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Agency

Salmonella in animals and feed in Great Britain

2022

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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.

Contents

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 2022 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 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 enforces Regulation (EC) No. 2160/2003 and Regulation (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

Salmonella isolated from animals and feed is biochemically or serologically confirmed and serotyped by micro, tube and, or slide agglutination tests. Each culture is 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, using conventional methods.

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 and people

This chapter provides information on *Salmonella* isolated from livestock from samples taken from all types of premises, including farms, hatcheries, veterinary practices and slaughterhouses. 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). There are a number of factors that influence the reporting of these data by clinical diagnostic laboratories. These are discussed in the Zoonoses Report UK 2017 (PHE 2018) and footnotes of Figure 1.1.

Figure 1.1 shows the most common *Salmonella* serovars isolated from livestock in Great Britain in 2022 alongside the most common serovars isolated from human cases of salmonellosis in Great Britain. Figures 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, serovars commonly associated with human cases are generally reported relatively less commonly from British livestock. However, *S*. Infantis which was the third most frequently reported serovar in humans in 2022 was the second most commonly reported from dogs in 2022.

In 2022, a total of 9,225 isolations of *Salmonella* from humans were reported to UK Health Security Agency (UKHSA), Public Health Wales and Public Health Scotland. This is a 64.0% increase in the total cases reported in 2021 (5,625 isolations) and 72.0% higher than in 2020 (5,362 isolations). 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. Data for 2020 and 2021 therefore cannot 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 2020, 2021 and 2022 data with previous years.

Figures showing the relative frequency of the most common *Salmonella* serovars in each animal species during 2022 (Figure 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 2022, the total number of *Salmonella* isolation reports from cattle, sheep, pigs and poultry increased by 22.9% compared with 2021 (3,461 isolations versus 2,809 isolations) and increased by 5.3% compared with 2020 (3,278 isolations) (Table 1.1). Compared to 2021 there was a decrease in isolations from cattle and sheep but this was offset by increases in isolations from pigs, chickens, turkeys and ducks. Trends were also variable across serovars, for example, reports of *S*. Mbandaka and *S*. Infantis were over double that of 2021, reports of *Salmonella* 13,23:i:- increased by 22.9% and reports of *S*. Enteritidis increased to 25 isolations from 11 in 2021. However, reports of *S*. Newport fell by 46.7% in 2022 compared to 2021. Reports of *S*. Typhimurium were similar to during 2021 (185 isolations versus 200 isolations) and 22.6% higher than during 2020 (159 isolations).

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 decreased by 3.4% in 2022 compared with 2021. This decrease was seen for cattle, sheep, pigs and goats with the greatest decrease being in cattle (15.8% decrease). The number of submissions increased for miscellaneous species (15.7% increase) and for poultry (10.3% increase). 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 4,529 isolations of *Salmonella* in livestock and dogs in 2022 which represents an increase of 21.1% compared with 2021 (3,740 isolations). This comprised 4,390 isolations from species covered by the statutory reporting requirements of the Zoonoses Order 1989 (2,404 isolations from chickens, 857 isolations from dogs, 430 isolations from cattle, 214 isolations from pigs, 188 isolations from turkeys, 121 isolations from ducks, 94 isolations from sheep, 60 isolations from horses, 17 isolations from pigeons, 2 isolations each from goats and rabbits and one isolation from a pheasant) plus 139 isolations from non-statutory species (for example, cats and reptiles, which are not reported in detail in this publication).

Relative to 2021, there were more isolations from chickens (2,404 versus 1,671 isolations), turkeys (188 versus 140 isolations) and ducks (121 versus 110 isolations). In contrast, there were fewer isolations from cattle (430 versus 521 isolations) sheep (94 versus 144 isolations) and pigs (214 versus 223 isolations).

The surveillance data for 2022 shows that 20.2% of the isolations of *Salmonella* reported to APHA resulted from samples taken due to clinical disease in livestock. This is lower than during both 2021 where 28.1% of isolations were from clinical disease investigations and 2020 when 23.1% 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 (92.9% and 88.8%, respectively) during 2022 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 2022, all of the *Salmonella* isolations from ducks resulted from voluntary surveillance.

Reports of *S*. Enteritidis increased by more than two-fold in 2022 compared with 2021 (25 versus 11 isolations), though decreased by 26.5% compared with 2020 (34 isolations). As in previous years, the majority of *S*. Enteritidis isolations in 2022 were reported from chickens (2 of 25 isolations), but there were also 2 isolations from sheep. This is similar to 2021 when most isolations of *S*. Enteritidis came from chickens (9 of 11), with one isolation each from cattle and ducks (Figure 1.4). As in most years since 2019, PT8 was the most common *S.* Enteritidis phage type isolated. The total number of *S*. Typhimurium isolations from cattle, sheep, pigs and poultry fell by 7.5% in 2022 (185 isolations) relative to 2021 (200 isolations). There was a decrease in the number of isolations from 3 sectors relative to the previous year. Isolations from sheep more than halved (8 versus 17 in 2021), isolations from cattle decreased by 10.8% (58 versus 65) and there was one isolation from turkeys compared with 3 in 2021 (Figure 1.5). However, isolations of *S*. Typhimurium in chickens were 20.0% higher in 2022 compared to 2021 (18 versus 15 isolations). Isolations of *S*. Typhimurium in pigs remained the same in 2022 as in 2021 (100 versus 100 isolations). There were no isolations of *S.* Typhimurium from ducks in 2022, as was the case in 2021. 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 DT105 in ruminants.

Total isolations of the monophasic strain *Salmonella* 4,5,12:i:- decreased by 4.2% in 2022 compared to 2021 (46 versus 48 isolations, Figure 1.6). Although, there was a marked increase in isolations of *Salmonella* 4,5,12:i:- in chickens in 2022 compared to 2021 (18 versus 8 isolations). Isolations of the monophasic strain *Salmonella* 4,12:i:- also decreased (by 36.5%, 33 versus 52 isolations) compared to 2021, with decreases in cattle, chickens and pigs (Figure 1.7).

Highlights

Cattle

Isolations of *Salmonella* from cattle in 2022 were 17.5% fewer than during 2021 (430 versus 521 isolations) and 10.3% higher than during 2020 (390 isolations).

As in previous years, *S*. Dublin remained the most common serovar in cattle (265 isolations, 61.6% of total cattle isolations). The number of isolations of *S*. Dublin decreased by 13.4%, compared with 2021 and increased by 17.8%, compared with 2020.

Salmonella Mbandaka was the second most commonly isolated serovar from cattle during 2022 (59 isolations, 13.7% of total cattle isolations) and *S*. Typhimurium was the third most commonly isolated (58 isolations, 13.5% of total cattle isolations). This is the same as 2021, 2020 and 2019 and similar to 2018 (Figure 2.2).

There were 58 isolations of *S.* Typhimurium from cattle in 2022, which is a decrease of 10.8% compared with 2021. The most common phage types of *S*. Typhimurium reported from cattle during 2022 were DT105 (22 isolations, 37.9% of isolations), DT75 (11 isolations, 19.0% of isolations) and DT104 and UNTY (both 6 isolations, 10.3% of isolations each).

There were 2 isolations of *Salmonella* 4,12:i:- (0.5% of total cattle isolations) during 2022 compared with 10 isolations during 2021, and one isolation of *Salmonella* Typhimurium 4,5,12:i:- (0.2% of total cattle isolations) compared with 5 isolations during 2021. This means that there were 3 isolations of the monophasic variants of *S*. Typhimurium during 2022 compared with 15 isolations during 2021. All 3 isolations in 2022 were phage type DT193.

There were no isolations of *S.* Enteritidis from cattle during 2022 compared with one isolation (NOPT) in 2021.

Small ruminants

Isolations of *Salmonella* from sheep in 2022 were 34.7% fewer than during 2021 (94 versus 144 isolations) and 22.1% higher than during 2020 (77 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, 69.1% of total sheep isolations).

Salmonella Typhimurium was the second most commonly isolated serovar from sheep in 2022 (8 isolations, 8.5% of total isolations), with around half the number of isolations recorded compared to 2021 (17 isolations, 11.8% of total sheep isolations). The phage types reported during 2022 were DT105 (2 isolations), DT75 (2 isolations) and one isolation each of DT104, U289, U308 and RDNC.

Salmonella Montevideo and *S*. Dublin were the next most commonly isolated serovars from sheep in 2022, both with 5 isolations (5.3% each of total isolations).

There were 2 isolations from goats in 2022 (both were *S. enterica* subspecies *diarizonae* 61:(k):1,5,(7)) compared to 2 isolations during 2021 (*S.* Dublin and *S. enterica* subspecies *diarizonae* 61:k:1,5) and no isolations during 2020.

Pigs

The number of *Salmonella* isolations from pigs in 2022 was similar to 2021 (214 isolations versus 223 isolations) and 13.2% higher than during 2020 (189 isolations) (Table 4.1).

Salmonella Typhimurium and its monophasic variants (*Salmonella* 4,[5],12:i:-) were together responsible for 70.6% of all isolations from pigs in 2022 (151 isolations). This is similar to previous years. However, for the third time since 2014 (and the third year in a row), the number of *S*. Typhimurium isolations (100 isolations) exceeded isolations of both monophasic variations combined (51 isolations).

The most common phage type of *S*. Typhimurium isolated from pigs in 2022 was DT193 (27 isolations, 27.0% of total *S*. Typhimurium isolations in pigs), followed by U308a (18 isolations). Most typable isolations of both monophasic variants of *S*. Typhimurium from pigs in 2022 were phage type DT193 (45 isolations) but there were also single isolations of DT120 and U311.

Deer, horses and rabbits

There were no isolations of *Salmonella* from deer during 2022, this was also the case during 2021 and 2020 (Table 5.1).

There were 2 isolations of *Salmonella* from rabbits 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 60 isolations of *Salmonella* from horses during 2022, 33.3% higher than during 2021 (45 isolations) and 46.3% higher than during 2020 (41 isolations) (Table 5.3).

Salmonella Typhimurium was the most common serovar isolated from horses in 2022 (18 isolations, 30.0% of total horse isolations). This is similar to the number of isolations in 2021 and 2020 (15 and 16 respectively). The most common phage types of *S*. Typhimurium in 2022 were DT105 and RDNC (3 isolations each, 16.7% of *S*. Typhimurium isolations each).

Salmonella Newport was the second most commonly reported serovar from horses during 2022 (6 isolations, 10.0% of total horse isolations), representing a large increase on 2021 (one isolation) but broadly similar to 2020 (7 isolations, 17.0% of total horse isolations).

There were 2 isolations of *Salmonella* 4,5,12:i:- in horses in 2022 (both DT104), compared with no isolations during 2021 and 3 isolations during 2020 (all DT193). There were no isolations of *Salmonella* 4,12:i:- from horses during 2022, which was also the case during 2021 and 2020.

Chickens

Including both NCP and non-statutory surveillance data, there were 2,404 isolations of *Salmonella* from chickens in 2022. This is an increase of 43.9% compared with 2021 (1,671 isolations) and an increase of 8.2% compared with 2020 (2,221 isolations) (Table 6.1).

The most commonly reported serovars were:

- *S*. Mbandaka (695 isolations, 28.9% of total chicken isolations)
- *S*. Montevideo (460 isolations, 19.1% of total chicken isolations)
- *Salmonella* 13,23:i:- (343 isolations, 14.3% of total chicken isolations)
- *S*. Kedougou (277 isolations, 11.5% of total chicken isolations)
- *S*. Agona (128 isolations, 5.3% of total chicken isolations)

There were 23 isolations of *S*. Enteritidis in 2022 compared with 9 isolations during 2021 and 31 isolations during 2020. The most commonly reported phage type in 2022 was PT8 (19 isolations).

There were 18 isolations of *S*. Typhimurium compared with 15 isolations in 2021. The most commonly reported phage types were DT75 (8 isolations) and RDNC (7 isolations). There also were 19 isolations of monophasic strains of *S*. Typhimurium, including 18 isolations of *Salmonella* 4,5,12:i:- (all DT193) and one isolation of *Salmonella* 4,12:i:- (DT120). This compares with 8 isolations and 4 isolations, respectively, of each monophasic variant during 2021.

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 (0.26% for breeders, 0.27% for layers and 0.03% for broilers).

Turkeys

Including both NCP and non-statutory surveillance data, there were 188 isolations of *Salmonella* from turkeys in 2022. This is an increase of 34.3% compared with 2021 (140 isolations) and a small decrease of 4.1% compared within 2020 (196 isolations) (Table 7.1).

During 2022 the most common serovar isolated from turkeys was *S.* Anatum (66 isolations, 35.1% of total turkey isolations), the second most common serovar was *S.* Kedougou (30 isolations, 16.0% of total turkey isolations) and the third most common was *S.* Senftenberg (26 isolations, 13.8% of total turkey isolations).

Salmonella Derby, which was the second most commonly reported serovar from turkeys in 2021, was only the fourth most common in 2022 (12 isolations, 6.4% of total turkey isolations).

There was one isolation of *S*. Typhimurium during 2022 (DT99), compared within 3 isolations during 2021 (all U203) and two isolations during 2020 (one isolation of RDNC and one of DT9). There were also 2 isolations of *Salmonella* 4,12:i:- and 2 isolations of *Salmonella* 4,5,12:i:- during 2022, compared with one isolation of *Salmonella* 4,12:i:- and 8 isolations of *Salmonella* 4,5,12:i:- 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 0.10% for turkey fatteners and 0.00% for turkey breeders. This is well below the EU target of 1% for each of these turkey production sectors.

Ducks and geese

There were 121 isolations of *Salmonella* from ducks in 2022. This is a 10.0% increase compared with 2021 (110 isolations) and 41.3% decrease compared within 2020 (206 isolations) (Table 8.1).

The most commonly isolated serovars from ducks in 2022 were *S.* Indiana (38 isolations, 31.4% of total duck isolations), *S.* Hadar (17 isolations, 14.0% of total duck isolations), *S.* Bovismorbificans, *S*. Give var. 15^+ and *S.* Orion var. 15^+ (each with 15 isolations, 12.4% 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 decline in isolations of *S*. Hadar has not continued in 2022 given that there were 17 isolations.

There were no isolations of *S*. Typhimurium from ducks in 2022. This was also the case during 2021 when for the first time *S*. Typhimurium was not recorded from ducks in Great Britain since 2001. There were no isolations of *S*. Enteritidis from ducks in 2022 compared with one isolation during 2021 (PT9b) and one isolation during 2020 (also PT9b).

There were no isolations of *Salmonella* from geese in 2022, compared with no isolations in 2021 and 2 isolations during 2020 (one isolation each of *S.* Beaudesert and *S*. Typhimurium DT193).

Other statutory birds (as specified in the Zoonoses Order)

There was one isolation of *Salmonella* from game birds in 2022, which is 85.7% fewer than during 2021 (7 isolations) and a 90.9% decrease compared within 2020 (11 isolations). The isolation in 2022 was *S*. Dublin from a pheasant. Game birds include guinea fowl, partridges, pheasants and quail.

Compared with 2021 there was a decrease in the number of isolations from pheasants (1 versus 7 isolations), but the same number of isolations were reported from partridges, quail and guinea fowl (no isolations in either year from any of the species).

There were 17 *Salmonella* isolations from pigeons in 2022, which is over double the number of reports in 2021 (8 isolations) and the same as in 2020 (17 isolations) (Table 9.4). All of the isolations were *S*. Typhimurium (13 isolations of DT2 and 4 of DT99).

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. Reports of *Salmonella* in dogs are therefore included in this publication for only the second time (Chapter 10). Due to this change in legislation, comparison of the data for 2021 and 2022 with previous years is not possible.

There were 857 isolations of *Salmonella* from dogs in 2022, the majority of which (94.2%) were from reports of clinical disease. This is an increase of 17.2% compared to 2021 (731 isolations).

The most common serovars reported were *S*. Typhimurium (116 isolations, 13.5% of total isolations from dogs), *S.* Infantis (109 isolations, 12.7% of isolations from dogs) and *S.* Dublin and *S*. Derby (each with 55 isolations, 8.3% each of total isolations from dogs).

The most common phage types of *S*. Typhimurium from dogs during 2022 were DT104 and RDNC (each with 26 isolations, 22.4% each of isolations), DT193 (15 isolations, 12.9% of isolations) and DT105 (11 isolations, 9.5% of isolations). There were also 41 isolations of *Salmonella* 4,5,12:i:- (80.5% of which were DT193) and 23 isolations of *Salmonella* 4,12:i:- (73.9% of which were DT193).

There were 15 isolations of *S*. Enteritidis from dogs during 2022. The most common phage types were PT8 (6 isolations, 40.0% of isolations) and PT9a (2 isolations, 13.3% of total isolations).

Wildlife

There were 2 isolations of *Salmonella* from wildlife during 2022, one isolation of *S.* Enteritidis (PT11) from a hedgehog and one isolation of *Salmonella* 4,12:-:- from a harbour porpoise. This is lower than in 2021 when there were 19 isolations of *Salmonella* from wildlife but the same as in 2020 (2 isolations).

Feedingstuffs

There were 801 isolations of *Salmonella* from feedingstuffs during 2022, including 110 isolations from compound feeds (Tables 12.3 to 12.6) and 691 from feed ingredients or products associated with testing under Animal By-Products Regulations (ABPR). This is a decrease of 4.1% compared with 2021 (835 isolations) and an increase of 6.0% compared with 2020 (756 isolations).

There were 187 isolations of regulated *Salmonella* serovars from animal feedingstuffs and related products during 2022. Regulated serovars are key serovars of public health importance targeted by the NCPs. This is 50.8% higher than in 2021 (124 isolations) and 74.8% higher than in 2020 (107 isolations). There were 61 isolations of *S*. Infantis, 53 isolations of *S.* Typhimurium, 32 isolations of *Salmonella* 4,5,12:i:-, 31 isolations of *Salmonella* 4,12:i:-, 6 isolations of *S.* Enteritidis, 3 isolations of *S*. Virchow and one isolation of *S.* Hadar.

The most commonly reported serovars from animal feedingstuffs and compound feed during 2022 were *S*. Kedougou (68 isolations), *S.* Infantis (61 isolations) and *S*. Typhimurium (53 isolations).

There were 406 reports of *Salmonella* from raw meat pet food (Table 12.8b). This is higher than during 2021 (295 reports) and 2020 (273 reports). The most common serovars reported during 2022 were *S*. Indiana (49 isolations), *S*. Infantis (38 isolations) *S*. Typhimurium (38 isolations), *S*. Derby (26 isolations), and *Salmonella* 4,12:i:- (21 isolations). Overall there were 123 isolations of regulated serovars from raw meat pet food in 2022. This is an increase of 73.2% compared with 2021 (71 isolations) and almost double the number of isolations in 2020 (62 isolations).

The isolation rate of *Salmonella* from domestic processed animal protein in 2022 was 0.66%, which is lower than during 2021 when it was 2.34%.

No batches of imported processed animal protein were tested during 2022, which is the same as during 2021 and 2020.

Antimicrobial resistance

Of the 5,562 *Salmonella* isolates examined during 2022, 75.7% were susceptible to all 16 antimicrobial compounds tested against. This is similar to 2021, when 67.7% of isolates were susceptible to all 16 antimicrobials.

A total of 494 cultures of *S.* Typhimurium were examined in 2022, of which 47.8% were susceptible to all the antimicrobials tested against which is a decrease from the 2019 (49.2%), and 2018 figures (54.4%), but higher than the figures reported in 2020 (39.9%) and 2021 (44.3%).

A total of 250 cultures of *S*. Dublin from cattle were examined in 2022, of which 96.4% were susceptible to all the antimicrobials tested against. This is higher than in 2021 when 88.3% were susceptible to all antimicrobials tested against.

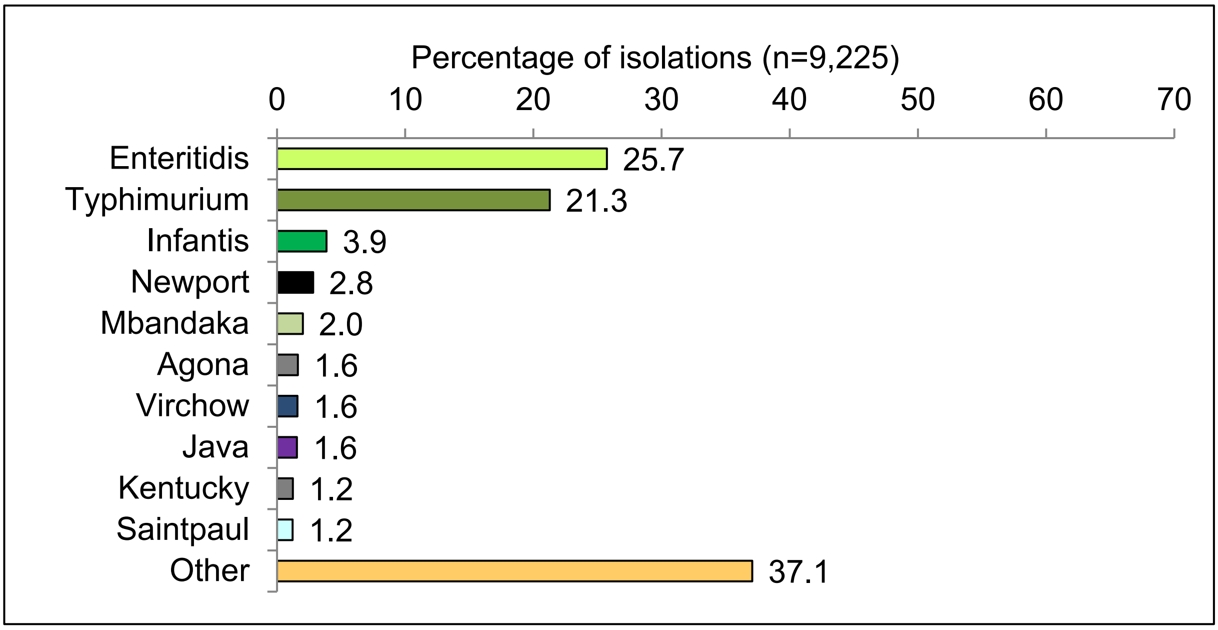
In total, 4,375 cultures of serovars other than *S*. Dublin or *S*. Typhimurium were tested in 2022 and 77.2% of these were sensitive to all the antimicrobials tested against. This is higher than in 2021 when 68.5% of cultures were fully sensitive.

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 2022 was 0.6%. Cefotaxime, ceftazidime or ciprofloxacin resistance was not detected in *S*. Enteritidis from animals in 2022. Cefotaxime and ceftazidime resistance was detected in 9 *Salmonella* isolates in 2022 (*S*. Infantis (4 isolations), *S.* Kentucky (2 isolations), *S.* Seftenberg (1 isolation) *S.* Bredeney (1 isolation) and *Salmonella* Minnesota (1 isolation)).

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 2022

Figure 1.1.1: Isolations from people

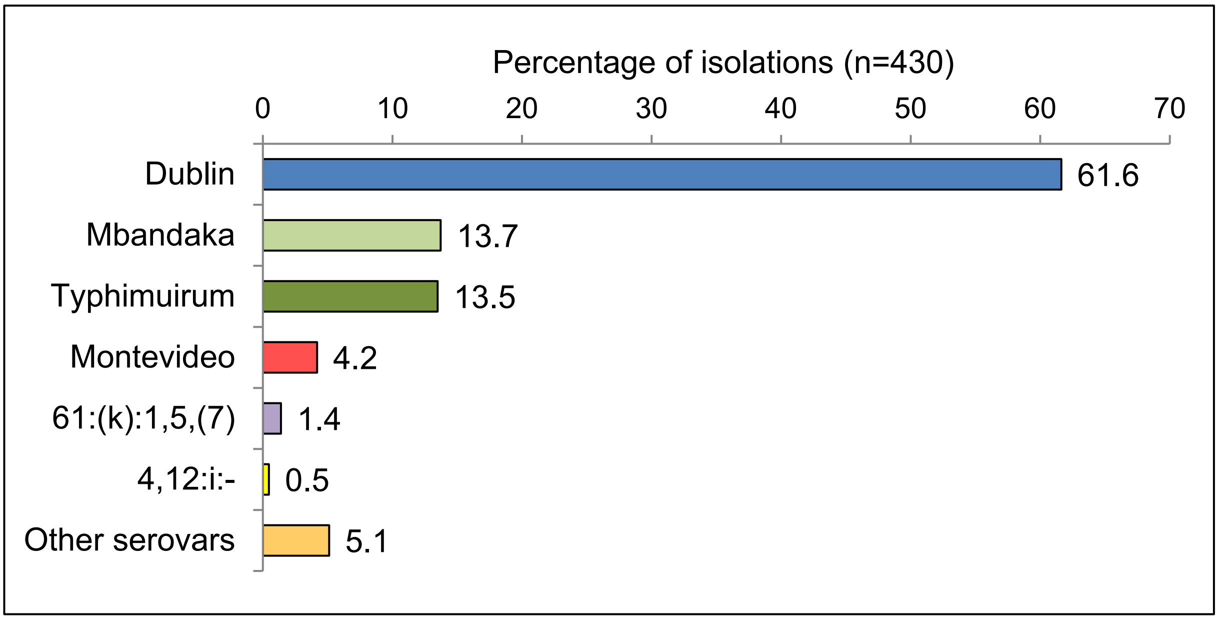


In 2022 the most common *Salmonella* serovar in people was *S.* Enteritidis, accounting for 25.7% of total isolations, followed by *S.* Typhimurium (21.3%), *S.* Infantis (3.9%) and *S.* Newport (2.8%).

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

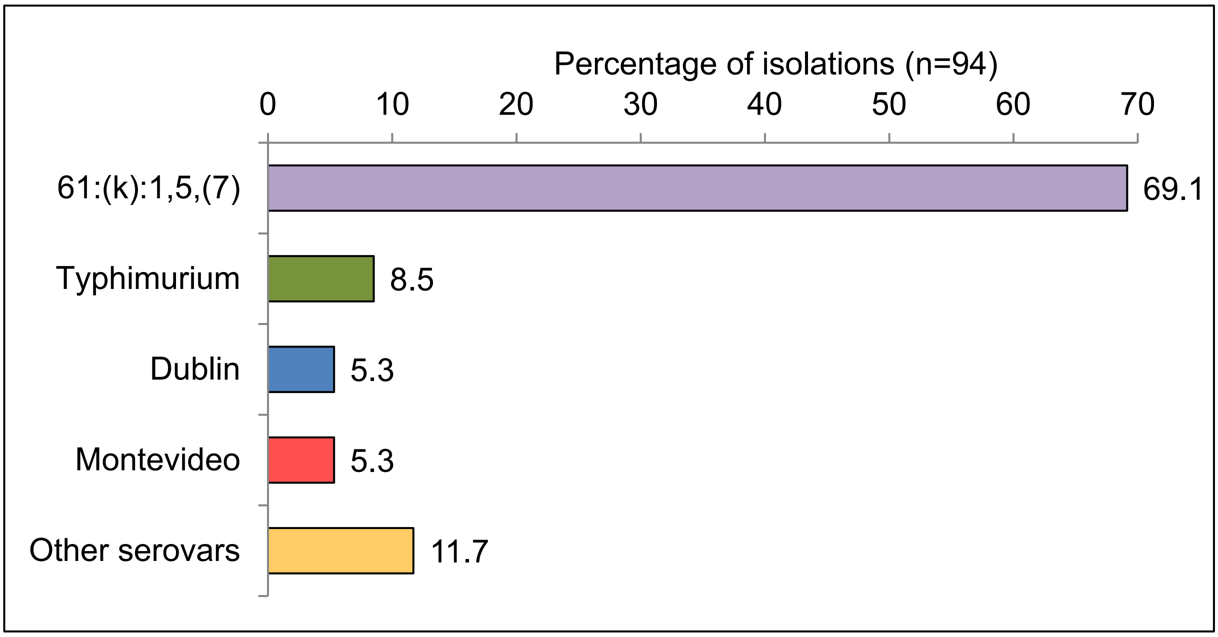
Data on human isolates was provided by UK Health Security Agency (UKHSA), Public Health Wales and Public Health Scotland. The UKHSA Second-Generation System (SGSS) is a live laboratory reporting system therefore numbers are subject to change and may not be directly comparable with data reported in previous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

Figure 1.1.2: Isolations from cattle



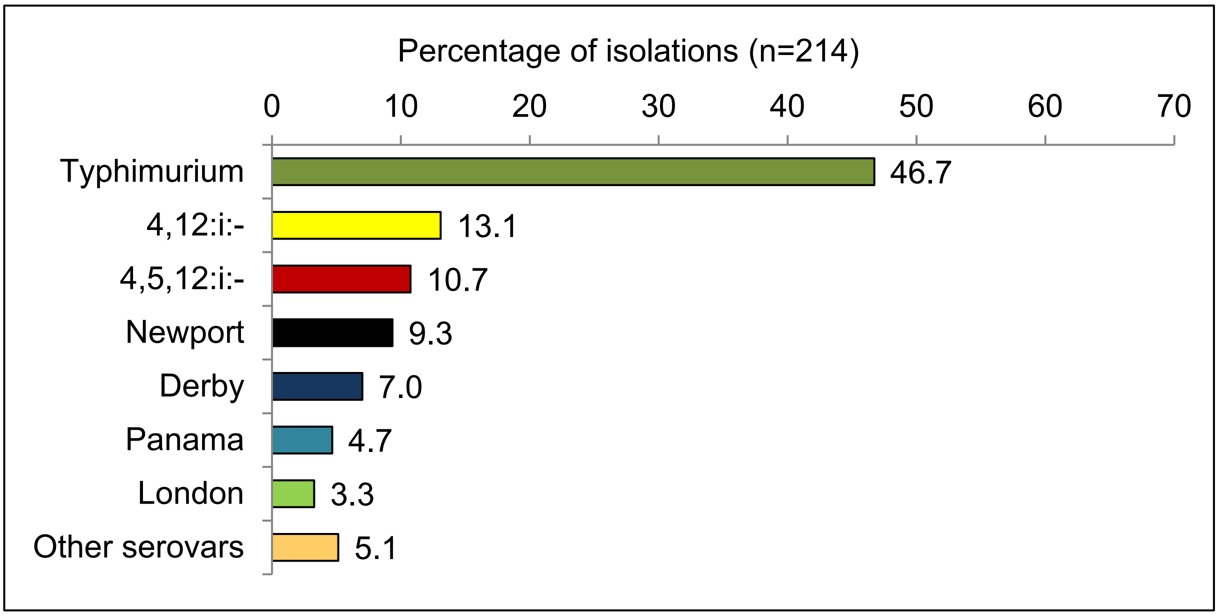
In 2022 the most common *Salmonella* serovar in cattle was *S.* Dublin (61.6% of total isolations), followed by *S.* Mbandaka (13.7%), *S.* Typhimurium (13.5%) and *S.* Montevideo (4.2%).

Figure 1.1.3: Isolations from sheep



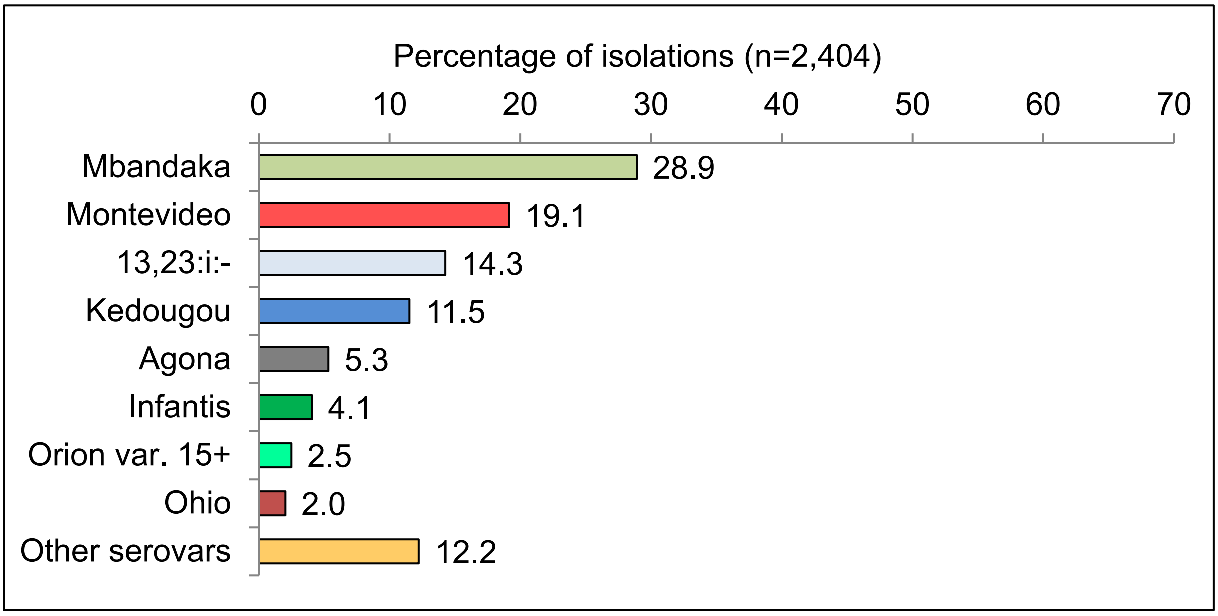
In 2022 the most common *Salmonella* serovar in sheep was *S.* 61:(k):1,5,(7) which includes enterica diarizonae and variants (69.1% of total isolations), followed by *S.* Typhimurium (8.5%) and *S.* Dublin and *S.* Montevideo (5.3% each).

Figure 1.1.4: Isolations from pigs



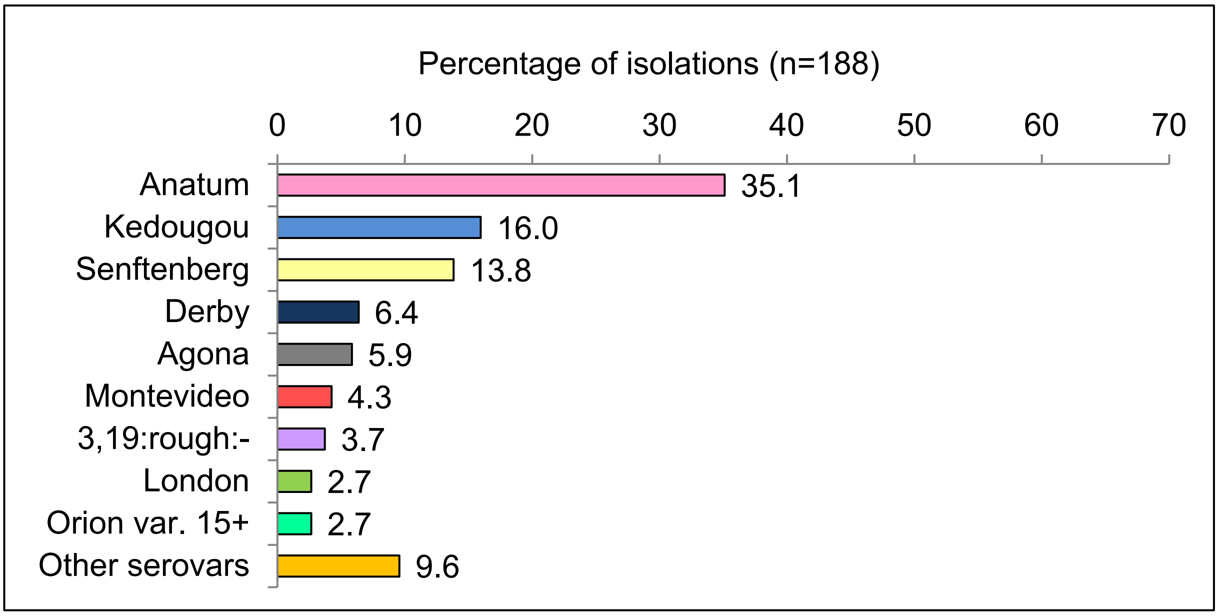
In 2022 the most common *Salmonella* serovar in pigs was *S.* Typhimurium (46.7% of total isolations), followed by *S.* 4,12:i:- (13.1%), *S.* 4,5,12:i:- (10.7%) and *S.* Newport (9.3%).

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



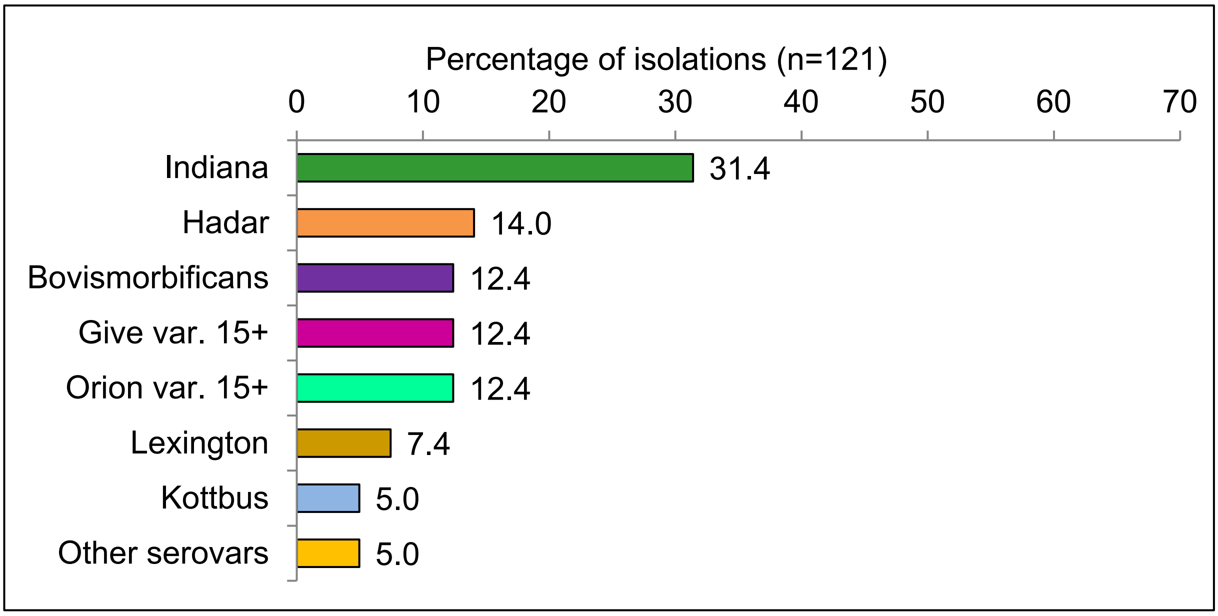
In 2022 the most common *Salmonella* serovar in chickens was *S.* Mbandaka (28.9% of total isolations), followed by *S.* Montevideo (19.1%), *S.* 13,23:i:- (14.3%) and *S.* Kedougou (11.5%).

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



In 2022 the most common *Salmonella* serovar in turkeys was *S.* Anatum (35.1% of total isolations), followed by *S.* Kedougou (16.0%), *S.* Senftenberg (13.8%) and *S.* Derby (6.4%).

Figure 1.1.7: Isolations from ducks



In 2022 the most common *Salmonella* serovar in ducks was *S.* Indiana (31.4% of total isolations), followed by *S.* Hadar (14.0%) and *S.* Bovismorbificans, *S.* Give var. 15^+ and *S.* Orion var. 15^+ (12.4% each).

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 2018 to 2022. Poultry includes chickens, turkeys and ducks.

The data includes statutory and non-statutory results.

***Salmonella* serovar**	**2018 isolations**	**2019 isolations**	**2020 isolations**	**2021 isolations**	**2022 isolations**
Africana	0	1	0	0	0
Agama	7	12	7	5	3
Agona	17	40	102	42	139
Ajiobo	0	0	0	2	0
Albany	0	2	0	0	0
Albert	2	0	0	0	0
Anatum	8	12	52	42	70
Bardo	1	1	14	10	5
Bareilly	0	0	0	1	0
Berta	0	1	1	0	2
Bovismorbificans	17	20	43	30	18
Braenderup	0	0	1	2	2
Brandenburg	0	0	0	0	1
Bredeney	0	0	3	1	0
Budapest	1	0	0	0	0
Chester	0	0	1	0	0
Coeln	4	2	3	1	4
Corvallis	0	0	0	0	3
Derby	441	183	39	49	40
Dublin	329	268	235	321	274
Eastbourne	0	4	0	0	0
Eboko	0	0	1	0	1
Enteritidis	30	50	34	11	25
Essen	0	0	0	1	0
Ferruch	0	0	0	2	0
Fresno	0	1	0	0	0
Gaminara	0	0	0	1	1
Give	64	11	9	6	3
Give var. 15^{+}	55	57	36	23	23
Glostrup	0	0	1	0	0
Goldcoast	0	0	0	1	0
Hadar	44	39	21	1	17
Havana	3	1	1	2	6
Idikan	13	17	9	5	45
Indiana	126	101	65	44	40
Infantis	2	2	1	42	98
Isangi	1	0	0	3	0

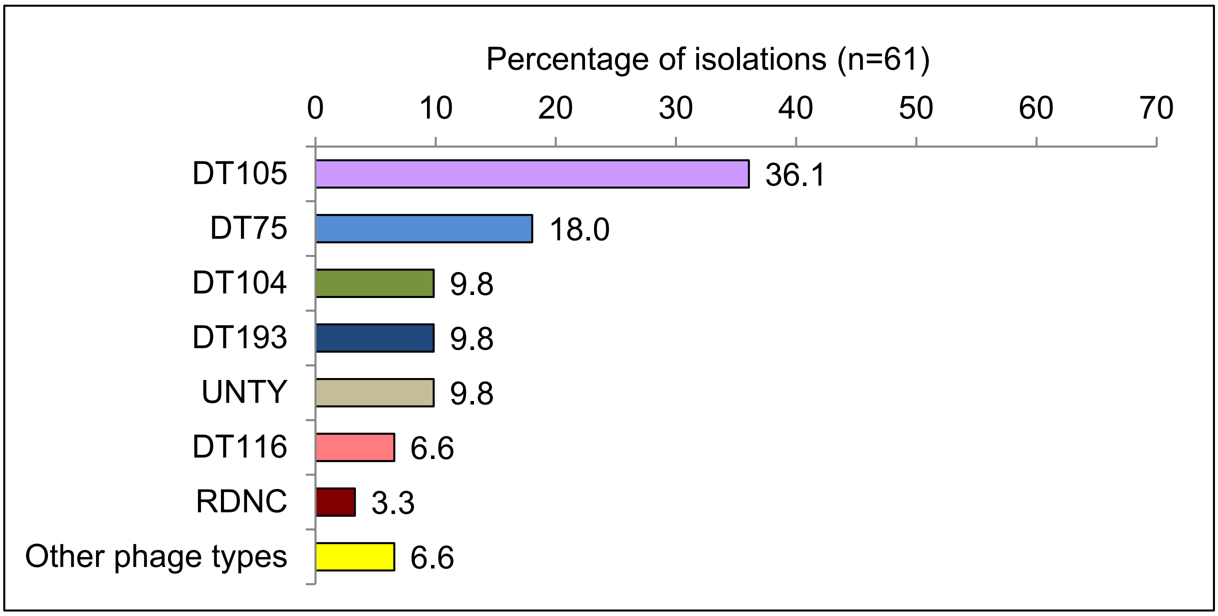
Salmonella serovar	2018 isolations	2019 isolations	2020 isolations	2021 isolations	2022 isolations
Istanbul	1	0	0	0	0
Kedougou	203	409	499	235	310
Kentucky	1	1	1	0	4
Kingston	2	4	3	1	3
Kottbus	31	22	13	15	7
Lagos	0	1	0	0	0
Lexington	6	2	7	10	9
Liverpool	0	0	2	0	1
Livingstone	12	11	13	18	3
London	0	3	6	12	14
London var 15^+	0	0	0	0	1
Mapo	1	0	0	0	0
Mbandaka	514	451	326	369	754
Menston	0	0	0	2	0
Minnesota	0	0	0	1	0
Mikiwasima	0	0	1	0	0
Mokola	1	0	0	0	0
Molade	0	0	0	1	0
Monschaui	4	4	2	0	0
Montevideo	143	203	270	454	491
Muenchen	0	1	8	4	9
Nchanga	1	0	0	0	0
Newport	24	23	66	62	33
Nima	0	1	0	0	0
Nottingham	9	13	0	7	4
Odozi	0	0	0	4	0
Offa	0	1	0	0	0
Ohio	94	76	34	55	50
Oranienburg	0	0	0	0	0
Orion	50	19	16	12	3
Orion var. 15^+	50	51	44	47	80
Oslo	6	15	6	3	0
Panama	3	1	2	5	13
Paratyphi B var. Java	0	0	2	0	0
Poona	2	0	1	0	0
Ramatgan	0	0	1	0	0
Reading	2	2	3	3	4
Rissen	7	1	0	0	1
Saintpaul	0	0	1	0	0
Schwarzengrund	0	0	1	0	0
Senftenberg	84	120	111	84	63
Soerenga	7	0	0	0	0
Stanley	1	1	0	0	1
Stanleyville	0	0	1	0	1
Stourbridge	1	0	1	3	1

Salmonella serovar	2018 isolations	2019 isolations	2020 isolations	2021 isolations	2022 isolations
Takoradi	0	0	0	0	1
Tennessee	0	2	1	0	1
Typhimurium	170	124	159	200	195
Uganda	0	2	0	0	0
Virchow	1	0	0	0	0
Wangata	2	0	0	0	0
4,5,12:i:-	55	43	56	48	46
4,12:i:-	55	58	39	52	33
13,23:i:-	681	436	716	279	343
61:k:1,5	5	5	11	40	4
61:k:1,5,7	9	10	4	2	17
61:-:1,5	10	11	18	32	0
61:-:1,5,7	37	37	17	0	50
untypable strains	70	52	100	68	59
rough strains	15	5	37	33	32
Total	**3,535**	**3,046**	**3,278**	**2,809**	**3,461**

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.

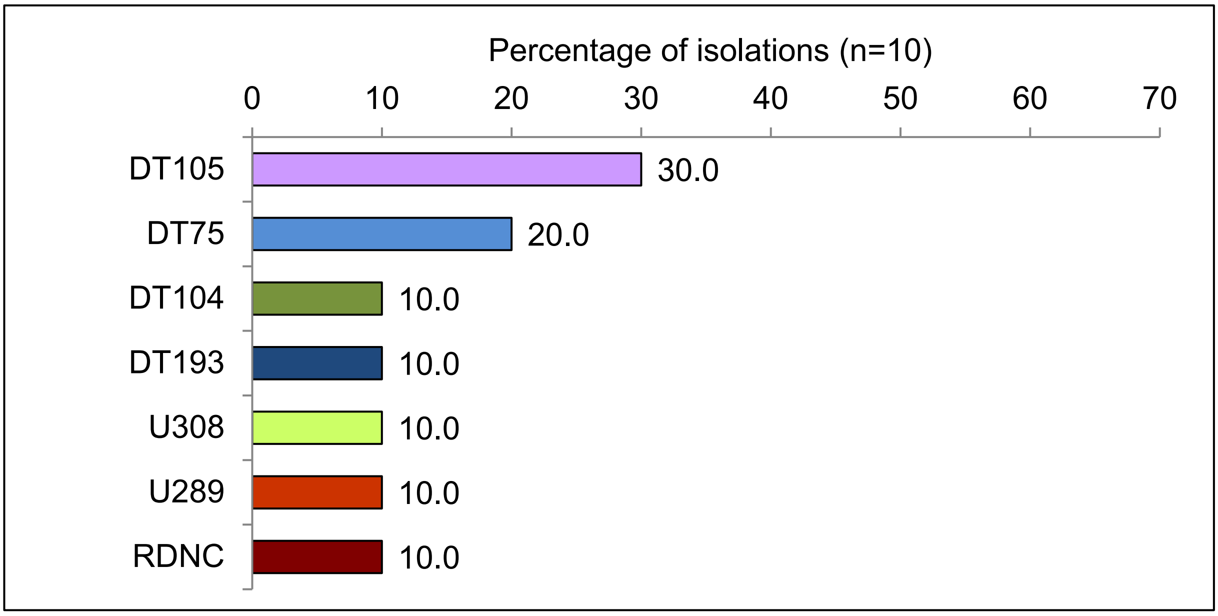
Figure 1.2: Isolations of the most common *S.* Typhimurium phage types (including monophasic strains) in livestock in 2022

Figure 1.2.1: Isolations from cattle



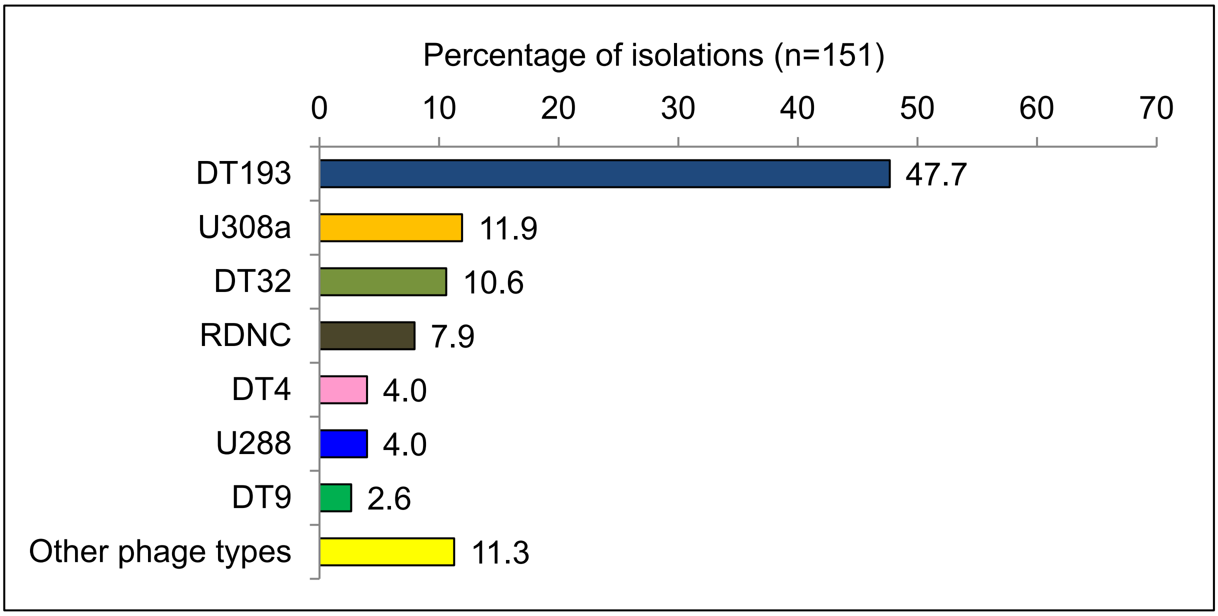
The most common *S.* Typhimurium phage type in cattle in 2022 was DT105 (36.1% of all cattle isolations), followed by DT75 (18.0%) and DT108, DT193 and UNTY (9.8% each).

Figure 1.2.2: Isolations from sheep



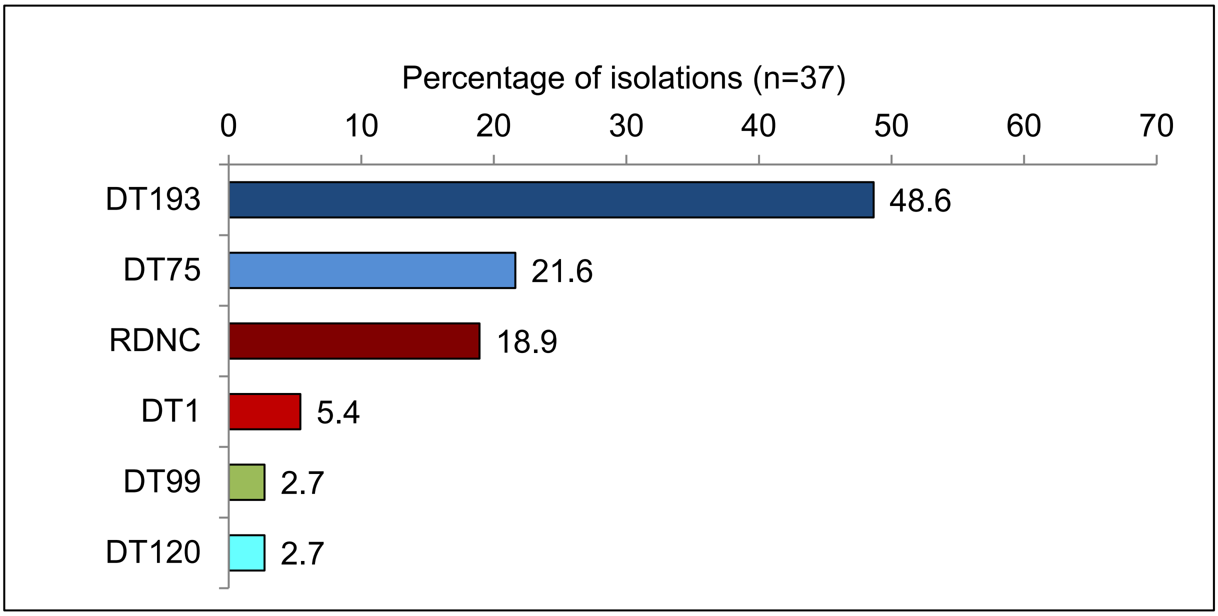
The most common *S.* Typhimurium phages type in sheep in 2022 was DT105 (30.0% of all sheep isolations), followed by DT75 (20.0%), DT104, DT193, U308, U289 and RDNC (10.0% each).

Figure 1.2.3: Isolations from pigs



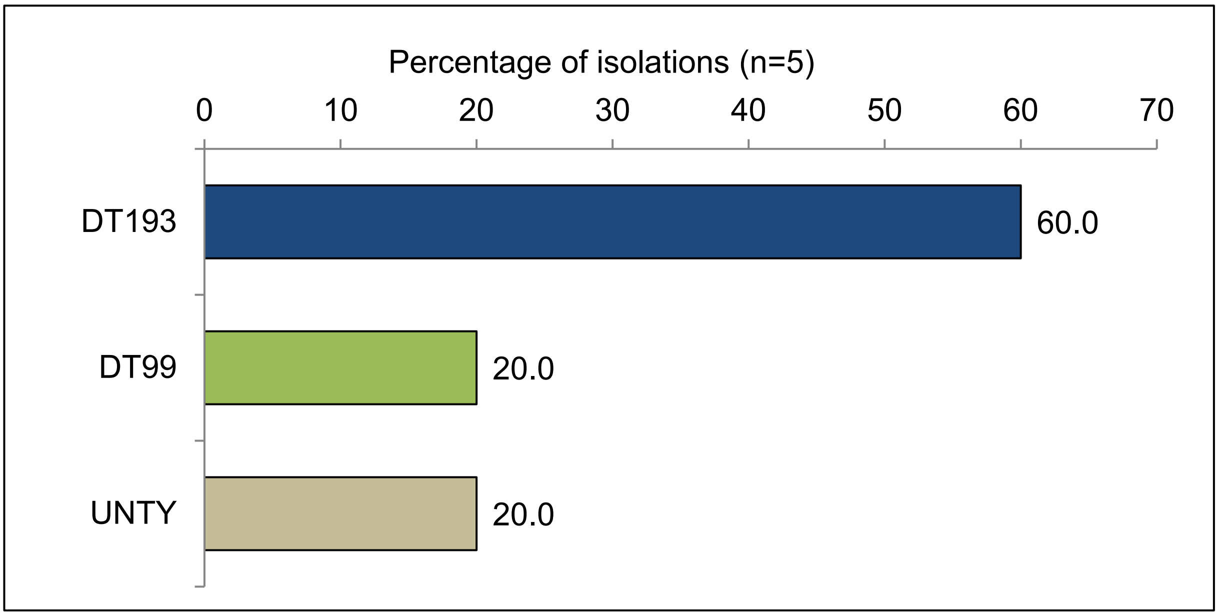
The most common *S.* Typhimurium phages type in pigs in 2022 was DT193 (47.7% of all pig isolations), followed by U308a (11.9%), DT32 (10.6%) and RDNC (7.9%).

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



The most common *S.* Typhimurium phages type in chickens in 2022 was DT193 (48.6% of all chicken isolations), followed by DT75 (21.6%), RDNC (18.9%) and DT1 (5.4%).

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

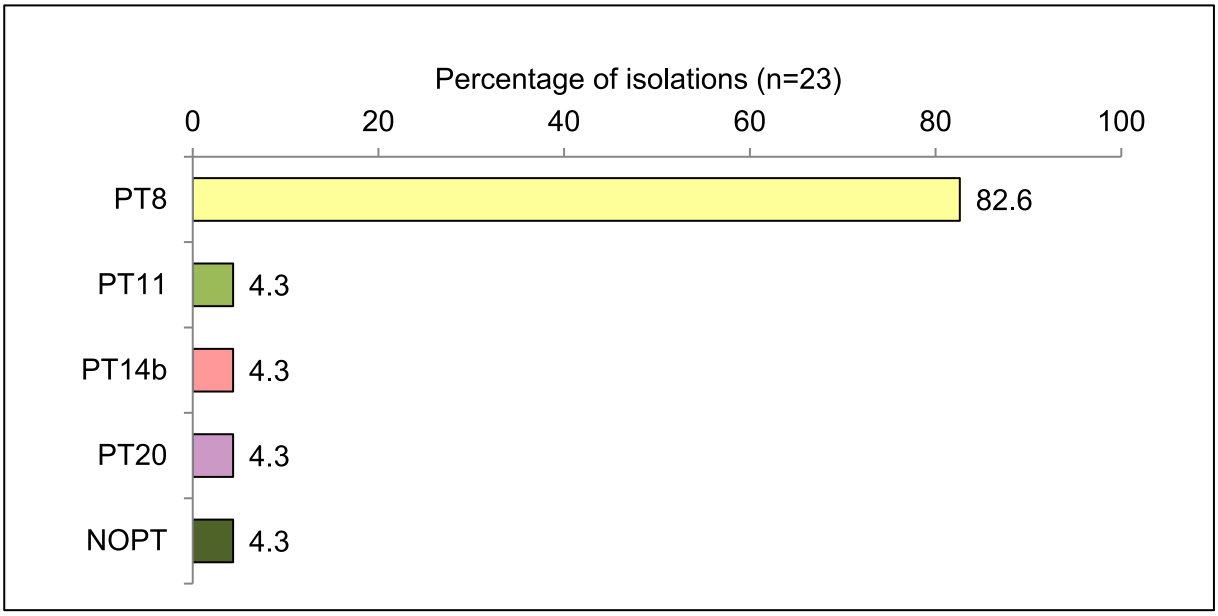


The most common *S.* Typhimurium phages type in turkeys in 2022 was DT193 (60.0% of all turkey isolations), followed by DT99 and UNTY (20.0% each).

There were no isolations of *S*. Typhimurium (including the monophasic forms) in ducks in 2022.

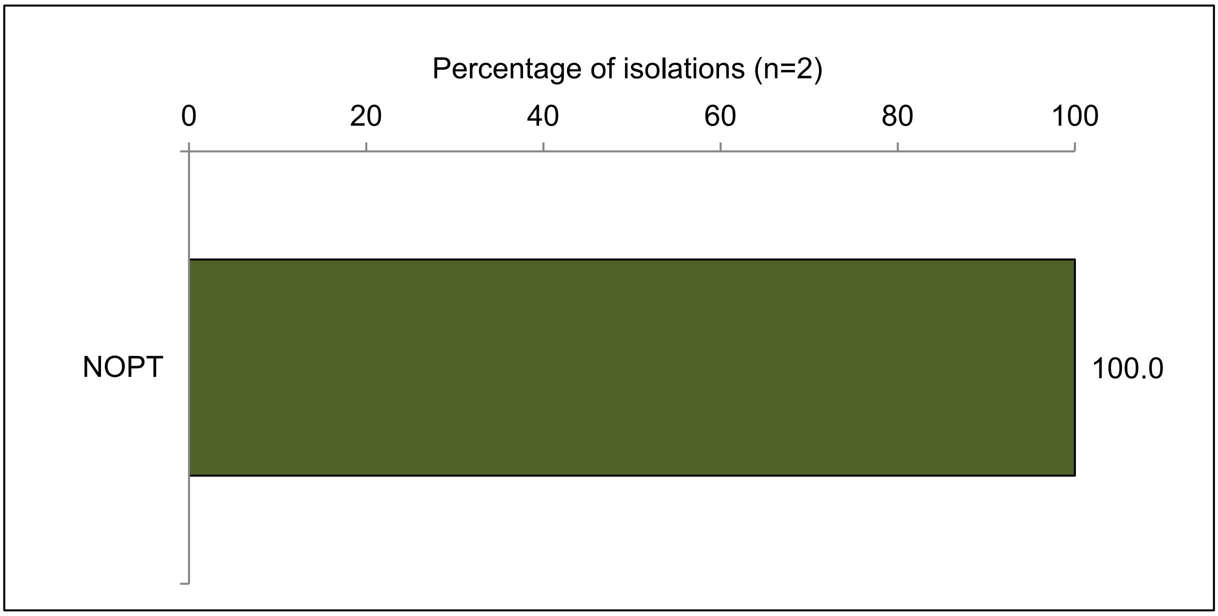
Figure 1.3: Isolations of the most common *S*. Enteritidis phage types in livestock in 2022

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



The most common *S*. Enteritidis phages type in chickens in 2022 was PT8 (82.6% of all chicken isolations), followed by PT11, PT14b, PT20 and NOPT (4.3% each).

Figure 1.3.2 Isolations from sheep



The most common *S*. Enteritidis phages type in sheep in 2022 was NOPT (100.0% of all sheep isolations).

There were no isolations of *S*. Enteritidis in cattle, ducks, pigs or turkeys in 2022.

Figure 1.4: Isolations of *S*. Enteritidis in livestock in Great Britain 2020 to 2022

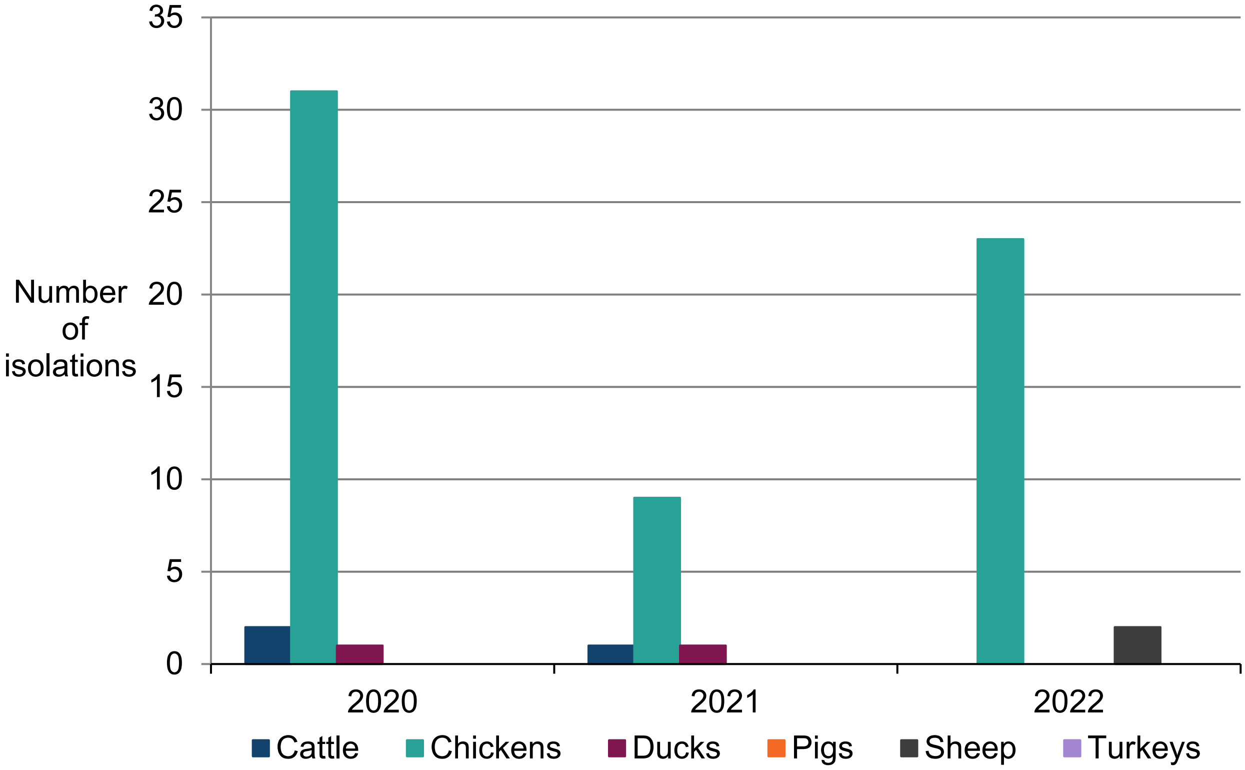


Figure 1.4 shows *Salmonella* Enteritidis was most commonly isolated from chickens during 2022, and in fewer numbers from sheep. This compares to chickens also being the most commonly isolated species in 2021 and 2020. *S*. Enteritidis was isolated from cattle and ducks in 2021 and 2020, though not in 2022. *S*. Enteritidis was not isolated in pigs or turkeys in 2020, 2021 or 2022.

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

Figure 1.5: Isolations of *S*. Typhimurium in livestock in Great Britain 2020 to 2022

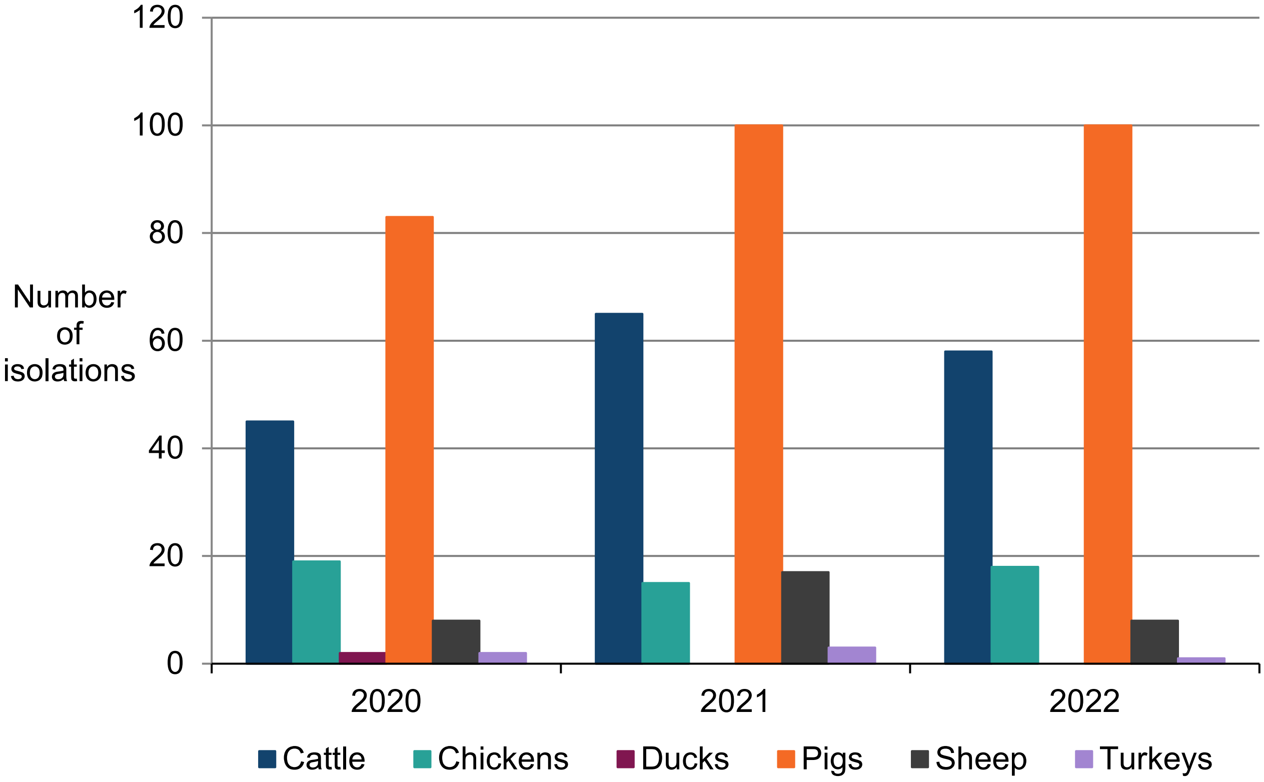


Figure 1.5 shows *Salmonella* Typhimurium was most commonly isolated from pigs amongst livestock species during 2022, and in lesser numbers from cattle, chickens, sheep and turkeys. This compares to pigs also being the most commonly isolated species in 2021 and 2020. *S*. Typhimurium was also isolated from cattle, chickens, sheep and turkeys in 2021 and 2020, and from ducks in 2020.

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

Figure 1.6: Isolations of *S*. 4,5,12:i:- in livestock in Great Britain 2020 to 2022

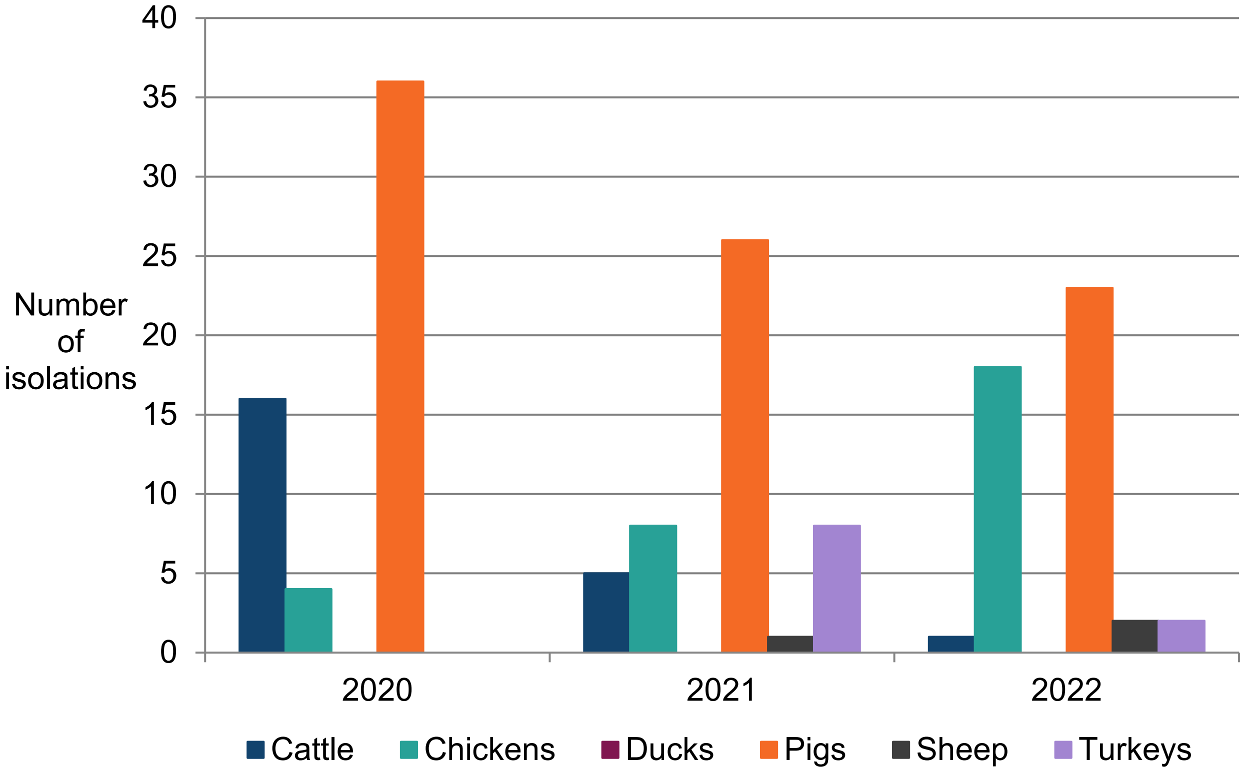


Figure 1.6 shows *Salmonella* 4,5,12:i:- was most commonly isolated from pigs amongst livestock species during 2022, and in lesser numbers from chickens, sheep, turkeys and cattle. This compares to pigs also being the most commonly isolated species in 2021 and 2020. *S*. 4,5,12:i:- was also isolated from chickens, turkeys, cattle and sheep in 2021 and from cattle and chickens in 2020.

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

Figure 1.7: Isolations of *S.* 4,12:i:- in livestock in Great Britain 2020 to 2022

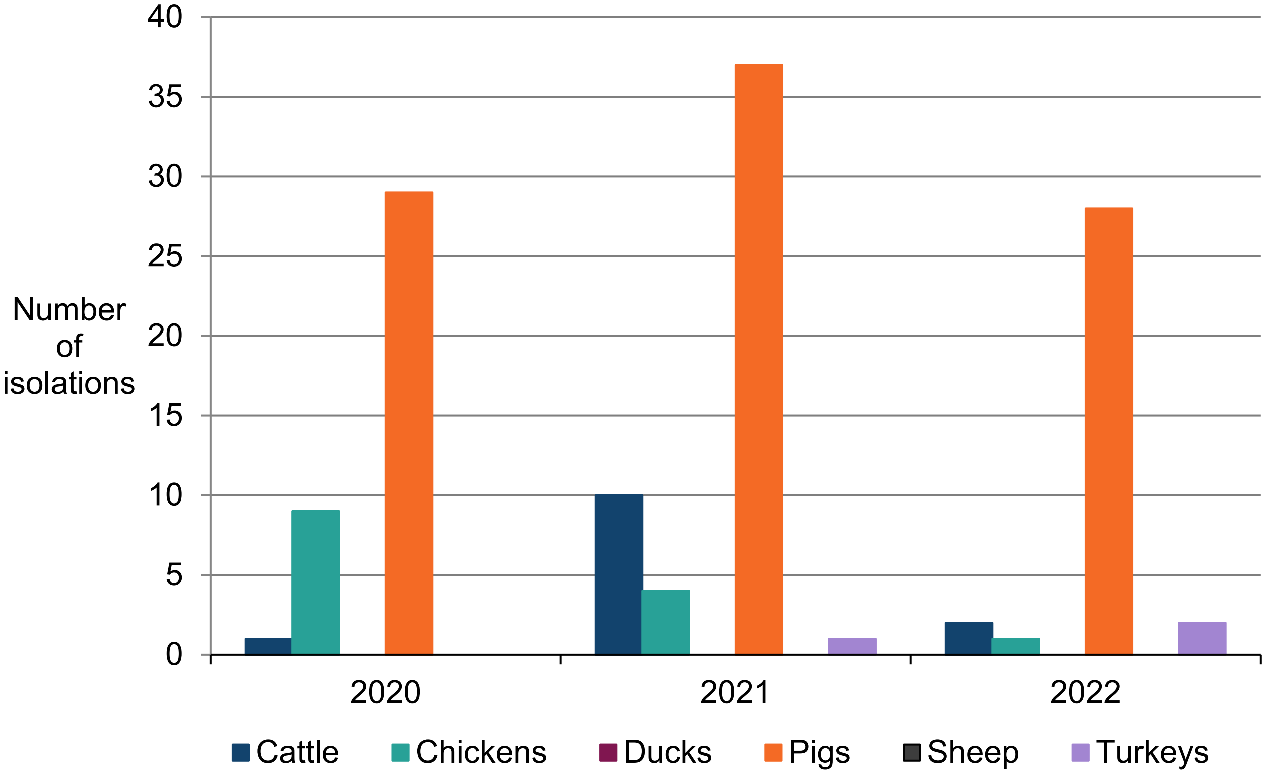


Figure 1.7 shows *Salmonella* 4,12:i:- was most commonly isolated from pigs amongst livestock species during 2022, and in lesser numbers from cattle, turkeys and chickens. This compares to pigs also being the most commonly isolated species in 2021 and 2020. *S.* 4,12:i:- was also isolated from cattle, chickens and turkeys in 2021 and from chickens and cattle in 2020.

