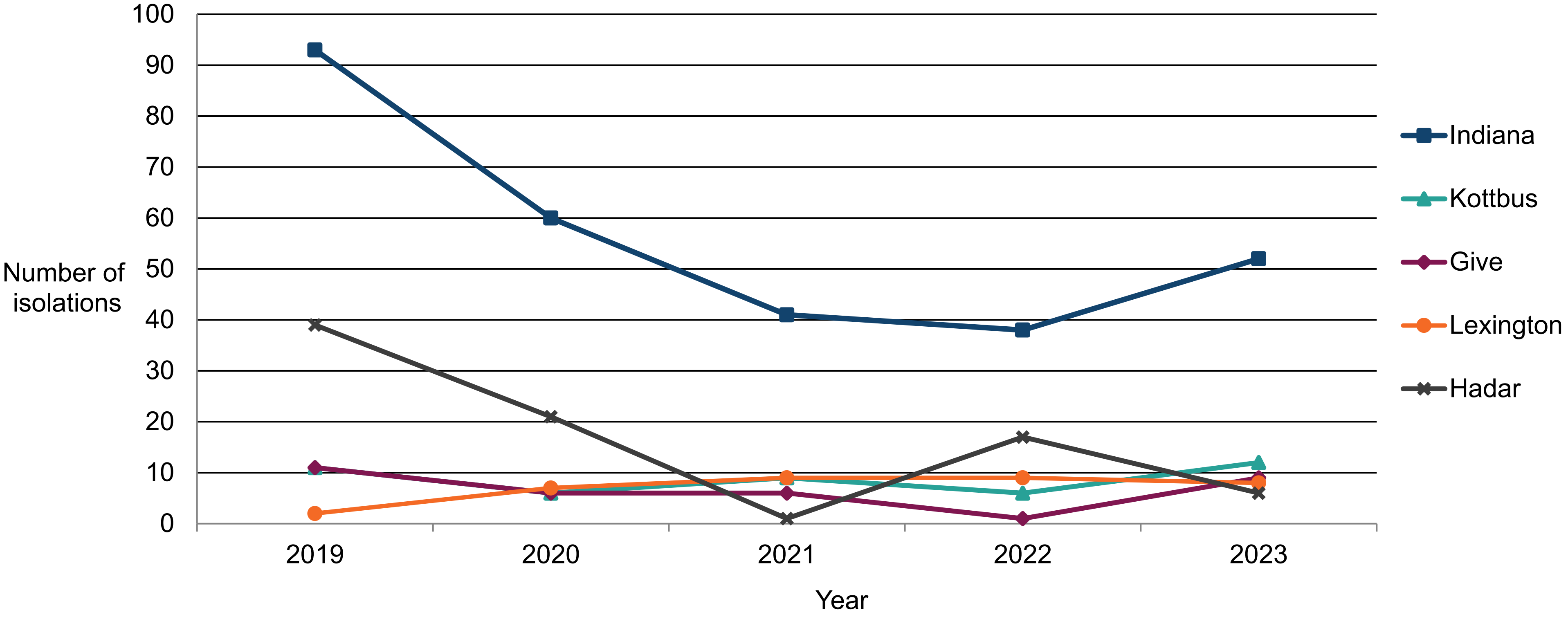


Figure 8.2 shows that *S.* Indiana remains the most common serovar isolated from ducks although numbers have declined overall from 93 isolations in 2019 to 52 in 2023. *S.* Kottbus has remained stable in recent years, 11 isolations in 2019 and 12 isolations in 2023 and was the second most common serovar in 2023. *S.* Give isolations have declined since 2019 from 11 isolations to 9 isolations in 2023. *S.* Lexington isolations have increased since 2019 from 2 isolations to 6 isolations in 2023. *S.* Hadar was the least common of the 5 in 2023 and isolations have declined since 2019 from 39 isolations to 6 isolations in 2023.

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 2003 to 2023

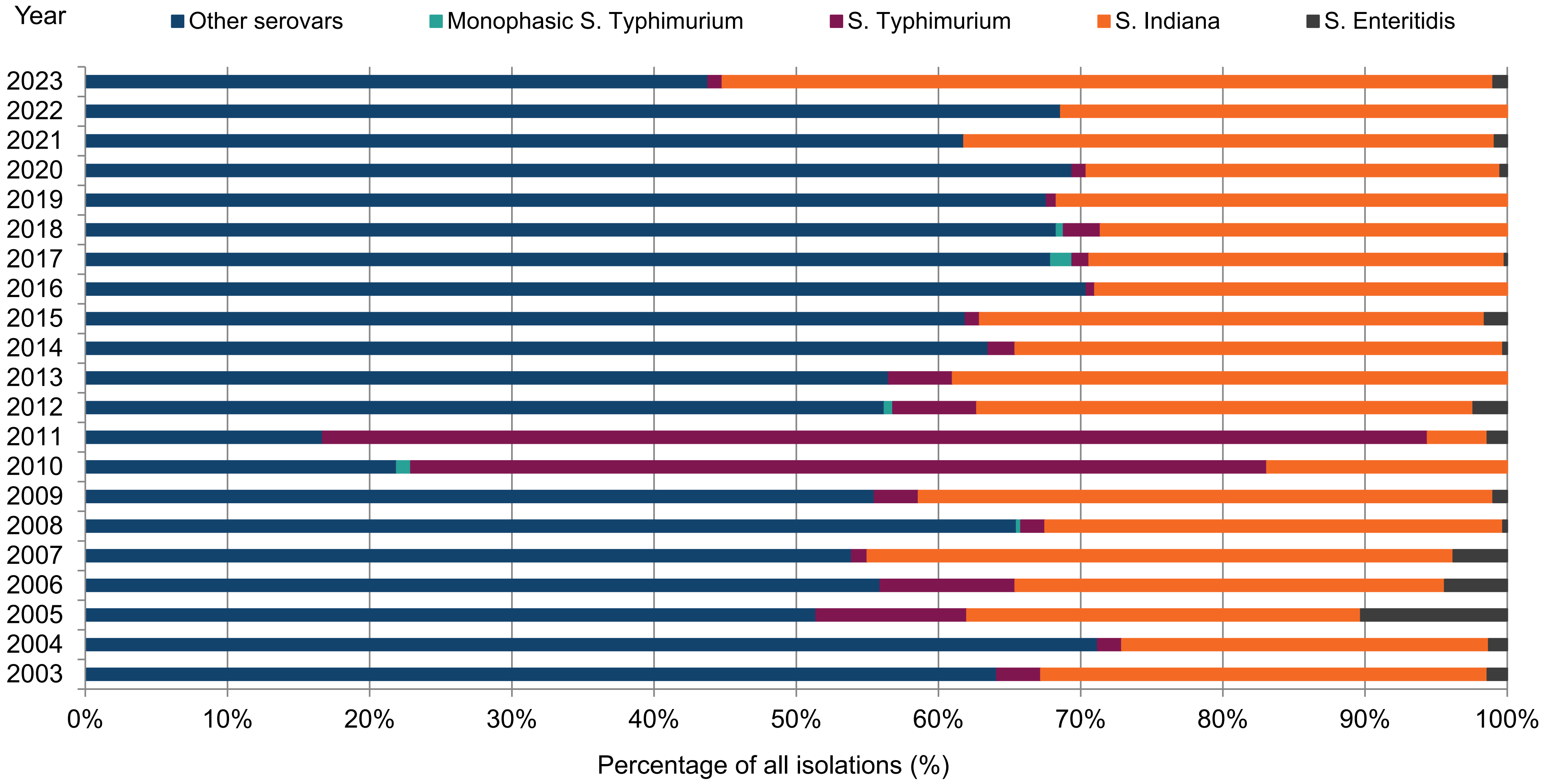


Figure 8.3 shows that *S.* Indiana accounts for the highest proportion of single serovar isolations in all years except 2010 and 2011, exceeding 25.0% every year since 2012. *S.* Typhimurium has accounted for less than 11.0% of all duck isolations every year except for 2010 and 2011 when it was 60.2% 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
2003	64.1%	0.0%	3.1%	31.4%	1.4%
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%

Table 8.3: *S*. Typhimurium phage types in ducks and geese in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT1	0	0	0	0	0	0	0	0	1	1
DT9	0	0	2	2	0	0	0	0	0	0
DT193	0	0	1	1	0	0	0	0	0	0
UNTY	2	2	0	0	0	0	0	0	0	0
Total	**2**	**2**	**3**	**3**	**0**	**0**	**0**	**0**	**1**	**1**

Table 8.4: *S*. Enteritidis phage types in ducks and geese in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
PT9	0	0	0	0	0	0	0	0	1	1
PT9b	0	0	1	1	1	1	0	0	0	0
Total	**0**	**0**	**1**	**1**	**1**	**1**	**0**	**0**	**1**	**1**

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 2023 which is an increase compared to 2022 (18 isolations) and 2021 (15 isolations).

Game birds

The total number of VIDA submissions from game birds (guinea fowl, partridges, pheasants and quail) to APHA and SRUC increased by 5.2% to 181 submissions in 2023, compared to 172 submissions in 2022. As in previous years, the greatest number of submissions were from pheasants, increasing by 4.5% compared with 2022 (116 versus 111 submissions). During 2023 there were also 38 submissions from grouse, which was an increase of 8.6% compared with 2022 (35 submissions), and 17 submissions from partridges which was similar to 2022 (16 submissions).

Two quail submissions were received during 2023, which is less than the submissions reported in 2022 (6 submissions). No guinea fowl submissions were reported in 2023 which is the same as in 2022. A further 8 submissions in 2023 were from birds reported as “other game” which is twice as many as in 2022 (8 versus 4 submissions).

There is no statutory *Salmonella* monitoring of game birds in Great Britain and the majority of submissions in 2023 were for diagnostic purposes (65.7%), which is less than during 2022 (79.6%). There had been a decreasing trend in the number of *Salmonella* isolations from game birds in recent years, across all species. However, there were 4 isolations in 2023, 4 times more than during 2022 (1 isolation) and 42.9% fewer than in 2021 (7 isolations). Two isolations from game birds in 2023 were from pheasants and 2 isolations were from partridges.

Pheasants

There were 2 isolations of *Salmonella* (*S*. Sentfenberg and *S*. Typhimurium NOPT) from pheasants in 2023, which is an increase from 2022 when there was one isolation and a decrease from 2021 when there were 7 isolations (Table 9.1). The 2023 isolates arose from clinical disease investigations, the presenting signs were not given.

The most common serovar usually associated with pheasants is *S*. Senftenberg.

Partridges

There were 2 isolations of *Salmonella* in partridges in 2023 (*S.* Sentfenberg and *S*. Typhimurium DT11), a change from 2021 and 2022 when there were no isolations. Prior to this the number of *Salmonella* isolations from partridges in Great Britain had been 5 isolations per year in 2019 and 2020 (Table 9.2).

Quail

There were no isolations of *Salmonella* from quail in 2023. The last reported isolation from this category of game birds was 5 isolations in 2019 (Table 9.3).

Guinea fowl

There were no isolations from guinea fowl in 2023, The last time *Salmonella* was isolated from guinea fowl was in 2015 when there was one isolation.

Pigeons

There were 68 VIDA submissions from pigeons to APHA and SRUC in 2023 which is a 20.0% decrease compared to 2022 (85 submissions) and a 78.9% increase compared to 2021 (38 submissions).

There were 18 *Salmonella* isolations from pigeons in 2023, which is similar to that in 2022 (17 isolations) but more than double that in 2021 (8 isolations) (Table 9.4). Two of these isolations were from clinical disease investigations with swollen joints and diarrhoea being the presenting signs for one isolation and no available presenting signs for the other isolation. The other 15 isolations were from voluntary surveillance submissions. All isolations in 2023 were *S*. Typhimurium, which is consistently the most commonly isolated serovar from pigeons. Thirteen isolations were phage type DT2, 3 were DT99 and one isolation each were DT105 and DT193 (Table 9.8).

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

***Salmonella* serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Dublin	0	0	0	0	0	0	1	1	0	0
Monophasic Typhimurium	0	0	0	0	1	1	0	0	0	0
Montevideo	0	0	1	1	0	0	0	0	0	0
Orion	0	0	1	1	1	1	0	0	0	0
Orion var 15⁺	2	2	0	0	0	0	0	0	0	0
Senftenberg	5	5	3	2	4	3	0	0	1	1
Typhimurium	1	1	1	0	1	1	0	0	1	1
Total	**8**	**8**	**6**	**4**	**7**	**6**	**1**	**1**	**2**	**2**

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

***Salmonella* serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Monophasic Typhimurium	1	1	3	1	0	0	0	0	0	0
Senftenberg	3	3	2	2	0	0	0	0	1	1
Soerenga	1	1	0	0	0	0	0	0	0	0
Typhimurium	0	0	0	0	0	0	0	0	1	1
Total	**5**	**5**	**5**	**3**	**0**	**0**	**0**	**0**	**2**	**2**

Table 9.3: Isolations and incidents of *Salmonella* in quail on all premises in Great Britain

***Salmonella* serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Bredeney	3	2	0	0	0	0	0	0	0	0
Enteritidis	1	1	0	0	0	0	0	0	0	0
Senftenberg	1	1	0	0	0	0	0	0	0	0
Total	**5**	**4**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Table 9.4: Isolations and incidents of *Salmonella* in pigeons on all premises in Great Britain

***Salmonella* serovar**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**	**2023 isolations**	**2023 incidents**
Enteritidis	0	0	0	0	1	1	0	0	0	0
Kedouogu	0	0	1	1	0	0	0	0	0	0
Orion	0	0	1	1	0	0	0	0	0	0
Typhimurium	11	11	13	13	6	6	17	17	18	18
Untypable strains	0	0	2	2	1	1	0	0	0	0
Total	**11**	**11**	**17**	**17**	**8**	**8**	**17**	**17**	**18**	**18**

Table 9.5: *S.* Typhimurium phage types in pheasants in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT2	1	1	0	0	0	0	0	0	0	0
DT193	0	0	1	0	0	0	0	0	0	0
NOPT	0	0	0	0	1	1	0	0	1	1
Total	**1**	**1**	**1**	**0**	**1**	**1**	**0**	**0**	**1**	**1**

Table 9.6: *S.* Typhimurium phage types in partridges in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT11	0	0	0	0	0	0	0	0	1	1
Total	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**1**

Table 9.7: *S.* Typhimurium phage types in pigeons in Great Britain 2019 to 2023

Phage types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT2	5	5	9	9	6	6	13	13	13	13
DT99	3	3	0	0	0	0	4	4	3	3
DT105	0	0	0	0	0	0	0	0	1	1
DT193	3	3	2	2	0	0	0	0	1	1
RDNC	0	0	1	1	0	0	0	0	0	0
UNTY	0	0	1	1	0	0	0	0	0	0
Total	**11**	**11**	**13**	**13**	**6**	**6**	**17**	**17**	**18**	**18**

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 2023 annual summary therefore represents the second 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 2023, the UK dog population was estimated to be around 12 million, with 31% 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 689 *Salmonella* isolations from dogs in 2023 (Table 10.1). This is a decrease of 19.6% compared to 2022 (857 isolations), and a decrease of 5.7% compared to 2021 (731 isolations). In total, 79 different serovars were reported (excluding untypable and rough strains), which is slightly higher than 2022 (71 serovars) and 2021 (71 serovars). The majority of isolations (681 isolations, 98.8%) arose from clinical investigations with the remainder from monitoring submissions (8 isolations, 1.2%).

The most commonly reported serovar from dogs in 2023 was *S*. Typhimurium (90 isolations, 13.1% 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 (116 isolations in 2022, 97 isolations in 2021, 11 isolations in 2020, and 5 isolations in 2019). The second most commonly reported serovar was *S*. Infantis (79 isolations, 11.5% of all isolations). Other commonly reported serovars were monophasic *S.* Typhimurium (42 isolations) *S*. Derby (37 isolations), *S.* Montevideo (35 isolations), *S*. Dublin (35 isolations), *S*. Anatum (32 isolations), and *S.* Enteritidis (26 isolations) (Table 10.1, Figure 10.2).

Salmonella Typhimurium and monophasic *S.* Typhimurium

There were 90 isolations of *S*. Typhimurium during 2023 comprising 14 different phage types. 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) (Table 10.2). This is compared to 2022 when the most common phage types were RDNC (26 isolations, 22.4% of all *S*. Typhimurium in dogs), DT104 (26 isolations, 22.4% of all *S*. Typhimurium in dogs), DT193 (15 isolations, 12.9% of all *S*. Typhimurium in dogs), and DT105 (11 isolations, 9.5% of all *S*. Typhimurium in dogs). Two *S*. Typhimurium phage types were reported for the first time in dogs from Great Britain during 2023 (DT21 and DT104b).

Since the start of 2023 following the move to whole genome sequencing, the monophasic variants *Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:- are 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.

There were 42 isolations of monophasic *S*. Typhimurium reported from dogs during 2023 comprising 6 different phage types. The most common phage type was DT193 (33 isolations, 78.6% of all monophasic *S.* Typhimurium in dogs) (Table 10.4).

Other notable serovars

The number of *Salmonella* Infantis isolations from dogs was 79 in 2023 down from 109 isolation in 2022 but still higher than previous years (51 isolations in 2021, 3 isolations in 2020, and one isolation in 2019) (Table 10.1 and Figure 10.2). *Salmonella* Enteritidis was isolated 26 times from dogs in 2023, which is an increase from 2022 (15 isolations). The most common phage type of *S*. Enteritidis was PT8 (5 isolations in 2023) (Table 10.3).

Public health significance

The change to make *Salmonella* in dogs reportable was made to improve the protection of public health. In 2023, *Salmonella* isolations in dogs accounted for 15.6% 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*. Infantis, which were the 3 most commonly reported serovars isolated from people in Great Britain in 2023 (see Chapter 1).

Notably, while dogs and cats may become clinically ill when infected (Morley et al., 2006), they are often asymptomatic carriers of these bacteria (Finley et al., 2007). Therefore, while the vast majority of dog isolations this year arose from clinical investigations (98.8%), 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.* Isolations of *Salmonella* from raw meat pet food (RMPF) have increased over recent years, with 331 isolations in 2023 (see Chapter 12, Table 12.8b). Consistent with 2022, *Salmonella* Typhimurium (30 isolations) and *S.* Infantis (29 isolations) were amongst the top 4 serovars isolated from RMPF in 2023, 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, especially if insufficient hygiene measures are adopted.

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

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Aarhus	0	0	0	0	3	3	0	0	0	0
Abony	0	0	0	0	0	0	1	1	0	0
Adelaide	0	0	0	0	0	0	0	0	2	2
Agama	2	2	2	2	14	14	11	11	13	13
Agona	0	0	1	1	16	16	27	27	15	15
Ajiobo	0	0	0	0	4	4	2	2	1	1
Altona	0	0	0	0	0	0	1	1	0	0
Amersfoort	0	0	0	0	1	1	0	0	0	0
Anatum	0	0	1	1	20	20	22	22	32	32
Ank	0	0	0	0	0	0	0	0	4	4
Apeyeme	0	0	0	0	0	0	0	0	1	1
Ball	0	0	0	0	0	0	1	1	0	0
Bardo	0	0	0	0	0	0	1	1	0	0
Bareilly	0	0	0	0	1	1	1	1	1	1
Berta	0	0	0	0	2	2	1	1	3	3
Bonn	0	0	0	0	1	1	0	0	3	3
Bovismorbificans	0	0	1	1	25	25	9	9	12	12
Brandenburg	0	0	3	3	11	11	10	10	4	4
Bredeney	0	0	0	0	3	3	10	10	2	2
Budapest	0	0	0	0	0	0	1	1	0	0
Cannstatt	0	0	0	0	0	0	1	1	0	0
Cerro	1	1	3	3	2	2	5	5	0	0
Chester	0	0	0	0	0	0	0	0	1	1
Coeln	0	0	0	0	3	3	11	11	3	3

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Concord	0	0	0	0	2	2	1	1	1	1
Corvallis	0	0	0	0	0	0	0	0	1	1
Cotham	0	0	0	0	0	0	0	0	1	1
Cubana	0	0	0	0	1	1	0	0	0	0
Derby	0	0	2	2	26	26	55	55	37	36
Dublin	1	1	5	5	61	61	55	54	35	35
Durham	0	0	1	1	1	1	1	1	0	0
Ealing	0	0	0	0	3	3	8	8	1	1
Eboko	0	0	0	0	1	1	0	0	1	1
Enteritidis	0	0	2	2	26	26	15	15	26	26
Fluntern	0	0	0	0	0	0	1	1	0	0
Fulica	0	0	0	0	0	0	1	1	1	1
Give	0	0	2	2	4	4	0	0	6	6
Give var 15+	0	0	0	0	0	0	3	3	0	0
Goelzau	0	0	0	0	0	0	0	0	1	1
Goldcoast	0	0	0	0	9	9	2	2	3	3
Gueuletapee	0	0	0	0	0	0	1	1	1	1
Hadar	0	0	0	0	8	8	5	5	2	2
Haifa	0	0	0	0	0	0	2	2	0	0
Havana	0	0	0	0	1	1	3	3	3	3
Hessarek	0	0	0	0	2	2	1	1	3	3
Hvittingfoss	0	0	0	0	0	0	0	0	1	1
Idikan	0	0	0	0	0	0	0	0	4	4
Indiana	0	0	2	2	13	13	20	20	7	7
Infantis	1	1	3	3	51	51	109	107	79	78
Isangi	0	0	0	0	1	1	2	2	0	0

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Javiana	0	0	0	0	2	2	1	1	1	1
Kapemba	0	0	0	0	0	0	1	1	1	1
Kedougou	0	0	0	0	8	8	1	1	9	9
Kentucky	0	0	0	0	0	0	8	8	4	4
Kingston	0	0	0	0	4	4	1	1	2	2
Kisarawe	0	0	0	0	0	0	20	20	0	0
Kottbus	0	0	2	2	11	11	0	0	12	12
Larochelle	0	0	1	1	0	0	0	0	0	0
Lexington	0	0	0	0	0	0	1	1	0	0
Litchfield	0	0	0	0	0	0	1	1	0	0
Liverpool	0	0	0	0	0	0	1	1	0	0
Livingstone	0	0	0	0	12	12	14	14	19	19
Lome	0	0	0	0	0	0	0	0	1	1
Lomita	0	0	0	0	1	1	0	0	0	0
London	0	0	0	0	7	7	13	13	5	5
Matopeni	0	0	0	0	1	1	0	0	0	0
Mbandaka	1	1	1	1	7	7	11	11	30	30
Meleagridis	0	0	0	0	1	1	0	0	0	0
Miami	0	0	0	0	1	1	0	0	0	0
Mikawasima	0	0	0	0	0	0	0	0	1	1
Mishmarhaemek	0	0	0	0	0	0	0	0	1	1
Molade	0	0	0	0	0	0	0	0	1	1
Monophasic Typhimurium	6	6	10	10	71	71	64	64	42	42
Montevideo	2	2	1	1	17	17	27	26	35	35
Muenchen	4	3	0	0	0	0	2	2	1	1