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 7.9 million in June 2022 according to Defra figures, an increase of 3.4% compared to June 2021 and contrary to the gradual reduction seen in the cattle population since 2016 (Figure 2.1).

On the VIDA database there were 17,624 submissions recorded from cattle in 2022, which was a decrease of 14.3% when compared with 2021 (20,574). There is no active surveillance for Salmonellae in cattle, with nearly all isolations being made from diagnostic submissions (animals with clinical disease).

There were 430 *Salmonella* isolations from cattle in 2022, a 17.5% decrease from 2021 when there were 521 isolations but 10.3% higher than during 2020 (390 isolations). The 3 most commonly reported serovars were *S*. Dublin, *S*. Mbandaka and *S*. Typhimurium, which have been the most common serovars isolated from cattle every year since 2013. The number of *S.* Dublin isolations, the most commonly reported serovar in cattle, fell by 13.4% compared to 2021 from 306 to 265 isolations in 2022. However, as a proportion of total isolates from cattle, there was a rise from 58.7% (2021) to 61.6% (2022). Isolates of *S.* Mbandaka and *S.* Typhimurium also fell in 2022 (by 19.2% and 10.8% respectively) compared to 2021 (Table 2.1).

Salmonella Dublin

The most common serovar isolated from cattle in Great Britain was *Salmonella* Dublin for the 24th successive year. There were 265 isolations of *Salmonella* Dublin, representing 61.6% of the total 430 *Salmonella* isolates from cattle.

As in previous years, the number of isolations peaked in the autumn. In 2022 the highest numbers were recorded in October with September and November also recording high incidences compared to the rest of the year. The rising prices and costs faced by farming enterprises saw an extended grazing period with warmer weather likely to impact organism survivability. Alimentary tract disease was the most common presentation, with the majority of incidents arising from cases of enteritis. This was recorded in all ages of animals, compared with isolations from abortions, a diagnosis restricted to adult cattle.

Salmonella Mbandaka

The second most common serovar in cattle was *S.* Mbandaka (59 isolations, 13.7% of total cattle isolations), with the number of isolations falling by 19.2% compared with 2021 (59 versus 73). Overall, the proportion of *S.* Mbandaka isolates did not alter compared with 2021 figures, making up approximately 14% in both years.

Salmonella Typhimurium

The third most common serovar isolated from cattle submissions was *S.* Typhimurium, with the number of isolates falling by 10.8% in 2022 from 65 in 2021 to 58 isolates. But the proportion of *S.* Typhimurium as a proportion of the total isolates for cattle rose by 1.0% in 2022 (12.5% in 2021 to 13.5% in 2022).

There was a marked change in phage types identified in 2022 compared with previous years. There were 22 isolations of DT105 and 11 isolations of DT75. DT105 was identified for the first time in 2021 (1 isolation) and DT75 has not been identified previously in cattle in Great Britain. The number of RDNC phage isolates fell dramatically, from 11 in 2021 to 2 in 2022. Having been first recorded as a single incident in 2020, *S.* Typhimurium U308 was recovered in 11 incidents in 2021, with a total of 14 isolates. In 2022 there were no isolations of this phage type. There was one incident of *S.* Typhimurium U289 in 2022 which was last reported in Cattle in 2011. There were no isolations of *S.* Typhimurium UNTY in 2022, which is the same as in 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 organism.

There were 3 isolations of the monophasic variants of *S.* Typhimurium in cattle in 2022, 2 isolations of 4,12:i:- (0.5% of total cattle isolates) and one isolation of *Salmonella* Typhimurium 4,5,12:i:- (0.2% of total cattle isolations). This compares with 15 isolations of these serovars in 2021. All 3 isolations in 2022 were phage type DT193.

Other serovars

The number of *Salmonella* Montevideo isolates, the fourth most commonly isolated serovar in cattle in 2022, fell 21.7% from 23 isolates in 2021 to 18 in 2022 but this did not have a large impact on the overall proportion of this serovar among total cattle isolations (5.4% of total cattle isolations in 2021 versus 4.2% in 2022) (Table 2.1).

For the first time since 2016, there were no isolations of *S.* Enteritidis in cattle in 2022, compared to a single isolation in 2021 (NOPT). There was one isolation of *S.* Panama in 2022, the last isolation of this serovar in cattle was in 2013.

Reports of non-Great Britain origin

There was one report of *S*. Mbandaka (from a clinical disease investigation) in cattle imported from Germany and one report of *S*. Montevideo (also associated with clinical disease) in cattle imported from Luxembourg. 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 2022

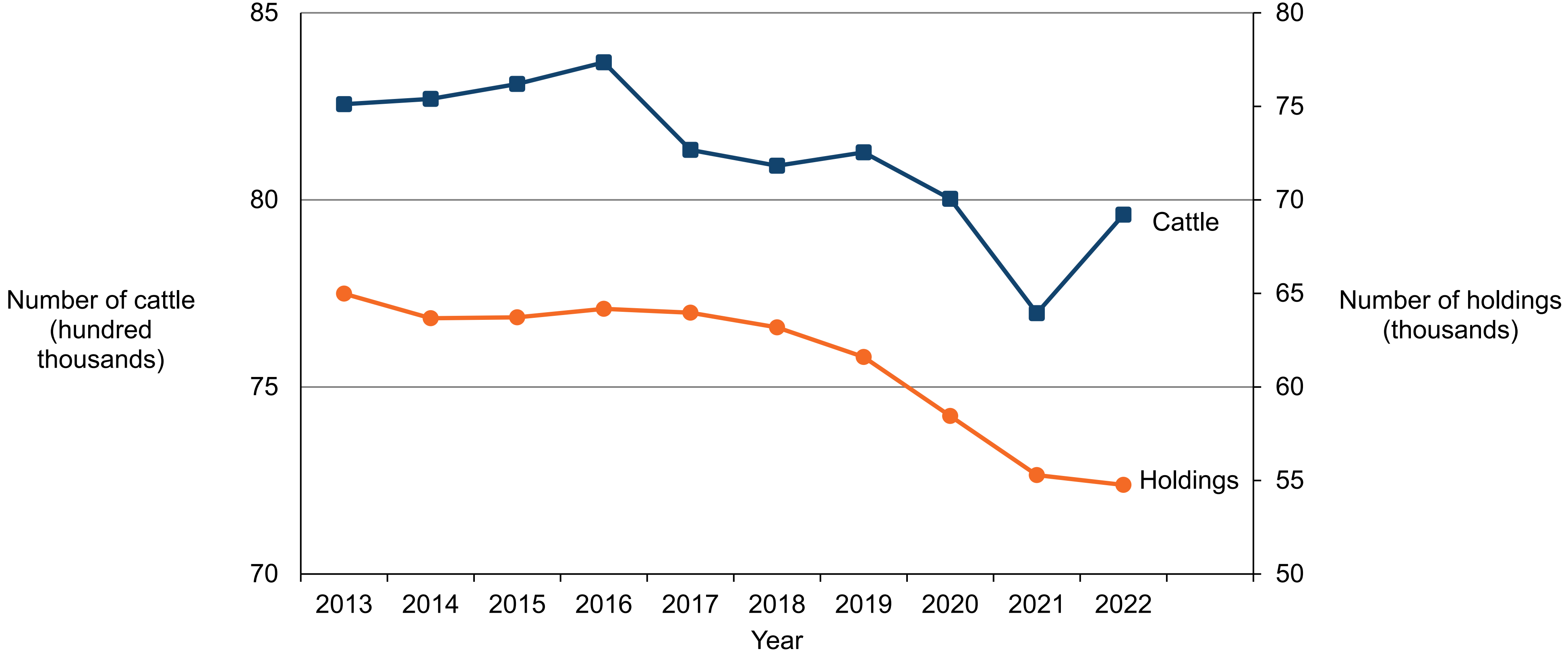


Figure 2.1 shows a steady decline in the number of cattle holdings since 2013 and while the number of cattle has also declined there was an upturn in 2022 to near the same level as in 2020.

Source: June 2021 and 2022 Agricultural Census.

Number of holdings in 2020 is estimated. Wales (holdings) and Scotland (animals and holdings) 2021 census data used for 2022.

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

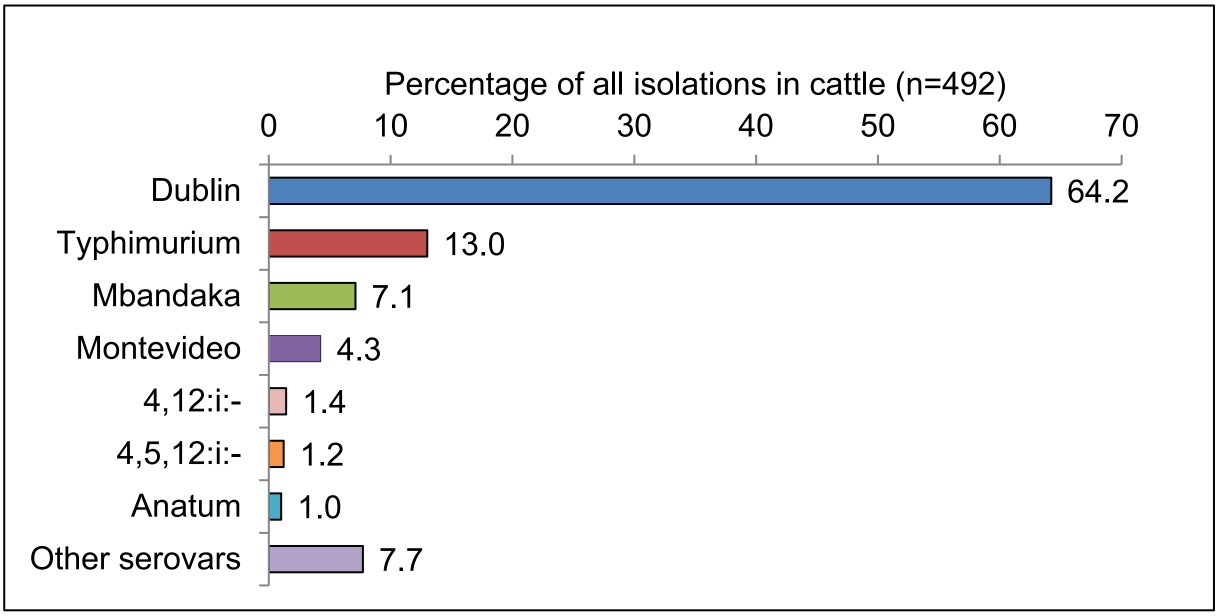
***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Agama	4	4	1	1	1	1	1	1	0	0
Ajiobo	0	0	0	0	0	0	0	0	0	0
Anatum	5	5	2	2	2	2	5	4	1	1
Bardo	0	0	1	1	0	0	0	0	0	0
Berta	0	0	1	1	0	0	0	0	0	0
Bovismorbificans	0	0	0	0	1	1	0	0	0	0
Bredeney	0	0	0	0	2	2	1	1	0	0
Chester	0	0	0	0	1	1	0	0	0	0
Coeln	4	3	0	0	0	0	1	1	0	0
Derby	0	0	0	0	1	1	0	0	0	0
Dublin	316	271	261	223	225	199	306	253	265	219
Durham	0	0	0	0	0	0	0	0	0	0
Eboko	0	0	0	0	1	1	0	0	0	0
Enteritidis	3	2	1	0	2	2	1	1	0	0
Gaminara	0	0	0	0	0	0	1	1	1	1
Glostrup	0	0	0	0	1	1	0	0	0	0
Indiana	0	0	0	0	1	1	0	0	1	1
Infantis	0	0	2	1	0	0	0	0	0	0
Kingston	0	0	2	1	0	0	1	1	0	0
Kottbus	1	1	3	3	2	2	6	6	0	0
Lagos	0	0	1	1	0	0	0	0	0	0
London	0	0	0	0	1	1	0	0	0	0
Mbandaka	35	28	78	59	63	56	73	64	59	54
Menston	0	0	0	0	0	0	2	2	0	0
Mokola	1	1	0	0	0	0	0	0	0	0
Montevideo	21	18	18	16	5	4	23	19	18	17

Salmonella serovar	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
Newport	4	4	6	6	2	2	2	2	0	0
Nottingham	0	0	3	2	0	0	0	0	0	0
Oslo	1	1	4	3	1	1	1	1	0	0
Panama	0	0	0	0	0	0	0	0	1	1
Paratyphi B var. Java	0	0	0	0	2	2	0	0	0	0
Rissen	1	1	0	0	0	0	0	0	0	0
Saintpaul	0	0	0	0	1	1	0	0	0	0
Stourbridge	1	1	0	0	0	0	0	0	0	0
Typhimurium	64	46	54	34	45	35	65	46	58	48
Uganda	0	0	1	1	0	0	0	0	0	0
Virchow	1	1	0	0	0	0	0	0	0	0
Wangata	1	1	0	0	0	0	0	0	0	0
4,5,12:i:-	6	4	7	6	16	9	5	5	1	1
4,12:i:-	7	5	7	6	1	1	10	9	2	2
61:k:1,5,7	0	0	1	1	0	0	0	0	2	2
61:-:1,5,7	2	2	1	1	1	1	0	0	4	4
61:k:1,5	0	0	0	0	1	1	3	3	0	0
61:-:1,5	1	0	1	1	3	3	2	2	0	0
untypable strains	9	9	10	10	7	5	9	9	12	12
rough strains	4	4	1	1	1	1	3	3	5	5
Total	**492**	**412**	**467**	**381**	**390**	**337**	**521**	**434**	**430**	**368**

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.

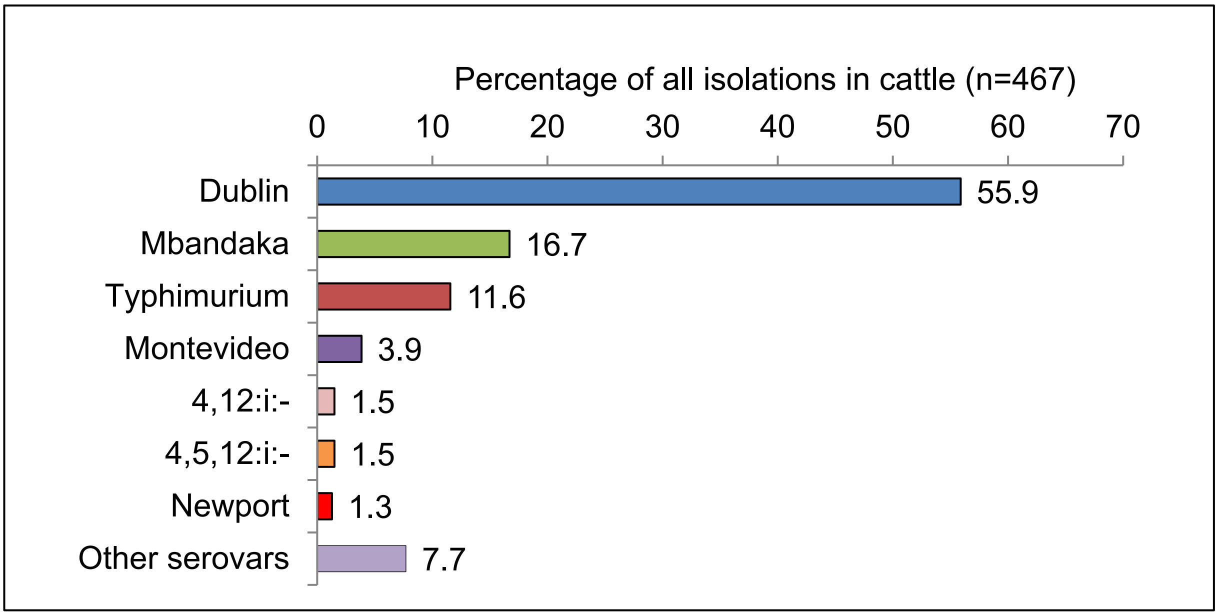
Figure 2.2: Isolations of the most common serovars in cattle in Great Britain 2018 to 2022

Figure 2.2.1: Isolations in 2018



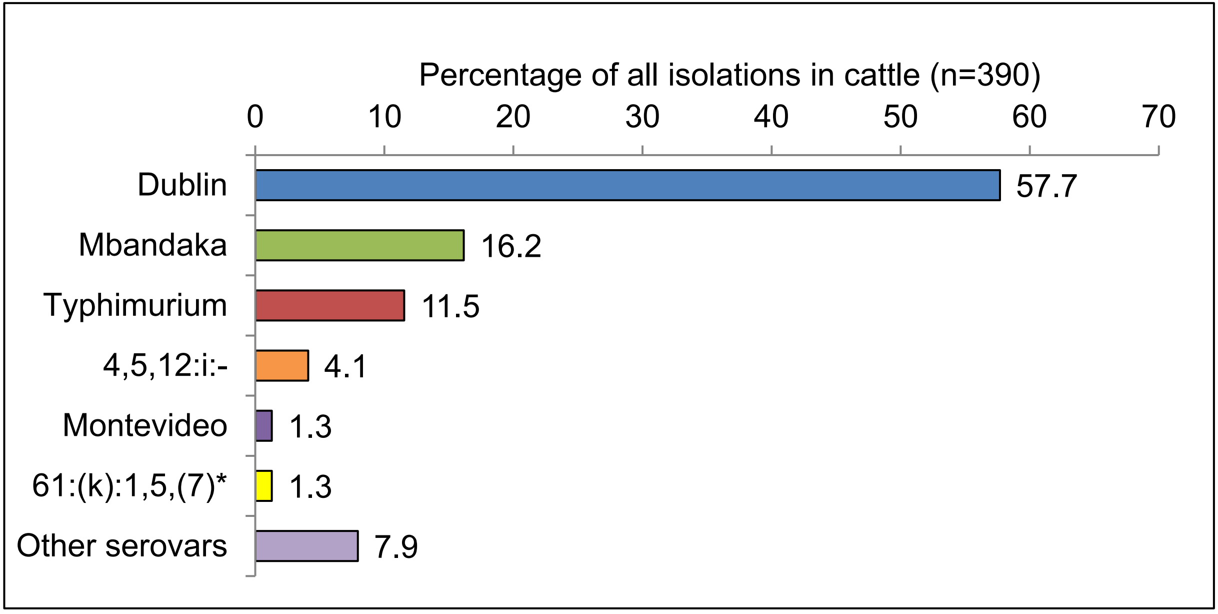
The most common serovar in cattle in 2018 was *S.* Dublin (64.2% of isolations), followed by *S.* Typhimurium (13.0% of isolations), *S.* Mbandaka (7.1% of isolations) *and S.* Montevideo (4.3% of isolations).

Figure 2.2.2: Isolations in 2019



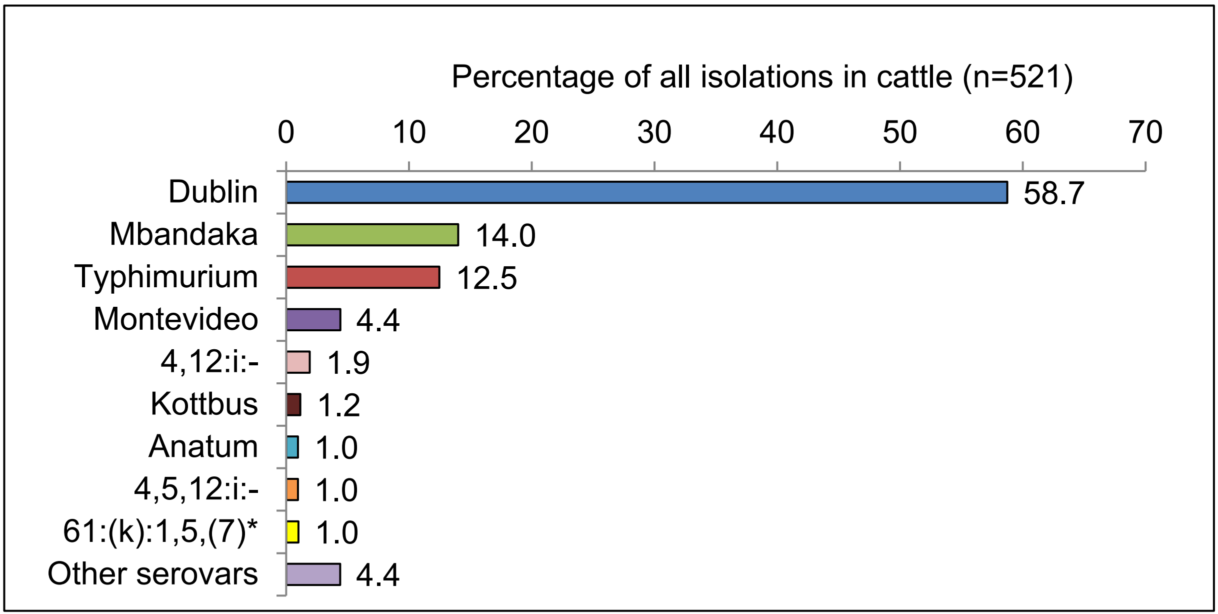
The most common serovar in cattle in 2019 was *S.* Dublin (55.9% of isolations), followed by *S.* Mbandaka (16.7% of isolations), *S.* Typhimurium (11.6% of isolations) and *S.* Montevideo (3.9% of isolations).

Figure 2.2.3: Isolations in 2020



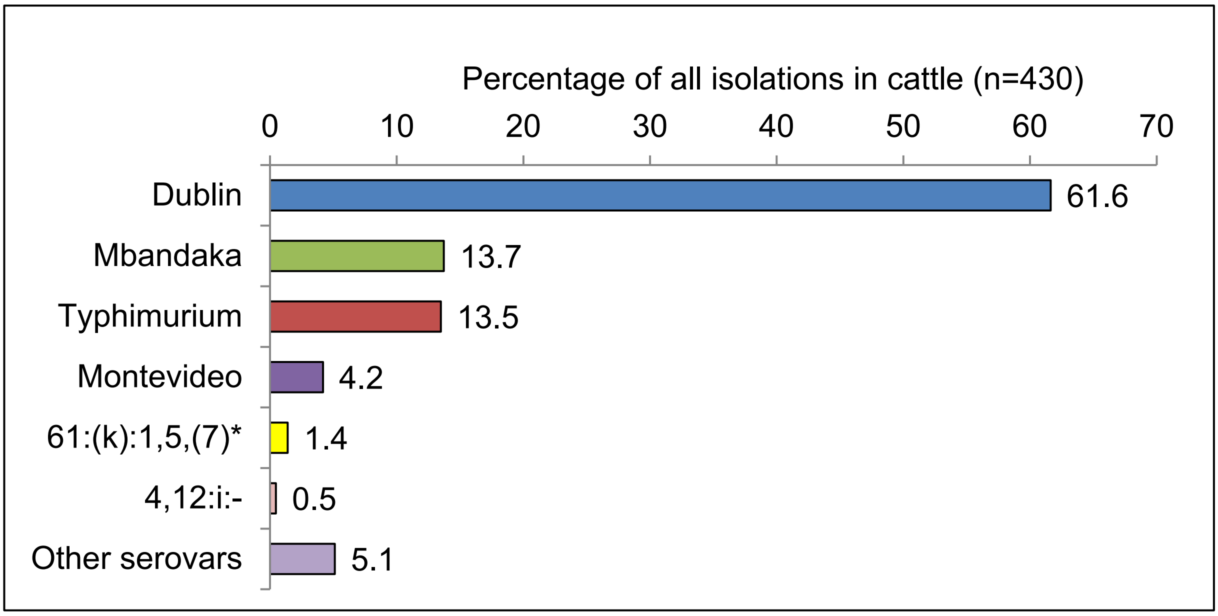
The most common serovar in cattle in 2020 was *S.* Dublin (57.7% of isolations), followed by *S.* Mbandaka (16.2% of isolations), *S.* Typhimurium (11.5% of isolations) and *S.* 4,5,12:i:- (4.1% of isolations).

Figure 2.2.4: 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 2.2.5: 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).

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 2022 and their trends over time since 2018

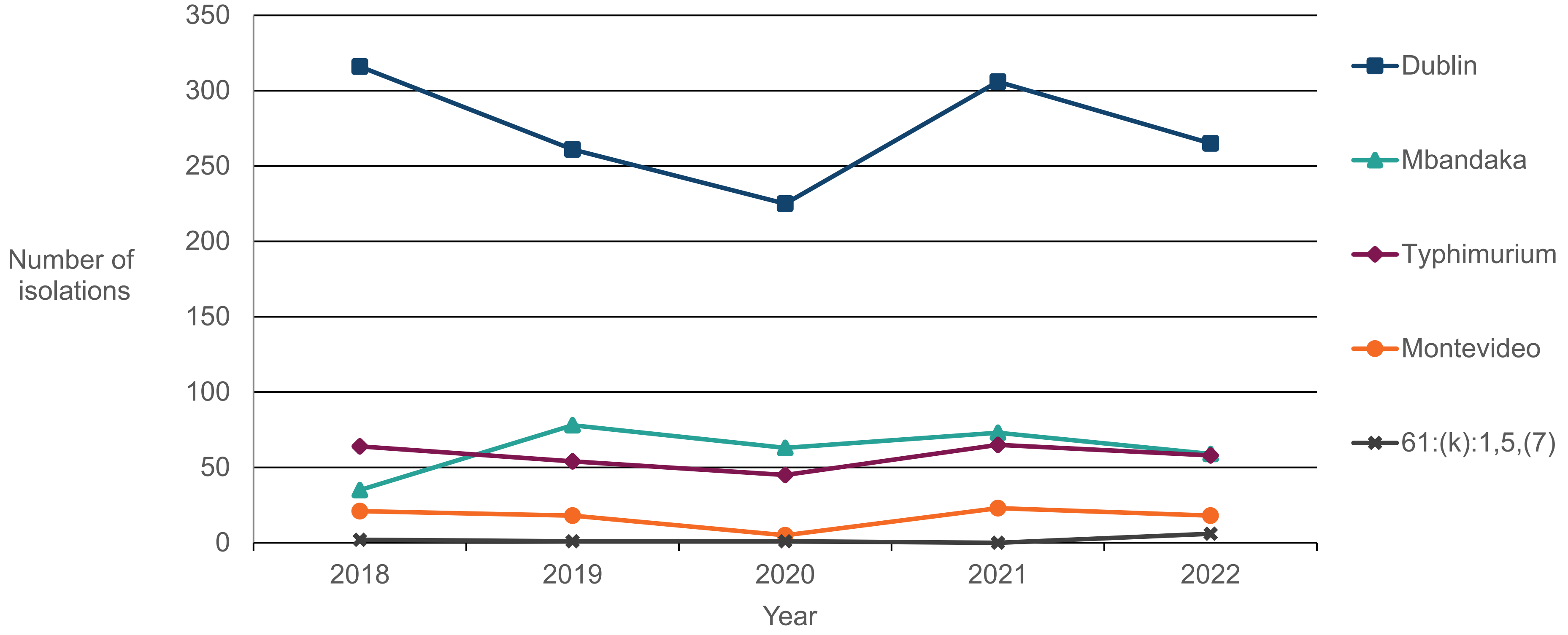


Figure 2.3 shows the most common serovar in cattle for all years was *S.* Dublin with over 225 isolations. There was a dip in isolations in 2020 and 2022 when there were 265 isolations. The number of isolations of *S.* Mbandaka, *S.* Typhimurium, *S.* Montevideo and *S.* 61:(k):1,5(7) showed less fluctuation 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 2018 to 2022

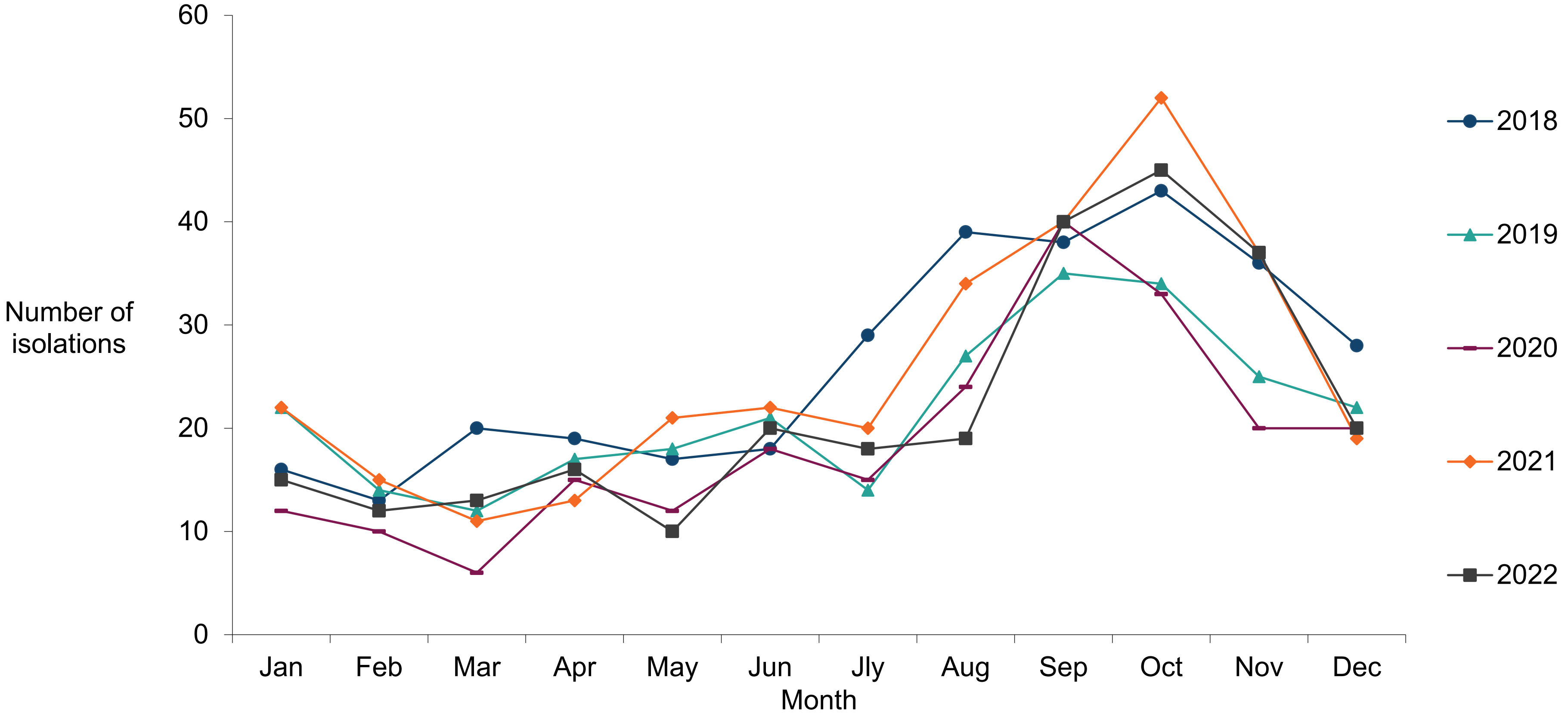


Figure 2.4 shows a marked seasonality in *S.* Dublin in all years with a peak in September and October, dropping to lower levels in January to June.

Figure 2.5: *S*. Dublin, *S*. Enteritidis, *S*. Typhimurium and *Salmonella* 4,(5),12:i:- as a proportion of all isolations in cattle in Great Britain 2002 to 2022

Figure 2.5 shows that as a proportion of all isolates in cattle in Great Britain between 2002 and 2022:

- *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 and made up 13.5% in 2022
- *S.* 4,12:i:- increased as a proportion of the total until 2021 when it was 1.9% but dropped in 2022 0.5%
- *S.* 4,5,12:i:- was also more variable but dropped in 2022 to 0.2% from 4.1% in 2021
- 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	*S.* 4,12:i:-	*S.* 4,5,12:i:-	*S.* Typhimurium
2002	9.0%	75.6%	0.5%	0.2%	0.3%	14.4%
2003	9.3%	77.7%	0.9%	0.0%	0.0%	12.1%
2004	13.4%	71.5%	0.6%	0.2%	0.0%	14.3%
2005	10.4%	70.4%	0.7%	0.3%	0.0%	18.2%
2006	21.6%	54.9%	0.0%	0.0%	0.2%	23.3%
2007	23.1%	58.9%	1.1%	0.1%	2.6%	14.2%
2008	22.6%	62.1%	0.3%	0.1%	1.5%	13.4%
2009	20.7%	67.5%	0.3%	0.3%	2.7%	8.5%
2010	22.3%	65.0%	0.5%	0.7%	4.2%	7.3%
2011	22.1%	64.7%	0.9%	0.6%	4.3%	7.4%
2012	23.8%	66.3%	0.5%	1.2%	3.4%	4.8%
2013	18.5%	72.5%	0.5%	0.7%	2.8%	5.0%
2014	25.2%	66.4%	0.2%	1.1%	1.7%	5.4%
2015	29.9%	62.5%	0.5%	1.0%	1.6%	4.5%
2016	22.1%	69.8%	0.0%	1.1%	1.6%	5.4%
2017	17.6%	65.9%	0.7%	1.8%	1.1%	12.9%
2018	19.5%	64.3%	0.6%	1.4%	1.2%	13.0%
2019	29.3%	55.9%	0.2%	1.5%	1.5%	11.6%

Year	Other serovars	*S.* Dublin	*S.* Enteritidis	*S.* 4,12:i:-	*S.* 4,5,12:i:-	*S.* Typhimurium
2020	25.9%	57.7%	0.5%	0.3%	4.1%	11.5%
2021	25.7%	58.7%	0.2%	1.9%	1.0%	12.5%
2022	24.2%	61.6%	0.0%	0.5%	0.2%	13.5%

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

Phage type	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
2	1	1	2	2	1	1	6	4	2	2
9	0	0	0	0	1	1	0	0	0	0
11	0	0	0	0	0	0	1	1	0	0
12	5	3	0	0	0	0	0	0	0	0
19	1	1	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	1	1	0	0
41	1	1	0	0	0	0	0	0	0	0
41b	0	0	0	0	1	1	0	0	0	0
46	0	0	0	0	0	0	1	1	0	0
75	0	0	0	0	0	0	0	0	11	10
104	17	15	18	14	15	10	8	6	6	6
105	0	0	0	0	0	0	1	1	22	17
116	0	0	0	0	10	5	4	3	4	3
120	0	0	0	0	0	0	1	1	0	0
189	0	0	1	1	1	1	0	0	1	1
193	2	2	4	4	2	2	6	3	3	2
204b	0	0	1	1	1	1	0	0	0	0
U289	0	0	0	0	0	0	0	0	1	1
U300	0	0	0	0	0	0	2	2	0	0
U302	8	8	1	1	1	1	0	0	0	0
U308	0	0	0	0	1	1	14	11	0	0
NOPT	2	0	4	0	10	10	9	5	6	4
RDNC	13	6	8	7	1	1	11	7	2	2
UNTY	14	9	15	4	0	0	0	0	0	0
Total	**64**	**46**	**54**	**34**	**45**	**35**	**65**	**46**	**58**	**48**

Figure 2.6: *Salmonella* Typhimurium DT104 and related strains as a proportion of all isolations of *S.* Typhimurium and *S.* 4,(5),12:i:- in cattle in Great Britain 2002 to 2022

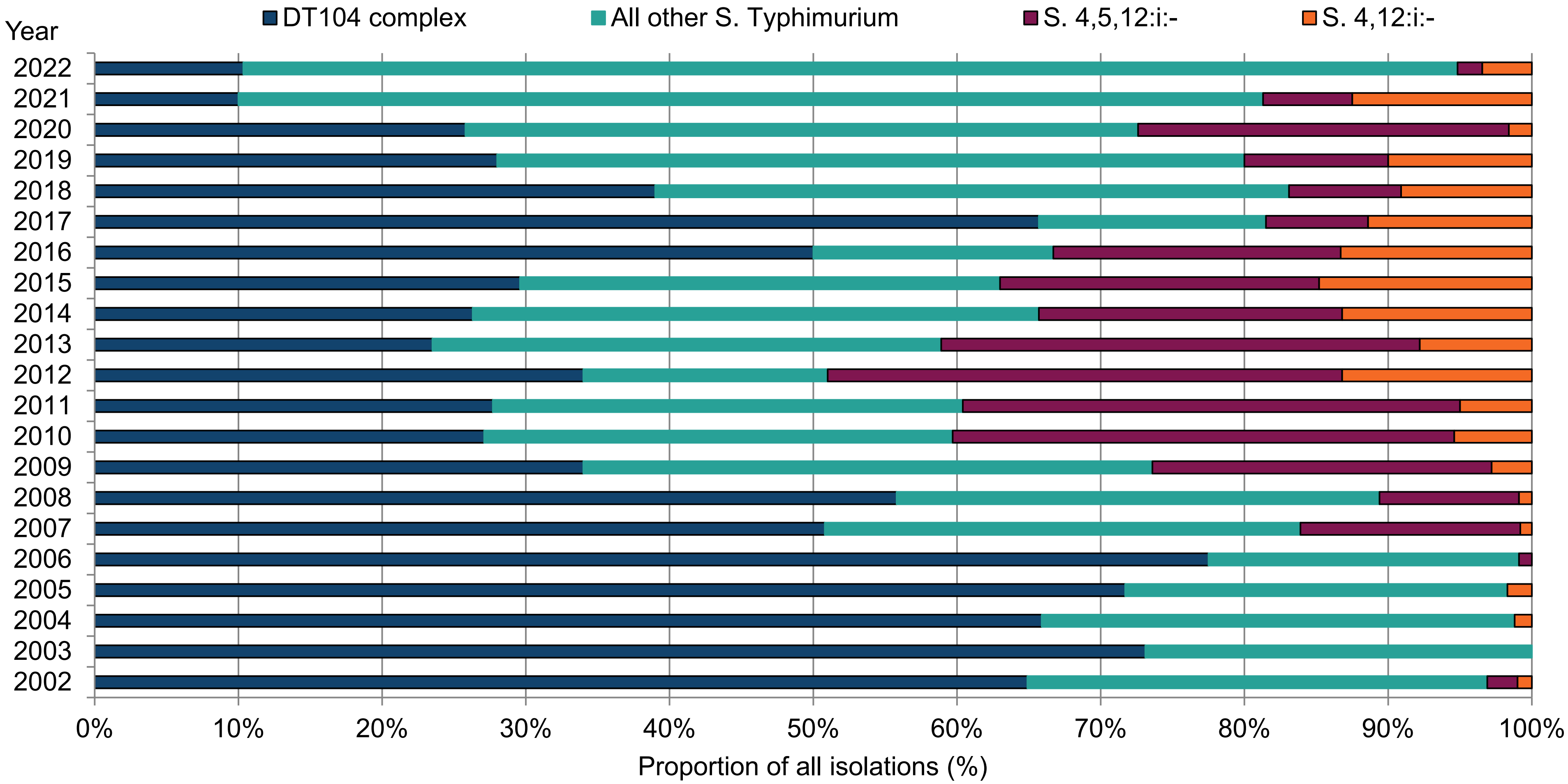


Figure 2.6 shows the proportion of all isolates of *S.* Typhimurium DT104 (and related strains), other *S.* Typhimurium strains and *S.* 4,(5),12:i:- in cattle in Great Britain between 2002 and 2022:

- 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 and 2022 (approx. 10% of all isolates)
- all other *S.* Typhimurium showed an increase from 2017 onwards, with the highest proportion of 84.5% in 2022
- *S.* 4,12:i:- showed a gradual increase from 2008 to 2015 but then declined to 3.4% in 2022
- *S.* 4,5,12:i:- increased from 2006 but then declined from 2012 (35.8%) to 1.7% in 2022

Figure 2.6: Table of data

Year	DT104 complex	All other *S.* Typhimurium	*S.* 4,5,12:i:-	*S.* 4,12:i:-
2002	64.9%	32.0	2.1%	1.0%
2003	73.1%	26.9	0.0%	0.0%
2004	65.9%	32.9	0.0%	1.2%
2005	71.7%	26.6	0.0%	1.7%
2006	77.5%	21.6	0.9%	0.0%
2007	50.8%	33.1	15.3%	0.8%
2008	55.8%	33.6	9.7%	0.9%
2009	34.0%	39.6	23.6%	2.8%
2010	27.1%	32.6	34.9%	5.4%
2011	27.7%	32.7	34.6%	5.0%
2012	34.0%	17.0	35.8%	13.2%
2013	23.5%	35.4	33.3%	7.8%
2014	26.3%	39.4	21.1%	13.2%
2015	29.6%	33.4	22.2%	14.8%
2016	50.0%	16.7	20.0%	13.3%
2017	65.7%	15.8	7.1%	11.4%

Year	DT104 complex	All other *S.* Typhimurium	*S.* 4,5,12:i:-	*S.* 4,12:i:-
2018	39.0%	44.1%	7.8%	9.1%
2019	28.0%	52.0%	10.0%	10.0%
2020	25.8%	46.8%	25.8%	1.6%
2021	10.0%	71.3%	6.2%	12.5%
2022	10.3%	84.5%	1.7%	3.4%

DT104 complex includes DT104, DT104b, DT12 and U302.

Table 2.3: *Salmonella* 4,5,12:i:- phage types in cattle in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
U311	1	1	0	0	2	1	0	0	0	0
DT194	0	0	0	0	3	1	0	0	0	0
DT193	4	2	4	3	10	6	3	3	1	1
UNTY	1	1	3	3	1	1	1	1	0	0
RDNC	0	0	0	0	0	0	1	1	0	0
Total	6	4	7	6	16	9	5	5	1	1

Table 2.4: *Salmonella* 4,12:i:- phage types in cattle in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
DT193	7	5	6	5	1	1	8	7	2	2
DT120	0	0	0	0	0	0	1	1	0	0
UNTY	0	0	1	1	0	0	1	1	0	0
Total	7	5	7	6	1	1	10	9	2	2

Table 2.5: *S*. Enteritidis phage types in cattle in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
NOPT	1	0	1	0	1	1	1	1	0	0
PT11	1	1	0	0	1	1	0	0	0	0
PT8	1	1	0	0	0	0	0	0	0	0
Total	3	2	1	0	2	2	1	1	0	0

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

Sheep

There was an increase in total numbers of sheep in Great Britain in 2022, rising from 30.9 million animals in 2021 to 31.1 million animals in 2022 according to the June agricultural census (Figure 3.1).

There were 6,076 ovine diagnostic submissions recorded on the VIDA database in Great Britain in 2022 compared to 6,198 in 2021, a decrease of 2.0%. This continues the decreasing trend in submission numbers seen since 2016 (with the exception of 2020 when submissions increased).

A total of 94 isolations of *Salmonella* were reported from sheep in 2022. Although this is a 34.7% decrease from 2021 (144 isolations), the figure is comparable to previous years (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 2022 (Figure 3.2). It was isolated on 65 occasions in 2022, again one of the highest recorded compared to previous years but well within the annual range of 37 to 109 isolations seen since 2008. *Salmonella* Typhimurium (8 isolations), *S.* Dublin (5 isolations) and *S.* Montevideo (5 isolations) were the next most commonly isolated serovars. The number of isolations of these 3 serovars fluctuate every year with them regularly swapping between second, third and fourth places. All 3 showed fewer isolations compared to 2021, but isolation numbers fell 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 2022 there were 65 isolations, accounting for 69.1% of the total number of isolates obtained from sheep samples (Figure 3.2), the highest percentage contribution compared to the preceding 4 years. It is considered a sheep adapted strain and of relatively low pathogenicity. The organism can be isolated from the reproductive, enteric, and occasionally the respiratory tracts of healthy sheep and 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 2022, diarrhoea was the most common presenting sign, and it was typically detected in association with parasitic gastroenteritis. Abortion was the second most frequently described presenting sign.

Salmonella Typhimurium

Salmonella Typhimurium was the second most common serovar isolated from sheep in 2022, representing 8.5% of the total *Salmonella* isolations (Figure 3.2). Isolations were lower this year compared to 2021 (8 versus 17), but comparable to those reported during 2019 (8 isolations) and 2020 (4 isolations). As expected, and like previous years, many of the cases were digestive system related, with diarrhoea and wasting the most common reasons for submission. Cases were reported in both adult animals and neonates.

Phage-typing was carried out on all 8 *S.* Typhimurium isolates from sheep in 2022 (Table 3.3). No single phage-type predominated. Only single isolations of the previously reported predominant phage-types DT104 and U308 were recorded in 2022. Three other *S.* Typhimurium phage-types identified this year, DT105 (2 isolates), DT75 (2 isolates) and U289 (one isolate) that have not been previously reported from sheep in Great Britain. One isolate did not conform to any phage types in the current typing scheme (RDNC).

There were 2 isolations of monophasic *S.* Typhimurium, 4,5,12:i:- in 2022. Phage-typing identified these as DT105 and DT193. This is comparable to other single monophasic variant isolations in 2018 (4,12:i:- DT193) and 2019 (4,12:i:- not phage-typed) Tables 3.4 and 3.5).

Salmonella Dublin

There were 5 isolations of *S.* Dublin in sheep in 2022, representing 5.3% of the total *Salmonella* isolations from sheep (Figure 3.2) and putting it as joint third most common serovar alongside *S.* Montevideo. The predominant presenting signs associated with diagnoses of *S.* Dublin this year were diarrhoea and malaise.

Salmonella Montevideo

Recorded isolations of *Salmonella* Montevideo in 2022 decreased by 82.1% with 5 isolations reported in 2022 compared to 28 isolations in 2021, accounting for 5.3% of the total number of *Salmonella* isolations and the lowest contribution since 2020 (Figure 3.2). Some strains of *S.* Montevideo are considered endemic within the Great Britain sheep population. As in all previous years, abortion was the principal presenting sign in diagnosed cases. This serovar can also be found in birds and poultry and as a contaminant of animal feed.

Salmonella Agama

Continuing the trend from 2020 and 2021 there was a single isolation of *Salmonella* Agama in 2022, diagnosed from a case of abortion. Numbers of isolations of this organism have been in single figures since 2018, ranging from one to 4 isolations per year. This serovar is typically associated with badgers.

Other serovars

Salmonella Enteritidis (NOPT) was isolated on 2 occasions during 2022. This is the first reported isolation of this serovar from sheep since 2007. Both were isolated from pre-weaned lambs with a history of diarrhoea.

Other serovars reported in sheep as single isolations during 2022 included: *S.* Derby (also reported in 2021) from an adult ewe with a history of wasting and *S.* Kingston (last reported in 2019) from a lamb with diarrhoea. *S.* Ohio was also isolated (last reported in 2020).

Goats

The Great Britain goat population fell slightly during 2022 to 107,876, compared to 107,989 in 2021 (June 2022 Agricultural Census).

There were 502 diagnostic submissions from goats recorded on the VIDA database in 2022 compared to 528 in 2021, a decrease of 4.9%.

Salmonellae are seldom isolated from goats, in most years single or zero isolations are reported. However, as in 2021 there were 2 isolations of *Salmonella* in goats during 2022. Both isolates were *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 2013 to 2022

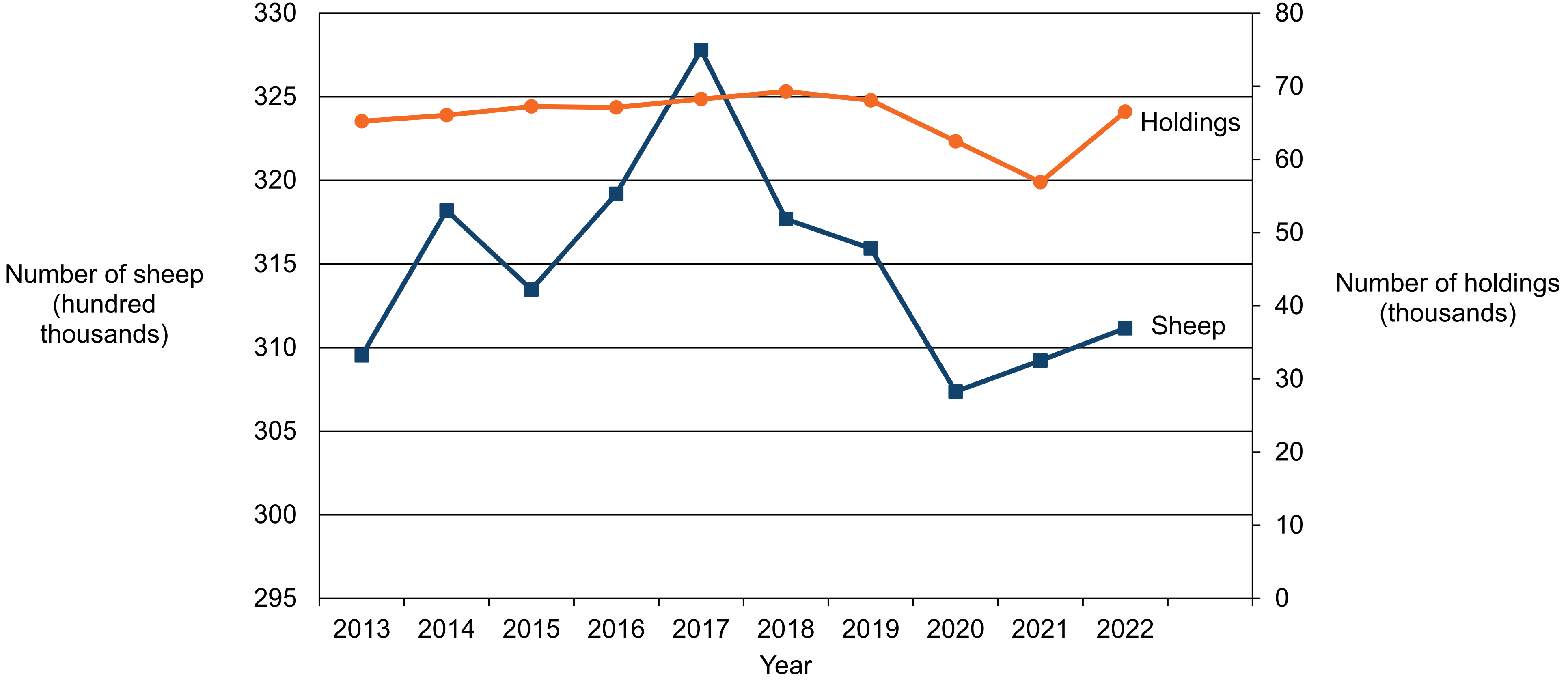


Figure 3.1 shows a relatively constant level of sheep holdings until 2019 when it starts to decline but with an upturn in 2022 to 67,000 holdings. The number of sheep in Great Britain increased until 2017 after which it declined until 2020 and 2022 when there was an increase

to just over 31,100,000. Data is sourced from the June 2021 and 2022 Agricultural Census. The number of holdings in 2020 is estimated and Wales (holdings) and Scotland (animals and holdings) 2021 census data used for 2022.

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

Salmonella serovar	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
Agama	2	2	4	4	1	1	1	1	1	1
Ajiobo	0	0	0	0	0	0	1	1	0	0
Anatum	0	0	0	0	0	0	1	1	0	0
Berta	0	0	0	0	1	1	0	0	0	0
Derby	0	0	0	0	0	0	1	1	1	1
Dublin	13	13	6	6	10	9	14	12	5	4
Enteritidis	0	0	0	0	0	0	0	0	2	2
Indiana	0	0	0	0	0	0	1	1	0	0
Kingston	0	0	1	1	0	0	0	0	1	1
Mbandaka	1	1	1	1	0	0	1	1	0	0
Minnesota	0	0	0	0	0	0	0	0	0	0
Montevideo	10	9	16	13	3	3	28	18	5	5
Newport	0	0	1	1	1	1	0	0	0	0
Ohio	0	0	0	0	1	1	0	0	1	1
Stourbridge	0	0	0	0	0	0	1	1	0	0
Typhimurium	15	9	4	2	8	5	17	13	8	8
4,5,12:i:-	0	0	0	0	0	0	1	1	2	2
4,12:i:-	1	1	1	1	0	0	0	0	0	0
61:k:1,5	5	4	5	4	10	10	37	35	4	4
61:k:1,5,7	9	9	9	9	4	4	2	2	15	13
61:-:1,5	9	7	10	7	15	15	30	29	0	0
61:-:1,5,7	35	31	35	31	16	16	0	0	46	44
untypable strains	9	9	10	10	7	5	8	8	1	1
rough strains	1	1	0	0	0	0	0	0	2	2

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Total	**110**	**96**	**103**	**90**	**77**	**71**	**144**	**125**	**94**	**89**

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.

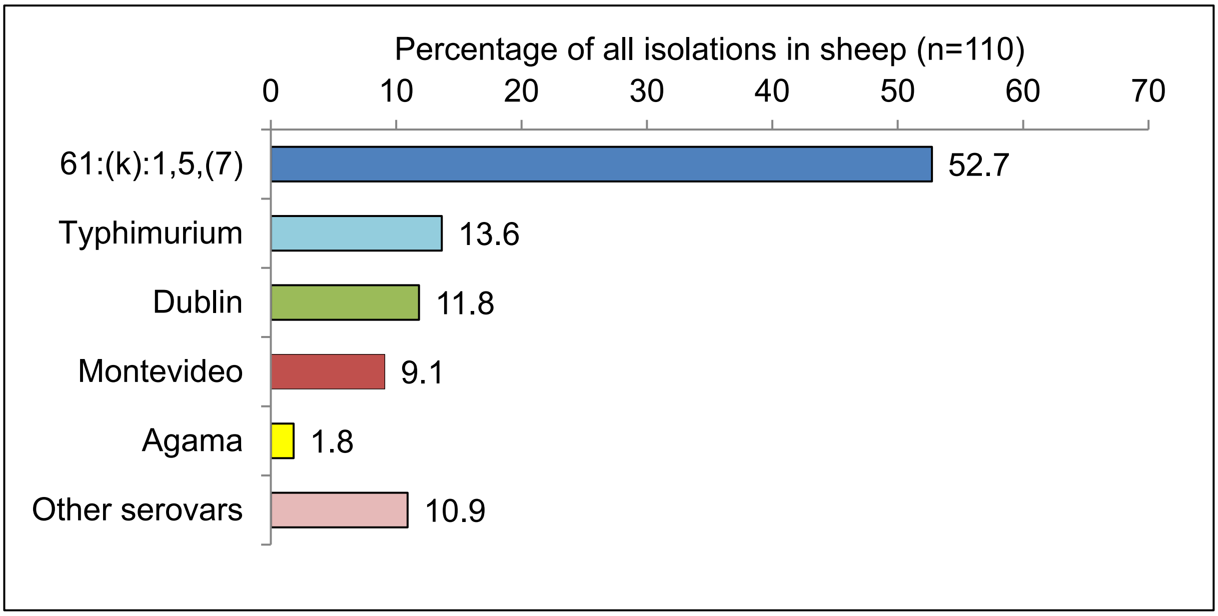
Table 3.2: Isolations and incidents of *Salmonella* in goats on all premises in Great Britain

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Dublin	0	0	0	0	1	1	1	1	0	0
61:-:1,5,7	0	0	0	0	0	0	0	0	1	1
61:k:1,5	0	0	0	0	0	0	1	1	1	1
untypable strains	0	0	1	1	0	0	0	0	0	0
Total	**0**	**0**	**1**	**1**	**1**	**1**	**2**	**2**	**2**	**2**

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.

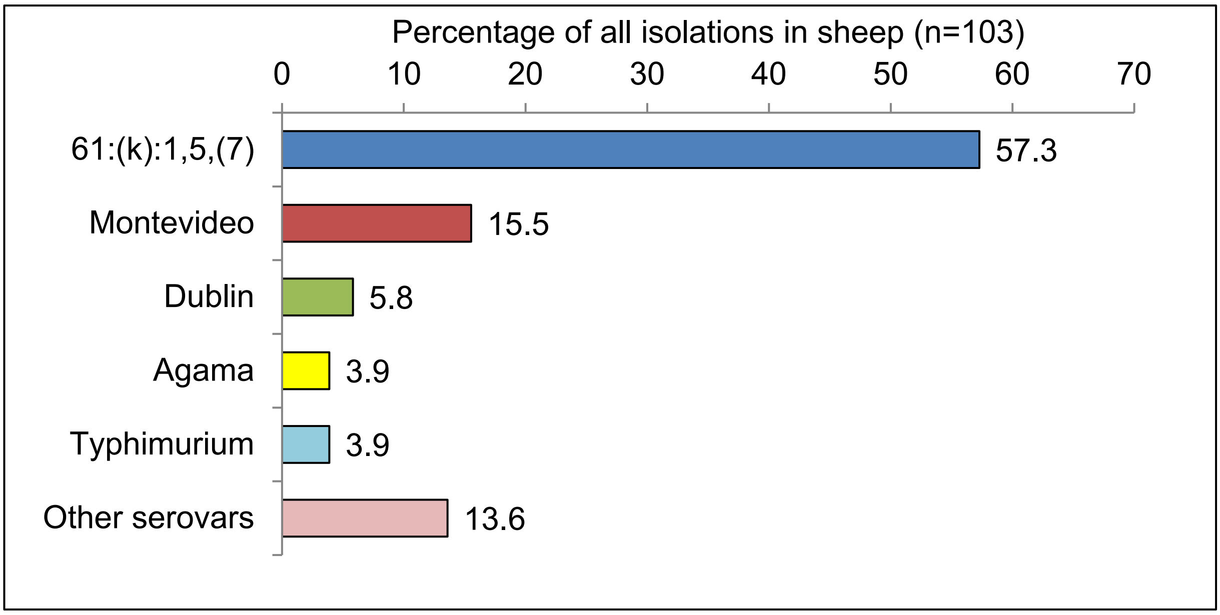
Figure 3.2: Isolations of the most common serovars in sheep in Great Britain 2018 to 2022

Figure 3.2.1: Isolations in 2018



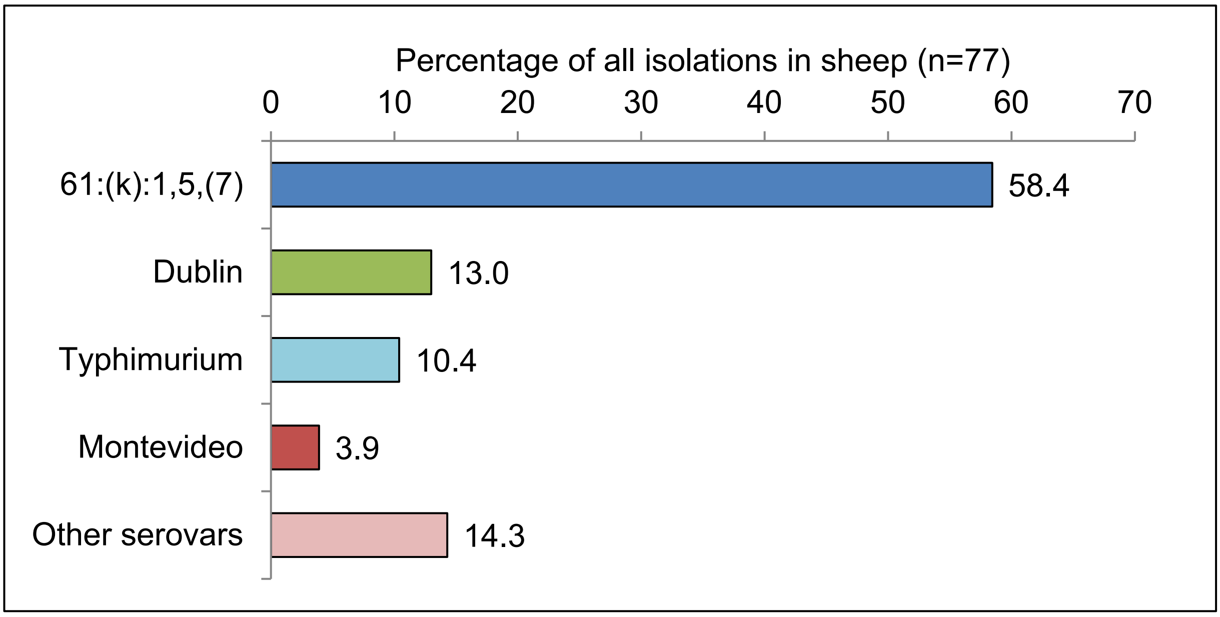
The most common serovar in sheep in 2018 was *Salmonella* 61:(k):1,5,(7) (52.7% of isolations), followed by *S.* Typhimurium (13.6% of isolations), *S.* Dublin (11.8% of isolations) and *S.* Montevideo (9.1% of isolations).

Figure 3.2.2: Isolations in 2019



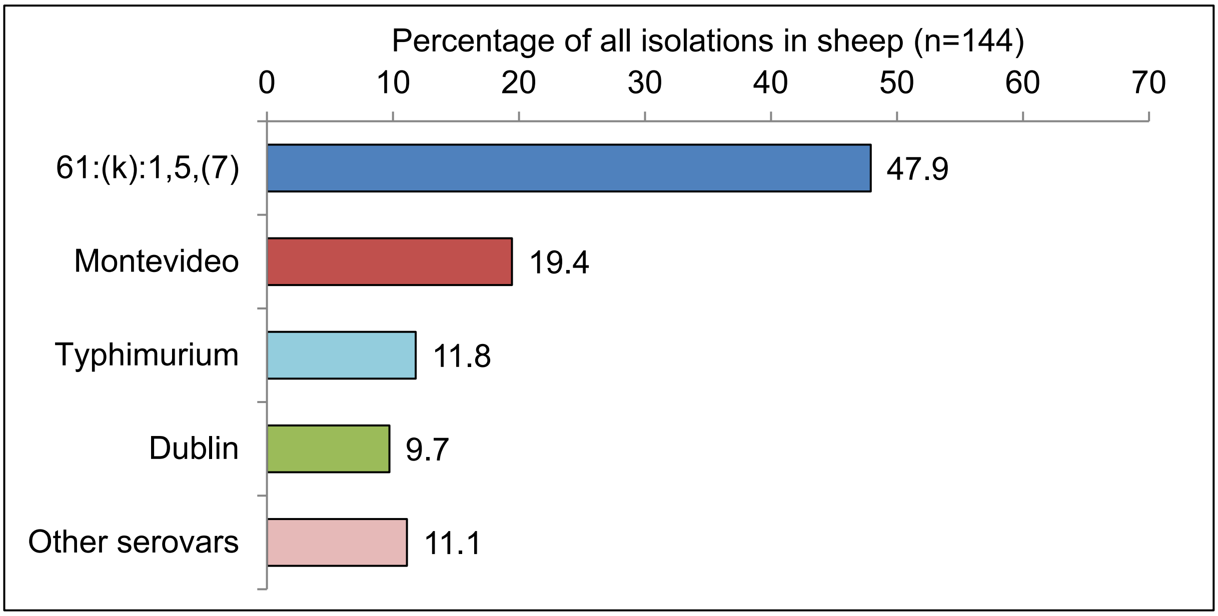
The most common serovar in sheep in 2019 was *Salmonella* 61:(k):1,5,(7) (57.3% of isolations), followed by *S.* Montevideo (15.5% of isolations), *S.* Dublin (5.8% of isolations) and *S.* Agama (3.9% of isolations).

Figure 3.2.3: Isolations in 2020



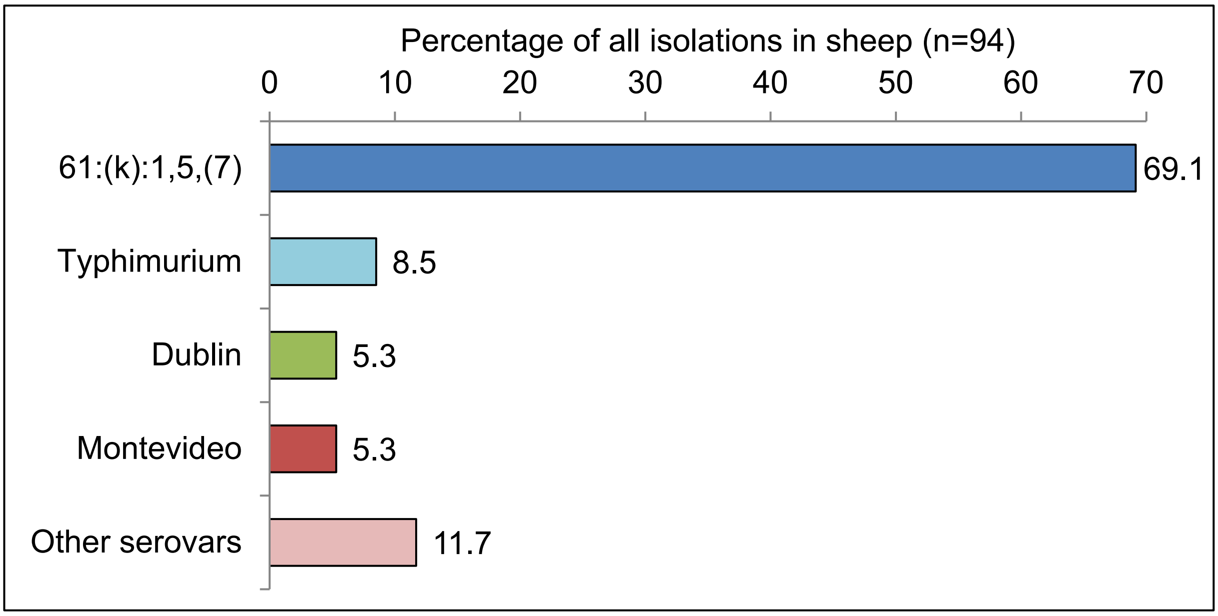
The most common serovar in sheep in 2020 was *Salmonella* 61:(k):1,5,(7) (58.4% of isolations), followed by *S.* Dublin (13.0% of isolations), *S.* Typhimurium (10.4% of isolations) and *S.* Montevideo (3.9% of isolations).

Figure 3.2.4: 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 3.2.5: 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).

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 2022 and their trends over time since 2018

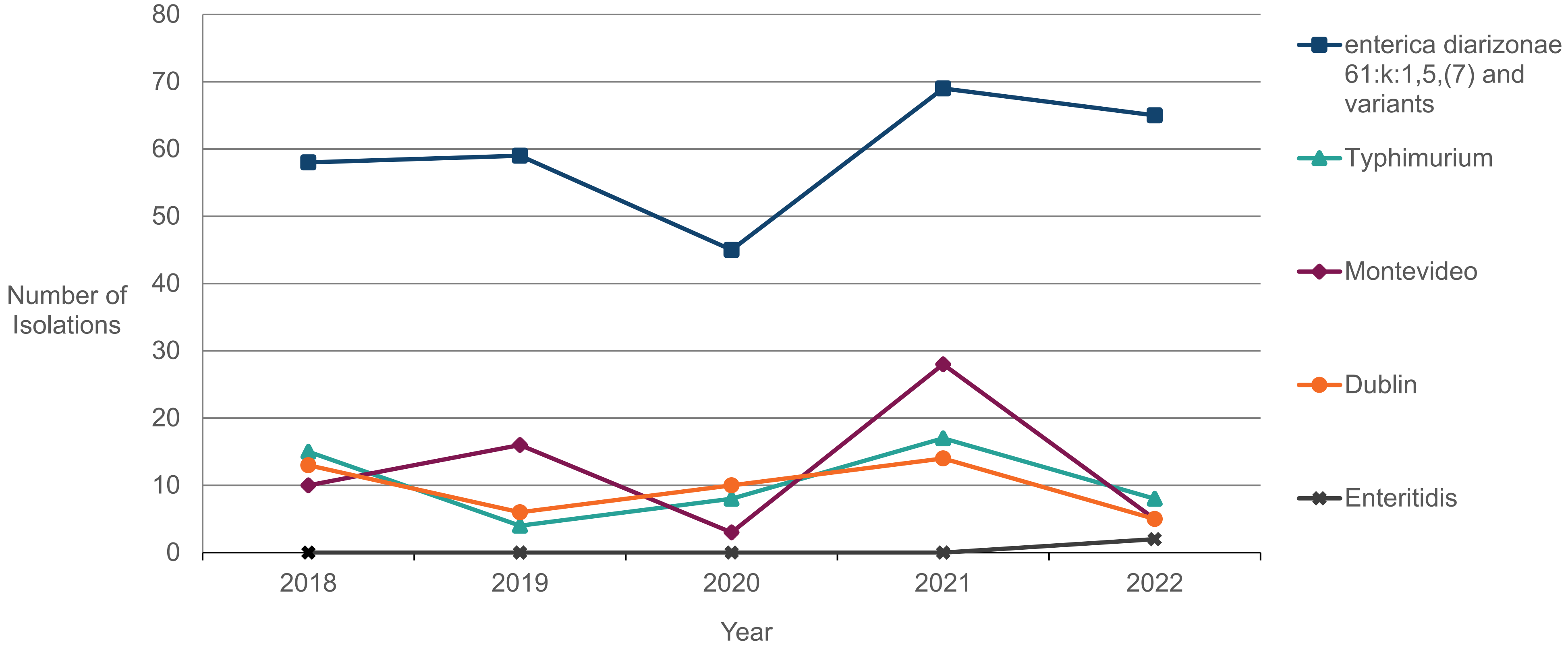


Figure 3.3 shows the most common serovar in sheep for all years was *S.* enterica diarizonae 61:k:1,5,(7) and its variants with 65 isolations in 2022. The number of isolations of *S.* Typhimurium, *S.* Montevideo, *S.* Dublin and *S.* Enteritidis was much lower and all fell below 10 isolations in 2022.

Figure 3.4: *S*. Dublin, *S*. *enterica diarizonae*, *S*. Enteritidis, *S*. Montevideo, *S*. Typhimurium and *Salmonella* 4,(5),12:i:- as a proportion of all isolations in sheep in Great Britain 2002 to 2022

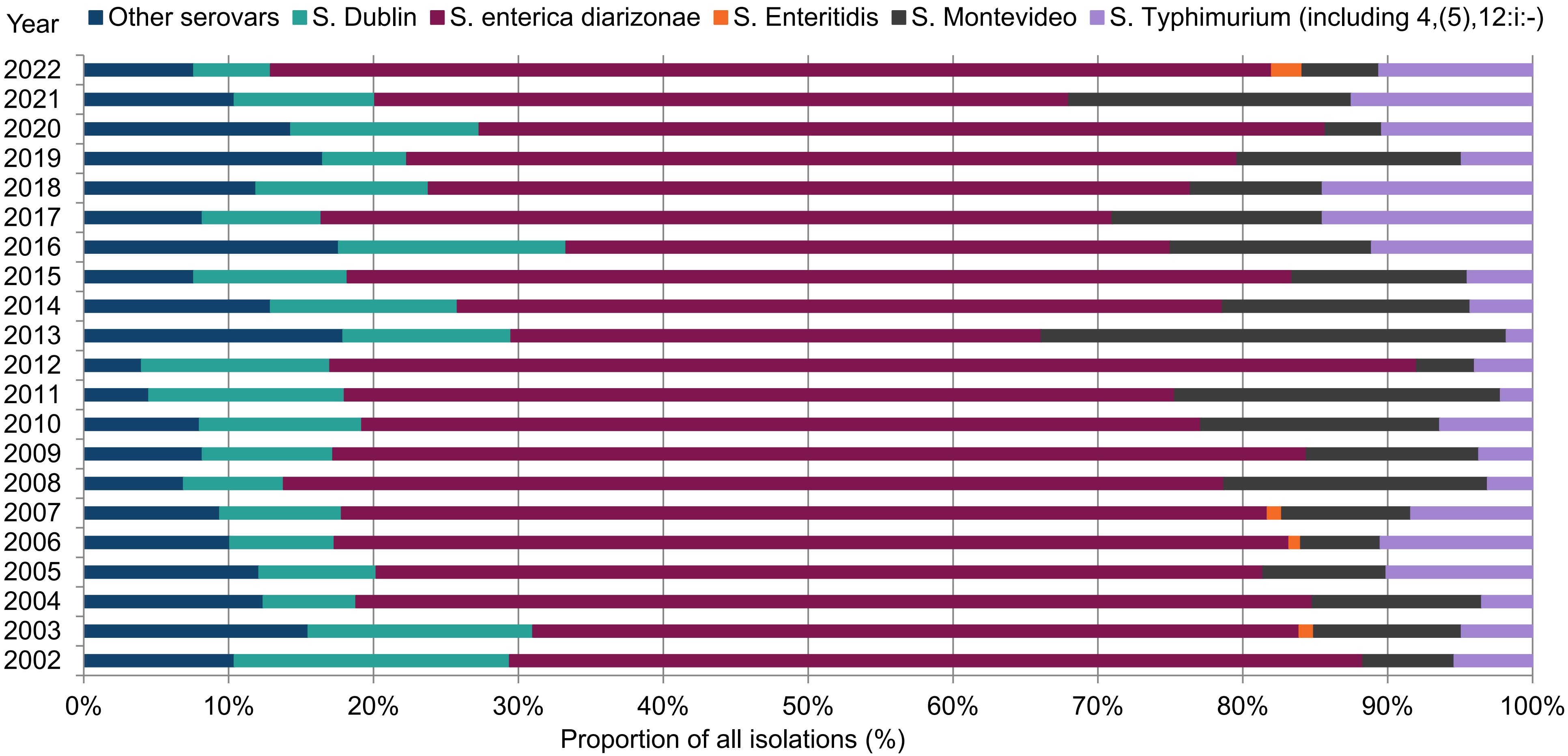


Figure 3.4 shows the proportion of all isolates of *S.* Dublin, *S. enterica diarizonae*, *S.* Enteritidis, *S.* Montevideo, *S.* Typhimurium and *Salmonella* 4,(5),12:i:- in pigs in Great Britain between 2002 and 2022:

- *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 5.3% in 2022
- *S.* Typhimurium (including 4,(5),12:i:-) increased as a proportion of the total until 2017 when it was 14.5% but dropped in 2022 to 10.6%
- *S.* Enteritidis was also more variable and was only isolated in 2003, 2006, 2007 and 2022
- other serovars have accounted for between 4.0% 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 4,(5),12:i:-)
2002	10.4%	19.0%	58.9	0.0%	6.3%	5.4%
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%
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%

Year	Other serovars	*S.* Dublin	*S. enterica diarizonae*	*S.* Enteritidis	*S.* Montevideo	*S.* Typhimurium (including 4,(5),12:i:-)
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%

Table 3.3: *S.* Typhimurium phage types in sheep in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
UNTY	6	1	1	1	0	0	0	0	0	0
RDNC	1	1	0	0	2	1	0	0	1	1
NOPT	0	0	0	0	0	0	1	1	0	0
U320	0	0	2	1	0	0	0	0	0	0
U308	0	0	0	0	0	0	10	7	1	1
U300	0	0	0	0	0	0	1	1	0	0
U289	0	0	0	0	0	0	0	0	1	1
DT116	0	0	0	0	0	0	2	2	0	0
DT105	0	0	0	0	0	0	0	0	2	2
DT104	6	5	1	0	4	3	3	2	1	1
DT75	0	0	0	0	0	0	0	0	2	2
DT41	2	0	0	0	0	0	0	0	0	0
DT2	0	0	0	0	2	1	0	0	0	0
Total	**15**	**7**	**4**	**2**	**8**	**5**	**17**	**13**	**8**	**8**

Table 3.4: *Salmonella* 4,5,12:i:- phage types in sheep in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
DT105	0	0	0	0	0	0	0	0	1	1
DT193	0	0	0	0	0	0	0	0	1	1
NOPT	0	0	0	0	0	0	1	1	0	0
Total	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**2**

Table 3.5: *Salmonella* 4,12:i:- phage types in sheep in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
DT193	1	1	0	0	0	0	0	0	0	0
NOPT	0	0	1	1	0	0	0	0	0	0
Total	**1**	**1**	**1**	**1**	**0**	**0**	**0**	**0**	**0**	**0**

Chapter 4: Reports of *Salmonella* in pigs

Compared with 2021, there was a small decrease of 2.8% in the total Great Britain pig herd in 2022 to just under 4.5 million animals according to the 2022 agricultural census (Figure 4.1). The year 2022 began with the cost of pig production exceeding pig prices at slaughter which was exacerbated by increased input costs relating to energy and pig feed prices and uncertainties about supply, associated with the war in the Ukraine. These challenges have contributed to the reduction in the breeding sow population.

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 database (VIDA). 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 a small increase (0.65%) in the total number of pig submissions from Great Britain to APHA and SRUC during 2022 (3,267 submissions) compared to 2021 (3,246 submissions). Conversely, there was a slight decrease (1.04%) in diagnostic pig submissions during 2022 (1,441 submissions) compared to 2021 (1,456 submissions).

There were 214 isolations of *Salmonella* from pigs in 2022. This is similar to 2021 when there were 223 isolations (but higher than the preceding years 2018 to 2020). The different serovars isolated, are detailed in Table 4.1 and Figure 4.2.

Salmonella Typhimurium and Monophasic *S.* Typhimurium variants

As has been the case in previous years, isolations of *S*. Typhimurium and its monophasic variants (*Salmonella* 4,5,12:i:- and *Salmonella* 4,12:i:-) together accounted for the majority of isolations of *Salmonella* from pigs in 2022 (70.6% of all isolations from pigs, Figures 4.2 and 4.4).

However, isolations in this category have represented a gradually decreasing proportion of total *Salmonella* isolations over recent years (73.1% in 2021 compared to 79.9% in 2018), and this decline has continued in 2022, albeit at a slow rate (70.6% of total pig isolations). As in 2021, the number of *S*. Typhimurium isolations (100 isolations, 46.7% of total pig isolations) exceeded isolations of both monophasic variants combined (51 isolations, 23.8% of total pig isolations). Prior to 2020, monophasic variants of *S*. Typhimurium accounted for a higher percentage of all pig isolations than *S*. Typhimurium (Table 4.1)

As in previous years, the most common serovar isolated from pigs in 2022 was *S*. Typhimurium (100 isolations). This is the same number of *S*. Typhimurium isolations reported in 2021 (100 isolations) and a 20.5% increase compared with 2020 (83 isolations).

Phage type DT193 (27 isolations), which is particularly associated with pigs, was the most commonly isolated phage type of *S*. Typhimurium in 2022. This was followed by U308a (18 isolations) and DT32 (16 isolations). Phage type U308a had not been reported from surveillance in pigs in Great Britain until 2021 although it was detected during project work in 2002. This contrasts with 2021 when the most common phage type was U288 (36 isolations in 2021 compared to just 6 in 2022) with DT193 and U308 as second and third most frequently identified respectively (Table 4.2).

An increasing number of different *S.* Typhimurium phage types have been identified each year since 2018 and 2019 when there were 5 in each year, to 8 in 2020, 10 in 2021 and 13 in 2022 (Table 4.2). In addition to the 13 identified phage types in 2022, 12 isolations did not conform to a recognised phage type in the current typing scheme (classified as RDNC). Three phage types, DT105, DT118 and DT181, identified in 2022 have not been recorded previously in pigs in Great Britain.

The next most common *Salmonella* serovar isolated from pigs in 2022 after *S*. Typhimurium, was monophasic *Salmonella* 4,12:i:- (28 isolations) which decreased by 24.3% from 37 isolations in 2021. There were 23 isolations of the other monophasic variant 4,5,12:i:- in 2022, down 11.5% from 26 isolations in 2021. Isolations of both these serovars were lower in 2022 than in any other year from 2018 to 2021.

Figures 4.5 and 4.6 show that 95.7% (45 of 47) of the monophasic *S.* Typhimurium variants that could be phage typed were DT193, which represents the ‘epidemic’ type that emerged in Europe from 2006 and has been dominant amongst monophasic strains of *S.* Typhimurium in Great Britain pigs. Four monophasic variant isolates (2 isolates of 4,12:i:- and 2 isolates of 4,5,12:i:-) were not typable in 2022.

Other serovars

After *S*. Typhimurium and its monophasic variants, the most frequently isolated serovar from pigs in 2022 was *S*. Newport (Table 4.1 and Figure 4.2). This was isolated 20 times (9.3% of all pig isolations), which is very similar to the situation for this serovar in 2021 (19 isolations, 8.5% of all pig isolations) but almost 3 times the number seen in 2020 (7 isolations, 3.7% of all pig isolations). Isolations of *S*. Derby from pigs in 2022 did not continue the rise seen between 2021 and 2022 with 15 isolations in 2022 compared to 17 in 2021). Isolations of *S*. Panama more than doubled in 2022 to 10 isolations from 4 in 2021 continuing an upward trend in the last 3 years (Table 4.1 and Figure 4.2).

Eleven different serovars were identified in 2022 with 2 untypable strains (Table 4.1). This is no more than in the years 2018 to 2021 in which the number of different serovars identified each year ranges from 11 to 13. However, one isolation was made of *S*. London var. 15^+, a serovar that has never previously been identified in Great Britain pigs. *S*. London has been identified with increasing frequency since 2019, with 7 isolations in 2022.

The other serovars identified in 2022 in lower numbers were *S*. Reading (3 isolations), *S*. Kedougou (3 isolations) and *S*. Bovismorbificans (2 isolations). There were no isolations of *S*. Enteritidis in 2022, which was last isolated in pigs in 2019 (Table 4.1).

Figure 4.1: Pig population and number of holdings with pigs in Great Britain 2013 to 2022

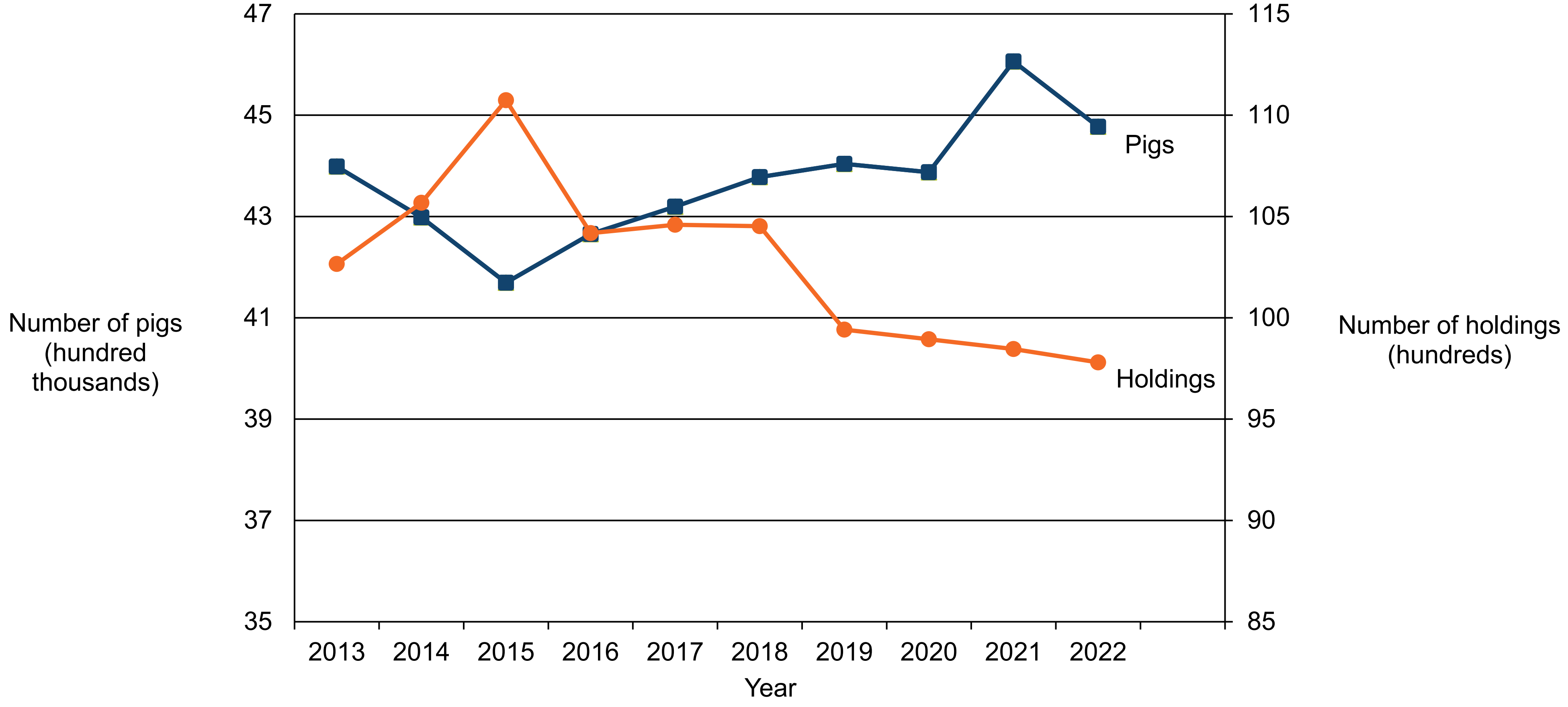


Figure 4.1 shows a variable number of pig holdings until 2019 when it starts to slowly decline to 9,780 holdings in 2022. The number of pigs in Great Britain increased until 2021 after which there was a decline in 2022 to just over 4,470,000. Data is sourced from the June 2021 and

2022 Agricultural Census. The number of holdings in 2020 is estimated and Wales (holdings) and Scotland (animals and holdings) 2021 census data used for 2022.

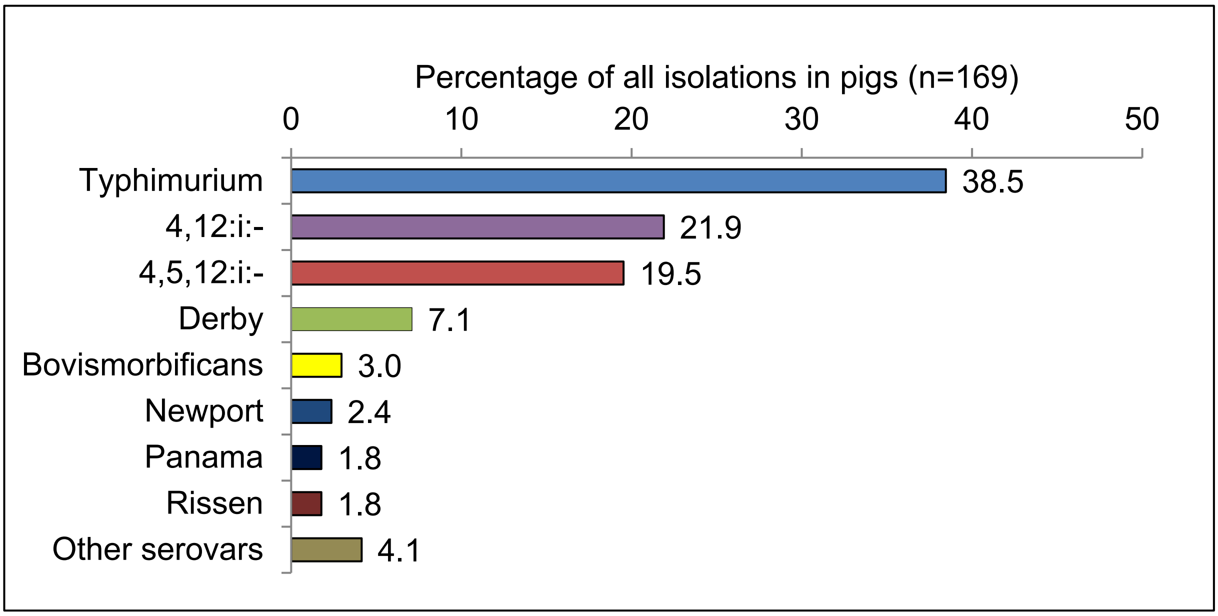
Table 4.1: Isolations and incidents of *Salmonella* in pigs on all premises in Great Britain

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Bardo	1	1	0	0	1	1	0	0	0	0
Bovismorbificans	5	3	12	10	5	5	7	6	2	2
Derby	12	12	6	5	12	11	17	16	15	13
Dublin	0	0	0	0	0	0	1	1	0	0
Enteritidis	0	0	1	1	0	0	0	0	0	0
Indiana	0	0	0	0	1	1	2	1	0	0
Kedougou	1	0	8	8	1	1	1	1	3	2
Livingstone	0	0	1	1	0	0	1	1	0	0
London	0	0	1	1	5	5	5	5	7	6
London var. 15^+	0	0	0	0	0	0	0	0	1	1
Nchanga	1	1	0	0	0	0	0	0	0	0
Newport	4	3	6	6	7	7	19	18	20	19
Panama	3	3	1	1	2	2	4	4	10	9
Reading	2	2	1	1	2	2	2	2	3	3
Rissen	3	2	0	0	0	0	0	0	0	0
Typhimurium	65	47	50	47	83	76	100	93	100	97
Uganda	0	0	1	1	0	0	0	0	0	0
4,5,12:i:-	33	28	30	27	36	34	26	25	23	19
4,12:i:-	37	28	47	45	29	28	37	32	28	25
rough strains	0	0	0	0	3	3	1	1	0	0
untypable strains	2	1	2	2	2	2	0	0	2	2
Total	**169**	**131**	**167**	**156**	**189**	**178**	**223**	**206**	**214**	**198**

In 2018, 4 of 37 isolations (all UNTY) were not confirmed as monophasic *S*. Typhimurium by PCR.

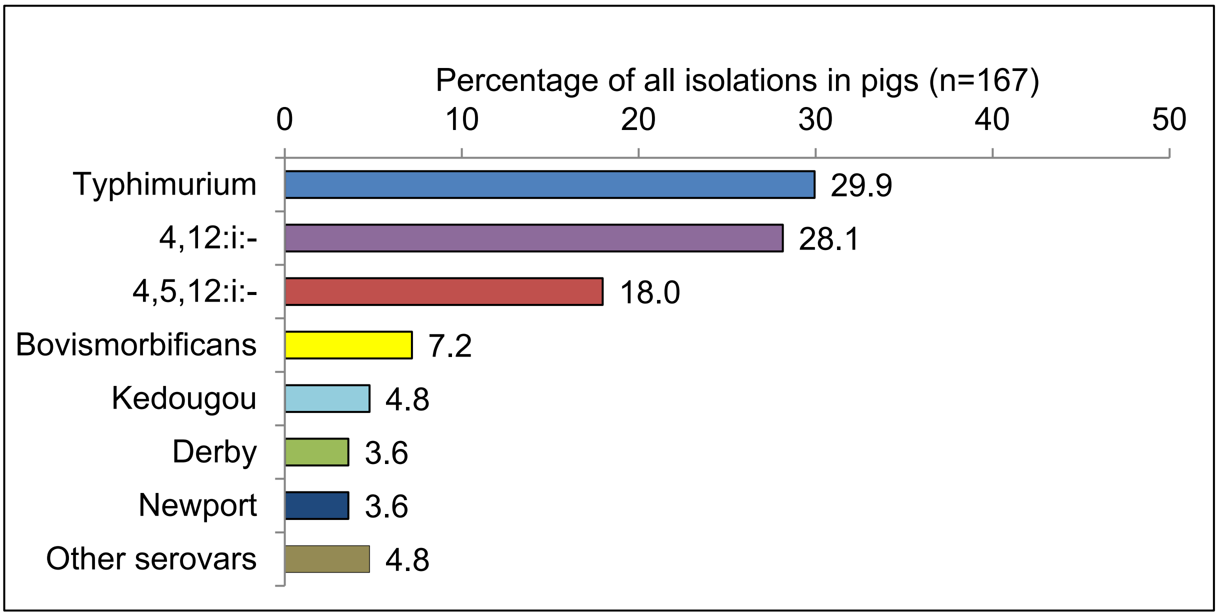
Figure 4.2: Isolations of the most common serovars in pigs in Great Britain 2018 to 2022

Figure 4.2.1: Isolations in 2018



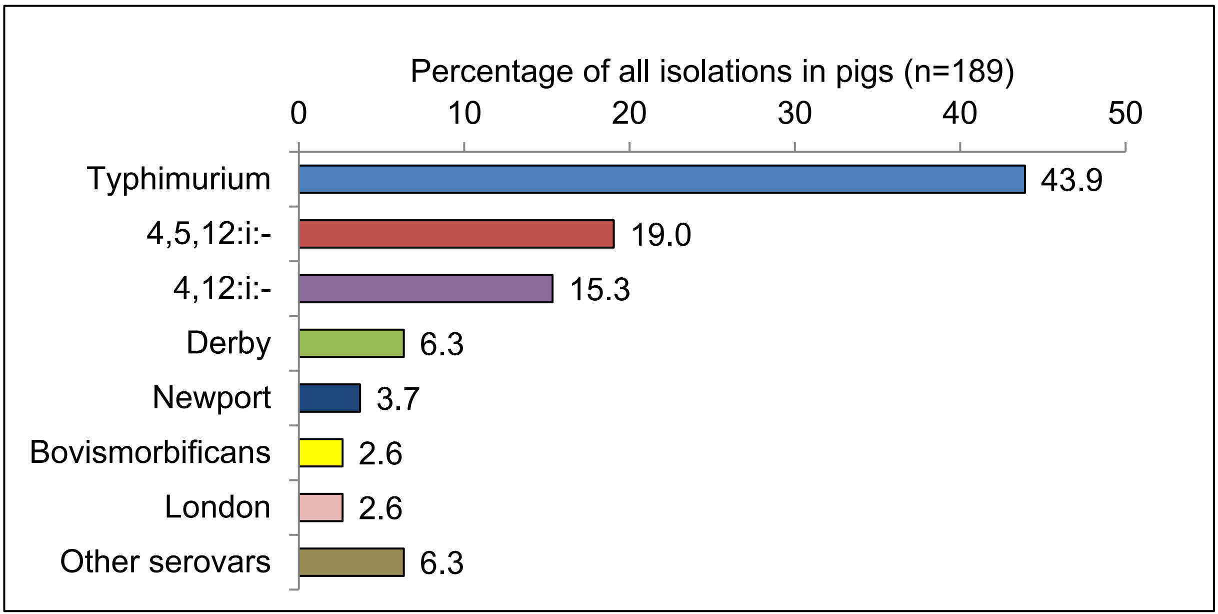
The most common serovar in pigs in 2018 was *S.* Typhimurium (38.5% of isolations), followed by *Salmonella* 4,12:i:- (21.9% of isolations), *Salmonella* 4,5,12:i:- (19.5% of isolations) and *S.* Derby (7.1% of isolations).

Figure 4.2.2: Isolations in 2019



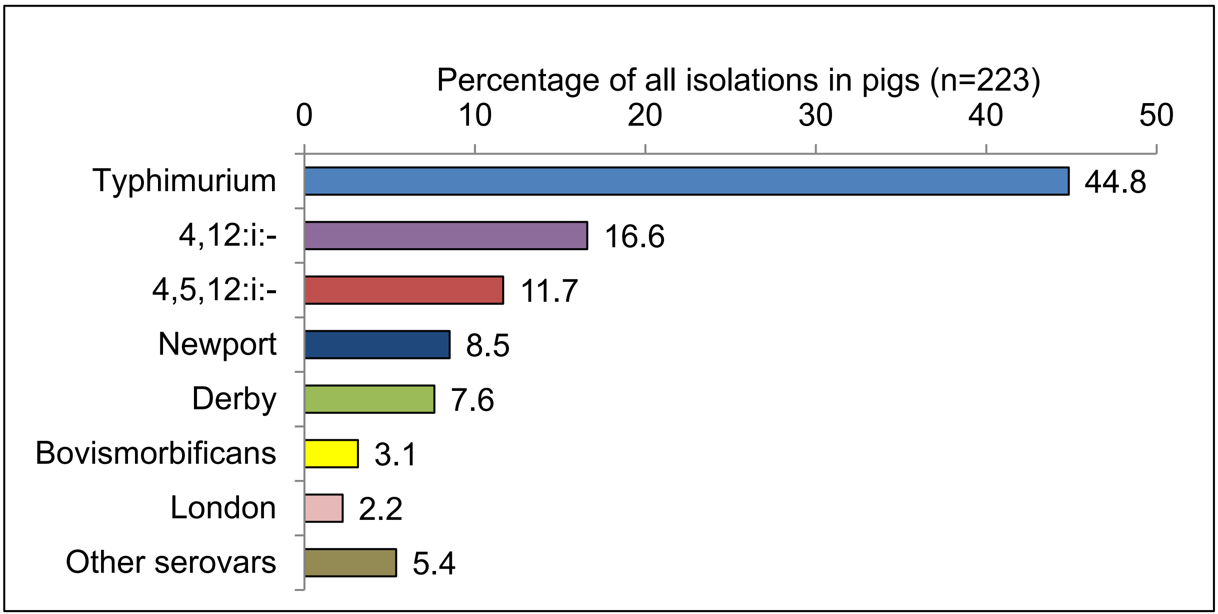
The most common serovar in pigs in 2019 was *S.* Typhimurium (29.9% of isolations), followed by *Salmonella* 4,12:i:- (28.1% of isolations), *Salmonella* 4,5,12:i:- (18.0% of isolations) and *S.* Bovismorbificans (7.2% of isolations).

Figure 4.2.3: Isolations in 2020



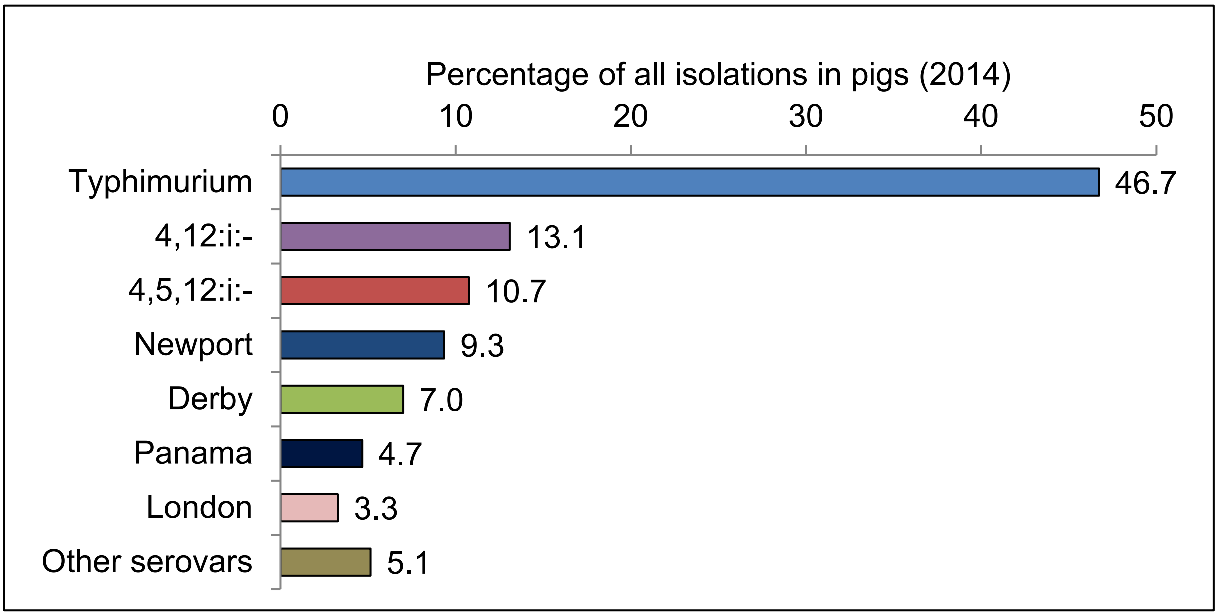
The most common serovar in pigs in 2020 was *S.* Typhimurium (43.9% of isolations), followed by *Salmonella* 4,5,12:i:- (19.0% of isolations), *Salmonella* 4,12:i:- (15.3% of isolations) and *S.* Derby (6.3% of isolations).

Figure 4.2.4 Isolations in 2021



The most common serovar in pigs in 2021 was *S.* Typhimurium (44.8% of isolations), followed by *Salmonella* 4,12:i:- (16.6% of isolations), *Salmonella* 4,5,12:i:- (11.7% of isolations) and *S.* Newport (8.5% of isolations).

Figure 4.2.5: Isolations in 2022



The most common serovar in pigs in 2022 was *S.* Typhimurium (46.7% of isolations), followed by *Salmonella* 4,12:i:- (13.1% of isolations), *Salmonella* 4,5,12:i:- (10.7% of isolations) and *S.* Newport (9.3% of isolations).

Figure 4.3: The 5 most common *Salmonella* serovars in pigs in Great Britain in 2022 and their trends over time since 2018

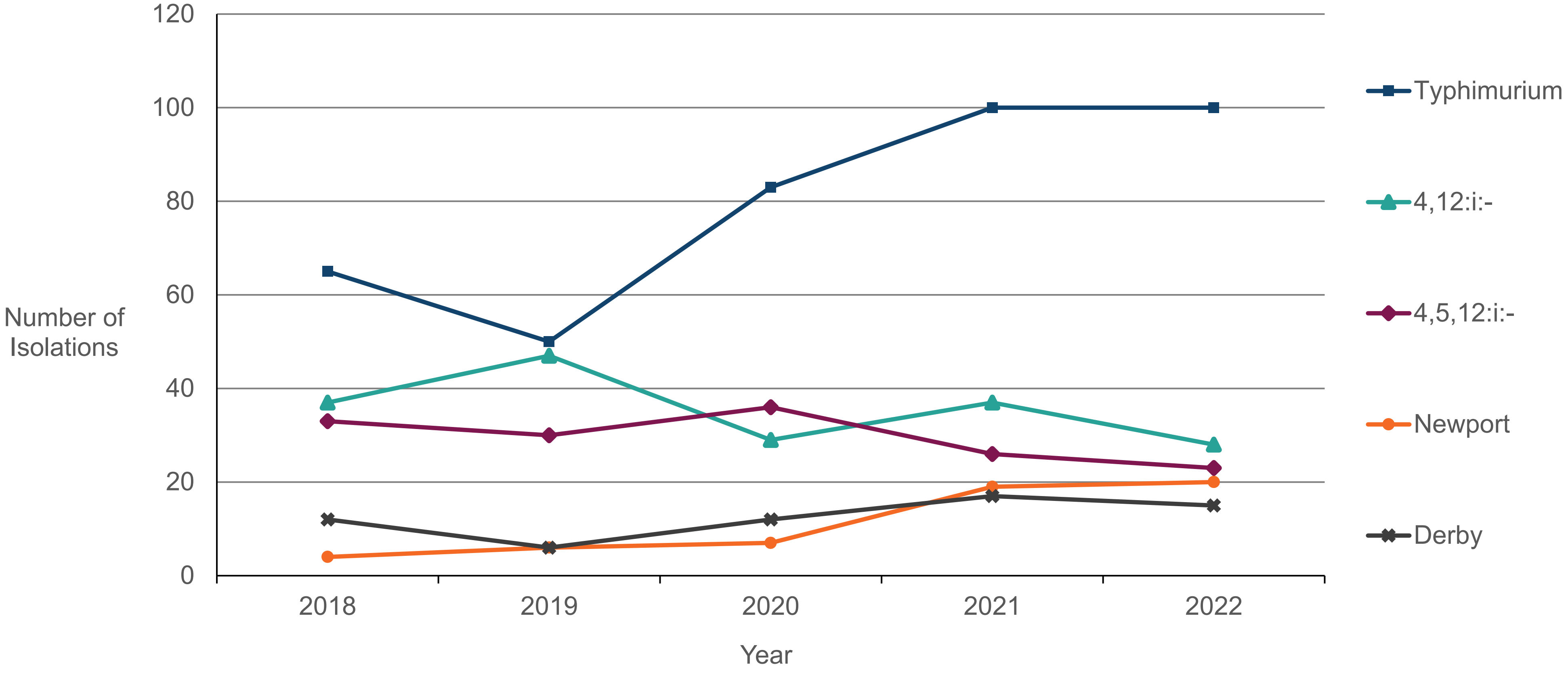


Figure 4.3 shows the most common serovars in pigs for all years was *S.* Typhimurium peaking at 100 isolations in 2021 and 2022. The number of isolations of the monophasic variants of *S.* Typhimurium (4,12:i:- and 4,5,12:i:-), *S.* Newport and *S.* Derby remained lower at below 30 isolations in 2022.

Figure 4.4: *S.* Derby, *S.* Enteritidis, *S.* Typhimurium and *Salmonella* 4,(5),12:i:- as a proportion of all isolations in pigs in Great Britain 2002 to 2022

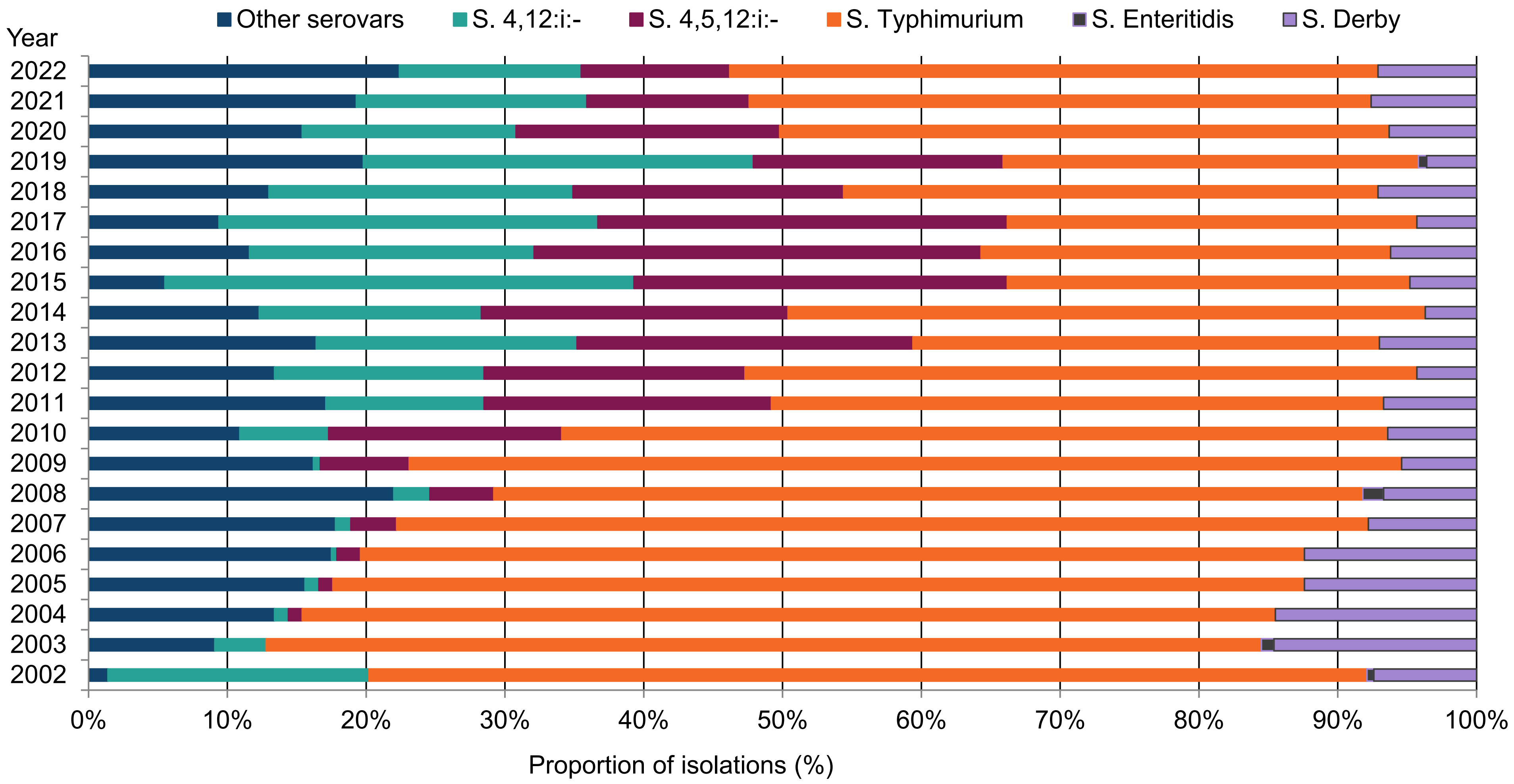


Figure 4.4 shows that as a proportion of all isolates in cattle in Great Britain between 2002 and 2022:

- *S.* Typhimurium accounted for the greatest proportion of isolates and varied across the years from 29 to 72%
- *S.* 4,5,12:i:- accounted for 32.2% of isolations in 2016 but has since declined and made up 10.7 in 2022
- *S.* 4,12:i:- was far more variable across the years with a high of 33.8% in 2015 and low of 0.4% in 2006
- *S.* Derby decreased as a proportion of the total until 2022, when it was 7.1% from a high of 14.6 2003
- *S.* Enteritidis was isolated in low numbers in 2002, 2003, 2008 and 2018
- 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	*S.* 4,12:i:-	*S.* 4,5,12:i:-	*S.* Typhimurium	*S.* Enteritidis	*S.* Derby
2002	1.4%	18.8%	0.0%	71.9%	0.5%	7.4%
2003	9.1%	3.7%	0.0%	71.7%	0.9%	14.6%
2004	13.4%	1.0%	1.0%	70.1%	0.0%	14.5%
2005	15.6%	1.0%	1.0%	70.0%	0.0%	12.4%
2006	17.5%	0.4%	1.7%	68.0%	0.0%	12.4%
2007	17.8%	1.1%	3.3%	70.0%	0.0%	7.8%
2008	22.0%	2.6%	4.6%	62.6%	1.5%	6.7%
2009	16.2%	0.5%	6.4%	71.5%	0.0%	5.4%
2010	10.9%	6.4%	16.8%	59.5%	0.0%	6.4%
2011	17.1%	11.4%	20.7%	44.1%	0.0%	6.7%
2012	13.4%	15.1%	18.8%	48.4%	0.0%	4.3%
2013	16.4%	18.8%	24.2%	33.6%	0.0%	7.0%
2014	12.3%	16.0%	22.1%	45.9%	0.0%	3.7%
2015	5.5%	33.8%	26.9%	29.0%	0.0%	4.8%
2016	11.6%	20.5%	32.2%	29.5%	0.0%	6.2%
2017	9.4%	27.3%	29.5%	29.5%	0.0%	4.3%
2018	13.0%	21.9%	19.5%	38.5%	0.0%	7.1%

Year	**Other serovars**	***S.* 4,12:i:-**	***S.* 4,5,12:i:-**	***S.* Typhimurium**	***S.* Enteritidis**	***S.* Derby**
2019	19.8%	28.1%	18.0%	29.9%	0.6%	3.6%
2020	15.4%	15.4%	19.0%	43.9%	0.0%	6.3%
2021	19.3%	16.6%	11.7%	44.8%	0.0%	7.6%
2022	22.4%	13.1%	10.7%	46.7%	0.0%	7.1%

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

Phage Types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
4	0	0	0	0	5	5	5	4	6	6
8	0	0	0	0	0	0	1	1	0	0
9	0	0	0	0	0	0	2	2	4	3
32	2	2	2	2	0	0	2	2	16	16
52	0	0	0	0	0	0	1	1	1	1
104	1	1	1	1	4	4	0	0	1	1
105	0	0	0	0	0	0	0	0	2	2
118	0	0	0	0	0	0	0	0	1	1
120	0	0	0	0	0	0	1	1	2	2
181	0	0	0	0	0	0	0	0	1	1
193	18	17	17	17	26	26	27	27	27	25
204b	0	0	0	0	1	1	0	0	0	0
U288	28	20	22	21	36	33	36	35	6	6
U302	5	5	4	4	1	1	0	0	0	0
U308	0	0	0	0	1	1	8	6	3	3
U308a	0	0	0	0	0	0	7	7	18	18
U323	0	0	0	0	1	1	0	0	0	0
NOPT	8	0	2	0	2	0	2	1	0	0
RDNC	0	0	1	1	5	3	8	6	12	12
UNTY	3	2	1	1	1	1	0	0	0	0
Total	**65**	**47**	**50**	**47**	**83**	**76**	**100**	**93**	**100**	**97**

Table 4.3: *Salmonella* 4,5,12:i:- phage types in pigs in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
UNTY	2	1	2	2	0	0	0	0	2	1
RDNC	0	0	0	0	2	2	2	2	0	0
NOPT	0	0	0	0	2	2	2	2	0	0
U311	0	0	0	0	0	0	1	1	1	1
DT193	31	27	28	25	32	30	18	18	20	17
DT120	0	0	0	0	0	0	2	1	0	0
Total	**33**	**28**	**30**	**27**	**36**	**34**	**25**	**24**	**23**	**19**

Table 4.4: *Salmonella* 4,12:i:- phage types in pigs in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
UNTY	4	4	3	3	4	4	5	4	2	2
NOPT	0	0	1	0	1	1	0	0	0	0
U302	0	0	1	1	0	0	0	0	0	0
DT208	0	0	0	0	0	0	1	1	0	0
DT193	32	23	40	39	24	23	30	26	25	22
DT120	1	1	2	2	0	0	1	1	1	1
Total	**37**	**28**	**47**	**45**	**29**	**28**	**37**	**32**	**28**	**25**

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.

Deer

There were no isolations of *Salmonella* from deer during 2022, the same as during 2021. Prior to that there were 2 isolations in 2019 (*S*. Montevideo and *Salmonella* 4,5,12:i:-) and one isolation during 2018 (*S.* Dublin, Table 5.1). APHA received 99 diagnostic submissions from deer in 2022.

Horses

The number of horses recorded as being kept in Great Britain at the June 2022 Agricultural Census was 212,252, which is an increase of 2.7% compared to 2021 (206,705 animals).

There were 60 isolations of *Salmonella* from horses during 2022, all a result of clinical disease investigations. This represents a 33.3% increase on the total number of isolations recorded from horses during 2021 (45 isolations) and 46.3% more than in 2020 (41 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 2022 were *S*. Typhimurium (18 isolations, 30.0% of total horse isolations), *S*. Newport (6 isolations, 10% of total horse isolations), *S.* Agama (4 isolations, 6.7% of total horse isolations), *S*. Bovismorbificans (4 isolations, 6.7% of total horse isolations), *S.* Enteritidis (4 isolations, 6.7% of total horse isolations) and *S.* Oslo (4 isolations, 6.7% of total horse isolations). In contrast, during 2021 the most common serovars were *S*. Bovismorbificans (16 isolations, 35.6% of total horse isolations) followed by *S*. Typhimurium (15 isolations, 33.3% of total horse isolations).

The number of *S.* Typhimurium isolations during 2022 was slightly higher than that reported in 2021 (18 versus 15 isolations) and 2020 (16 isolations) but just under half of those reported in 2019 (34 isolations). As in 2021 there were no isolations of the monophasic strain of *Salmonella* Typhimurium, *Salmonella* 4,12:i:- in 2022. However, there were 2 isolations of the monophasic strain *Salmonella* 4,5,12:i:- (both DT104) in 2022, which compares to no isolations in 2021 (Figure 5.5).

The 18 isolations of *S*. Typhimurium reported from horses during 2022 comprised 8 different phage types (excluding RDNC) (Table 5.4 and Figure 5.3). The most common phage type was DT105 (3 isolations). This phage type has not been previously identified by APHA in horses in Great Britain and the isolations originated from 3 different incidents. One incident stated diarrhoea as the main clinical sign, no information was available for the other 2 incidents. There were 2 isolations of DT1 which is often associated with wild birds, 2 isolations each of DT8, DT109, DT116 and DT193 and one isolation each of DT32 and DT104.

There were 4 isolations of *S*. Enteritidis (1x PT13a, 1x PT8 and 2x PT9a) in 2022, double that seen in 2021 when there were 2 isolations (1x PT13a and 1x NOPT). All isolations resulted from clinical disease investigations, but clinical presentation was not recorded. *S*. Enteritidis PT8 is often associated with feed and poultry.

There were single isolations each of *S.* Anatum, *S.* Braenderup and *S.* Durham in 2022, all resulting from clinical disease investigations. Neither *S.* Braenderup nor *S.* Durham have been reported in horses since 2017. *S*. Braenderup is a more common serovar of humans but is occasionally associated with poultry and feed.

Notably, the number of *S*. Bovismorbificans isolations recorded during 2022 was 75% lower than in 2021 (4 versus 16). *S.* Bovismorbificans is often associated with pigs and there was a similar decrease of 71.4% in the number of isolations from pigs in 2022 compared to 2021 (7 versus 2).

There were 6 isolations of *S.* Newport in 2022 compared to a single isolation in 2021 but consistent with 2020 numbers (7 isolations). All 6 isolations in 2022 were susceptible to all antimicrobials tested. In some parts of the country, *S.* Newport can be associated with badgers.

Rabbits

APHA received 12 diagnostic rabbit submissions in 2022. Of these there were 2 isolations of *Salmonella*, one each of *S.* Fluntern and *S.* Newport (Table 5.2) arising from separate incidents. The *S.* Newport isolate was fully susceptible to all antimicrobials tested. The last isolation from rabbits was in 2016 (*Salmonella* 21:g,t:-). Prior to that there was a single isolation in 2012 (*S*. Monschaui).

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

Salmonella **serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Dublin	1	1	0	0	0	0	0	0	0	0
Montevideo	0	0	1	1	0	0	0	0	0	0
4,5,12:i:-	0	0	1	1	0	0	0	0	0	0
Total	**1**	**1**	**2**	**2**	**0**	**0**	**0**	**0**	**0**	**0**

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

Salmonella **serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Fluntern	0	0	0	0	0	0	0	0	1	1
Newport	0	0	0	0	0	0	0	0	1	1
Total	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2**	**2**

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

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Agama	0	0	1	1	4	4	0	0	4	4
Agona	0	0	0	0	0	0	1	1	0	0
Anatum	2	2	0	0	2	2	0	0	1	1
Bovismorbificans	7	6	19	11	0	0	16	10	4	4
Braenderup	0	0	0	0	0	0	0	0	1	1
Coeln	0	0	2	2	0	0	0	0	2	2
Concord	0	0	0	0	0	0	1	1	0	0
Dublin	0	0	1	1	0	0	1	1	2	2
Durham	0	0	0	0	0	0	0	0	1	1
Eboko	0	0	0	0	0	0	0	0	3	3
Enteritidis	1	1	5	5	1	1	2	2	4	4
Hessarek	0	0	1	1	0	0	0	0	0	0
Javiana	0	0	0	0	1	1	0	0	0	0
Kingston	0	0	5	4	3	3	2	2	3	2
Kottbus	0	0	0	0	1	1	1	1	3	3
London	1	1	0	0	0	0	0	0	0	0
Mbandaka	0	0	3	2	0	0	0	0	0	0
Mokola	0	0	0	0	1	1	0	0	0	0
Montevideo	0	0	0	0	0	0	1	1	0	0
Newport	2	2	12	8	7	6	1	1	6	6
Oslo	0	0	23	7	1	1	1	1	4	4
Paratyphi B var. Java	0	0	0	0	1	1	1	1	0	0
Stanleyville	0	0	0	0	0	0	1	1	0	0
Typhimurium	7	4	34	23	16	15	15	12	18	17

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
4,5,12:i:-	0	0	6	1	3	1	0	0	2	1
4,12:i:-	0	0	12	7	0	0	0	0	0	0
untypable strains	1	1	2	2	0	0	1	1	2	2
Total	**21**	**17**	**126**	**75**	**41**	**37**	**45**	**36**	**60**	**57**

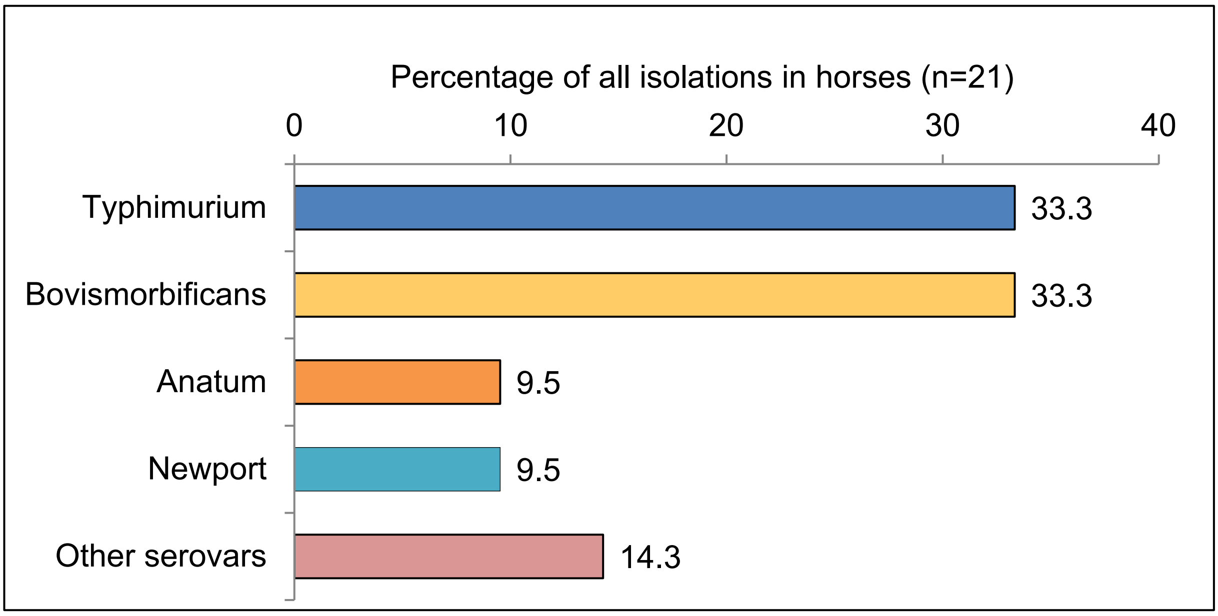
Table 5.4: Isolations and incidents of *S.* Typhimurium in horses on all premises in Great Britain

Phage types	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
1	0	0	2	1	1	1	5	5	2	2
2	0	0	0	0	0	0	2	2	0	0
8	0	0	3	3	0	0	0	0	2	1
12	1	1	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	1	1
29	0	0	0	0	0	0	1	1	0	0
40	0	0	4	2	0	0	0	0	0	0
41	1	1	3	3	0	0	0	0	0	0
104	0	0	3	3	0	0	0	0	1	1
105	0	0	0	0	0	0	0	0	3	3
109	0	0	0	0	0	0	0	0	2	2
116	0	0	0	0	5	4	0	0	2	2
135	0	0	1	1	0	0	0	0	0	0
193	0	0	4	2	2	2	0	0	2	2
U188	0	0	2	2	0	0	0	0	0	0
U302	0	0	6	3	0	0	1	1	0	0

Phage types	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
U320	1	1	0	0	1	1	0	0	0	0
UNTY	0	0	1	1	0	0	0	0	0	0
RDNC	4	1	5	2	7	7	6	3	3	3
Total	**7**	**4**	**34**	**23**	**16**	**15**	**15**	**12**	**18**	**17**

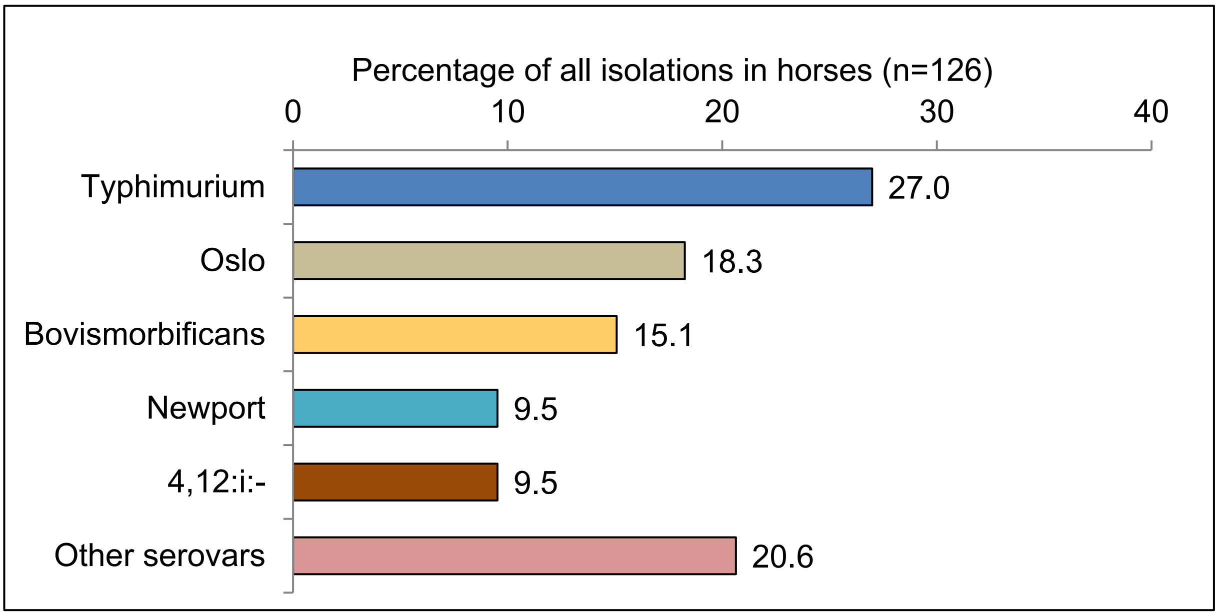
Figure 5.1: Isolations of the most common serovars in horses in Great Britain 2018 to 2022

Figure 5.1.1: Isolations in 2018



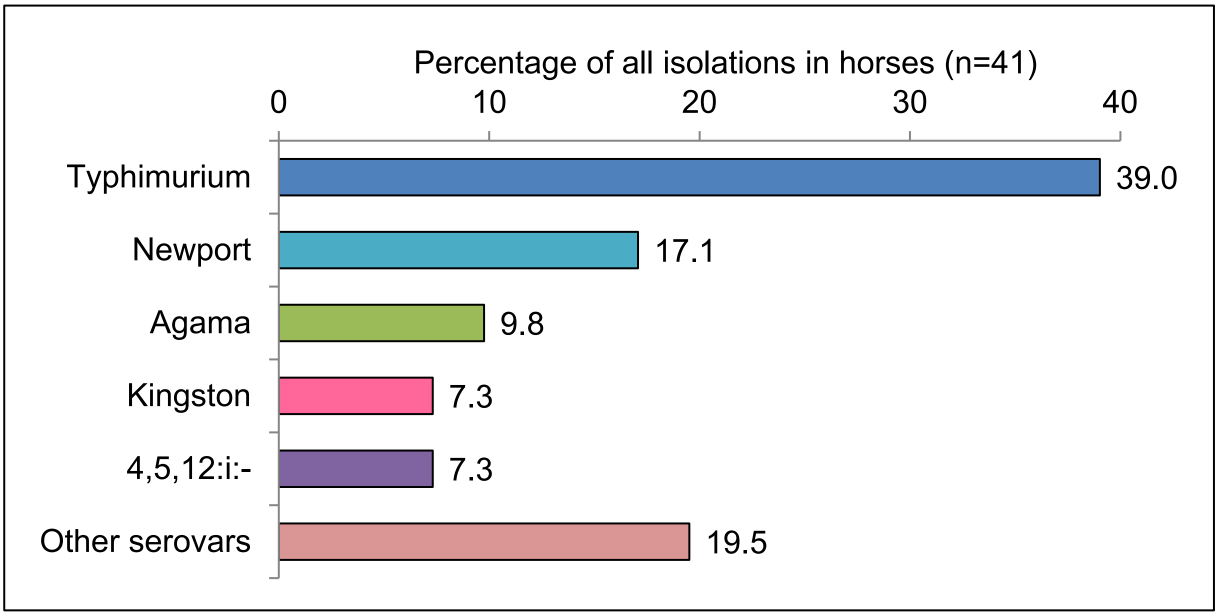
The most common serovars in horses in 2018 were *S.* Typhimurium and *S*. Bovismorbificans (33.3% of isolations each), followed by *S.* Anatum and *S*. Newport (9.5% of isolations each).

Figure 5.1.2: Isolations in 2019



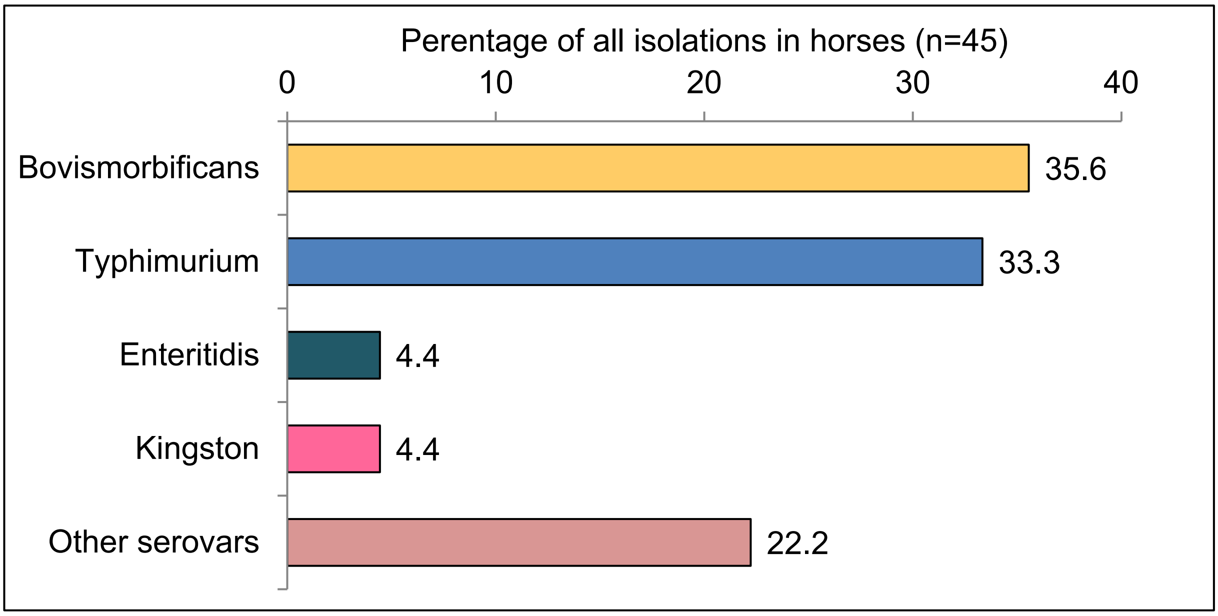
The most common serovar in horses in 2019 was *S.* Typhimurium (27.0% of isolations), followed by *S*. Oslo (18.3% of isolations), *S.* Bovismorbificans (15.1% of isolations) and *S*. Newport and *Salmonella* 4,12:i:- (9.5% of isolations each).

Figure 5.1.3: Isolations in 2020



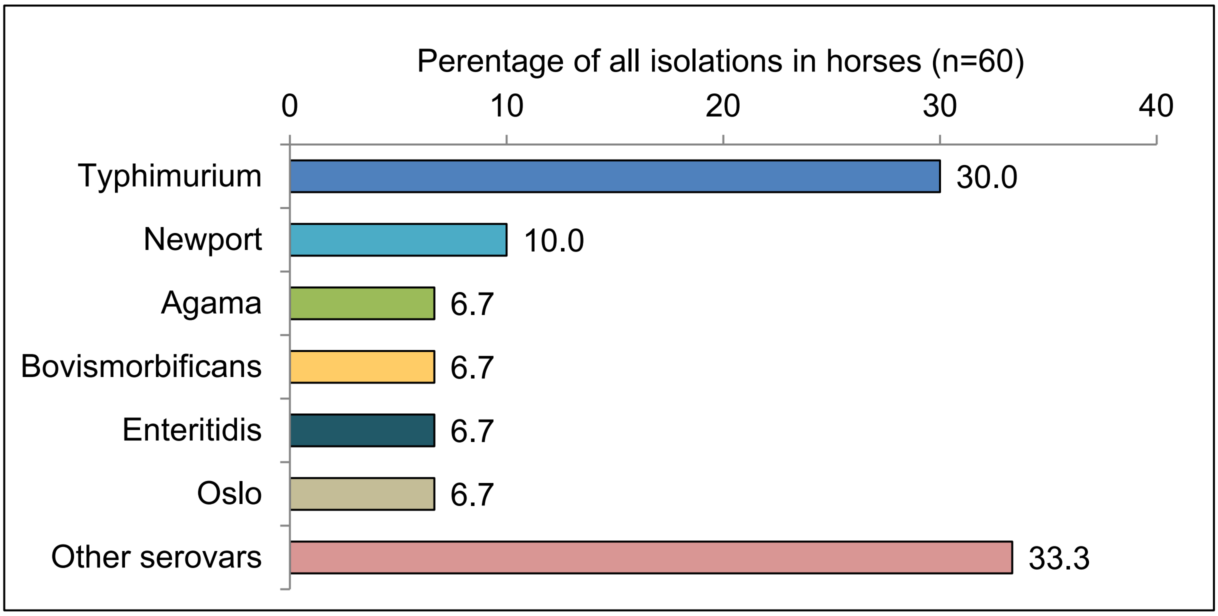
The most common serovar in horses in 2020 was *S.* Typhimurium (39.0% of isolations), followed by *S*. Newport (17.1% of isolations), *S.* Agama (9.8% of isolations) and *S*. Kingston and *Salmonella* 4,5,12:i:- (7.3% of isolations each).

Figure 5.1.4: 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 5.1.5: 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 5.2: The 6 most common *Salmonella* serovars in horses in Great Britain in 2022 and their trends over time since 2018

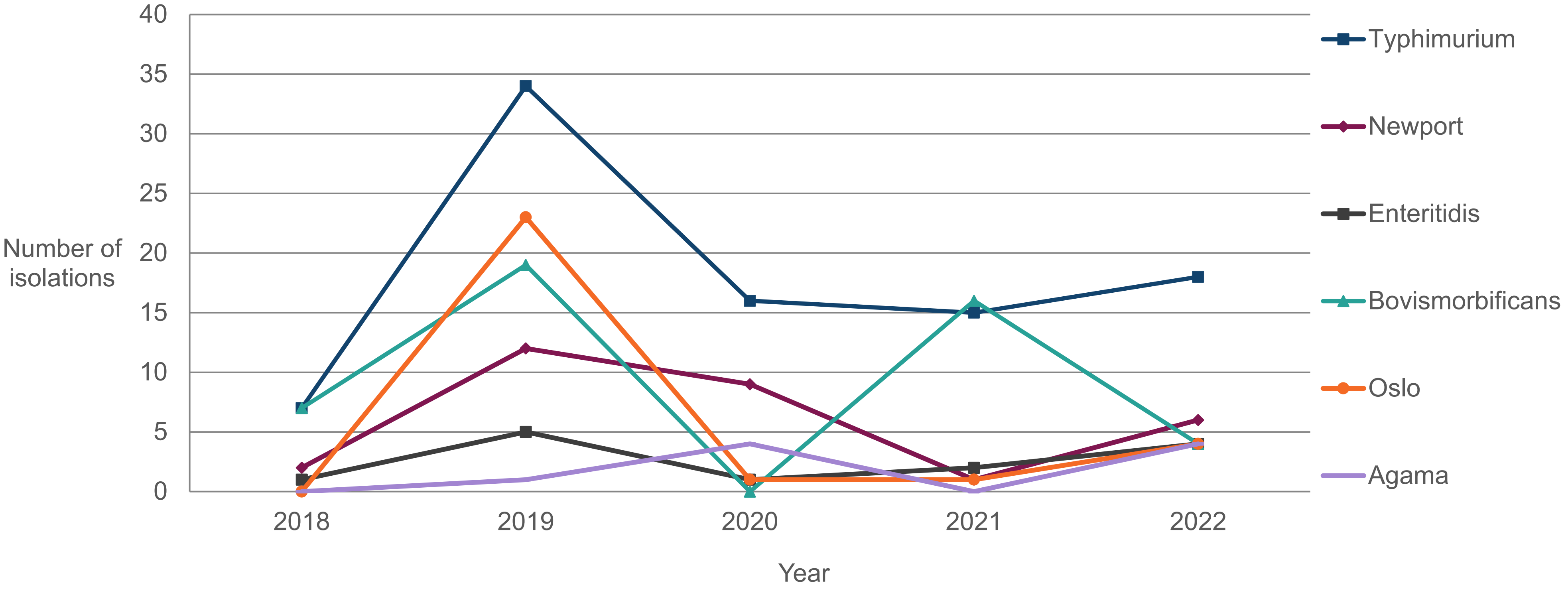


Figure 5.2 shows that *S.* Typhimurium remains the top serovar in horses with 18 isolations in 2022, remaining relatively stable since 2020. The second most common serovar in horses in 2022 was *S.* Newport which has decreased from 12 isolations in 2019 to 6 in 2022. *S.* Agama and *S*. Enteritidis typically have low numbers (less than 5) of isolations across all years and were joint third most common serovar in horses in 2022 along with *S.* Oslo and *S.* Bovismorbificans, all with 4 isolations.

Figure 5.3: *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and *Salmonella* 4,(5),12:i:- as a proportion of all isolations in horses in Great Britain 2002 to 2022

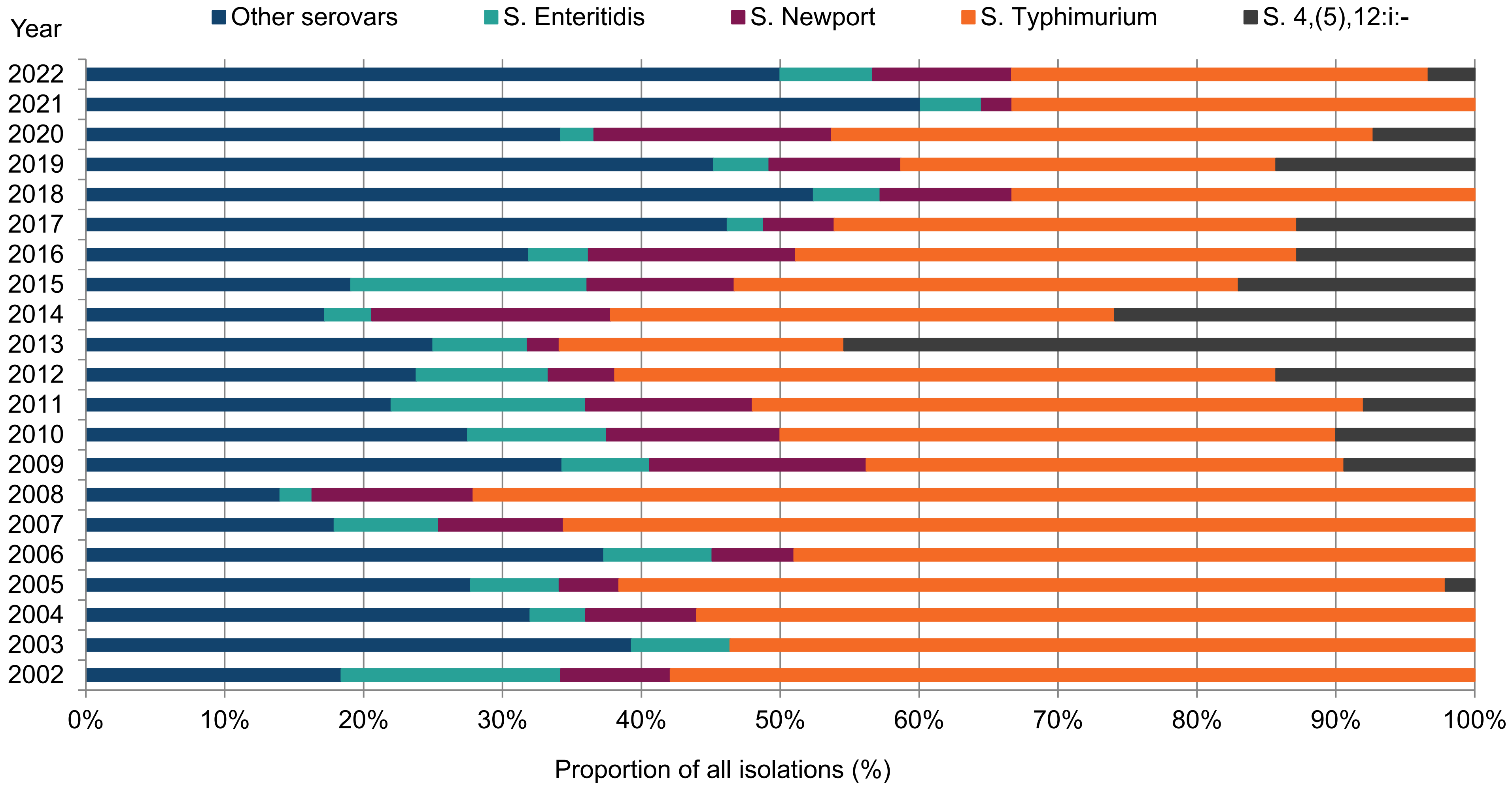


Figure 5.3 shows the proportion of all isolates of *S*. Enteritidis, *S*. Newport, *S*. Typhimurium and *Salmonella* 4,(5),12:i:- in horses in Great Britain between 2002 and 2022:

- *S*. Typhimurium accounted for the greatest proportion of isolates and varied stable across the years at 20-72%
- *S*. 4,(5),12:i:- in was variable across the years with a high of 45.4% in 2013 and no isolations in 2002 to 2004, 2006 to 2008, 2018 and 2021
- *S*. Newport accounted for 17.2% of isolations in 2014, with less in other years and no isolations in 2003
- *S*. Enteritidis was also more variable with a low of 2.3% in 2008 and a high of 17.0% in 2015
- other serovars have accounted for between 14.0% and 60.1% since with fluctuations year on year but an overall increase

Figure 5.3: Table of data

Year	Other serovars	*S.* Enteritidis	*S.* Newport	*S.* Typhimurium	*S.* 4,(5),12:i:-
2002	18.4%	15.8%	7.9%	57.9%	0.0%
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%
2016	31.9%	4.3%	14.9%	36.1%	12.8%

Year	Other serovars	*S.* Enteritidis	*S.* Newport	*S.* Typhimurium	*S.* 4,(5),12:i:-
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%

Table 5.5: *Salmonella* 4,5,12:i:- phage types in horses in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
DT193	0	0	6	1	3	1	0	0	0	0
DT104	0	0	0	0	0	0	0	0	2	1
Total	**0**	**0**	**6**	**1**	**3**	**1**	**0**	**0**	**2**	**1**

Table 5.6: *Salmonella* 4,12:i:- phage types in horses in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
DT193	0	0	12	7	0	0	0	0	0	0
Total	**0**	**0**	**12**	**7**	**0**	**0**	**0**	**0**	**0**	**0**

Table 5.7: *S.* Enteritidis phage types in horses in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
UNTY	0	0	0	0	0	0	0	0	0	0
NOPT	0	0	0	0	0	0	1	1	0	0
PT21	0	0	1	1	0	0	0	0	0	0
PT13a	0	0	3	3	0	0	1	1	1	1
PT11	0	0	1	1	0	0	0	0	0	0
PT9A	0	0	0	0	0	0	0	0	2	2
PT8	0	0	0	0	1	1	0	0	1	1
PT4	1	1	0	0	0	0	0	0	0	0
Total	1	1	5	5	1	1	2	2	4	4

Chapter 6: Reports of *Salmonella* in chickens

During 2022 there was significant disruption to the poultry industry as a result of Avian Influenza. The outbreak was long running affecting all industry sectors country wide. Altered management and biosecurity measures were necessary. This is likely to have impacted submission numbers. During 2020 and 2021 there was a reduction in submissions for non-statutory surveillance and a reduction in diagnostic submissions in many species as a consequence of the Covid-19 pandemic and associated lockdown measures. This should therefore be borne in mind when comparing 2020, 2021 and 2022 data with previous years.

According to the June Agricultural Census, the total number of chickens held in Great Britain was 153.5 million birds in 2022, comprising approximately 44.1 million breeding and laying hens, and 109.5 million broiler chickens (Figure 6.1). This compares to 135.3 million chickens in 2021, an increase of 13.5%.

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 very small proportion of the total isolates reported in Great Britain. Results from the NCPs are reported in a way that ensures that every flock with a *Salmonella*-positive result is counted only once. Numbers of positive flocks reported within the NCP are, therefore, expected to differ from the number of reported isolations. For example, some flocks may be positive for more than one serovar, in which case they are still only counted once as positive flocks for the NCP. This also applies if there is a long interval between positive tests from the same flock.

There was a total of 5,414 chicken diagnostic and monitoring submissions received by APHA and SRUC laboratories in 2022, a decrease of 5.1% compared to 5,703 in 2021. 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.

There were 2,404 isolations of *Salmonella* from chickens in 2022 (Table 6.1) an increase of 43.9 % compared with 2021 (1,671 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 and is possibly linked to the ban on using formaldehyde based products in animal feed production since January 2018, across the EU and more recently in retained Great Britain legislation, as well as emergence of strains that are more persistent in farms and hatcheries.

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 2022 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 2,234 (92.9%)
- voluntary surveillance: 169 (7.0%)
- clinical disease: 1 (0.04%)

The percentage of *Salmonella* isolations reported through statutory surveillance in 2022 was similar to 2021 data when 87.3% of total chicken isolations arose from statutory surveillance.

Forty-five different *Salmonella* serovars were isolated in 2022, accounting for 2,356 of the 2,404 isolations. Forty-eight isolations involved untypable *Salmonella* cultures (including 18 rough strains). Table 6.1 shows the *Salmonella* serovars isolated from chickens between 2018 and 2022. Figure 6.2 shows the relative percentages of the most common serovars isolated from chickens between 2018 and 2022.

The 4 most common serovars isolated from chickens in 2022 is consistent with 2018-2021, however the relative contribution of each serovar varied (Figure 6.3). *Salmonella* Mbandaka was the most frequently isolated serovar in 2022 (695 isolations, 28.9% of all chicken isolations) having increased by over two-fold compared to 2021 (294 isolations), which will have contributed to the overall increase in number of *Salmonella* isolations in 2022 compared with previous years. Isolations of *S*. Mbandaka, which is a 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.

There were 460 isolations of *S*. Montevideo in 2022 accounting for 19.1% of all chicken isolations and the second most frequently isolated serovar compared to the most frequently isolated in 2021 (403 isolations, 24.1% of all chicken isolations) (Figure 6.2).

Isolations of this serovar have been increasing year-on-year since 2015 (when there were 31 isolations). Isolations rose sharply in 2021 when there was a 53.8% increase compared with 2020 (262 isolations), and a 14.1% increase in 2022 compared to 2021 continues this trend (Figure 6.3).

In 2022 there were 343 isolations of *Salmonella* 13,23:i:- accounting for 14.3% of all *Salmonella* isolations and making it the third most frequently isolated serovar, consistent with 2021. For the 3 years previous to 2021 *Salmonella* 13,23:i:- had been the most frequently isolated serovar and in 2020 the number of isolations peaked (716 isolations) (Figure 6.3). Isolations of this serovar increased in 2022 compared with the low numbers in 2021 (279 isolations). Having first been isolated in 2009, this is the first time since 2017 that the relative proportion of isolations of *Salmonella* 13,23:i:- has fallen below 15%. 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).

Salmonella Kedougou accounted for 277 isolations in 2022 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). Although isolations in 2022 have increased compared to 2021 (217 isolations) the relative proportion associated with this serovar has reduced from 13.0% to 11.5% in 2022. 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 *S*. Agona from chickens increased by more than three-fold in 2022 (128 isolations) compared to 2021 (34 isolations). This is the highest number of isolations of this serovar ever reported, though similar to numbers in 2020 (101 isolations). Since 2018 there has been large fluctuations in numbers of this serovar which is usually associated with feed contamination.

In 2022, there was a sharp rise in the number of isolations of *S.* Idikan (45 isolations) in the Great Britain chicken population compared with 2021 (5 isolations) which were largely associated with single incursions isolated from broiler flocks as part of the NCP (40 flocks). This serovar is often associated with imported vegetable protein feed ingredients. There were 60 isolations of *S.* Orion var. 15^+ in 2022, which is a marked increase compared to 2021 (34 isolations) and more than a four-fold increase in the number of isolations in 2019 (14 isolations) and years previous. *Salmonella* Orion var. 15^+ isolations originate mainly from broiler flocks and are likely related to the feed source. There was a three-fold increase in isolations of *S*. Havana in 2022 (6 isolations) compared with 2021 (2 isolations). Other notable increases in serovars isolated from chickens in 2022 compared with 2021 included *S.* Infantis (98 versus 42 isolations), *S.* Enteritidis (23 versus 9 isolations), the monophasic *Salmonella* Typhimurium variant *Salmonella* 4,5,12:i:- (18 versus 8 isolations).

There were 23 isolations of *S.* Enteritidis in 2022 representing more than a two-fold increase compared to 2021 (9 isolations) when isolations were at a 5 year low. Recently, isolations of *S*. Enteritidis peaked in 2019 with 48 isolations. These isolations in 2022 were associated with 6 flocks (5 of which were from the layer sector), one more flock than in 2021 (5 flocks). There was less diversity of phage types of *S.* Enteritidis isolated in 2022 compared to 2021 with 19 of 23 isolations of PT8 (Table 6.5), also the most common phage type in 2109 and 2020. The remaining typeable phage types isolated in 2022 were associated with single isolations of PT20, PT14b (last reported from chickens in Great Britain in 2009) and PT11 (last isolated from chickens in 2014).

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 2022, there were approximately double the number of isolations of *Salmonella* 4,5,12:i:- (18 isolations) compared with 2021 (8 isolations), which follows a doubling of isolations compared with the year previous (4 isolations in 2020). All isolations were phage type DT193 (Table 6.3). This has been the only phage type isolated since 2019. Eleven of these eighteen isolations occurred on one broiler holding detected via NCP testing. The cases of monophasic *S.* Typhimurium are considered likely to be associated with contamination originating from pig herds.

Isolations of *S*. Infantis in chickens were markedly increased across all chicken sectors in 2022 with 98 isolations compared with 42 isolations in 2021 and one isolation in 2020. *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.

Other notable trends include decreases in isolations of *S*. Bovismorbificans, *S.* Newport, *S*. Senftenberg, *Salmonella* 4,12:i:-, *S.* Livingstone from chickens in 2022 compared to 2021.