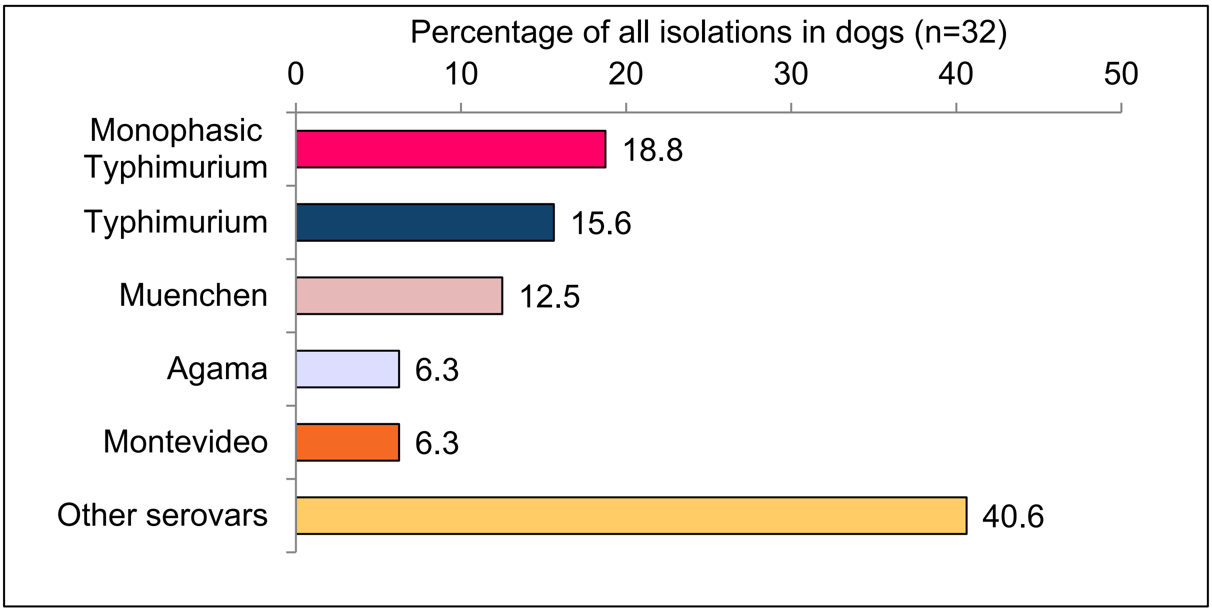
Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Muenster	0	0	0	0	2	2	2	2	9	9
Nagoya	0	0	0	0	0	0	0	0	1	1
Newport	0	0	4	4	43	43	52	52	25	25
Ohio	0	0	0	0	3	3	0	0	1	1
Oranienburg	0	0	0	0	1	1	4	4	4	4
Orion	0	0	0	0	3	3	1	1	3	3
Orion var 15+	0	0	0	0	0	0	0	0	1	1
Oslo	1	1	2	2	6	6	10	10	7	7
Panama	1	1	0	0	5	5	9	9	4	4
Paratyphi B var Java	0	0	0	0	11	11	9	9	1	1
Pomona	0	0	0	0	1	1	0	0	0	0
Poona	0	0	0	0	0	0	0	0	1	1
Putten	0	0	0	0	1	1	0	0	0	0
Reading	0	0	0	0	1	1	1	1	0	0
Rissen	0	0	0	0	10	9	6	6	3	3
Saintpaul	0	0	0	0	0	0	1	1	1	1
Saphra	0	0	0	0	1	1	0	0	0	0
Schwarzengrund	0	0	0	0	2	2	1	1	1	1
Senftenberg	0	0	1	1	3	3	0	0	0	0
Soerenga	0	0	0	0	3	3	1	1	0	0
Stanley	0	0	1	1	1	1	10	10	4	4
Stanleyville	0	0	0	0	4	4	0	0	1	1
Stendal	0	0	0	0	0	0	1	1	0	0
Stourbridge	1	1	0	0	2	2	0	0	1	1
Szentes	0	0	0	0	0	0	0	0	1	1

Salmonella serovar	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
Tennessee	0	0	0	0	1	1	1	1	0	0
Thompson	1	1	0	0	1	1	0	0	22	20
Typhimurium	5	3	11	10	97	87	116	116	90	90
Uganda	0	0	2	2	7	7	3	3	1	1
Utah	0	0	0	0	0	0	0	0	1	1
Virchow	0	0	0	0	7	7	3	3	1	1
Wangata	0	0	0	0	1	1	0	0	0	0
Yoruba	0	0	0	0	0	0	0	0	3	3
4,5,12:b:-	0	0	0	0	5	5	2	2	1	1
6,7:-:-	0	0	0	0	17	17	23	23	1	1
6,8:-:-	0	0	0	0	3	3	0	0	2	2
61:k:1,5,7	0	0	0	0	0	0	0	0	3	3
61:-:1,5,7	0	0	0	0	0	0	8	7	0	0
untypable strains	5	5	0	0	22	22	19	19	18	18
rough strains	0	0	0	0	8	8	8	8	1	1
Total	**32**	**29**	**64**	**63**	**731**	**720**	**857**	**852**	**689**	**685**

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.

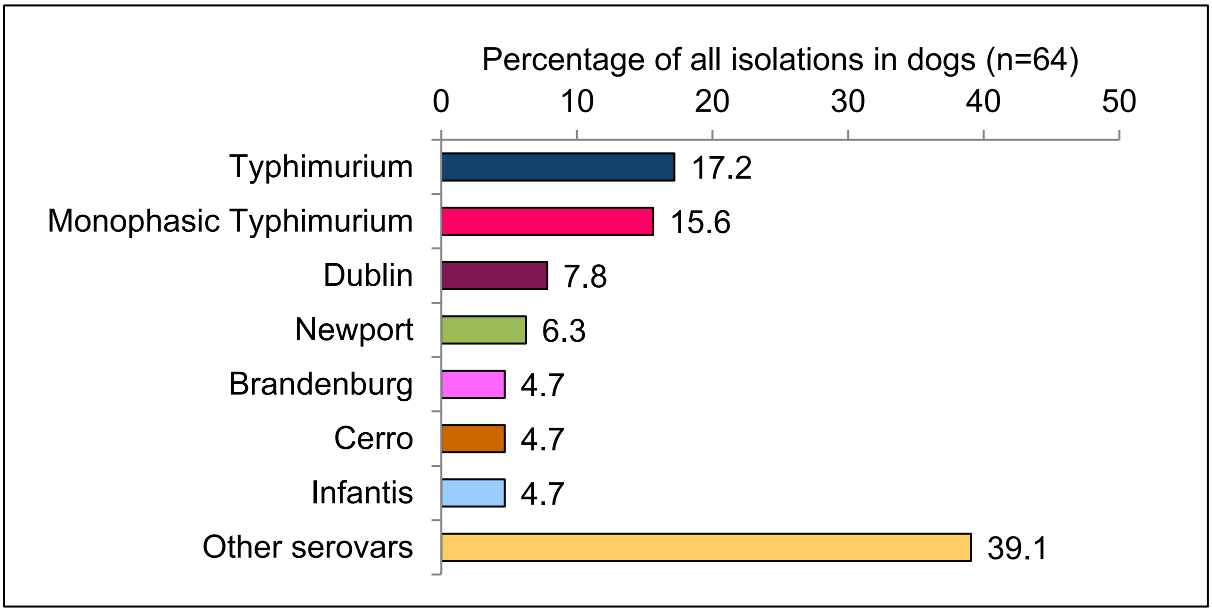
Figure 10.1: Isolations of the most common serovars in dogs in Great Britain 2019 to 2023

Figure 10.1.1: Isolations in 2019



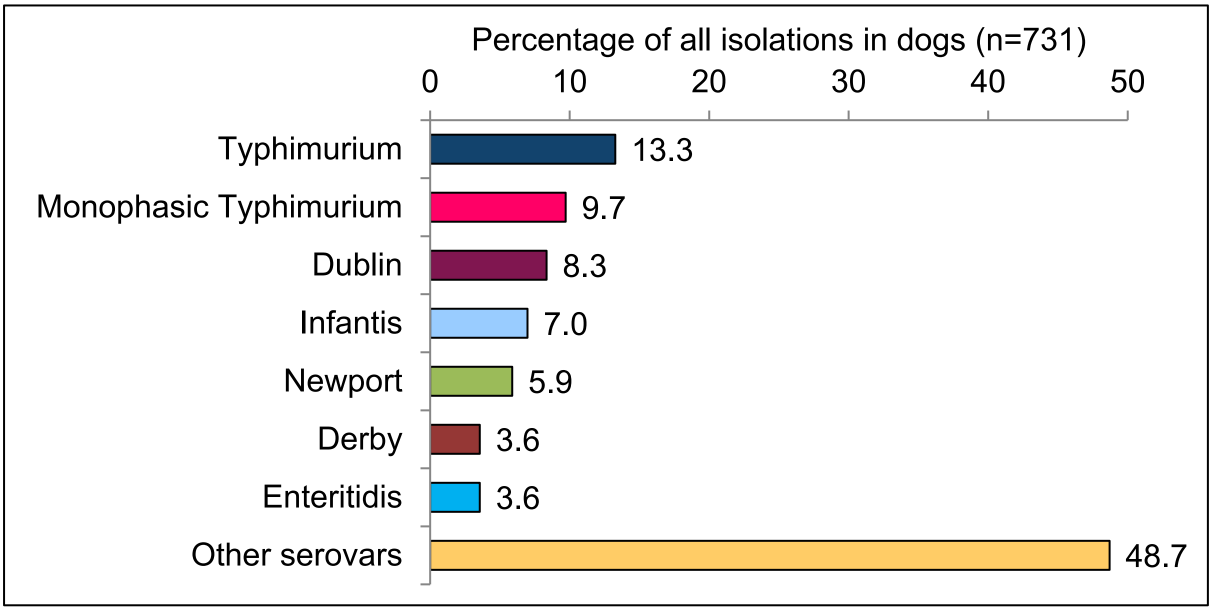
In 2019 the most common *Salmonella* serovar in dogs was monophasic *S.* Typhimurium, accounting for 18.8% of total isolations, followed by *S*. Typhimurium (15.6%), *S*. Muenchen (12.5%), and *S.* Agama (6.3%).

Figure 10.1.2: Isolations in 2020



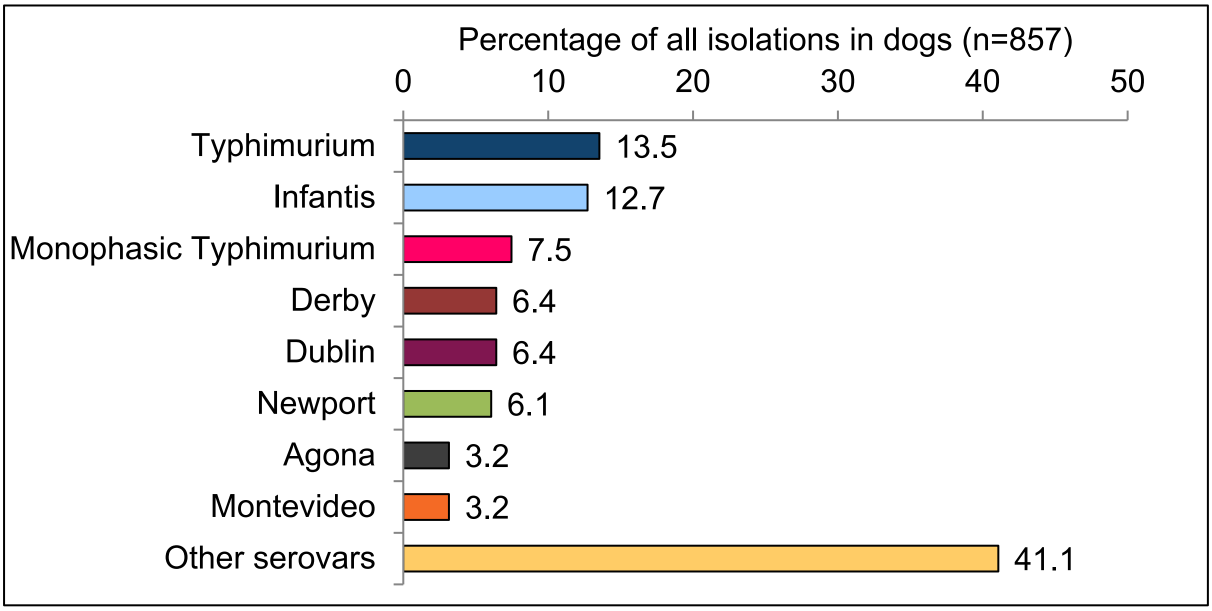
In 2020 the most common *Salmonella* serovar in dogs was *S.* Typhimurium, accounting for 17.2% of total isolations, followed by monophasic *S*. Typhimurium (15.6%), *S.* Dublin (7.8%) and *S*. Newport (6.3%).

Figure 10.1.3: Isolations in 2021



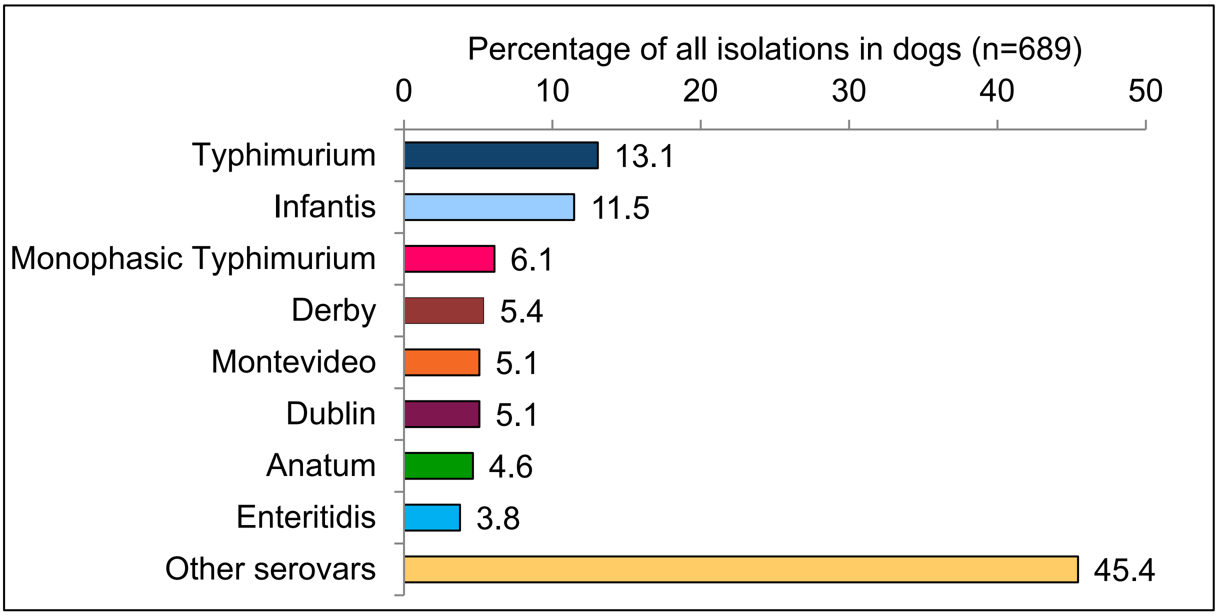
In 2021 the most common *Salmonella* serovar in dogs was *S*. Typhimurium, accounting for 13.3% of total isolations, followed by monophasic *S.* Typhimurium (9.7%), *S*. Dublin (8.3%) and *S*. Infantis (7.0%).

Figure 10.1.4: Isolations in 2022



In 2022 the most common *Salmonella* serovar in dogs 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 2023



In 2023 the most common *Salmonella* serovar in dogs 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%) and *S*. Montevideo (5.1%).

Figure 10.2: The 5 most common *Salmonella* serovars in dogs in Great Britain in 2023 and their trends over time since 2019

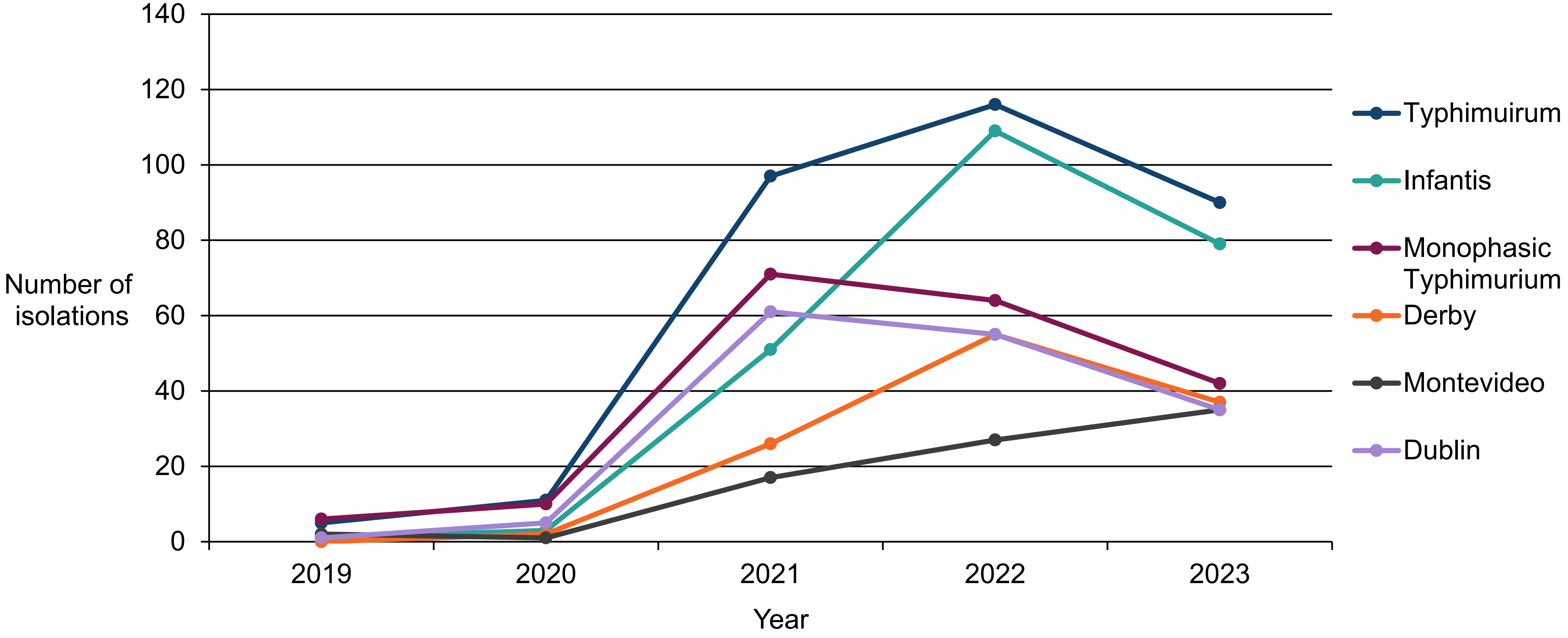


Figure 10.2 shows a very low number of isolations for all serovars until 2021 when reporting of *Salmonella* in dogs became statutory with *S*. Typhimurium being the most common at 21 isolations (2018) or less. All of the 5 most common serovars have increased significantly since then with *S.* Typhimurium still being the most common in 2023 (90 isolations), followed by *S*. Infantis (79 isolations), monophasic *S.* Typhimurium(42 isolations), *S*. Derby (37 isolations), *S*. Dublin and *S*. Montevideo (both 35 isolations).

Table 10.2: Isolations and incidents of *S*. Typhimurium in dogs on all premises in Great Britain

Phage Types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT1	0	0	0	0	2	2	9	9	6	6
DT2	0	0	3	3	14	10	8	8	9	9
DT2a	0	0	0	0	1	1	0	0	0	0
DT3	0	0	0	0	1	1	0	0	0	0
DT4	0	0	0	0	0	0	1	1	0	0
DT5	0	0	0	0	0	0	1	1	0	0
DT8	0	0	0	0	3	3	1	1	0	0
DT9	0	0	0	0	1	1	0	0	1	1
DT11	0	0	0	0	1	1	0	0	0	0
DT21	0	0	0	0	0	0	0	0	1	1
DT41	1	1	0	0	1	1	0	0	0	0
DT42	0	0	0	0	0	0	1	1	0	0
DT56	0	0	0	0	1	1	0	0	0	0
DT75	0	0	0	0	0	0	6	6	16	16
DT99	0	0	0	0	1	1	3	3	3	3
DT101	0	0	0	0	1	1	0	0	0	0
DT104	1	1	1	1	18	18	26	26	6	6
DT104b	0	0	0	0	0	0	0	0	1	1
DT105	0	0	1	1	5	5	11	11	8	8
DT106	0	0	0	0	0	0	1	1	0	0
DT115	0	0	1	1	0	0	0	0	0	0
DT116	0	0	0	0	2	2	1	1	5	5

Phage Types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT120	0	0	0	0	0	0	2	2	1	1
DT189	0	0	2	1	1	1	1	1	0	0
DT193	1	1	0	0	13	13	15	15	10	10
DT194	0	0	0	0	0	0	1	1	0	0
U208	0	0	0	0	0	0	1	1	0	0
U288	0	0	0	0	1	1	0	0	0	0
U289	0	0	0	0	1	1	0	0	0	0
U308	0	0	1	1	4	4	0	0	0	0
U308a	0	0	0	0	1	1	0	0	0	0
U311	0	0	0	0	2	2	1	1	0	0
NOPT	1	0	0	0	1	0	0	0	0	0
RDNC	1	1	1	1	19	14	26	26	22	22
UNTY	0	0	1	1	2	2	0	0	1	1
Total	**5**	**4**	**11**	**10**	**97**	**87**	**116**	**116**	**90**	**90**

Reporting of *Salmonella* in dogs became statutory in 2021

Table 10.3: Isolations and incidents of *S*. Enteritidis in dogs on all premises in Great Britain

Phage Types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
PT2	0	0	0	0	1	1	0	0	1	1
PT3	0	0	0	0	2	2	1	1	0	0
PT4	0	0	0	0	0	0	1	1	1	1
PT4b	0	0	0	0	0	0	1	1	0	0
PT8	0	0	0	0	2	2	6	6	5	5
PT9	0	0	0	0	0	0	1	1	3	3
PT9a	0	0	0	0	0	0	2	2	3	3
PT11	0	0	1	1	6	6	0	0	1	1
PT11b	0	0	0	0	0	0	1	1	2	2
PT13a	0	0	0	0	1	1	0	0	1	1
PT14b	0	0	0	0	0	0	0	0	1	1
PT21	0	0	0	0	1	1	0	0	3	3
PT28	0	0	0	0	1	1	0	0	0	0
PT31	0	0	1	1	0	0	0	0	0	0
PT33	0	0	0	0	0	0	1	1	0	0
PT35	0	0	0	0	0	0	0	0	1	1
NOPT	0	0	0	0	2	2	1	1	2	2
RDNC	0	0	0	0	6	6	0	0	2	2
UNTY	0	0	0	0	4	4	0	0	0	0
Total	**0**	**0**	**2**	**2**	**26**	**26**	**15**	**15**	**26**	**26**

Reporting of *Salmonella* in dogs became statutory in 2021.

Table 10.4: Monophasic *Salmonella* Typhimurium phage types in dogs in in Great Britain 2019 to 2023

Phage Types	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents	2023 isolations	2023 incidents
DT35	0	0	0	0	0	0	1	1	0	0
DT104	0	0	0	0	0	0	0	0	1	1
DT120	0	0	0	0	1	1	1	1	1	1
DT193	6	6	8	8	52	52	50	50	33	33
DT194	0	0	1	1	0	0	0	0	0	0
U308a	0	0	0	0	0	0	0	0	1	1
U311	0	0	0	0	4	4	6	6	0	0
RDNC	0	0	1	1	3	3	4	4	2	2
NOPT	0	0	0	0	2	2	0	0	0	0
UNTY	0	0	0	0	9	9	2	2	4	4
Total	**6**	**6**	**10**	**10**	**71**	**71**	**64**	**64**	**42**	**42**

Reporting of *Salmonella* in dogs became statutory in 2021.

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 and 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), and Great Britain Wildlife Health Partnership (Great Britain WDHP), 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's (APHA) Diseases of Wildlife Scheme (DoWS).

Wild mammals

Hedgehogs

Two *Salmonella* isolates (*S*. Enteritidis PT11) were reported in 2 European hedgehogs (*Erinaceus europaeus*). Unfortunately, additional information regarding clinical findings or pathology are unavailable. *S*. Enteritidis PT11 is reported to be the most common *Salmonella* spp. isolated from hedgehogs and is common and widespread in hedgehogs in England (Keymer et al., 1991). Robinson and Routh (1999) suggest that *S*. Enteritidis PT11 appears to be endemic in hedgehogs.

European badgers

Two European badgers (*Meles meles*) submitted to the Starcross Veterinary Investigation Centre in Autumn 2023 had a variety of *Salmonella* serovars isolated: *S.* Agama, *S.* Anatum, *S.* Berta (multiple serovars present in one badger) and *S.* Newport (single serovar present in one badger). No further information on the clinical findings or pathology are available. A wide range of *Salmonella* spp. are known to be commonly present in badgers in the UK (Wray et al., 1977; Euden, 1990; Wilson et al., 2003, O'Hagan et al., 2021). The reported range of serovars is broad, with *S.* Agama being the most commonly isolated serovar in badgers (Euden, 1990; O'Hagan et al., 2021).