There were 12 isolations of *S.* Newport, a reduction of 67.6% on the number in 2021 (37 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 2022 with 37 isolations compared to 63 isolations in 2021 and 96 isolations in 2020. Isolations of *Salmonella* Senftenberg peaked in 2017 (238 isolations) and are often related to hatchery contamination. There was a single isolation of *Salmonella* 4,12:i:- in 2022 compared with 4 in 2021, the lowest number of isolations of this serovar since 2012. This isolation was phage type DT120 (Table 6.4) which was last isolated from chickens in 2012. As with *Salmonella* 4,5,12:i:-, cases of this monophasic variant of *S*. Typhimurium in chickens are likely to be associated with contamination originating from pig herds. Isolations of *S*. Livingstone reduced from 17 isolations in 2021 to 3 isolations in 2022. Whilst this is a large reduction in the number of isolations it should be noted that the 17 isolations in 2021 came from 4 flocks compared to 3 flocks in 2022. Nonetheless, this is the lowest number of isolations of this serovar since before 2012.

There were eighteen *S.* Typhimurium isolations from chickens in 2022, accounting for 0.75% of all *Salmonella* isolations and similar to 2021 (0.9% of all *Salmonella* isolations, 15 isolations). There was less variability in phage types in 2022 (4 phage types) compared with 2021 (7 phage types) (Table 6.2). The most common phage type in 2022 was DT75 (8 isolations), which has not previously been reported from chickens in Great Britain. Isolations originated from 5 flocks including layer and broiler flocks as part of the NCP. Seven further isolates did not conform to any phage reaction pattern in the current typing scheme (RDNC). Many of these strains are likely to be associated with wild birds.

In 2022 the following serovars were isolated from chickens in Great Britain for the first time: *S.* Eboko (1 isolation) and *S*. Takoradi (1 isolation). Other unusual serovars included *S*. Berta (last reported from chickens in 2013) and *S*. Corvallis (last reported from chickens in 2007).

There was one reported isolation of *Salmonella* (*S*. Infantis) from chickens imported into Great Britain in 2022 compared to 11 reports in 2021. This single isolation was associated with chicken meat products originating in the EU. These data are excluded from the tables and figures of this report.

National Control Programme for *Salmonella* in chickens

The Zoonoses Regulation EC No. 2160/2003, 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 the Great Britain law and are referenced as the retained EU legislation. 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 EC 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 2022

In 2022, 17 adult breeding flocks, on 13 separate holdings, tested positive for *Salmonella* spp. under the statutory testing programme. This is an increase compared with recent years including 2021 and 2020 (7 positive flocks), 2019 (13 positive flocks), and 2018 (12 positive flocks) and the highest number of positive flocks since 2009 when 19 flocks tested positive (overall prevalence 1.38%). 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 recent years (Figure 6.4).

Three adult breeding flocks tested positive for a regulated *Salmonella* serovar in 2022 (Table 6.6). *Salmonella* Typhimurium DT75 was identified in 2 layer parent breeding flocks (via routine annual official sampling) on the same premise and *S*. Infantis was identified in a broiler parent breeding flock (via routine annual official sampling). Having first been isolated in 2021, this is the second year that *S*. Infantis has been isolated from a chicken breeder flock since the inception of the NCP. *Salmonella* Typhimurium was last identified in chicken breeder flocks as part of the NCP in 2020 from a broiler grandparent breeding flock. *Salmonella* 4,12:i:- and *Salmonella* 4,5,12:i:- were last detected in 2014 and 2010, respectively. *Salmonella* Enteritidis has never been detected in the breeding chicken NCP.

Fourteen adult breeding flocks on 11 separate holdings, compared with 9 flocks in 2021, were positive for non-regulated *Salmonella* serovars in 2022 (Table 6.6). Five broiler parent breeding flocks on 3 separate holdings tested positive for *Salmonella* 13,23:i:-, the most common serovar to be isolated from chicken breeders via NCP sampling this year. In most cases, this serovar is a monophasic variant of *S*. Idikan and can be a resident strain in some hatcheries and feed mills. The isolation of *Salmonella* 13,23:i:- in multiple flocks on the same holding may indicate a single incursion or common source linked to feed in these flocks. 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 (9 positive flocks). There has been a decreasing trend in occurrence of this serovar over recent years, but there was a reversal of this trend in 2022 (5 positive flocks compared to 1 positive flock in 2021).

Salmonella Give var. 15^+ (Newbrunswick) was isolated from 2 broiler parent flocks on 2 different holdings in 2022, which compares to 5 broiler parent flocks positive for this serovar on one holding in 2021. One of these flocks also tested positive for *S*. Agona via operator sampling on the same date. Prior to 2021*, S*. Give var. 15^+ had never been isolated from breeding chicken flocks in the NCP, but it is occasionally isolated from animal feed and is thought to have become resident on some duck farms.

Four non-regulated *Salmonella* serovars identified in adult parent breeding flocks during 2022 have never previously been reported via NCP sampling: *S*. Anatum, *S*. Corvallis, *S.* Idikan and *S*. Orion var. 15^+ (Binza). In addition, *S*. Agona was isolated from 2 broiler parent flocks in 2022, having most recently been isolated in 2017.

No immature (in-rear) breeding flocks tested positive for *Salmonella* spp. during 2022 compared with one in 2021 and 2 in 2020.

A comparison of the serovars identified in adult breeding flocks testing positive under the NCP between 2018 and 2022 is shown in Table 6.6 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, with the exception that *Salmonella* 13,23:i:- has been identified every year since 2013 (and always in broiler breeder flocks).

In Great Britain, a total of 1,156 adult breeding flocks on 284 premises were registered in 2022, and a total of 879 flocks were subject to *Salmonella* testing via routine annual official sampling visits*.* In 2022 there was a shortfall of approximately 24% in the number of flocks subject to annual official sampling, which is more than in 2021 when there was a shortfall of 13%. The shortfall in 2022 was largely due to the large Avian Influenza outbreak which impacted the number of official sampling visits that could take place. Using the number of registered flocks as the denominator population, the estimated prevalence of *Salmonella* spp. in adult breeding flocks within the NCP was 1.47% (17 of 1,156) in 2022. This is the highest number of positive flocks since 2009 when 19 flocks tested positive (prevalence of 1.38%) (Table 6.6, 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 retained EU 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 2022

During 2022, a total of 42 adult laying hen flocks, originating from 35 separate holdings, tested positive for *Salmonella* under the statutory testing programme. This is 37.3% lower than the number of flocks testing positive in 2008 when the NCP was first implemented (67 positive flocks), an increase of 10.5% compared to 2021 (38 positive flocks) (Table 6.7) and is the first increase in the number of positive flocks in the NCP since 2019 (Figure 6.6).

A total of 10 adult flocks, from 8 separate holdings, tested positive for regulated *Salmonella* serovars during 2022, similar to 2021 (9 positive flocks from 9 separate holdings) but fewer than in 2020 (14 flocks) and 2019 when prevalence of regulated serovars were at the highest levels since 2010 (16 positive flocks) (Table 6.7 and Figure 6.6). Five adult flocks from 4 separate holdings tested positive for *S.* Enteritidis (PT8 (x3), PT14b (x1), PT20 (x1)) in 2022. This is a slight increase compared to 2021 (3 positive flocks on 3 holdings), but is still 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). *Salmonella* Enteritidis PT14b and *S*. Enteritidis PT20 were both isolated for the first time as part of the layer NCP. 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.

Five adult flocks, from 4 separate holdings, tested positive for *S.* Typhimurium (RDNC (x4), DT75 (x1)) in 2022. This is a slight decrease from 6 flocks in 2021 and reverses an increasing trend seen in recent years in the number of flocks testing positive for this serovar: 4 positive flocks in 2020, and one positive flock in each of 2019 and 2018 (Table 6.7). Prior to 2018, *S*. Typhimurium had not been isolated from NCP samples collected from adult laying flocks since 2012, when 2 flocks on 2 different holdings tested positive.

No adult flocks of laying hens were positive for *Salmonella* 4,5,12:i:- or *Salmonella* 4,12:i:- in 2022. This is consistent with 2021 and 2020 and compares to just one flock testing positive for *Salmonella* 4,5,12:i:- (DT193) in 2019. 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 2018 and 2022 is shown in Table 6.7 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, 15 different non-regulated serovars were identified from adult laying chickens in 2022, from 32 flocks on 27 separate holdings. One flock tested positive for 2 different non-regulated serovars (*S*. Newport and *S*. Bardo).

The most common serovar, *S*. Mbandaka, was isolated from 6 flocks on 6 different holdings. This is the highest number of adult laying flocks that have tested positive for this serovar in the NCP since its inception. Contaminated compound feed may be a source of infection with *S*. Mbandaka in these flocks. Management factors, and in particular the large number of free-range flocks affect biosecurity which increases the risk of *Salmonella* introduction via wildlife and vermin.

Four adult flocks on 3 holdings tested positive for *S*. Derby and 3 adult flocks on 3 holdings tested positive for *S.* Infantis. This represents a marked increase in both serovars compared to recent years which are usually associated with single isolations when present. *S*. Dublin was isolated in 4 flocks in 2022 compared with no flocks since 2018 with the exception of 2019 when it was isolated from one flock.

Three adult flocks on 2 separate holdings tested positive for *S*. Bardo in 2022. This is the second year (first year 2021) that *S*. Bardo has been isolated from adult laying flocks in the NCP, though it was isolated from 2 immature layer flocks and a layer parent breeder flock in 2020. *Salmonella* Bardo is a variant of *S*. Newport, and one of the 3 adult flocks in 2022 also tested positive for *S*. Newport. This was also consistent with 2021 when 3 of the 5 positive adult flocks also tested positive for *S*. Newport. *Salmonella* Newport can often be associated with badgers and is also found in the layer breeding pyramid.

In 2022, no new serovars were isolated from adult laying flocks as part of the NCP compared with 8 the previous year.

Three immature (in-rear) laying flocks from 3 separate holdings were positive for *Salmonella* in 2022. All were *S*. Senftenberg, a known hatchery contaminant. This is the lowest numbers of immature flocks testing positive since 2018, and a large reduction compared with 2021 and 2020 (14 flocks and 25 flocks, respectively). The number of in-rear flocks testing positive for *Salmonella* each year between 2013 and 2019 was 8 or fewer. No in-rear layer flocks tested positive for regulated serovars in 2022. 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. Overall, 2022 saw a 79% reduction in positive flocks compared to 2021 when 14 in-rear flocks from 12 holdings tested positive.

Using the number of NCP-eligible adult flocks of laying hens in production in Great Britain during 2022 as the denominator population, the estimated prevalence of *Salmonella* spp. in laying flocks was 1.13% (42 of 3,721) in 2022. Prior to 2022, there had been a decreasing trend in flocks testing positive since 2019 (0.96% in 2021, 1.06% in 2020, 1.20% in 2019), but 2022 sees a slight reversal of this trend (Figure 6.6). The estimated prevalence of regulated *Salmonella* serovars in adult laying flocks was 0.27% (10 of 3,721) in 2022. This figure remains well below the target of 2.00% and is consistent with 2021 (0.23%) and lower than the previous 2 years (0.35% in 2020, 0.40% in 2019).

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 retained 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 2022

During 2022, a total of 1,960 broiler flocks from 478 separate holdings tested positive for *Salmonella* under NCP testing. This represents an increase of 56.3% compared to 2021 (1,254 flocks) and the highest prevalence since the inception of the NCP in 2009. The increase in 2022 continues a generally increasing trend (with exception of 2021) in positive flocks since 2017 (Table 6.8 and Figure 6.8). The increase in 2022 compared with 2021 is attributable to increases in the number of flocks positive for several different serovars, including *S.* Idikan (40 versus 5 flocks), *S.* Infantis (77 versus 22 flocks), *S.* Agona (114 versus 33 flocks, respectively), and *S.* Mbandaka (579 versus 238 flocks).

Fifteen broiler flocks, on 11 separate holdings, tested positive for regulated serovars in 2022. This is consistent with 2021, 2019 and 2018 (15 flocks tested positive in 2021, 17 flocks positive in both 2019 and 2018) but a five-fold increase in the number identified in 2020 (3 flocks positive) (Table 6.8 and Figure 6.8). Although the same number of flocks tested positive for regulated serovars in 2022 as in 2021 the proportion of different regulated serovars varied.

Four flocks from 4 separate holdings tested positive for *S.* Typhimurium (DT75 x2, DT99 x1, and DT1 x1) in 2022 the same as in 2021 (Table 6.8). This is the first time DT75 has been isolated from broiler flocks as part of the NCP having also been isolated from chicken layer and chicken breeding flocks in 2022.

Ten flocks, from 6 separate holdings, tested positive for monophasic *S*. Typhimurium 4,5,12:i:- (all DT193) in 2022. This compares with 6 flocks (from a single holding) testing positive for this serovar in 2021, and none in 2020. No flocks tested positive for monophasic *S*. Typhimurium 4,12:i:- in 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.

One flock tested positive for *S.* Enteritidis (PT11) in 2022 (Table 6.8). This is similar to 2021, when there were 2 positive flocks (on a single holding), and overall maintains the trend for very few broiler flocks testing positive for this serovar in recent years. This represents a considerable decrease compared to 2015, when 50 flocks tested positive for *S*. Enteritidis after an outbreak related to imported hatching eggs, which also happened in 2018 to a lesser extent (7 positive flocks). 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.

A comparison of the serovars identified in broiler flocks in the NCP between 2018 and 2022 is shown in Table 6.8 and Figure 6.9. Data for years prior to this are available in the *Salmonella* in Livestock Production reports from the relevant year. There were 1,945 broiler flocks positive for non-regulated *Salmonella* serovars in 2022, including fourteen flocks that tested positive for more than one non-regulated serovar. The 4 most common serovars isolated from broiler chickens in 2022 was consistent across all years since 2019.

Salmonella Mbandaka was the most frequently isolated serovar in 2022 (579 flocks) accounting for 29.5% of all *Salmonella* positive flocks. This is almost 2.5 times the number of positive flocks compared to 2021 (238 flocks) and is the highest number of flocks associated with this serovar since the inception of the NCP. In 2022, *S*. Mbandaka was identified on 193 premises, of which 60 (31.1%) premises were repeatedly positive for this serovar in subsequent flocks. *Salmonella* Mbandaka is a feed-related serovar, typically 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.

Salmonella Montevideo was the second most frequently reported serovar from broiler flocks in 2022 (409 flocks). This is an increase of 24.0% compared to 2021 (330 flocks).

There have been year on year increases in flocks testing positive for this serovar from 51 positive flocks in 2017 (Table 6.8). *Salmonella* Montevideo was identified on 142 premises in 2022, of which 46 (32.4%) were repeatedly positive for the same serovar in subsequent flocks. Multiple incursions of *S.* Montevideo were observed on individual premises. Of the 142 premises which had at least one positive flock for *S.* Montevideo, 19.7% (28 flocks) had 2 incursions of this serovar in 2022. Up to 7 incursions of *S.* Montevideo were observed on 3 premises, with 9.2% (13 of 142), 4.9% (7 of 142), 3.5% (5 of 142) and 1.4% (2 of 142) of premises having three, four, 5 and 6 incursions respectively. *Salmonella* Montevideo, which is commonly associated with feed, appears to be an efficient environmental persister and is able to colonise cooling systems for heat processed feed ingredients and finished feed, as well as hatcher cabinets and feeding systems on farms*.*

The occurrence of *Salmonella* 13,23:i:- has increased in 2022, with 301 flocks compared to 252 flocks in 2021, a 19.4% increase. 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 2022, *Salmonella* 13,23:i:- was identified on 113 premises, of which 41 (36.3%) were repeatedly positive for the same serovar in subsequent flocks.

Other notable increases in the number of broiler flocks testing positive in 2022 compared to 2021 include: *S*. Infantis (77 versus 22 flocks), *S*. Agona (114 versus 33 flocks), *S*. Idikan (40 versus 5 flocks) and *S*. Kedougou (232 versus 192 flocks). *Salmonella* Infantis is an unusual serovar in food animals in the Great Britain, but has been associated with imported feed ingredients, as well as raw meat pet food and dogs. It is one of the most frequently isolated serovars in broiler chickens across mainland Europe. *Salmonella* Kedougou is associated with feed mill environments and can be found in ingredients such as oilseed meals. *Salmonella* Agona is usually associated with feed contamination.

There were no new serovars reported from broiler flocks from NCP samples during 2022. Despite increases in most serovars in 2022 there was a notable decrease in flocks testing positive for *S*. Senftenberg from 29 flocks in 2021 to 18 flocks in 2022, a 37.9% reduction and the lowest number of flocks positive since 2017.

An estimated 45,741 broiler flocks were tested in Great Britain according to the requirements of the *Salmonella* NCP during 2022. Using this as the denominator population, the estimated prevalence of *Salmonella*-positive broiler flocks was 4.28% (1,960 of 45,741). This is an increase compared to recent years (2.41% in 2021, 3.38% in 2020 and 3.01% in 2019) and is the highest since the inception of the NCP in 2009 (Table 6.8, Figure 6.8).

The estimated prevalence of regulated *Salmonella* serovars in broiler flocks in Great Britain during 2022 was 0.03% (15 of 45,741). This is consistent with the prevalence in 2021 (0.03%) but slightly higher than in 2020 (0.01%) (Table 6.8, Figure 6.7). The prevalence of regulated *Salmonella* serovars in broiler chickens in 2022 was well below the definitive EU target of below 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 2013 to 2022

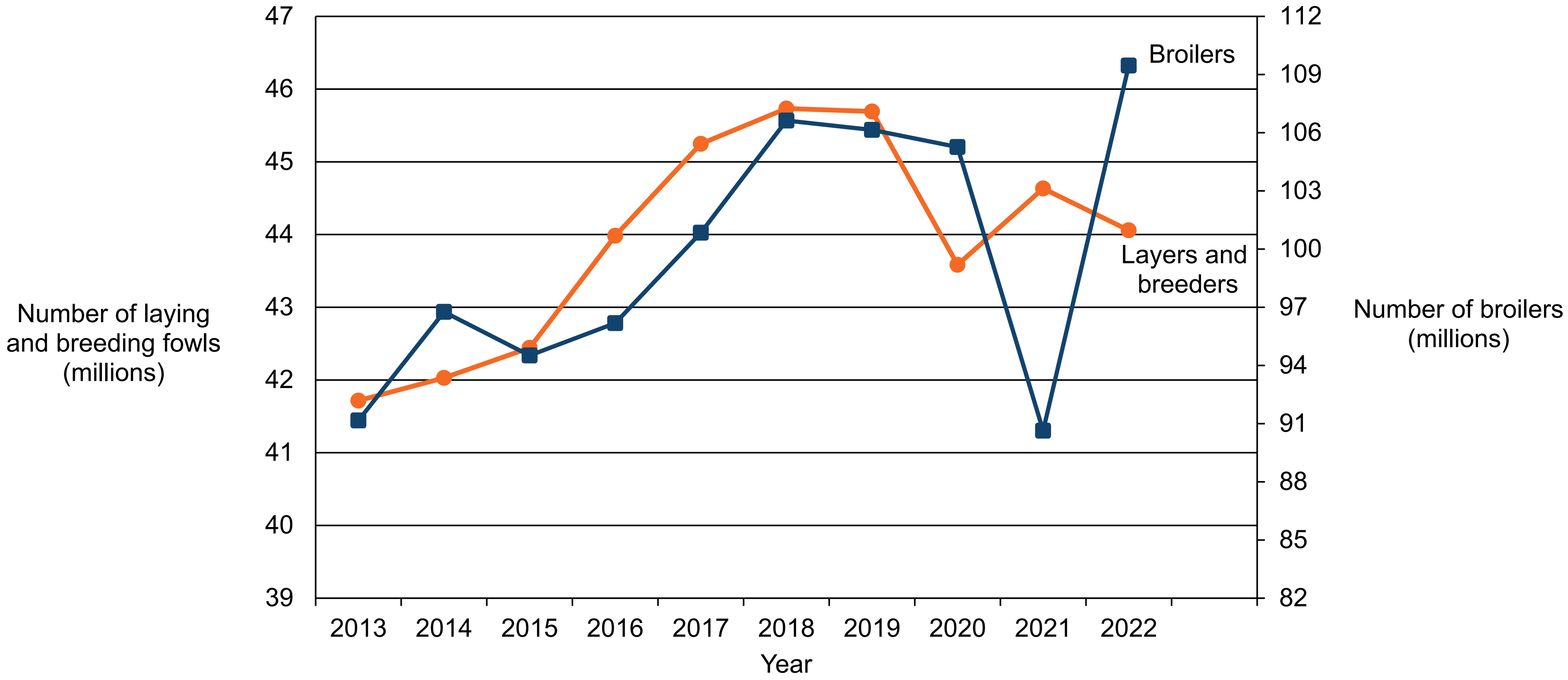


Figure 6.1 shows that the number of broiler, laying and breeding fowl in Great Britain increased steadily from 2013 to 2018 peaking at just over 106 million broilers and 45 million laying and breeding fowl in 2018. After this there was a slight decline in the number of layers and broilers to 44 million in 2022 but the number of broilers was at its highest level of 109 million birds in 2022.

Source: June 2021 (Scotland) and 2022 (England and Wales) 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	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
Africana	0	0	1	1	0	0	0	0	0	0
Agama	1	1	7	7	4	4	1	1	1	1
Agona	4	6	29	31	73	101	33	34	117	128
Ajiobo	0	0	0	0	0	0	0	1	0	0
Anatum	1	1	5	5	6	8	4	5	2	3
Bareilly	0	0	0	0	0	0	1	1	0	0
Bardo	0	0	0	0	1	13	5	10	3	5
Berta	0	0	0	0	0	0	0	0	1	1
Bovismorbificans	0	0	0	0	16	21	7	21	0	0
Braenderup	0	0	0	0	1	1	2	2	2	2
Bredeney	0	0	0	0	1	1	0	0	0	0
Budapest	1	1	0	0	0	0	0	0	0	0
Coeln	0	0	1	1	2	3	0	0	4	4
Corvallis	0	0	0	0	0	0	0	0	2	3
Derby	18	26	30	44	4	4	8	9	11	12
Dublin	0	0	1	1	0	0	0	0	4	4
Eastbourne	0	0	3	3	0	0	0	0	0	0
Eboko	0	0	0	0	0	0	0	0	1	1
Enteritidis	10	27	16	48	12	31	5	9	6	23
Essen	0	0	0	0	0	0	0	1	0	0
Ferruch	0	0	0	0	0	0	2	2	0	0
Fresno	0	0	0	1	0	0	0	0	0	0
Give	4	8	0	0	2	3	0	0	0	0
Give var.15^{+}	0	0	4	4	4	4	6	16	8	8

Salmonella serovar	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
Goldcoast	0	0	0	0	0	0	1	1	0	0
Havana	3	3	1	1	1	1	2	2	5	6
Idikan	9	13	16	17	5	8	5	5	41	45
Indiana	3	3	7	7	2	3	0	0	1	1
Infantis	1	2	0	0	0	1	24	42	81	98
Isangi	1	1	0	0	0	0	1	3	0	0
Kedougou	190	197	335	357	342	430	192	217	233	277
Kentucky	0	1	1	1	0	1	0	0	4	4
Kingston	1	1	1	1	2	2	0	0	2	2
Kottbus	5	6	2	4	2	5	0	0	1	1
Lexington	0	0	0	0	0	0	1	1	0	0
Liverpool	0	0	0	0	1	2	0	0	1	1
Livingstone	9	12	7	10	9	11	4	17	2	3
London	0	0	2	2	0	0	1	1	2	2
Mbandaka	353	472	335	367	232	261	240	294	586	695
Mikawasima	0	0	0	0	1	1	0	0	0	0
Minnesota	0	0	0	0	0	0	0	1	0	0
Molade	0	0	0	0	0	0	1	1	0	0
Montevideo	69	113	146	169	246	262	332	403	411	460
Muenchen	0	0	1	1	6	8	4	4	9	9
Newport	7	8	5	5	13	52	10	37	10	12
Nima	0	0	1	1	0	0	0	0	0	0
Nottingham	4	9	4	9	0	0	0	7	2	4
Odozi	0	0	0	0	0	0	2	4	0	0
Offa	0	0	1	1	0	0	0	0	0	0
Ohio	87	94	71	75	33	33	54	55	44	49
Orion	13	14	3	4	0	0	0	0	1	1
Orion var.15^{+}	11	15	12	14	28	30	33	34	55	60

Salmonella serovar	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
Oslo	2	2	2	2	2	2	2	2	0	0
Panama	0	0	0	0	0	0	1	1	1	2
Poona	1	2	0	0	1	1	0	0	0	0
Ramatgan	0	0	0	0	1	1	0	0	0	0
Reading	0	0	1	1	1	1	1	1	0	1
Rissen	2	2	1	1	0	0	0	0	1	1
Schwarzengrund	0	0	0	0	1	1	0	0	0	0
Senftenberg	19	56	33	72	53	96	29	63	19	37
Soerenga	1	1	0	0	0	0	0	0	0	0
Stanley	1	1	1	1	0	0	0	0	1	1
Stanleyville	0	0	0	0	1	1	0	0	0	1
Stourbridge	0	0	0	0	1	1	2	2	1	1
Takoradi	0	0	0	0	0	0	0	0	0	1
Tennessee	0	0	2	2	0	1	0	0	0	1
Typhimurium	5	9	11	14	6	19	10	15	11	18
4,5,12:i:-	1	2	3	4	0	4	6	8	10	18
4,12:i:-	5	8	3	3	1	9	3	4	0	1
13,23:i:-	459	681	426	436	600	716	253	279	306	343
61:-:1,5,7	0	0	1	1	0	0	0	0	0	0
Untypable strains	26	33	16	19	38	37	27	28	32	35
Rough strains	4	7	1	1	1	26	1	27	0	18
Total	**1321**	**1838**	**533**	**1749**	**1727**	**2221**	**1302**	**1671**	**2019**	**2404**

10 flocks were positive for more than one serovar in 2018.

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

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

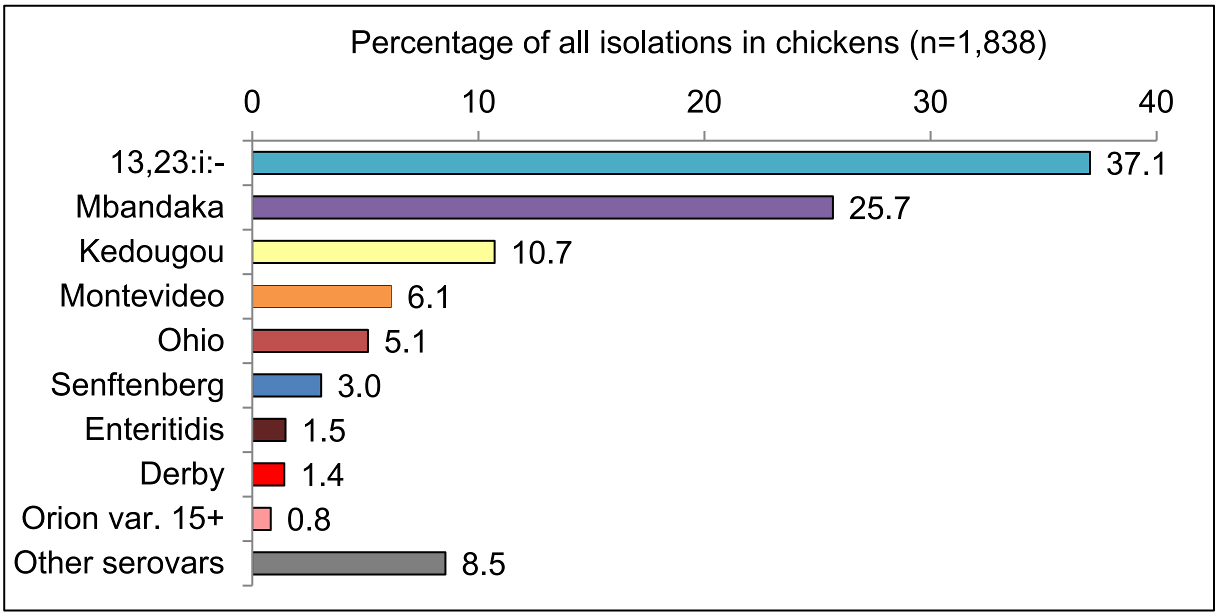
14 flocks were positive for more than one serovar in 2021.

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

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

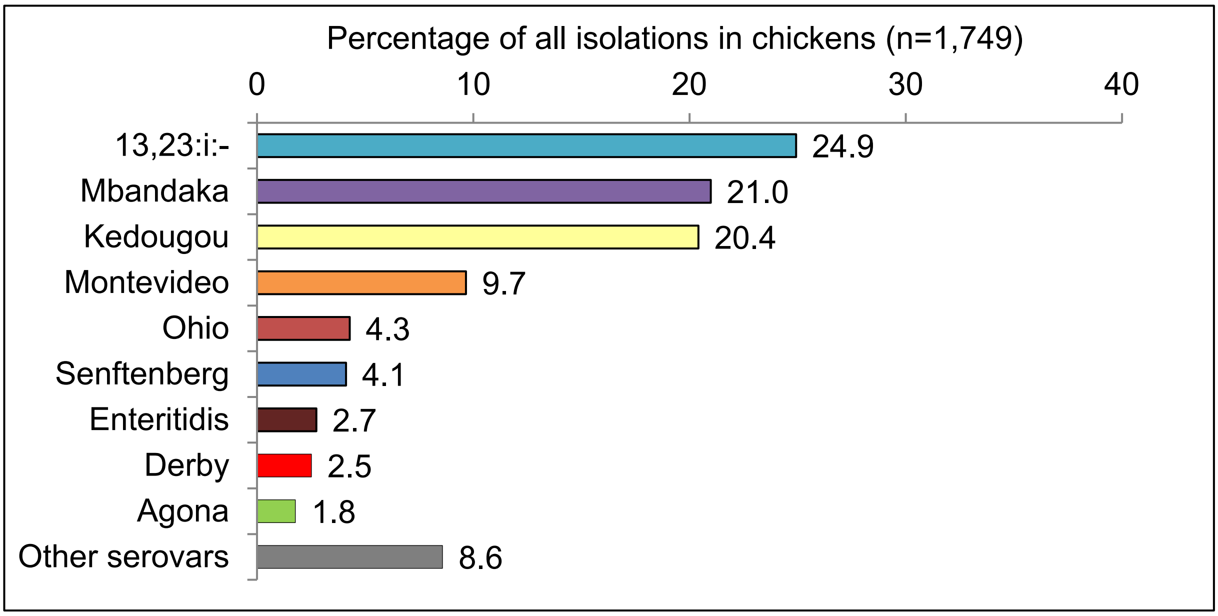
Figure 6.2: Isolations of the most common serovars in chickens in Great Britain 2018 to 2022 (statutory and non-statutory testing)

Figure 6.2.1: Isolations in 2018



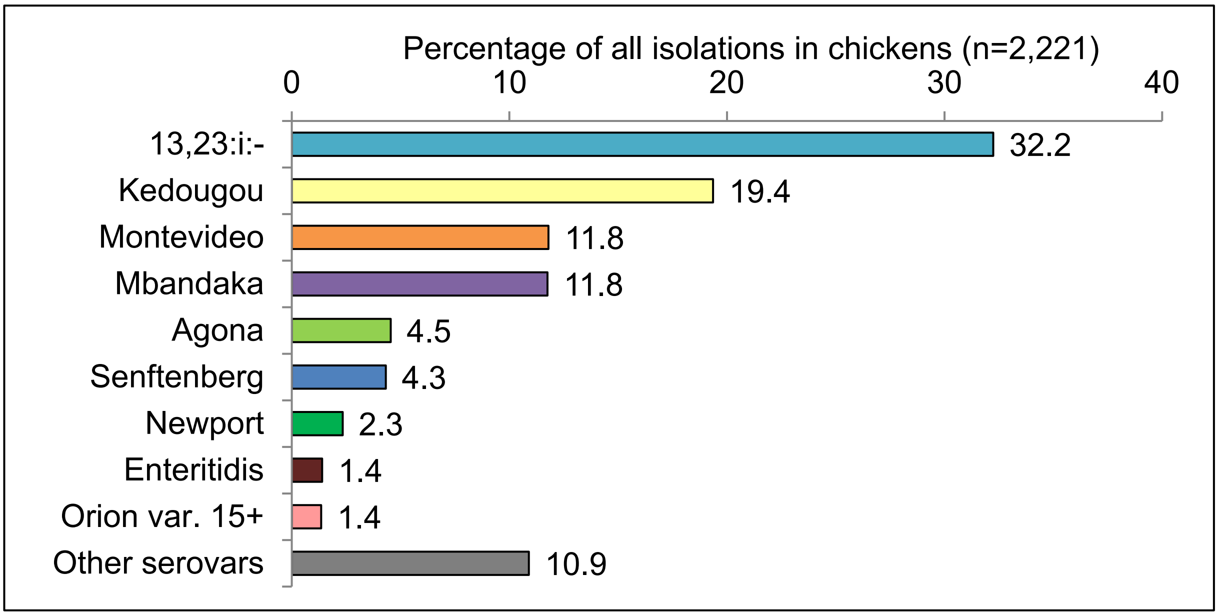
In 2018 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:-, accounting for 37.1% of total isolations, followed by *S.* Mbandaka (25.7%), *S.* Kedougou (10.7%) and *S.* Montevideo (6.1%).

Figure 6.2.2: Isolations in 2019



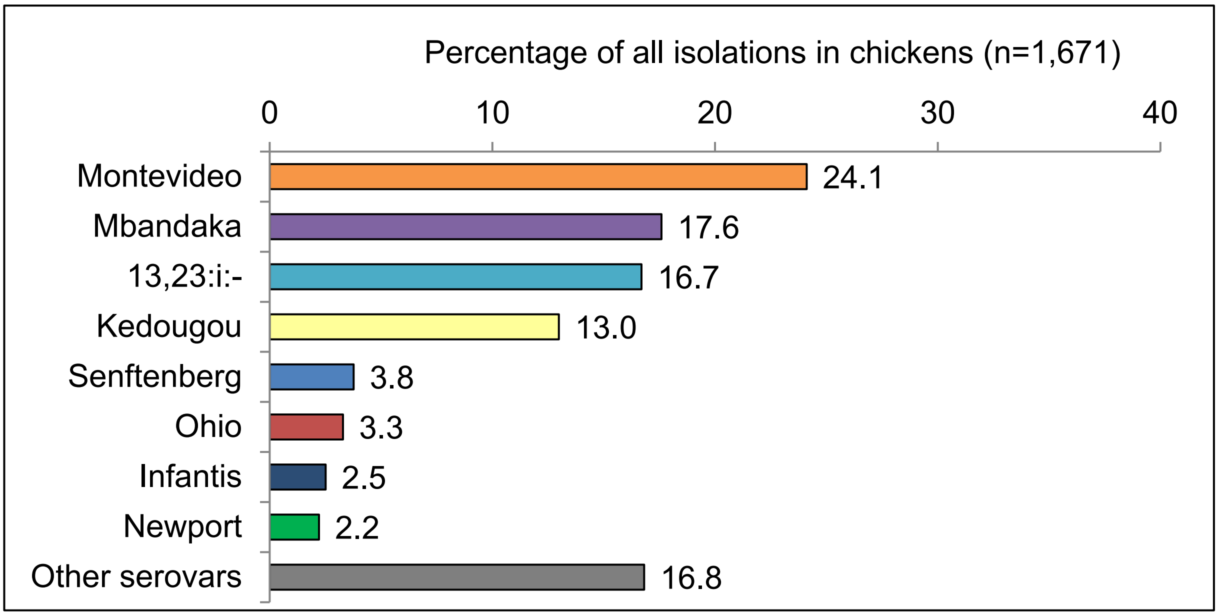
In 2019 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:-, accounting for 24.9% of total isolations, followed by *S.* Mbandaka (21.0%), *S.* Kedougou (20.4%) and *S.* Montevideo (9.7%).

Figure 6.2.3: Isolations in 2020



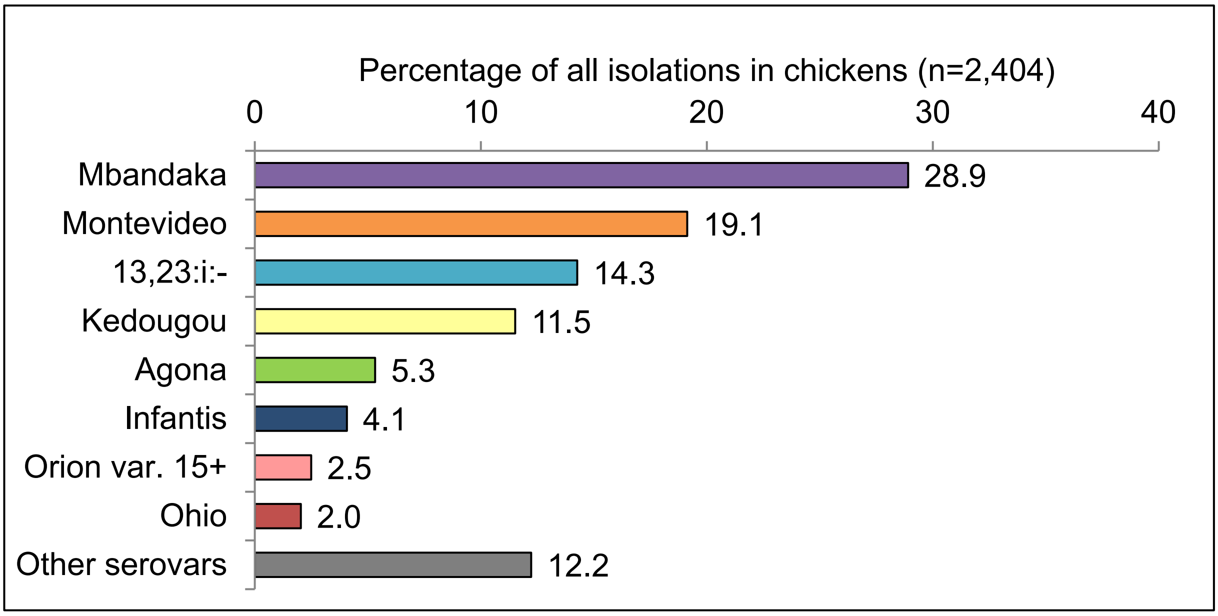
In 2020 the most common *Salmonella* serovar in chickens was *S.* 13,23:i:-, accounting for 32.2% of total isolations, followed by *S.* Kedougou (19.4%), *S.* Montevideo (11.8%) and *S.* Mbandaka (11.8%).

Figure 6.2.4: 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 6.2.5: **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 6.3: The 5 most common *Salmonella* serovars in chickens in Great Britain in 2022 and their trends over time since 2018

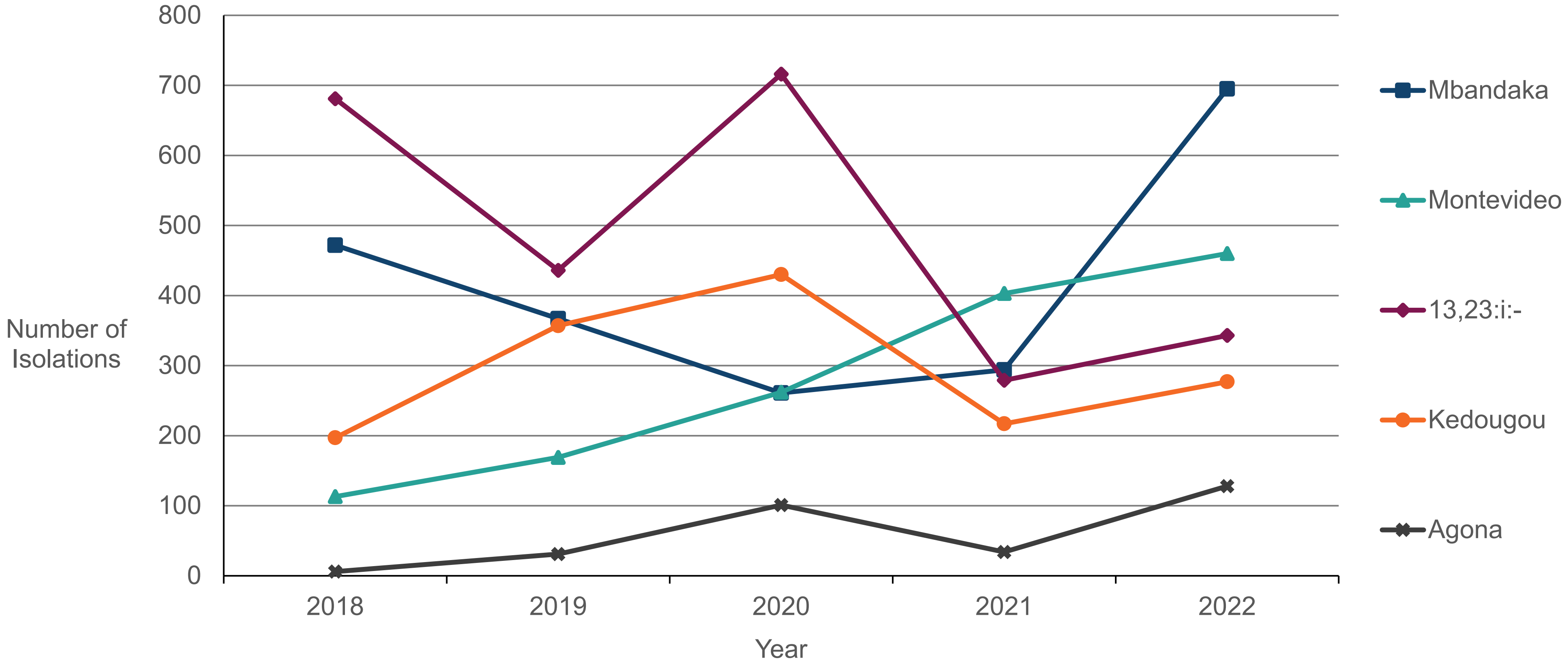


Figure 6.3 shows that from 2018 to 2020 *S.* 13,23:i:- was the most common serovar isolated from chickens but fell to third most common in 2022 (343 isolations). *S.* Mbandaka, which has typically been second or third most common was the most frequently isolated serovar in 2022 with 695 isolations. *S.* Montevideo has steadily increased over time to be the second most common in 2022 (450 isolations) and *S.*

Agona remains the fifth most commonly isolated (128 isolations). *S.* Kedougou isolations fluctuate and it was fourth most common in 2022 (227 isolations).

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

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
1	0	0	0	0	0	0	1	2	1	2
2	0	0	1	1	3	9	3	4	0	0
13	0	0	0	1	0	0	0	0	0	0
35	0	0	1	1	0	0	0	0	0	0
36	0	0	1	1	0	0	0	0	0	0
75	0	0	0	0	0	0	0	0	5	8
99	0	0	4	4	0	0	0	0	1	1
104	0	0	0	0	0	0	2	2	0	0
116	0	0	0	0	0	0	0	1	0	0
193	1	1	1	2	2	6	1	1	0	0
U308	0	0	0	0	0	2	0	0	0	0
U320	0	0	0	0	0	0	1	1	0	0
NOPT	0	1	0	0	0	0	0	0	0	0
RDNC	4	7	3	4	1	2	4	4	4	7
Total	**5**	**9**	**11**	**14**	**6**	**19**	**10**	**15**	**11**	**18**

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

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

Table 6.3: *Salmonella* 4,5,12:i:- phage types in chickens in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
DT193	0	1	3	4	0	4	6	8	10	18
UNTY	1	1	0	0	0	0	0	0	0	0
Total	**1**	**2**	**3**	**4**	**0**	**4**	**6**	**8**	**10**	**18**

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

Table 6.4: *Salmonella* 4,12:i:- phage types in chickens in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
UNTY	1	1	2	2	0	0	0	0	0	0
RDNC	0	0	0	0	0	1	0	0	0	0
NOPT	0	0	0	0	0	0	0	0	0	0
DT193	4	7	1	1	1	8	3	4	0	0
DT120	0	0	0	0	0	0	0	0	0	1
Total	**5**	**8**	**3**	**3**	**1**	**9**	**3**	**4**	**0**	**1**

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

Table 6.5: *S.* Enteritidis in chickens on all premises in Great Britain

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
2	0	0	1	1	0	0	0	0	0	0
4	5	13	0	1	0	2	3	3	0	0
7	1	2	0	0	0	0	0	0	0	0
8	3	6	12	35	9	22	0	2	3	19
8a	0	0	0	0	0	0	1	1	0	0
9b	0	0	0	0	0	0	0	1	0	0
11	0	0	0	0	0	0	0	0	1	1
11b	0	0	1	1	0	0	0	0	0	0
13	0	0	1	1	3	5	0	0	0	0
13a	0	1	2	8	0	0	0	1	0	0
14b	0	0	0	0	0	0	0	0	1	1
20	0	0	0	0	0	0	1	1	1	1
62	0	2	0	0	0	0	0	0	0	0
NOPT	1	2	0	0	0	0	0	0	0	1
UNTY	0	1	0	1	1	2	0	0	0	0
Total	**10**	**27**	**16**	**48**	**12**	**31**	**5**	**9**	**6**	**23**

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

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

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

Figure 6.4: Prevalence of *Salmonella* in breeding chicken flocks tested under NCP in Great Britain 2007 to 2022

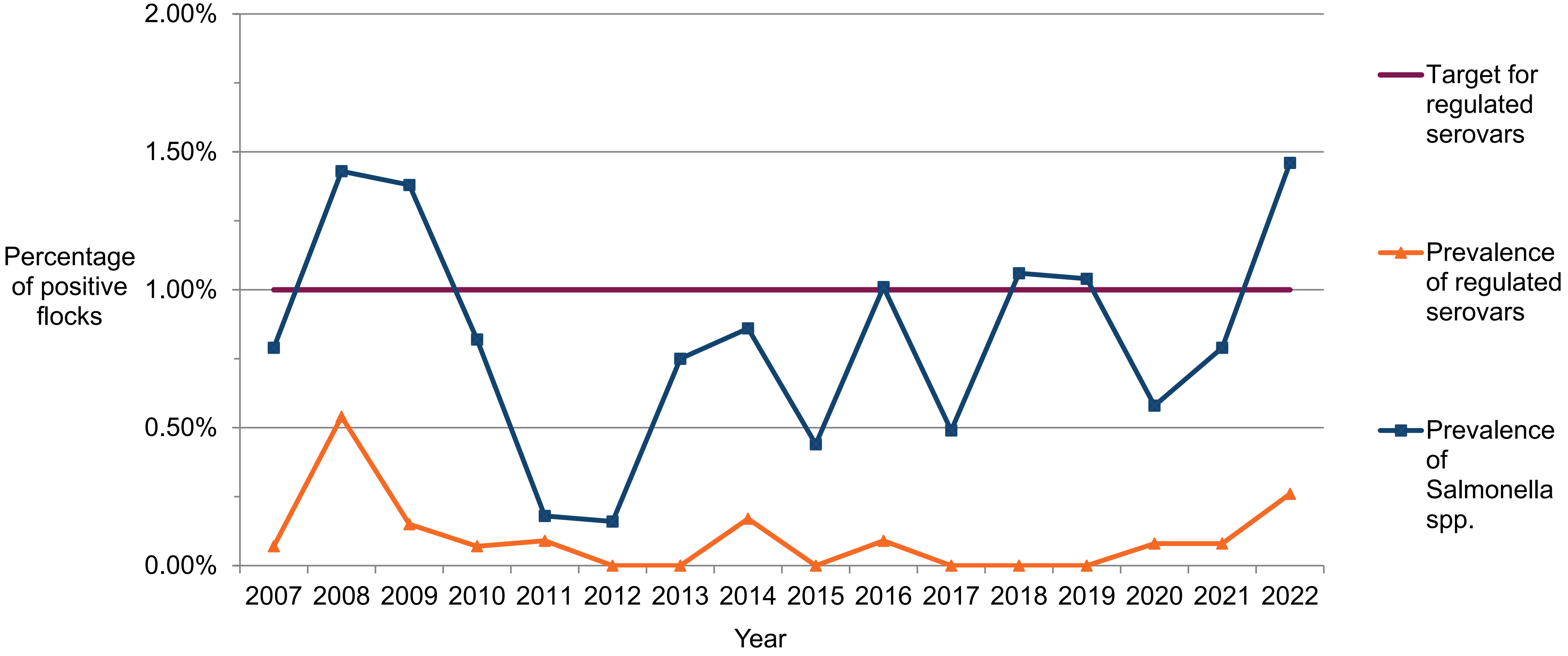


Figure 6.4 shows a variable prevalence of *Salmonella spp.* in breeding chicken flocks of between 0.16% and 1.43% but a more constant, lower prevalence of regulated serovars of between 0.0% and 0.54% which does not exceed the target of 1% prevalence.

Table 6.6: Chicken breeding flocks in Great Britain. Number of flocks reported positive with each *Salmonella* serovar, NCP testing 2018 to 2022

The following table shows the number of chicken breeding flocks reported positive with each *Salmonella* serovar from 2018 to 2022 and serovar rank in that year.

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
13,23:i:-	1	9	1	7	1	2	2	1	1	5
Agona	0	0	0	0	0	0	0	0	2	2
Give var. 15^+	0	0	0	0	0	0	1	5	2	2
Typhimurium	0	0	0	0	2	1	0	0	2	2
Anatum	0	0	0	0	0	0	0	0	3	1
Corvallis	0	0	0	0	0	0	0	0	3	1
Idikan	0	0	0	0	0	0	0	0	3	1
Infantis	0	0	0	0	0	0	2	1	3	1
Mbandaka	2	1	0	0	2	1	2	1	3	1
Ohio	0	0	2	2	0	0	0	0	3	1
Orion var. 15^+(Binza)	0	0	0	0	0	0	0	0	3	1
3,19:z27:-	0	0	3	1	0	0	0	0	0	0
6,7:-:enz15	0	0	3	1	0	0	0	0	0	0
6,8:e,h:-	0	0	0	0	2	1	0	0	0	0
Bardo	0	0	0	0	2	1	0	0	0	0
Kedougou	2	1	0	0	1	2	0	0	0	0
Kottbus	0	0	3	1	0	0	0	0	0	0
London	0	0	0	0	0	0	2	1	0	0
Newport	0	0	0	0	2	1	2	1	0	0
Nottingham	0	0	3	1	0	0	0	0	0	0
O rough:g,m,t:-	2	1	0	0	0	0	0	0	0	0

For details of chicken breeding flocks reported positive in 2010 to 2017, see the 2017 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
2018	1.06%	0.00%
2019	1.04%	0.00%
2020	0.58%	0.08%
2021	0.79%	0.08%
2022	1.47%	0.26%

Flocks testing positive for more than one serovar

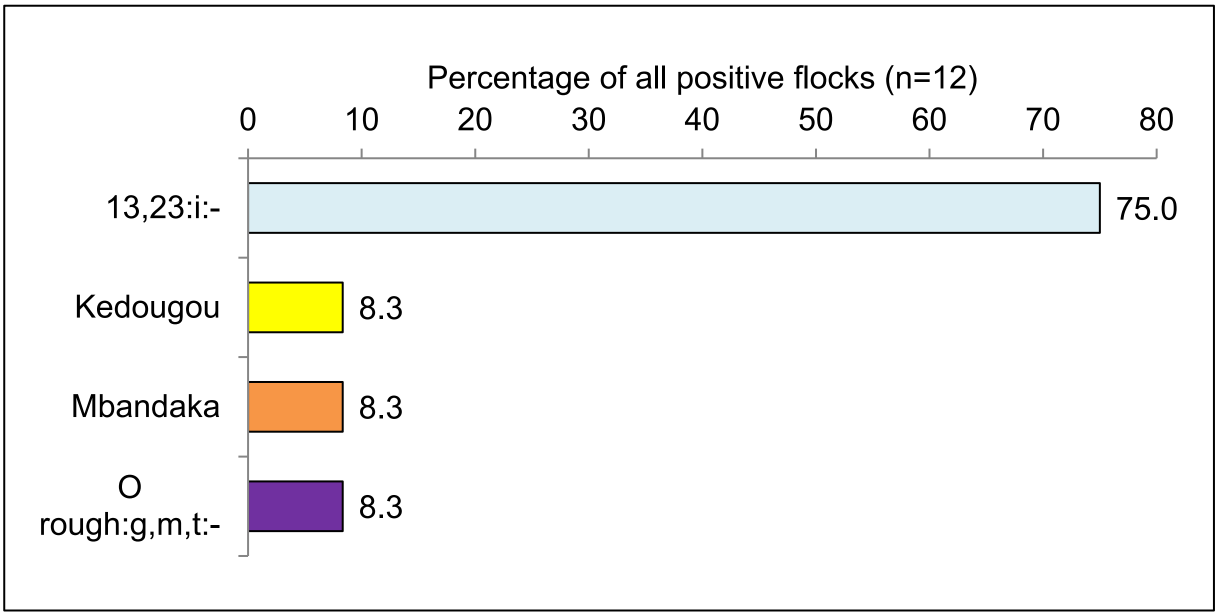
Some flocks tested positive for more than one serovar. Each flock was counted only once in the overall figure to calculate prevalence.

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^+.

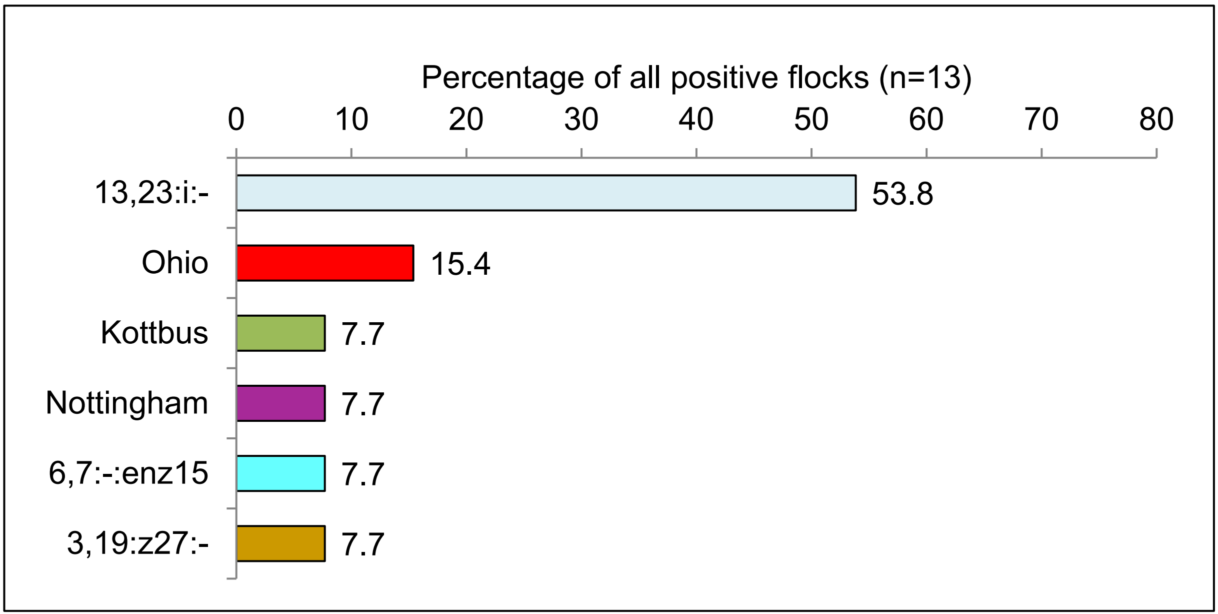
Figure 6.5: Serovars identified in adult chicken breeding flocks in Great Britain 2018 to 2022 reported from NCP testing

Figure 6.5.1: Isolations in 2018



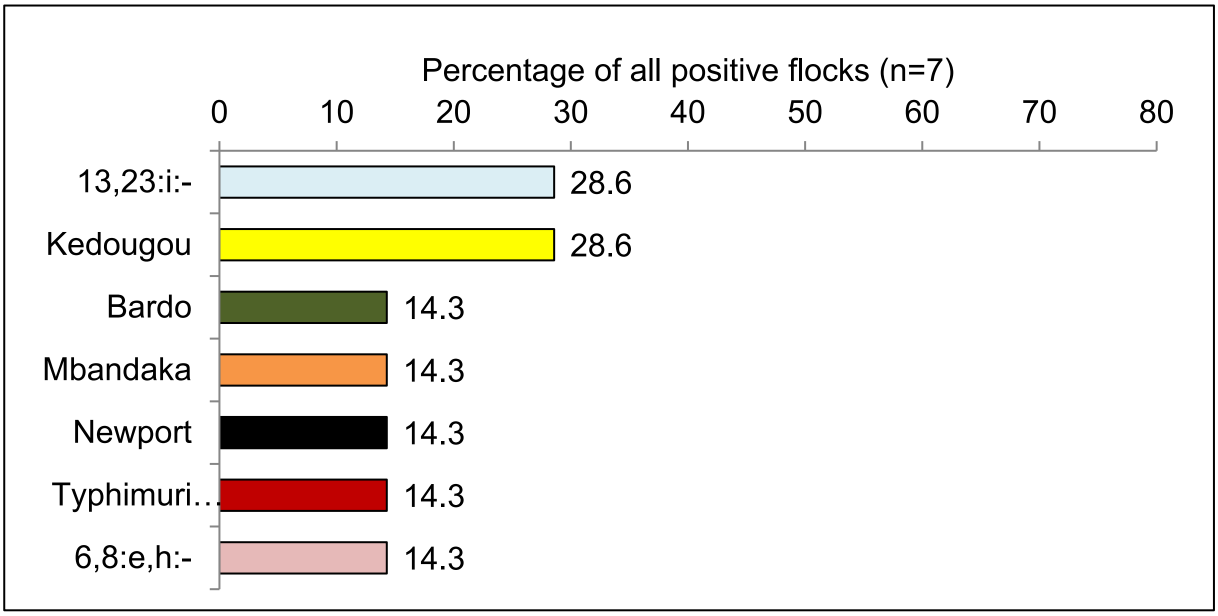
In 2018 the most common *Salmonella* serovar in all positive flocks was *S.* 13,23:i:- accounting for 75.0% of total isolations, followed by *S.* Kedougou (8.3%), *S*. Mbandaka, (8.3%) and *S.* rough:g,m,t:- (8.3%).

Figure 6.5.2: Isolations in 2019



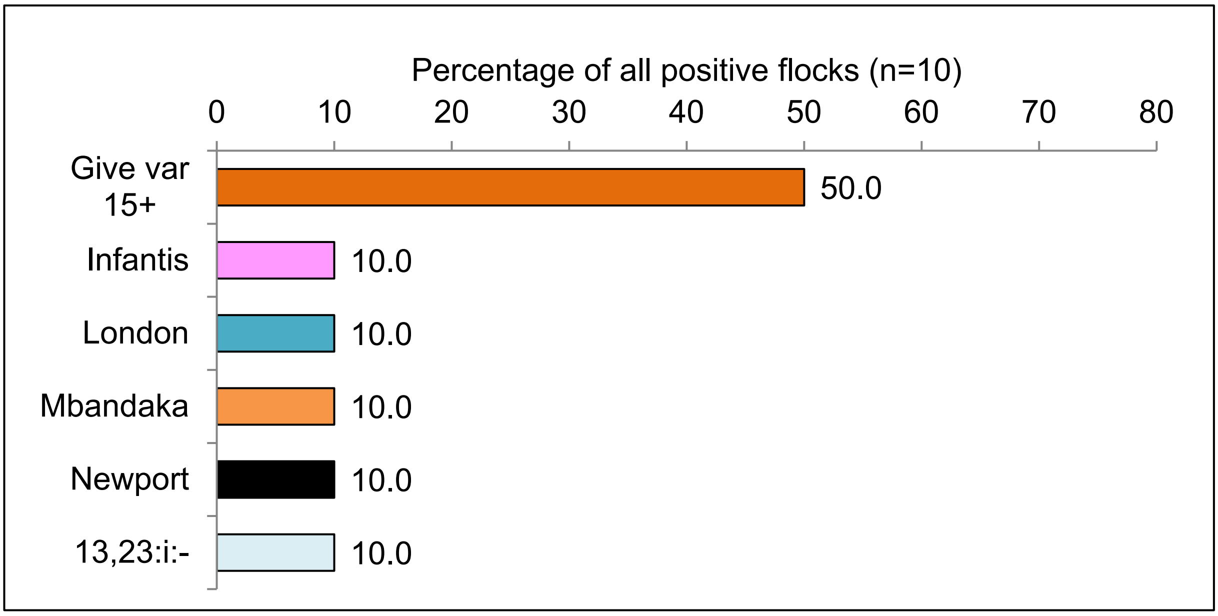
In 2019 the most common *Salmonella* serovar in all positive flocks was *S.* 13,23:i:- accounting for 53.8% of total isolations, followed by *S.* Ohio (15.4%). All other Serovars made up the remaining 30.8%

Figure 6.5.3: Isolations in 2020



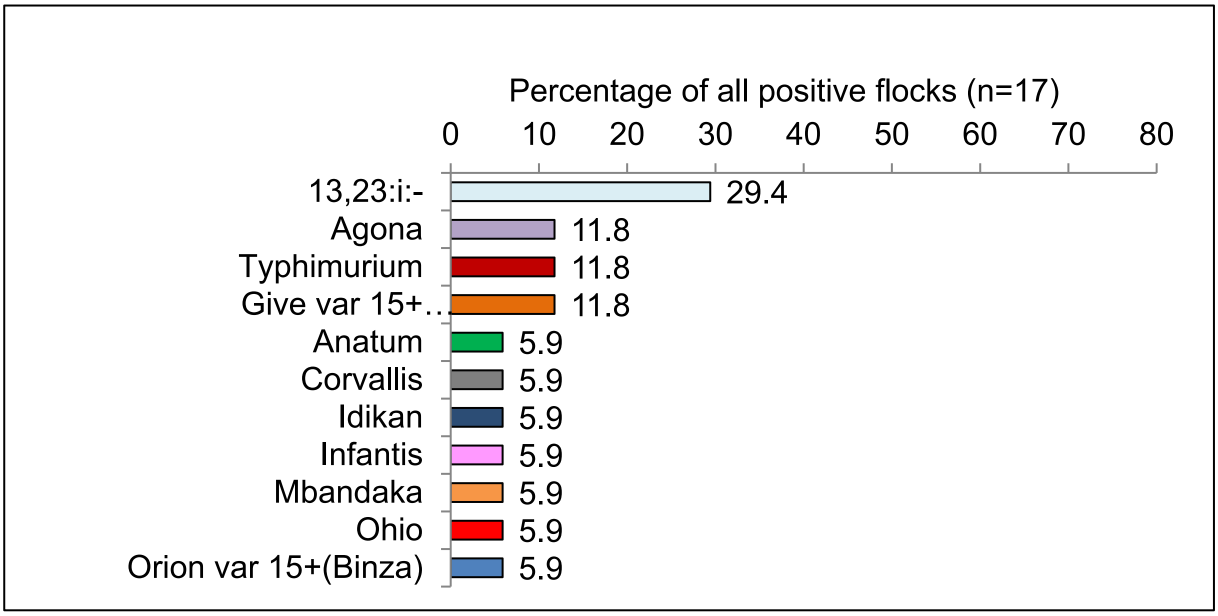
In 2019 the most common *Salmonella* serovars in all positive flocks was *S.* 13,23:i:- and *S.* Kedougou both accounting for 28.6% of total isolations each. All other Serovars made up the remaining 71.5%

Figure 6.5.4: 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 6.5.5: 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%

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 2022

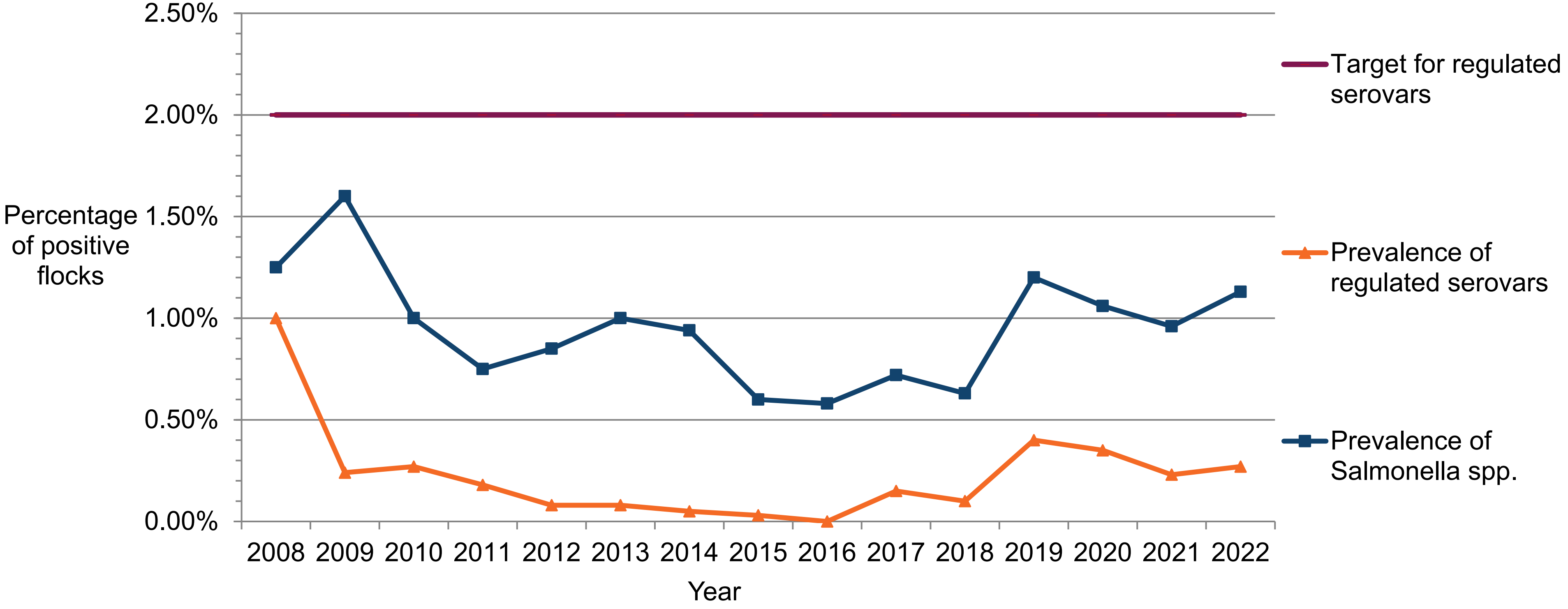


Figure 6.6 shows a variable prevalence of *Salmonella spp.* in laying hen flocks of between 0.58% and 1.60% and a similar but lower prevalence of regulated serovars of between 0.0% and 1.0% which does not exceed the target of 2% prevalence across all years.

Table 6.7: Laying hen flocks in Great Britain. Number of flocks reported positive with each *Salmonella* serovar, NCP testing 2018 to 2022

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
Mbandaka	3	2	5	1	0	0	6	1	1	6
Enteritidis	2	3	1	14	1	11	4	3	2	5
Typhimurium	4	1	5	1	3	4	2	6	2	5
Derby	0	0	5	1	5	1	6	1	3	4
Dublin	0	0	5	1	0	0	0	0	3	4
Bardo	0	0	0	0	0	0	3	5	4	3
Infantis	0	0	0	0	0	0	6	1	4	3
Newport	2	3	3	3	4	2	1	7	4	3
Montevideo	0	0	4	2	5	1	5	2	5	2
Agama	4	1	2	4	4	2	6	1	6	1
Agona	0	0	0	0	2	6	0	0	6	1
Indiana	4	1	0	0	0	0	0	0	6	1
Kedougou	0	0	2	4	5	1	0	0	6	1
Kentucky	0	0	0	0	0	0	0	0	6	1
Livingstone	0	0	0	0	4	2	0	0	6	1
Senftenberg	3	2	5	1	0	0	0	0	6	1
Stourbridge	0	0	0	0	0	0	6	1	6	1
13,23:i:-	1	5	5	1	5	1	0	0	0	0
4,5,12:b:-	0	0	5	1	0	0	0	0	0	0
4,5,12:i:-	0	0	5	1	0	0	0	0	0	0
6,7:-:enz15	0	0	0	0	0	0	6	1	0	0
Africana	0	0	5	1	0	0	0	0	0	0
Anatum	0	0	4	2	5	1	6	1	0	0
Bareilly	0	0	0	0	0	0	6	1	0	0

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
Bovismorbificans	0	0	0	0	4	2	4	3	0	0
Bredeney	0	0	0	0	5	1	0	0	0	0
Budapest	4	1	0	0	0	0	0	0	0	0
Coeln	0	0	0	0	5	1	0	0	0	0
Havana	0	0	0	0	0	0	6	1	0	0
Idikan	4	1	5	1	5	1	0	0	0	0
Isangi	0	0	0	0	0	0	6	1	0	0
Kingston	4	1	0	0	5	1	0	0	0	0
Kottbus	0	0	5	1	5	1	0	0	0	0
Lexington	0	0	0	0	0	0	6	1	0	0
Liverpool	0	0	0	0	5	1	0	0	0	0
London	0	0	5	1	0	0	0	0	0	0
Molade	0	0	0	0	0	0	6	1	0	0
Nima	0	0	5	1	0	0	0	0	0	0
Nottingham	4	1	4	2	0	0	0	0	0	0
O Rough:z38:-	0	0	0	0	0	0	6	1	0	0
O rough:g,m:-	4	1	0	0	0	0	0	0	0	0
Odozi	0	0	0	0	0	0	5	2	0	0
Oslo	4	1	0	0	5	1	6	1	0	0
Ramatgam	0	0	0	0	5	1	0	0	0	0
Reading	0	0	5	1	5	1	0	0	0	0
Rissen	3	2	5	1	0	0	0	0	0	0
Schwarzengrund	0	0	0	0	5	1	0	0	0	0
Soerenga	4	1	0	0	0	0	0	0	0	0
Stanleyville	0	0	0	0	5	1	0	0	0	0
Tennessee	0	0	4	2	0	0	0	0	0	0

For details of laying hen flocks reported positive in 2013 to 2017, see the 2017 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
2018	0.63%	0.10%
2019	1.20%	0.40%
2020	1.06%	0.35%
2021	0.96%	0.23%
2022	1.13%	0.27%

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:-.

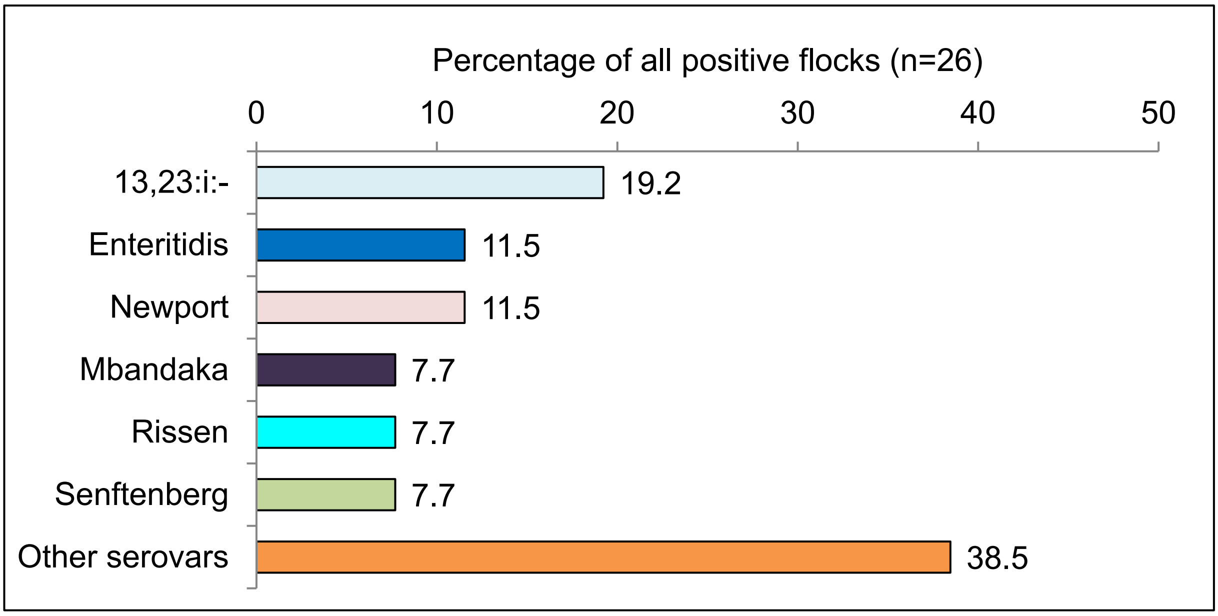
In 2020 1 flock tested positive for both *S*. Enteritidis and *S*. Agama and 1 flock tested positive for *S*. Enteritidis, *S.* Typhimurium and *S*. Bovismorbificans.

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.

Figure 6.7: Serovars identified in adult laying hen flocks in Great Britain 2018 to 2022 reported from NCP testing

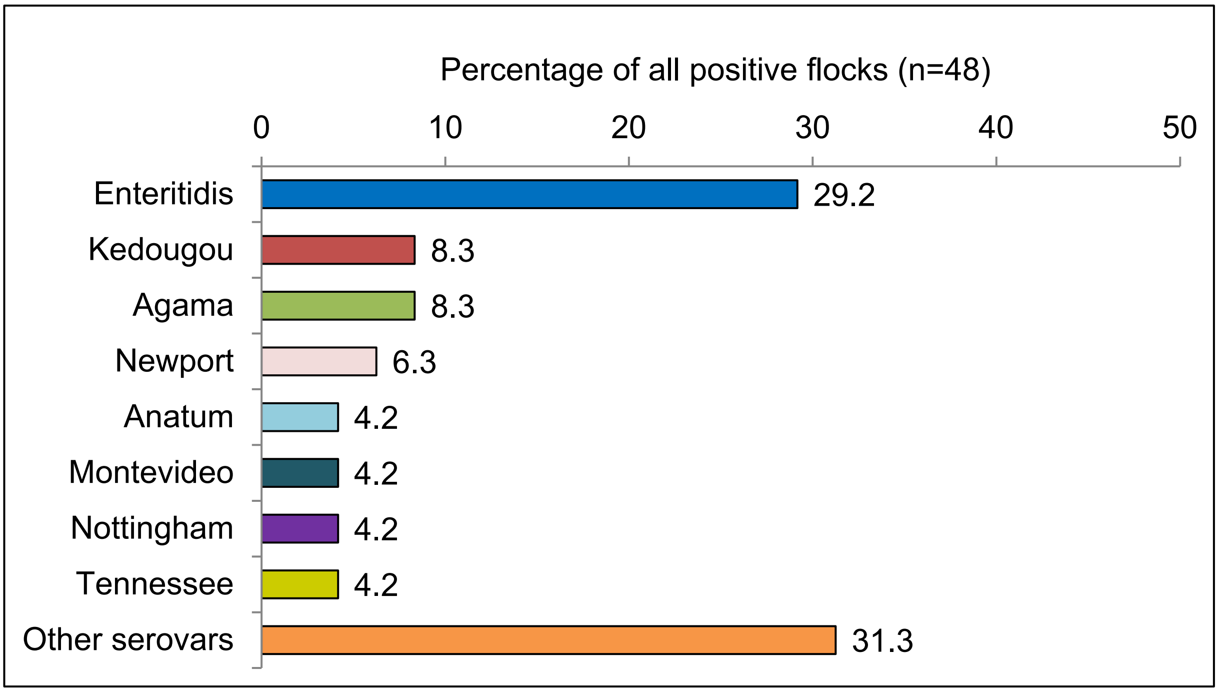
Figure 6.7.1: Isolations in 2018



In 2018 the most common *Salmonella* serovar in adult laying hen flocks was *S.* 13,23:i:- accounting for 19.2% of total isolations, followed by *S.* Enteritidis (11.5%) and *S.* Newport (11.5%).

In 2018 1 flock was positive for 2 serovars (counted once in total). Summed percentages of all serovars therefore exceeds 100%

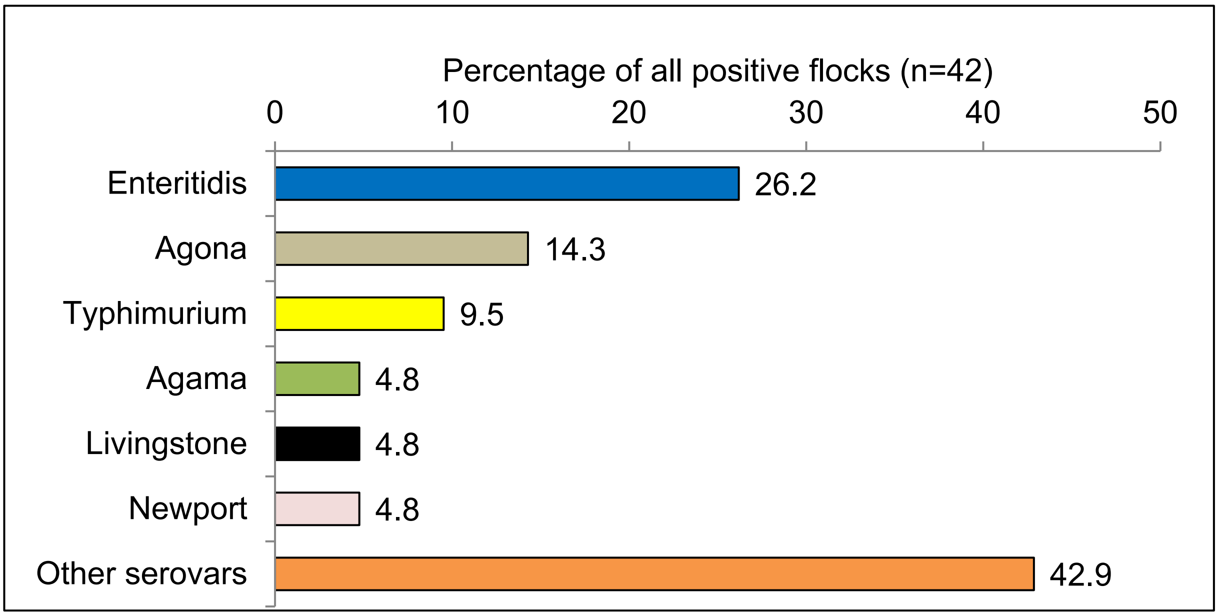
Figure 6.7.2: Isolations in 2019



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%

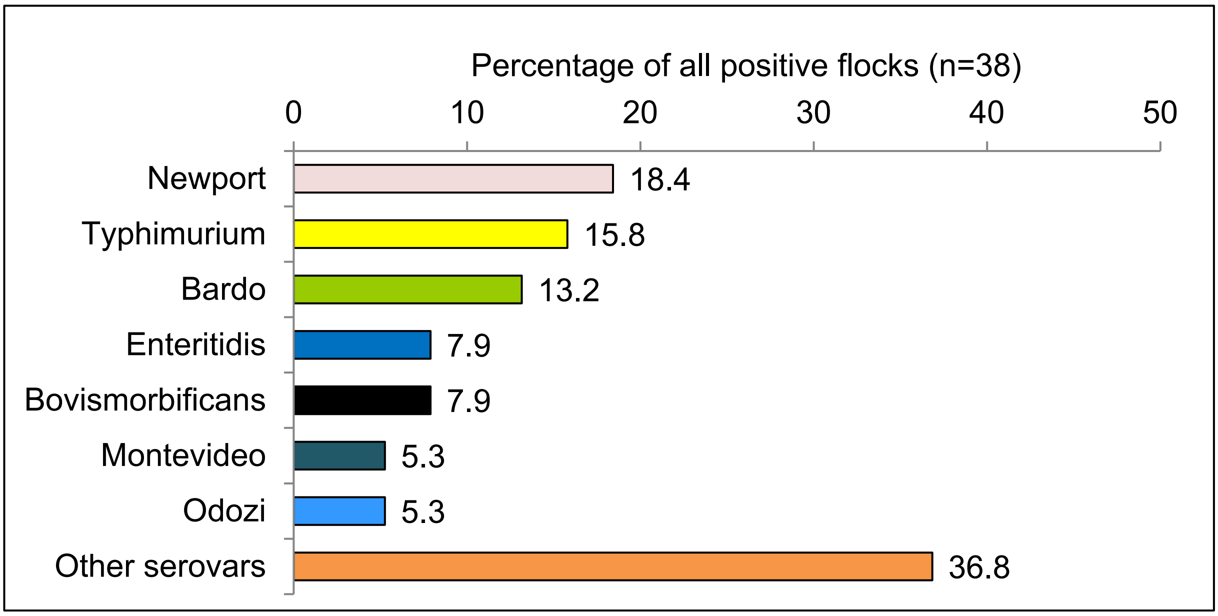
Figure 6.7.3: Isolations in 2020



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%).

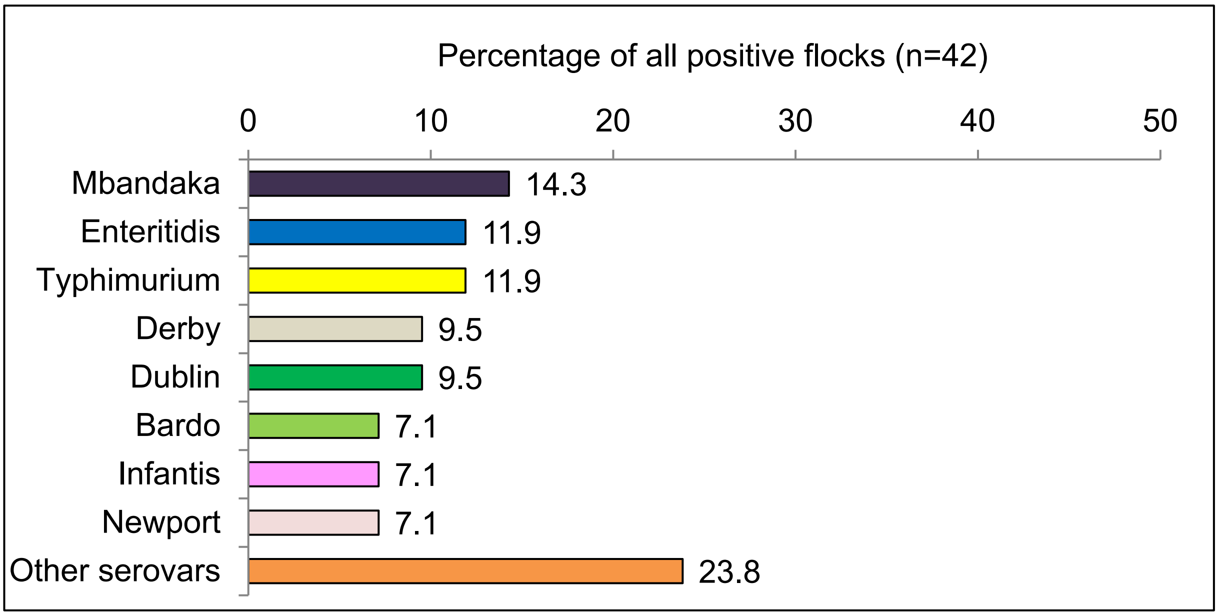
In 2020 4 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%

Figure 6.7.4: 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 6.7.5: 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 6.8: Prevalence of *Salmonella* in broiler chicken flocks tested under NCP in Great Britain 2009 to 2022

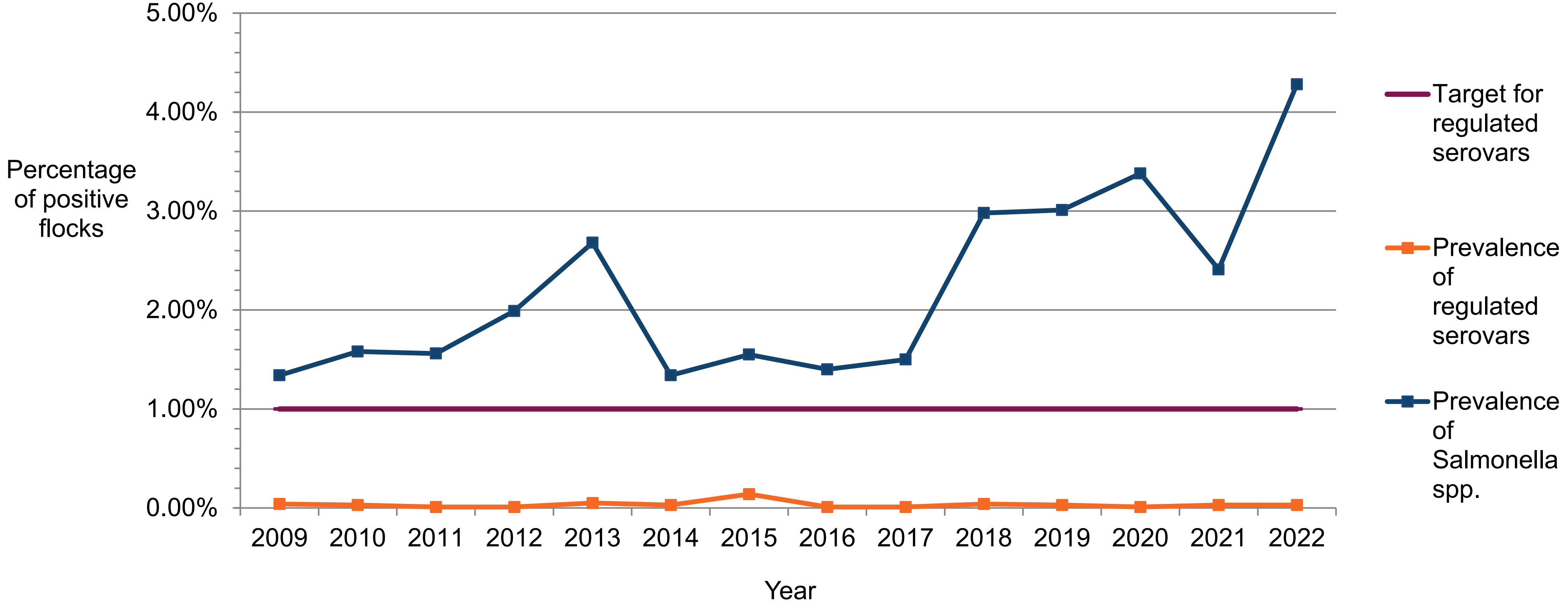


Figure 6.8 shows a variable prevalence of *Salmonella spp.* in broiler chicken flocks of between 1.34% and 4.28% (in 2022) but a more constant, lower prevalence of regulated serovars of between 0.01% and 0.14% which does not exceed the target of 1% prevalence

Table 6.8: Broiler chicken flocks in Great Britain. Number of flocks positive for each *Salmonella* serovar, NCP testing 2018 to 2022

The following table shows the number of broiler chicken flocks reported positive with each *Salmonella* serovar from 2018 to 2022 and the rank within that year. This data comes from NCP testing.

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
Mbandaka	2	350	2	334	4	231	3	238	1	579
Montevideo	5	69	4	144	3	245	1	330	2	409
13,23:i:-	1	445	1	418	1	597	2	252	3	301
Kedougou	3	189	3	331	2	339	4	192	4	232
Agona	14	4	7	29	5	67	6	33	5	114
Infantis	17	1	0	0	0	0	9	22	6	77
Orion var. 15^{+}	9	11	9	12	8	28	6	33	7	54
Ohio	4	87	5	69	7	33	5	54	8	43
Idikan	11	8	8	15	15	4	12	5	9	40
6,7:z10:-	15	3	13	3	9	21	8	23	10	21
Senftenberg	7	17	6	32	6	53	7	29	11	18
4,5,12:i:-	17	1	14	2	0	0	11	6	12	10
Muenchen	0	0	15	1	13	6	13	4	13	9
Derby	6	18	7	29	16	3	10	7	14	7
Newport	14	4	14	2	11	10	15	2	14	7
6,7:-:-	0	0	0	0	0	0	0	0	15	6
Give var. 15^{+}	0	0	12	4	15	4	16	1	15	6
Havana	15	3	15	1	18	1	16	1	16	5
Coeln	0	0	15	1	18	1	0	0	17	4
Typhimurium	14	4	10	10	18	1	13	4	17	4
Kentucky	0	0	15	1	0	0	0	0	18	3

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
4,12:d:-	7	17	11	7	14	5	16	1	19	2
Braenderup	0	0	0	0	18	1	15	2	19	2
Kingston	0	0	15	1	18	1	0	0	19	2
London	0	0	15	1	0	0	0	0	19	2
Nottingham	15	3	15	1	0	0	0	0	19	2
47:z4,z23:-	0	0	0	0	0	0	0	0	20	1
6,7:d:-	0	0	0	0	0	0	0	0	20	1
6,8:d:-	0	0	0	0	0	0	0	0	20	1
Anatum	17	1	13	3	14	5	14	3	20	1
Berta	0	0	0	0	0	0	0	0	20	1
Corvallis	0	0	0	0	0	0	0	0	20	1
Eboko	0	0	0	0	0	0	0	0	20	1
Enteritidis	12	7	14	2	18	1	15	2	20	1
Kottbus	14	5	0	0	18	1	0	0	20	1
Liverpool	0	0	0	0	0	0	0	0	20	1
Livingstone	10	9	11	7	12	7	13	4	20	1
Orion	8	13	13	3	0	0	0	0	20	1
Panama	0	0	0	0	0	0	16	1	20	1
Rissen	0	0	0	0	0	0	0	0	20	1
Stanley	17	1	15	1	0	0	0	0	20	1
13,22:-:1,6	0	0	0	0	18	1	0	0	0	0
13,23:-:-	0	0	0	0	18	1	0	0	0	0
13,23:-:l,w	0	0	14	2	0	0	0	0	0	0
28:-:-	0	0	15	1	0	0	0	0	0	0
3,10:e,h:-	0	0	15	1	0	0	0	0	0	0
3,15:l,v:-	0	0	0	0	18	1	0	0	0	0
3,19:-:-	0	0	0	0	0	0	15	2	0	0

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
4,12:e,h:-	0	0	0	0	13	6	0	0	0	0
4,12:i:-	14	5	13	3	18	1	14	3	0	0
6,7:-:enz15	0	0	0	0	17	2	0	0	0	0
61:-:1,5,7	0	0	15	1	0	0	0	0	0	0
Agama	0	0	13	3	17	2	0	0	0	0
Bovismorbificans	0	0	0	0	10	14	13	4	0	0
Eastbourne	0	0	13	3	0	0	0	0	0	0
Ferruch	0	0	0	0	0	0	15	2	0	0
Give	14	4	0	0	17	2	0	0	0	0
Goldcoast	0	0	0	0	0	0	16	1	0	0
Indiana	15	2	11	7	17	2	0	0	0	0
Isangi	17	1	0	0	0	0	0	0	0	0
Mikawasima	0	0	0	0	18	1	0	0	0	0
O rough:l,v:1,7	0	0	0	0	18	1	0	0	0	0
O rough:z10:e,n,z15	16	2	15	1	0	0	0	0	0	0
Offa	0	0	15	1	0	0	0	0	0	0
Oslo	17	1	14	2	18	1	16	1	0	0
Poona	17	1	0	0	18	1	0	0	0	0
Reading	0	0	0	0	0	0	16	1	0	0
Stourbridge	0	0	0	0	18	1	16	1	0	0
Structure only	13	6	0	0	0	0	0	0	0	0

For details of broiler chicken flocks reported positive in 2013 to 2017, see the 2017 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
2018	2.98%	0.04%
2019	3.01%	0.03%
2020	3.38%	0.01%
2021	2.41%	0.03%
2022	4.28%	0.03%

Flocks testing positive for more than one serovar

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

In 2018:

- 3 flocks tested positive for both *S*. Mbandaka and *S*. 13,23:i:-
- 2 flocks tested positive for both *S*. Kedougou and *S*. 13,23:i:-
- 1 flock tested positive for both *S*. 6,7:z10:- and *S*. 13,23:i:-
- 1 flock tested positive for both *S*. Mbandaka and *S*. Enteritidis
- 1 flock tested positive for both *S*. 13,23:i:- and *S*. Enteritidis
- 1 flock tested positive for both *S*. 13,23:i:- and *S*. Orion var. 15^+

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^+ (Binza) 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^+ (Binza)
- 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:

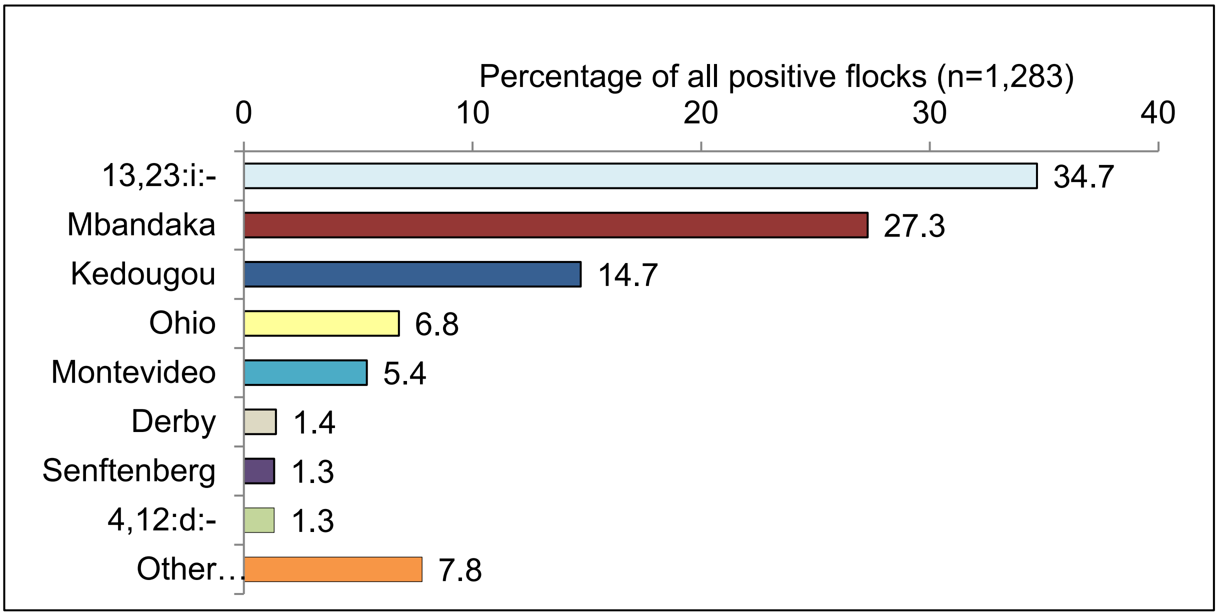
- 3 flocks tested positive for both *S*. Mbandaka and *S*. 6,7:z10:-
- 2 flocks tested positive for both *S*. Montevideo and *S*. 13,23:i:-
- 1 flock tested positive for both *S*. Mbandaka and *S*. Montevideo
- 1 flock tested positive for both *S*. 13,23:i:- and *S*. Orion var. 15^{+} (Binza)
- 1 flock 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^{+} (Binza), *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

Figure 6.9: Serovars identified in broiler chickens in Great Britain 2018 to 2022 reported from NCP testing

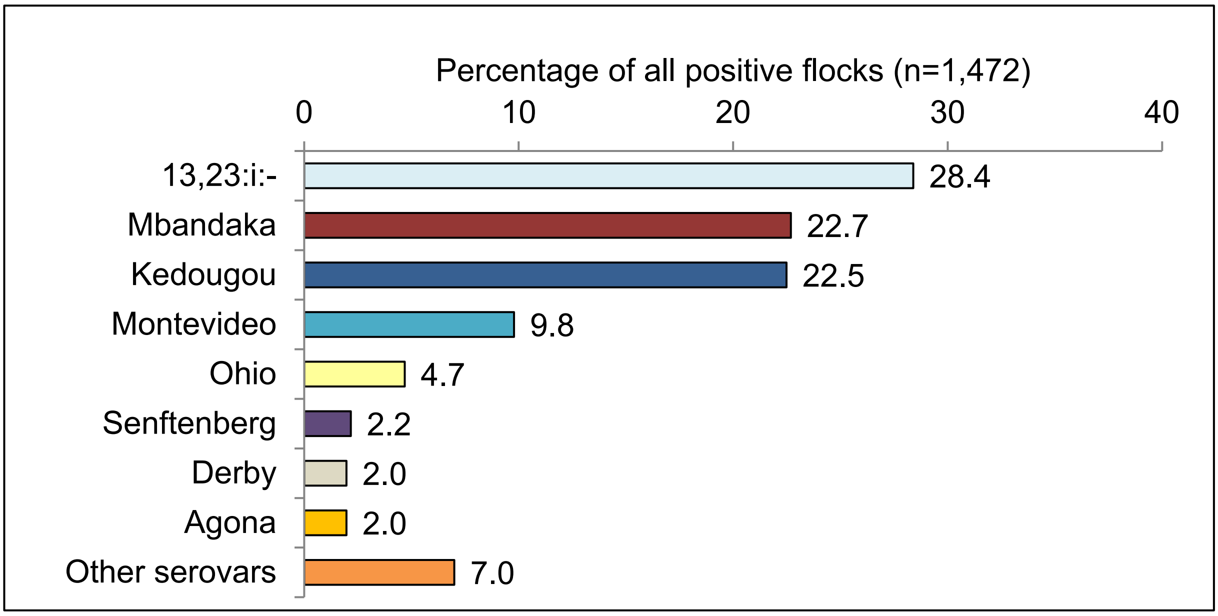
Figure 6.9.1: Isolations in 2018



In 2018 the most common *Salmonella* serovar in broiler flocks was *S.* 13,23:i:- accounting for 34.7% of total isolations, followed by *S.* Mbandaka (27.3%), *S.* Kedougou (14.7%) and *S.* Ohio (6.7%).

In 2018 9 flocks were positive for 2 serovars (each counted once in total). Summed percentages of all serovars therefore exceeds 100%.

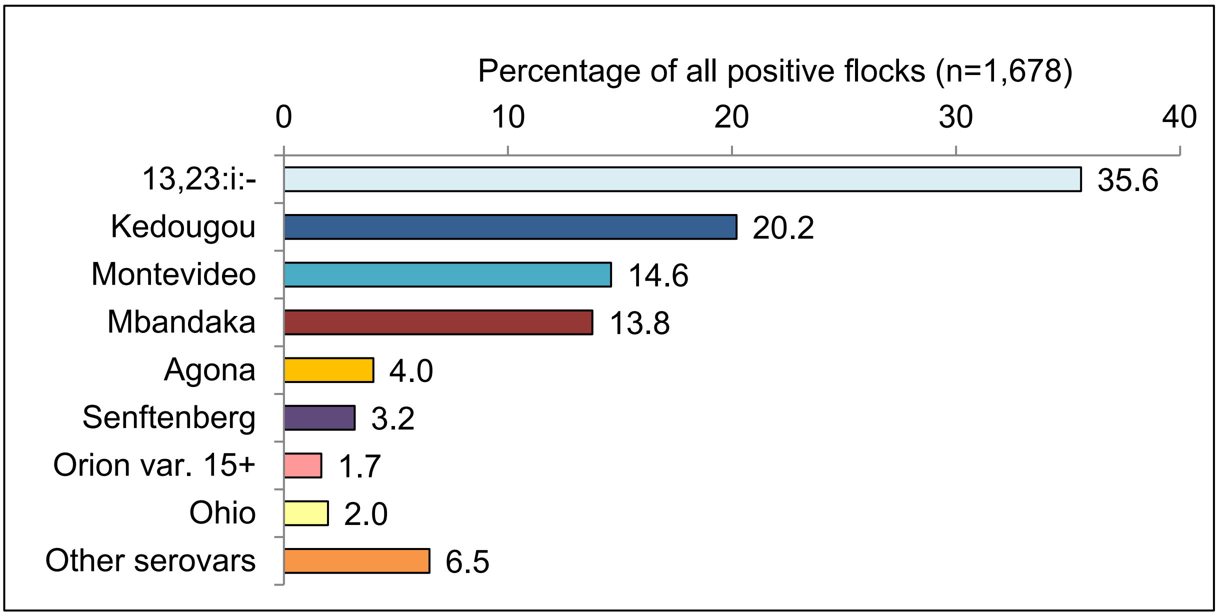
Figure 6.9.2: Isolations in 2019



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%.

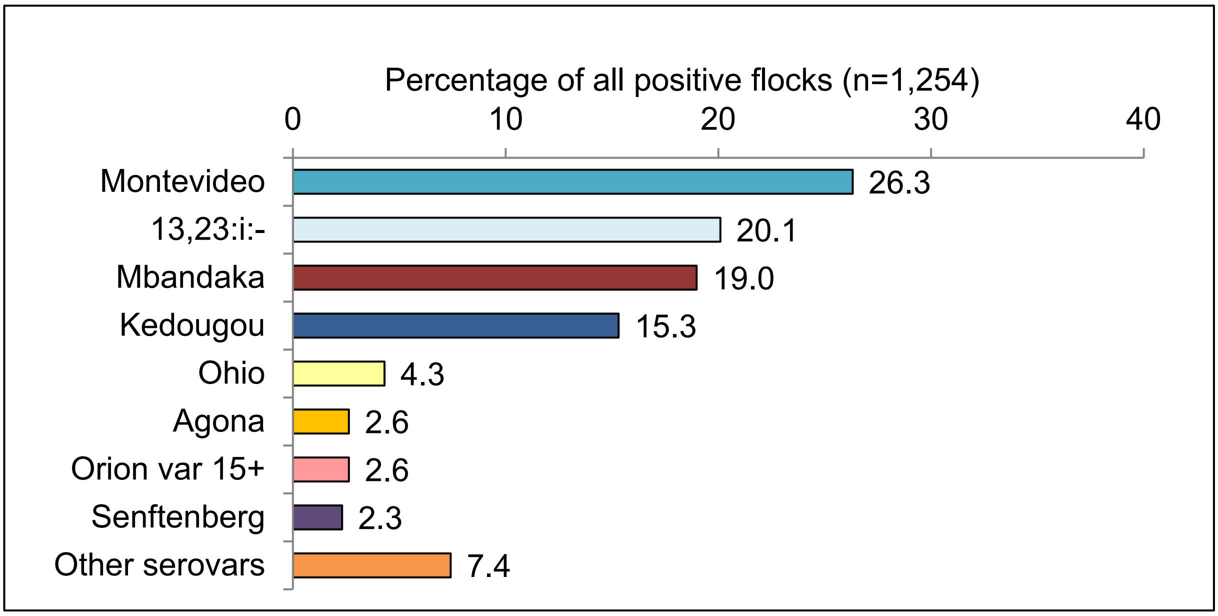
Figure 6.9.3: Isolations in 2020



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%.

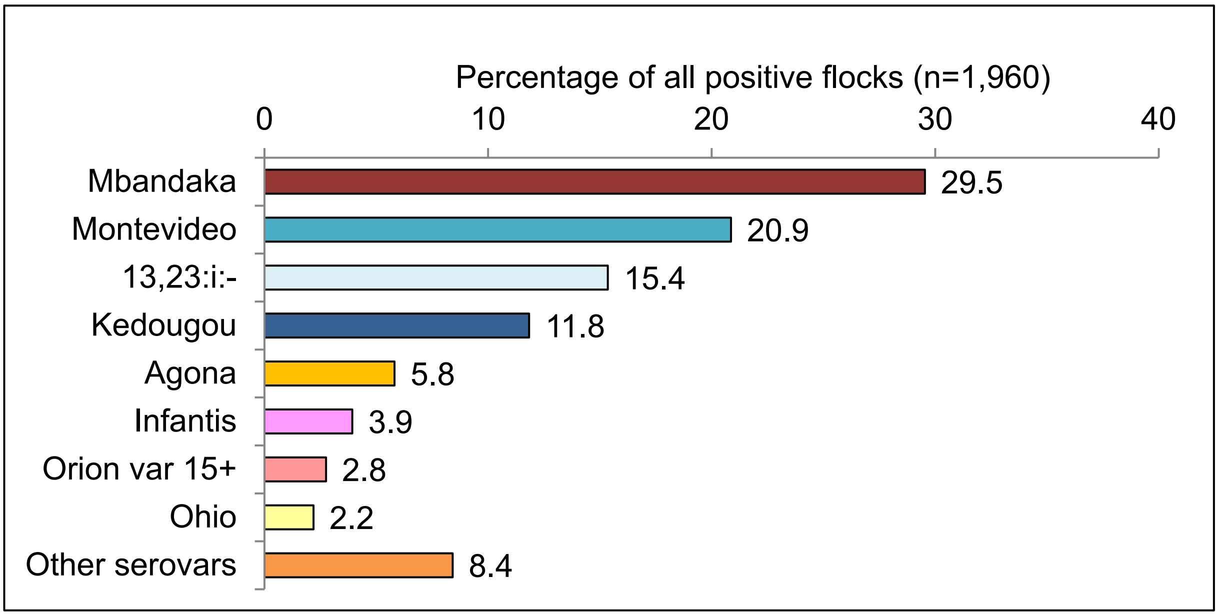
Figure 6.9.4: Isolations in 2021



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 6.9.5: 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%.

Chapter 7: Reports of *Salmonella* in turkeys

During 2022 there was significant disruption to the poultry industry as a result of Avian Influenza. The outbreak was long running affecting all industry sectors country wide. Altered management and biosecurity measures were necessary. This is likely to have impacted submission numbers. During 2020 and 2021 there was 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 and 2022 data with previous years.

According to the June Agricultural Census, there were 3.73 million turkeys in Great Britain in 2022 compared with 3.72 million in 2021, 3.65 million in 2020, and 3.91 million in 2019.

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 283 turkey diagnostic and monitoring submissions made to APHA and SRUC laboratories in 2022. This compares to 307 in 2021, representing a decrease of 7.8%. 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 188 *Salmonella* isolations were reported from turkeys in 2022 (Table 7.1), which represents a 34.3% increase compared to 2021 (140 isolations) but similar to the number of isolations in 2020 (196 isolations). This is the first increase in isolations since 2015 following a decreasing trend in the number of *Salmonella* isolations in recent years from turkeys.

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. Despite an increase in isolations in 2022, this was not associated with an increase in *S*. Derby isolations.

The total number of isolations in 2022 was distributed between the following categories according to the reason for submission:

- statutory surveillance: 167 (88.8%)
- voluntary surveillance: 20 (10.6%)
- investigations of clinical disease: 1 (0.5%)

Seventeen different serovars of *Salmonella* were isolated in 2022, accounting for 175 of the 188 isolations. The remaining 13 isolations involved un-typable and rough *Salmonella* strains. Table 7.1 shows the absolute number of isolations of each *Salmonella* serovar isolated from turkeys, from 2018 to 2022, and Figure 7.1 shows the relative percentages of the most common.

Salmonella Anatum (66 isolations, 35.1% of all isolations) was the most frequently isolated serovar in 2022. This was also the most frequently isolated serovar in 2021, but this represents more than a two-fold increase in the number of isolations compared to 2021 (31 isolations). Isolations of this serovar have increased dramatically since 2019 (4 isolations), which is likely to be associated with contaminated feed (Figure 7.2).

Salmonella Kedougou (30 isolations, 16.0% of all isolations), a feed related serovar, was the second most common serovar in 2022. There was an 87.5% increase in the number of isolations compared with 2021 (16 isolations but fewer than in 2020 (68 isolations) when it was the most frequently isolated serovar (Figure 7.2).

Isolations of *S.* Senftenberg accounted for 13.8% of all isolations (26 isolations) in 2022. Although the number of isolations was higher than in 2021 (20 isolations), the relative contribution of this serovar was similar (14.3% of all isolations), increasing from 7.7% in 2020 (15 isolations). However, there were still fewer than half the number of isolations of *S*. Senftenberg compared to 2019 (48 isolations) (Figure 7.2). *Salmonella* Senftenberg is a hatchery-related serovar that is also able to colonise feedmills*.*

Salmonella Derby, the most common serovar isolated from turkeys from 2007-2019, and the second most common in 2021, was only the fourth most common serovar in 2022. There were 12 isolations of *S*. Derby in 2022, an 45.5% reduction compared with 2021 (22 isolations) and representing just 6.4% of all isolations compared with 15.7% in 2021 (Figure 7.1). Isolations of *S*. Derby peaked in 2016 with 501 isolations, and since then there has been a general decreasing trend in isolations (Figure 7.2). This reduction follows more successful 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 seems to have 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.

In 2022 there were 5 isolations of regulated serovars from turkeys. There was one isolation of *S*. Typhimurium (from a turkey fattening site), compared to 3 isolations (from a single turkey fattener site) in 2021. 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 2018 and 2022 are illustrated in Table 7.2. The isolation of *S*. Typhimurium reported in 2022 was DT99 which has not been reported from turkeys in Great Britain since 2004.

The remaining 4 isolations of regulated serovars originated from 2 turkey fattening holdings. There were 2 isolations of the monophasic strain of *S.* Typhimurium 4,5,12:i:- (both DT193 from the same flock) and 2 isolations of monophasic *S.* Typhimurium 4,12:i:- (DT193 x1 and UNTY x1 from a single flock). This compares with 9 isolations of monophasic strains of *S.* Typhimurium from turkeys in 2021 (Tables 7.3 and 7.4). These strains are typically associated with pigs and were first reported from turkeys in 2011. The number of isolations from turkeys each year has typically been between 2 and five, but there were peaks in 2014 (20 isolations) and 2018 (15 isolations) (Table 7.1).

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

Notably, *S*. Berta (1 isolation from voluntary surveillance in a breeder flock) and *S*. Brandenburg (1 isolation from statutory sampling in a fattener flock) have never previously been reported from turkeys in Great Britain. There were also 5 isolations of *S.* London (from 3 fattening flocks) in 2022. Prior to 2021 when there were 6 isolations this serovar had never previously been reported from turkeys in Great Britain. There were 2 isolations of *S*. Give (voluntary surveillance in fattener flocks), which was last reported from turkeys in 2015 and 8 isolations of *S.* Montevideo in 2022 (last isolated from turkeys was 2016 when there was one isolation).

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 retained as Great Britain legislation, aim to protect public health, through a reduction in levels of *Salmonella* in turkey flocks.

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 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. There is equivalent national legislation for Scotland and Wales although there has been close collaboration throughout the development of the legislative proposals and implementation.

Positive flocks identified in the NCP for breeding turkeys 2022

Four adult turkey breeding flocks tested positive for *Salmonella* in 2022. This is double the number compared to 2021 (2 positive flocks), but a 42.9% reduction compared with 2020 (7 positive flocks) (Table 7.5).

No turkey breeding flocks tested positive for any regulated serovar in 2022, consistent with 2021 and 2020. This compares with 2 flocks on one site testing positive for *Salmonella* 4,5,12:i:- DT193 in 2019 and 6 positive flocks (all in same ownership with 3 flocks each kept on 2 nearby sites) in 2018. Prior to this no regulated serovars had ever been isolated from turkey breeding flocks in the NCP since it began in 2010.

All 4 adult turkey breeding flocks tested positive for *S.* Senftenberg in 2022, which is similar to 3 flocks in 2020 (no flocks tested positive for this serovar in 2021). Whilst prevalence of this serovar in generally low in turkey breeding flocks, *S*. Senftenberg has been the most frequently isolated serovar across the last 10 years and identified in 7 of the last 10 years (Table 7.5). All positive flocks were identified through routine annual official testing.

Six immature breeding flocks tested positive for *Salmonella* in 2022 compared with 7 positive flocks in 2021 and none in 2020. Three immature flocks of day-old birds on the same premises tested positive for *S.* Senftenberg, with a fourth flock positive for this serovar on a separate holding. *Salmonella* Senftenberg is a known hatchery contaminant, which is rarely found in breeding or fattening birds (though has been the most frequently identified serovar in fattening flocks over the past 10 years). It is therefore likely that the number of positive rearing flocks reported reflects contamination of the hatchery of origin. In addition, one immature flock tested positive for *S.* Anatum and one immature flock tested positive for *Salmonella* 3,10:e,h:-. These flocks were on the same premises on which 3 immature flocks tested positive for *S.* Senftenberg, as detailed above. This is the first time either of these serovars has been isolated in a turkey breeding flock since the NCP started for breeding turkeys in 2010.

For comparison, the serovars identified in the adult turkey breeder NCP between 2018 and 2022 are shown in Table 7.5. Figure 7.5 shows the relative percentages of the serovars in the turkey breeder NCP from 2018 to 2022.

A total of 203 adult turkey breeding flocks were in production in Great Britain in 2022 and were included in the NCP. Therefore, the estimated prevalence for regulated serovars was 0.0% (0 of 203) which is below the target of a maximum of 1% of flocks testing positive. This figure is consistent with 2021 and 2020 (0%) and a decrease compared to 2019 (0.73%). The estimated prevalence for all serovars in 2022 was 1.97% (4 of 203), an increase from 0.83% in 2021 (2 flocks) but a decrease from 2.62% (7 flocks) in 2020. Figure 7.6 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 2022

In total, 97 fattening turkey flocks (on 46 different holdings) were positive for *Salmonella* in 2022. This is a 3.19% increase from 2021 (94 positive flocks on 48 different holdings) and interrupts a year-on-year decreasing trend in the proportion of flocks testing positive from

2016-2021 (Table 7.6, Figure 7.4). Figure 7.9 illustrates the most common serovars isolated from fattening flocks from 2018-2022.

In 2022, 2 flocks on 2 holdings tested positive for regulated serovars compared to 12 flocks in 2021, representing an 83.3% reduction and a notable reduction in the number of flocks testing positive for *S*. Typhimurium and monophasic *S*. Typhimurium. The detection of regulated serovars in 2022 and 2021 follows 2 years in which no flocks tested positive for regulated serovars. 2019 was the first year since the NCP began that no regulated serovars were isolated from turkey fattening flocks, although only one was isolated in both 2012 and 2013.

One turkey fattening flock tested positive for the monophasic *S.* Typhimurium strain 4,5,12:i:- DT193 (via operator sampling) and one flock tested positive for monophasic *S*. Typhimurium 4,12:i:- DT193 (via operator sampling). Both serovars were isolated from turkey fatteners in 2021 (*S.* Typhimurium strain 4,5,12:i:- from 8 flocks, *S*. Typhimurium 4,12:i:- from 1 flock). No turkey fattening flocks tested positive for either *S*. Enteritidis or *S.* Typhimurium in 2022.This is consistent with 2019 and 2020 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 95 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 2018 and 2022 are shown in Table 7.6. The relative percentages of the most common serovars from turkey fattening flocks each year from 2018 to 2022 are shown in Figure 7.6. The 3 most commonly isolated serovars in 2022 was consistent with 2020 and 2021, although the relative contribution of each serovar has varied.

For the third consecutive year, *S.* Anatum was the most frequently isolated serovar from turkey fattening flocks in the NCP in 2022. There was an increase in the number of flocks testing positive for this serovar in 2022 (40 flocks) compared to 2021 (31 flocks) with isolations remaining 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.

Salmonella Kedougou was the second most common serovar, isolated from 21 turkey fattening flocks in 2022. This is more than double the number of flocks testing positive for this serovar in 2021 (9 flocks) although a reduction of 36.4% compared to 2020 (33 flocks). In 2020, *S*. Kedougou also ranked as the second most common serovar.

Salmonella Derby was the third most common serovar and was isolated in 7 turkey fattening flocks in 2022. This represents a near three-fold reduction in number of positive flocks compared with 2021 and 2020 when 19 positive flocks were identified in each year. This continues a dramatic reduction in the number of flocks testing positive for this serovar since 2018 (259 flocks). This is the third year in a row since the NCP began in 2010 that *S*. Derby was not the most common serovar isolated from turkey fattening flocks. This reduction follows more successful control of *S.* Derby in adult turkey breeding flocks and hatcheries and gradual resolution of persistent contamination of some fattening farms.

The number of samples testing positive for *S.* Agona has gradually increased in recent years from 2 in 2020, 4 in 2021, and 7 in 2022. This follows a gradual decline in flocks testing positive from 7 in 2018 to 2 in 2020. The proportion of positive flocks that were positive for this serovar has also increased from 1.7% in 2020 to 7.2% in 2022.

Salmonella Senftenberg, a known hatchery contaminant, was isolated from 5 flocks in 2022, a 66.7% increase compared to 2021 (3 positive flocks). 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.

Salmonella London was isolated from 3 flocks, the second consecutive year this serovar has been isolated from fattening flocks since the NCP began. One flock tested positive for *Salmonella* Brandenburg which is the first time this serovar has been isolated from turkeys in Great Britain since the inception of the NCP in 2010. In addition, 3 flocks tested positive for *S*. Montevideo, which was last isolated from turkey fatteners in 2010.

A total of 2,017 turkey fattening flocks were in production in Great Britain in 2022 and were included in the NCP. Therefore, the estimated prevalence for regulated *Salmonella* serovars was 0.10% (2 of 2,017), which is well below the target of a maximum of 1% of flocks positive for regulated serovars. The estimated prevalence of all *Salmonella* spp. In 2022 was 4.81% (97 of 2,017).

Figure 7.7 shows the change in prevalence of turkey fattening flocks testing positive for *Salmonella* since 2013. Estimated prevalence of regulated serovars in 2022 (0.10%) was lower than in 2021 (0.48%) but higher than in 2020 and 2019 (0.00% in both years). Estimated prevalence of all *Salmonella* serovars in 2022 (4.81%) was higher than in 2021 (3.76%) and 2020 (4.76%), but a 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	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
Agama	0	0	0	0	1	1	2	2	0	1
Agona	7	11	5	9	2	2	4	7	7	11
Albany	0	0	1	2	0	0	0	0	0	0
Albert	1	1	0	0	0	0	0	0	0	0
Anatum	2	2	4	4	38	42	31	31	40	66
Berta	0	0	0	0	0	0	0	0	0	1
Bovismorbificans	3	4	0	0	0	0	2	2	0	1
Brandenburg	0	0	0	0	0	0	0	0	1	1
Coeln	0	0	0	1	0	0	0	0	0	0
Derby	259	401	105	132	20	22	19	22	7	12
Eastbourne	0	0	1	1	0	0	0	0	0	0
Give	0	0	0	0	0	0	0	0	0	2
Give var. 15^{+}	0	0	0	0	0	0	1	1	0	0
Idikan	0	0	0	0	0	1	0	0	0	0
Indiana	0	0	1	1	0	0	0	0	0	0
Kedougou	5	5	28	44	33	68	9	16	21	30
Kingston	0	0	0	0	1	1	0	0	0	0
Kottbus	1	1	4	4	0	0	0	0	0	0
Livingstone	0	0	0	0	0	2	0	0	0	0
London	0	0	0	0	0	0	1	6	3	5
Mbandaka	4	6	0	5	1	2	1	1	0	0
Montevideo	0	0	0	0	0	0	0	0	3	8
Newport	0	5	1	5	1	2	2	3	1	1
Nottingham	0	0	1	1	0	0	0	0	0	0

Salmonella serovar	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
Ohio	0	0	0	1	0	0	0	0	0	0
Orion var. 15^{+}	0	1	0	1	1	2	4	5	3	5
Senftenberg	24	28	36	48	9	15	3	20	9	26
Soerenga	0	6	0	0	0	0	0	0	0	0
Typhimurium	4	6	0	0	0	2	3	3	0	1
Wangata	1	1	0	0	0	0	0	0	0	0
4,5,12:i:-	9	14	2	2	0	0	8	8	1	2
4,12:i:-	1	1	0	0	0	0	1	1	1	2
untypable strains	0	2	4	5	19	29	6	10	5	6
rough strains	2	2	0	1	3	5	1	2	2	7
Total	**318**	**497**	**190**	**267**	**124**	**196**	**96**	**140**	**101**	**188**

In 2018 the isolations of *S.* Derby include presumptive *S.* Derby. This affects 172 flocks and 230 isolations in 2018.

In 2018 5 flocks tested positive for 2 different *Salmonella* serovars. These flocks are included in the table under both serovars but only once in the overall total.

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.

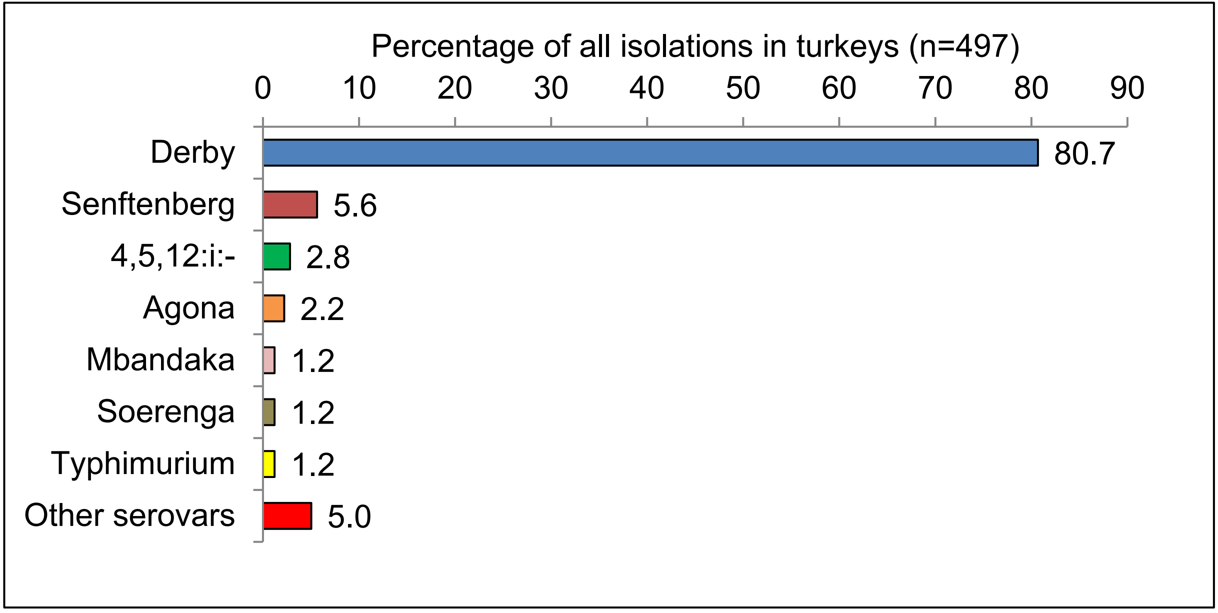
In 2020 5 flocks tested positive for 2 different *Salmonella* serovars. These are included in the table under both serovars but only once in the overall total.

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.

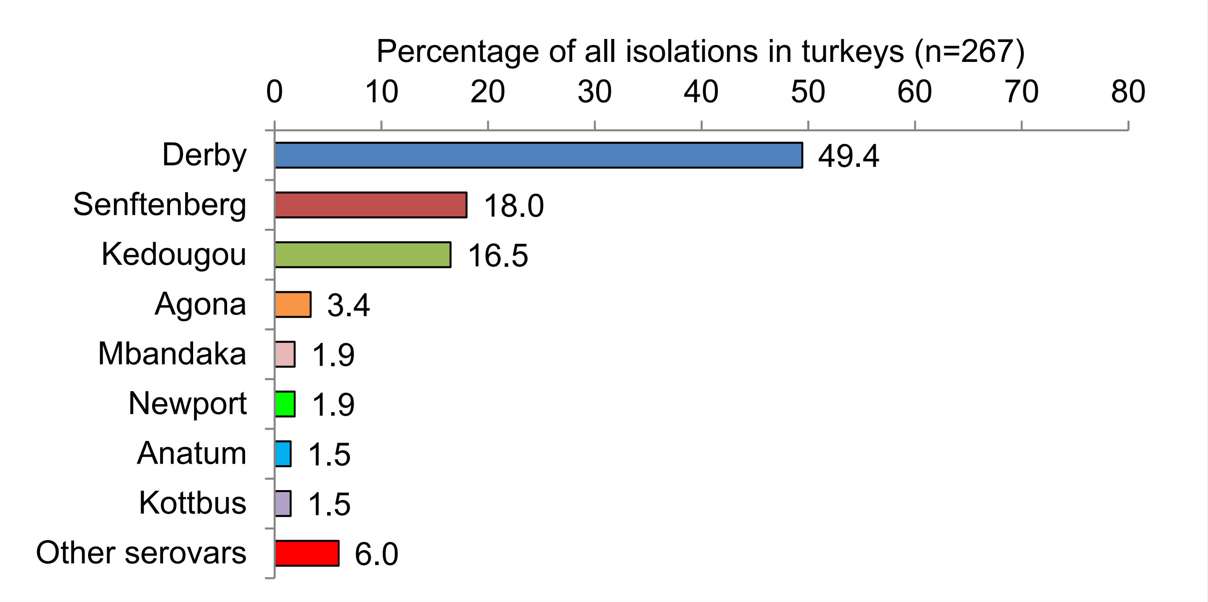
Figure 7.1: The most common serovars in turkeys by number of isolations in Great Britain 2018 to 2022 (statutory and non-statutory testing)

Figure 7.1.1: Isolations in 2018



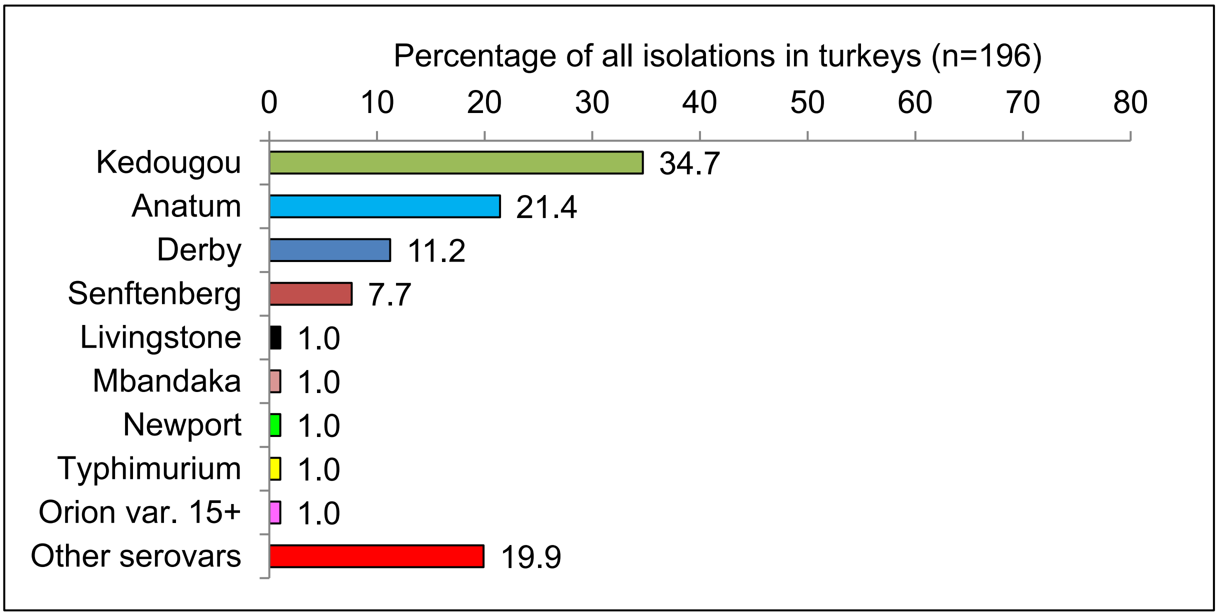
In 2018 the most common *Salmonella* serovar in turkeys was *S.* Derby (including presumptive *S.* Derby), accounting for 80.7% of total isolations, followed by *S*. Senftenberg (5.6%), *S.* 4,5,12:i:- (2.8%) and *S.* Agona (2.2%).

Figure 7.1.2: Isolations in 2019



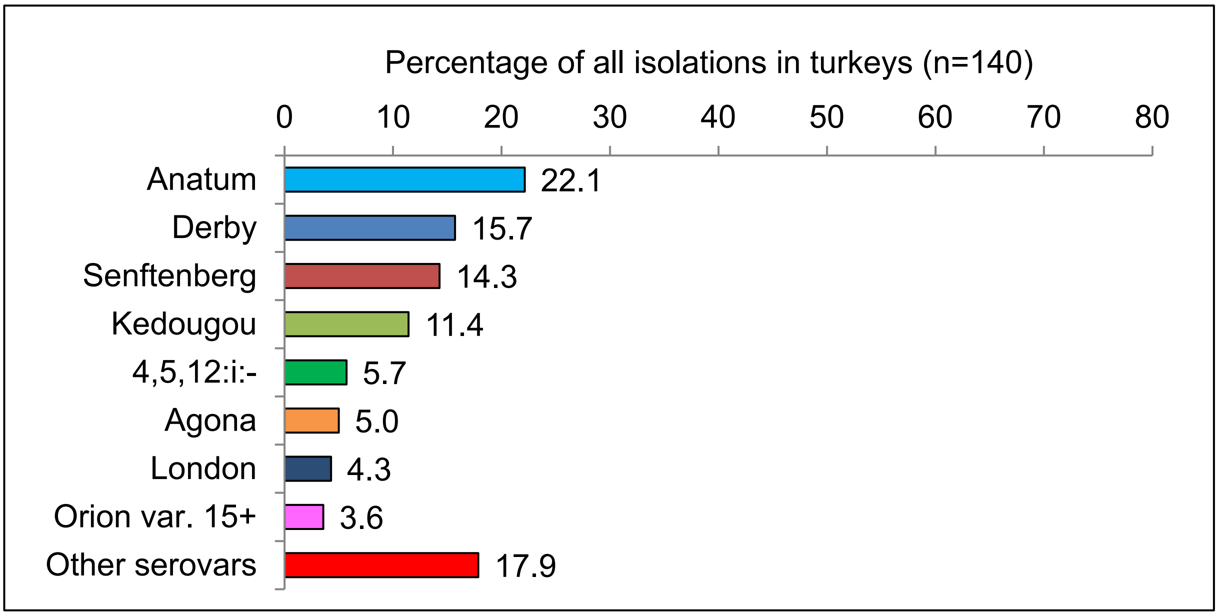
In 2019 the most common *Salmonella* serovar in turkeys was *S.* Derby, accounting for 49.4% of total isolations, followed by *S*. Senftenberg (18.0%), *S.* Kedougou (16.5%) and *S.* Agona (3.4%).

Figure 7.1.3: Isolations in 2020



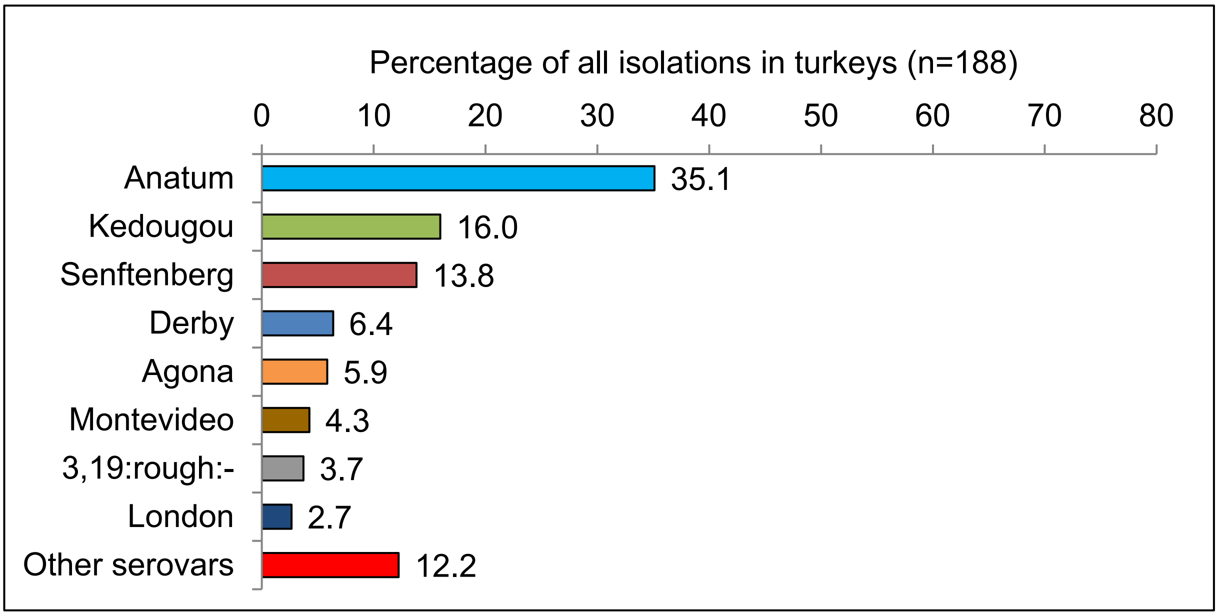
In 2020 the most common *Salmonella* serovar in turkeys was *S.* Kedougou, accounting for 34.7% of total isolations, followed by *S*. Anatum (21.4%), *S.* Derby (11.2%) and *S.* Senftenberg (7.7%).

Figure 7.1.4: 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 7.1.5: 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 7.2: The 5 most common *Salmonella* serovars in turkeys in Great Britain in 2022 and their trends over time since 2018

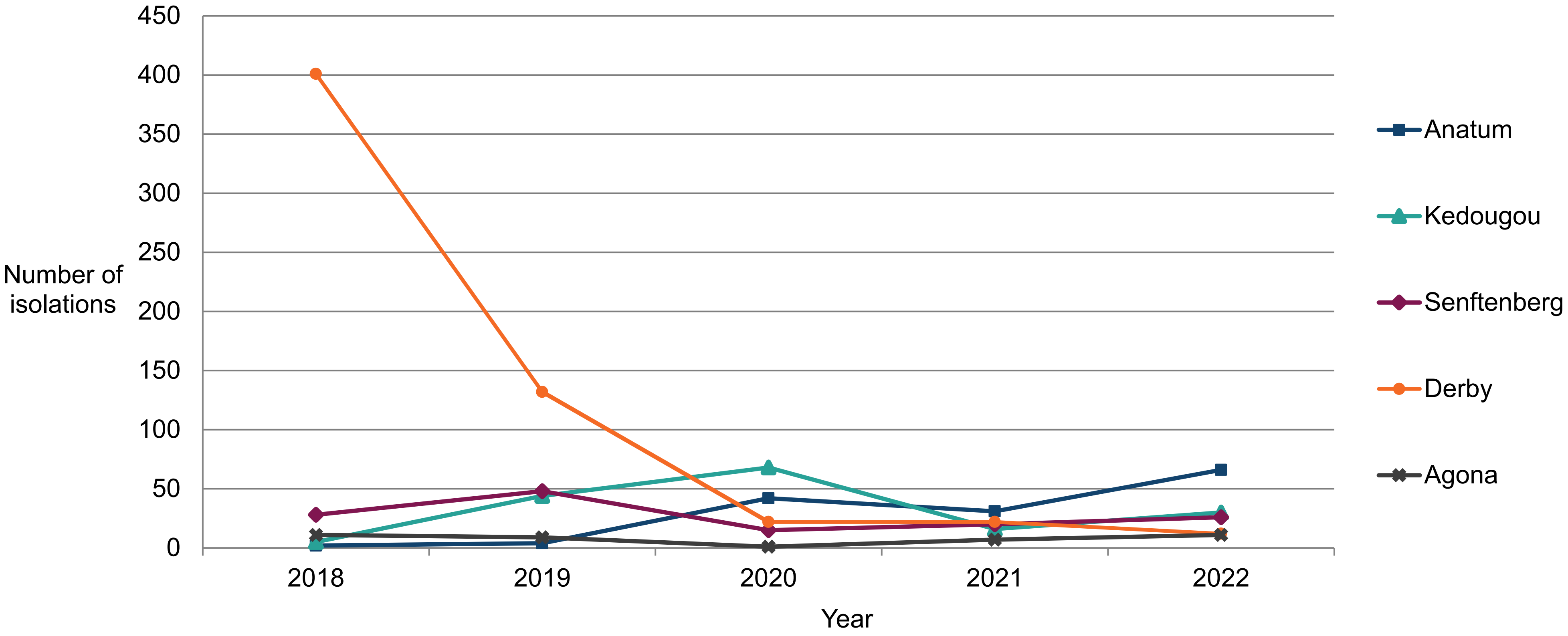


Figure 7.2 shows that despite a very high number of isolations in 2018 (401) *S.* Derby has declined to fourth most common in 2022. The position of the other top 5 serovars varies year on year with *S.* Anatum having the most isolations in 2022 (66), followed by *S.* Kedougou (30), *S.* Senftenberg (26) and finally *S.* Agona (11).

Table 7.2: *S.* Typhimurium phage types in turkeys in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
RDNC	0	0	0	0	0	1	0	0	0	0
U302	0	0	0	0	0	0	3	3	0	0
DT193	1	1	0	0	0	0	0	0	0	0
DT99	0	0	0	0	0	0	0	0	0	1
DT12	3	5	0	0	0	0	0	0	0	0
DT9	0	0	0	0	0	1	0	0	0	0
Total	**4**	**6**	**0**	**0**	**0**	**2**	**3**	**3**	**0**	**1**

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

Table 7.3: *Salmonella* 4,5,12:i:- phage types in turkeys in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
UNTY	0	0	0	0	0	0	1	1	0	0
NOPT	0	1	0	0	0	0	0	0	0	0
DT193	9	13	2	2	0	0	7	7	1	2
Total	**9**	**14**	**2**	**2**	**0**	**0**	**8**	**8**	**1**	**2**

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

Table 7.4: *Salmonella* 4,12:i:- phage types in turkeys in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
UNTY	0	0	0	0	0	0	0	0	0	1
DT193	1	1	0	0	0	0	1	1	1	1
Total	**1**	**1**	**0**	**0**	**0**	**0**	**1**	**1**	**1**	**2**

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 2013 to 2022

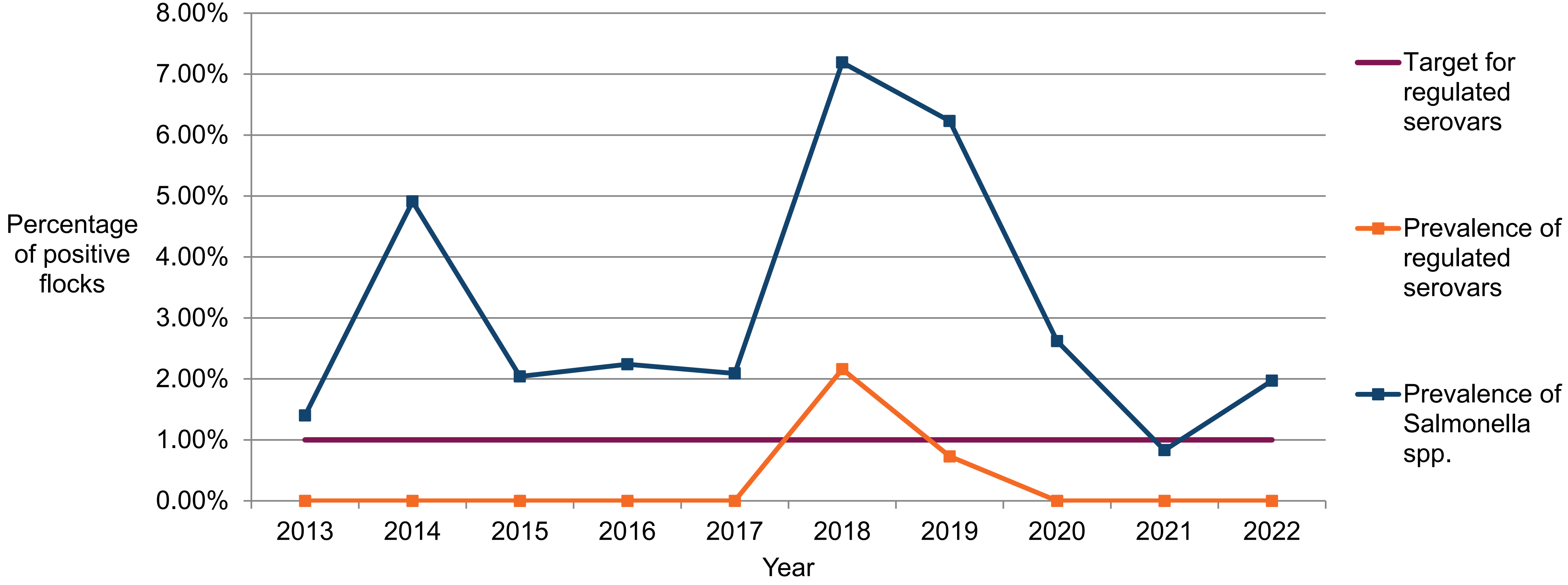


Figure 7.3 shows a peak in the prevalence of *Salmonella spp.* In breeding turkey flocks of 7.19% in 2018 but a subsequent decline thereafter to 1.97% in 2022.The prevalence of regulated serovars remains at 0.0% despite a small peak in 2018 to 2.16% which was above the target of 1% prevalence. The absolute 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 2013 to 2022

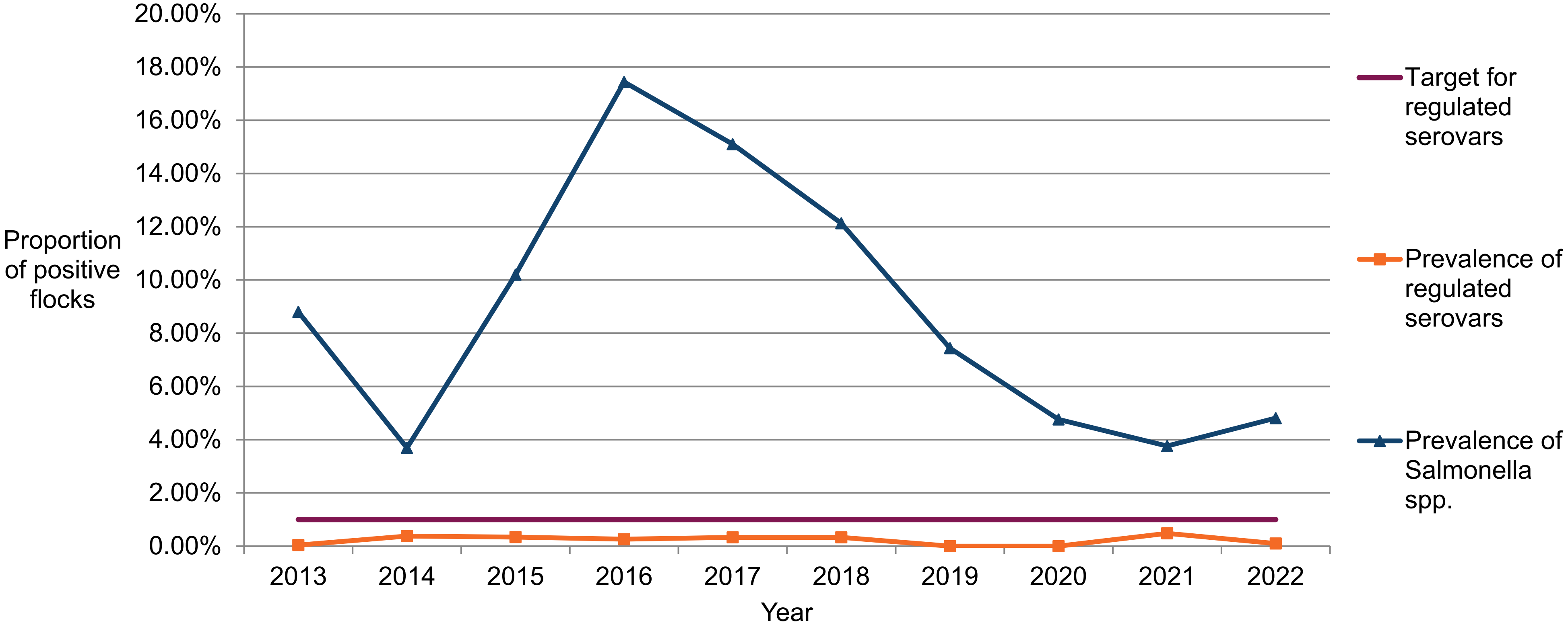


Figure 7.4 shows a peak in the prevalence of *Salmonella spp.* In fattening turkey flocks of 17.4% in 2016 but a subsequent decline thereafter to 4.8% in 2022.The prevalence of regulated serovars remains very low and below the target of 1% prevalence across all years.

Table 7.5: Turkey breeding flocks in Great Britain (number of adult flocks reported positive for each *Salmonella* serovar, NCP testing 2018 to 2022)

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
Senftenberg	1	12	1	15	1	3	0	0	1	4
13,23:i:-	0	0	0	0	2	2	0	0	0	0
4,5,12:i:-	2	6	2	2	0	0	0	0	0	0
Agama	0	0	0	0	3	1	1	1	0	0
Derby	0	0	0	0	3	1	0	0	0	0
Mbandaka	3	4	0	0	0	0	2	1	0	0

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

For details of turkey breeding flocks reported positive in 2013 to 2017, see the 2017 edition of *Salmonella* in livestock production in Great Britain.

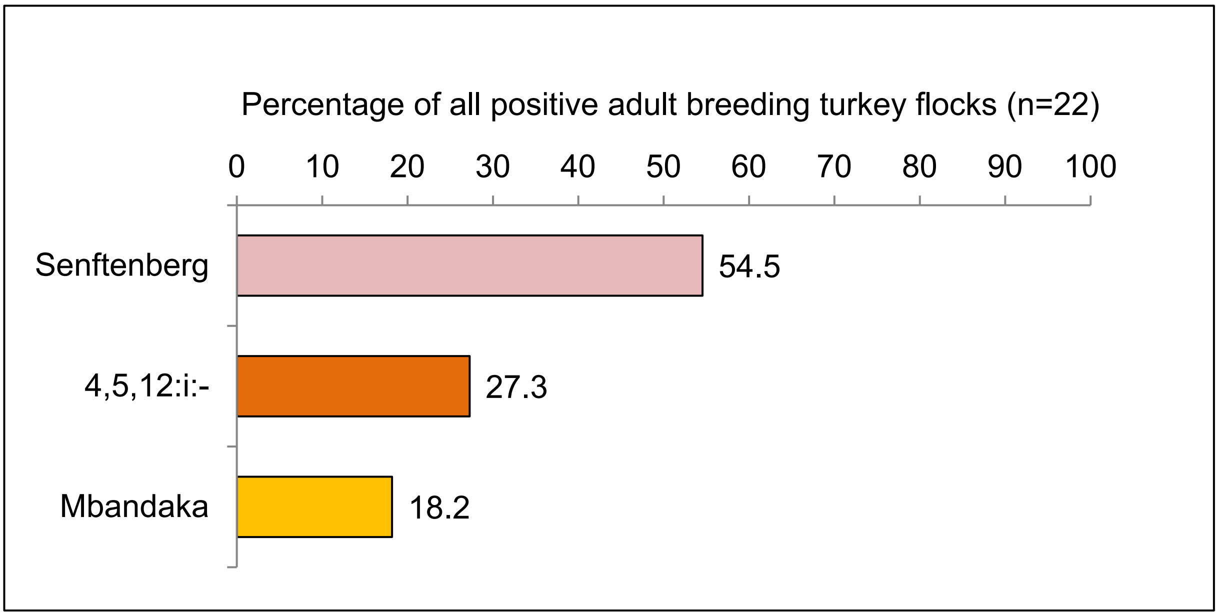
Prevalence of all serovars and regulated serovars

Year	Prevalence of all serovars	Prevalence of regulated serovars
2018	7.91%	2.16%
2019	6.23%	0.73%
2020	2.62%	0.00%
2021	0.83%	0.00%

Year	Prevalence of all serovars	Prevalence of regulated serovars
2022	1.97%	0.00%

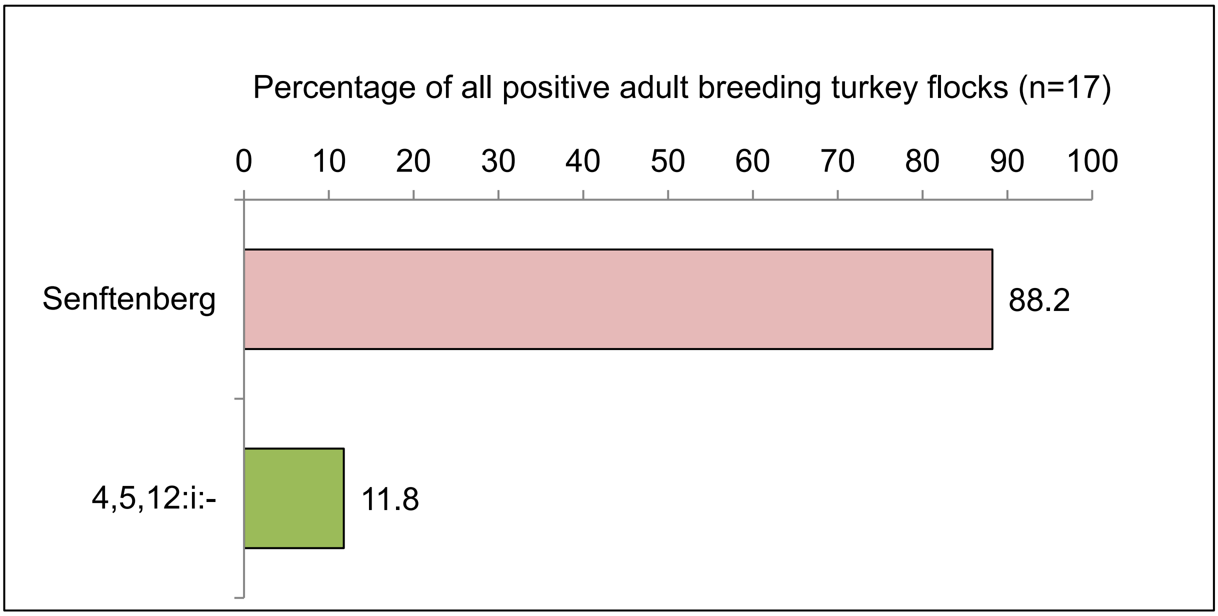
Figure 7.5: The most common serovars identified in adult turkey breeding flocks in Great Britain 2018 to 2022 reported from NCP testing

Figure 7.5.1: Isolations in 2018



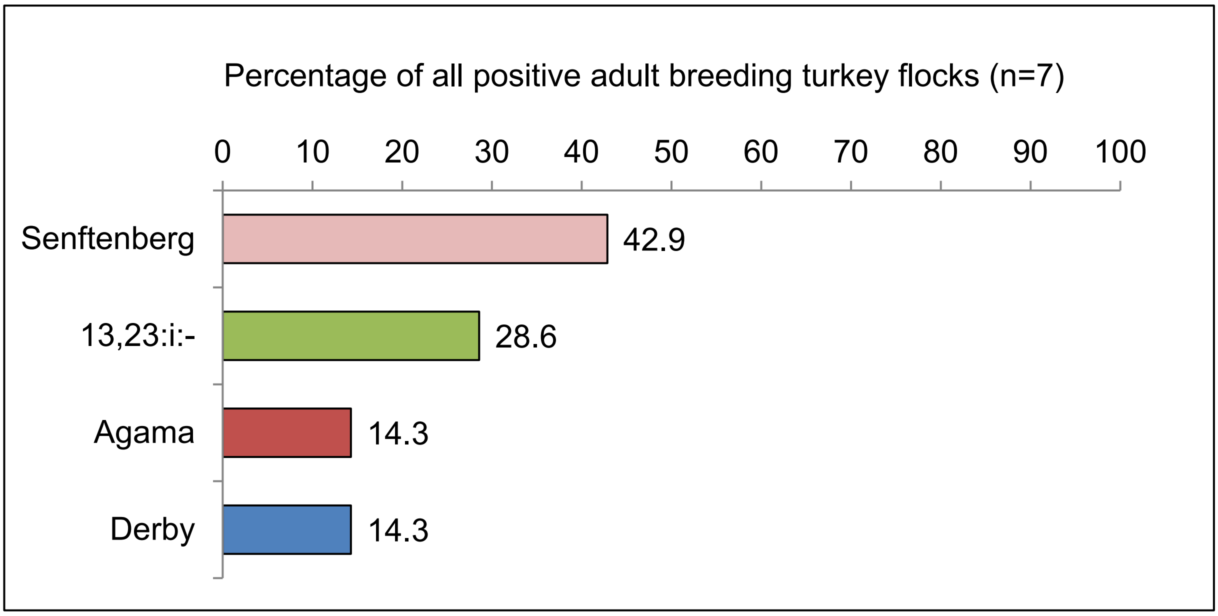
In 2018 the most common *Salmonella* serovar in breeding turkey flocks was *S.* Senftenberg accounting for 54.5% of isolations followed by *S.* 4,5,12:i:- (27.3%) and *S.* Mbandaka (18.2%).