Red squirrel

Salmonella Typhimurium RDNC was detected in a female Red squirrel (*Sciurus vulgaris*) submitted to the Penrith Veterinary Investigation Centre that died with an extensive mandibular abscess. This squirrel also had pleuritis and pneumonia, with *S*. Typhimurium cultured from the lung tissue, which is an unusual bacterium to isolate from a squirrel.

Wild birds

There were 2 isolations of *Salmonella* from wild birds in 2023, although it should be noted that handling of wild bird submissions during the Avian influenza outbreak was primarily to screen for AI. Further testing of these carcases is delayed until AI has been ruled out in these submissions. Such a delay will have adversely affected the condition of the carcasses and the bacterial examination for *Salmonella*.

One *Salmonella* isolate (*S*. Typhimurium DT2) was reported in a Common Buzzard (*Buteo buteo*) that was submitted as part of the Avian Influenza (AI) monitoring scheme and tested AI negative. The buzzard was in poor body condition and had severe necrotising pharyngitis and oesophagitis caused by trichomonads, in addition to *S*. Typhimurium isolated from its intestinal contents. A variety of *Salmonella* species and serotypes have been isolated in European raptors (including Common Buzzards) with *S*. Typhimurium commonly identified in several raptor species (Molina-Lopez et al., 2011; Botti et al., 2013; Giacopello et al., 2016).

A heavy growth of *S*. Typhimurium RDNC was the confirmed cause of septicaemia, enteritis and death in an immature Herring gull (*Larus argentatus*) submitted to the Shrewsbury Veterinary Investigation Centre. A wide range of *Salmonella* serotypes are carried by Herring gulls that are also found in humans (including *S*. Typhimurium), and it is likely that the gulls 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 2019 to 2023

Species	Serovar and phage type	2019	2020	2021	2022	2023
Badger	Agama	0	0	1	0	1
Badger	Anatum	0	0	0	0	1
Badger	Berta	0	0	0	0	1
Badger	Newport	0	0	1	0	1
Hedgehog	Enteritidis PT11	3	1	10	1	2
Hedgehog	Enteritidis PT20	0	0	1	0	0
Hedgehog	Enteritidis PT183	1	0	0	0	0
Porpoise	4,12:-:-	0	0	0	1	0
Squirrel	Typhimurium RDNC	0	0	0	0	1
Total	Not applicable	**4**	**1**	**13**	**2**	**7**

Table 11.2: Isolations of *Salmonella* in wild birds in Great Britain 2019 to 2023

Species	Serovar and phage type	2019	2020	2021	2022	2023
Buzzard	Typhimurium DT2	0	0	0	0	1
Egret	Typhimurium DT2	0	1	0	0	0
Finch	Typhimurium DT193	0	0	2	0	0
Gull	Typhimurium RDNC	0	0	0	0	1
Heron	Typhimurium DT193	0	0	1	0	0
Mixed species	Typhimurium NOPT	0	0	1	0	0
Swan	Typhimurium DT1	0	0	1	0	0
Swan	Typhimurium U308	0	0	1	0	0
Total	Not applicable	**0**	**1**	**6**	**0**	**2**

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

From 2020 onwards, the total number of samples of animal feedingstuffs 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 897 isolations of *Salmonella* from feedingstuffs during 2023, including 94 isolations from compound feeds (Tables 12.3 - 12.6) and 759 from feed ingredients or products associated with testing under Animal By-Products Regulations (ABPR) (Table 12.7). Isolations from feedingstuffs increased by 12.0% compared with 2022 (801 isolations) and increased by 7.4% compared with 2021 (835 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 feedingstuffs and products tested under the ABPR increased by 41.7% in 2023 compared with 2022 (265 isolations versus 187 isolations) and by 113.7% compared with 2021 (124 isolations) (Table 12.1). In 2023, these comprised 132 isolations of *S.* Infantis, 70 isolations of *S.* Typhimurium, 29 isolations of monophasic *S.* Typhimurium, 19 isolations of *S.* Enteritidis, 14 isolations of *S.* Hadar, 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 several other species, including dogs. Details of these isolations are given in Table 12.6.

There were 8 *Salmonella* isolations from compound ruminant feed during 2023, a small increase from 2022 (7 isolations), and a 60% decrease from 2021 (20 isolations). The reported serovars were *S.* Tennessee (7 isolations, 87.5% of isolations) and a single isolation of *S.* Molade (12.5% of isolations). Neither of these serovars have been isolated from cattle or small ruminants (Figure 12.4, also see Chapters 2 and 3), however during 2022, *S.* Tennessee was isolated once from ruminant feed (Table 12.3).

There was a 92.9% decrease in the number of *Salmonella* isolations from compound pig feed during 2023 compared to 2022 (1 isolation versus 14 isolations), and a 95.2% decrease in number of isolations compared to 2021 (21 isolations) (Table 12.4). The single *Salmonella* isolation during 2023 was of *S.* Derby. Isolations of *S.* Derby represented 6.6% of total *Salmonella* isolations in pigs in 2023 (Figure 12.5, also see Chapter 4).

There were 9 isolations of *Salmonella* from compound poultry feed during 2023, which is 40% fewer than 2022 (15 isolations) and 62.5% fewer than 2021 (24 isolations) (Table 12.5). Five different serovars were reported, the most common being *S*. Typhimurium (5 isolations, accounting for 55.6% of total isolations), followed by one isolation each of *S*. 4,12:b:-, *S.* Cubana, *S.* Senftenberg, and *S.* Utah (each accounting for 11.1% of isolations from compound poultry feed). A comparison of the serovars recorded from compound poultry feed and the most common serovars found in chickens and turkeys tested under the NCP in 2023 is shown in Figure 12.6. No chicken or turkey flocks tested under the NCP in 2023 tested positive for *S*. Utah. *Salmonella* Cubana and *S*. 4,12:b:- were both isolated on single occasions from laying flocks. *Salmonella* Typhimurium was isolated from chicken breeding and laying flocks (but not broiler), in addition to turkeys (Figure 12.6, also see Chapters 6 and 7). 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 is the usual situation in poultry.

Isolations from feedingstuff ingredients

During 2023, there was a total of 44 *Salmonella* isolations arising from 12 different feedingstuff ingredient types (Table 12.8a). This is a decrease of 61.4% compared to 2022 (114 isolations). *Salmonella* was most commonly isolated from soya (12 isolations), followed by feed additives and mixed vegetables (6 isolations each), and maize and rapeseed (4 isolations each).

There was an 88.6% reduction in isolations from rapeseed in 2023 compared to 2022 (4 versus 35 isolations), and a 94.5% reduction compared to 2021 (73 isolations). There was a reduction in *Salmonella* isolation from malt (3 in 2023 versus 5 in 2022). In 2023, there were 6 isolations in mixed vegetables compared to 0 in 2022 and 2021.

The most commonly isolated serovars from feedingstuff ingredients during 2023 were *S.* Typhimurium (10 isolations), *S*. Derby (6 isolations), *S.* Montevideo, *S.* Agama and *S.* Agona (3 isolations each). There was a single isolate of *S.* Rissen, compared to 26 isolations in 2022. During 2023, *S.* Typhimurium was isolated from soya (5 isolations), rapeseed (1 isolations) and maize (4 isolations). *S.* Derby was isolated from feed additives (4 isolations) and mixed vegetables (2 isolations). Isolations of *S.* Tennessee decreased from 9 isolations in 2022 and 2021, to 2 isolations in 2023 while there was just a single isolate of *S.* Rissen in 2023 (from oilseeds) compared to 26 in 2023, 23 of which were from rapeseed (Table 12.8a).

Isolations from products associated with ABPR

During 2023, there were 759 *Salmonella* isolations arising from 18 different product types plus feedmill environments tested under ABPR in Great Britain (Table 12.8b). This is 31.5% higher than the number of isolations in 2022 (577 isolations) and more than twice that of 2021 (504 isolations). The highest number of isolations was from raw meat pet food (331 isolations), followed by samples from feed mill environments (289 isolations), unspecified products (35 isolations), and digestate (34 isolations).

Compared with 2022, there was an increase in the number of *Salmonella* isolates from several different products controlled under the ABPR, including feedmill environments (289 versus 133 isolations) and digestate (34 versus 4 isolations). There were fewer isolations of *Salmonella* from raw meat pet food in 2023 compared to 2022 (331 versus 406 isolations) (Table 12.8b).

The most commonly isolated serovars from products tested under the ABPR were *S.* Infantis (120 isolations), *S.* Kedougou (90 isolations), *S*. Ohio (76 isolations), and *S.* Indiana (47 isolations). The majority of *S*. Kedougou isolations were from samples collected from feed mill environments (82 isolations) and are likely to indicate resident contamination within some mills. Likewise, 89.5% of *S.* Ohio isolations (68 isolations) were from feed mill environments, digestate (2 isolates, 2.6%) and unspecified (6 isolates, 7.9%). All except one *S.* Indiana isolate came from raw meat pet food, the remaining isolate being from raw meat. *S.* Infantis isolations were from a variety of sources including 29 isolations (24.2%) from raw pet food, 22 isolations (18.3%) from digestate, and 20 isolations (16.7%) from the feedmill environment (Table 12.8b).

Isolations from raw meat pet food

During 2023 there were 331 reports of *Salmonella* from raw meat pet food (Table 12.8b and figure 12.7). This is lower than during 2022 (406 reports) but an increase from 2021 (293 reports). The most common serovars isolated from raw meat pet food during 2023 were *S*. Indiana (46 isolations), *S.* Derby (31 isolations), and *S.* Infantis (29 isolations) (Figure 12.7). In comparison, *Salmonella* Typhimurium, *S.* Infantis and monophasic *S.* Typhimurium were the 3 most commonly isolated serovars in dogs in 2022 (Chapter 10).

There were 99 isolations of regulated serovars from raw meat pet food in 2023 (Table 12.2) which was 19.5% higher than in 2022 (123 isolations) but a 39% increase from 2021 (71 isolations). Regulated serovars comprise *S*. Enteritidis, *S*. Hadar, *S*. Infantis, monophasic *S*. Typhimurium, *S*. Typhimurium and *S*. Virchow. These included 30 isolations of *S*. Typhimurium, 29 isolations of *S.* Infantis and monophasic *S.* Typhimurium respectively and 19 isolations of *S.* Enteritidis. (Table 12.2, Figure 12.2).

Regulated serovars originating from raw meat pet food during 2023 accounted for 37.4% of total regulated serovars isolated from all feedingstuffs and products associated with the

ABPR (Table 12.2). This is a lower proportion than during 2022 (65.8% of total regulated serovars) and 2021 (57.3% of total regulated serovars). Many isolates of *Salmonella* from this category of animal feedingstuff were multi-drug resistant, please see Chapter 13 for further information.

Testing of processed animal protein

A total of 323 batches of domestically produced processed animal protein were tested during 2023. This is a 7.3% increase compared with 2022 (301 batches) and a 15.9% decrease compared with 2021 (384 batches) (Table 12.9 and Figure 12.8). Four batches tested positive for *Salmonella* in 2023 (1.24%), which is twice the number in 2022 (2 positive batches; 0.66%) but lower than during 2021 (9 positive batches, 2.34% positive). Three different serovars were isolated in 2023 including *S.* Typhimurium (one isolation each of DT75 and DT105), *S.* Infantis (one isolation) and *S.* Gueuletapee (one isolation) (Table 12.10)

No batches of imported animal protein were tested during 2023, which is the same as during both 2022 and 2021.The last batches of imported animal protein testing positive for *Salmonella* were reported during 2009.

Table 12.1: Regulated *Salmonella* serovars in animal feedingstuffs in Great Britain 2021 to 2023

Salmonella serovar	2021 Finished feed	2021 Vegetable material	2021 Misc.	2022 Finished feed	2022 Vegetable material	2022 Misc.	2023 Finished feed	2023 Vegetable material	2023 Misc.
Enteritidis PT2	0	0	1	0	0	0	0	0	0
Enteritidis PT3	0	0	0	0	0	0	0	0	1
Enteritidis PT3a	0	0	1	0	0	0	0	0	0
Enteritidis PT4	0	1	0	0	1	0	1	0	0
Enteritidis PT5	0	0	0	0	0	0	0	0	1
Enteritidis PT6	0	0	0	0	0	0	0	0	2
Enteritidis PT8	0	0	0	1	0	1	0	0	1
Enteritidis PT9	0	0	0	0	0	0	0	0	1
Enteritidis PT9b	0	1	0	0	0	0	0	0	1
Enteritidis PT11b	0	0	0	0	0	0	0	0	2
Enteritidis PT13a	0	0	0	0	0	0	0	0	3
Enteritidis PT21	0	0	0	0	0	1	0	0	3
Enteritidis PT22	0	0	0	0	0	0	0	0	1
Enteritidis NOPT	0	0	1	0	0	0	0	0	1
Enteritidis RDNC	0	0	0	1	0	1	0	0	1
Enteritidis UNTY	0	0	1	0	0	0	0	0	0
Hadar	0	0	3	0	0	1	1	0	13
Infantis	0	0	40	11	0	50	10	1	121
Monophasic Typhimurium DT59	0	0	0	0	0	0	0	0	1

Salmonella serovar	2021 Finished feed	2021 Vegetable material	2021 Misc.	2022 Finished feed	2022 Vegetable material	2022 Misc.	2023 Finished feed	2023 Vegetable material	2023 Misc.
Monophasic Typhimurium DT104	0	0	0	0	0	3	0	0	0
Monophasic Typhimurium DT120	0	0	1	0	0	1	0	0	3
Monophasic Typhimurium DT193	0	0	16	8	0	42	2	1	20
Monophasic Typhimurium DT208	0	0	0	0	0	1	0	0	0
Monophasic Typhimurium U311	0	0	1	0	0	1	0	0	0
Monophasic Typhimurium NOPT	0	0	0	0	0	0	0	0	1
Monophasic Typhimurium RDNC	0	0	1	0	0	0	0	0	0
Monophasic Typhimurium UNTY	0	0	5	0	0	7	0	0	1
Typhimurium DT1	1	0	1	0	0	0	0	1	2
Typhimurium DT2	0	2	5	1	3	5	1	4	13
Typhimurium DT3	0	0	1	0	0	0	0	0	0
Typhimurium DT4	0	0	0	0	0	0	0	0	1
Typhimurium DT8	0	0	0	0	0	2	0	0	1
Typhimurium DT9	0	0	0	0	0	3	0	0	1
Typhimurium DT32	0	0	0	0	0	0	0	0	1
Typhimurium DT75	0	0	0	0	0	3	0	0	2
Typhimurium DT99	0	0	0	0	4	3	4	5	6
Typhimurium DT104	0	0	4	0	1	3	0	0	0

Salmonella serovar	2021 Finished feed	2021 Vegetable material	2021 Misc.	2022 Finished feed	2022 Vegetable material	2022 Misc.	2023 Finished feed	2023 Vegetable material	2023 Misc.
Typhimurium DT105	0	0	0	1	0	5	0	0	4
Typhimurium DT116	0	0	3	0	0	0	0	0	2
Typhimurium DT120	0	0	0	0	0	2	0	0	1
Typhimurium DT130	0	0	0	0	0	0	0	0	1
Typhimurium DT193	0	2	3	0	0	3	0	0	4
Typhimurium U208	0	0	1	0	0	0	0	0	0
Typhimurium U281	0	0	1	0	0	0	0	0	0
Typhimurium U288	0	0	1	0	0	0	0	0	0
Typhimurium U302	0	0	1	0	0	0	0	0	0
Typhimurium U308	0	2	3	0	0	0	0	0	0
Typhimurium U310	0	0	0	0	0	0	0	0	1
Typhimurium U311	0	0	0	0	0	3	0	0	0
Typhimurium U322	0	0	0	0	0	0	0	0	4
Typhimurium NOPT	0	0	6	0	0	2	0	0	3
Typhimurium RDNC	1	2	10	1	0	8	0	0	7
Typhimurium UNTY	0	0	1	0	0	0	0	0	1
Virchow	0	0	0	0	0	3	0	0	1
Total	**2**	**10**	**112**	**24**	**9**	**154**	**19**	**12**	**234**

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, 2023

Salmonella serovar	Feedingstuff	N
Enteritidis PT3	Pet food (raw)	1
Enteritidis PT4	Compound feed (species unknown)	1
Enteritidis PT5	Feedmill environmental	1
Enteritidis PT6	Feedmill environmental	2
Enteritidis PT8	Pet food (raw)	1
Enteritidis PT9	Feedmill environmental	1
Enteritidis PT9a	Pet food (raw)	1
Enteritidis PT11b	Feedmill environmental	1
Enteritidis PT11b	Pet food (raw)	1
Enteritidis PT13a	Pet food (raw)	2
Enteritidis PT13a	Raw meat	1
Enteritidis PT21	Pet food (raw)	2
Enteritidis PT21	Unspecified	1
Enteritidis PT22	Pet food (raw)	1
Enteritidis NOPT	Feedmill environmental	1
Enteritidis RDNC	Feedmill environmental	1
Hadar	Compound feed (species unknown)	1
Hadar	Feedmill environmental	1
Hadar	Minerals	1
Hadar	Pet food (raw)	11
Infantis	Aeration tank	4
Infantis	Biogas	1
Infantis	Centrate liquor	13
Infantis	Compost	2
Infantis	Compound feed (species unknown)	10
Infantis	Digestate	22
Infantis	Digestate liquor	18
Infantis	Dog treat	1
Infantis	Feed additive	1
Infantis	Feedmill environmental	20
Infantis	Oilseeds	1
Infantis	Pasteurised liquor	4
Infantis	Pet food (raw)	29
Infantis	Process water tank	5

Salmonella serovar	Feedingstuff	N
Infantis	Unspecified	1
Monophasic Typhimurium DT59	Raw meat	1
Monophasic Typhimurium DT120	Pet food (raw)	3
Monophasic Typhimurium DT193	Compound feed (species unknown)	2
Monophasic Typhimurium DT193	Digestate	1
Monophasic Typhimurium DT193	Feedmill environmental	3
Monophasic Typhimurium DT193	Mixed vegetables	1
Monophasic Typhimurium DT193	Pet food (raw)	16
Monophasic Typhimurium NOPT	Feedmill environmental	1
Monophasic Typhimurium UNTY	Feedmill environmental	1
Typhimurium DT1	Pet food (raw)	2
Typhimurium DT1	Soya	1
Typhimurium DT2	Compound chicken feed	1
Typhimurium DT2	Feedmill environmental	4
Typhimurium DT2	Maize	3
Typhimurium DT2	Pet food (raw)	8
Typhimurium DT2	Rapeseed	1
Typhimurium DT2	Unspecified	1
Typhimurium DT32	Pet food (raw)	1
Typhimurium DT4	Pet food (raw)	1
Typhimurium DT75	Biogas	1
Typhimurium DT75	Pet food (raw)	1
Typhimurium DT8	Pet food (raw)	1
Typhimurium DT9	Pet food (raw)	1
Typhimurium DT99	Compound chicken feed	4
Typhimurium DT99	Feedmill environmental	4
Typhimurium DT99	Maize	1
Typhimurium DT99	Pet food (raw)	2
Typhimurium DT99	Soya	4
Typhimurium DT105	Feedmill environmental	2
Typhimurium DT105	Pet food (raw)	1
Typhimurium DT105	Unspecified	1
Typhimurium DT116	Pet food (raw)	2
Typhimurium DT120	Pet food (raw)	1
Typhimurium DT130	Digestate	1
Typhimurium DT193	Pet food (raw)	3
Typhimurium DT193	Unspecified	1
Typhimurium U310	Pet food (raw)	1
Typhimurium U322	Feedmill environmental	4
Typhimurium NOPT	Feedmill environmental	1

Salmonella serovar	Feedingstuff	N
Typhimurium NOPT	Pet food (raw)	2
Typhimurium RDNC	Feedmill environmental	4
Typhimurium RDNC	Pet food (raw)	3
Typhimurium UNTY	Feedmill environmental	1
Virchow	Pet food (raw)	1
Total	Not applicable	**265**

Figure 12.1: Number of isolations of regulated *Salmonella* serovars in animal feedingstuffs and products associated with the ABPR 2019 to 2023

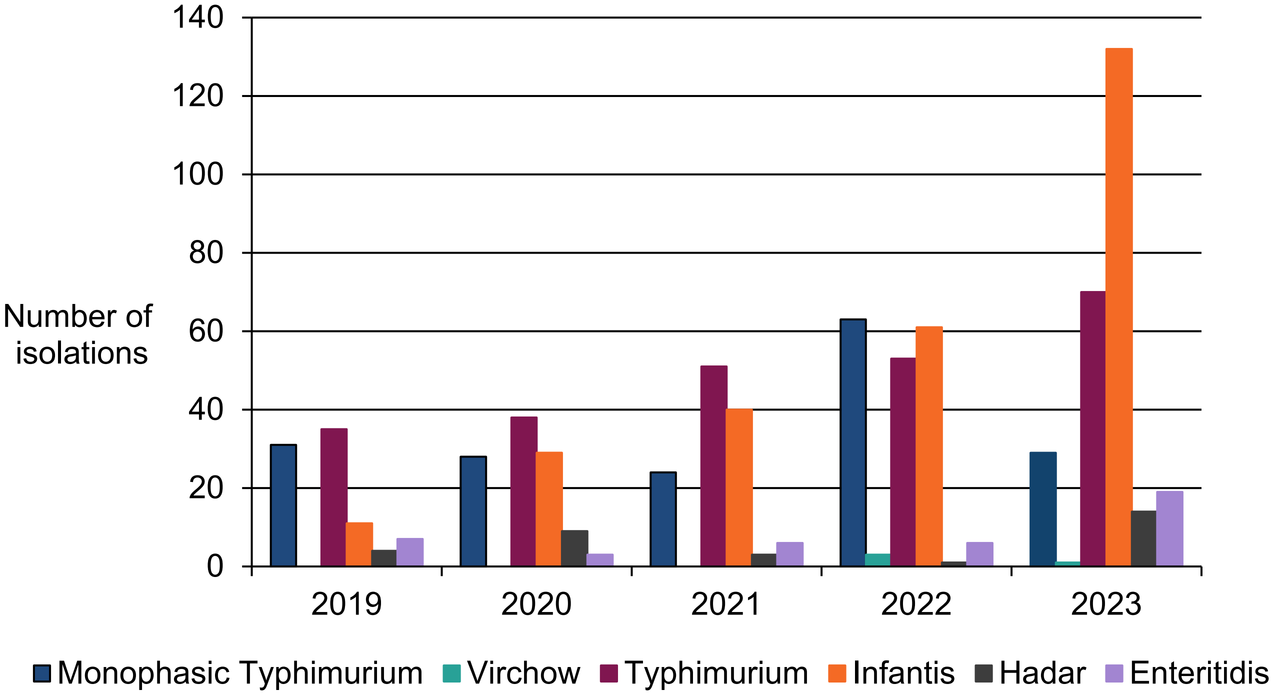
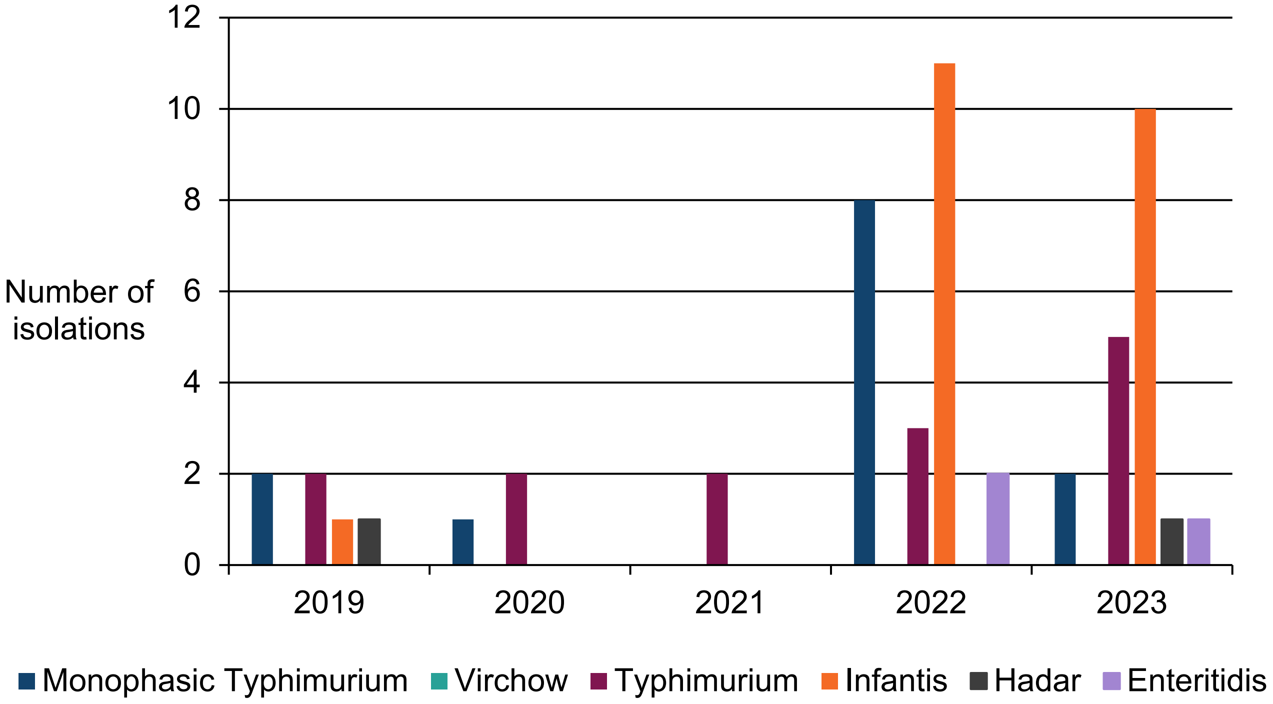


Figure 12.1 shows the number of isolations of monophasic *S*. Typhimurium and *S.* Virchow have decreased since 2022. Isolations of *S.* Infantis have increased since 2019 from 11 isolations to 132 in 2023, with more than twice as many isolations during 2023 compared to 2022 (132 versus 61). *S*. Enteritidis isolations have tripled since 2022 (19 versus 6). *S*. Hadar isolations have peaked during 2023, with 14 isolations compared to 1 in 2022.

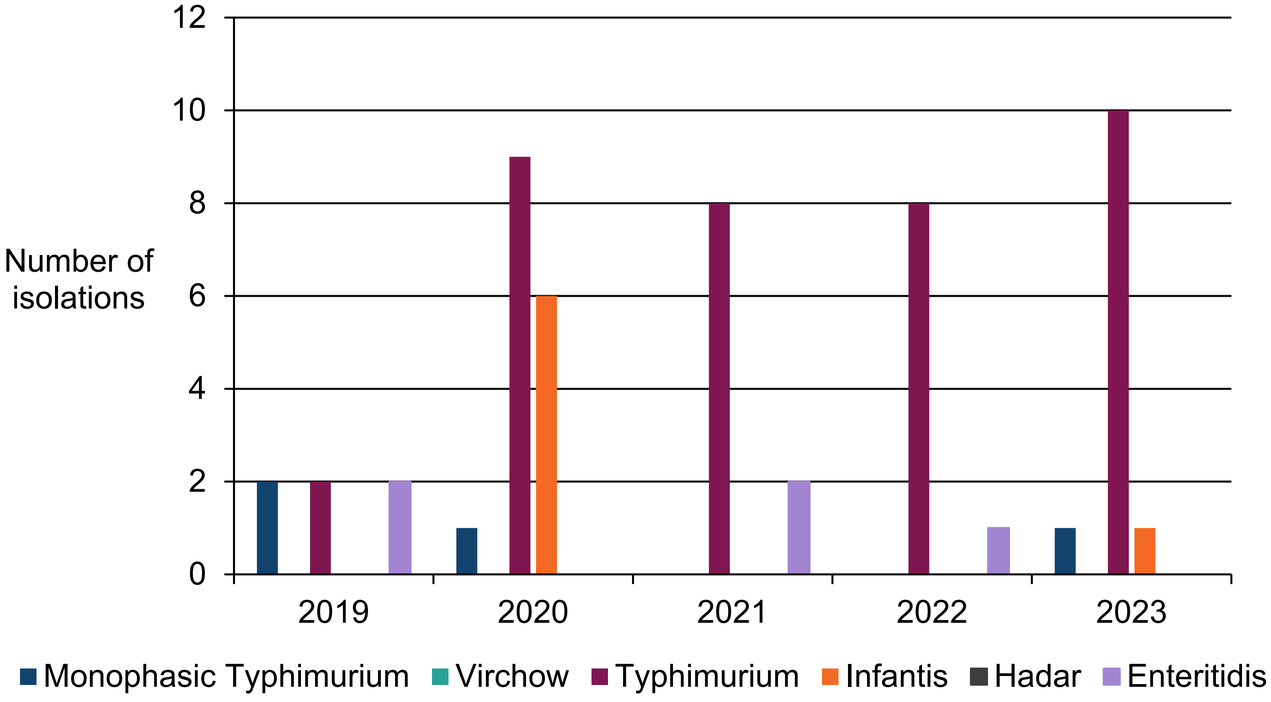
Figure 12.2: Number of isolations of regulated *Salmonella* serovars in animal feedingstuffs and products associated with the ABPR, 2019 to 2023 by type of feedingstuff

Figure 12.2.1 Finished feed



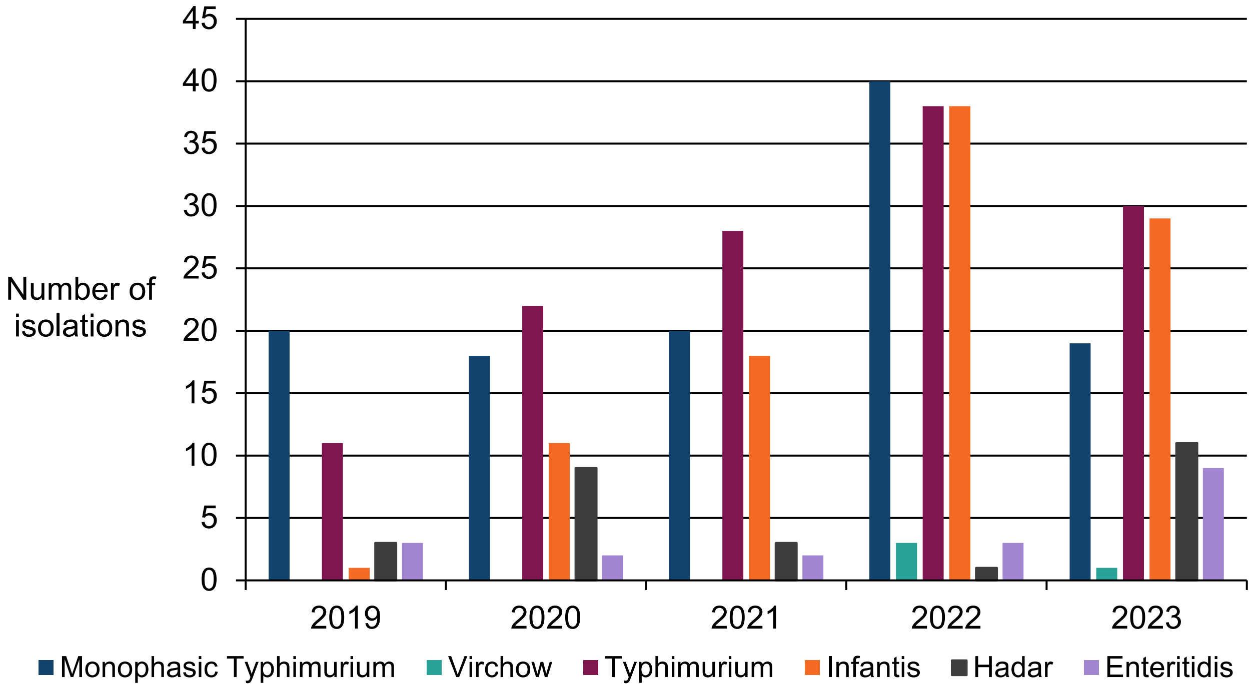
There were 19 isolations of regulated serovars from finished feed during 2023, a 20.1% decrease from 2022 (24 isolations). Isolations of monophasic *S.* Typhimurium decreased by 75% compared to 2022 (2 isolations versus 8). The number of isolations of the regulated serovar *S*. Typhimurium from finished feed has been increasing since 2019. Isolations of *S.* Infantis decreased to 10 isolations during 2023 from a peak of 11 isolations in 2022. There was one isolation of *S*. Enteritidis in 2023 after being isolated for the first time in 2022. There have been no isolations of *S.* Virchow in finished feed.

Figure 12.2.2 Vegetable material



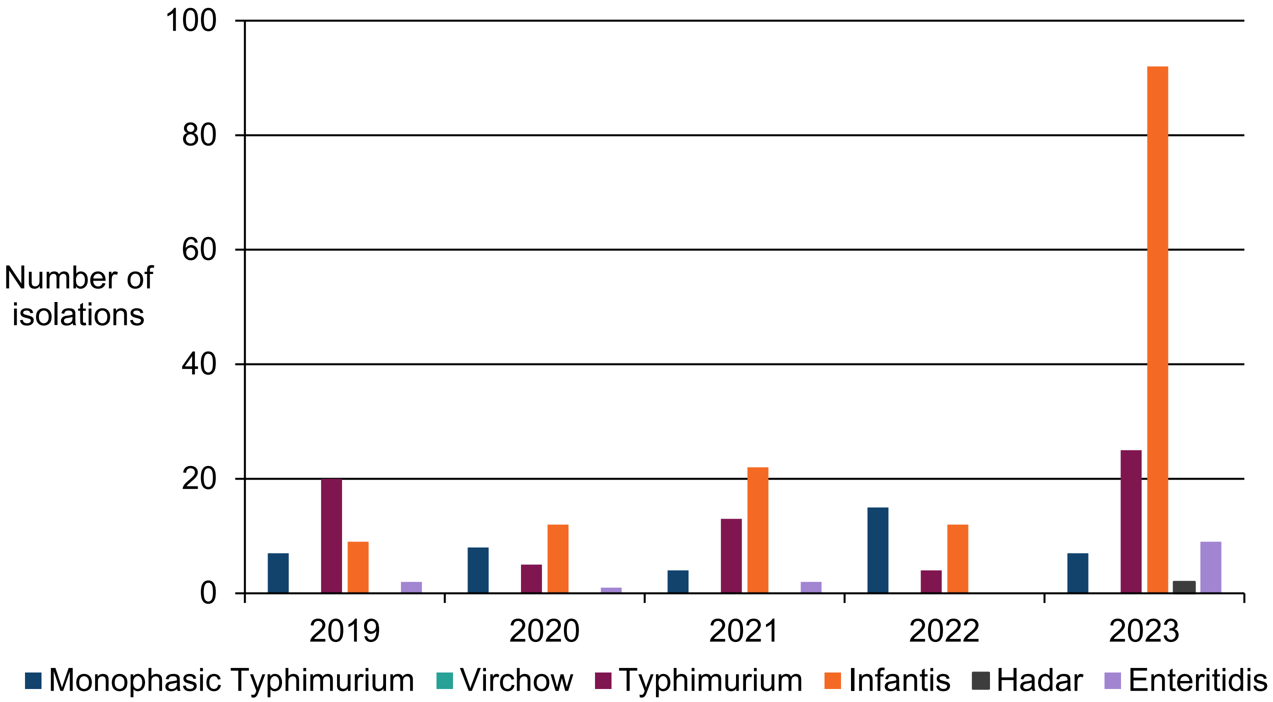
S. Infantis was isolated from vegetable material in 2020 (6 isolations) and 2023 (1 isolation). Since 2019, *S*. Enteritidis has been isolated every year except 2020 and 2023. *S.* Typhimurium was isolated 10 times in 2023, an increase from 8 isolations in 2021 and 2022. Neither *S*. Hadar nor *S.* Virchow have been isolated in vegetable material between 2019 and 2023. There was a single isolation of monophasic *S.* Typhimurium in 2023, the first isolation of this serovar in vegetable material since 2020.

Figure 12.2.3 Pet food (raw)



S. Typhimurium, monophasic *S.* Typhimurium and *S.* Infantis have been the most frequently isolated serovars from raw pet food across all years since 2020. The numbers of all 3 have risen steadily and peaked in 2022 but dropped in 2023. Neither *S.* Hadar nor *S.* Virchow are frequently isolated from raw pet food with *S.* Virchow only isolated in 2022 and 2023. Numbers of *S.* Enteritidis have been steady at less than 5 for the last 4 years but increased to 9 in 2023.

Figure 12.2.4 Miscellaneous



The number of isolations of *S*. Enteritidis has remained relatively stable with between 3 and 5 isolations per year since 2019 but increased to 9 in 2023. Isolations of *S.* Infantis have increased in miscellaneous feedstuffs from 9 in 2019 to 92 in 2023. *S.* Typhimurium isolations have also increased since 2022, from 4 to 25 in 2023. There have been no isolations of *S.* Virchow between 2019 and 2023. Isolations of monophasic *S.* Typhimurium have halved since 2022, from 15 to 7 in 2023.

Figure 12.3: Number of isolations of *Salmonella* in compound animal feedingstuffs, 2019 to 2023

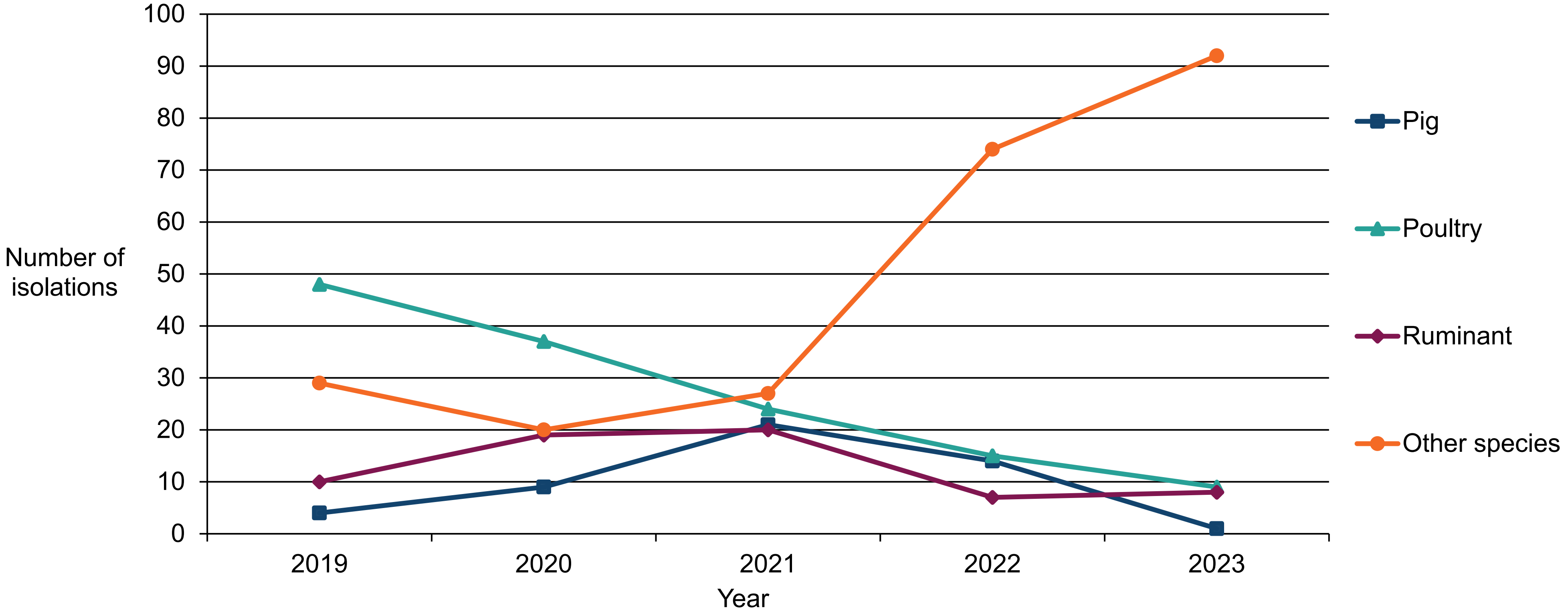


Figure 12.3 shows a decreasing trend in the number of isolations of *Salmonella* in compound poultry feed in recent years from 48 in 2019 to 9 in 2023. The number of isolations in ruminant feed has fluctuated since 2019, doubling from 10 to 20 between 2019 and 2021, before declining in 2022 to 7 isolations. There were 8 isolations of *Salmonella* in ruminant feed in 2023. Isolations in compound pig feed have remained below 21 since 2019 and was one in 2023, whilst the number of isolations in other species increased significantly in 2023 to 92 (from 74 in 2022) compared to just 29 in 2019.

Table 12.3: Serovars of *Salmonella* isolated from compound ruminant feed in Great Britain in 2023, compared with the previous 2 years

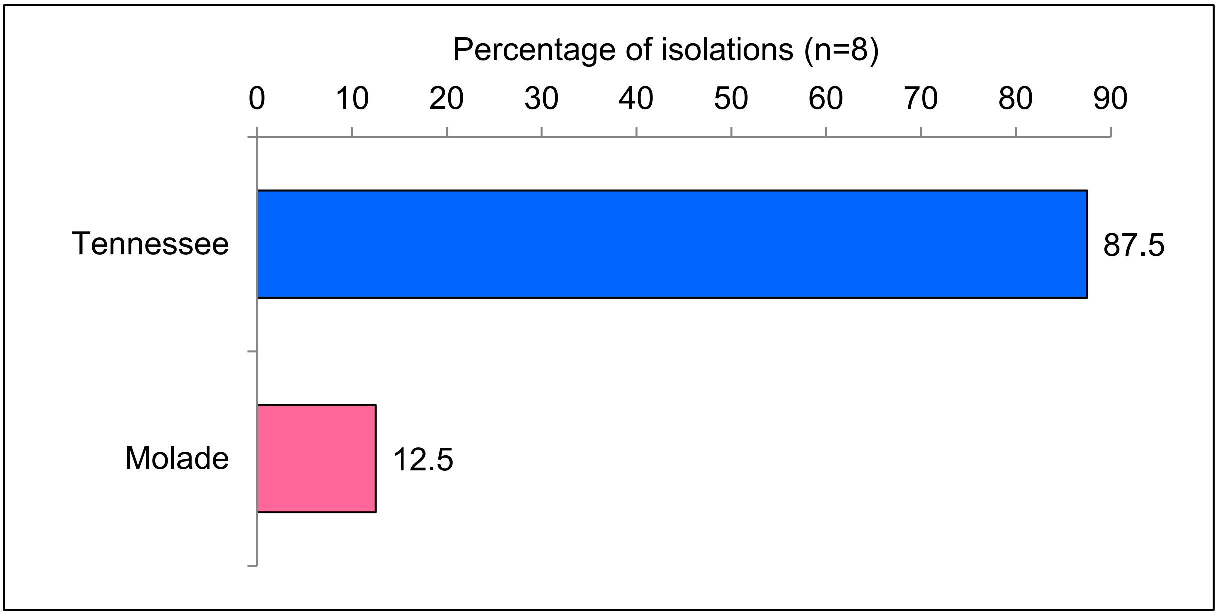
Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
Agona	0	2	0
Derby	2	1	0
Kedougou	0	1	0
Kentucky	0	2	0
Korlebu	1	0	0
Mbandaka	3	0	0
Molade	0	0	1
Rissen	10	0	0
Senftenberg	1	0	0
Tennessee	3	1	7
Total	**20**	**7**	**8**

Table 12.4: Serovars of *Salmonella* isolated from compound pig feed in Great Britain in 2023, compared with the previous 2 years

Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
4,5,12:i:-	0	1	0
6,7,:-:-	1	0	0
Agona	1	0	0
California	1	0	0
Derby	0	2	1
Enteritidis	0	1	0
Hindmarsh	0	1	0
Kedougou	0	3	0
Ohio	3	1	0
Panama	1	0	0
Rissen	11	5	0
Tennessee	3	0	0
Total	**21**	**14**	**1**

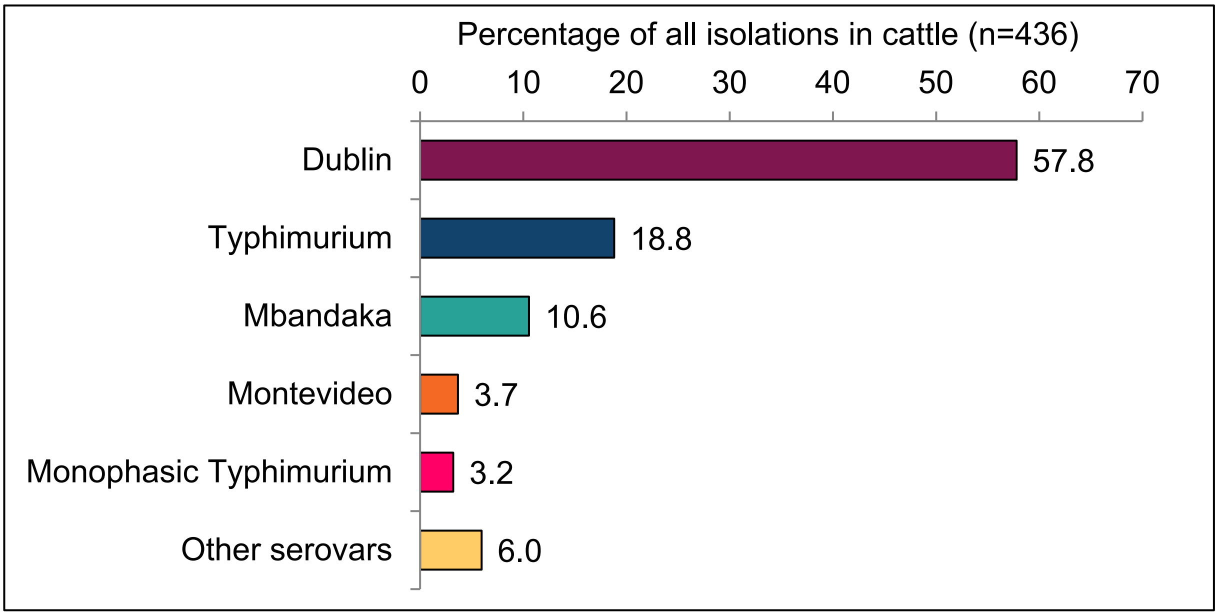
Figure 12.4: Isolations of the most common serovars in compound ruminant feed, cattle and sheep in Great Britain in 2023

Figure 12.4.1: Isolations from compound ruminant feed



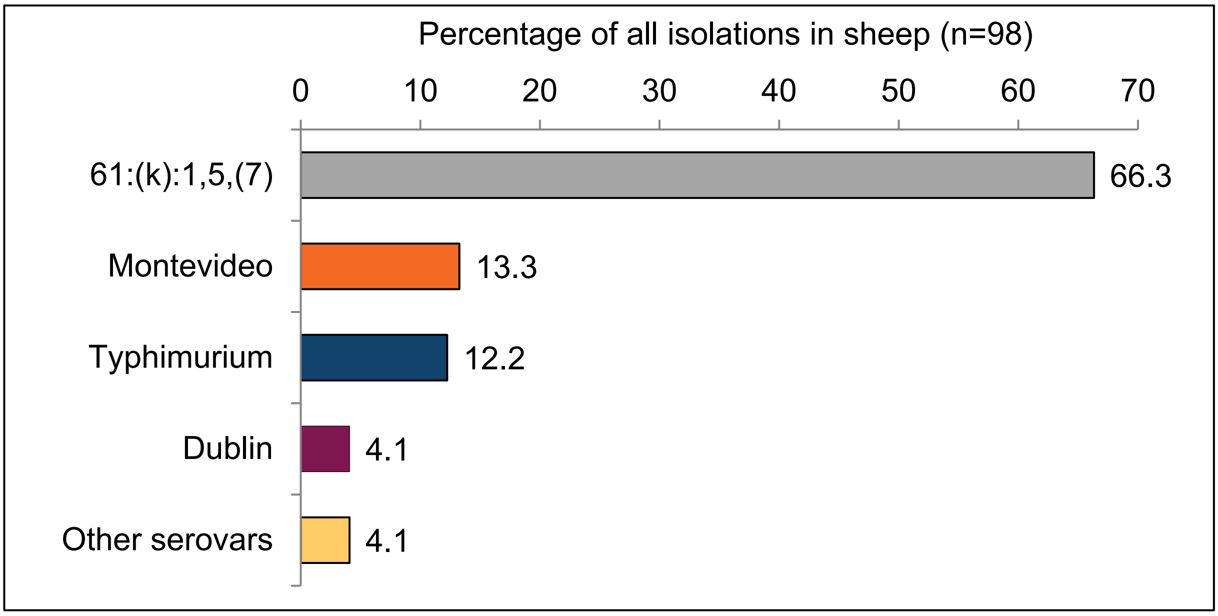
In 2023 the most common *Salmonella* serovar in compound ruminant feed was *S.* Tennessee, accounting for 87.5% of total isolations within this feed type. *S.* Molade represented 12.5% of total isolations.