Figure 7.5.2: Isolations in 2019



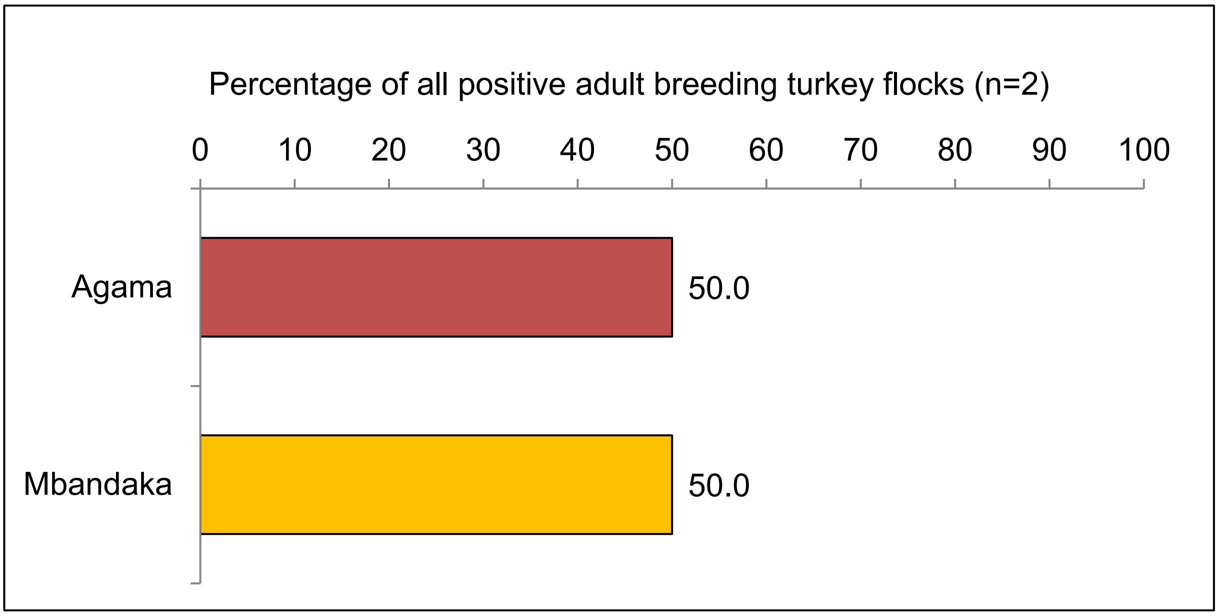
In 2019 the most common *Salmonella* serovar in breeding turkey flocks was *S*. Senftenberg accounting for 88.2% of isolations followed by *S*. 4,5,12:i:- which accounted for the remaining 11.8%.

Figure 7.5.3: Isolations in 2020



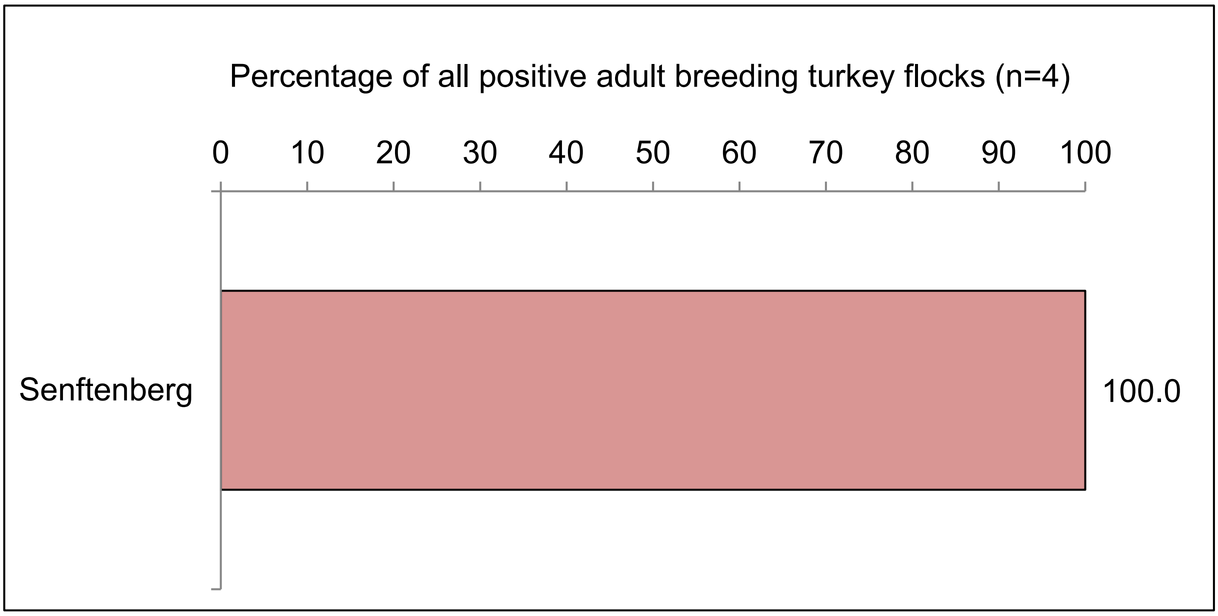
In 2020 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Senftenberg, accounting for 42.9% of total isolations, followed by *S*. 13,23:i:- (28.6%), *S.* Agama (14.3%) and *S*. Derby (14.3%).

Figure 7.5.4: 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 7.5.5: Isolations in 2022



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

Table 7.6: Turkey fattening flocks in Great Britain (number of flocks reported positive for each *Salmonella* serovar, NCP testing 2018 to 2022)

The following table shows the number of turkey fattening flocks reported positive with each *Salmonella* serovar from 2018 to 2022 and the rank within that year. This data comes from NCP testing.

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
Anatum	7	2	5	4	1	38	1	31	1	40
Kedougou	4	5	2	28	2	33	3	9	2	21
Agona	3	7	4	5	7	2	5	4	3	7
Derby	1	259	1	105	3	19	2	19	3	7
Senftenberg	2	12	3	21	5	6	6	3	4	5
3,10:e,h:-	0	0	7	1	4	11	6	3	6	3
London	0	0	0	0	0	0	8	1	5	3
Montevideo	0	0	0	0	0	0	0	0	5	3
Orion var. 15^+	0	0	0	0	8	1	5	4	5	3
13,23:i:-	0	0	6	3	6	4	7	2	6	2
3,19:rough:-	0	0	0	0	8	1	0	0	6	2
4,12:i:-	8	1	0	0	0	0	8	1	6	1
4,5,12:i:-	6	3	0	0	0	0	4	8	6	1
Brandenburg	0	0	0	0	0	0	0	0	6	1
Newport	0	0	7	1	8	1	7	2	6	1
6,8:e,h:-	0	0	0	0	8	1	8	1	0	0
Agama	0	0	0	0	0	0	8	1	0	0
Albany	0	0	7	1	0	0	0	0	0	0
Albert	8	1	0	0	0	0	0	0	0	0
Bovismorbificans	6	3	0	0	0	0	7	2	0	0
Eastbourne	0	0	7	1	0	0	0	0	0	0

Serovar	Rank 2018	Flocks 2018	Rank 2019	Flocks 2019	Rank 2020	Flocks 2020	Rank 2021	Flocks 2021	Rank 2022	Flocks 2022
Give var. 15^+	0	0	0	0	0	0	8	1	0	0
Indiana	0	0	7	1	0	0	0	0	0	0
Kingston	0	0	0	0	8	1	0	0	0	0
Kottbus	8	1	5	4	0	0	0	0	0	0
Mbandaka	0	0	0	0	8	1	0	0	0	0
Nottingham	0	0	7	1	0	0	0	0	0	0
O rough:e,g:1,6	0	0	0	0	8	1	0	0	0	0
O rough:f,g:-	7	2	0	0	7	2	0	0	0	0
Typhimurium	5	4	0	0	0	0	6	3	0	0
Wangata	8	1	0	0	0	0	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 2017, see the 2017 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
2018	12.13%	0.33%
2019	7.44%	0.00%
2020	4.76%	0.00%
2021	3.76%	0.48%

Year	Prevalence of all serovars	Prevalence of regulated serovars
2022	4.81%	0.10%

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 *S*. Derby and *S*. Kedougou
- 1 flock tested positive for *S*. Derby and *S*. O rough:f,g:-
- 1 flock tested positive for *S*. Derby and *S*. 4,12:i:-
- 1 flock tested positive for *S*. Derby and *S*. Typhimurium
- 1 flock tested positive for *S*. Derby and *S*. 4,5,12:i:-

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:

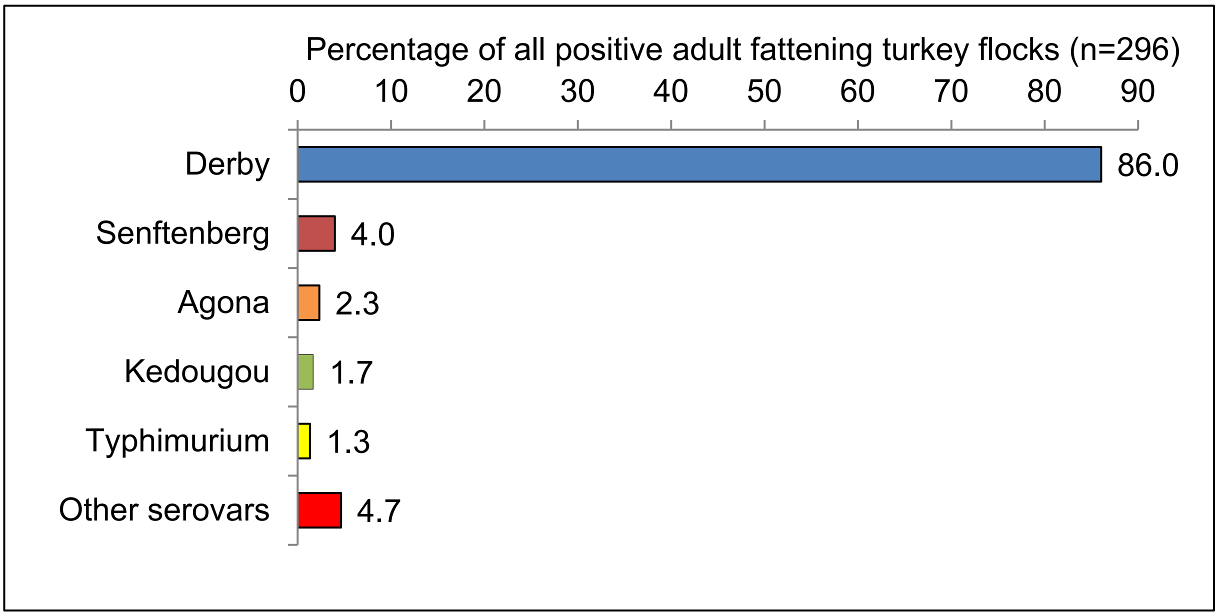
- 1 flock tested positive for *S*. Derby and *S*. Newport
- 1 flock tested positive for *S*. Give var. 15^+ and *S*. Orion var. 15^+

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

Figure 7.6: The most common serovars identified in turkey fattening flocks in Great Britain 2018 to 2022 reported from NCP testing

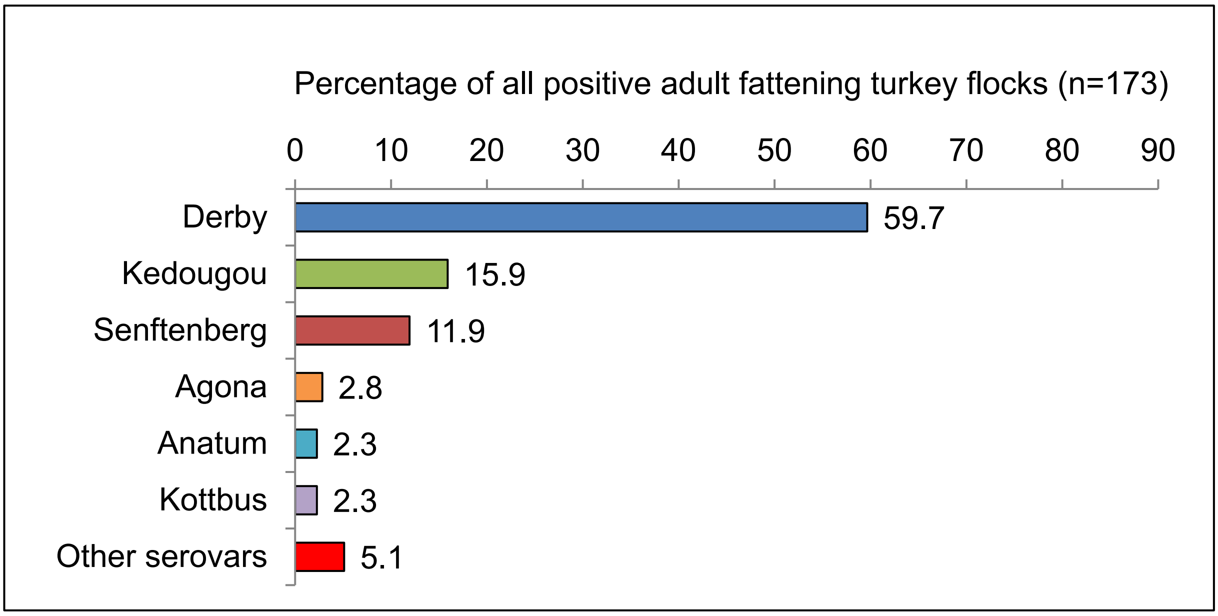
Figure 7.6.1: Isolations in 2018



In 2018 the most common *Salmonella* serovar in fattening turkey flocks was *S.* Derby (including presumptive *S.* Derby), accounting for 86.0% of total isolations, followed by *S.* Senftenberg (4.0%), *S.* Agona (2.3%) and *S.* Kedougou (1.7%).

In 2018 5 flocks were positive for 2 serovars (each counted once in the total). Summed percentages of all serovars therefore exceeds 100%.

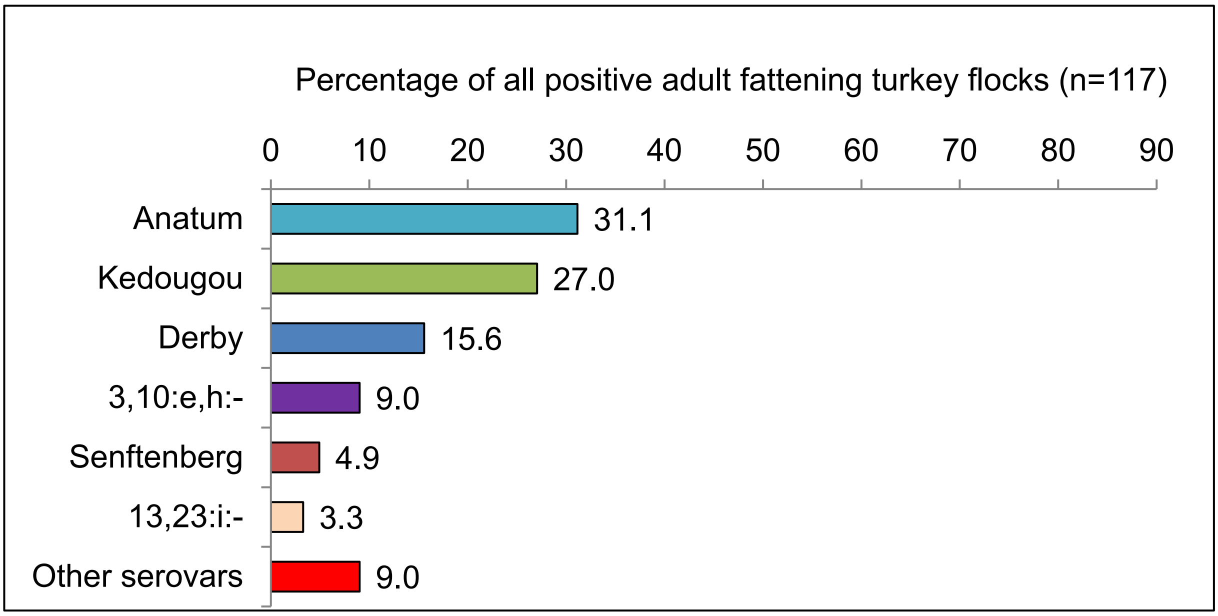
Figure 7.6.2: Isolations in 2019



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%.

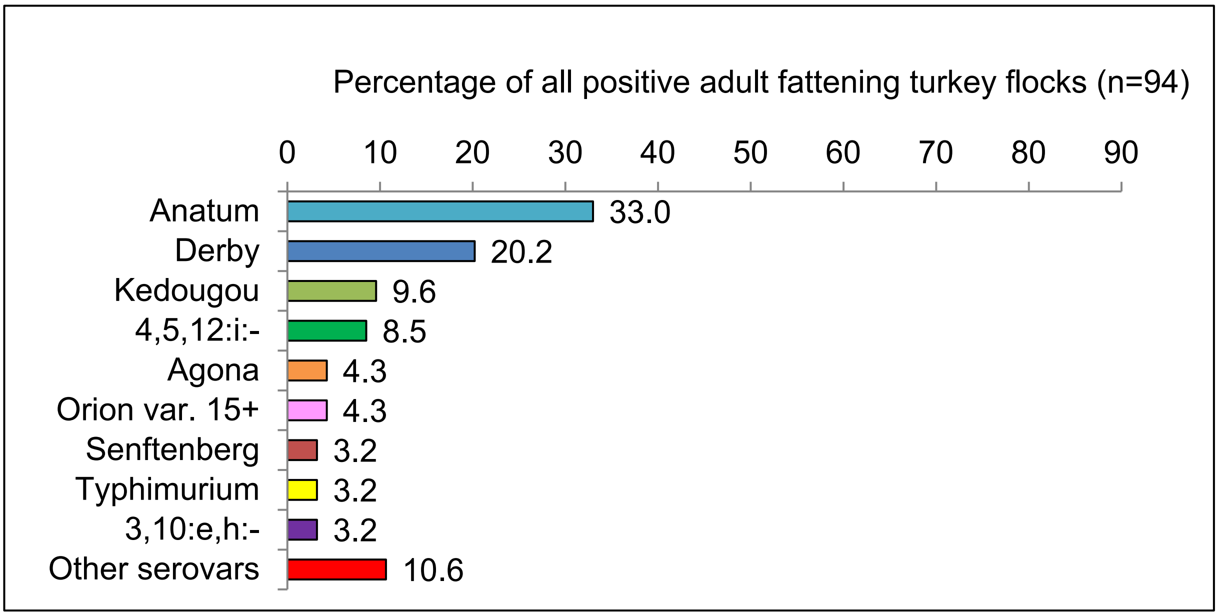
Figure 7.6.3: Isolations in 2020



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%.

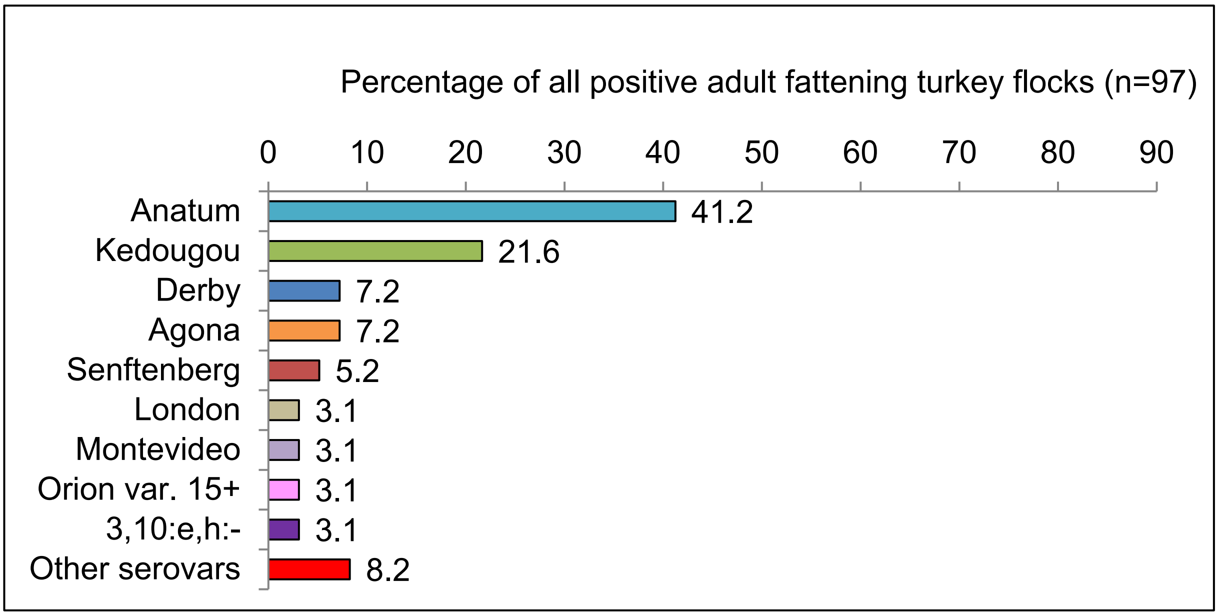
Figure 7.6.4: Isolations in 2021



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 *S*. 4,5,12:i:- (8.5%).

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

Figure 7.6.5: 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%.

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

During 2020 there was a reduction in non-statutory surveillance and clinical diagnosis submissions in many species which was a consequence of the Covid-19 pandemic and associated lockdown measures. During 2021 and 2022 there was a reduction in non-statutory surveillance and clinical diagnosis submissions in many avian species as consequence of the large Avian Influenza outbreak and associated control measures. 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. *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 2022 there were 121 isolations of *Salmonella* from ducks in Great Britain, which is 10.0% more than in 2021 (110 isolations) and 41.3% fewer than in 2020 (206 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, most likely due to the Covid-19 pandemic and the large Avian Influenza outbreak.

The most common serovars isolated from ducks during 2022 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) and *S*. Orion var 15$^+$ (15 isolations, 12.4% of duck isolations). Together these serovars accounted for 82.6% of all *Salmonella* isolations from ducks (Figure 8.1). In contrast, during 2021 the most common serovars were *S*. Indiana (41 isolations, 37.3% of duck isolations), *S.* Orion (12 isolations, 10.9% of duck isolations), *S*. Kottbus (9 isolations, 8.2% of duck isolations) and *S*. Lexington (9 isolations, 8.2% of duck isolations).

Salmonella Indiana remained the most commonly reported serovar from ducks during 2022 (38 isolations). However, this is the fourth consecutive year that the number of *S*. Indiana isolations has fallen and represents the lowest number since 2011 when there were 3 isolations. This serovar accounted for a slightly lower proportion of total isolations from ducks in 2022 (31.4%) compared to 2021 (37.3%) (Figure 8.1 and Figure 8.3).

There were 17 isolations of *S.* Hadar during 2022, the second most common serovar isolated from ducks. Despite an increase in isolations compared to 2021 (1 isolation), this is similar to the number of isolations in 2020 (21 isolations). However, in general there has been a declining trend in the number of *S*. Hadar isolations since 2018 (44 isolations) (Figure 8.1).

Isolations of *Salmonella* Give var.15^+ increased in 2022 (15 isolations) compared to 2021 (6 isolations) but in recent years there has been a general decline in isolations since 2017 (70 isolations). Despite fewer isolations in 2022, *S*. Give var.15^+ was the joint third most common serovar to be isolated from ducks.

There were 15 isolations of *S*. Orion var. 15^+ from ducks in 2022 representing the highest number of isolations since 2019 but still lower than in previous years (2014 to 2018) when there were greater than 20 isolations. However, the proportion of isolations associated with *S*. Orion var. 15^+ in 2022 (12.4%) was increased compared with recent years (7.3% in 2021, 5.8% in 2020).

There were 15 isolations of *S*. Bovismorbificans in 2022 compared to no isolations during 2021 and 16 isolations in 2020. This serovar was associated with 12.4% of isolations, joint third (with *S*. Give var.15^+) most common serovar in ducks in 2022 (Figure 8.1) which is the highest proportion since before 2009.

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

There were no isolations of *S*. Enteritidis from ducks in 2022, the first year since 2019 this serovar has not been isolated having been isolated once each in 2020 and 2021 (Figure 8.3 and Table 8.4). There were no isolations of *S*. Typhimurium from ducks during 2022, which is the second year this serovar has been absent from ducks in Great Britain since 2001, decreasing from 2 isolations in 2020 (both phage type DT9, Table 8.3). Isolations of *S*. Typhimurium from ducks have decreased substantially since 2010 when there were 119 isolations representing 60.4% of total isolations. It is thought that this overall reduction may be associated with the inception of the duck assurance scheme in 2010. There were no isolations of *Salmonella* 4,12:i:- from ducks during 2022, consistent with 2019 to 2021, and compares with one isolation (DT120) in 2018 (Table 8.5). *Salmonella* 4,5,12:i:- has not been isolated from ducks since 2010.

There were 2 isolations of *S.* Orion during 2022 (1.7% of duck isolations) compared with 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). *S.* Give isolations continued to decline with 1 isolation in 2022 compared with a peak of 56 isolations in 2018.

Other reported serovars from ducks in 2022 included *S*. Kottbus (6 isolations). *Salmonella* Kottbus has been isolated from ducks every year since 2013 but there has been a generally declining trend in the number of isolations since 2018 (Table 8.1). There were no isolations of *S*. Newport during 2022, the first time since 2019, though there have been relatively few isolations of this serovar in recent years (1 isolation in 2021 and 2 isolations in 2020).

Geese

There were no isolations of *Salmonella* from geese in 2022. This is consistent with 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 2022 there 289 diagnostic submissions from Geese recorded on the VIDA database in Great Britain compared to 130 in 2021.

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

Salmonella serovar	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
Agona	0	0	0	0	0	0	1	1	0	0
Albert	1	1	0	0	0	0	0	0	0	0
Anatum	0	0	1	1	0	0	0	0	0	0
Bovismorbificans	8	8	8	5	16	8	0	0	15	3
Derby	2	2	1	1	0	0	0	0	0	0
Enteritidis	0	0	0	0	1	1	1	1	0	0
Give	56	20	11	9	6	6	6	5	1	1
Give var. 15$^+$	55	36	53	41	32	21	6	5	15	13
Hadar	44	34	39	36	21	20	1	1	17	10
Indiana	123	95	93	79	60	53	41	33	38	28
Istanbul	1	1	0	0	0	0	0	0	0	0
Kedougou	0	0	0	0	0	0	1	1	0	0
Kottbus	24	17	11	9	6	5	9	9	6	5
Lexington	6	5	2	2	7	5	9	7	9	8
Mapo	1	1	0	0	0	0	0	0	0	0
Monschaui	4	4	4	4	2	2	0	0	0	0
Newport	3	3	0	0	2	2	1	1	0	0
Orion	36	22	15	13	16	15	12	11	2	2
Orion var. 15$^+$	34	32	36	32	12	12	8	6	15	8
Oslo	3	3	9	8	3	2	0	0	0	0
Rissen	1	1	0	0	0	0	0	0	0	0
Senftenberg	0	0	0	0	0	0	1	0	0	0
Typhimurium	11	5	2	2	2	2	0	0	0	0
4,12:i:-	1	1	0	0	0	0	0	0	0	0

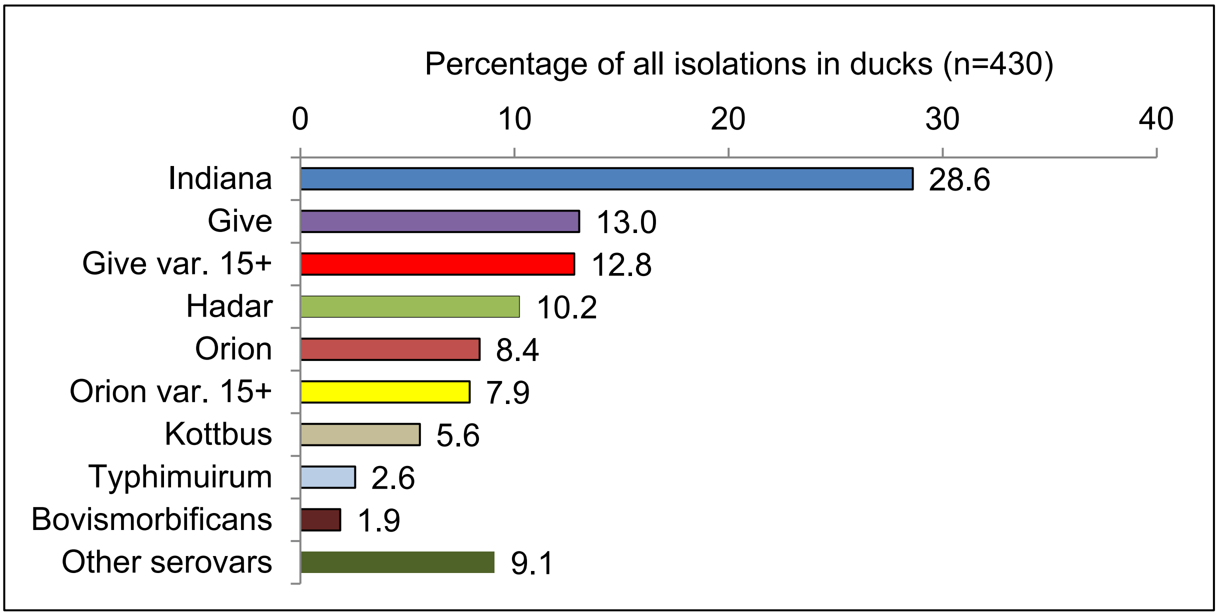
Salmonella serovar	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
untypable strains	15	13	6	5	18	18	13	13	3	3
rough strains	1	1	2	2	2	2	0	0	0	0
Total	**430**	**305**	**293**	**249**	**206**	**174**	**110**	**94**	**121**	**81**

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

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 Isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Beaudesert	0	0	0	0	1	1	0	0	0	0
Indiana	2	2	0	0	0	0	0	0	0	0
Kottbus	1	1	0	0	0	0	0	0	0	0
Typhimurium	0	0	0	0	1	1	0	0	0	0
4,12:i:-	1	0	0	0	0	0	0	0	0	0
Total	**4**	**3**	**0**	**0**	**2**	**2**	**0**	**0**	**0**	**0**

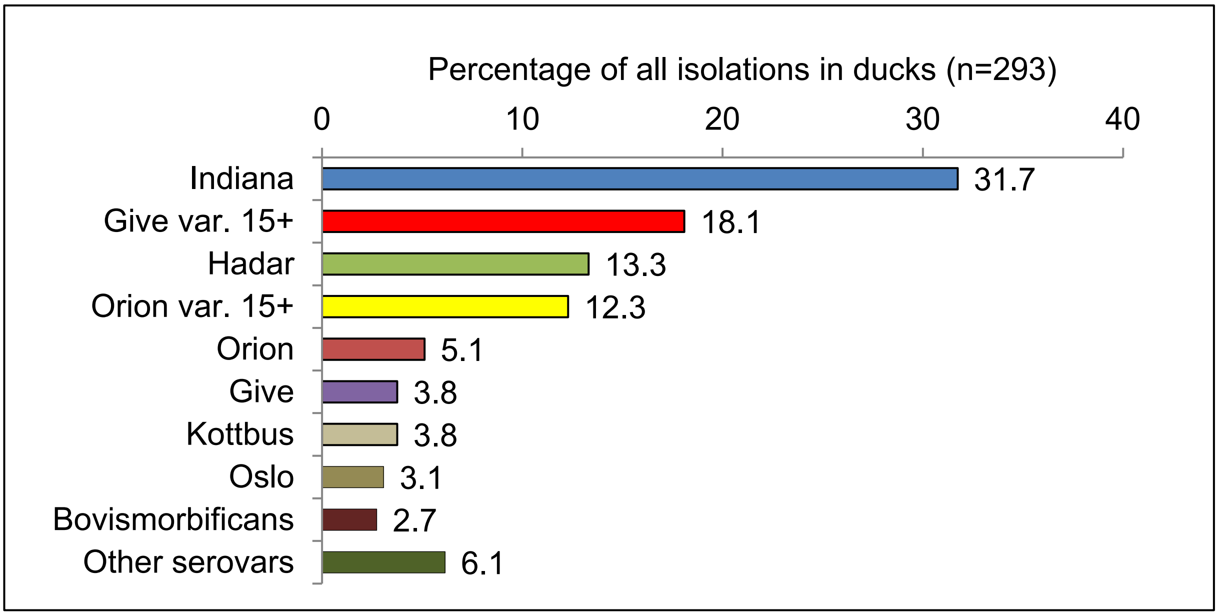
Figure 8.1: Isolations of the most common serovars in ducks in Great Britain 2018 to 2022

Figure 8.1.1: Isolations in 2018



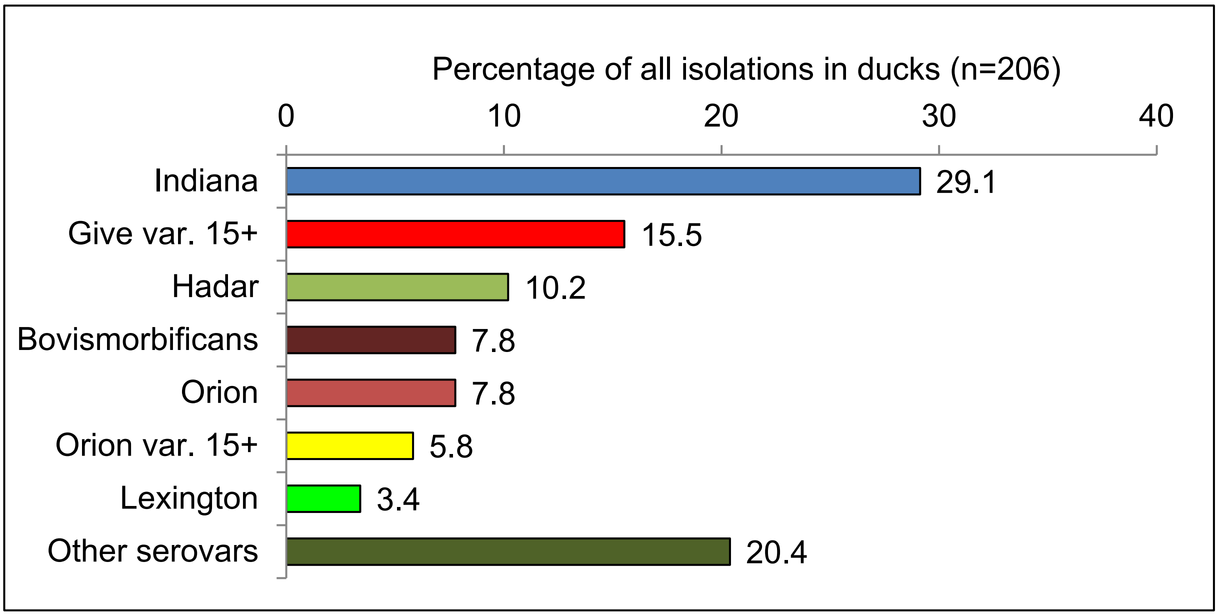
In 2018 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 28.6% of total isolations, followed by *S.* Give (13.0%), *S.* Give var. 15^{+} (12.8%) and *S.* Hadar (10.2%).

Figure 8.1.2: Isolations in 2019



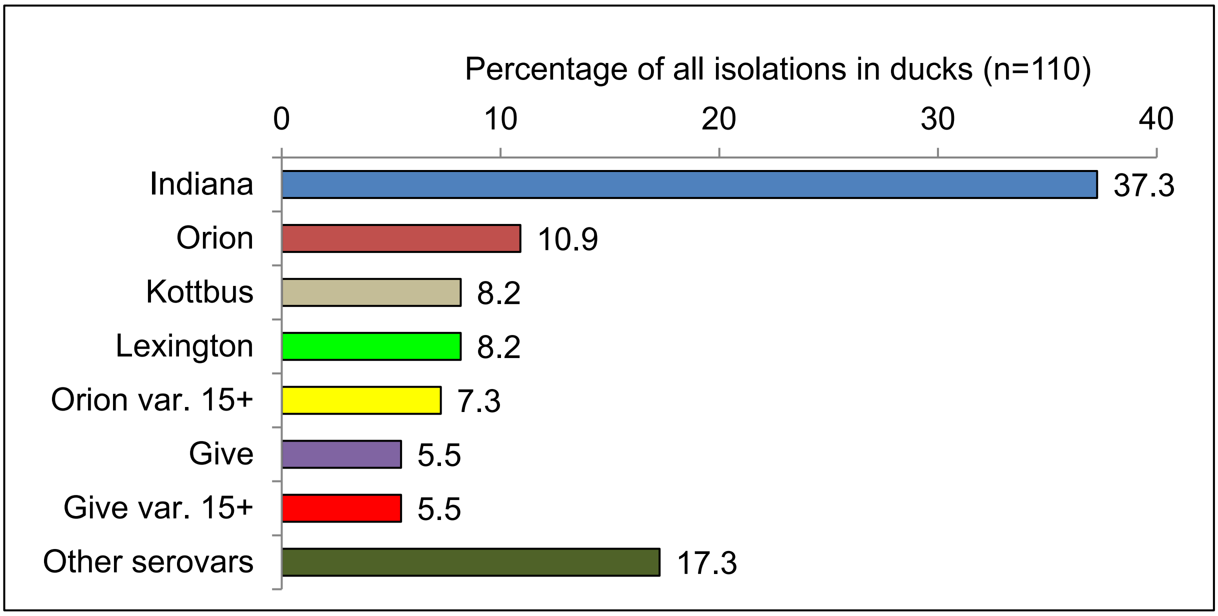
In 2019 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 31.7% of total isolations, followed by *S*. Give var. 15^+ (18.1%), *S.* Hadar (13.3%) and *S.* Orion var. 15^+ (12.3%).

Figure 8.1.3: Isolations in 2020



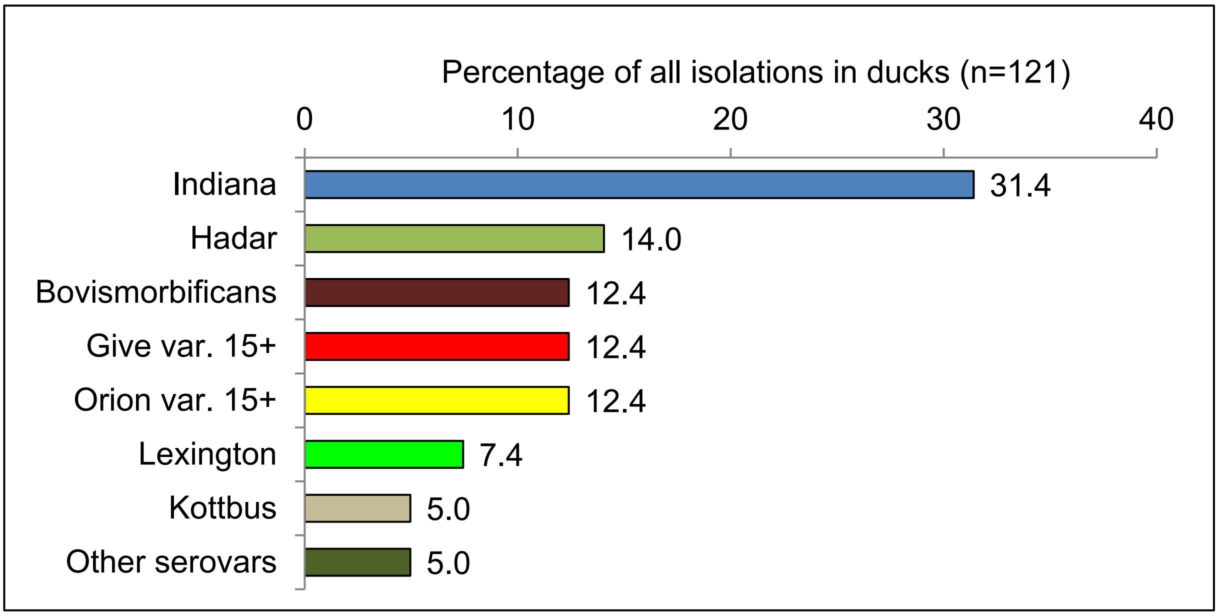
In 2020 the most common *Salmonella* serovar in ducks was *S.* Indiana, accounting for 29.1% of total isolations, followed by *S*. Give var. 15^+ (15.5%), *S.* Hadar (10.2%) and *S.* Bovismorbificans (7.8%).

Figure 8.1.4: 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 8.1.5: 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 8.2: The 5 most common *Salmonella* serovars in ducks in Great Britain in 2022 and their trends over time since 2018

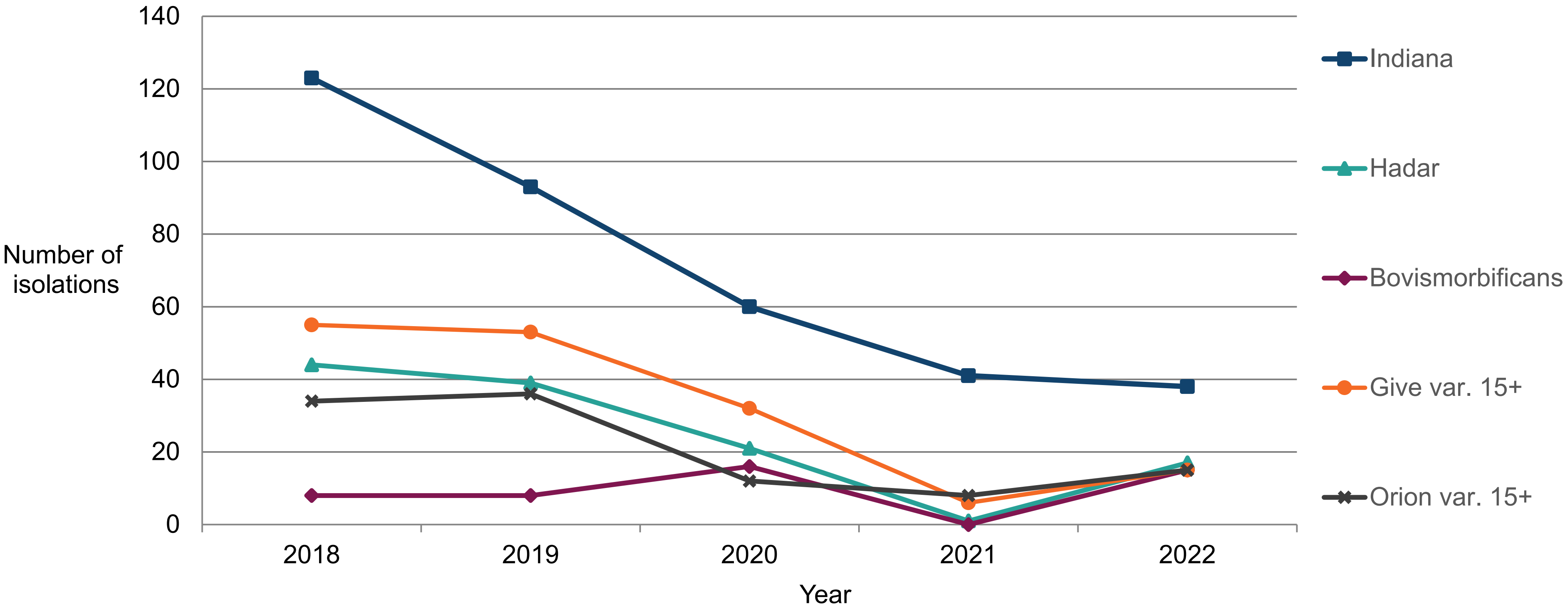


Figure 8.2 shows that *S.* Indiana remains the most common serovar isolated from ducks although numbers have declined from 123 isolations in 2018 to 38 in 2022. *S.* Hadar isolations have also declined since 2018 from 44 isolations to 17 isolations in 2022 making it

the second most common serovar in ducks. *S.* Give var. 15^+ and *S.* Orion var. $15^{+,}$ both had 15 isolations in 2022, lower than in 2019 but higher than 2021. *S.* Bovismorbificans was typically the least common of the 5 but increased from 8 in 2018 to 15 isolations in 2022.

Figure 8.3: *S*. Enteritidis, *S*. Indiana, *S*. Typhimurium, *S*. 4,(5),12:i:- and other serovars as a percentage of all isolations in ducks in Great Britain 2002 to 2022

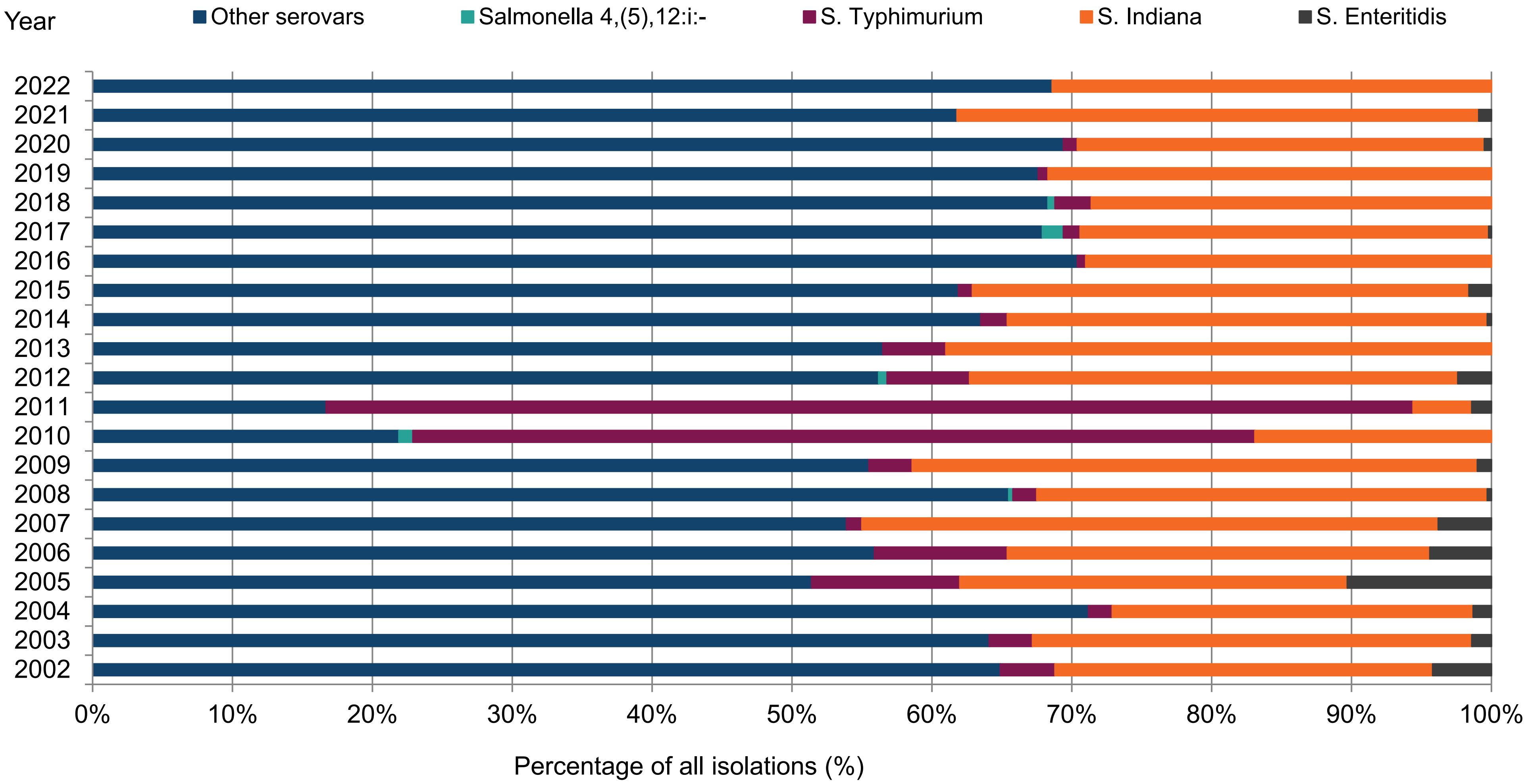


Table 8.3 shows that *S.* 4,(5),12:i:- (including monophasic variants *S.* 4,12:i:- and 4,5,12:i:-) account for a very low proportion of isolations from ducks in all years, the highest being 1.5% in 2017. *S.* Enteritidis is also typically low with the highest proportion being 10.3% in 2005. *S.* Indiana 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.

Figure 8.3: Table of data

Year	Other serovars	*Salmonella* 4,(5),12:i:-	S. Typhimurium	S. Indiana	S. Enteritidis
2002	64.9%	0.0%	3.9%	27.0%	4.2%
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%

Year	Other serovars	*Salmonella* 4,(5),12:i:-	S. Typhimurium	S. Indiana	S. Enteritidis
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%

Table 8.3: *S*. Typhimurium phage types in ducks and geese in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
UNTY	0	0	2	2	0	0	0	0	0	0
RDNC	2	0	0	0	0	0	0	0	0	0
NOPT	1	0	0	0	0	0	0	0	0	0
DT193	0	0	0	0	1	1	0	0	0	0
DT12	8	5	0	0	0	0	0	0	0	0
DT9	0	0	0	0	2	2	0	0	0	0
Total	**11**	**5**	**2**	**2**	**3**	**3**	**0**	**0**	**0**	**0**

Table 8.4: *S*. Enteritidis phage types in ducks and geese in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
PT9b	0	0	0	0	1	1	1	1	0	0
Total	**0**	**0**	**0**	**0**	**1**	**1**	**1**	**1**	**0**	**0**

Table 8.5: *Salmonella* 4,12:i:- phage types in ducks and geese in Great Britain 2018 to 2022

Phage types	2018 flocks	2018 isolations	2019 flocks	2019 isolations	2020 flocks	2020 isolations	2021 flocks	2021 isolations	2022 flocks	2022 isolations
DT193	1	0	0	0	0	0	0	0	0	0
DT120	1	1	0	0	0	0	0	0	0	0
Total	**2**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

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 1 isolation of *Salmonella* was reported from these species during 2022 which is a reduction compared to 2021 (15 isolations) and 2020 (28 isolations).

Game birds

The total number of VIDA submissions from game birds (guinea fowl, partridges, pheasants and quail) to APHA and SRUC increased by 8.2% to 172 submissions in 2022, compared to 159 submissions in 2021. As in previous years, the greatest number of submissions were from pheasants, increasing by 16.8% compared with 2021 (111 versus 95 submissions). During 2022 there were also 35 submissions from grouse, which was an increase of 16.7% compared with during 2021 (30 submissions), and 16 submissions from partridges which was a decrease of 46.7% compared to 2021 (30 submissions).

Six quail submissions and no guinea fowl submissions were received during 2022, which is similar to 2020 (5 quail and no guinea fowl). A further 4 submissions in 2022 were from birds reported as “other game” which is half as many as in 2021 (4 versus 8 submissions).

There is no statutory *Salmonella* monitoring of game birds in Great Britain and the majority of submissions in 2022 were for diagnostic purposes (79.6%), which is similar to 2021 (78.5%). There has been a decreasing trend in the number of *Salmonella* isolations from game birds in recent years, across all species. There was one isolation in 2022, which is 85.7% fewer than during 2021 (7 isolations) and 90.9% fewer than in 2020 (11 isolations). All isolations from game birds in 2022 were from pheasants.

Pheasants

There was one isolation of *Salmonella* (*S.* Dublin) from pheasants in 2022, which is a decrease from 2021 when there were 7 isolations and 2020 when the lowest previous annual number of isolations from pheasants in Great Britain was reported (6 isolations) (Table 9.1). The 2022 isolate arose from a clinical disease investigation with wasting and poor condition the main presenting sign.

S. Dublin was last reported in pheasants in 2016, the most common serovar usually associated with pheasants is *S*. Senftenberg.

Partridges

There were no isolations of *Salmonella* in partridges in 2022, the same as in 2021. Prior to this the number of *Salmonella* isolations from partridges in Great Britain had previously remained stable at 5 isolations per year since 2018 (Table 9.2).

Quail

There were no isolations of *Salmonella* from quail in 2022. 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 2022, the same as during 2021 and 2020. The last time *Salmonella* was isolated from guinea fowl was in 2015 when there was one isolation.

Pigeons

There were 85 VIDA submissions from pigeons to APHA and SRUC in 2022 which is more than double that in 2021 (38 submissions) and over 3 times that in 2020 (25 submissions).

There were 17 *Salmonella* isolations from pigeons in 2022, which is more than double that in 2021 (8 isolations) but the same as in 2020 (17 isolations) (Table 9.4). Six of these isolations were from clinical disease investigations with no available presenting signs and 11 were from voluntary surveillance. All isolations in 2022 were *S*. Typhimurium, which is consistently the most commonly isolated serovar from pigeons. Thirteen isolations were phage type DT2 and 4 were DT99 (Table 9.8).

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

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Dublin	0	0	0	0	0	0	0	0	1	1
Montevideo	0	0	0	0	1	1	0	0	0	0
Orion	0	0	0	0	1	1	1	1	0	0
Orion var. 15^{+}	1	1	2	2	0	0	0	0	0	0
Pullorum	1	1	0	0	0	0	0	0	0	0
Senftenberg	4	4	5	5	3	2	4	3	0	0
Typhimurium	4	2	1	1	1	0	1	1	0	0
4,5,12:i:-	0	0	0	0	0	0	1	1	0	0
Total	**10**	**8**	**8**	**8**	**6**	**4**	**7**	**6**	**1**	**1**

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

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Orion var. 15^{+}	1	1	0	0	0	0	0	0	0	0
Senftenberg	1	1	3	3	2	2	0	0	0	0
Soerenga	1	1	1	1	0	0	0	0	0	0
Typhimurium	2	1	0	0	0	0	0	0	0	0
4,5,12:i:-	0	0	0	0	3	1	0	0	0	0
4,12:i:-	0	0	1	1	0	0	0	0	0	0
Total	**5**	**3**	**5**	**5**	**5**	**3**	**0**	**0**	**0**	**0**

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

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Bredeney	0	0	3	2	0	0	0	0	0	0
Enteritidis	0	0	1	1	0	0	0	0	0	0
Senftenberg	0	0	1	1	0	0	0	0	0	0
Typhimurium	2	2	0	0	0	0	0	0	0	0
Total	2	**2**	**5**	**4**	**0**	**0**	**0**	**0**	**0**	**0**

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

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Enteritidis	0	0	0	0	0	0	1	1	0	0
Kedougou	0	0	0	0	1	1	0	0	0	0
Orion	0	0	0	0	1	1	0	0	0	0
Typhimurium	7	6	11	11	13	13	6	6	17	17
4,12:i:-	2	2	0	0	0	0	0	0	0	0
Untypable strains	0	0	0	0	2	2	1	1	0	0
Total	**9**	**8**	**11**	**11**	**17**	**17**	**8**	**8**	**17**	**17**

Table 9.5: *S.* Typhimurium phage types in pheasants in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
NOPT	0	0	0	0	0	0	1	1	0	0
DT193	0	0	0	0	1	0	0	0	0	0
DT41	1	0	0	0	0	0	0	0	0	0
DT40	2	2	0	0	0	0	0	0	0	0
DT2a	1	0	0	0	0	0	0	0	0	0
DT2	0	0	1	1	0	0	0	0	0	0
Total	**4**	**2**	**1**	**1**	**1**	**0**	**1**	**1**	**0**	**0**

Table 9.6: *S.* Typhimurium phage types in partridges in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
NOPT	1	0	0	0	0	0	0	0	0	0
DT2a	1	1	0	0	0	0	0	0	0	0
Total	**2**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Table 9.7: *S.* Typhimurium phage types in quail in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
DT104	2	2	0	0	0	0	0	0	0	0
Total	**2**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Table 9.8: *S.* Typhimurium phage types in pigeons in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
UNTY	1	1	0	0	1	1	0	0	0	0
RDNC	0	0	0	0	1	1	0	0	0	0
NOPT	1	0	0	0	0	0	0	0	0	0
DT193	0	0	3	3	2	2	0	0	0	0
DT99	0	0	3	3	0	0	0	0	4	4
DT11	1	1	0	0	0	0	0	0	0	0
DT2	4	4	5	5	9	9	6	6	13	13
Total	**7**	**6**	**11**	**11**	**13**	**13**	**6**	**6**	**17**	**17**

Chapter 10: Reports of *Salmonella* in dogs

Salmonella in dogs became reportable through 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 2022 annual summary therefore represents the first 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 2022, the UK dog population was estimated to be around 13 million, with 34% of UK adults owning a dog. 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 857 *Salmonella* isolations from dogs in 2022 (Table 10.1). This is an increase of 17.2% compared to 2021 (731 isolations), and more than a 13-fold increase compared to 2020 (64 isolations). In total, 72 different serovars were reported (excluding untypable and rough strains), which is much higher than previous years (25 serovars in 2020 and 14 serovars in 2019) though similar to 2021 (72 serovars). The majority of isolations (807 isolations, 94.2%) arose from clinical investigations with the remainder from voluntary surveillance (2 isolations, 0.2%), unknown (1 isolation, 0.1%), or other reasons (47 isolations, 5.5%).

The most commonly reported serovar from dogs in 2022 was *S*. Typhimurium (116 isolations, 13.5% of all isolations). *S*. Typhimurium has been the most commonly reported serovar for the past 5 years though for some previous years the number of isolations was much lower (97 isolations in 2021, 11 isolations in 2020, 5 isolations in 2019 and 21 isolations in 2018). The second most commonly reported serovar was *S*. Infantis (109 isolations 12.7% of all isolations). Other commonly reported serovars were *S*. Derby (55 isolations), *S*. Dublin (55 isolations), *S*. Newport (52 isolations), and *Salmonella* 4,5,12:i:- (41 isolations) (Table 10.1, Figure 10.2). The majority of *S*. Newport isolates (48 of 52, 92.3%) were fully sensitive to all antimicrobials tested against. This is a higher percentage sensitive than in 2021 (34 of 43, 79.1%).

Salmonella Typhimurium and monophasic *S.* Typhimurium

There were 116 isolations of *S*. Typhimurium during 2022 comprising 19 different phage types. 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) (Table 10.2). This is compared to 2021 when the most common phage types were RDNC (19 isolations, 19.6% of all *S*. Typhimurium in dogs), DT104 (18 isolations, 18.6% of *S*. Typhimurium in dogs), DT2 (14 isolations, 14.4% of *S*. Typhimurium in dogs) and DT193 (13 isolations, 13.4% of *S*. Typhimurium in dogs) Eight *S*. Typhimurium phage types were reported for the first time in dogs from Great Britain during 2022 (U208, DT194, DT120, DT106, DT75, DT42, DT4, and DT5).

There were 41 isolations of monophasic *S*. Typhimurium 4,5,12:i:- and 23 isolations of monophasic *S.* Typhimurium 4,12:i:- reported from dogs during 2022. The dominant phage type for both of these *S.* Typhimurium variants was DT193 (33 isolations, 80.5% of *S.* 4,5,12:i:- and 17 isolations, 73.9% of *S.* 4,12:i:-) (Table 10.4 and Table 10.5).

Other notable serovars

The number of *Salmonella* Infantis isolations from dogs increased in 2022 to 109 isolations (51 isolations in 2021, 3 isolations in 2020, and 1 isolation in 2019) (Table 10.1 and Figure 10.2). *S.* Enteritidis was isolated 15 times from dogs in 2022, which is a decrease from 2021 (26 isolations). The most common phage types of *S*. Enteritidis was PT8 (6 isolations in 2022) (Table 10.3).

Public health significance

The change to make *Salmonella* in dogs reportable was made to improve the protection of public health. In 2022, *Salmonella* isolations in dogs accounted for approximately one fifth (18.9%) of *Salmonella* isolations from all animals. The most common serovars isolated included those which are important causes of human disease, including *S*. Typhimurium, *S*. Enteritidis and *S*. Infantis, which were the most common serovars isolated from people in Great Britain in 2022 (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 majority of dog isolations this year arose from clinical investigations (94.2%), 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 the highest number so far in 2022 (406 isolations, see Chapter 12). *Salmonella* Typhimurium and *S.* Infantis were amongst the top 4 serovars isolated from RMPF in 2022, 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**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Aarhus	0	0	0	0	0	0	3	3	0	0
Abony	0	0	0	0	0	0	0	0	1	1
Agama	4	4	2	2	2	2	14	14	11	11
Agona	0	0	0	0	1	1	16	16	27	27
Ajiobo	1	1	0	0	0	0	4	4	2	2
Altona	0	0	0	0	0	0	0	0	1	1
Amersfoort	0	0	0	0	0	0	1	1	0	0
Anatum	1	1	0	0	1	1	20	20	22	22
Ball	0	0	0	0	0	0	0	0	1	1
Bardo	0	0	0	0	0	0	0	0	1	1
Bareilly	0	0	0	0	0	0	1	1	1	1
Berta	0	0	0	0	0	0	2	2	1	1
Bonn	0	0	0	0	0	0	1	1	0	0
Bovismorbificans	1	1	0	0	1	1	25	25	9	9
Brandenburg	0	0	0	0	3	3	11	11	10	10
Bredeney	0	0	0	0	0	0	3	3	10	10
Budapest	0	0	0	0	0	0	0	0	1	1
Cannstatt	0	0	0	0	0	0	0	0	1	1
Cerro	0	0	1	1	3	3	2	2	5	5
Coeln	0	0	0	0	0	0	3	3	11	11
Concord	1	1	0	0	0	0	2	2	1	1
Cubana	0	0	0	0	0	0	1	1	0	0
Derby	2	2	0	0	2	2	26	26	55	55
Dublin	6	6	1	1	5	5	61	61	55	54
Durham	0	0	0	0	1	1	1	1	1	1

Salmonella serovar	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
Ealing	0	0	0	0	0	0	3	3	8	8
Eboko	0	0	0	0	0	0	1	1	0	0
Enteritidis	1	1	0	0	2	2	26	26	15	15
Fluntern	0	0	0	0	0	0	0	0	1	1
Fulica	0	0	0	0	0	0	0	0	1	1
Give	0	0	0	0	2	2	4	4	0	0
Give var. 15^{+} (Newbrunswick)	0	0	0	0	0	0	0	0	3	3
Goldcoast	0	0	0	0	0	0	9	9	2	2
Gueuletapee	0	0	0	0	0	0	0	0	1	1
Hadar	1	1	0	0	0	0	8	8	5	5
Haifa	0	0	0	0	0	0	0	0	2	2
Havana	0	0	0	0	0	0	1	1	3	3
Hessarek	0	0	0	0	0	0	2	2	1	1
Indiana	1	1	0	0	2	2	13	13	20	20
Infantis	1	1	1	1	3	3	51	51	109	107
Isangi	0	0	0	0	0	0	1	1	2	2
Javiana	0	0	0	0	0	0	2	2	1	1
Kapemba	0	0	0	0	0	0	0	0	1	1
Kedougou	1	1	0	0	0	0	8	8	1	1
Kentucky	1	1	0	0	0	0	0	0	8	8
Kingston	0	0	0	0	0	0	4	4	1	1
Kisarawe	0	0	0	0	0	0	0	0	20	20
Kottbus	0	0	0	0	2	2	11	11	0	0
Larochelle	0	0	0	0	1	1	0	0	0	0
Lexington	0	0	0	0	0	0	0	0	1	1
Litchfield	0	0	0	0	0	0	0	0	1	1
Liverpool	0	0	0	0	0	0	0	0	1	1

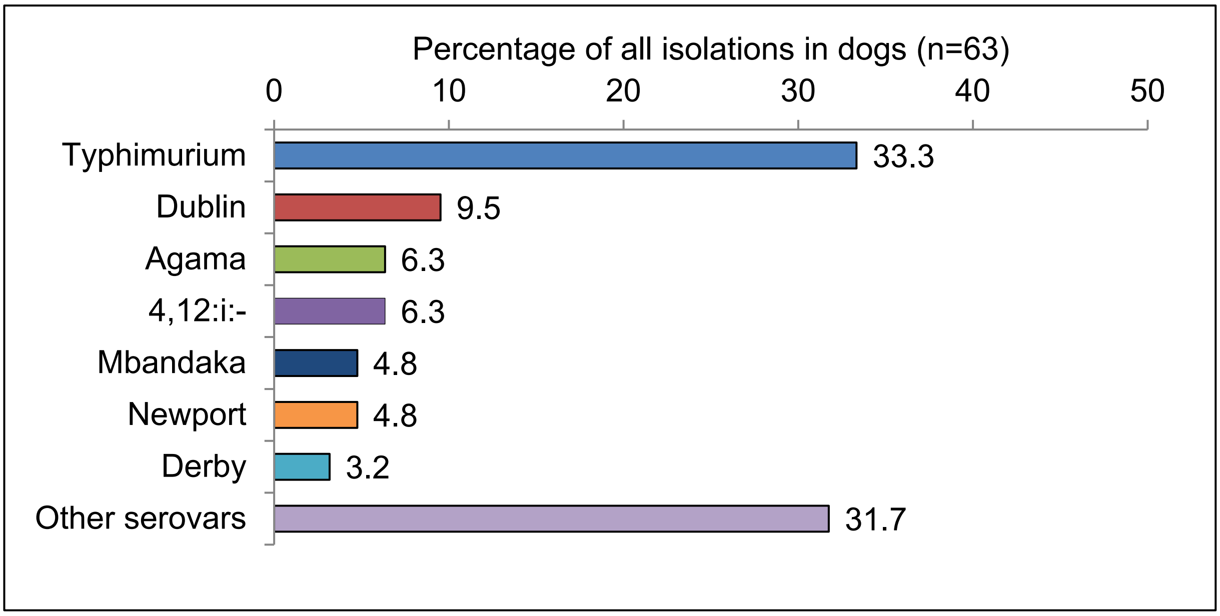
Salmonella serovar	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
Livingstone	0	0	0	0	0	0	12	12	14	14
Lomita	0	0	0	0	0	0	1	1	0	0
London	0	0	0	0	0	0	7	7	13	13
Matopeni	0	0	0	0	0	0	1	1	0	0
Mbandaka	3	3	1	1	1	1	7	7	11	11
Meleagridis	0	0	0	0	0	0	1	1	0	0
Miami	0	0	0	0	0	0	1	1	0	0
Montevideo	1	1	2	2	1	1	17	17	27	26
Munchen	0	0	4	3	0	0	0	0	2	2
Muenster	0	0	0	0	0	0	2	2	2	2
Newport	3	3	0	0	4	4	43	43	52	52
Ohio	0	0	0	0	0	0	3	3	0	0
Oranienburg	0	0	0	0	0	0	1	1	4	4
Orion	1	1	0	0	0	0	3	3	1	1
Oslo	0	0	1	1	2	2	6	6	10	10
Panama	0	0	1	1	0	0	5	5	9	9
Paratyphi B var. Java	0	0	0	0	0	0	11	11	9	9
Pomona	0	0	0	0	0	0	1	1	0	0
Putten	0	0	0	0	0	0	1	1	0	0
Reading	1	1	0	0	0	0	1	1	1	1
Riggil	1	1	0	0	0	0	0	0	0	0
Rissen	0	0	0	0	0	0	10	9	6	6
Saintpaul	0	0	0	0	0	0	0	0	1	1
Saphra	0	0	0	0	0	0	1	1	0	0
Schwarzengrund	0	0	0	0	0	0	2	2	1	1
Senftenberg	0	0	0	0	1	1	3	3	0	0
Soerenga	0	0	0	0	0	0	3	3	1	1

***Salmonella* serovar**	**2018 isolations**	**2018 incidents**	**2019 isolations**	**2019 incidents**	**2020 isolations**	**2020 incidents**	**2021 isolations**	**2021 incidents**	**2022 isolations**	**2022 incidents**
Stanley	1	1	0	0	1	1	1	1	10	10
Stanleyville	0	0	0	0	0	0	4	4	0	0
Stendal	0	0	0	0	0	0	0	0	1	1
Stourbridge	0	0	1	1	0	0	2	2	0	0
Tennessee	0	0	0	0	0	0	1	1	1	1
Thompson	0	0	1	1	0	0	1	1	0	0
Typhimurium	21	16	5	3	11	10	97	87	116	116
Uganda	0	0	0	0	2	2	7	7	3	3
Virchow	0	0	0	0	0	0	7	7	3	3
Wangata	0	0	0	0	0	0	1	1	0	0
4,5,12:b:-	0	0	0	0	0	0	5	5	2	2
4,5,12:i:-	1	1	4	4	8	8	38	38	41	41
4,12:i:-	4	4	2	2	2	2	33	33	23	23
6,7:-:-	0	0	0	0	0	0	17	17	23	23
6,8:-:-	0	0	0	0	0	0	3	3		
61:-:1,5,7	0	0	0	0	0	0	0	0	8	7
untypable strains	4	3	5	5	0	0	22	22	19	19
rough strains	0	0	0	0	0	0	8	8	8	8
Total	**63**	**57**	**32**	**29**	**64**	**63**	**731**	**720**	**857**	**852**

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.

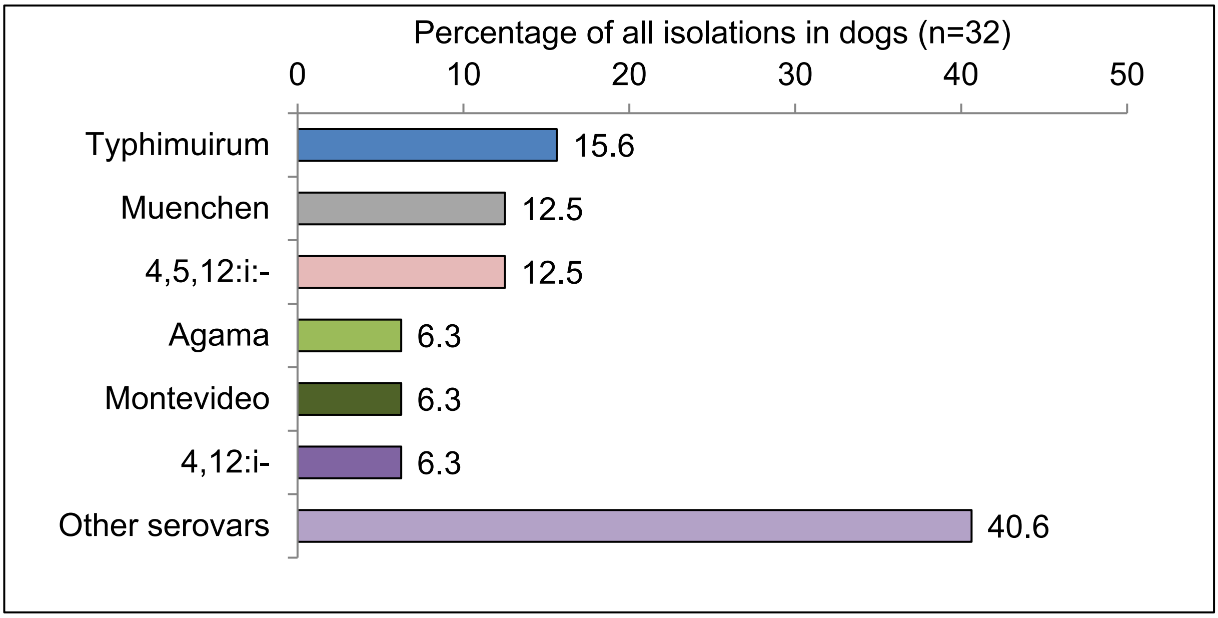
Figure 10.1: Isolations of the most common serovars in dogs in Great Britain 2018 to 2022

Figure 10.1.1: Isolations in 2018



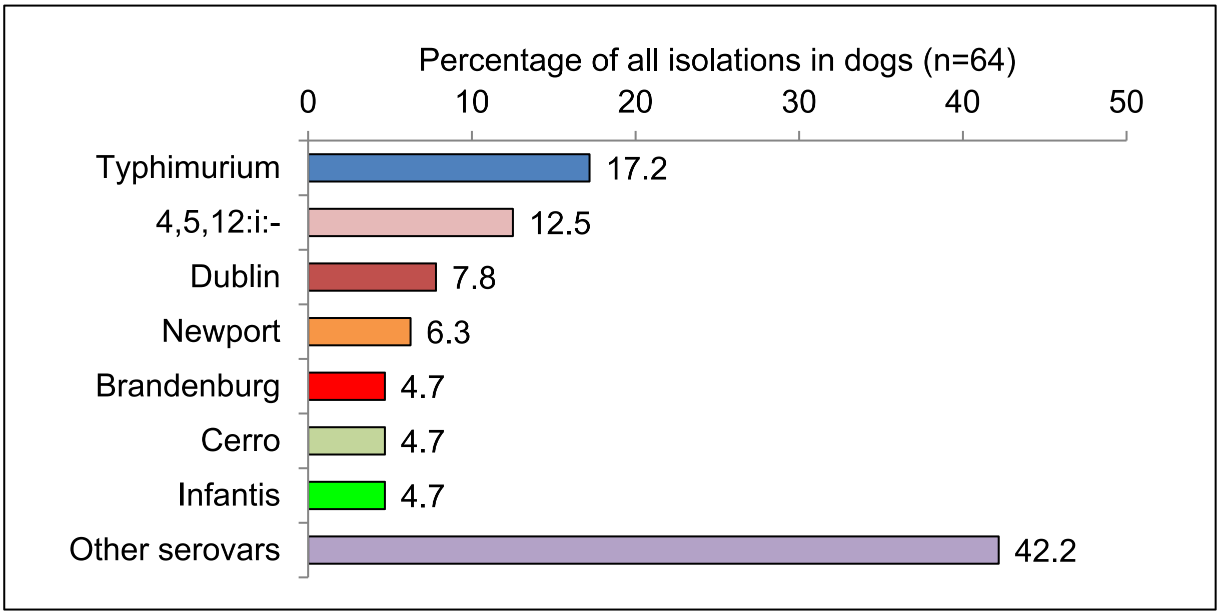
In 2018 the most common *Salmonella* serovar in dogs was *S.* Typhimurium, accounting for 33.3% of total isolations, followed by *S*. Dublin (9.5%), *S.* Agama (6.3%) and *S.* 4,12:i:- (6.3%).