Figure 12.4.2: Isolations from cattle



In 2023, the most common *Salmonella* serovar in cattle was *S.* Dublin accounting for 57.8% of total isolations, followed by *S.*Typhimurium (18.8%), and *S.* Mbandaka, (10.6%).

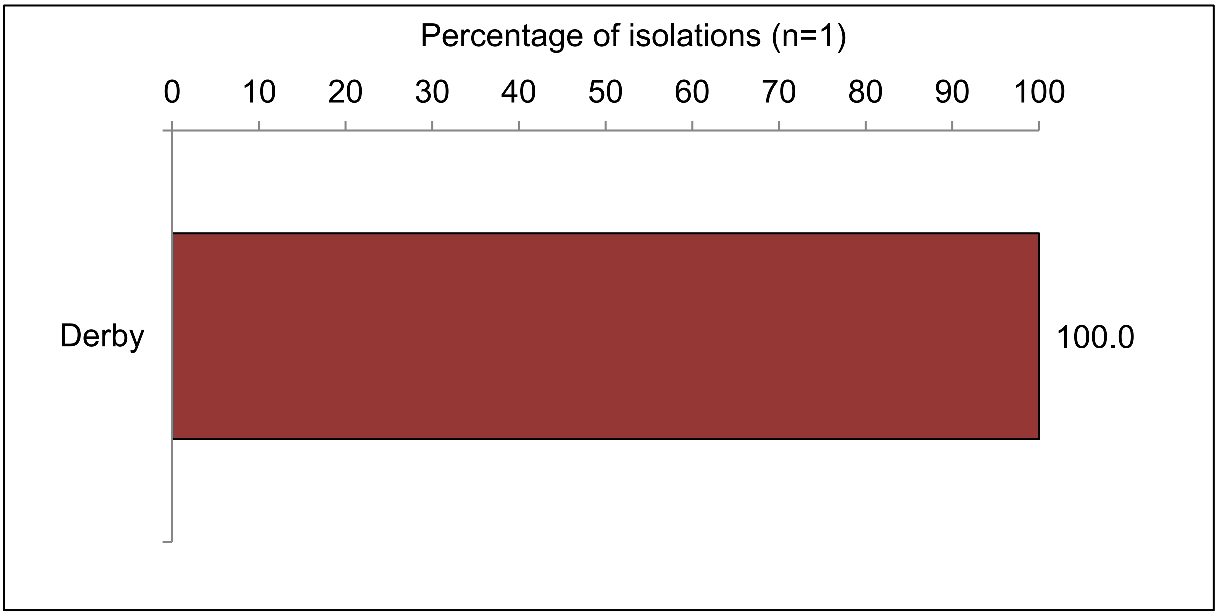
Figure 12.4.3: Isolations from sheep



The most common *Salmonella* serovar in sheep was *S.* 61:(k):1,5,(7) (variants of *Salmonella* enterica subspecies diarizonae), accounting for 66.3% of total isolations, followed by *S.* Montevideo (13.3%), and *S.* Typhimurium (12.2%).

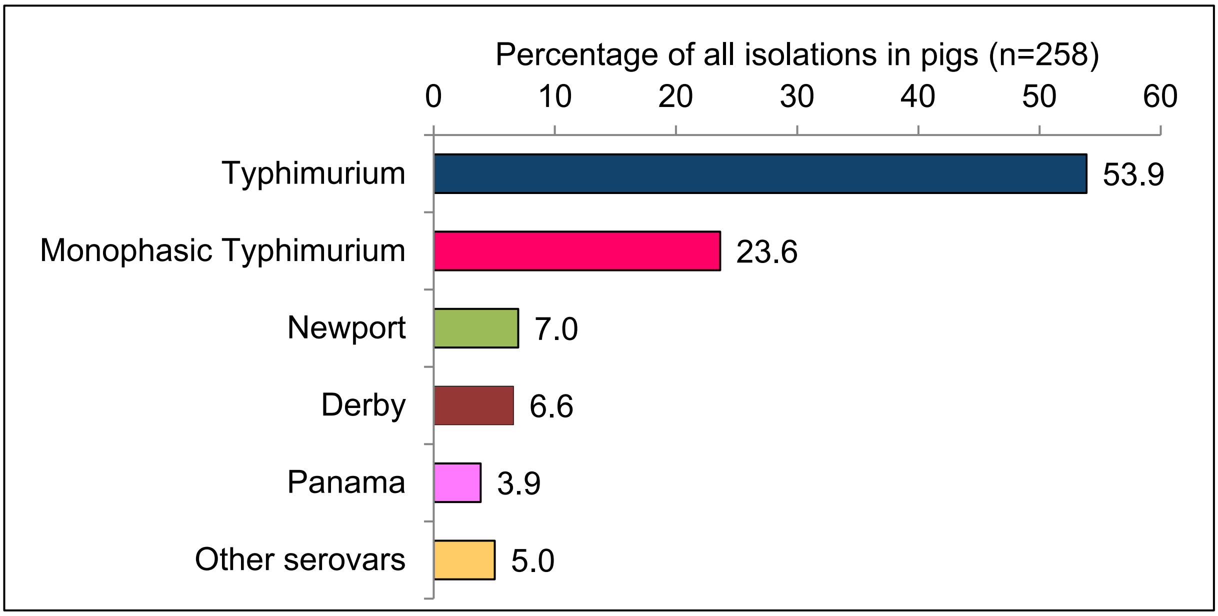
Figure 12.5: Isolations of the most common serovars in compound pig feed and pigs in Great Britain in 2023

Figure 12.5.1: Isolations from compound pig feed



There was a single isolation of *S.* Derby in compound pig feed.

Figure 12.5.2: Isolations from pigs



In 2023 the most common *Salmonella* serovar in pigs was *S.* Typhimurium, accounting for 53.9% of total isolations, followed by monophasic *S.* Typhimurium (23.6%), *S.* Newport (7.0%), and *S.* Derby (6.6%).

Table 12.5: Serovars of *Salmonella* isolated from compound poultry feed in Great Britain in 2023 compared with the previous 2 years

Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
4,12:b:-	0	0	1
6,7:-:-	1	0	0
6,7:-:enz15	0	1	0
Agama	0	2	0
Agona	0	1	0
Anatum	1	0	0
Bredeney	6	0	0
Cubana	0	0	1
Derby	0	1	0
Enteritidis	0	1	0
Havana	1	0	0
Idikan	0	1	0
Infantis	0	1	0
Kedougou	1	2	0
Korlebu	1	0	0
Lexington	1	0	0
Mbandaka	2	0	0
Montevideo	1	0	0
Newport	1	1	0
Odozi	2	0	0
Rissen	2	0	0
Ruiru	1	0	0
Senftenberg	0	0	1
Soerenga	0	2	0
Tennessee	1	0	0
Typhimurium	2	1	5
Utah	0	1	1
Total	**24**	**15**	**9**

Table 12.6: Serovars of *Salmonella* isolated from compound feed for other species feed in Great Britain in 2023, compared with the previous 2 years

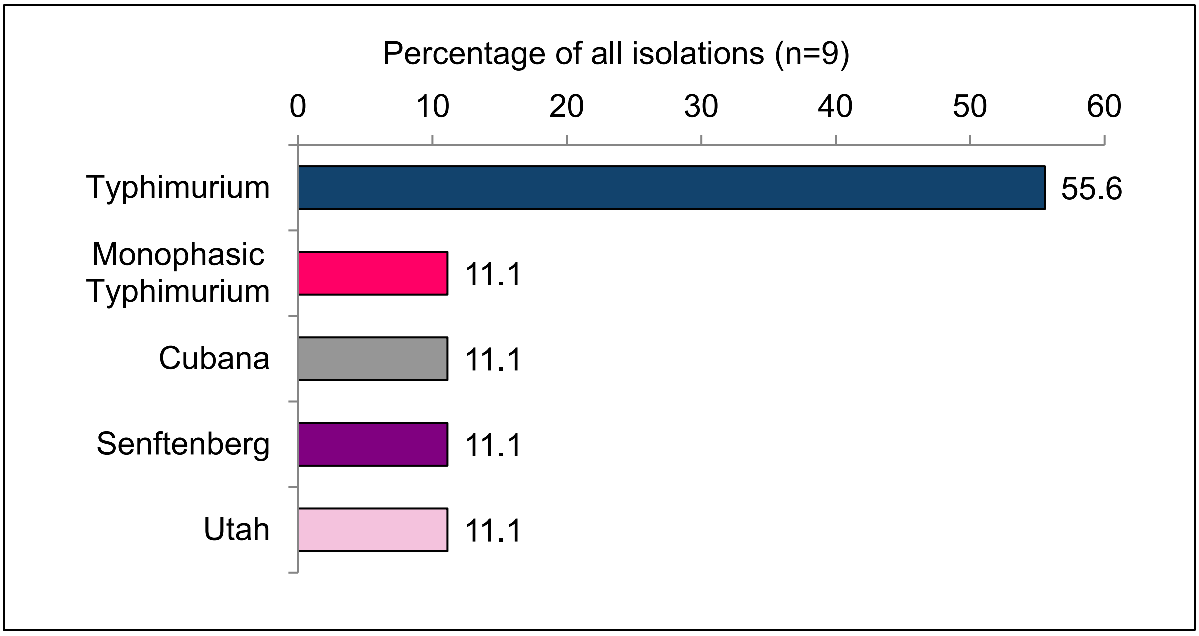
Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
13,23:i:-	0	0	2
3,10:-:1,5	0	0	1
6,7:-:-	0	7	0
6,7:r:-	0	1	0
Aarhus	1	0	0
Aba	0	1	0
Agama	2	0	0
Agona	1	1	1
Anatum	0	1	0
Bovismorbificans	3	2	0
Brancaster	0	1	0
Cerro	0	1	0
Coeln	0	1	0
Derby	2	5	9
Duisburg	0	0	1
Enteritidis PT4	0	0	1
Give	0	0	1
Hadar	0	0	1
Havana	2	0	1
Ibadan	0	1	0
Idikan	0	1	0
Indiana	0	0	4
Infantis	0	10	10
Isangi	0	1	0
Kedougou	1	5	2
Kentucky	1	1	1
Kingston	0	1	0
Lexington	0	0	1
Livingstone	4	1	0
London	0	0	1
Mbandaka	0	3	0
Molade	1	1	0
Monophasic Typhimurium	0	7	2
Mons	1	0	0
Montevideo	1	3	4
Morbihan	0	0	1
Muenster	0	0	1

Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
Newport	0	2	3
Nottingham	1	1	1
O rough:g,p:-	0	1	0
Ohio	0	0	6
Panama	0	2	0
Poona	0	0	1
Putten	0	0	2
Rissen	5	4	0
Senftenberg	0	0	13
Soerenga	0	0	3
Takoradi	0	1	0
Tennessee	1	3	1
Thompson	0	2	0
Typhimurium	0	2	0
Worthington	0	0	1
Total	**27**	**74**	**76**

Other species in 2023 were: cats (1 isolation), dogs (10 isolations), mixed species (1 isolation), fish (1 isolation) and unspecified (63 isolations).

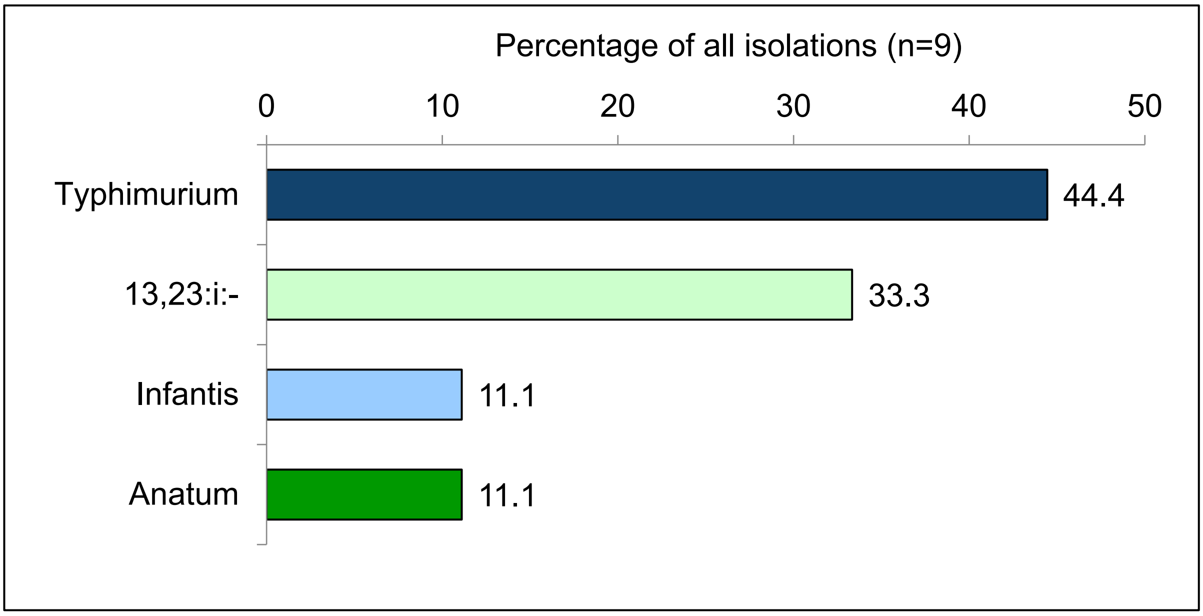
Figure 12.6: Isolations of the most common serovars in compound poultry feed and positive flocks of chickens and turkeys from NCP testing in Great Britain in 2023

Figure 12.6.1: Isolations from compound poultry feed



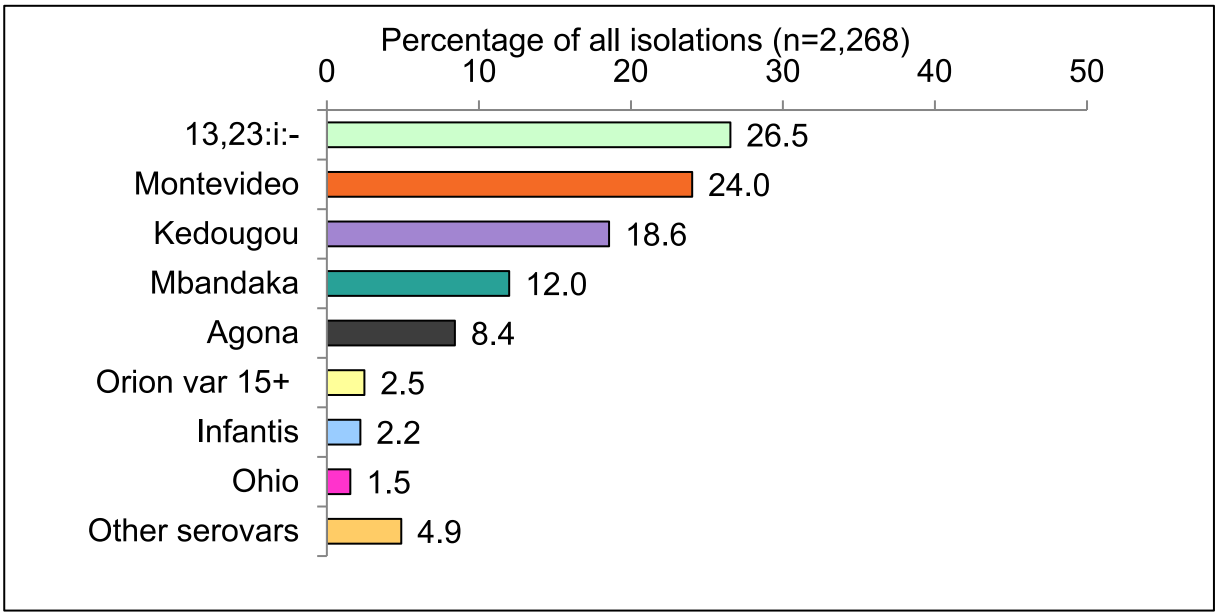
In 2023 the most commonly isolated serovar from compound poultry feed was *S.* Typhimurium (55.6%), followed by a single isolation each of: monophasic *S.* Typhimurium, *S.* Cubana, *S.* Senftenberg, and *S.* Utah.

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



The most common *Salmonella* serovar in (adult) breeder chickens was *S.* Typhimurium, accounting for 44.4% of total isolations, followed by *S.* 13,23:i:- (33.3%). *S.* Infantis and *S.* Anatum each accounted for 11.1% of total isolations.

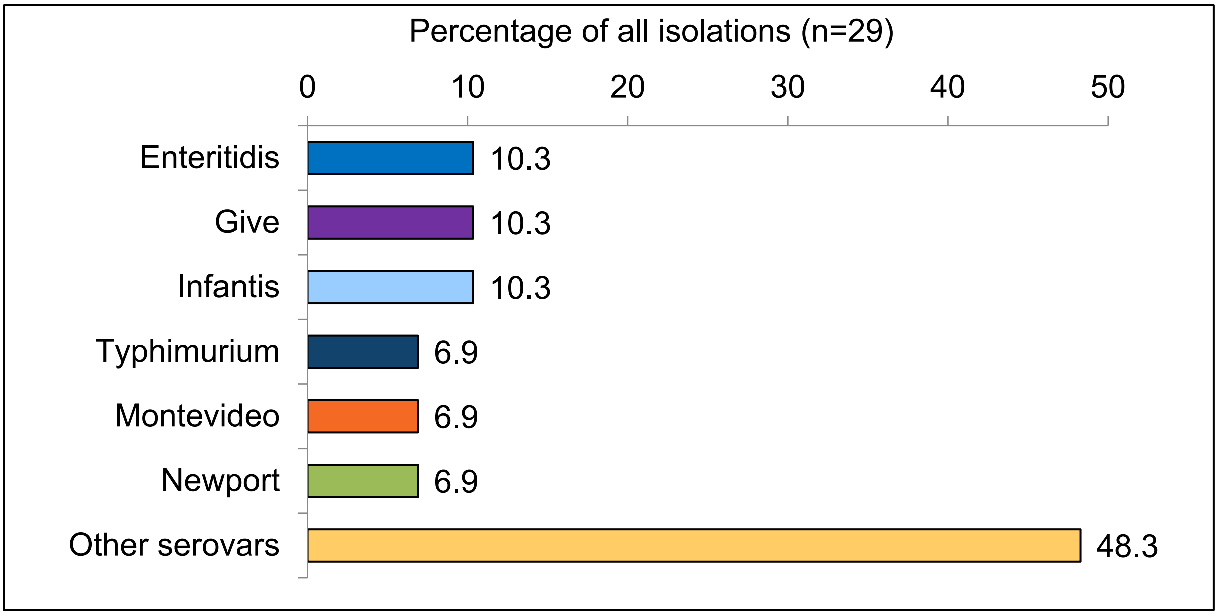
Figure 12.6.3: Isolations from broiler chickens (NCP testing only)



The most common *Salmonella* serovar in broiler Chickens was *S.* 13,23:i:-, accounting for 26.5% of total isolations, followed by *S.* Montevideo (24.0%), *S.* Kedougou (18.6%), and *S.* Mbandaka (12.0%).

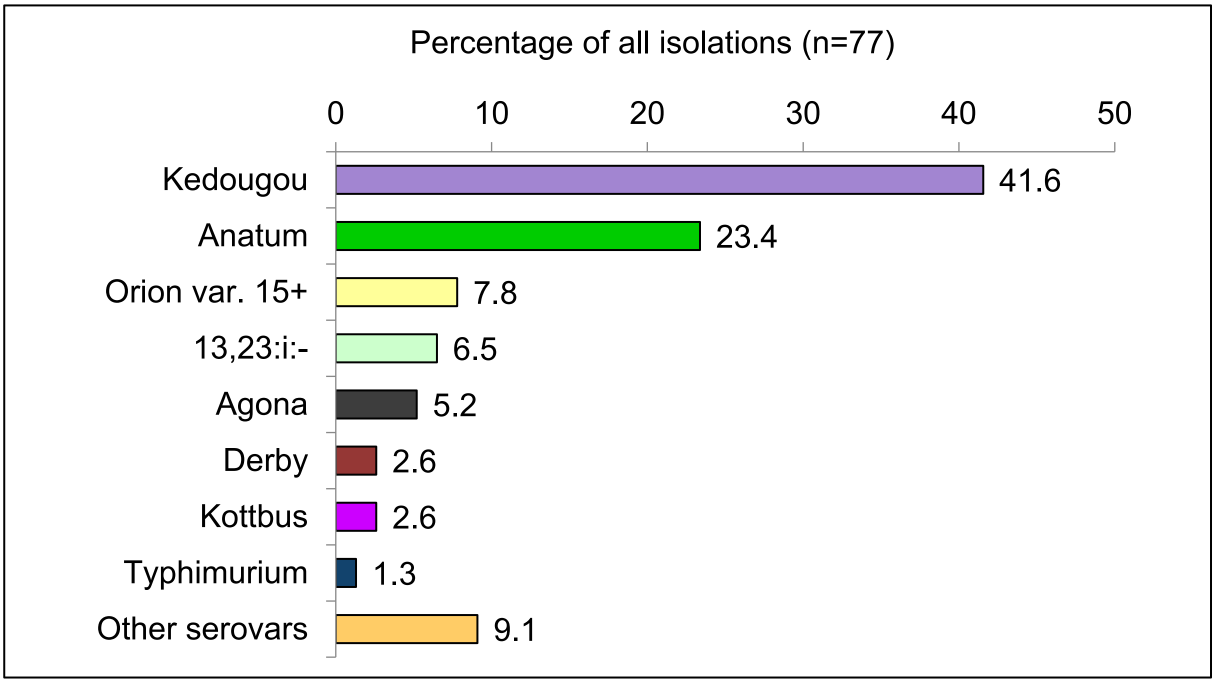
15 broiler chicken flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

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



Other *Salmonella* serovars accounted for 48.3% of all isolations in adult layer chickens. *S.* Enteritidis, *S*. Give*, and S*. Infantis each accounted for 10.3% of total isolations.

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



The most common *Salmonella* serovar in breeder and fattening turkeys was *S.* Kedougou, accounting for 41.6% of total isolations, followed by *S.* Anatum (23.4%).