Figure 10.1.2: Isolations in 2019



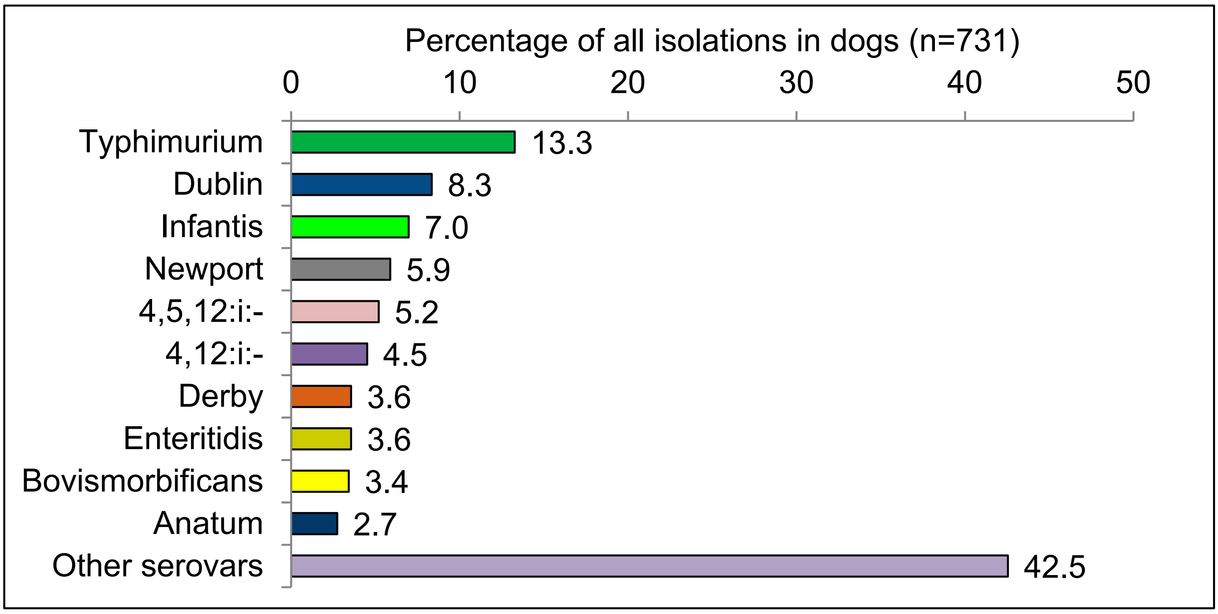
In 2019 the most common *Salmonella* serovar in dogs was *S.* Typhimurium, accounting for 15.6% of total isolations, followed by *S*. Muenchen (12.5%), *S.* 4,5,12:i:- (12.5%) and *S.* Agama (6.3%).

Figure 10.1.3: Isolations in 2020



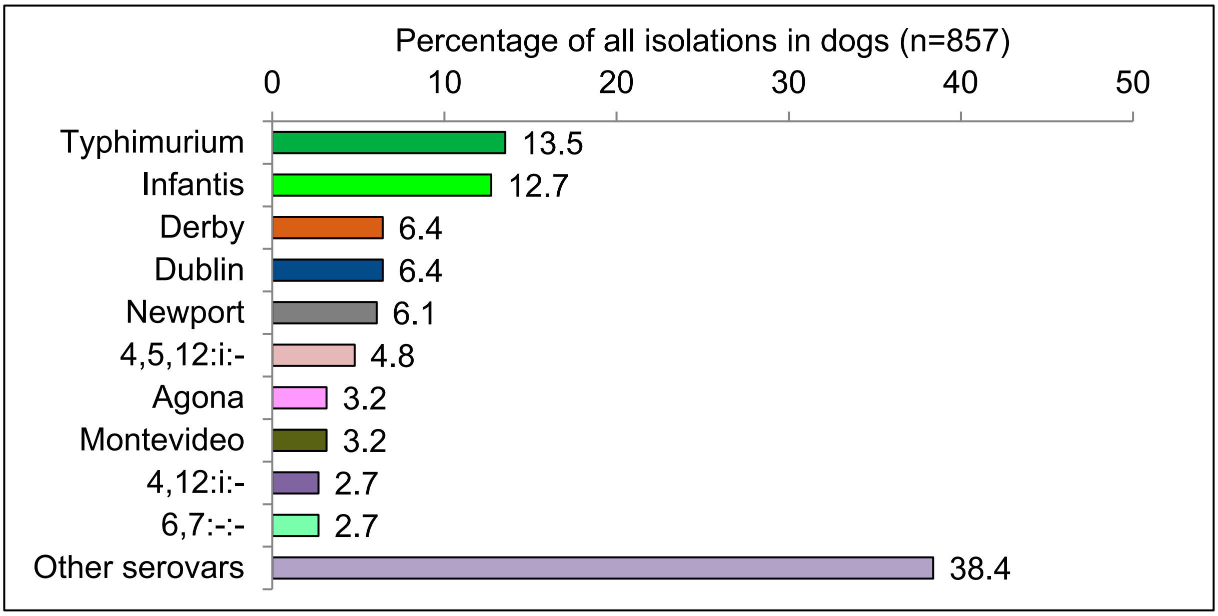
In 2020 the most common *Salmonella* serovar in dogs was *S.* Typhimurium, accounting for 17.2% of total isolations, followed by *S.* 4,5,12:i:- (12.5%), *S.* Dublin (7.8%) and *S.* Newport (6.3%).

Figure 10.1.4 Isolations in 2021



In 2021 the most common *Salmonella* serovar in dogs was *S.* Typhimurium, accounting for 13.3% of total isolations, followed by *S.* Dublin (8.3%), *S.* Infantis (7.0%) and *S.* Newport (5.9%).

Figure 10.1.5: 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%), *S.* Derby (6.4%) and *S.* Dublin (6.4%).

Figure 10.2: The 5 most common *Salmonella* serovars in dogs in Great Britain in 2022 and their trends over time since 2018

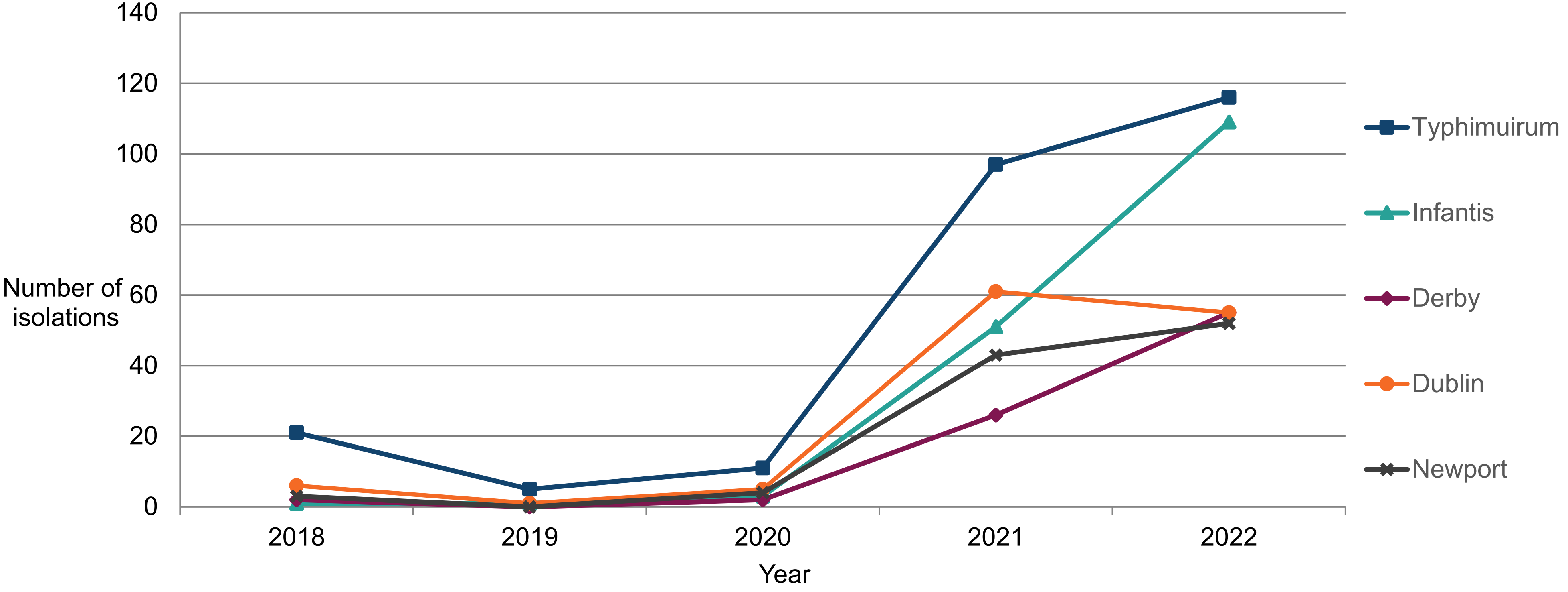


Figure 10.2 shows a very low number of isolations for all serovars until 2021 when reporting of *Salmonella* in dogs became statutory with *S.* Typhimurium being the most common at 21 isolations (2018) or less. All of the 5 most common serovars have increased significantly since then with *S.* Typhimurium still being the most common in 2022 (116 isolations), followed by *S.* Infantis (109 isolations), *S.* Dublin and *S.* Derby (55 isolations each) and *S.* Newport (52 isolations).

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

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
1	1	1	0	0	0	0	2	2	9	9
2	5	3	0	0	3	3	14	10	8	8
2a	0	0	0	0	0	0	1	1	0	0
3	0	0	0	0	0	0	1	1	0	0
4	0	0	0	0	0	0	0	0	1	1
5	0	0	0	0	0	0	0	0	1	1
8	0	0	0	0	0	0	3	3	1	1
9	0	0	0	0	0	0	1	1	0	0
11	0	0	0	0	0	0	1	1	0	0
41	1	1	1	1	0	0	1	1	0	0
42	0	0	0	0	0	0	0	0	1	1
56	0	0	0	0	0	0	1	1	0	0
66	1	1	0	0	0	0	0	0	0	0
75	0	0	0	0	0	0	0	0	6	6
99	0	0	0	0	0	0	1	1	3	3
101	0	0	0	0	0	0	1	1	0	0
104	3	2	1	1	1	1	18	18	26	26
105	0	0	0	0	1	1	5	5	11	11
106	0	0	0	0	0	0	0	0	1	1
115	0	0	0	0	1	1	0	0	0	0
116	0	0	0	0	0	0	2	2	1	1
120	0	0	0	0	0	0	0	0	2	2
189	0	0	0	0	2	1	1	1	1	1
193	3	3	1	1	0	0	13	13	15	15
194	0	0	0	0	0	0	0	0	1	1

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
U208	0	0	0	0	0	0	0	0	1	1
U288	0	0	0	0	0	0	1	1	0	0
U289	0	0	0	0	0	0	1	1	0	0
U302	2	2	0	0	0	0	0	0	0	0
U308	0	0	0	0	1	1	4	4	0	0
U308a	0	0	0	0	0	0	1	1	0	0
U311	0	0	0	0	0	0	2	2	1	1
NOPT	1	0	1	0	0	0	1	0	0	0
RDNC	4	3	1	1	1	1	19	14	26	26
UNTY	0	0	0	0	1	1	2	2	0	0
Total	**21**	**16**	**5**	**4**	**11**	**10**	**97**	**87**	**116**	**116**

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	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
2	0	0	0	0	0	0	1	1	0	0
3	0	0	0	0	0	0	2	2	1	1
4	1	1	0	0	0	0	0	0	1	1
4b	0	0	0	0	0	0	0	0	1	1
8	0	0	0	0	0	0	2	2	6	6
9	0	0	0	0	0	0	0	0	1	1
9a	0	0	0	0	0	0	0	0	2	2
11	0	0	0	0	1	1	6	6	0	0
11b	0	0	0	0	0	0	0	0	1	1
13a	0	0	0	0	0	0	1	1	0	0
21	0	0	0	0	0	0	1	1	0	0
28	0	0	0	0	0	0	1	1	0	0
31	0	0	0	0	1	1	0	0	0	0
33	0	0	0	0	0	0	0	0	1	1
NOPT	0	0	0	0	0	0	2	2	1	1
RDNC	0	0	0	0	0	0	6	6	0	0
UNTY	0	0	0	0	0	0	4	4	0	0
Total	**1**	**1**	**0**	**0**	**2**	**2**	**26**	**26**	**15**	**15**

Table 10.4: *Salmonella* 4,5,12:i:- phage types in dogs in in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
RDNC	0	0	0	0	1	1	2	2	2	2
NOPT	0	0	0	0	0	0	1	1	0	0
U311	1	1	0	0	0	0	4	4	5	5
DT194	0	0	0	0	1	1	0	0	0	0
DT193	0	0	4	4	6	6	31	31	33	33
DT35	0	0	0	0	0	0	0	0	1	1
Total	1	1	4	4	8	8	38	38	41	41

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

Table 10.5: *Salmonella* 4,12:i:- phage types in dogs in Great Britain 2018 to 2022

Phage types	2018 isolations	2018 incidents	2019 isolations	2019 incidents	2020 isolations	2020 incidents	2021 isolations	2021 incidents	2022 isolations	2022 incidents
UNTY	0	0	0	0	0	0	9	9	2	2
RDNC	0	0	0	0	0	0	1	1	2	2
NOPT	0	0	0	0	0	0	1	1	0	0
U311	0	0	0	0	0	0	0	0	1	1
DT193	2	2	2	2	2	2	21	21	17	17
DT120	1	1	0	0	0	0	1	1	1	1
DT32	1	1	0	0	0	0	0	0	0	0
Total	4	4	2	2	2	2	33	33	23	23

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

Chapter 11: Reports of *Salmonella* in wildlife

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

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

Wild mammals

Hedgehogs

One *Salmonella* isolate (*S.* Enteritidis PT11) was reported in a European hedgehog (*Erinaceus europaeus*) in 2022 in Great Britain. *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.

Porpoises

There was one isolation of a monophasic type B *Salmonella* (*S.* 4,12:-:-) from a harbour porpoise (*Phocoena phocoena*) submitted by a private laboratory for serotyping. Unfortunately, additional information regarding clinical findings or pathology are unavailable. Monophasic group B *Salmonella* have previously been reported in porpoises found in British waters (Davison *et al.*, 2010).

Wild birds

There were no isolations of *Salmonella* from wild birds in 2022, 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 was not possible until AI was ruled out in these submissions. Such a delay will have adversely affected the bacterial isolation of *Salmonella*.

Table 11.1: Isolations and incidents of *Salmonella* in wild mammals in Great Britain in 2022

Wildlife species	Enteritidis PT11 isolations	Enteritidis PT11 incidents	4,12:-:- isolations	4,12:-:- incidents
Hedgehog	1	1	0	0
Porpoise	0	0	1	1
Total	**1**	**1**	**1**	**1**

Table 11.2: Isolations of *Salmonella* in wild mammals in Great Britain 2018 to 2022

Isolations from badgers

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium DT12a	0	0	0	0	0
Livingstone	0	0	0	0	0
Kedougou	0	0	0	0	0
Enteritidis RDNC	0	0	0	0	0
Enteritidis PT183	0	0	0	0	0
Enteritidis PT20	0	0	0	0	0
Enteritidis PT11	0	0	0	0	0
Hadar	0	0	0	0	0
Newport	0	0	0	1	0
Agama	0	0	0	1	0
4,12:-:-	0	0	0	0	0
Total	**0**	**0**	**0**	**2**	**0**

Isolations from ferrets (feral)

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium DT12a	0	0	0	0	0
Livingstone	0	0	0	0	0
Kedougou	1	0	0	0	0
Enteritidis RDNC	0	0	0	0	0
Enteritidis PT183	0	0	0	0	0
Enteritidis PT20	0	0	0	0	0
Enteritidis PT11	0	0	0	0	0
Hadar	0	0	0	0	0
Newport	0	0	0	0	0
Agama	0	0	0	0	0
4,12:-:-	0	0	0	0	0
Total	**1**	**0**	**0**	**0**	**0**

Isolations from hedgehogs

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium DT12a	1	0	0	0	0
Livingstone	1	0	0	0	0
Kedougou	0	0	0	0	0
Enteritidis RDNC	1	0	0	0	0
Enteritidis PT183	0	1	0	0	0
Enteritidis PT20	0	0	0	1	0
Enteritidis PT11	1	3	1	10	1
Hadar	0	0	0	0	0
Newport	0	0	0	0	0
Agama	0	0	0	0	0
4,12:-:-	0	0	0	0	0
Total	**4**	**4**	**1**	**11**	**1**

Isolations from porpoises

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium DT12a	0	0	0	0	0
Livingstone	0	0	0	0	0
Kedougou	0	0	0	0	0
Enteritidis RDNC	0	0	0	0	0
Enteritidis PT183	0	0	0	0	0
Enteritidis PT20	0	0	0	0	0
Enteritidis PT11	0	0	0	0	0
Hadar	0	0	0	0	0
Newport	0	0	0	0	0
Agama	0	0	0	0	0
4,12:-:-	0	0	0	0	1
Total	**0**	**0**	**0**	**0**	**1**

Table 11.3: Isolations of *Salmonella* in wild birds in Great Britain 2018 to 2022

Isolations from egrets

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium NOPT	0	0	0	0	0
Typhimurium U308	0	0	0	0	0
Typhimurium DT193	0	0	0	0	0
Typhimurium DT2	0	0	1	0	0
Typhimurium DT1	0	0	0	0	0
Mbandaka	0	0	0	0	0
Total	**0**	**0**	**1**	**0**	**0**

Isolations from finches

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium NOPT	1	0	0	0	0
Typhimurium U308	0	0	0	0	0
Typhimurium DT193	0	0	0	2	0
Typhimurium DT2	0	0	0	0	0
Typhimurium DT1	0	0	0	0	0
Mbandaka	0	0	0	0	0
Total	**1**	**0**	**0**	**2**	**0**

Isolations from gulls

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium NOPT	0	0	0	0	0
Typhimurium U308	0	0	0	0	0
Typhimurium DT193	0	0	0	0	0
Typhimurium DT2	0	0	0	0	0
Typhimurium DT1	0	0	0	0	0
Mbandaka	1	0	0	0	0
Total	**1**	**0**	**0**	**0**	**0**

Isolations from herons

Serovar and Phage type	2018	2019	2020	2021	2022
Typhimurium NOPT	0	0	0	0	0
Typhimurium U308	0	0	0	0	0
Typhimurium DT193	0	0	0	1	0
Typhimurium DT2	0	0	0	0	0
Typhimurium DT1	0	0	0	0	0
Mbandaka	0	0	0	0	0
Total	**0**	**0**	**0**	**1**	**0**

Isolations from mixed species

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium NOPT	0	0	0	1	0
Typhimurium U308	0	0	0	0	0
Typhimurium DT193	0	0	0	0	0
Typhimurium DT2	0	0	0	0	0
Typhimurium DT1	0	0	0	0	0
Mbandaka	0	0	0	0	0
Total	**0**	**0**	**0**	**1**	**0**

Isolations from swans

Serovar and phage type	2018	2019	2020	2021	2022
Typhimurium NOPT	0	0	0	0	0
Typhimurium U308	0	0	0	1	0
Typhimurium DT193	0	0	0	0	0
Typhimurium DT2	0	0	0	0	0
Typhimurium DT1	0	0	0	1	0
Mbandaka	0	0	0	0	0
Total	**0**	**0**	**0**	**2**	**0**

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 so it is 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 801 isolations of *Salmonella* from feedingstuffs during 2022, including 110 isolations from compound feeds (Tables 12.3 to 12.6) and 702 from feed ingredients or products associated with testing under Animal By-Products Regulations (ABPR) (Table 12.7). This is a decrease of 4.1% compared with 2021 (835 isolations) and an increase of 6.0% compared with 2020 (756 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 50.8% in 2022 compared with 2021 (187 isolations versus 124 isolations) and by 74.8% compared with 2020 (107 isolations) (Table 12.1). In 2022, these comprised 61 isolations of *S*. Infantis, 53 isolations of *S.* Typhimurium, 32 isolations of *Salmonella* 4,5,12:i:-, 31 isolations of *Salmonella* 4,12:i:-, 6 isolations of *S.* Enteritidis, 3 isolations of *S*. Virchow and one isolation of *S.* Hadar. The 3 *S*. Virchow isolations were reported from raw meat pet food, this serovar was last isolated in 2011 from brewers yeast. 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 7 *Salmonella* isolations from compound ruminant feed during 2022, which is less than half of the number of isolations seen in 2021 (20 isolations) and in 2020 (19 isolations). The reported serovars were *S*. Agona (2 isolations, 28.6% of isolations), *S*. Kentucky (2 isolations, 28.6% of isolations), and single isolations of *S*. Derby, *S*. Kedougou and *S*. Tennessee (14.3% of isolations each) (Table 12.3). *Salmonella* Derby was isolated once from sheep during 2022 but not from cattle. Neither *S*. Agona, *S*. Kentucky, *S*. Kedougou nor *S*. Tennessee were isolated from cattle or sheep during 2022 (Figure 12.4, also see Chapters 2 and 3).

There were 14 isolations of *Salmonella* from compound pig feed during 2022, which is one third less than the number of isolations in 2021 (21 isolations) and a 55.6% increase compared to the number of isolations during 2020 (9 isolations). The most common serovars reported were *S*. Rissen (5 isolations, 35.7% of isolations), *S*. Kedougou (3 isolations, 21.4% of isolations) and *S*. Derby (2 isolations, 14.3% of isolations) (Table 12.4). There was also one isolation each of *S*. Enteritidis (PT8), *S*. Hindmarsh, *S*. Ohio and *Salmonella* 4,5,12:i:-, each representing 7.1% of total isolations. Of these serovars, *S*. Derby, *S*. Kedougou and *Salmonella* 4,5,12:i:- were isolated from pigs during 2022 (Figure 12.5, also see Chapter 4).

There were 15 isolations of *Salmonella* from compound poultry feed during 2022, which is 37.5% fewer than during 2021 (24 isolations) and 59.5% less than during 2020 (37 isolations) (Table 12.5). Twelve different serovars were reported, the most common being *S*. Agama, *S*. Kedougou and *S*. Soerenga (2 isolations of each, each accounting for 13.3% of total isolations) followed by *S*. Agona, *S*. Derby, *S*. Enteritidis, *S*. Idikan, *S*. Infantis, *S*. Newport, *S*. Typhimurium, *S*. Utah and *Salmonella* 6,7:-:enz$_{15}$ (1 report of each, 6.7% of isolations from compound poultry feed each). 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 2022 is shown in Figure 12.6. No chicken or turkey flocks tested under the NCP in 2022 tested positive for *S*. Soerenga, *S*. Utah or *Salmonella*. 6,7:-:enz$_{15}$. However, all of the other serovars reported from compound poultry feeds were also isolated from poultry in 2022, across all sectors. These include *S*. Typhimurium in chicken breeding, laying and broiler flocks, *S.* Enteritidis in chicken breeding and laying flocks, *S*. Derby, *S*. Kedougou and *S.* Newport in chicken broiler, layer flocks and turkey fattening flocks and *S.* Agona in chicken breeder, layer, broiler and turkey fattening flocks (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 2022, there were a total of 114 *Salmonella* isolations arising from 24 different feedingstuff ingredients (see Table 12.8a for details). This is a decrease of 52.3% compared to 2021, when there were 239 isolations. The highest number of isolations was from rapeseed (35 isolations), followed by soya bean meal (30 isolations), and mixed oil seed (11 isolations).

Isolations from rapeseed fell by just over half in 2022 compared to 2021 (35 versus 73 isolations) and fell by around two thirds compared to 2020 (108 isolations). The number of isolations from soya bean meal in 2022 decreased by 21.1% compared to 2021 (30 versus

38 isolations) and decreased by 23.1% compared to 2020 (39 isolations). Isolations from mixed oil seeds fell significantly in 2022 (11 isolations) compared to 2021 (69 isolations) and fell by over a third compared to 2020 (18 isolations).

The most commonly isolated serovars from feedingstuff ingredients during 2022 were *S*. Rissen (26 isolations) and *S*. Tennessee (9 isolations), which is the same as 2021. Isolations of *S*. Rissen decreased by 65.3% in 2022 compared to 2021 (26 versus 75 isolations). During 2022 most isolations of this serovar were from rapeseed (23 isolations), but there were also 2 isolations from mixed oilseed and a single isolation from barley. Isolations of *S.* Tennessee fell by 84.2% compared to 2021 (9 versus 57 isolations). Most isolations during 2022 came from rapeseed (5 isolations), but there were also single isolations from liquorice root, minerals, soya bean meal and sunflower (Table 12.8a). Such contamination usually originates from persistent *Salmonella* within oil extraction plant cooling systems.

Isolations from products associated with ABPR

During 2022, there were a total of 577 *Salmonella* isolations arising from 5 different product types plus feedmill environments tested under ABPR in Great Britain (see Table 12.8b for details). This is 14.5% higher than the number of isolations in 2021 (504 isolations) and an increase of 24.9% compared with 2020 (462 isolations). The highest number of isolations was from raw meat pet food (406 isolations), followed by samples from feed mill environments (133 isolations) and blood products (26 isolations).

Compared with 2021, there was an increase in the number of *Salmonella* isolations in 2022 from several different products controlled under the ABPR including raw meat pet food (406 versus 295 isolations), feedmill environments (133 versus 115 isolations), blood products (26 versus 5 isolations) and meat and tallow (2 versus 0 isolations). In contrast, there were fewer isolations from samples collected from digestate (4 versus 56 isolations), rendering plant material (0 versus 11 isolations), bone meal (0 versus 11 isolations) and meat meal (0 versus 11 isolations) (see Table 12.8b).

The most commonly isolated serovars from products tested under the ABPR were *S*. Kedougou (55 isolations), *S*. Indiana (49 isolations), *S*. Infantis (48 isolations), *S.* Typhimurium (41 isolations) and *S*. Derby (34 isolations). The majority of *S*. Kedougou isolations were from samples collected from feed mill environments (50 isolations) and are likely to indicate resident contamination within some mills. All *S.* Indiana isolations came from raw meat pet food. Overall, 79.2% of *S*. Infantis isolations (38 isolations) came from raw meat pet food with the rest from feedmill environments (8 isolations) and meat and tallow (2 isolations). The majority of *S*. Typhimurium and *S*. Derby isolations were from raw meat pet food (38 and 26 isolations, respectively) (Table 12.8b).

Isolations from raw meat pet food

During 2022 there were 406 reports of *Salmonella* from raw meat pet food (Table 12.8b). This is higher than during 2021 (295 reports) and 2020 (273 reports). The most common serovars reported during 2022 were *S*. Indiana (49 isolations), *S*. Infantis (38 isolations) *S*. Typhimurium (38 isolations), *S*. Derby (26 isolations), and *Salmonella* 4,12:i:- (21 isolations). *Salmonella* Indiana was also the most common serovar reported during 2021 and 2020 (34 and 29 isolations, respectively). In comparison, *Salmonella* Typhimurium, *S.* Infantis and *S.* Derby were the 3 most commonly isolated serovars in dogs in 2022.

There were 123 isolations of regulated serovars from raw meat pet food in 2022 (Tables 12.2 and 12.8b). This is an increase of 73.2% compared with 2021 (71 isolations) and almost double the number of isolations in 2020 (62 isolations). There were 38 isolations of *S*. Typhimurium (DT2 (x5), DT105 (x5), DT9 (x3), DT75 (x3), DT104 (x3), U311 (x3), DT8 (x2), DT120 (x2), DT193 (x2), DT99 (x1), NOPT (x2) and RDNC (x7)), 38 isolations of *S*. Infantis, 21 isolations of *Salmonella* 4,12:i:- (DT193 (x17), DT104 (x1) and UNTY (x3)), 19 isolations of *Salmonella* 4,5,12:i:- (DT193 (x12), DT104 (x1), DT120 (x1), U208 (x1), U311 (x1) and UNTY (x3)), 3 isolations of *S*. Enteritidis (PT8 (x1), PT21 (x1) and RDNC (x1)), 3 isolations of *S*. Virchow and one isolation of *S*. Hadar.

Regulated serovars originating from raw meat pet food during 2022 accounted for 65.8% of total regulated serovars isolated from all feedingstuffs and products associated with the ABPR (Table 12.2). This is a higher proportion than during 2021 (57.3% of total regulated serovars) and a higher proportion than in 2020 (57.9% 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 301 batches of domestically produced processed animal protein were tested during 2022. This is a 21.6% decrease compared with 2021 (384 batches) and a 25.1% decrease compared with 2020 (402 batches) (Table 12.9 and Figure 12.7). Two batches tested positive for *Salmonella* in 2022 (0.66%), which is lower than during 2021 (9 positive batches, 2.34% positive), and similar to 2020 (3 positive batches, 0.8% positive). Two different serovars were isolated in 2022. These, and the serovars isolated in previous years, are shown in Table 12.10. There was one isolation of *S*. Derby and one isolation of *S*. Tennessee in 2022 but no reports of regulated serovars. This is different to 2021 when there were 2 isolations of the regulated serovar *S*. Typhimurium but similar to 2020 when there were no isolations of regulated serovars from processed animal protein.

No batches of imported animal protein were tested during 2022, which is the same as during both 2021 and 2020.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 2020 to 2022

***Salmonella* serovar**	**2020 Finished feed**	**2020 Vegetable material**	**2020 Misc.**	**2021 Finished feed**	**2021 Vegetable material**	**2021 Misc.**	**2022 Finished feed**	**2022 Vegetable material**	**2022 Misc.**
Enteritidis PT2	0	0	0	0	0	1	0	0	0
Enteritidis PT3a	0	0	0	0	0	1	0	0	0
Enteritidis PT4	0	0	2	0	1	0	0	1	0
Enteritidis PT8	0	0	0	0	0	0	1	0	1
Enteritidis PT9b	0	0	1	0	1	0	0	0	0
Enteritidis PT21	0	0	0	0	0	0	0	0	1
Enteritidis NOPT	0	0	0	0	0	1	0	0	0
Enteritidis RDNC	0	0	0	0	0	0	1	0	1
Enteritidis UNTY	0	0	0	0	0	1	0	0	0
Hadar	0	0	9	0	0	3	0	0	1
Infantis	0	6	23	0	0	40	11	0	50
Typhimurium DT1	0	1	0	1	0	1	0	0	0
Typhimurium DT2	0	3	2	0	2	5	1	3	5
Typhimurium DT3	0	0	0	0	0	1	0	0	0
Typhimurium DT8	0	0	0	0	0	0	0	0	2
Typhimurium DT9	0	0	0	0	0	0	0	0	3
Typhimurium DT41b	0	0	1	0	0	0	0	0	0
Typhimurium DT75	0	0	0	0	0	0	0	0	3
Typhimurium DT99	0	0	0	0	0	0	0	4	3
Typhimurium DT104	0	0	7	0	0	4	0	1	3
Typhimurium DT105	0	0	0	0	0	0	1	0	5
Typhimurium DT116	0	0	0	0	0	3	0	0	0
Typhimurium DT120	0	0	0	0	0	0	0	0	2
Typhimurium DT193	1	4	4	0	2	3	0	0	3

***Salmonella* serovar**	**2020 Finished feed**	**2020 Vegetable material**	**2020 Misc.**	**2021 Finished feed**	**2021 Vegetable material**	**2021 Misc.**	**2022 Finished feed**	**2022 Vegetable material**	**2022 Misc.**
Typhimurium DT208	0	0	1	0	0	0	0	0	0
Typhimurium U208	0	0	0	0	0	1	0	0	0
Typhimurium U281	0	0	0	0	0	1	0	0	0
Typhimurium U288	0	0	1	0	0	1	0	0	0
Typhimurium U302	0	0	0	0	0	1	0	0	0
Typhimurium U308	0	0	0	0	2	3	0	0	0
Typhimurium U311	0	0	0	0	0	0	0	0	3
Typhimurium NOPT	0	1	1	0	0	6	0	0	2
Typhimurium RDNC	1	0	8	1	2	10	1	0	8
Typhimurium UNTY	0	0	1	0	0	1	0	0	0
Virchow	0	0	0	0	0	0	0	0	3
4,5,12:i:- DT104	0	0	0	0	0	0	0	0	1
4,5,12:i:- DT120	0	0	0	0	0	0	0	0	1
4,5,12:i:- DT193	1	1	14	0	0	10	4	0	20
4,5,12:i:- DT208	0	0	0	0	0	0	0	0	1
4,5,12:i:- U311	0	0	0	0	0	1	0	0	1
4,5,12:i:- NOPT	0	0	1	0	0	0	0	0	0
4,5,12:i:- UNTY	0	0	0	0	0	0	0	0	4
4,12:i:- DT104	0	0	0	0	0	0	0	0	2
4,12:i:- DT120	0	0	0	0	0	1	0	0	0
4,12:i:- DT193	0	0	11	0	0	6	4	0	22
4,12:i:- RDNC	0	0	0	0	0	1	0	0	0
4,12:i:- UNTY	0	0	0	0	0	5	0	0	3
Total	**3**	**16**	**87**	**2**	**10**	**112**	**24**	**9**	**154**

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, 2022

***Salmonella* serovar**	**Feedingstuff**	**N**
Enteritidis PT4	Buckwheat	1
Enteritidis PT8	Compound pig feed	1
Enteritidis PT8	Pet food (raw)	1
Enteritidis PT21	Pet food (raw)	1
Enteritidis RDNC	Compound chicken feed	1
Enteritidis RDNC	Pet food (raw)	1
Hadar	Pet food (raw)	1
Infantis	Compound cat feed	1
Infantis	Compound dog feed	8
Infantis	Compound poultry feed	1
Infantis	Compound unknow species feed	1
Infantis	Environmental	8
Infantis	Malt	2
Infantis	Meat and tallow	2
Infantis	Pet food (raw)	38
Typhimurium DT2	Broken brown rice	1
Typhimurium DT2	Compound chicken feed	1
Typhimurium DT2	Rapeseed	1
Typhimurium DT2	Pet food (raw)	5
Typhimurium DT2	Soya	1
Typhimurium DT8	Pet food (raw)	2
Typhimurium DT9	Pet food (raw)	3
Typhimurium DT75	Pet food (raw)	3
Typhimurium DT99	Environmental	2
Typhimurium DT99	Maize	1
Typhimurium DT99	Mixed oil seed	1
Typhimurium DT99	Rapeseed	1
Typhimurium DT99	Pet food (raw)	1
Typhimurium DT99	Soya	1
Typhimurium DT104	Oats	1
Typhimurium DT104	Pet food (raw)	3
Typhimurium DT105	Compound dog feed	1
Typhimurium DT105	Pet food (raw)	5
Typhimurium DT120	Pet food (raw)	2
Typhimurium DT193	Biscuit	1
Typhimurium DT193	Pet food (raw)	2
Typhimurium U311	Pet food (raw)	3
Typhimurium NOPT	Pet food (raw)	2
Typhimurium RDNC	Compound dog feed	1

Salmonella serovar	Feedingstuff	N
Typhimurium RDNC	Environmental	1
Typhimurium RDNC	Pet food (raw)	7
Virchow	Pet food (raw)	3
4,5,12:i:- DT104	Pet food (raw)	1
4,5,12:i:- DT120	Pet food (raw)	1
4,5,12:i:- DT193	Blood products	6
4,5,12:i:- DT193	Meat and tallow	2
4,5,12:i:- DT193	Compound mixed species feed	3
4,5,12:i:- DT193	Compound pig feed	1
4,5,12:i:- DT193	Pet food (raw)	12
4,5,12:i:- U208	Pet food (raw)	1
4,5,12:i:- U311	Pet food (raw)	1
4,5,12:i:- UNTY	Blood products	1
4,5,12:i:- UNTY	Pet food (raw)	3
4,12:i:- DT104	Pet food (raw)	1
4,12:i:- DT104	Protein blend	1
4,12:i:- DT193	Blood Products	2
4,12:i:- DT193	Compound mixed species feed	4
4,12:i:- DT193	Digestate	2
4,12:i:- DT193	Environmental	1
4,12:i:- DT193	Pet food (raw)	17
4,12:i:- UNTY	Pet food (raw)	3
Total	Not applicable	**187**

Figure 12.1: Number of isolations of regulated *Salmonella* serovars in animal feedingstuffs and products associated with the ABPR 2018 to 2022

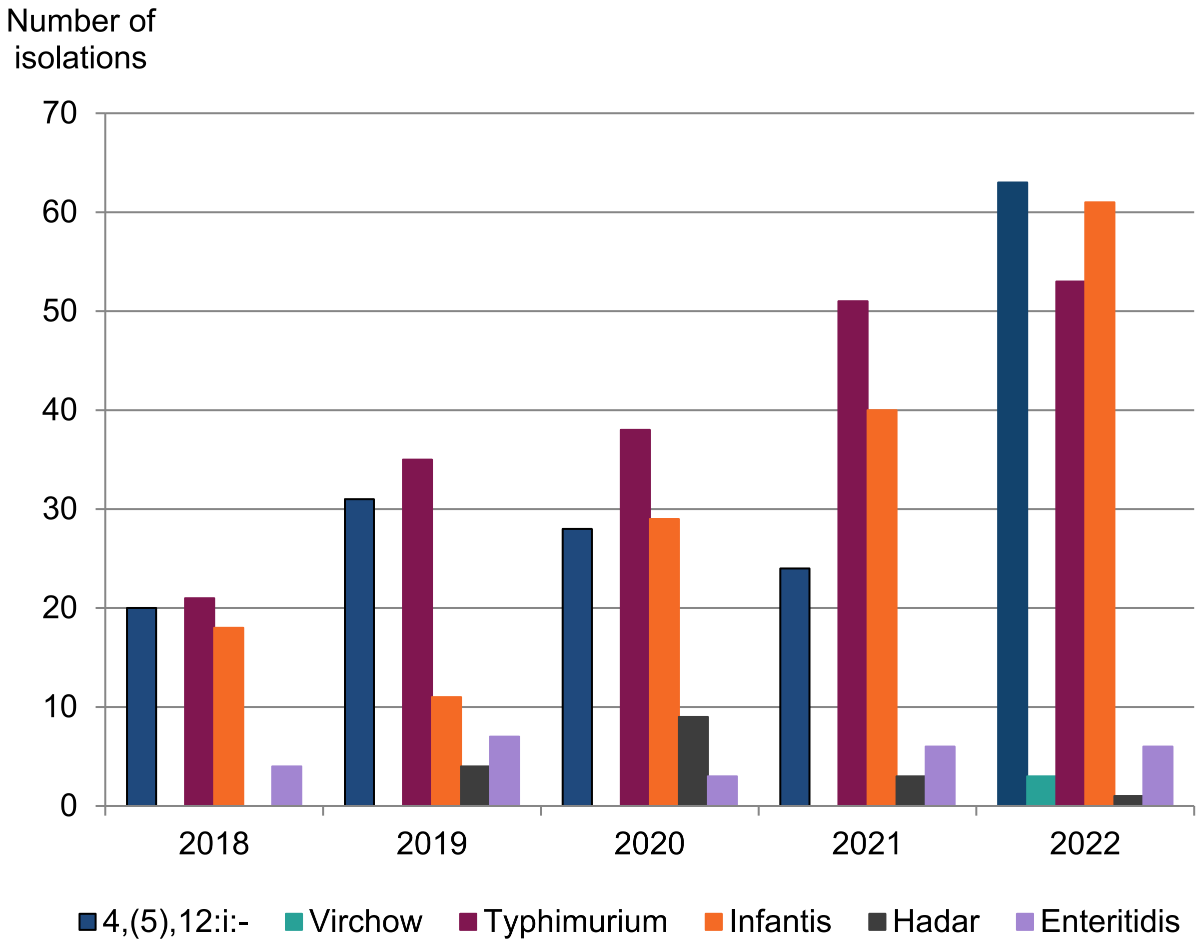
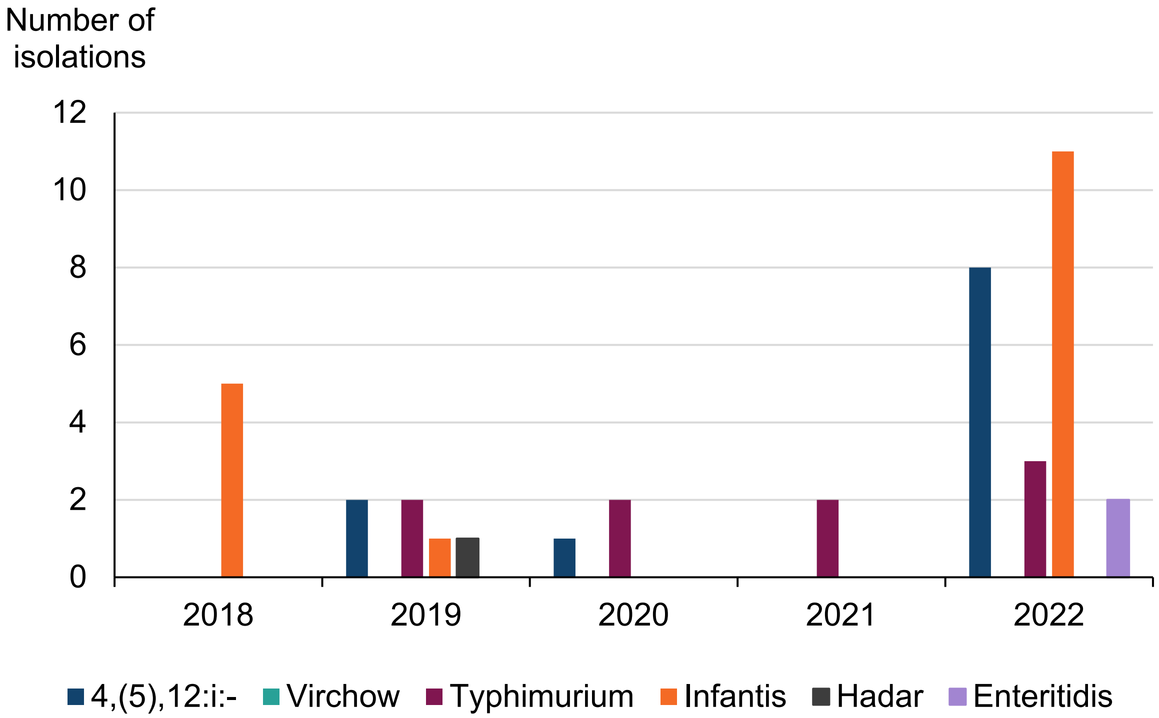


Figure 12.1 shows the number of isolations of *S*. 4,(5),12:i:- (including 4,12:i:- and 4,5,12:i:-), *S*. Typhimurium and *S*. Infantis have all increased since 2018 from around 20 isolations to over 50 in 2022. *S*. Enteritidis has remained low at 7 isolations or lower. *S*. Hadar peaked in 2020 with 9 isolations but fell to just 1 in 2022.

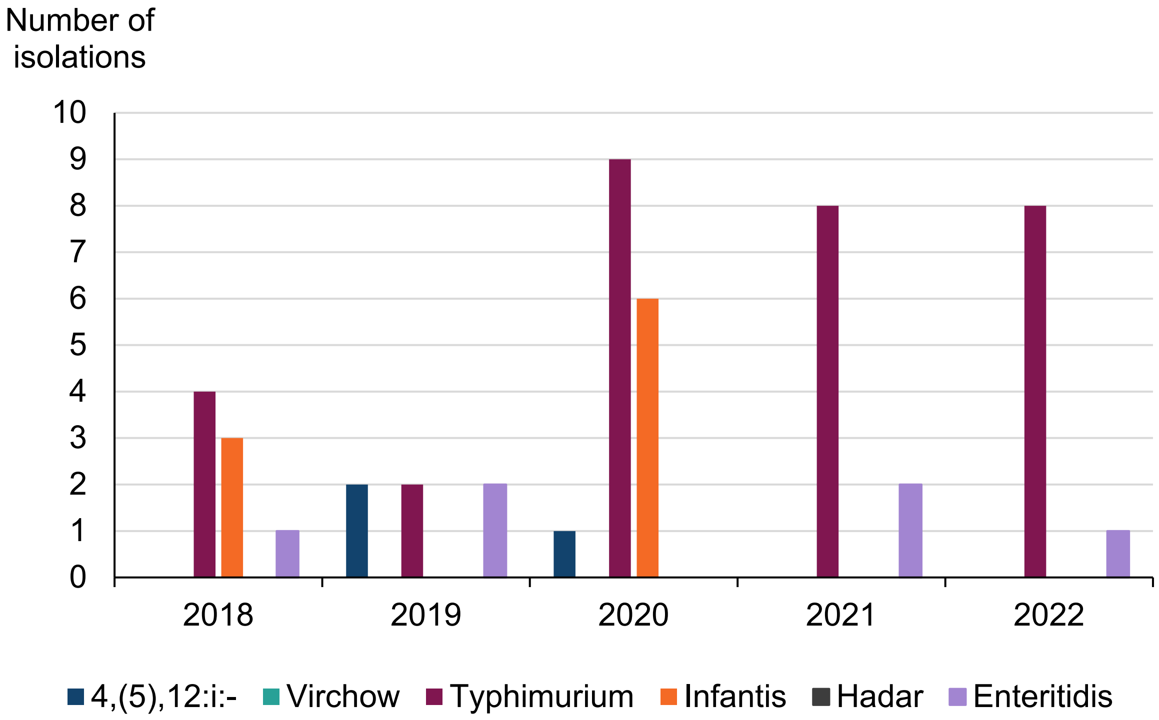
Figure 12.2: Number of isolations of regulated *Salmonella* serovars in animal feedingstuffs and products associated with the ABPR 2018 to 2022 by type of feedingstuff

Finished feed



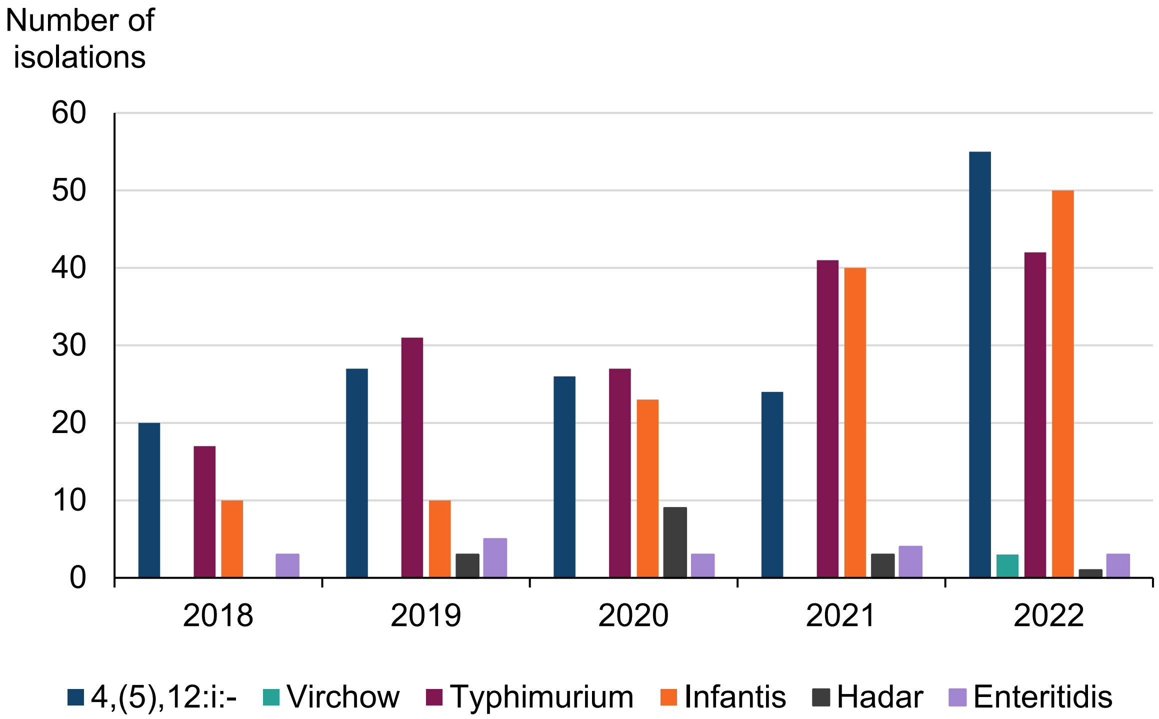
The number of isolations of regulated serovars from finished feed has increased since 2018 for *S*. 4,(5),12:i: (including *S*. 4,12:i:- and *S*. 4,5,12:i:-), *S*. Typhimurium and *S*. Infantis. *S*. Enteritidis was isolated twice for the first time in 2022 and there have been no isolations of *S.* Virchow in finished feed.

Vegetable material



S. Infantis was isolated from vegetable material in 2018 (3 isolations) and 2020 (6 isolations) and *S*. 4,(5),12:i:- in 2019 (2 isolations) and 2020 (1 isolation). *S*. Enteritidis has been isolated every year except 2020 and was isolated once in 2022. *S.* Typhimurium was isolated 8 times in 2022, the same as 2021. *S*. Hadar was isolated twice in 2019 and once in 2020 and *S.* Virchow has not been isolated in vegetable material from 2018 to 2022.

Miscellaneous



The number of isolations of *S*. Enteritidis has remained relatively stable across the years with 3 isolations in 2022. *S.* 4,(5),21:i:-, *S*. Typhimurium and *S.* Infantis has increased in miscellaneous feedstuffs from 20 isolations or less in 2018 to over 40 in 2022. There were 3 isolations of *S.* Virchow in 2022, the first isolation of this serovar in the last 5 years.

Figure 12.3: Number of isolations of *Salmonella* in compound animal feedingstuffs 2018 to 2022

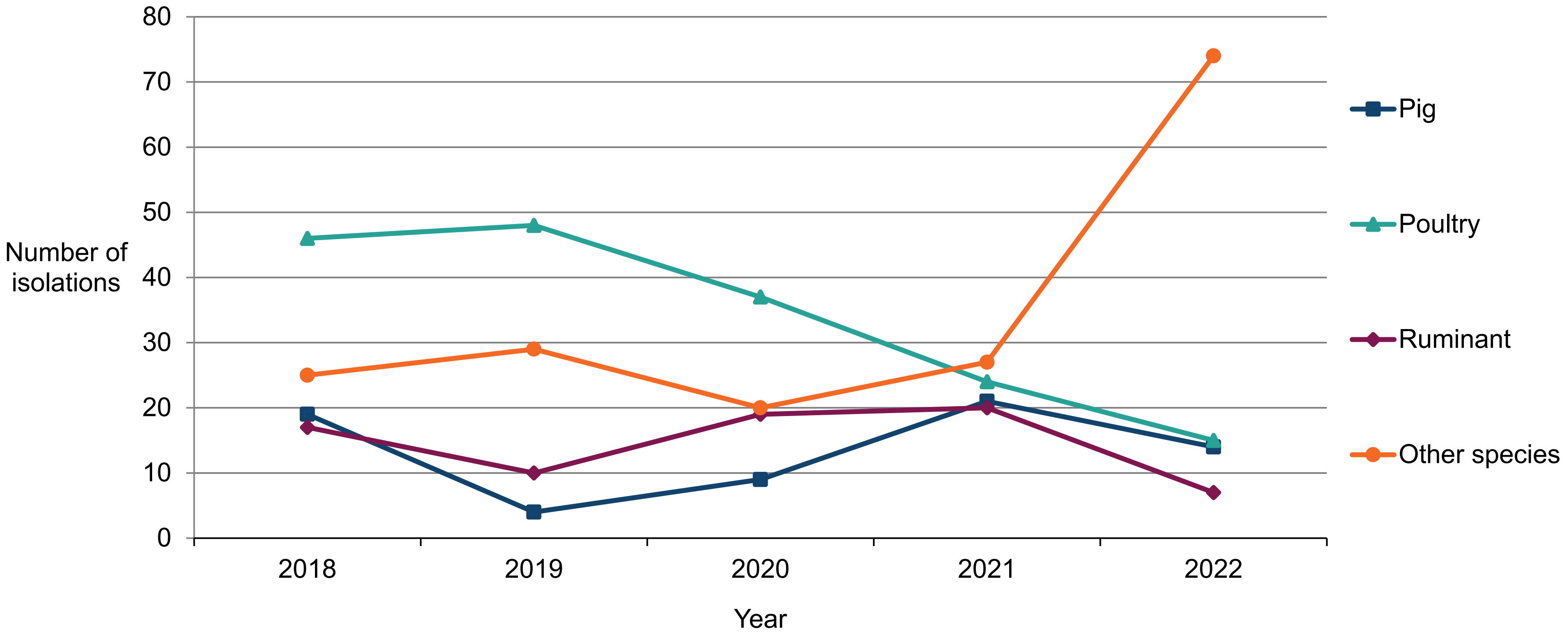


Figure 12.3 shows the number of isolations of *Salmonella* in compound poultry feed has declined in recent years from 48 in 2019 to 15 in 2022. Likewise, the number of isolations in ruminant feed has also declined from 17 in 2018 to 7 in 2022. Isolations in compound pig feed have remained below 21 since 2018 and was 14 in 2022 while the number of isolations in other species increased significantly in 2022 to 74 compared to just 25 in 2018.

Table 12.3: Serovars of *Salmonella* isolated from compound ruminant feed in Great Britain in 2022, compared with the previous 2 years

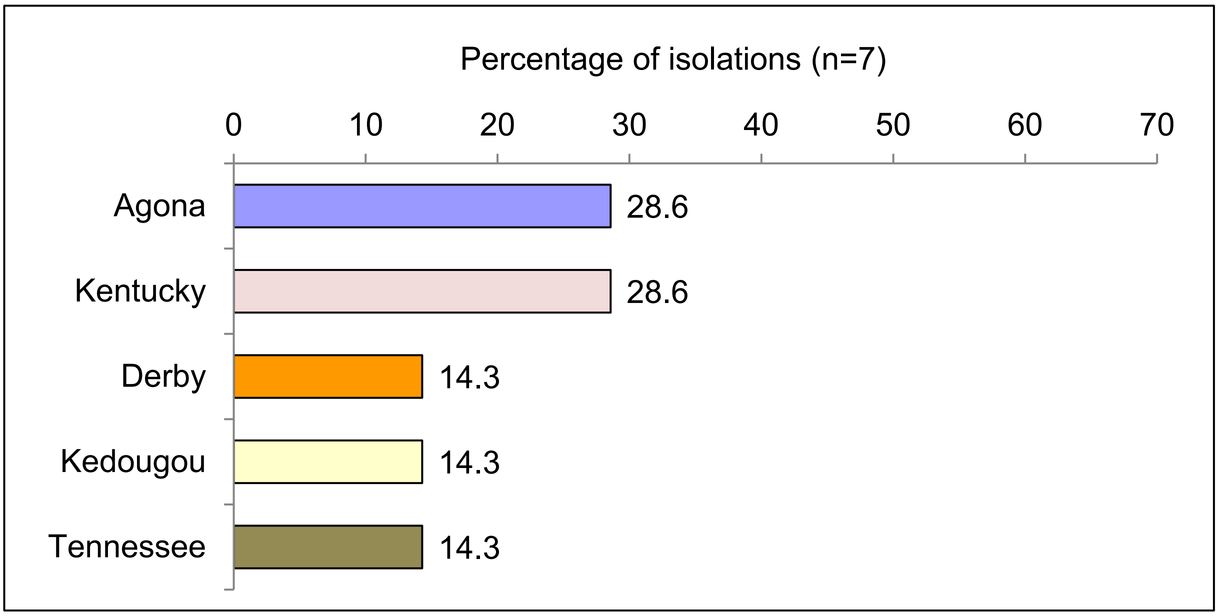
***Salmonella* Serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
3,19:rough:-	1	0	0
4,12:d:-	1	0	0
Aarhus	1	0	0
Agama	1	0	0
Agona	1	0	2
Budapest	1	0	0
Derby	1	2	1
Emek	1	0	0
Kedougou	0	0	1
Kentucky	0	0	2
Korlebu	0	1	0
London	1	0	0
Mbandaka	1	3	0
Newport	1	0	0
Poona	1	0	0
Rissen	1	10	0
Senftenberg	2	1	0
Tennessee	3	3	1
Typhimurium DT193	1	0	0
Total	**19**	**20**	**7**

Table 12.4: Serovars of *Salmonella* isolated from compound pig feed in Great Britain in 2022, compared with the previous 2 years

***Salmonella* Serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
4,5,12:i:-	0	0	1
6,7,:-:-	0	1	0
Agona	0	1	0
California	0	1	0
Derby	0	0	2
Enteritidis	0	0	1
Hindmarsh	0	0	1
Kedougou	0	0	3
Odozi	1	0	0
Ohio	0	3	1
Panama	0	1	0
Rissen	6	11	5
Senftenberg	1	0	0
Tennessee	1	3	0
Total	**9**	**21**	**14**

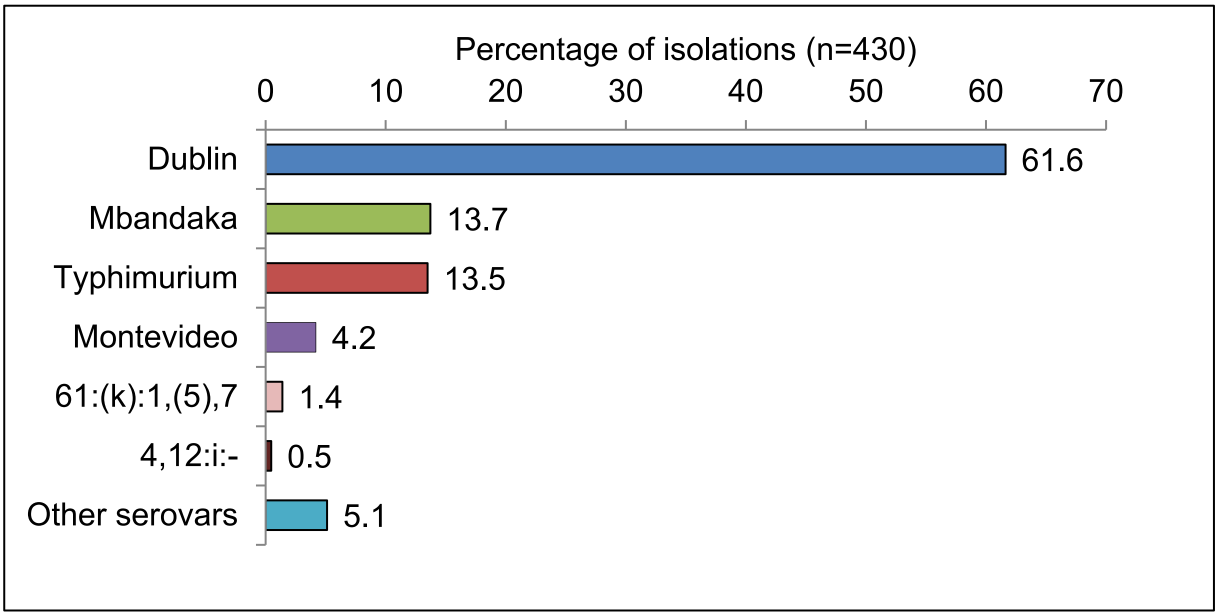
Figure 12.4: Isolations of the most common serovars in compound ruminant feed, cattle and sheep in Great Britain 2022

Figure 12.4.1: Isolations from compound ruminant feed



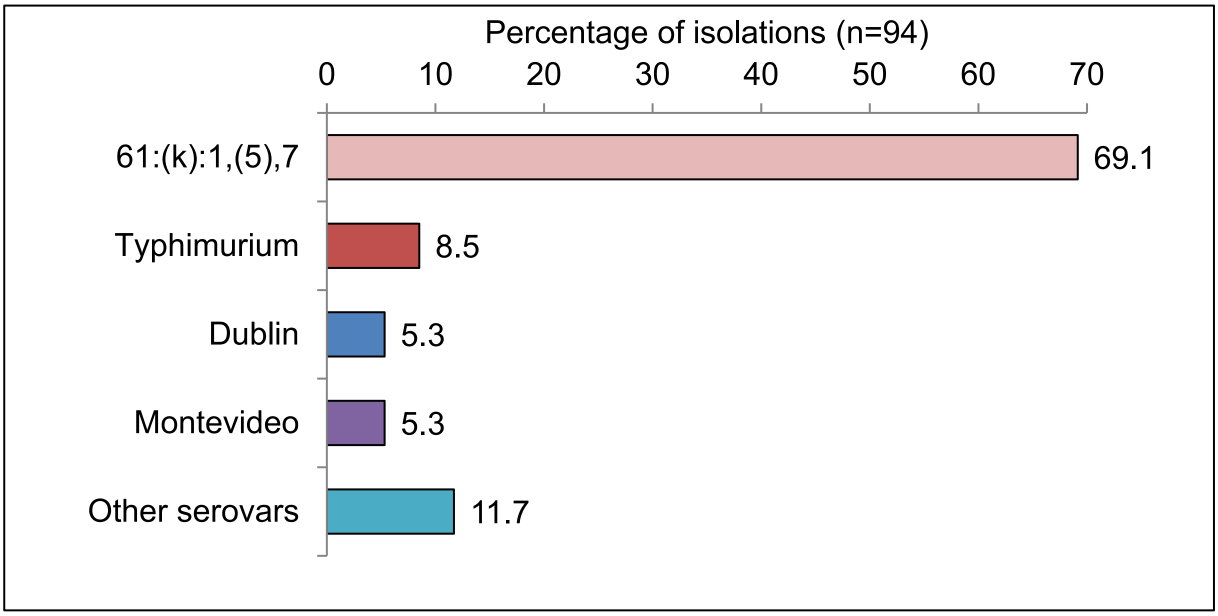
In 2022 the most common *Salmonella* serovars in compound ruminant feed, were *S.* Agona and *S*. Kentucky, accounting for 28.6% of total isolations each. Other serovars made up the remaining 42.9%

Figure 12.4.2: Isolations from cattle



In 2022 the most common *Salmonella* serovars in cattle, was *S.* Dublin accounting for 61.6% of total isolations, followed by *S*. Mbandaka, (13.7%), *S.* Typhimurium (13.5%) and *S.* Montevideo (4.2%).

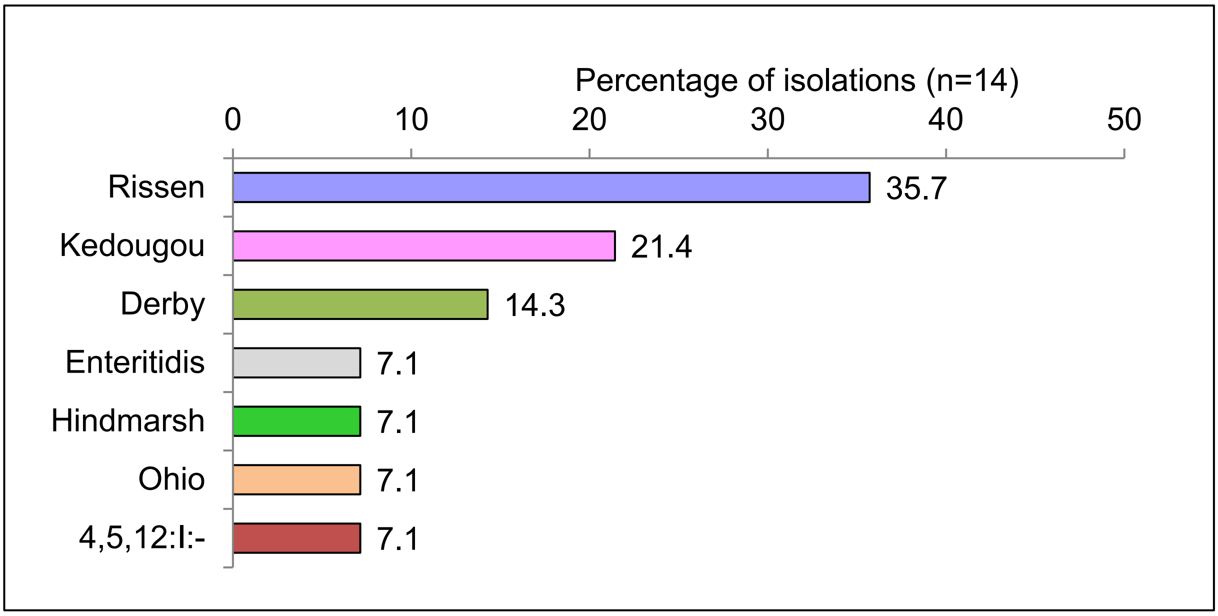
Figure 12.4.3: Isolations from sheep



The most common *Salmonella* serovar in sheep was *S.* 61:(K):1,(5),7 (variants of *Salmonella* enterica subspecies diarizonae), accounting for 69.1% of total isolations, followed by *S.* Typhimurium (8.5%), *S.* Dublin (5.3%) and *S.* Montevideo (5.3%).

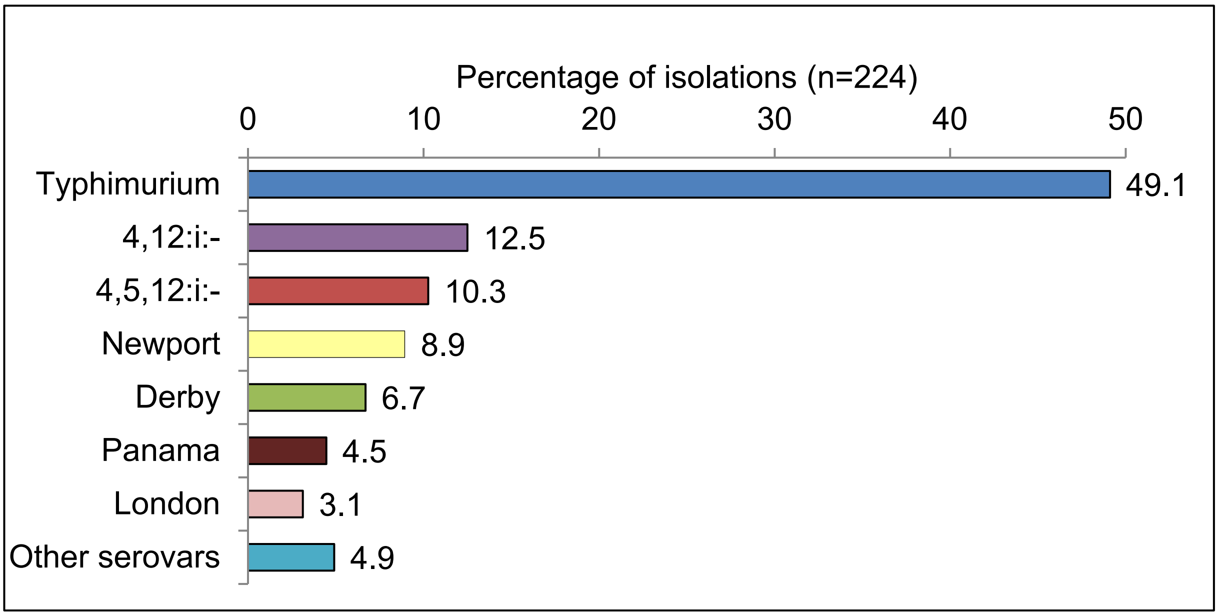
Figure 12.5: Isolations of the most common serovars in compound pig feed and pigs in Great Britain 2022

Figure 12.5.1: Isolations from compound pig feed



In 2022 the most common *Salmonella* serovar in pig feed was *S.* Rissen, accounting for 35.7% of total isolations, followed by *S.* Kedougou (21.4%) and *S.* Derby (14.3%).

Figure 12.5.2: Isolations from pigs



In 2022 the most common *Salmonella* serovar in pigs was *S.* Typhimurium, accounting for 49.1% of total isolations, followed by *S.* 4,12:i:- (12.5%), *S.* 4,5,12:i:- (10.3%) and *S.* Newport (8.9%).

Table 12.5: Serovars of *Salmonella* isolated from compound poultry feed in Great Britain in 2022 compared with the previous 2 years

Salmonella **Serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
13,23:i:-	5	0	0
4,12:d:-	1	0	0
6,7:-:-	1	1	0
6,7:-:enz15	0	0	1
66:-:-	1	0	0
Agama	0	0	2
Agona	2	0	1
Anatum	0	1	0
Bredeney	0	6	0
Coeln	1	0	0
Cubana	1	0	0
Derby	0	0	1
Enteritidis	0	0	1
Give	2	0	0
Havana	1	1	0
Idikan	1	0	1
Infantis	0	0	1
Kedougou	4	1	2
Korlebu	0	1	0
Lexington	0	1	0
Litchfield	1	0	0
Liverpool	1	0	0
Mbandaka	0	2	0
Montevideo	0	1	0
Newport	2	1	1
Odozi	0	2	0
Ohio	2	0	0
Rissen	3	2	0
Ruiru	0	1	0
Soerenga	0	0	2
Stockholm	1	0	0
Taksony	1	0	0
Tennessee	5	1	0
Typhimurium RDNC	1	0	0
Typhimurium	0	2	1
Utah	0	0	1
Total	**37**	**24**	**15**

Table 12.6: Serovars of *Salmonella* isolated from compound feed for other species in Great Britain in 2022, compared with the previous 2 years

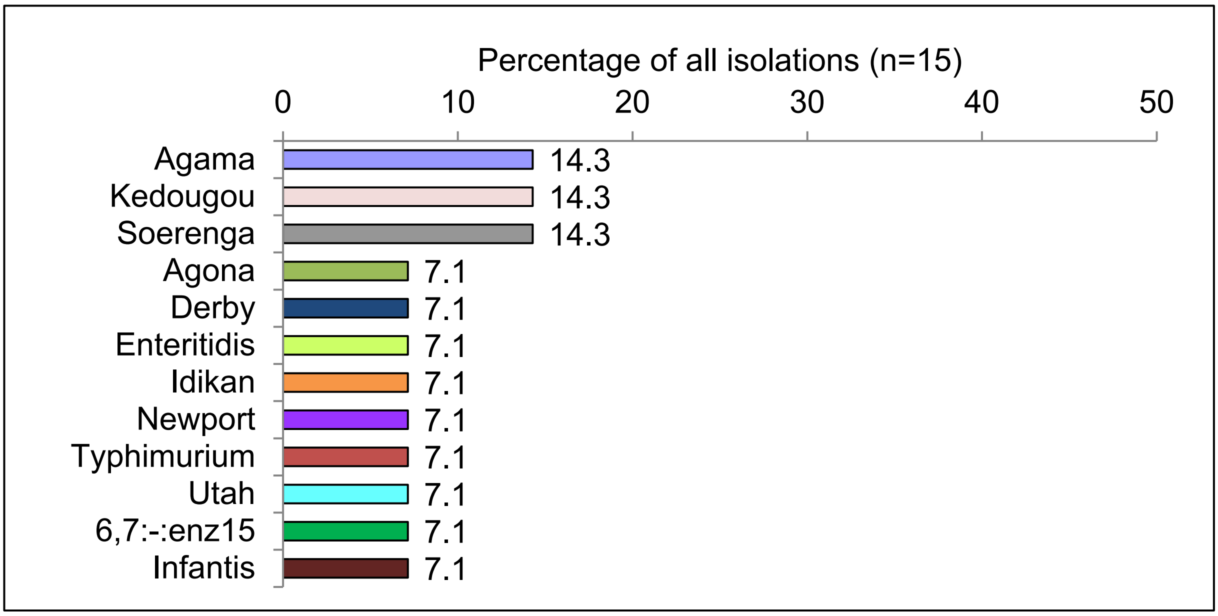
***Salmonella* Serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
13,23:i:-	1	0	0
4,12:d:-	2	0	0
4,12:i:-	0	0	4
4,12:z:-	1	0	0
4,5,12:i:-	0	0	3
4,5,12:i:- DT193	1	0	0
42:z:1,5	1	0	0
6,7:-:-	1	0	7
6,7:r:-	0	0	1
61:-:-	1	0	0
Aarhus	0	1	0
Aba	0	0	1
Agama	1	2	0
Agona	2	1	1
Anatum	0	0	1
Bovismorbificans	0	3	2
Brancaster	0	0	1
Cerro	0	0	1
Coeln	0	0	1
Cubana	1	0	0
Derby	0	2	5
Havana	0	2	0
Ibadan	0	0	1
Idikan	0	0	1
Indiana	1	0	0
Infantis	0	0	10
Isangi	0	0	1
Kedougou	0	1	5
Kentucky	0	1	1
Kingston	0	0	1
Livingstone	2	4	1
Mbandaka	0	0	3
Molade	0	1	1
Mons	0	1	0
Montevideo	0	1	3
Newport	1	0	2
Nottingham	0	1	1
O rough:g,p:-	0	0	1
Ohio	2	0	0

***Salmonella* Serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Panama	0	0	2
Rissen	0	5	4
Takoradi	0	0	1
Taksony	1	0	0
Tennessee	1	1	3
Thompson	0	0	2
Typhimurium	0	0	2
Total	**20**	**27**	**74**

Other species in 2022 were: cats (4 isolations), dogs (24 isolations), horse (1 isolation), mixed avian species (4 isolations), mixed species (30 isolations) and unspecified (11 isolations).