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

Table 12.7: *Salmonella* serovars reported from animal feedingstuff ingredients and products associated with the ABPR in Great Britain, 2021 to 2023

Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
Aarhus	0	0	0
Aba	0	1	0
Agama	5	1	4
Agona	16	13	13
Ajiobo	0	1	0
Albert	0	0	0
Alachua	1	0	0
Anatum	8	9	10
Banana	0	1	0
Bareilly	2	1	0
Bere	0	1	0
Bochum	1	0	0
Bonn	0	2	1
Bovismorbificans	0	6	4
Brancaster	0	0	0
Branderup	2	0	0
Brandenburg	1	2	1
Bredeney	2	0	2
Budapest	0	0	0
California	8	0	0
Cannstatt	2	0	0
Carmel	0	1	0
Cerro	0	6	5
Coeln	5	0	1
Cubana	4	6	1
Dallgow	0	0	0
Derby	19	37	57
Denver	0	0	0
Dublin	10	4	5
Duisburg	0	1	1
Durban	0	0	0
Ealing	11	3	0
Eastbourne	0	0	1
Elomrane	0	0	0
Enteritidis	6	4	19
Fresno	0	2	2
Give	8	7	13

Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
Give var 15+	0	10	1
Glostrup	0	0	0
Goldcoast	1	3	0
Hadar	3	1	14
Havana	3	3	3
Heidelberg	0	0	1
Ibadan	0	0	0
Idikan	4	4	3
Indiana	35	49	53
Infantis	40	61	132
Isangi	0	0	2
Kedougou	38	57	94
Kentucky	4	2	6
Kiambu	0	0	1
Kingston	0	2	1
Korlebu	2	0	0
Kottbus	23	17	12
Larochelle	1	0	0
Leeuwarden	0	0	0
Lexington	2	8	2
Lille	0	0	0
Litchfield	0	0	3
Liverpool	0	3	0
Livingstone	6	9	9
Lomita	1	0	0
London	5	10	3
Mbandaka	31	21	13
Meleagridis	2	0	1
Miami	0	0	1
Molade	0	0	1
Monophasic Typhimurium	24	55	29
Montevideo	18	10	26
Morbihan	0	0	1
Morehead	0	0	1
Muenchen	0	0	1
Muenster	0	5	6
Nagoya	0	0	1
Neunkirchen	0	0	1
Newport	18	20	32
Nottingham	0	0	19
Odozi	0	0	0
Ohio	30	22	82

Salmonella serovar	Isolations 2021	Isolations 2022	Isolations 2023
Oranienburg	1	1	1
Ordonez	23	0	0
Orion	16	6	2
Orion var 15^{+}	1	1	1
O rough:f,g:-	3	0	0
O rough:g,p:-	2	0	0
O rough:i:z	2	0	0
O rough:k:z	4	0	0
O rough:z_{10}:enz_{15}	0	2	0
O rough:z_{29}:-	0	1	0
Oslo	2	1	1
Ouakam	1	1	0
Panama	10	15	5
Paratyphi B var. Java	3	2	5
Poona	0	0	1
Putten	0	0	2
Reading	0	1	2
Riggil	1	0	0
Rissen	90	35	8
Rublislaw	0	2	0
Ruiru	4	0	0
Saintpaul	0	1	0
Schwarzengrund	1	2	1
Senftenberg	27	15	41
Senftenberg (z_{27})	0	1	0
Soerenga	1	1	3
Stanley	2	1	2
Stanleyville	1	0	1
Szentes	1	1	0
Tennessee	47	11	12
Teshie	0	1	0
Tsevie	0	1	0
Thompson	0	0	1
Typhimurium	49	50	70
Uganda	0	1	3
Utah	0	0	1
Vinohrady	1	0	0
Virchow	0	3	1
Weltevreden	1	0	0
Westhampton	3	0	0
Wilhelmsberg	0	1	2
Worthington	0	0	1

***Salmonella* serovar**	**Isolations 2021**	**Isolations 2022**	**Isolations 2023**
Yoruba	1	0	0
3,10:z_{10}:-	0	1	0
3,10:-:-	1	0	0
3,10:-:1,5	0	0	1
3,15:rough:-	0	1	0
3,19:z_{27}:-	0	4	0
3,19:-:-	0	1	0
3,19:rough:-	2	0	0
4,5,12:b:-	1	0	0
4,5,12::-:1,2	1	0	0
4,12:b:-	0	0	3
4,12:z:-	0	2	0
4,12,[27]:b:e,n,x	1	0	0
4,12:rough:-	0	1	0
6,7:b:-	0	1	0
6,7:enz$_{15}$	2	6	0
6,7:k:-	1	0	0
6,7:r:-	4	0	0
6,7:rough:-	2	0	0
6,7:-:-	4	10	0
6,8:e,h:-	0	3	0
9,12:l,v:-	1	0	0
13,23:i:-	3	5	15
17:b:-	0	0	1
38:l,v,z_{13}:-	0	1	0
38:rz	1	0	0
41:z_4,z_{24}:-	0	1	0
42:b:e,n,x,z15	0	0	1
47:z4,z23:-	0	0	1
47:z_4,z_{23}:-	1	0	0
61:k:1,5	4	0	0
61:k:1,5,7	0	9	12
61:-:1,5	14	0	0
61:-:1,5,7	0	17	1
Total	**743**	**702**	**897**

Table 12.8a: Serovars of *Salmonella* in feedingstuff ingredients in Great Britain, 2021 to 2023

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Barley	Bovismorbificans	0	1	0
Barley	Enteritidis PT9b	1	0	0
Barley	Kottbus	1	1	0
Barley	Panama	0	1	0
Barley	Rissen	0	1	0
Biscuit	Bochum	1	0	0
Biscuit	Rissen	1	0	0
Biscuit	Typhimurium DT193	0	1	0
Broken rice	Riggil	1	0	0
Broken rice	Typhimurium DT2	1	1	0
Buckwheat	Enteritidis PT4	0	1	0
Cocoa	$41:z_4,z_{24}:-$	0	1	0
Feed additive	Derby	0	0	4
Feed additive	Infantis	0	0	1
Feed additive	Nottingham	0	0	1
Feeder mice	Montevideo	0	1	0
Fishmeal	Montevideo	0	0	2
Fishmeal	Schwarzengrund	0	1	0
Ginger root	Teshie	0	1	0
Guar protein	Orion	1	0	0
Guar protein	Senftenberg	0	1	0
Herbs	Enteritidis PT4	1	0	0
Herbs	Szentes	1	0	0
Licorice root	Anatum	0	1	0
Licorice root	Montevideo	0	1	0
Licorice root	Tennessee	0	1	0
Locust bean meal	Newport	1	0	0
Maize	Typhimurium DT2	0	0	3
Maize	Typhimurium DT99	0	1	1
Malt	Agama	1	0	3
Malt	Anatum	0	3	0
Malt	Infantis	7	2	0
Malt	Kottbus	2	0	0
Malt	Orion	1	0	0
Meat meal	Braenderup	1	0	0
Meat meal	6,7,:r:-	1	0	0
Minerals	Derby	0	1	0

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Minerals	Hadar	0	0	1
Minerals	Kedoudou	0	1	0
Minerals	Tennessee	0	1	0
Mixed cereals	Anatum	0	1	0
Mixed ingredients	Agama	1	0	0
Mixed ingredients	Cubana	1	0	0
Mixed ingredients	Lexington	0	1	0
Mixed oil seeds	Banana	0	1	0
Mixed oil seeds	Budapest	0	0	0
Mixed oil seeds	Cubana	1	1	0
Mixed oil seeds	Ealing	5	0	0
Mixed oil seeds	Idikan	1	0	0
Mixed oil seeds	Kottbus	1	0	0
Mixed oil seeds	Livingstone	0	1	0
Mixed oil seeds	Montevideo	2	0	0
Mixed oil seeds	Paratyphi B var. Java	1	0	0
Mixed oil seeds	Rissen	49	2	0
Mixed oil seeds	Senftenberg	4	4	0
Mixed oil seeds	Soerenga	0	1	0
Mixed oil seeds	Tennessee	1	0	0
Mixed oil seeds	Typhimurium DT99	0	1	0
Mixed oil seeds	Typhimurium DT193	1	0	0
Mixed oil seeds	Typhimurium U308	1	0	0
Mixed oil seeds	3,19:-:rough:-	1	0	0
Mixed oil seeds	6,7:rough:-	1	0	0
Mixed vegetables	Derby	0	1	2
Mixed vegetables	Indiana	0	0	2
Mixed vegetables	Newport	0	1	0
Mixed vegetables	Monophasic Typhimurium DT193	0	0	1
Mixed vegetables	Montevideo	0	0	1
Mixed vegetables	Panama	0	1	0
Oats	Newport	1	0	0
Oats	Oslo	1	0	0
Oats	Panama	1	0	0
Oats	Typhimurium DT104	0	1	0
Oilseeds	Infantis	0	0	1
Oilseeds	Rissen	0	0	1
Palm kernel	Senftenberg	0	0	1
Peas	Tennessee	1	0	0
Poultry offal meal	Coeln	2	0	0
Poultry offal meal	Infantis	11	0	0

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Poultry offal meal	Livingstone	1	0	0
Poultry offal meal	Mbandaka	1	0	0
Premix	Ohio	1	0	0
Premix	Senftenberg	1	0	0
Protein blend	Derby	0	1	0
Protein blend	London	0	1	0
Protein blend	Rissen	1	0	0
Protein blend	4,12:i:- DT104	0	1	0
Rapeseed	Agona	0	0	1
Rapeseed	Bredeney	2	0	0
Rapeseed	Ealing	3	1	0
Rapeseed	Havana	1	0	0
Rapeseed	Idikan	0	1	0
Rapeseed	Kedougou	0	0	1
Rapeseed	Kingston	0	1	0
Rapeseed	Mbandaka	1	0	0
Rapeseed	Montevideo	2	0	0
Rapeseed	Rissen	21	23	0
Rapeseed	Senftenberg	4	1	0
Rapeseed	Tennessee	35	5	1
Rapeseed	Typhimurium DT2	1	1	1
Rapeseed	Typhimurium DT99	0	1	0
Rapeseed	Typhimurium RDNC	1	0	0
Rapeseed	Westhampton	1	0	0
Rapeseed	6,7:-:-	0	1	0
Rapeseed	6,7,:rough:-:-	1	0	0
Separated fibre	Agona	0	0	1
Soya	Agona	0	0	1
Soya	Fresno	0	0	1
Soya	Havana	0	0	1
Soya	Livingstone	0	0	1
Soya	Mbandaka	0	0	1
Soya	Senftenberg	0	0	1
Soya	Tennessee	0	0	1
Soya	Typhimurium DT1	0	0	1
Soya	Typhimurium DT99	0	0	4
Soya bean meal	Agona	3	0	0
Soya bean meal	Alachua	1	0	0
Soya bean meal	Anatum	2	1	0
Soya bean meal	Bareilly	0	1	0
Soya bean meal	Bere	0	1	0

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Soya bean meal	California	3	0	0
Soya bean meal	Cannstatt	1	0	0
Soya bean meal	Carmel	0	1	0
Soya bean meal	Cerro	0	2	0
Soya bean meal	Cubana	1	4	0
Soya bean meal	Duisburg	0	1	0
Soya bean meal	Fresno	0	2	0
Soya bean meal	Havana	1	1	0
Soya bean meal	Kedougou	0	1	0
Soya bean meal	Kentucky	2	1	0
Soya bean meal	Korlebu	2	0	0
Soya bean meal	Lexington	1	0	0
Soya bean meal	Livingstone	0	2	0
Soya bean meal	Mbandaka	2	1	0
Soya bean meal	Montevideo	3	0	0
Soya bean meal	Ohio	0	1	0
Soya bean meal	Orion	3	0	0
Soya bean meal	O rough:f,g:-:-	1	0	0
Soya bean meal	Rissen	2	0	0
Soya bean meal	Senftenberg	2	0	0
Soya bean meal	Tennessee	4	1	0
Soya bean meal	Typhimurium DT2	0	1	0
Soya bean meal	Typhimurium DT99	0	1	0
Soya bean meal	Typhimurium RDNC	1	0	0
Soya bean meal	Uganda	0	1	0
Soya bean meal	Weltevreden	1	0	0
Soya bean meal	Yoruba	1	0	0
Soya bean meal	3,15:rough:-	0	1	0
Soya bean meal	3,19:-:-	0	1	0
Soya bean meal	3,19:z_{27}:-	0	3	0
Soya bean meal	6,7:b:-	0	1	0
Soya bean meal	6,7:z_4,z_{23}:-	0	0	0
Soya bean meal	47:z_4,z_{23}:-	1	0	0
Sunflower	Cannstatt	1	0	0
Sunflower	Cubana	1	0	0
Sunflower	Liverpool	0	1	0
Sunflower	Llandoff	1	0	0
Sunflower	Mbandaka	1	0	0
Sunflower	Montevideo	2	0	0
Sunflower	Tennessee	0	1	0
Sunflower	Typhimurium DT2	0	0	0

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Sunflower	Typhimurium DT193	1	0	0
Sunflower	Vinohady	1	0	0
Sunflower	3,19:rough:-	1	0	0
Wheat	Agama	1	0	0
Wheat	Agona	0	2	0
Wheat	Kedougou	0	0	1
Wheat	Kingston	0	0	1
Wheat	Rissen	1	0	0
Wheat	Typhimurium U308	1	0	0
Yucca	Mbandaka	0	1	0
Total	Not applicable	**239**	**114**	**44**

Table 12.8b: Serovars of *Salmonella* in other products associated with the ABPR in Great Britain, 2021 to 2023

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Aeration tank	Infantis	0	0	4
Beef concentrate	Isangi	0	0	1
Biogas	Infantis	0	0	1
Biogas	Typhimurium DT75	0	0	1
Blood products	Cerro	0	2	0
Blood products	Derby	0	7	0
Blood products	Panama	0	6	0
Blood products	Rissen	0	2	0
Blood products	Senftenberg	1	0	0
Blood products	Tennessee	2	0	0
Blood products	Typhimurium DT2	2	0	0
Blood products	4,12:i:- DT193	0	2	0
Blood products	4,5,12:i:- DT193	0	6	0
Blood products	4,5,12:i:- UNTY	0	1	0
Bone meal	Idikan	1	0	0
Bone meal	Infantis	2	0	0
Bone meal	Mbandaka	3	0	0
Bone meal	Senftenberg	3	0	0
Bone meal	Tennessee	1	0	0
Bone meal	6,7:r:-	1	0	0
Centrate liquor	Infantis	0	0	13
Compost	Aba	0	1	0
Compost	Agona	1	0	0
Compost	Give	1	0	0
Compost	Indiana	1	0	0
Compost	Infantis	0	0	2
Compost	Kottbus	1	0	0
Compost	London	0	1	0
Compost	Senftenburg	0	1	0
Compost	Tennessee	0	1	0
Compost	13,23:i:-	0	0	1
Digestate	Agona	10	0	1
Digestate	Bareilly	2	0	0
Digestate	Bovismorbificans	0	0	1
Digestate	Branderup	1	0	0
Digestate	Derby	1	0	0
Digestate	Eastbourne	0	0	1

Feedingstuff	***Salmonella* serovar**	**Isolations 2021**	**Isolations 2022**	**Isolations 2023**
Digestate	Infantis	0	0	22
Digestate	Kedougou	1	0	0
Digestate	Kentucky	0	0	1
Digestate	Livingstone	0	0	2
Digestate	Mbandaka	1	0	0
Digestate	Monophasic Typhimurium DT193	0	2	1
Digestate	Montevideo	2	0	0
Digestate	Newport	3	1	1
Digestate	Ohio	0	0	2
Digestate	Ordonez	23	0	0
Digestate	Oslo	0	0	1
Digestate	Panama	3	0	0
Digestate	Rissen	2	0	0
Digestate	Senftenberg	1	0	0
Digestate	Typhimurium DT116	2	0	0
Digestate	Typhimurium DT130	0	0	1
Digestate	Typhimurium NOPT	3	0	0
Digestate	Typhimurium RDNC	1	0	0
Digestate	61:k:1,5,7	0	1	0
Digestate liquor	Infantis	0	0	18
Dog treat	Derby	0	0	1
Dog treat	Infantis	0	0	1
Dog treat	Montevideo	0	0	1
Dog treat	Nottingham	0	0	1
Effluent tank	13,23:i:-	0	0	1
Feedmill environment	Agama	1	1	0
Feedmill environment	Agona	1	2	1
Feedmill environment	Ajiobo	0	1	0
Feedmill environment	Anatum	2	2	0
Feedmill environment	Bonn	0	0	1
Feedmill environment	California	5	0	0
Feedmill environment	Cerro	0	1	3
Feedmill environment	Coeln	2	0	0
Feedmill environment	Cubana	1	1	0
Feedmill environment	Derby	1	1	5
Feedmill environment	Ealing	1	1	0
Feedmill environment	Enteritidis PT5	0	0	1
Feedmill environment	Enteritidis PT6	0	0	2
Feedmill environment	Enteritidis PT9	0	0	1
Feedmill environment	Enteritidis PT11b	0	0	1

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Feedmill environment	Enteritidis NOPT	0	0	1
Feedmill environment	Enteritidis RDNC	0	0	1
Feedmill environment	Give	0	0	1
Feedmill environment	Hadar	0	0	1
Feedmill environment	Havana	1	0	0
Feedmill environment	Heidelberg	0	0	1
Feedmill environment	Idikan	1	2	3
Feedmill environment	Infantis	2	8	20
Feedmill environment	Kedougou	33	50	82
Feedmill environment	Kentucky	0	1	4
Feedmill environment	Kiambu	0	0	1
Feedmill environment	Kottbus	0	1	1
Feedmill environment	Liverpool	0	1	0
Feedmill environment	Livingstone	0	1	1
Feedmill environment	Mbandaka	2	9	3
Feedmill environment	Monophasic Typhimurium DT193	0	1	3
Feedmill environment	Monophasic Typhimurium NOPT	0	0	1
Feedmill environment	Monophasic Typhimurium UNTY	0	0	1
Feedmill environment	Montevideo	0	0	7
Feedmill environment	Morehead	0	0	1
Feedmill environment	Nagoya	0	0	1
Feedmill environment	Neunkirchen	0	0	1
Feedmill environment	Newport	0	1	4
Feedmill environment	Nottingham	0	0	16
Feedmill environment	Ohio	27	20	68
Feedmill environment	Oranienburg	1	1	1
Feedmill environment	Oslo	1	1	0
Feedmill environment	Ouakam	0	1	0
Feedmill environment	Paratyphi var. java	0	1	1
Feedmill environment	Rissen	7	3	2
Feedmill environment	Ruiru	2	0	0
Feedmill environment	Senftenberg	11	2	9
Feedmill environment	Senftenberg (z_{27})	0	1	0
Feedmill environment	Stanleyville	0	0	1
Feedmill environment	Szentes	0	1	0
Feedmill environment	Tennessee	2	0	1
Feedmill environment	Typhimurium DT2	0	0	4
Feedmill environment	Typhimurium DT99	0	2	4

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Feedmill environment	Typhimurium DT105	0	0	2
Feedmill environment	Typhimurium U288	1	0	0
Feedmill environment	Typhimurium U322	0	0	4
Feedmill environment	Typhimurium NOPT	0	0	1
Feedmill environment	Typhimurium RDNC	1	1	4
Feedmill environment	Typhimurium UNTY	0	0	1
Feedmill environment	Uganda	0	0	3
Feedmill environment	Williamsberg	0	0	1
Feedmill environment	Westhampton	1	0	0
Feedmill environment	3,19:z_{27}:-	0	1	0
Feedmill environment	4,5,12:b:-	1	0	0
Feedmill environment	6,7:enz$_{15}$	1	2	0
Feedmill environment	6,7:k:-	1	0	0
Feedmill environment	6,7:r:-	1	0	0
Feedmill environment	6,7:-:-	3	4	1
Feedmill environment	13,23:i:-	1	5	8
Feedmill environment	61:k:1,5,7	0	0	1
Feedmill environment	61:-:1,5,7	0	1	0
Feedmill environment	42:b:e,n,x,z15	0	0	1
Feedmill environment	47:z4,z23:-	0	0	1
Fertilizer - tea fungal additive	Anatum	0	0	1
Landfill	Derby	0	0	1
Meat and bone	Derby	0	0	1
Meat & bone meal	Livingstone	1	0	0
Meat & tallow	4,5,12:i:- DT193	0	2	0
Meat & tallow	Infantis	0	2	0
Pasteurised liquor	Infantis	0	0	4
Pet food (raw)	Agama	1	0	1
Pet food (raw)	Agona	1	9	7
Pet food (raw)	Anatum	4	1	8
Pet food (raw)	Bonn	0	2	0
Pet food (raw)	Bovismorbificans	0	5	2
Pet food (raw)	Brandenburg	1	2	1
Pet food (raw)	Bredeney	0	0	1
Pet food (raw)	Cerro	0	1	0
Pet food (raw)	Coeln	1	0	0
Pet food (raw)	Derby	17	26	31
Pet food (raw)	Dublin	10	4	5
Pet food (raw)	Ealing	2	1	0
Pet food (raw)	Enteritidis PT2	1	0	0

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Pet food (raw)	Enteritidis PT3a	0	0	1
Pet food (raw)	Enteritidis PT8	0	1	1
Pet food (raw)	Enteritidis PT9a	0	0	1
Pet food (raw)	Enteritidis PT11b	0	0	1
Pet food (raw)	Enteritidis PT13a	0	0	2
Pet food (raw)	Enteritidis PT21	0	1	2
Pet food (raw)	Enteritidis PT22	0	0	1
Pet food (raw)	Enteritidis RDNC	0	1	0
Pet food (raw)	Enteritidis UNTY	1	0	0
Pet food (raw)	Give	7	7	10
Pet food (raw)	Give var 15^+	0	10	1
Pet food (raw)	Goldcoast	1	3	0
Pet food (raw)	Hadar	3	1	11
Pet food (raw)	Havana	0	2	1
Pet food (raw)	Idikan	1	1	0
Pet food (raw)	Indiana	34	49	46
Pet food (raw)	Infantis	18	38	29
Pet food (raw)	Isangi	0	0	1
Pet food (raw)	Kedougou	4	5	2
Pet food (raw)	Kentucky	2	0	0
Pet food (raw)	Kingston	0	1	0
Pet food (raw)	Kottbus	18	15	11
Pet food (raw)	Larochelle	1	0	0
Pet food (raw)	Lexington	1	7	1
Pet food (raw)	Litchfield	0	0	3
Pet food (raw)	Liverpool	0	1	0
Pet food (raw)	Livingstone	4	5	3
Pet food (raw)	London	5	8	2
Pet food (raw)	Mbandaka	19	10	8
Pet food (raw)	Meleagridis	2	0	1
Pet food (raw)	Miami	0	0	1
Pet food (raw)	Monophasic Typhimurium DT104	0	2	0
Pet food (raw)	Monophasic Typhimurium DT120	1	1	3
Pet food (raw)	Monophasic Typhimurium DT193	14	29	16
Pet food (raw)	Monophasic Typhimurium U208	0	1	0
Pet food (raw)	Monophasic Typhimurium U311	1	1	0

Feedingstuff	***Salmonella* serovar**	**Isolations 2021**	**Isolations 2022**	**Isolations 2023**
Pet food (raw)	Monophasic Typhimurium NOPT	3	0	0
Pet food (raw)	Monophasic Typhimurium RDNC	1	0	0
Pet food (raw)	Monophasic Typhimurium UNTY	0	6	0
Pet food (raw)	4,5,12:-1,2 DT1	1	0	0
Pet food (raw)	Montevideo	7	8	8
Pet food (raw)	Muenchen	0	0	1
Pet food (raw)	Muenster	0	5	5
Pet food (raw)	Newport	13	17	22
Pet food (raw)	Ohio	2	1	0
Pet food (raw)	Orion	11	6	2
Pet food (raw)	Orion var. 15^+	1	1	1
Pet food (raw)	O rough:f,g:-	2	0	0
Pet food (raw)	O rough:g,p:-	1	0	0
Pet food (raw)	O rough:i:z	2	0	0
Pet food (raw)	O rough:k:z	4	0	0
Pet food (raw)	O rough:z_{10}:enz_{15}	0	2	0
Pet food (raw)	Panama	6	7	4
Pet food (raw)	Paratyphi var. Java	2	1	3
Pet food (raw)	Reading	0	1	2
Pet food (raw)	Rissen	6	4	4
Pet food (raw)	Rubislaw	0	2	0
Pet food (raw)	Ruiru	2	0	0
Pet food (raw)	Saintpaul	0	1	0
Pet food (raw)	Schwarzengrund	0	1	0
Pet food (raw)	Senftenberg	0	6	13
Pet food (raw)	Stanley	2	1	2
Pet food (raw)	Stanleyville	1	0	0
Pet food (raw)	Tennessee	0	1	0
Pet food (raw)	Tsevie	0	1	0
Pet food (raw)	Typhimurium DT1	1	0	2
Pet food (raw)	Typhimurium DT2	3	5	8
Pet food (raw)	Typhimurium DT3	1	0	0
Pet food (raw)	Typhimurium DT4	0	0	1
Pet food (raw)	Typhimurium DT8	0	2	1
Pet food (raw)	Typhimurium DT9	0	3	1
Pet food (raw)	Typhimurium DT32	0	0	1
Pet food (raw)	Typhimurium DT75	0	3	1
Pet food (raw)	Typhimurium DT99	0	1	2

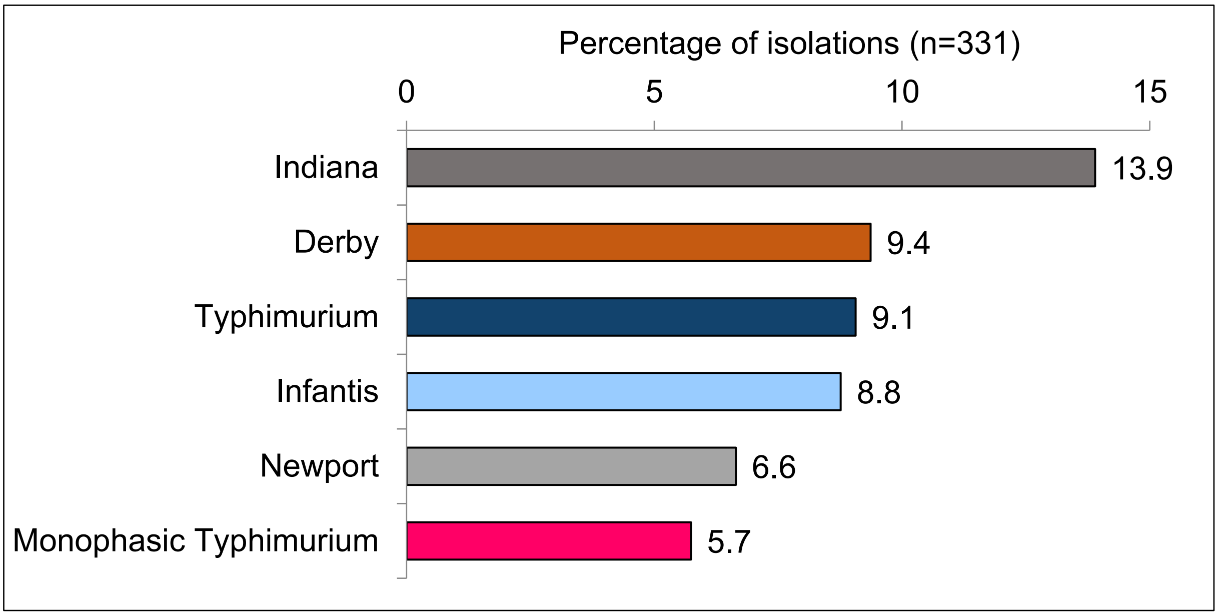
Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Pet food (raw)	Typhimurium DT104	0	3	0
Pet food (raw)	Typhimurium DT105	3	5	1
Pet food (raw)	Typhimurium DT116	1	0	2
Pet food (raw)	Typhimurium DT120	0	2	1
Pet food (raw)	Typhimurium DT193	2	2	3
Pet food (raw)	Typhimurium U208	1	0	0
Pet food (raw)	Typhimurium U281	1	0	0
Pet food (raw)	Typhimurium U302	1	0	0
Pet food (raw)	Typhimurium U308	3	0	0
Pet food (raw)	Typhimurium U311	0	3	1
Pet food (raw)	Typhimurium NOPT	3	2	2
Pet food (raw)	Typhimurium RDNC	7	7	3
Pet food (raw)	Typhimurium UNTY	1	0	0
Pet food (raw)	Virchow	0	3	1
Pet food (raw)	Westhampton	1	0	0
Pet food (raw)	Wilhelmsberg	0	1	1
Pet food (raw)	3,10:z_{10}:-	0	1	0
Pet food (raw)	4,12:b:-	0	0	2
Pet food (raw)	4,12,[27]:b:e,n,x	1	0	0
Pet food (raw)	4,12:rough	0	1	0
Pet food (raw)	4,12:z:-	0	2	0
Pet food (raw)	6,7:-:enz$_{15}$	0	4	0
Pet food (raw)	6,7:-:-	1	5	0
Pet food (raw)	6,8:e,h:-	0	3	0
Pet food (raw)	9,12:l,v:-	1	0	0
Pet food (raw)	13,23:i:-	2	0	3
Pet food (raw)	38:l,v,z_{13}:-	0	1	0
Pet food (raw)	38:r:z	1	0	0
Pet food (raw)	61:-:1,5	12	0	0
Pet food (raw)	61:-:1,5,7	4	16	1
Pet food (raw)	61:k:1,5,7	0	8	11
Process water tank	Infantis	0	0	5
Raw meat	Bovismorbificans	0	0	1
Raw meat	Enteritidis	0	0	1
Raw meat	Indiana	0	0	1
Raw meat	Livingstone	0	0	2
Raw meat	Mbandaka	0	0	1
Raw meat	Monophasic Typhimurium DT59	0	0	1
Raw meat	Montevideo	0	0	1
Raw meat	Newport	0	0	2

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Raw meat	Paratyphi b variant Java	0	0	1
Raw meat	Schwarzengrund	0	0	1
Rendering plant material	Enteritidis PT3a	1	0	0
Rendering plant material	Mbandaka	1	0	0
Rendering plant material	O rough:g,p:-	1	0	0
Rendering plant material	Soerenga	1	0	0
Rendering plant material	Typhimurium DT104	1	0	0
Rendering plant material	Typhimurium DT193	1	0	0
Rendering plant material	Monophasic Typhimurium DT193	2	0	0
Rendering plant material	6,7:-:enz$_{15}$	1	0	0
Rendering plant material	61:-1,5	2	0	0
Unspecified	Anatum	0	0	1
Unspecified	Bredeney	0	0	1
Unspecified	Cerro	0	0	2
Unspecified	Coeln	0	0	1
Unspecified	Derby	0	0	2
Unspecified	Enteritidis PT21	0	0	1
Unspecified	Enteritidis NOPT	1	0	0
Unspecified	Fresno	0	0	1
Unspecified	Give	0	0	1
Unspecified	Infantis	0	0	1
Unspecified	Kedougou	0	0	6
Unspecified	Monophasic Typhimurium NOPT	2	0	0
Unspecified	Montevideo	0	0	2
Unspecified	Ohio	0	0	6
Unspecified	Panama	0	0	1
Unspecified	Rissen	0	0	1
Unspecified	Senftenberg	0	0	3
Unspecified	Tennessee	1	0	1
Unspecified	Thompson	0	0	1
Unspecified	Typhimurium DT2	0	0	1
Unspecified	Typhimurium DT015	0	0	1

Feedingstuff	*Salmonella* serovar	Isolations 2021	Isolations 2022	Isolations 2023
Unspecified	Typhimurium DT193	0	0	1
Unspecified	Typhimurium RDNC	1	0	0
Unspecified	3,10:-:-	1	0	0
Total	Not applicable	**502**	**577**	**759**

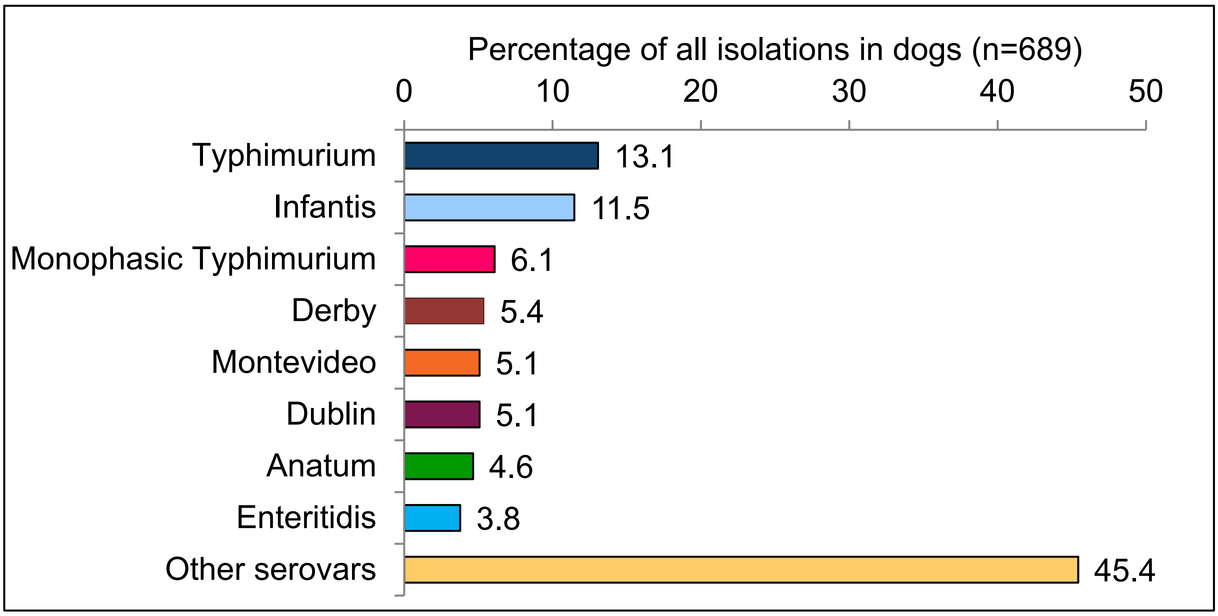
Figure 12.7: Isolations of the most common serovars in raw pet food and dogs in Great Britain in 2023

Figure 12.7.1: Isolations from raw pet food



The most common *Salmonella* serovar in raw pet food was *S.* Indiana, accounting for 13.9% of total isolations, followed by *S.* Derby (9.4%), *S.* Typhimurium (9.1%), *S.* Infantis (8.8%), *S.* Newport (6.6%) and monophasic *S.* Typhimurium (5.7%).

Figure 12.7.2: Isolations from dogs



In 2023 the most common *Salmonella* serovar in dogs 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*. Montevideo (5.1%) and *S* Dublin (5.1%).

Table 12.9: Animal By-Products (Enforcement) Regulations 2013, domestic protein official testing and contamination rates in Great Britain, 2021 to 2023

Sample Type	2021 Batches	2021 number +ve	2021 % +ve	2022 Batches	2022 number +ve	2022 % +ve	2023 Batches	2023 number +ve	2023 % +ve
Blood meal	4	1	25.0	0	0	0	2	0	0
Bone meal	0	0	0	0	0	0	0	0	0
Feather meal	1	0	0	1	0	0	9	0	0
Greaves	3	0	0	1	0	0	0	0	0
Meat & bone meal	10	0	0	3	0	0	2	0	0
Meat meal	0	0	0	0	0	0	0	0	0
Poultry offal meal	1	0	0	0	0	0	7	0	0
White fish meal	7	0	0	14	0	0	15	0	0
Other fish meal	0	0	0	1	0	0	0	0	0
Others	358	8	2.23	281	2	0.71	288	4	1.39
Total	**384**	**9**	**2.34**	**301**	**2**	**0.66**	**323**	**4**	**1.24**

This table excludes the results of private testing.

Table 12.10: Animal By-Products (Enforcement) Regulations, 2013. Serovars isolated during 2021 to 2023 from official and private testing of domestic protein and other products associated with the regulations in Great Britain

Serovar	Isolations 2021	Isolations 2022	Isolations 2023
Agona	1	0	0
Bovismorbificans	0	0	0
Cerro	0	0	0
Derby	0	1	0
Durban	1	0	0
Gueuletapee	0	0	1
Indiana	1	0	0
Infantis	0	0	1
Isangi	0	0	0
Kedougou	1	0	0
Kottbus	1	0	0
Livingstone	1	0	0
Tennessee	0	1	0
Typhimurium DT2	1	0	0
Typhimurium DT75	0	0	1
Typhimurium DT105	0	0	1
Typhimurium NOPT	1	0	0
Untypable	1	0	0
Total	**9**	**2**	**4**

The total number of batches positive was the same as the total number of isolations positive in 2021, 2022 and 2023.

Figure 12.8: Contamination rate for domestic processed animal protein (batches tested) in Great Britain, 2014 to 2023

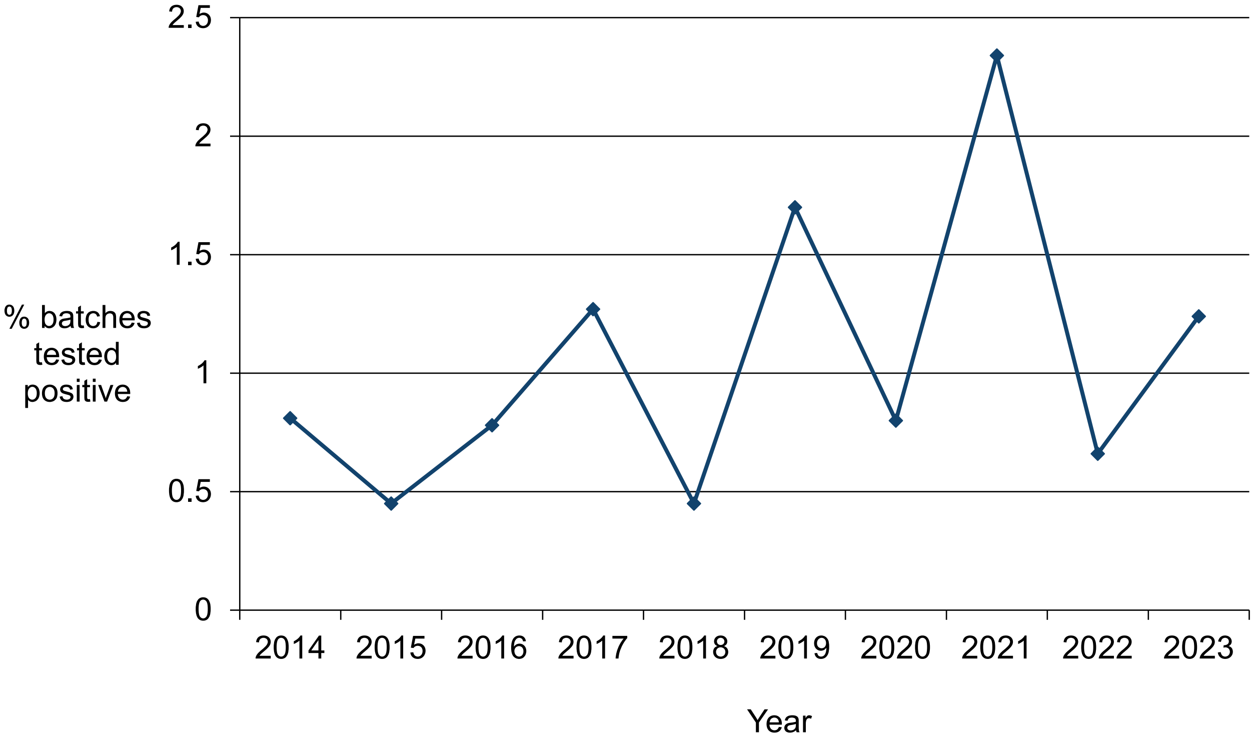


Figure 12.8 shows the proportion of positive batches for domestic processed animal protein had fluctuated year on year with an overall increase in positivity. 2021 saw the highest proportion of contaminated batches (2.34%) but fell in 2022 to 0.66% of batches which is lower than 2013 with 0.75% of batches. There was an increase in the proportion of batches testing positive in 2023 (1.24%) compared with 2022 but less than in 2021.

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 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 $\leq$ 13mm used in previous years, to the BSAC breakpoint of resistant or intermediate $\leq$ 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 2021 provides further details in an annex and is available on GOV.UK.

The sole change made to the zone size breakpoints and disc concentrations used over the period 2008 to 2021 related to the ceftazidime disc for which the zone size was reduced from 29mm to 26mm in 2012, in line with BSAC recommendations. The BSAC disc diffusion method is no longer being supported, but the BSAC clinical breakpoints were fully harmonised with those of the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and will remain valid, unless EUCAST clinical breakpoints for the antimicrobials included in this report are subsequently revised.

Table 13.1: Details of antimicrobials

Antimicrobial	Concentration (µg per ml)	Code	Zone size (R≤x mm)
Nalidixic acid	30	NA	13
Tetracycline	10	T	13
Neomycin	10	N	13
Ampicillin	10	AM	14
Furazolidone	15	FR	13
Ceftazidime	30	CAZ	26
Sulphamethoxazole and trimethoprim combination	25	TM	15
Chloramphenicol	30	C	20
Amikacin	30	AK	18
Amoxicillin and clavulanic acid combination	30	AMC	14
Gentamicin	10	CN	19
Streptomycin	10	S	13
Sulphonamide compounds	300	SU	13
Cefotaxime	30	CTX	29
Apramycin	15	APR	13
Ciprofloxacin	1	CIP	16

Prior to 1996, all *Salmonella* isolates received were tested for antimicrobial susceptibility, but since then only the first isolate of a given serotype or phage type from each incident has usually been tested. 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.

Salmonella Dublin

A total of 317 cultures of *Salmonella* Dublin underwent antimicrobial sensitivity testing in 2023. As in previous years, most *S.* Dublin isolates (270, 85.2%) originated from cattle and 96.3% were susceptible to all 16 antimicrobials (Table 13.2). Although each of the resistant isolates showed resistance to only one antimicrobial from the panel, one isolate was resistant to nalidixic acid and another to apramycin. Apramycin resistance has not been detected in *S.* Dublin from cattle since 2011 (Table 13.2).

Salmonella Dublin isolates from species other than cattle, comprised 39 isolates from dogs, one from a chicken, one from a sheep, and one from a wildcat. Five isolates were also obtained from animal feed. Apart from 2 dog isolates (one resistant to streptomycin and the other with resistance pattern TAmTmC), all others were susceptible.

The percentage of *S.* Dublin isolates sensitive to all 16 antimicrobials has shown only slight fluctuations over the period 2006 to 2019. However, in 2020, a rise in the proportion of resistant isolates was observed and this increased level was maintained in 2021. In 2022, there was a return to pre-2020 susceptibility levels, which continued into 2023. This was mostly due to a decrease in *S.* Dublin isolates resistant to neomycin, chloramphenicol and tetracycline in cattle, which were not detected at all in 2023. The overall majority of *S.* Dublin isolates remain susceptible (96.8%), which has been consistent since surveillance began in 1971.

Salmonella Typhimurium

The number of isolates of *S.* Typhimurium tested in 2023 was 558. The most frequent definitive or undefined phage types subjected to susceptibility testing at APHA are given in Table 13.3. Overall, 5.0% of *S.* Typhimurium isolates were phage type DT104 or DT104b, while phage type U302 was not detected (Table 13.4). The percentage of the 8 most common definitive and undefined phage types of *S.* Typhimurium sensitive to all 16 antimicrobial agents in 2023 is given in Figure 13.1.

The percentage of *S.* Typhimurium cultures sensitive to all the antimicrobials tested was 55.0% (Table 13.4). This finding is consistent with the upward trend that followed the drop in susceptibility observed in 2020 (39.9%).

Dogs and pigs accounted for 48.7% of *S.* Typhimurium detected from animals. Only 1.7% of *S*. Typhimurium isolates from pigs (n=176) were susceptible, whereas 78.1% of canine isolates (n=96) were susceptible. The susceptibility of canine isolates versus porcine isolates reflected occurrence of the different phage types.

The generally high level of resistance of *S.* Typhimurium isolates observed in recent years has partly been a reflection of the contribution of DT104 and its variants DT104b and U302. These phage types, which are preferentially selected for susceptibility tests because of the importance of the pentavalent resistance pattern, have comprised more than a quarter of tested isolates in some years of the last decade. In 2023, no U302 *Salmonella* Typhimurium strains were detected, while one susceptible DT104b was isolated from a dog. Of the 27 DT104 strains tested in 2023, 7 were from cattle, 6 from dogs, 5 from pigs, 4 from chickens, 3 from cats, one from a horse and one from a lion.

Seven of the 27 DT104 isolates and the single DT104b isolate tested in 2023 were susceptible to all the antimicrobials in the panel. All remaining DT104 were resistant to at least one of the 16 antimicrobials tested. The proportion of *S.* Typhimurium isolates comprising DT104 and its variants, which had shown a general decline in 2007 to 2014, showed a resurgence in 2015 to 2017 (Table 13.4). However, levels have been decreasing steadily since 2019, reaching the lowest recorded level in 2023 (5,0%). The typical pentavalent resistance pattern AmCSSuT commonly seen in *S.* Typhimurium DT104 and its variants, was detected in 60.7% (17 of 28) of isolates.

The pentavalent resistance pattern above, with the addition of nalidixic acid resistance, was also common (32.1%, 9 of 28). Ten of the 28 DT104 and DT104b isolates were resistant to nalidixic acid and 6 to sulphamethoxazole and trimethoprim combination. Nalidixic acid resistance in *S.* Typhimurium DT104 by species of origin is listed in Table 13.5 for the main food-producing animal species over the last 11 years.

Salmonella Typhimurium U288 and DT193 from pigs accounted for 0.9% (5 isolates) and 7.0% (39 isolates) of the total numbers of *S.* Typhimurium isolates, respectively. None of the U288 or DT193 isolates from pigs were fully susceptible in 2023.

Considering all definitive types of *S.* Typhimurium, resistance to sulphamethoxazole and trimethoprim combination has fluctuated markedly in recent years (Table 13.6). The prevalence of resistance to sulphamethoxazole and trimethoprim combination in *S.* Typhimurium was 30.5% in 2023, with a high proportion of resistant isolates originating from pigs (Table 13.6).

The definitive and undefined phage types of *S.* Typhimurium resistant to sulphamethoxazole and trimethoprim combination and recovered from pigs in 2023 included contributions primarily from isolates of 2 phage types: U308a (61 isolates) and DT193 (33 isolates). Phage type U288 used to represent an important proportion of resistant isolates in pigs. However, detections of this phage type dropped in 2022 and remained low in 2023 (5 isolates), although all isolates tested resistant to sulphamethoxazole and trimethoprim combination (Table 13.7). AmCSSuTTm was a common resistance pattern observed in U308a (42 isolates), DT193 isolates (21 isolates) and U288 isolates (3 isolates) from pigs.

S. Typhimurium DT105 has increased in cattle in recent years. Forty of the 93 *S.* Typhimurium isolates detected from cattle in 2023 belonged to this definitive phage type, which often either showed the resistance pattern SSuT (21 of 23 resistant isolates) or was susceptible (17 isolates).

Apramycin resistance in *S.* Typhimurium in 2023 was 6.8%, a notable increase compared to the preceding 9 years (Table 13.4). However, this is still considerably lower than in 2012 when 20.4% of isolates were resistant to apramycin.

In 2023, a total of 16 *S.* Typhimurium isolates were resistant to nalidixic acid: 5 from cattle, 4 from chickens, 2 from dogs, 2 from feed, 2 from pigs, and one from a partridge. One of the 2 isolates from feed was a multidrug-resistant (MDR: resistant to at least 4 antimicrobials in the panel) DT193 *S.* Typhimurium from raw pet food which showed resistance to other 12 antimicrobials, including cefotaxime, ceftazidime, ciprofloxacin and apramycin.

Multiple antibiotic resistance was detected in definitive and undefined phage types DT104 (from cats, cattle, chickens, dogs, pigs, a horse, and a lion), DT105 (cats, cattle, and pigs), DT11 (a partridge and a pig), DT116 (dogs), DT120 (pigs), DT181 (pigs), DT193 (pigs, dogs and feed), DT2 (dogs and feed), DT20 (pigs), DT32 (pigs and feed), DT4 (pigs), RDNC (dogs, pigs and feed), U288 (pigs and sheep), U308 (pigs), U308a (pigs), U310 (feed) and from isolates which reacted with the phages but did not conform to a recognised pattern of lysis (RDNC) (dogs, pigs and feed).

Of the 26 different definitive and undefined phage types detected, 17 (namely DT1, 2, 4, 8, 9, 21, 32, 75, 99, 104, 105, 116, 120, 130, 182, 193, U322) were susceptible to all the antimicrobials in the test panel.

Monophasic *Salmonella* Typhimurium serovars

A total of 203 isolates of monophasic *Salmonella* Typhimurium were tested in 2023, belonging to phage types DT104 (2) , DT193 (150), DT120 (12), DT1 (1), DT191 (1), DT194 (1), DT59 (1), U302 (1), U308a (1), U323 (2), RDNC (6), UNTY (20), NOPT (3) and 2 untyped isolates. Most isolates originated from pigs (78 isolates), dogs (49 isolates) and feed (41 isolates). Overall, 7.4% were susceptible to all the antimicrobials in the panel and 70.4% were MDR. The most common pattern of resistance observed was AmSSuT, which occurred in 133 isolates. Considering the DT193 isolates, 104 of 150 (69.3%) showed the AmSSuT pattern alone, or with additional resistance.

Considering the aminoglycosides other than streptomycin, apramycin resistance was detected in 35 isolates and neomycin resistance in 39 isolates. Resistance to neomycin and apramycin was observed in 32 isolates (mainly DT193 or not typed (NOPT)), obtained from pigs (78.1%), environmental samples (15.6%), dogs (9.4%), chickens (3.1%) and feed (3.1%).