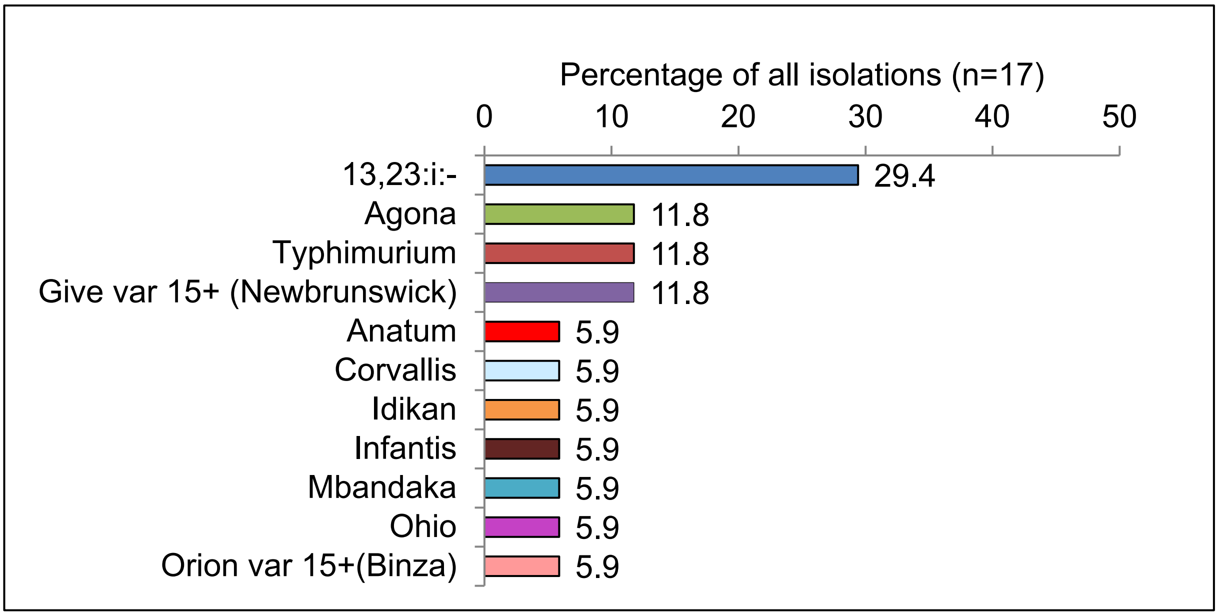
Figure 12.6: Isolations of the most common serovars in compound poultry feed and positive flocks of chickens and turkeys from NCP testing in Great Britain 2022

Figure 12.6.1: Isolations from compound poultry feed



In 2022 the top three *Salmonella* serovars isolated from compound poultry feed was *S.* Agama, *S.* Kedougou and *S.* Soerenga, each accounting for 14.3% of total isolations. Other serovars made up the remaining 63.9%

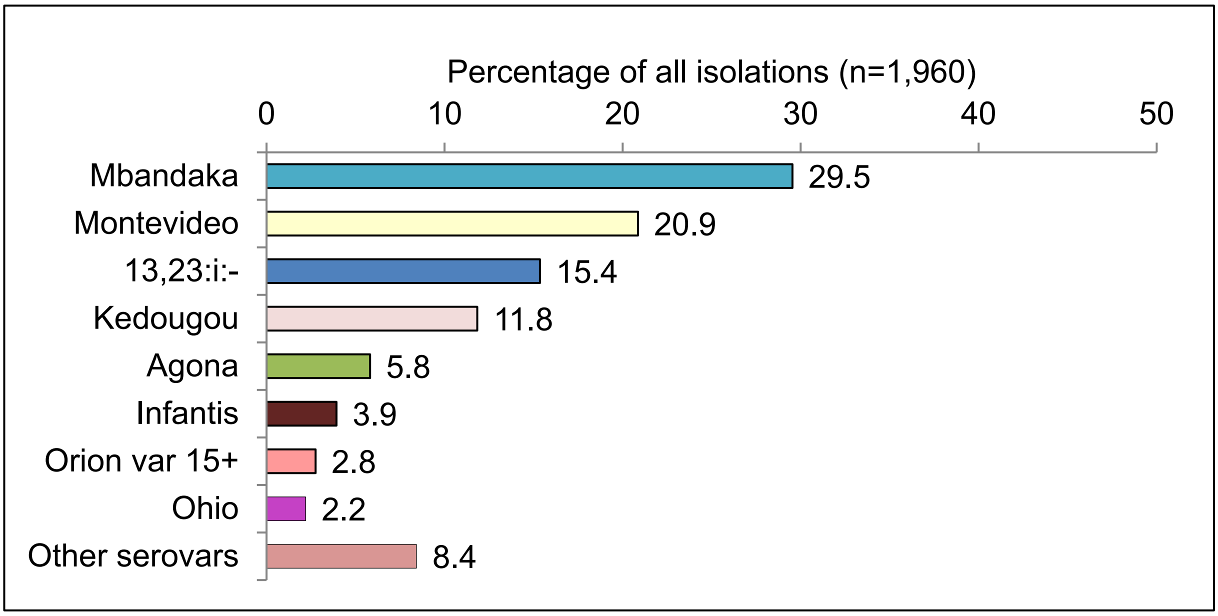
Figure 12.6.2: Isolations from (adult) breeder chickens (NCP testing only)



The most common *Salmonella* serovar in (adult) breeder Chickens was *S.* 13,23:i:-, accounting for 29.4% of total isolations, followed by *S.* Agona (11.8%), *S.* Typhimurium (11.8%) and *S.* Give var. 15^+ (Newbrunswick) (11.8%).

One breeder chicken flock was positive for 2 serovars (counted once in total). Summed percentages of all serovars therefore exceeds 100%.

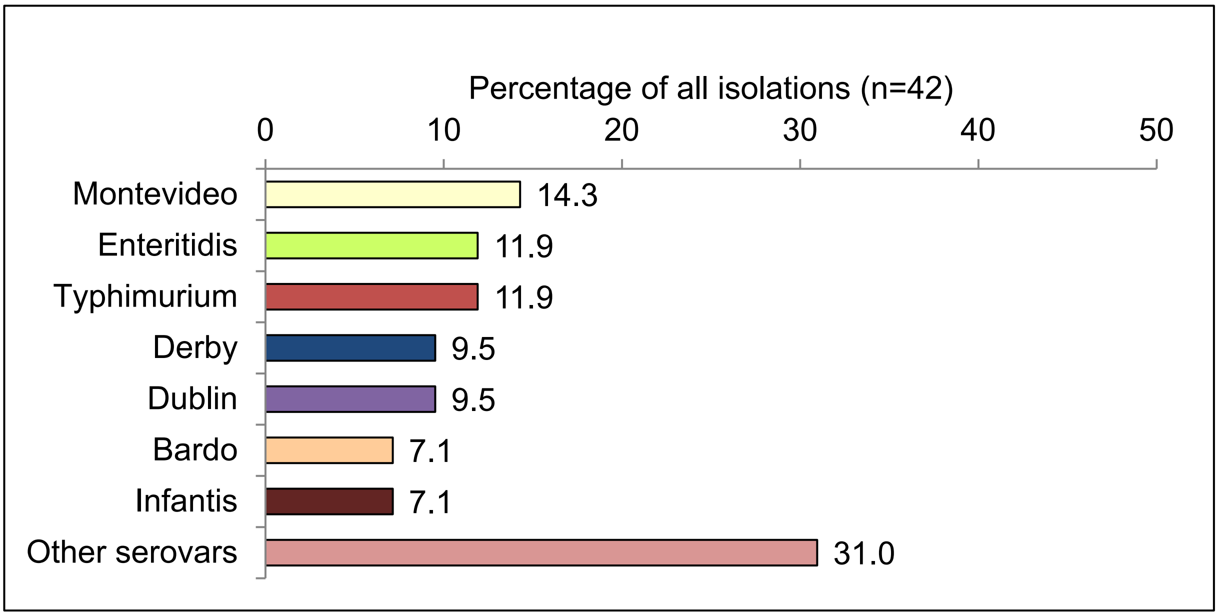
Figure 12.6.3: Isolations from broiler chickens (NCP testing only)



The most common *Salmonella* serovar in broiler Chickens 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%).

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

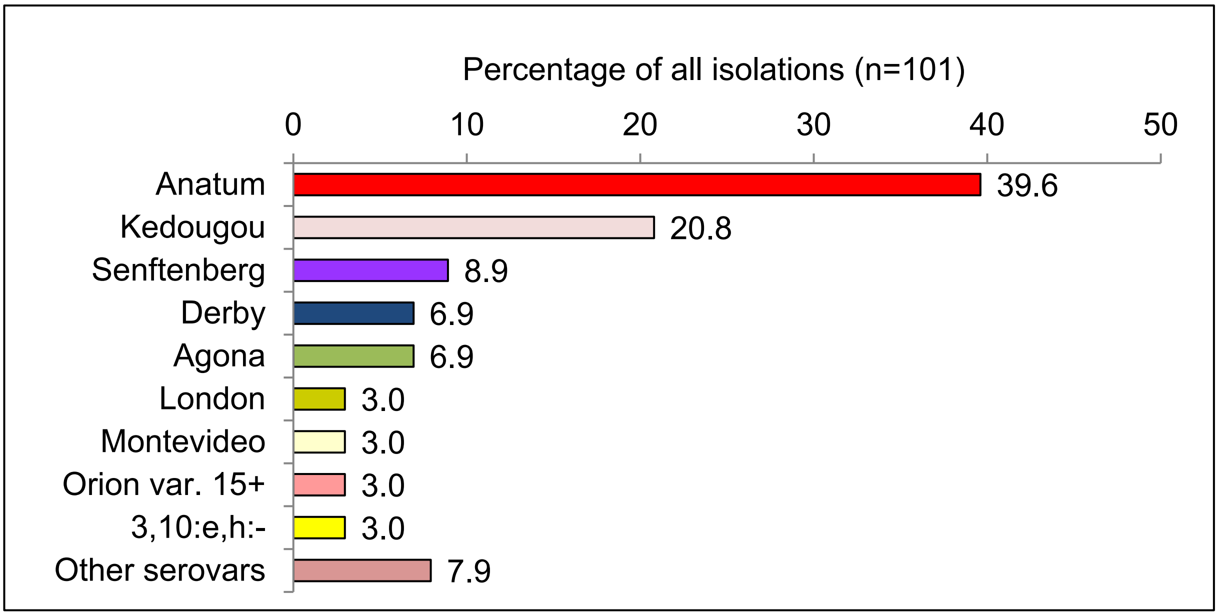
Figure 12.6.4: Isolations from (adult) layer chickens (NCP testing only)



The most common *Salmonella* serovar in (adult) layer chickens was *S.* Montevideo, accounting for 14.3% of total isolations, followed by *S.* Enteritidis (11.9%) and *S.* Typhimurium (11.9%).

One layer chicken flock was positive for 2 serovars (counted once in total). Summed percentages of all serovars therefore exceeds 100%.

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.* Anatum, accounting for 39.6% of total isolations, followed by *S.* Kedougou (20.8%) and *S.* Senftenberg (8.9%).

Three turkey flocks were positive for 2 serovars (each counted only once in 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 2020 to 2022

***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Aarhus	1	0	0
Aba	0	0	1
Agama	2	5	1
Agona	5	16	13
Ajiobo	0	0	1
Albert	1	0	0
Alachua	0	1	0
Anatum	9	8	9
Banana	2	0	1
Bareilly	1	2	1
Bere	0	0	1
Bochum	0	1	0
Bonn	0	0	2
Bovismorbificans	18	0	6
Brancaster	1	0	0
Branderup	0	2	0
Brandenburg	1	1	2
Bredeney	9	2	0
Budapest	16	0	0
California	0	8	0
Cannstatt	0	2	0
Carmel	0	0	1
Cerro	3	0	6
Coeln	0	5	0
Cubana	3	4	6
Dallgow	1	0	0
Derby	21	19	37
Denver	0	0	0
Dublin	5	10	4
Duisburg	0	0	1
Durban	1	0	0
Ealing	1	11	3
Elomrane	1	0	0
Enteritidis	3	6	4
Fresno	0	0	2
Give	9	8	7
Give var 15^+ (Newbrunswick)	0	0	10
Glostrup	1	0	0
Goldcoast	3	1	3

Salmonella serovar	Isolations 2020	Isolations 2021	Isolations 2022
Hadar	9	3	1
Havana	6	3	3
Ibadan	4	0	0
Idikan	3	4	4
Indiana	30	35	49
Infantis	29	40	61
Isangi	1	0	0
Kedougou	36	38	57
Kentucky	2	4	2
Kingston	3	0	2
Korlebu	0	2	0
Kottbus	14	23	17
Larochelle	0	1	0
Leeuwarden	1	0	0
Lexington	1	2	8
Lille	1	0	0
Liverpool	3	0	3
Livingstone	10	6	9
Lomita	0	1	0
London	4	5	10
Mbandaka	28	31	21
Meleagridis	1	2	0
Montevideo	8	18	10
Muenchen	1	0	0
Muenster	3	0	5
Newport	7	18	20
Nottingham	3	0	0
Odozi	1	0	0
Ohio	29	30	22
Oranienburg	0	1	1
Ordonez	0	23	0
Orion	10	16	6
Orion var 15^+	0	1	1
O rough:f,g:-	0	3	0
O rough:g,p:-	0	2	0
O rough:i:z	0	2	0
O rough:k:z	0	4	0
O rough:z_{10}:enz$_{15}$	0	0	2
O rough:z_{29}:-	0	0	1
Oslo	0	2	1
Ouakam	1	1	1
Panama	5	10	15
Paratyphi B var. Java	3	3	2
Poona	1	0	0
Reading	1	0	1

***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Riggil	0	1	0
Rissen	52	90	35
Rublislaw	0	0	2
Ruiru	2	4	0
Saintpaul	0	0	1
Schwarzengrund	1	1	2
Senftenberg	19	27	15
Senftenberg (z_{27})	0	0	1
Soerenga	1	1	1
Stanley	4	2	1
Stanleyville	0	1	0
Stockholm	1	0	0
Szentes	1	1	1
Taksony	3	0	0
Tennessee	72	47	11
Teshie	0	0	1
Tsevie	0	0	1
Typhimurium	36	49	50
Uganda	1	0	1
Vinohrady	0	1	0
Virchow	0	0	3
Weltevreden	0	1	0
Westhampton	0	3	0
Wilhelmsberg	0	0	1
Yoruba	0	1	0
3,10:e,h:-	1	0	0
3,10:lv:-	11	0	0
3,10:z_{10}:-	0	0	1
3,10:-:-	0	1	0
3,15:rough:-	0	0	1
3,19:z_{27}:-	1	0	4
3,19:-:-	2	0	1
3,19:rough:-	0	2	0
3,19:z_{45}:-	1	0	0
4,5,12:b:-	0	1	0
4,5,12::-:1,2	0	1	0
4,5,12:i:-	12	11	28
4,5,12:-:-	2	0	0
4,12:d:-	1	0	0
4,12:i:-	11	13	27
4,12:z:-	0	0	2
4,12,[27]:b:e,n,x	0	1	0
4,12:rough:-	0	0	1
6,7:b:-	0	0	1
6,7:enz_{15}	1	2	6

Salmonella serovar	Isolations 2020	Isolations 2021	Isolations 2022
6,7:k:-	1	1	0
6,7:r:-	0	4	0
6,7:rough:-	1	2	0
6,7:z_4,z_{23}:-	2	0	0
6,7:z:-	1	0	0
6,7:-:-	1	4	10
6,8:e,h:-	7	0	3
9,12:l,v:-	0	1	0
9,12:-:-	1	0	0
13,23:i:-	10	3	5
38:l,v,z_{13}:-	0	0	1
38:rz	0	1	0
41:z_4,z_{24}:-	0	0	1
47:z_4,z_{23}:-	2	1	0
61:k:1,5	7	4	0
61:k:1,5,7	0	0	9
61:-:1,5	17	0	0
61:-:1,5	0	14	0
61:-:1,5,7	9	0	17
Total	**672**	**743**	**702**

Table 12.8a: Serovars of *Salmonella* in feedingstuff ingredients in Great Britain 2020 to 2022

Feedingstuff	***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Barley	Bovismorbificans	0	0	1
Barley	Enteritidis PT9b	0	1	0
Barley	Glostrup	1	0	0
Barley	Kottbus	0	1	1
Barley	Panama	0	0	1
Barley	Rissen	0	0	1
Biscuit	Bochum	0	1	0
Biscuit	Rissen	0	1	0
Biscuit	Typhimurium DT193	0	0	1
Broken rice	Riggil	0	1	0
Broken rice	Typhimurium DT2	0	1	1
Buckwheat	Enteritidis PT4	0	0	1
Cocoa	$41:z_4,z_{24}:-$	0	0	1
Feeder mice	Montevideo	0	0	1
Fishmeal	Montevideo	1	0	0
Fishmeal	Schwarzengrund	0	0	1
Ginger root	Teshie	0	0	1
Guar protein	Montevideo	1	0	0
Guar protein	Orion	0	1	0
Guar protein	Senftenberg	0	0	1
Guar protein	$47:z_4,z_{23}:-$	1	0	0
Herbs	Enteritidis PT4	0	1	0
Herbs	Infantis	1	0	0
Herbs	Szentes	1	1	0
Liquorice root	Anatum	0	0	1
Liquorice root	Montevideo	0	0	1
Liquorice root	Tennessee	0	0	1
Linseed	Muenster	1	0	0
Locust bean meal	Newport	0	1	0
Maize	Cubana	1	0	0
Maize	Typhimurium DT99	0	0	1
Malt	Agama	0	1	0
Malt	Anatum	0	0	3
Malt	Indiana	1	0	0
Malt	Infantis	0	7	2
Malt	Kingston	1	0	0
Malt	Kottbus	0	2	0
Malt	Orion	1	1	0
Malt	4,5,12:i:- DT193	1	0	0
Meat meal	Braenderup	0	1	0
Meat meal	6,7,:r:-	0	1	0
Minerals	Derby	0	0	1

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Minerals	Kedougou	0	0	1
Minerals	Tennessee	0	0	1
Mixed cereals	Anatum	0	0	1
Mixed ingredients	Agama	0	1	0
Mixed ingredients	Cubana	0	1	0
Mixed ingredients	Lexington	0	0	1
Mixed ingredients	Taksony	1	0	0
Mixed oil seeds	Banana	0	0	1
Mixed oil seeds	Budapest	1	0	0
Mixed oil seeds	Cubana	0	1	1
Mixed oil seeds	Ealing	0	5	0
Mixed oil seeds	Idikan	0	1	0
Mixed oil seeds	Infantis	1	0	0
Mixed oil seeds	Kedougou	1	0	0
Mixed oil seeds	Kottbus	0	1	0
Mixed oil seeds	Livingstone	0	0	1
Mixed oil seeds	Montevideo	0	2	0
Mixed oil seeds	Paratyphi B var. Java	0	1	0
Mixed oil seeds	Rissen	12	49	2
Mixed oil seeds	Senftenberg	1	4	4
Mixed oil seeds	Soerenga	0	0	1
Mixed oil seeds	Tennessee	1	1	0
Mixed oil seeds	Typhimurium DT2	1	0	0
Mixed oil seeds	Typhimurium DT99	0	0	1
Mixed oil seeds	Typhimurium DT193	0	1	0
Mixed oil seeds	Typhimurium U308	0	1	0
Mixed oil seeds	3,19:-:rough:-	0	1	0
Mixed oil seeds	6,7:rough:-	0	1	0
Mixed vegetables	Derby	0	0	1
Mixed vegetables	Newport	0	0	1
Mixed vegetables	Panama	0	0	1
Oats	Newport	0	1	0
Oats	Oslo	0	1	0
Oats	Panama	0	1	0
Oats	Typhimurium DT104	0	0	1
Peas	Tennessee	0	1	0
Poultry offal meal	Coeln	0	2	0
Poultry offal meal	Infantis	0	11	0
Poultry offal meal	Livingstone	0	1	0
Poultry offal meal	Mbandaka	0	1	0
Premix	Ohio	0	1	0
Premix	Senftenberg	0	1	0
Protein blend	Derby	0	0	1
Protein blend	London	0	0	1
Protein blend	Rissen	1	1	0
Protein blend	4,12:i:- DT104	0	0	1

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Rapeseed	Agona	1	0	0
Rapeseed	Bredeney	4	2	0
Rapeseed	Budapest	2	0	0
Rapeseed	Ealing	1	3	1
Rapeseed	Havana	0	1	0
Rapeseed	Idikan	0	0	1
Rapeseed	Kingston	0	0	1
Rapeseed	Mbandaka	1	1	0
Rapeseed	Meleagridis	1	0	0
Rapeseed	Montevideo	2	2	0
Rapeseed	Muenchen	1	0	0
Rapeseed	Newport	1	0	0
Rapeseed	Paratyphi B var. Java	1	0	0
Rapeseed	Rissen	33	21	23
Rapeseed	Senftenberg	4	4	1
Rapeseed	Tennessee	55	35	5
Rapeseed	Typhimurium DT2	0	1	1
Rapeseed	Typhimurium DT99	0	0	1
Rapeseed	Typhimurium RDNC	0	1	0
Rapeseed	Westhampton	0	1	0
Rapeseed	3,19:-:-	1	0	
Rapeseed	6,7:-:-	0	0	1
Rapeseed	6,7,:rough:-:-	0	1	0
Soya bean meal	Aarhus	1	0	0
Soya bean meal	Agama	1	0	0
Soya bean meal	Agona	0	3	0
Soya bean meal	Alachua	0	1	0
Soya bean meal	Anatum	1	2	1
Soya bean meal	Banana	2	0	0
Soya bean meal	Bareilly	0	0	1
Soya bean meal	Bere	0	0	1
Soya bean meal	Budapest	8	0	0
Soya bean meal	California	0	3	0
Soya bean meal	Cannstatt	0	1	0
Soya bean meal	Carmel	0	0	1
Soya bean meal	Cerro	0	0	2
Soya bean meal	Cubana	1	1	4
Soya bean meal	Denver	0	0	0
Soya bean meal	Duisburg	0	0	1
Soya bean meal	Fresno	0	0	2
Soya bean meal	Havana	0	1	1
Soya bean meal	Infantis	3	0	0
Soya bean meal	Kedougou	0	0	1
Soya bean meal	Kentucky	0	2	1
Soya bean meal	Korlebu	0	2	0
Soya bean meal	Liverpool	1	0	0

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Soya bean meal	Lexington	0	1	0
Soya bean meal	Livingstone	1	0	2
Soya bean meal	Mbandaka	5	2	1
Soya bean meal	Montevideo	0	3	0
Soya bean meal	Ohio	0	0	1
Soya bean meal	Orion	0	3	0
Soya bean meal	O rough:f,g:-:-	0	1	0
Soya bean meal	Rissen	0	2	0
Soya bean meal	Senftenberg	3	2	0
Soya bean meal	Soerenga	1	0	0
Soya bean meal	Taksony	2	0	0
Soya bean meal	Tennessee	0	4	1
Soya bean meal	Typhimurium DT2	0	0	1
Soya bean meal	Typhimurium DT99	0	0	1
Soya bean meal	Typhimurium DT193	3	0	0
Soya bean meal	Typhimurium RDNC	0	1	0
Soya bean meal	Uganda	0	0	1
Soya bean meal	Weltevreden	0	1	0
Soya bean meal	Yoruba	0	1	0
Soya bean meal	3,15:rough:-	0	0	1
Soya bean meal	3,19:-:-	1	0	1
Soya bean meal	3,19:z_{27}:-	1	0	3
Soya bean meal	4,12:d:-	1	0	0
Soya bean meal	6,7:b:-	0	0	1
Soya bean meal	6,7:z_4,z_{23}:-	2	0	0
Soya bean meal	47:z_4,z_{23}:-	1	1	0
Sugar beet	Ohio	1	0	0
Sunflower	Agona	1	0	0
Sunflower	Bredeney	2	0	0
Sunflower	Cannstatt	0	1	0
Sunflower	Cubana	0	1	0
Sunflower	Dallgow	1	0	0
Sunflower	Give	2	0	0
Sunflower	Infantis	1	0	0
Sunflower	Kentucky	1	0	0
Sunflower	Liverpool	1	0	1
Sunflower	Llandoff	0	1	0
Sunflower	Mbandaka	1	1	0
Sunflower	Montevideo	1	2	0
Sunflower	Rissen	2	0	0
Sunflower	Ruiru	1	0	0
Sunflower	Senftenberg	3	0	0
Sunflower	Tennessee	0	0	1
Sunflower	Typhimurium DT2	2	0	0
Sunflower	Typhimurium DT193	0	1	0
Sunflower	Typhimurium NOPT	1	0	0

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Sunflower	Vinohady	0	1	0
Sunflower	3,19:rough:-	0	1	0
Wheat	Agama	0	1	0
Wheat	Agona	1	0	2
Wheat	Kedougou	1	0	0
Wheat	Kingston	1	0	0
Wheat	Ohio	1	0	0
Wheat	Rissen	0	1	0
Wheat	Senftenberg	1	0	0
Wheat	Tennessee	1	0	0
Wheat	Typhimurium DT1	1	0	0
Wheat	Typhimurium DT193	1	0	0
Wheat	Typhimurium U308	0	1	0
Yucca	Mbandaka	0	0	1
Total	Not applicable	**208**	**239**	**114**

Table 12.8b: Serovars of *Salmonella* in other products associated with the ABPR in Great Britain 2020 to 2022

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Blood products	Cerro	0	0	2
Blood products	Derby	1	0	7
Blood products	Panama	0	0	6
Blood products	Rissen	0	0	2
Blood products	Senftenberg	1	1	0
Blood products	Tennessee	0	2	0
Blood products	Typhimurium DT2	0	2	0
Blood products	4,12:i:- DT193	0	0	2
Blood products	4,5,12:i:- DT193	0	0	6
Blood products	4,5,12:i:- UNTY	0	0	1
Blood products	61:-:1,5,7	1	0	0
Bone meal	Idikan	0	1	0
Bone meal	Infantis	0	2	0
Bone meal	Livingstone	2	0	0
Bone meal	Mbandaka	0	3	0
Bone meal	Senftenberg	0	3	0
Bone meal	Tennessee	0	1	0
Bone meal	6,7:r:-	0	1	0
Compost	Aba	0	0	1
Compost	Agona	0	1	0
Compost	Bovismorbificans	2	0	0
Compost	Give	0	1	0
Compost	Indiana	0	1	0
Compost	Isangi	1	0	0
Compost	Kedougou	1	0	0
Compost	Kottbus	0	1	0
Compost	London	0	0	1
Compost	Mbandaka	1	0	0
Compost	Senftenberg	0	0	1
Compost	Tennessee	0	0	1
Digestate	Agona	0	10	0
Digestate	Anatum	2	0	0
Digestate	Bareilly	1	2	0
Digestate	Bovismorbificans	6	0	0
Digestate	Branderup	0	1	0
Digestate	Cannstatt	1	0	0
Digestate	Cerro	1	0	0
Digestate	Derby	0	1	0
Digestate	Durban	1	0	0
Digestate	Havana	1	0	0
Digestate	Kedougou	0	1	0
Digestate	Kentucky	1	0	0

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Digestate	Mbandaka	0	1	0
Digestate	Montevideo	0	2	0
Digestate	Newport	1	3	1
Digestate	Ordonez	0	23	0
Digestate	Panama	0	3	0
Digestate	Rissen	0	2	0
Digestate	Senftenberg	0	1	0
Digestate	Tennessee	1	0	0
Digestate	Typhimurium DT116	0	2	0
Digestate	Typhimurium NOPT	0	3	0
Digestate	Typhimurium RDNC	0	1	0
Digestate	4,12,:i:- DT193	0	0	2
Digestate	6,7:z:-	1	0	0
Digestate	61:k:1,5,7	0	0	1
Feedmill environment	Agama	0	1	1
Feedmill environment	Agona	1	1	2
Feedmill environment	Ajiobo	0	0	1
Feedmill environment	Albert	1	0	0
Feedmill environment	Anatum	4	2	2
Feedmill environment	Bovismorbificans	1	0	0
Feedmill environment	Bredeney	1	0	0
Feedmill environment	Budapest	4	0	0
Feedmill environment	California	0	5	0
Feedmill environment	Cerro	1	0	1
Feedmill environment	Coeln	0	2	0
Feedmill environment	Cubana	0	1	1
Feedmill environment	Derby	1	1	1
Feedmill environment	Ealing	0	1	1
Feedmill environment	Enteritidis PT9b	1	0	0
Feedmill environment	Havana	2	1	0
Feedmill environment	Idikan	1	1	2
Feedmill environment	Infantis	12	2	8
Feedmill environment	Kedougou	26	33	50
Feedmill environment	Kentucky	0	0	1
Feedmill environment	Kingston	1	0	0
Feedmill environment	Kottbus	2	0	1
Feedmill environment	Leeuwarden	1	0	0
Feedmill environment	Lille	1	0	0
Feedmill environment	Liverpool	0	0	1
Feedmill environment	Livingstone	0	0	1
Feedmill environment	Mbandaka	3	2	9
Feedmill environment	Montevideo	1	0	0
Feedmill environment	Newport	1	0	1
Feedmill environment	Nottingham	3	0	0
Feedmill environment	Odozi	1	0	0
Feedmill environment	Ohio	26	27	20

Feedingstuff	***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Feedmill environment	Oranienburg	0	1	1
Feedmill environment	Orion	1	0	0
Feedmill environment	Oslo	0	1	1
Feedmill environment	Ouakam	0	0	1
Feedmill environment	O_rough:z_{29}:-	0	0	1
Feedmill environment	Paratyphi var. java	0	0	1
Feedmill environment	Poona	1	0	0
Feedmill environment	Rissen	3	7	3
Feedmill environment	Ruiru	1	2	0
Feedmill environment	Senftenberg	6	11	2
Feedmill environment	Senftenberg (z_{27})	0	0	1
Feedmill environment	Stockholm	1	0	0
Feedmill environment	Szentes	0	0	1
Feedmill environment	Tennessee	11	2	0
Feedmill environment	Typhimurium DT99	0	0	2
Feedmill environment	Typhimurium DT104	2	0	0
Feedmill environment	Typhimurium U288	0	1	0
Feedmill environment	Typhimurium RDNC	0	1	1
Feedmill environment	Typhimurium UNTY	1	0	0
Feedmill environment	Westhampton	0	1	0
Feedmill environment	3,19:rough:-	1	0	0
Feedmill environment	3,19:z_{27}:-	0	0	1
Feedmill environment	4,5,12:b:-	0	1	0
Feedmill environment	4,5,12:i:- DT193	1	0	0
Feedmill environment	4,12:i:- DT193	0	0	1
Feedmill environment	6,7:enz$_{15}$	1	1	2
Feedmill environment	6,7:k:-	1	1	0
Feedmill environment	6,7:r:-	0	1	0
Feedmill environment	6,7:rough:-	1	0	0
Feedmill environment	6,7:-:-	1	3	4
Feedmill environment	13,23:i:-	8	1	5
Feedmill environment	61:-:1,5,7	0	0	1
Landfill	Budapest	1	0	0
Landfill	4,5,12:i:- DT193	1	0	0
Meat meal	Cerro	1	0	0
Meat meal	Derby	1	0	0
Meat meal	Goldcoast	1	0	0
Meat meal	Havana	1	0	0
Meat meal	Liverpool	1	0	0
Meat meal	London	1	0	0
Meat meal	Mbandaka	1	0	0
Meat meal	Ouakam	1	0	0
Meat meal	Tennessee	1	0	0
Meat meal	Typhimurium RDNC	1	0	0
Meat meal	61:-:1,5,7	1	0	0

Feedingstuff	***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Meat and bone meal	Havana	1	0	0
Meat and bone meal	Livingstone	2	1	0
Meat and tallow	4,5,12:i:- DT193	0	0	2
Meat and tallow	Infantis	0	0	2
Pet food (raw)	Agama	1	1	0
Pet food (raw)	Agona	1	1	9
Pet food (raw)	Anatum	2	4	1
Pet food (raw)	Bonn	0	0	2
Pet food (raw)	Bovismorbificans	9	0	5
Pet food (raw)	Brancaster	1	0	0
Pet food (raw)	Brandenburg	1	1	2
Pet food (raw)	Cerro	0	0	1
Pet food (raw)	Coeln	0	1	0
Pet food (raw)	Derby	18	17	26
Pet food (raw)	Dublin	5	10	4
Pet food (raw)	Ealing	0	2	1
Pet food (raw)	Elomrane	1	0	0
Pet food (raw)	Enteritidis PT2	0	1	0
Pet food (raw)	Enteritidis PT4	2	0	0
Pet food (raw)	Enteritidis PT8	0	0	1
Pet food (raw)	Enteritidis PT21	0	0	1
Pet food (raw)	Enteritidis RDNC	0	0	1
Pet food (raw)	Enteritidis UNTY	0	1	0
Pet food (raw)	Give	7	7	7
Pet food (raw)	Give var. 15^{+} (Newbrunswick)	0	0	10
Pet food (raw)	Goldcoast	2	1	3
Pet food (raw)	Hadar	9	3	1
Pet food (raw)	Havana	0	0	2
Pet food (raw)	Idikan	2	1	1
Pet food (raw)	Indiana	29	34	49
Pet food (raw)	Infantis	11	18	38
Pet food (raw)	Kedougou	7	4	5
Pet food (raw)	Kentucky	0	2	0
Pet food (raw)	Kingston	0	0	1
Pet food (raw)	Kottbus	12	18	15
Pet food (raw)	Larochelle	0	1	0
Pet food (raw)	Lexington	1	1	7
Pet food (raw)	Liverpool	0	0	1
Pet food (raw)	Livingstone	5	4	5
Pet food (raw)	London	3	5	8
Pet food (raw)	Mbandaka	15	19	10
Pet food (raw)	Meleagridis	0	2	0
Pet food (raw)	Montevideo	4	7	8
Pet food (raw)	Muenster	2	0	5
Pet food (raw)	Newport	4	13	17

Feedingstuff	***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Pet food (raw)	Ohio	1	2	1
Pet food (raw)	Orion	8	11	6
Pet food (raw)	Orion var. 15^+	0	1	1
Pet food (raw)	O rough:f,g:-	0	2	0
Pet food (raw)	O rough:g,p:-	0	1	0
Pet food (raw)	O rough:i:z	0	2	0
Pet food (raw)	O rough:k:z	0	4	0
Pet food (raw)	O rough:z_{10}:enz_{15}	0	0	2
Pet food (raw)	Oslo	0	0	0
Pet food (raw)	Panama	5	6	7
Pet food (raw)	Paratyphi var. Java	2	2	1
Pet food (raw)	Reading	1	0	1
Pet food (raw)	Rissen	1	6	4
Pet food (raw)	Rubislaw	0	0	2
Pet food (raw)	Ruiru	0	2	0
Pet food (raw)	Saintpaul	0	0	1
Pet food (raw)	Schwarzengrund	0	0	1
Pet food (raw)	Senftenberg	0	0	6
Pet food (raw)	Stanley	4	2	1
Pet food (raw)	Stanleyville	0	1	0
Pet food (raw)	Tennessee	1	0	1
Pet food (raw)	Tsevie	0	0	1
Pet food (raw)	Typhimurium DT1	0	1	0
Pet food (raw)	Typhimurium DT2	2	3	5
Pet food (raw)	Typhimurium DT3	0	1	0
Pet food (raw)	Typhimurium DT8	0	0	2
Pet food (raw)	Typhimurium DT9	0	0	3
Pet food (raw)	Typhimurium DT41b	1	0	0
Pet food (raw)	Typhimurium DT75	0	0	3
Pet food (raw)	Typhimurium DT99	0	0	1
Pet food (raw)	Typhimurium DT104	0	0	3
Pet food (raw)	Typhimurium DT105	5	3	5
Pet food (raw)	Typhimurium DT116	0	1	0
Pet food (raw)	Typhimurium DT120	0	0	2
Pet food (raw)	Typhimurium DT193	4	2	2
Pet food (raw)	Typhimurium DT194	1	0	0
Pet food (raw)	Typhimurium U208	1	1	0
Pet food (raw)	Typhimurium U281	0	1	0
Pet food (raw)	Typhimurium U288	1	0	0
Pet food (raw)	Typhimurium U302	0	1	0
Pet food (raw)	Typhimurium U308	0	3	
Pet food (raw)	Typhimurium U311	0	0	3
Pet food (raw)	Typhimurium NOPT	1	3	2
Pet food (raw)	Typhimurium RDNC	6	7	7
Pet food (raw)	Typhimurium UNTY	0	1	0

Feedingstuff	***Salmonella* serovar**	**Isolations 2020**	**Isolations 2021**	**Isolations 2022**
Pet food (raw)	Uganda	1	0	0
Pet food (raw)	Virchow	0	0	3
Pet food (raw)	Westhampton	0	1	0
Pet food (raw)	Wilhelmsberg	0	0	1
Pet food (raw)	3,10:e,h:-	1	0	0
Pet food (raw)	3,10:lv:-	11	0	0
Pet food (raw)	3,10:z_{10}:-	0	0	1
Pet food (raw)	4,5,12:i:- DT104	0	0	1
Pet food (raw)	4,5,12:i:- DT120	0	0	1
Pet food (raw)	4,5,12:i:- DT193	7	10	12
Pet food (raw)	4,5,12:i:- U208	0	0	1
Pet food (raw)	4,5,12:i:- U311	0	1	1
Pet food (raw)	4,5,12:i:- UNTY	0	0	3
Pet food (raw)	4,5,12:i:- NOPT	1	0	0
Pet food (raw)	4,5,12:-1,2 DT1	0	1	0
Pet food (raw)	4,5,12:-:- DT193	1	0	0
Pet food (raw)	4,5,12:-:- NOPT	1	0	0
Pet food (raw)	4,12:i:- DT104	0	0	1
Pet food (raw)	4,12:i:- DT120	0	1	0
Pet food (raw)	4,12:i:- DT193	10	4	17
Pet food (raw)	4,12:i:- NOPT	0	3	0
Pet food (raw)	4,12:i:- RDNC	0	1	0
Pet food (raw)	4,12:i:- UNTY	0	0	3
Pet food (raw)	4,12,[27]:b:e,n,x	0	1	0
Pet food (raw)	4,12:rough	0	0	1
Pet food (raw)	4,12:z:-	0	0	2
Pet food (raw)	6,7:e,h:-	1	0	0
Pet food (raw)	6,7:-:enz$_{15}$	0	0	4
Pet food (raw)	6,7:-:-	0	1	5
Pet food (raw)	6,8:e,h:-	7	0	3
Pet food (raw)	9,12:l,v:-	0	1	0
Pet food (raw)	9,12:-:-	1	0	0
Pet food (raw)	13,23:i:-	2	2	0
Pet food (raw)	38:l,v,z_{13}:-	0	0	1
Pet food (raw)	38:r:z	0	1	0
Pet food (raw)	61:k:1,5	7	0	0
Pet food (raw)	61:-:1,5	17	12	0
Pet food (raw)	61:-:1,5,7	6	4	16
Pet food (raw)	61:k:1,5,7	0	0	8
Rendering plant material	Bredeney	2	0	0
Rendering plant material	Enteritidis PT3a	0	1	0
Rendering plant material	Mbandaka	0	1	0
Rendering plant material	O rough:g,p:-	0	1	0
Rendering plant material	Soerenga	0	1	0
Rendering plant material	Typhimurium DT104	0	1	0

Feedingstuff	*Salmonella* serovar	Isolations 2020	Isolations 2021	Isolations 2022
Rendering plant material	Typhimurium DT193	0	1	0
Rendering plant material	4,5,12:i:- DT193	1	0	0
Rendering plant material	4,12:i:- DT193	1	2	0
Rendering plant material	6,7:-:enz$_{15}$	0	1	0
Rendering plant material	61:-1,5	0	2	0
Rendering plant material	61:-:1,5,7	1	0	0
Unspecified	Bredeney	1	0	0
Unspecified	Enteritidis NOPT	0	1	0
Unspecified	Schwarzengrund	1	0	0
Unspecified	Tennessee	1	1	0
Unspecified	Typhimurium RDNC	0	1	0
Unspecified	3,10:-:-	0	1	0
Unspecified	4,12:i:- NOPT	0	2	0
Total	Not applicable	**461**	**502**	**577**

Table 12.9: Animal By-Products (Enforcement) Regulations 2013, domestic protein official testing and contamination rates in Great Britain 2020 to 2022

Sample Type	2020 Batches	2020 number +ve	2020 % +ve	2021 Batches	2021 number +ve	2021 % +ve	2022 Batches	2022 number +ve	2022 % +ve
Blood meal	3	0	0.0	4	1	25.0	0	0	0.0
Bone meal	0	0	0.0	0	0	0.0	0	0	0.0
Feather meal	4	0	0.0	1	0	0.0	1	0	0.0
Greaves	3	0	0.0	3	0	0.0	1	0	0.0
Meat and bone meal	6	1	16.7	10	0	0.0	3	0	0.0
Meat meal	1	0	0.0	0	0	0.0	0	0	0.0
Poultry offal meal	3	0	0.0	1	0	0.0	0	0	0.0
White fish meal	9	0	0.0	7	0	0.0	14	0	0.0
Other fish meal	2	0	0.0	0	0	0.0	1	0	0.0
Others	371	2	0.5	358	8	2.23	281	2	0.71
Total	**402**	**3**	**0.8**	**384**	**9**	**2.34**	**301**	**2**	**0.66**

This table excludes the results of private testing.

Table 12.10: Animal By-Products (Enforcement) Regulations, 2013. Serovars isolated during 2020 to 2022 from official and private testing of domestic protein and other products associated with the regulations in Great Britain

Serovar	Isolations 2020	Isolations 2021	Isolations 2022
Agona	0	1	0
Bovismorbificans	1	0	0
Cerro	1	0	0
Derby	0	0	1
Durban	0	1	0
Indiana	0	1	0
Isangi	1	0	0
Kedougou	0	1	0
Kottbus	0	1	0
Livingstone	0	1	0
Tennessee	0	0	1
Typhimurium DT2	0	1	0
Typhimurium NOPT	0	1	0
Untypable	0	1	0
Total	**3**	**9**	**2**

The total number of batches positive was the same as the total number of isolations positive in 2020, 2021 and 2022.

Figure 12.7: Contamination rate for domestic processed animal protein (batches tested) in Great Britain 2013 to 2022

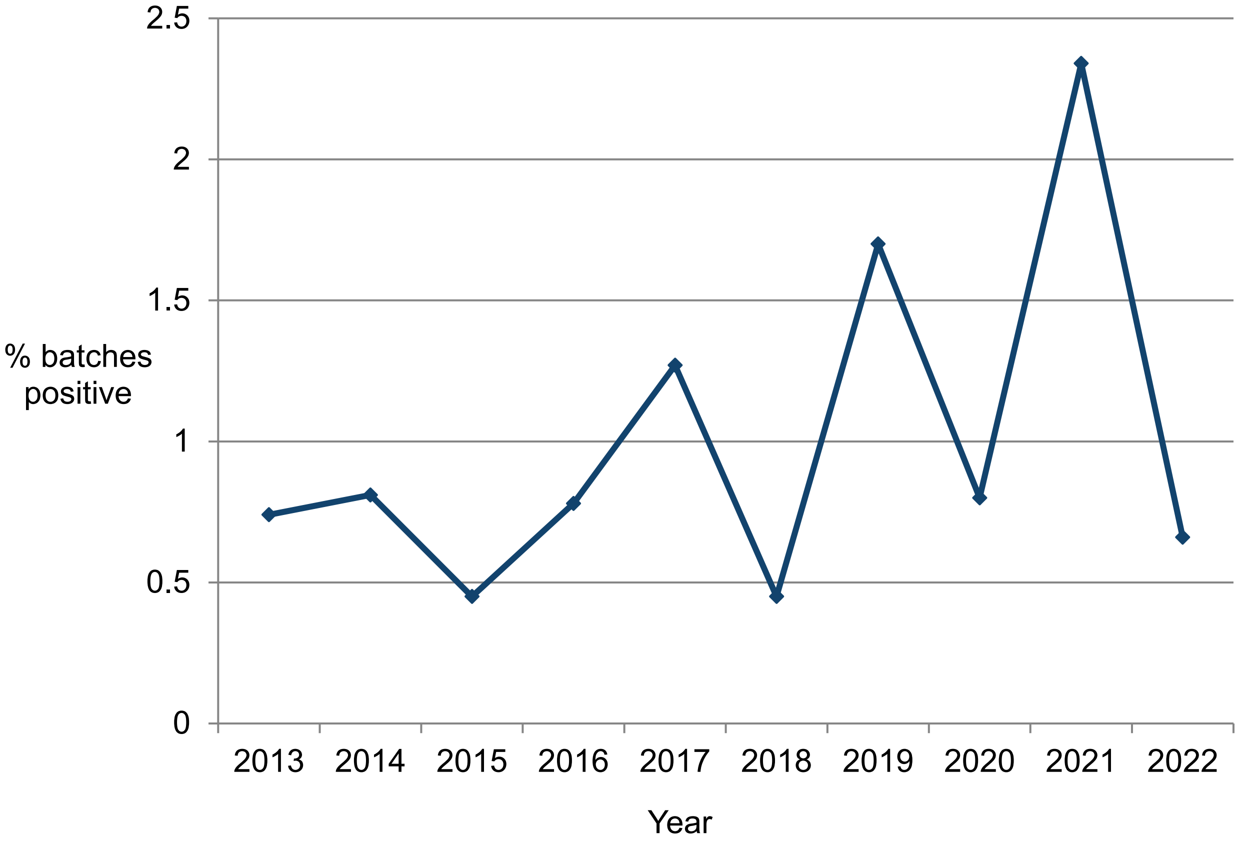


Figure 12.7 shows the proportion of positive batches for domestic processed animal protein had fluctuated year on year with an overall increase in positivity. 2021 saw the highest proportion of contaminated batches (2.34%) but fell in 2022 to 0.66% of batches which is lower than 2013 with 0.75% of batches.

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	13
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	19

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 333 cultures of *Salmonella* Dublin underwent antimicrobial sensitivity testing in 2022. As in previous years most *S.* Dublin isolates (250, 75.0%) originated from cattle. *Salmonella* Dublin isolates from species other than cattle in 2022, comprised 56 isolates from dogs, 7 isolates from sheep, 4 from chickens, 2 from horses, 2 from pheasants, one from a ferret, one from an alpaca, 9 from animal feed and one from an unspecified source. Of the 250 *Salmonella* Dublin cultures from cattle tested during 2022, 96.4% were susceptible to all 16 antimicrobials (Table 13.2). 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, an increase in the proportion of resistant isolates was observed and this increased level was maintained in 2021. In 2022, a return to susceptible levels pre-2020 was observed. The majority of isolates remain susceptible, which has been consistent since surveillance began in 1971.

Salmonella Typhimurium

The number of isolates of *S.* Typhimurium tested in 2022 was 494. The most frequent definitive or undefined phage types subjected to susceptibility testing at APHA are given in Table 13.3. A total of 11.7% of *S.* Typhimurium isolates were phage type DT104 or U302 (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 2022 is given in Figure 13.1.

The percentage of *S.* Typhimurium cultures that were sensitive to all of the antimicrobials tested was 47.8% (Table 13.4), which is a decrease from the 2019 (49.2%), and 2018 figures (54.4%), but higher than the figures reported in 2020 (39.9%) and 2021 (44.3%).

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 isolates in some years in the previous decade. In 2022, no DT104b or U302 *Salmonella* Typhimurium strains were isolated. Of the 58 DT104 strains tested in 2022, 8 were from cats and 30 from dogs, with only 8 originating from cattle and one from sheep, 2 from primates, 6 from feed, one from a pig and 2 from horses.

Only 11 of the 58 DT104 isolates tested in 2022 were sensitive to all of the antimicrobials. 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 but was at a lower level in 2022 (11.7%) (Table 13.4). The typical pentavalent resistance pattern

AmCSSuT was commonly seen in *S.* Typhimurium DT104, occurring in 43.1% (25 of 58) of isolates.

The pentavalent resistance pattern above, with the addition of Nalidixic acid resistance was also common (22.4%,13 of 58). Thirteen of the 58 DT104 isolates were resistant to nalidixic acid and 3 to sulphamethoxazole and trimethoprim combination. Nalidixic acid resistance in *S.* Typhimurium DT104 by species of origin is listed in Table 13.4 for the main food-producing animal species over the last 11 years.

Salmonella Typhimurium U288 and DT193 from pigs accounted for 1.0% (5) and 5.7% (28) of the total numbers of *S.* Typhimurium isolates respectively. None of the U288 or DT193 isolates from pigs were fully susceptible in 2022.

Considering all definitive types of *S.* Typhimurium, resistance to sulphamethoxazole and trimethoprim combination has fluctuated markedly in recent years (Table 13.5). The prevalence of resistance to sulphamethoxazole and trimethoprim combination was 22.9% in 2022. It has been predominantly isolates from pigs that have accounted for these fluctuations in sulphamethoxazole and trimethoprim combination resistance (Table 13.6). A high proportion of many definitive types of *S.* Typhimurium isolated from pigs are resistant to sulphamethoxazole and trimethoprim combination.

The definitive and undefined phage types of *S.* Typhimurium resistant to sulphamethoxazole and trimethoprim combination and recovered from pigs in 2022 included contributions primarily from isolates of 2 phage types DT193 and U288. The total numbers of isolates of these types and the percentage resistant to sulphamethoxazole and trimethoprim combination are shown in Table 13.7. AmCSSuTTm was a common resistance pattern observed in both DT193 isolates (10 isolates) and U288 isolates (3 isolates) from pigs.

Apramycin resistance in *S.* Typhimurium in 2022 was 4.4%, a notable increase compared to the preceding 9 years where it has been consistently less than 2.5%. However, this is still considerably lower than in 2012 when 20.4% of isolates were resistant to apramycin (Table 13.4).

No *S.* Typhimurium isolates in 2022 were resistant to cefotaxime and ceftazidime, and 22 isolates were resistant to nalidixic acid (mostly from feed (8 isolations) and dogs (11 isolations)).

Multiple antibiotic resistance (resistance to 4 or more antimicrobial agents in the panel of 16) was detected in definitive and undefined phage types DT104 (from cats, cattle, dogs, horses, feed, a pig, primates and a sheep), DT105 (dogs and pigs), DT118 (pig), DT120 (dogs, pigs and feed), DT181 (pig), DT193 (pigs, dogs, feed), DT194 (dog), DT32 (pigs, horse), DT4 (pigs), DT52 (pig), DT75 (cattle), U288 (pigs), U308 (pigs), U308a (pigs), U311 (dog and feed) and from isolates which did not react to phages (dogs, pigs, feed). Of the 33 different definitive and undefined phage types detected, 8 (namely 1, 106, 189, 42, 5, 9, U208, U289), several of which are mainly associated with wildlife, were susceptible to all of the antimicrobials in the test panel.

Monophasic *Salmonella* Typhimurium serovars

One hundred and sixteen isolates of *Salmonella* 4,12:i:- were tested, belonging to definitive phage types DT104 (x2), DT193 (x99), DT120 (x3), U311 (x1), 9 isolates that were not typable and 2 isolates for which a PT could not be determined. Most isolates were from feed, especially raw meat pet food (43.1%) with pigs (26.7%) and dogs (21.6%) being the next most common sources of origin. The most common pattern of resistance observed was AmSSuT, which occurred in 42/99 of DT193 isolates. Considering the DT193 isolates, 75 of 99 (75.7%) had the AmSSuT resistance pattern alone or with one or more additional resistances. Two isolates from pigs were resistant to Amikacin, in addition to 9 other antimicrobials in the panel tested against.

A total of 139 isolates of *Salmonella* 4,5,12:i:- were tested, including phage types DT104 (x3), DT105 (x1), DT120 (x3), DT193 (x112), DT208 (x1), DT35 (x1), DT311 (x9), 7 isolates that were untypable and 2 isolates for which no PT could be determined. The most common resistance pattern in DT193 isolates was AmSSuT, occurring in 45.3% of isolates (63 of 139). Most isolates of *Salmonella* 4,5,12:i:- DT193 were from feed (25.2%), dogs (20.9%) and pigs (14.4%).

Considering the aminoglycosides other than streptomycin, apramycin resistance was detected in 25.8% and neomycin resistance in 58.1% of *Salmonella* 4,12:i:- from pigs (n=31). Resistance to neomycin and apramycin was observed in 14.0% and 8.0%, respectively, of *Salmonella* 4,12:i:- isolates from feed, especially raw meat pet food, or feed constituents (n=50). Apramycin resistance was detected in 56.5% and neomycin resistance in 56.5% of *Salmonella* 4,5,12:i:- from pigs (n=23).

Resistance to apramycin was also observed in 2.3% of *Salmonella* 4,5,12:i:- isolates from feed or feed constituents, and resistance to neomycin was present in 62.3% of these isolates (n=44). Resistance to the aminoglycosides apramycin and neomycin was therefore detected in monophasic *S.* Typhimurium isolates from pigs, feed and raw meat pet food in 2022.

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

Of the 4,735 isolates of serovars other than *S.* Dublin and *S.* Typhimurium tested, 77.2% were sensitive to all the antimicrobials in the test panel (Table 13.8), an increase on the figure recorded in 2021, when 68.5% were fully sensitive. Sixty-three isolates (1.3% of the total) were *S.* Enteritidis of which 87.3% (55 of 63) were fully susceptible. Eight isolates were resistant to nalidixic acid: 5 PT21 from feed, one PT3 from a dog and 2 PT6b from chickens.

Neomycin resistant *Salmonella* isolates originated mainly from chickens (2,016 isolates tested, 1.9% resistant), pigs (137 isolates tested, 27.8% resistant), feed and pet food or feed constituents (1,156 tested, 1.5% resistant), and dogs (731 isolates tested, 1.6% resistant). In ducks, *S*. Give var. 15^{+} (Newbrunswick) and *S.* Indiana were the main serovars showing resistance to neomycin (1 of 108 isolates resistant for both serovars). *S.* Indiana isolates from ducks were also frequently resistant to furazolidone (1 of 108 isolates resistant) and this was similar to the situation observed in 2021.

Considering *Salmonella* isolates other than Typhimurium and Dublin from turkeys in 2022 (n=126), 35.7% were resistant to streptomycin, 26.2% to sulphonamides and 26.2% to tetracyclines. This is lower than the equivalent figures for pigs in 2022 (respectively 42.3%, 51.8% and 51.1%), but higher than those for chickens (respectively 7.5%, 9.3% and 5.5%) or cattle (4.5%, 1.8% and 1.8 % respectively). In 2022, the proportion of *Salmonella* isolates originating from feed or related samples (24.4%) was similar to 2021 (27.7%) and the proportion of fully susceptible isolates remained similar (69.6% in 2022 compared to 67.9% in 2021).

Individual antimicrobials

Of the 5,562 *Salmonella* isolates tested in 2022, 4,210 (75.7%) were sensitive to all of the antimicrobials tested (Table 13.9). This is similar to the situation in 2021 when 4,507 isolates were tested and 3,051 (67.7%) were sensitive to all of the antimicrobials tested.

Tetracycline resistance was most commonly found in *Salmonella* isolates originating from pigs and turkeys in 2022. This was also the situation for resistance to sulphonamides and streptomycin. Findings were similar in 2021.

Resistance to apramycin in all *Salmonella* serovars was 1.4% in 2022, similar to the level observed in 2021 (2.1%). *Salmonella* isolates from pigs, for which resistance was 19.8% in 2022, contributed most to the overall apramycin resistance figure. In pigs, apramycin resistance was observed in both monophasic *S.* Typhimurium variants 4,12:i:- and 4,5,12:i:- and in 2022, 25.8% of *Salmonella* 4,12:i:- isolates (n=31) and 56.5% of *Salmonella* 4,5,12:i:- isolates (n=23) from pigs were resistant to apramycin.

Overall, 1.7% of all *Salmonella* isolates were resistant to gentamicin. Resistance was detected to the aminoglycoside amikacin in 2 of 50 (4.0%) *Salmonella* 4,12:i:- isolates from feed, 2 of 31 (6.5%) *Salmonella* 4,12:i:- isolates from pigs and 1 of 125 (0.8%) *S*. Typhimurium isolates from pigs. All 4 of the *Salmonella* 4,12:i:- isolates were DT193 and were also resistant to tetracycline, neomycin, ampicillin, sulphamethoxazole and trimethoprim combination, chloramphenicol, amikacin, gentamycin, streptomycin, sulphonamides and apramycin. The *S*. Typhimurium isolate from a pig was also DT193 and also resistant to tetracycline, neomycin, ampicillin, sulphamethoxazole and trimethoprim combination, chloramphenicol, amikacin, gentamycin and sulphonamides.

The highest prevalence of resistance to nalidixic acid in 2022 was observed in *Salmonella* isolates from other non-avian species, feed (especially raw meat pet food), turkeys and dogs. In turkeys, 20 of 21 *S.* Senftenberg isolates, 1 of 21 *S*. Kedougou and 7 of 7 *Salmonella* 3,19:rough:- isolates were resistant to nalidixic acid in 2022. The situation in turkeys was similar in 2013 to 2021, with nalidixic acid resistance frequently detected in this serovar. In chickens, resistance to nalidixic acid was found in *Salmonella* 13,23:i:-, *S*. Agona, *S*. Bardo, *S.* Infantis, *S.* Enteritidis, *S*. Kedougou, *S*. Montevideo, and *S.* Senftenberg.

Ciprofloxacin resistant isolates detected in 2022 originated from cattle (*S*. Dublin (1 of 250 resistant)), chickens (*S*. 13,23:i:- (1 of 249 resistant), *S*. Agona (2 of 117 resistant), *S*. Bardo (1 of 4 resistant), *S*. Idikan (2 of 35 resistant), *S*. Infantis (2 of 103 resistant)), dogs (*S*. 4, 12:i:- (1 of 25 resistant), *S*. Infantis (2 of 115 resistant), *S*. Kentucky (5 of 9 resistant), *S*. Newport (2 of 54 resistant), *S*. O Rough:i:1,2 (1 of 3 resistant)), turkeys (*S*. 3,19:rough:- (1 of 7 resistant)) and feed and related samples (*S*. 4,12:i:- (2 of 50 resistant), *S*. Derby (1 of 78 resistant), *S*. Infantis (5 of 109 resistant), *S*. Typhimurium (1 of 69 resistant)).

Resistance to cefotaxime and ceftazidime was detected in 9 isolates in 2022, 3 *S*. Infantis and one *S*. Minnesota from chickens, one *S*. Bredeney and 2 *S*. Kentucky from dogs, one *S*. Infantis from feed (cefotaxime only) and one *S*. Senftenberg from feed (ceftazidime only). Apart from the *S*. Senftenberg from feed, all other strains were resistant to between 2 and 10 other antibiotics in addition to cefotaxime and ceftazidime.

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 2022 was 0.6%. Cefotaxime, ceftazidime or ciprofloxacin resistance was not detected in *S.* Enteritidis or *S*. Typhimurium from animals in 2022.

Two *S*. Kentucky isolated from dogs were highly ciprofloxacin resistant. This highly ciprofloxacin resistant *S*. Kentucky clone is established in the poultry industry in many countries worldwide but is not established in the UK poultry industry.

Cefotaxime and ceftazidime resistance was detected in 9 *Salmonella* isolates in 2022. Eight of these strains were multi-drug resistant (MDR: resistant to at least 4 antimicrobials in the panel). One isolate of *S*. Kentucky from a dog, and one isolate of *S*. Infantis from feed (raw pet food) were resistant to ciprofloxacin in addition to third generation cephalosporins.

Four *S.* Infantis isolates were MDR and resistant to cefotaxime, with 2 also resistant to ceftazidime. Three isolates originated from chickens and one from raw pet food. Two of the chicken isolates are similar to a *S*. Infantis clone that is circulating in continental Europe where in certain countries it is particularly well established in broilers. Advice and support were provided to the contaminated UK farm to achieve the elimination of this infection.

In 2022, 5 *Salmonella* isolates (2 *Salmonella* 4,12:i:- DT103 from feed, 2 *Salmonella* 4,12:i:- DT193 from pigs and one *S*. Typhimurium DT193 from a pig) were resistant to amikacin. Aminoglycoside resistance is of public health relevance, and amikacin resistance is rarely found in samples originating from livestock.

Susceptibility in *S.* Dublin isolates in cattle was 96.4% in 2022. This represents an increase of susceptibility for this serovar compared to 2020 and 2021 (88.9% in 2020 and 88.3% in 2021). This was mostly due to a decrease in *S.* Dublin resistant to neomycin and, or chloramphenicol and tetracycline.

Generally, several MDR strains, some including resistance to critically important antimicrobials, were detected in dogs, cats and raw pet food in 2022. 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 spill over 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 2013 to 2022

The table below shows the percentage of *S.* Dublin isolates from cattle resistant to each of the antimicrobials from 2013 to 2022. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
AM	0.3%	0.7%	1.7%	0.4%	0.0%	0.0%	0.0%	1.2%	1.1%	0.0%
C	0.0%	0.0%	0.4%	0.4%	0.0%	0.3%	0.4%	2.3%	1.1%	0.4%
NA	1.0%	0.0%	2.2%	1.2%	0.0%	2.2%	0.0%	1.6%	0.7%	0.0%
S	1.3%	2.4%	0.4%	1.6%	0.0%	0.3%	0.4%	0.8%	0.7%	3.2%
APR	0.0%	0.0%	0.0%	0.0%	0.0%	0%	0.0%	0.0%	0.0%	0.0%
CN	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
N	0.3%	0.3%	2.2%	0.0%	0.0%	0.3%	0.0%	5.1%	2.6%	0.0%
FR	0.0%	0.3%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.3%	0.0%
SU	0.0%	0.7%	0.0%	0.0%	0.0%	0.3%	0.4%	0.8%	0.4%	0.8%
TM	0.0%	0.7%	0.0%	0.0%	0.0%	0.0%	0.7%	0.8%	0.4%	0.4%
T	0.0%	1.1%	0.4%	0.4%	0.0%	0.3%	0.4%	3.9%	6.0%	0.0%
Susceptible to all 16 antimicrobials	96.9%	96.5%	94.2%	96.3%	100.0%	96.2%	99.6%	88.9%	88.3%	96.4%
Total isolates tested	393	286	226	245	272	320	269	256	267	250

Table 13.3: Number of isolates of *S*. Typhimurium of the most frequent phage types subjected to susceptibility testing at APHA 2013 to 2022

Phage type	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
UNTY	0	0	0	0	0	43	19	0	3	0
RDNC	0	0	0	0	0	201	24	53	88	70
U310	0	18	0	0	0	0	0	0	0	0
U308	0	7	0	0	0	0	0	5	51	0
U308a	0	0	0	0	0	0	0	0	0	25
U302	22	13	27	13	9	39	18	0	6	0
U288	22	28	24	30	26	40	27	58	48	0
DT193	30	21	19	13	19	34	38	65	69	60
DT120	16	0	0	0	0	0	0	0	2	0
DT116	0	0	0	0	0	0	0	22	16	0
DT104	21	19	12	40	59	47	45	52	60	58
DT99	0	0	0	0	7	0	0	0	1	22
DT73	0	0	0	0	0	0	14	0	0	0
DT41	6	0	0	0	4	0	0	0	1	0
DT40	0	13	7	0	5	0	0	0	0	0
DT12	0	0	0	5	2	28	0	0	0	0
DT9	0	17	0	0	0	0	0	5	3	0
DT8	5	0	7	5	2	0	0	0	7	0
DT4	0	0	0	0	0	0	0	5	0	0
DT2	8	17	25	24	19	13	13	39	42	41
DT1	1	9	9	8	4	0	0	0	15	0
DT105	0	0	0	0	0	0	0	0	0	51
DT75	0	0	0	0	0	0	0	0	0	42
DT32	0	0	0	0	0	0	0	0	0	19

Table 13.4: *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2013 to 2022

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	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
AM	57.6%	43.3%	46.7%	60.2%	58.3%	30.1%	46.1%	50.0%	43.0%	39.7%
C	35.2%	36.6%	46.0%	57.8%	53.5%	29.9%	44.1%	45.2%	37.0%	32.4%
NA	4.8%	0.9%	1.2%	0.0%	1.6%	0.4%	0.0%	3.0%	8.8%	4.4%
S	54.5%	39.7%	51.5%	63.9%	57.1%	40.7%	40.2%	49.7%	34.3%	37.2%
APR	1.8%	0.9%	0.0%	2.4%	0.0%	1.8%	0.8%	0.9%	1.5%	4.4%
N	0.6%	0.0%	2.4%	0.6%	0.0%	1.8%	0.8%	7.8%	9.9%	7.3%
FR	0.0%	0.0%	0.0%	0.6%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
SU	60.6%	43.8%	48.5%	66.3%	62.6%	44.0%	46.1%	58.4%	47.1%	43.9%
TM	44.8%	35.7%	32.1%	28.9%	19.8%	15.7%	24.0%	33.7%	25.3%	22.9%
T	61.2%	49.1%	46.7%	61.4%	54.5%	36.3%	42.1%	50.6%	39.0%	36.4%
Susceptible to all 16 antimicrobials	30.3%	44.2%	41.8%	30.1%	34.2%	54.4%	49.2%	39.9%	44.3%	47.8%
Total isolates tested	165	224	165	166	187	504	254	340	467	494

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

- 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)

Table 13.5: Nalidixic acid resistance in *Salmonella* Typhimurium DT104 from domestic livestock in 2012 to 2022.

The following table outlines the number of isolates tested in different species of livestock between 2012 and 2022 and the percentages of these that were resistant to nalidixic acid.

Year	Cattle	Sheep	Pigs	Chickens	Turkeys	Ducks
2012	6 (0.0%)	2 (0.0%)	5 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
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%)

Table 13.6: Sulphamethoxazole and trimethoprim combination resistance in *Salmonella* Typhimurium (all phage types) from domestic livestock in 2012 to 2022.

The following table outlines the number of *S.* Typhimurium isolates tested in different species of livestock between 2012 and 2022 and the percentages of these that were resistant to sulphamethoxazole and trimethoprim combination.

Year	Cattle	Sheep	Pigs	Chickens	Turkeys	Ducks
2012	15 (6.7%)	5 (0.0%)	99 (72.7%)	9 (22.2%)	0 (0.0%)	4 (0.0%)
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%)

Table 13.7: Trends in sulphamethoxazole and trimethoprim combination resistance in certain types of *Salmonella* Typhimurium from pigs over the period 2012 to 2022.

The following table outlines the number *S.* Typhimurium DT193, DT208 and U288 isolates tested in different species of livestock between 2012 and 2022 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
2012	24 (62.5%)	0 (0.0%)	34 (94.1%)
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%)

Figure 13.1: Percentage of the 8 most common definitive and undefined phage types of *Salmonella* Typhimurium susceptible to all 16 antimicrobial agents in 2022

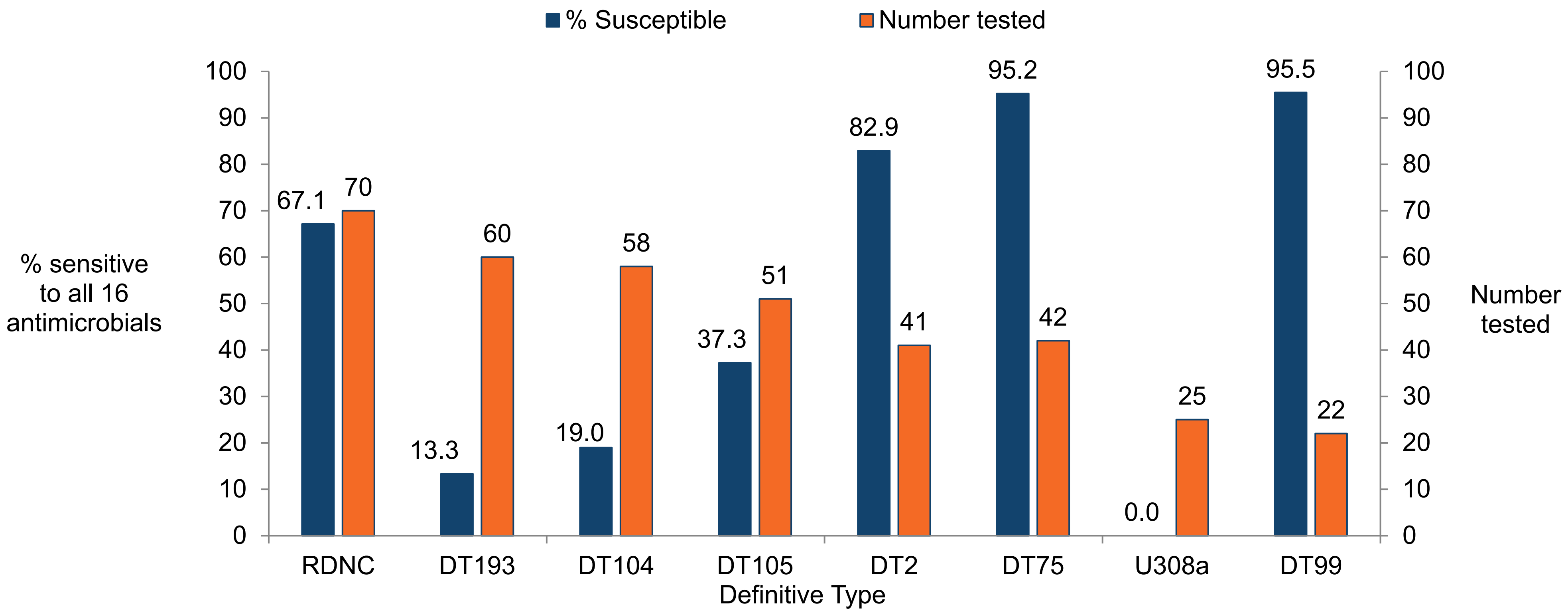


Figure 13.1 shows that the highest rates of isolates sensitive to all 16 antimicrobials were in found in DT99 (95.5%), DT75 (95.2%) and DT2 (82.9%). No isolates of U308a were fully susceptible.

Table 13.8: *Salmonella* other than *Salmonella* Dublin and *Salmonella* Typhimurium: antimicrobial susceptibility monitoring 2013 to 2022

The following table outlines the number *Salmonella* isolates other than *S.* Dublin and *S.* Typhimurium tested between 2013 and 2022 and the percentages of these that were resistant to the antimicrobials tested against. For a key to the antimicrobials used see table 13.1.

Antimicrobial	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
AM	12.3%	12.7%	13.3%	11.1%	10.3%	7.7%	7.4%	10.3%	11.2%	9.8%
C	1.7%	1.8%	2.4%	2.6%	2.0%	1.5%	2.1%	2.4%	2.6%	1.9%
NA	5.7%	4.0%	5.5%	2.6%%	5.8%	1.4%	2.7%	3.3%	5.5%	3.9%
S	19.2%	18.8%	22.6%	16.0%	13.1%	11.7%	15.0%	11.4%	13.4%	10.2%
APR	1.4%	1.6%	2.9%	2.0%	1.6%	0.8%	1.3%	1.2%	2.4%	1.2%
N	3.4%	2.0%	3.2%	2.2%	2.0%	1.8%	2.6%	3.0%	5.2%	2.3%
FR	3.1%	2.1%	1.9%	1.4%	1.6%	1.2%	1.6%	1.0%	2.0%	0.8%
SU	26.5%	20.9%	26.4%	23.7%	19.0%	15.7%	20.2%	19.8%	16.2%	13.3%
TM	12.2%	7.5%	10.4%	10.4%	6.2%	5.3%	10.2%	11.7%	6.4%	6.7%
TM	28.0%	20.0%	25.5%	22.9%	19.6%	14.9%	20.2%	19.3%	18.5%	11.8%
Percentage susceptible to all 16 antimicrobials	61.2%	68.2%	60.2%	68.9%	71.2%	77.7%	71.9%	69.5%	68.5%	77.2%
No of isolates	2,328	1,837	2,198	1,986	5,652	3,589	4,010	3,617	3,665	4,735

Table 13.9: All *Salmonella*: antimicrobial susceptibility 2022 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	3.7%	3.4%	69.5%	3.1%	30.7%	7.4%	10.2%	11.9%
AMC	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%
CAZ	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%	0.1%	0.1%
CTX	0.0%	0.0%	0.0%	0.2%	0.0%	0.0%	0.1%	0.1%
C	2.3%	3.4%	55.3%	0.8%	0.0%	0.0%	5.7%	4.5%
NA	0.2%	1.1%	0.0%	0.9%	22.0%	0.0%	1.6%	3.8%
CIP	0.2%	0.0%	0.0%	0.4%	0.8%	0.0%	0.3%	0.6%
S	11.1%	3.4%	50.0%	7.4%	34.5%	0.9%	12.5	12.2%
APR	0.0%	1.1%	19.8%	0.3%	0.0%	0.0%	1.9%	1.4%
CN	0.0%	1.1%	20.6%	0.5%	1.6%	0.0%	2.2%	1.7%
N	0.0%	1.1%	27.9%	1.9%	0.8%	1.9%	3.8%	2.6%
FR	0.0%	0.0%	0.0%	0.4%	0.0%	0.9%	0.3%	0.7%
SU	9.3%	3.4%	66.8%	9.2%	26.0%	6.5%	14.6%	15.3%
TM	0.2%	2.3%	56.1%	6.7%	3.1%	0.9%	9.6%	7.8%
T	8.8%	3.4%	55.0%	5.4%	26.0%	8.3%	11.0%	13.3%

Percentage susceptible to all 16 antimicrobials	86.8%	95.4%	27.9%	83.2%	22.8%	88.0%	77%	75.7%
No of isolates	431	87	262	2,040	127	108	3,055	5,562

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	2.9%	14.4%	8.4%	0.0%	15.5%	9.2%	11.4%	11.9%
AMC	0.0%	0.4%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%
CAZ	0.0%	0.3%	0.0%	0.0%	0.1%	0.0%	0.1%	0.1%
CTX	0.0%	0.3%	0.0%	0.0%	0.1%	0.0%	0.1%	0.1%
C	2.9%	4.3%	4.7%	0.0%	2.0%	3.1%	2.6%	4.5%
NA	0.0%	4.4%	4.7%	0.0%	9.1%	0.0%	5.3%	3.8%
CIP	0.0%	1.4%	0.0%	0.0%	0.8%	0.0%	0.8%	0.6%
S	11.4%	13.7%	12.6%	21.7%	10.4%	7.7%	9.7%	12.2%
APR	0.0%	0.9%	0.5%	0.0%	0.7%	4.6%	0.7%	1.4%
CN	0.0%	1.2%	0.5%	0.0%	0.7%	4.6%	0.8%	1.7%
N	0.0%	1.4%	0.0%	0.0%	1.4%	0.0%	1.0%	2.6%
FR	0.0%	1.2%	0.0%	0.0%	1.5%	0.0%	0.9%	0.7%
SU	11.4%	14.7%	8.4%	0.0%	18.5%	27.7%	13.3%	15.3%
TM	1.4%	3.9%	1.0%	0.0%	7.1%	21.5%	4.6%	7.8%
T	15.7%	15.1%	9.4%	0.0%	17.7%	21.5%	13.1%	13.3%
Percentage susceptible to all 16 antimicrobials	84.3%	78.2%	82.2%	78.3%	69.3%	70.8%	74.1%	75.7%
No of isolates	70	924	191	23	1234	65	2507	5562

Other non-avian species included ferret, fish, fox, wallaby, wildcat, zebra, alpaca, cat, snake, tortoise, porpoise, primate, rabbit, rat, reptile, amphibian, other, other carnivore, other mammal, otter, frog, goat, hedgehog, lion, lizard, mongoose, and mouse. Other avian species included owl, pheasant, pigeon, and unspecified avian.

In 2022, 5 *Salmonella* isolates (2 isolates of 4,12:i:- DT103 from feed, 2 isolates of 4,12:i:- DT193 from pigs and one *S*. Typhimurium DT193 from a pig) were resistant to amikacin.

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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 a range of specialist scientific services and products to the Government and other interested parties worldwide the provision of administrative services and control of technical services supporting regulation and enforcement of EU plant and seed directives' (certificate number LRQ 4001392). 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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Quality

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Source

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Title

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Additional report metadata elements and definitions

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Salmonella reports made in Great Britain

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Data collected under:

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Rights. copyright

Crown copyright

Subject. Category

Zoonoses, Animal Health

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Surveillance of *Salmonella* in animals (FZ2000)

Monitoring of Antimicrobial Resistance in Bacteria from Animals and their Environment (OM0190)

Microbiological monitoring of Animal By Products, laboratory inspection scheme and Quality Assurance sample supply (ABPR and IPAPO) (FZ2000)

Status

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(Francesca.Martelli@apha.gov.uk)

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Type

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 and Penrith
- 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.