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

Of the 4,638 isolates of serovars other than *S.* Dublin and *S.* Typhimurium tested, 73.9% were sensitive to all the antimicrobials in the test panel (Table 13.8). Susceptibility declined in 2023 in comparison to the previous year (77.2%), although still an increase on the figure recorded in 2021 (68.5%). Sixty-six isolates were *S.* Enteritidis, of which 74.2% (49 of 66) were fully susceptible.

Considering all serovars other than *Salmonella* Dublin and *Salmonella* Typhimurium, 158 isolates (3.4%) were resistant to nalidixic acid, mainly obtained from feed (101 isolates) and dogs (20 isolates). The main serovars involved were *S.* Indiana (50 isolates, all from feed) and *S.* Infantis (38 isolates from feed, dogs, and chickens). Resistance to nalidixic acid was also observed in 14 *S.* Enteritidis isolates: 7 PT21 from dogs and feed, 2 PT11b from dogs, one PT14b from a dog, one PT35 from a dog, one PT4 from feed, one RDNC from environmental samples, and one UNTY from a cat.

Thirty-eight isolates were resistant to ciprofloxacin, including 23 isolates from feed (mainly *S.* Infantis and *S.* Newport), 8 isolates from dogs (mainly *S.* Kentucky and *S.* Infantis), 5 isolates from chickens (mainly *S.* Agona), one *S.* Idikan from the chick environment, and one *S.* Infantis from a cat.

Seven isolates of serovars other than *Salmonella* Dublin and *Salmonella* Typhimurium were resistant to cefotaxime and ceftazidime, including 3 *S*. Kentucky, one *S*. Derby, one *S*. Livingstone, one *S*. Enteritidis, one *S*. Saintpaul. All isolates were obtained from dogs.

Of 4,638 isolates, 96 (2.1%) were resistant to neomycin and originated mainly from pigs (37 resistant out of 152 isolates tested), chickens (23 of 1923), dogs (18 of 622) and feed (14 of 1166).

Considering *Salmonella* isolates other than Typhimurium and Dublin from turkeys in 2023 (n=74), 23.0% were resistant to streptomycin, 40.5% to sulphonamides and 46.0% to tetracyclines. This is lower than the equivalent figures for pigs in 2023 (n=52 and 51.3% , 54.0%, 54.0% respectively), but higher than those for chickens (n= 1923 and 5.5%, 13.5% and 5.9%) or cattle (n=108 and 14.8%, 12.0% and 8.3% respectively).

Individual antimicrobials

Of the 5,513 *Salmonella* isolates tested in 2023, 4,042 (73.3%) were sensitive to all the antimicrobials tested (Table 13.9). This is a slight decrease in susceptibility in comparison to 2022 (75.7% of 5,562 isolates), but higher than levels recorded in 2021 (67% of 4,507 isolates).

Ampicillin resistance decreased from 11.9% of 5,562 isolates in 2022 to 9.9% of 5513 isolates in 2023 and across most sources of isolates (except for cattle, pigs, ducks, and non-avian species). A slight increase in resistance was observed for sulphonamides (from 15.3% in 2022 to 19.0% in 2023), tetracycline (from 13.3% to 15.4%) and sulphamethoxazole and trimethoprim combination (from 7.8% to 12.3%). This could be partially due to an increase in isolates resistant to these compounds originating from feed, particularly *S.* Kedougou which frequently features the resistance pattern TSuTm, or a combination of these compounds.

Pigs and turkeys showed the highest proportions of resistance to tetracycline (57.6% and 44.7%, respectively), sulphonamides (75.0% and 39.5%), streptomycin (57.9% and 22.4%) and sulphamethoxazole and trimethoprim combination (64.0% and 15.8%). Findings were similar in the previous 2 years.

Considering all *Salmonella* serovars tested in 2023, resistance to apramycin (1.7%), gentamicin (1.9%) and neomycin (3.0%) remained similar to the levels observed in 2022. *Salmonella* isolates from pigs (n=328), contributed most to the overall figures of resistance to these compounds, with 21.6% of pig isolates showing resistance to apramycin, 21.6% to gentamicin, 32.3% to neomycin and 40 isolates being resistant to all 3 antimicrobials. Pig isolates showing resistance to one or all 3 antimicrobials included the serovars *S.* Typhimurium, monophasic *S.* Typhimurium, *S.* Newport, *S.* Kedougou, and *S.* Panama. One *S.* London isolate showed resistance to apramycin and gentamicin, but not to neomycin. In 2023 apramycin resistance was detected in a *S.* Dublin isolate from cattle for the first time since 2011. None of the *Salmonella* isolates tested in 2023 was resistant to the aminoglycoside amikacin.

In 2023, 3.2% of isolates (n=5,513) were resistant to nalidixic acid, a slight decrease from the previous year (3.8% of 5,562). The main sources of isolates resistant to nalidixic acid in 2023 were feed and turkeys. In feed, *S.* Indiana (50 resistant isolates of 110 tested) and *S.* Infantis (12 of 180) were the main serovars involved. Results in 2023 from turkeys were consistent with findings from previous years, with isolates resistant to nalidixic acid belonging to the serovars *S.* 3,19:-:- (1 of 1) and *S.* 3,19:rough:- (1 of 1), *S*. Kedougou (1 of 28) and *S.* Senftenberg (2 of 3 isolates), *S.* Agona (1 of 8). In chickens, resistance to nalidixic acid was found in *S.* Infantis (8 of 60), *S.* Agona (4 of 142), *S.* Typhimurium (4 of 21), *S.* Montevideo (2 of 536), 13,23:i:- (2 of 420) and *S.* Mbandaka (1 of 279).

Forty-two (0.8%) of the isolates tested in 2023 were resistant to ciprofloxacin, an increase from 2022 (0.6% of 5562 isolates). Ciprofloxacin resistance was observed in 25 isolates from feed (14 *S.* Infantis, 8 *S.* Newport, 2 *S.* Typhimurium, one *S.* Litchfield), 8 from dogs (3 *S.* Kentucky, 2 *S.* Infantis, one *S.* Newport, one *S.* Saintpaul, and one 57:z4,z23:-), 5 from chickens (5 *S.* Agona, one *S.* 13,23:i:-), one *S.* Typhimurium from a pig, one isolate of *S.* Infantis from a cat, one *S.* Typhimurium from a partridge, and one *S.* Idikan from an environmental sample (chick environment).

Resistance to cefotaxime and ceftazidime remained stable in 2023 (0.1%) and it was detected in 7 dog isolates (3 *S*. Kentucky, one *S*. Derby, one *S*. Livingstone, one *S.*

Enteritidis, one *S*. Saintpaul) and in one *S*. Typhimurium isolate from feed. All isolates were MDR, with 5 showing a resistance pattern that involved 10 or more antimicrobials, including the *S.* Kentucky isolates (all 3 showing the same resistance pattern), the *S.* Saintpaul isolate and the *S*. Typhimurium 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 older methods of *Salmonella* typing for human isolates and is also being increasingly used to characterise and compare isolates from animals and humans*.* Ongoing liaison takes place between the Agencies concerned in relation to the strains detected and their resistance.

Regarding the antimicrobials referred to in this report, resistance to third generation cephalosporins and fluoroquinolones is considered of most importance, since these antimicrobials are particularly relevant for the treatment of human salmonellosis, when this is required. Most cases of non-typhoidal *Salmonella* infection in humans are non-invasive, limited to the gastro-intestinal tract and may not require treatment with antimicrobials. The percentage of *Salmonella* isolates that were resistant to ciprofloxacin in 2023 was 0.8%, including 4 *S*. Typhimurium from a pig, a partridge and 2 feed samples. One of the ciprofloxacin-resistant *S*. Typhimurium from feed, originated from raw pet food and had a MDR pattern involving also apramycin, nalidixic acid, cefotaxime, ceftazidime and other 8 antimicrobials. Resistance to third generation cephalosporins (cefotaxime and ceftazidime) was 0.1% (8 isolates) in 2023, with 7 isolates (including one *S.* Enteritidis) from a dog, as well as the above-mentioned *S*. Typhimurium isolate from feed.

Resistance to third generation cephalosporins was not detected in *S.* Infantis isolates (n= 349) in 2023. Of the 49 antimicrobial resistant isolates detected in 2023 (14% of the total), 40 were MDR. Seventeen isolates tested resistant to both nalidixic acid and ciprofloxacin, 14 originating from feed, 2 from dogs and one from a cat. In chickens (n=60), 8 out of the ten antimicrobial resistant *S.* Infantis isolates detected in 2023 were resistant to nalidixic acid.

Generally, several MDR strains, some including resistance to critically important antimicrobials, were detected in dogs, cats and raw pet food in 2023. This partly reflects the fact that *Salmonella* from dogs was made reportable in Great Britain in April 2021, and for this reason an increased number of *Salmonella* isolates from dogs were tested since 2021 when compared to previous years. These findings are however relevant for the potential of *Salmonella* transmission to people from pets and for the risk of spillover of these MDR *Salmonella* to UK livestock.

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.

Table 13.2: *Salmonella* Dublin in cattle: antimicrobial susceptibility monitoring 2014 to 2023

The table below shows the percentage of *S.* Dublin isolates from cattle resistant to each of the antimicrobials from 2014 to 2023. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
AM	0.7%	1.7%	0.4%	0.0%	0.0%	0.0%	1.2%	1.1%	0.0%	0.4%
C	0.0%	0.4%	0.4%	0.0%	0.3%	0.4%	2.3%	1.1%	0.4%	0.0%
NA	0.0%	2.2%	1.2%	0.0%	2.2%	0.0%	1.6%	0.7%	0.0%	0.4%
S	2.4%	0.4%	1.6%	0.0%	0.3%	0.4%	0.8%	0.7%	3.2%	1.9%
APR	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.4%
CN	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%
FR	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%	0.0%
SU	0.7%	0.0%	0.0%	0.0%	0.3%	0.4%	0.8%	0.4%	0.8%	0.0%
TM	0.7%	0.0%	0.0%	0.0%	0.0%	0.7%	0.8%	0.4%	0.4%	0.0%
T	1.1%	0.4%	0.4%	0.0%	0.3%	0.4%	3.9%	6.0%	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%
Total isolates tested	286	226	245	272	320	269	256	267	250	270

Table 13.3: Number of isolates of *S*. Typhimurium of the most frequent phage types subjected to susceptibility testing at APHA 2014 to 2023

Phage type	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
UNTY	0	0	0	0	43	19	0	3	0	2
RDNC	0	0	0	0	201	24	53	88	70	52
U310	18	0	0	0	0	0	0	0	0	1
U308	7	0	0	0	0	0	5	51	0	10
U308a	0	0	0	0	0	0	0	0	25	67
U302	13	27	13	9	39	18	0	6	0	0
U288	28	24	30	26	40	27	58	48	0	6
DT193	21	19	13	19	34	38	65	69	60	65
DT120	0	0	0	0	0	0	0	2	0	8
DT116	0	0	0	0	0	0	22	16	0	7
DT104	19	12	40	59	47	45	52	60	58	27
DT99	0	0	0	7	0	0	0	1	22	31
DT73	0	0	0	0	0	14	0	0	0	0
DT41	0	0	0	4	0	0	0	1	0	0
DT40	13	7	0	5	0	0	0	0	0	0
DT12	0	0	5	2	28	0	0	0	0	0
DT9	17	0	0	0	0	0	5	3	0	3
DT8	0	7	5	2	0	0	0	7	0	1
DT4	0	0	0	0	0	0	5	0	0	4
DT2	17	25	24	19	13	13	39	42	41	60
DT1	9	9	8	4	0	0	0	15	0	18
DT105	0	0	0	0	0	0	0	0	51	76
DT75	0	0	0	0	0	0	0	0	42	70
DT32	0	0	0	0	0	0	0	0	19	26
Total	162	130	138	156	445	198	304	412	388	534

Table 13.4: *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2014 to 2023

The table below shows the percentage of *S.* Typhimurium isolates that were resistant to each of the antimicrobials over the last 10 years. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
AM	43.3%	46.7%	60.2%	58.3%	30.1%	46.1%	50.0%	43.0%	39.7%	36.6%
C	36.6%	46.0%	57.8%	53.5%	29.9%	44.1%	45.2%	37.0%	32.4%	31.2%
NA	0.9%	1.2%	0.0%	1.6%	0.4%	0.0%	3.0%	8.8%	4.4%	2.9%
S	39.7%	51.5%	63.9%	57.1%	40.7%	40.2%	49.7%	34.3%	37.2%	31.4%
APR	0.9%	0.0%	2.4%	0.0%	1.8%	0.8%	0.9%	1.5%	4.4%	6.8%
N	0.0%	2.4%	0.6%	0.0%	1.8%	0.8%	7.8%	9.9%	7.3%	12.5%
FR	0.0%	0.0%	0.6%	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%
TM	35.7%	32.1%	28.9%	19.8%	15.7%	24.0%	33.7%	25.3%	22.9%	30.5%
T	49.1%	46.7%	61.4%	54.5%	36.3%	42.1%	50.6%	39.0%	36.4%	30.3%
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%
Total isolates tested	224	165	166	187	504	254	340	467	494	558

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

- 35 (18.3%) in 2012
- 47 (28.5%) in 2013
- 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)

Table 13.5: Nalidixic acid resistance in *Salmonella* Typhimurium DT104 from domestic livestock in 2013 to 2023.

The following table outlines the number of isolates tested in different species of livestock between 2013 and 2023 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)

Table 13.6: Sulphamethoxazole and trimethoprim combination resistance in *Salmonella* Typhimurium (all phage types) from domestic livestock in 2013 to 2023.

The following table outlines the number of *S.* Typhimurium isolates tested in different species of livestock between 2013 and 2023 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)

Table 13.7: Trends in sulphamethoxazole and trimethoprim combination resistance in certain types of *Salmonella* Typhimurium from pigs over the period 2013 to 2023.

The following table outlines the number *S.* Typhimurium DT193, DT208 and U288 isolates tested in different species of livestock between 2013 and 2023 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)

Figure 13.1: Percentage of the 8 most common definitive and undefined phage types of *Salmonella* Typhimurium susceptible to all 16 antimicrobial agents in 2023

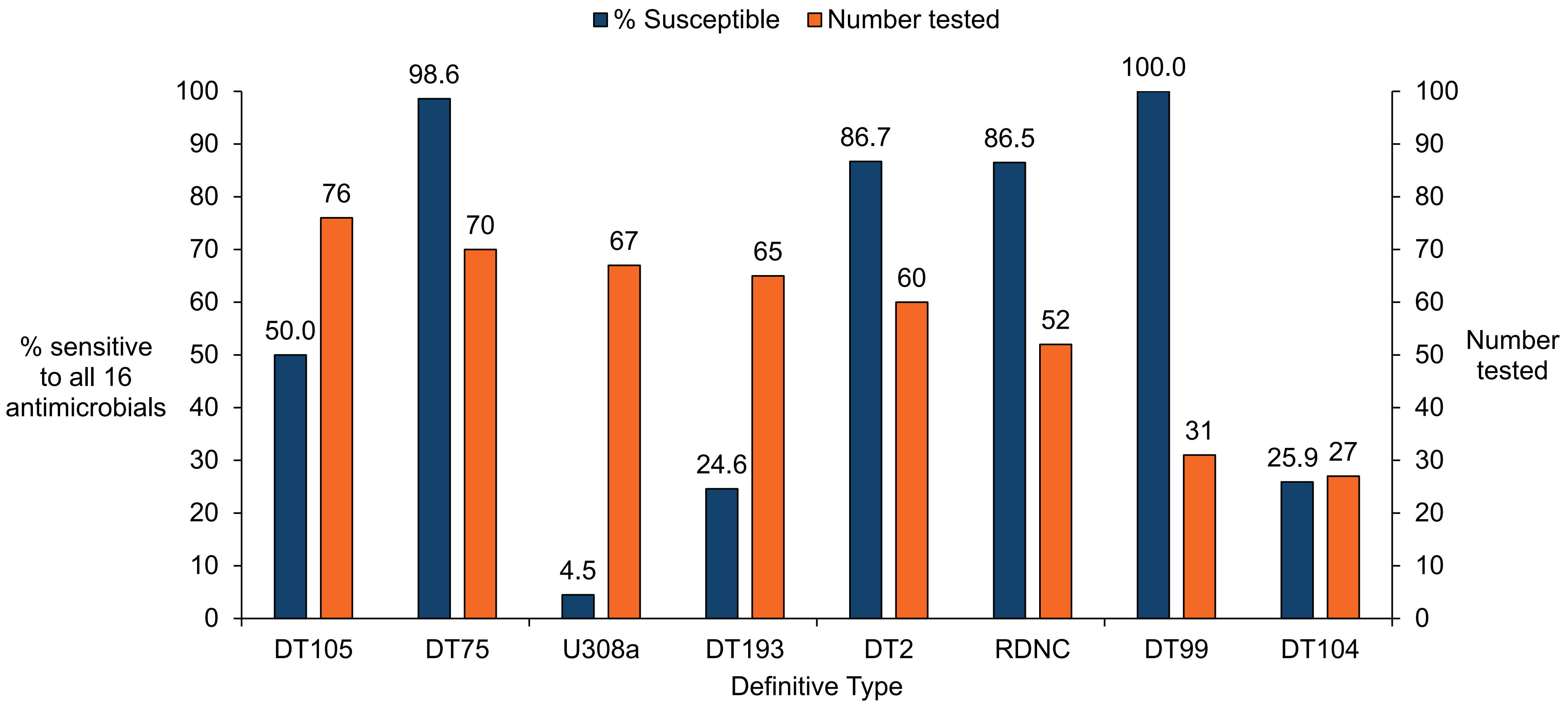


Figure 13.1 shows that the highest rates of isolates sensitive to all 16 antimicrobials were in found in DT99 (100.0%), DT75 (98.6%) and DT2 (86.7%). Only 4.5% if U308a isolates were fully susceptible.

Table 13.8: *Salmonella* other than *Salmonella* Dublin and *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2014 to 2023

The following table outlines the number *Salmonella* isolates other than *S.* Dublin and *S.* Typhimurium tested between 2014 and 2023 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	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
AM	12.7%	13.3%	11.1%	10.3%	7.7%	7.4%	10.3%	11.2%	9.8%	7.3%
C	1.8%	2.4%	2.6%	2.0%	1.5%	2.1%	2.4%	2.6%	1.9%	2.4%
NA	4.0%	5.5%	2.6%	5.8%	1.4%	2.7%	3.3%	5.5%	3.9%	3.4%
S	18.8%	22.6%	16.0%	13.1%	11.7%	15.0%	11.4%	13.4%	10.2%	9.8%
APR	1.6%	2.9%	2.0%	1.6%	0.8%	1.3%	1.2%	2.4%	1.2%	1.2%
N	2.0%	3.2%	2.2%	2.0%	1.8%	2.6%	3.0%	5.2%	2.3%	2.1%
FR	2.1%	1.9%	1.4%	1.6%	1.2%	1.6%	1.0%	2%	0.8%	1.0%
SU	20.9%	26.4%	23.7%	19.0%	15.7%	20.2%	19.8%	16.2%	13.3%	17.8%
TM	7.5%	10.4%	10.4%	6.2%	5.3%	10.2%	11.7%	6.4%	6.7%	10.9%
TM	20.0%	25.5%	22.9%	19.6%	14.9%	20.2%	19.3%	18.5%	11.8%	14.6%
Percentage susceptible to all 16 antimicrobials	68.2%	60.2%	68.9%	71.2%	77.7%	71.9%	69.5%	68.5%	77.2%	73.9%
No of isolates	1,837	2,198	1,986	5,652	3,589	4,010	3,617	3,665	4,735	4,638

Table 13.9: All *Salmonella*: antimicrobial susceptibility 2023 and resistances to individual antimicrobials

The tables below show the percentage of isolates resistant to each antimicrobial in 2022 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	4.5%	1.5%	75.3%	2.5%	21.1%	10.1%	11.5%	9.9%
AMC	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%
CAZ	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
CTX	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
C	1.7%	1.5%	60.4%	0.6%	0.0%	1.1%	7.4%	5.2%
NA	1.3%	0.0%	0.6%	1.1%	7.9%	0.0%	1.2%	3.2%
CIP	0.0%	0.0%	0.3%	0.3%	0.0%	0.0%	0.2%	0.8%
S	9.8%	3.0%	57.9%	5.6%	22.4%	1.1%	12.3%	11.5%
APR	0.2%	1.5%	21.6%	0.2%	0.0%	0.0%	2.6%	1.7%
CN	0.0%	1.5%	21.6%	0.4%	0.0%	0.0%	2.7%	1.9%
N	0.0%	0.0%	32.3%	1.2%	1.3%	0.0%	4.4%	3.0%
FR	0.0%	0.0%	0.0%	0.5%	0.0%	0.0%	0.3%	0.9%
SU	8.3%	1.5%	75.0%	13.6%	39.5%	3.4%	19.6%	19.0%
TM	0.4%	1.5%	64.0%	11.1%	15.8%	0.0%	14.8%	12.3%
T	7.2%	1.5%	57.6%	6.0%	44.7%	7.9%	12.8%	15.4%
Percentage susceptible to	89.4%	97.0%	19.2%	80.7%	30.3%	84.3%	74.5%	73.3%

Antimicrobial	Cattle	Sheep	Pigs	Chickens	Turkeys	Ducks	Total livestock	Total (livestock and non-livestock)
all 16 antimicrobials								
No of isolates	471	66	328	1,945	76	89	2,975	5,513

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	4.8%	9.8%	2.2%	5.3%	8.8%	3.9%	8.0%	9.9%
AMC	0.0%	0.5%	0.0%	0.0%	0.2%	0.0%	0.2%	0.1%
CAZ	0.0%	0.9%	0.0%	0.0%	0.1%	0.0%	0.3%	0.1%
CTX	0.0%	0.9%	0.0%	0.0%	0.1%	0.0%	0.3%	0.1%
C	1.6%	3.0%	2.2%	5.3%	2.0%	3.5%	2.5%	5.2%
NA	0.0%	3.4%	3.7%	2.6%	8.2%	1.8%	5.5%	3.2%
CIP	0.0%	1.1%	0.7%	2.6%	2.0%	0.4%	1.4%	0.8%
S	8.1%	9.8%	12.6%	13.2%	11.7%	7.7%	10.7%	11.5%
APR	0.0%	0.8%	0.0%	0.0%	0.4%	2.1%	0.7%	1.7%
CN	0.0%	1.3%	0.0%	0.0%	0.6%	1.8%	0.9%	1.9%
N	0.0%	2.4%	0.0%	0.0%	1.2%	1.1%	1.4%	3.0%
FR	0.0%	1.1%	2.2%	0.0%	2.0%	0.7%	1.5%	0.9%
SU	6.5%	9.9%	5.2%	0.0%	26.3%	17.2%	18.4%	19.0%
TM	0.0%	4.5%	0.0%	2.6%	13.2%	12.6%	9.4%	12.3%

Antimicrobial	Horses	Dogs	Other non-avian species	Other avian species	Feed	Environment	Total-non-livestock	Total (livestock and non-livestock)
T	6.5%	10.8%	9.6%	7.9%	25.5%	14.7%	18.3%	15.4%
Percentage susceptible to all 16 antimicrobials	91.9%	82.2%	80.0%	78.9%	62.3%	78.2%	72.0%	73.3%
No of isolates	62	757	135	38	1,261	285	2,538	5,513

Other non-avian species included Alpaca, badger, canine, cat, cheetah, deer, goat, hedgehog, leopard, lion, lizard, snake, squirrel, tortoise, turtle, wildcat, unspecified mammal and unspecified reptile/amphibian. Other avian species included Buzzard, gull, partridge, pheasant, pigeon, rhea, vulture and unspecified bird.

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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 3rd 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 3rd 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

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Source

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Title

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Additional report metadata elements and definitions

Coverage spatial

Salmonella reports made in Great Britain

Date. Issued

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Mandate authorising statutes

Data collected under:

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- CSPO 2007
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Rights. copyright

Crown copyright

Subject. Category

Zoonoses, Animal Health

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Surveillance of *Salmonella* in animals (FZ2000)

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Report

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Isolations were reported by Nominated Officers of the Animal and Plant Health Agency for England and Wales and Divisional Veterinary Managers for Scotland and, through them, by private laboratories.

Regional Veterinary Leads of the Animal and Plant Health Agency are responsible for the collection of samples of processed animal protein.

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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APHA is an Executive Agency of the Department for Environment, Food and Rural Affairs and was formed on 1 October 2014. Prior to this it was known as AHVLA.