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SCIENTIFIC REPORT

The European Union One Health 2024 Zoonoses Report

European Food Safety Authority (EFSA) | European Centre for Disease Prevention and Control (ECDC)

Correspondence: Ask a Question

Abstract

This report by the European Food Safety Authority and the European Centre for Disease Prevention and Control presents the results of zoonoses monitoring and surveillance activities carried out in 2024 in 27 Member States (MSs), the United Kingdom (Northern Ireland) and eight non-MSs, according to the Zoonoses Directive 2003/99/EC. Key statistics on zoonoses and zoonotic agents in humans, food, animals and feed are provided and interpreted historically. In 2024, the first and second most reported zoonoses in humans were campylobacteriosis and salmonellosis, respectively, followed by Shiga toxin-producing *Escherichia coli* (STEC) infections. Listeriosis was the fourth and most severe zoonotic disease, with the highest percentage of hospitalisations and the highest case fatality rate. The number of cases reported in the last 5 years showed a significant increasing trend in campylobacteriosis, salmonellosis, listeriosis and STEC infections. Fourteen MSs and the United Kingdom (Northern Ireland) met all targets for reducing *Salmonella* prevalence in poultry populations for the relevant serovars. *Salmonella* samples from various animal carcases, and samples for *Campylobacter* quantification in broiler carcases, were more frequently positive when carried out by the competent authorities than with food business operators' own checks. Twenty-seven MSs and the United Kingdom (Northern Ireland) reported more food-borne outbreaks, cases and hospitalisations in 2024 than in 2023, although the number of deaths decreased. *Salmonella* in 'eggs and egg products' was the agent/food pair of most concern. *Salmonella* was also the causative agent associated with the majority of multi-country outbreaks reported in the EU in 2024. Foods of non-animal origin, and in particular 'vegetables and other products thereof', caused the largest number of deaths in strong-evidence outbreaks. This report also provides updates on brucellosis, echinococcosis, trichinellosis, tuberculosis due to *Mycobacterium bovis,* rabies as well as other zoonotic bacteria, viruses and parasites in food and animals.

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INTRODUCTION

Legal basis for European Union-coordinated zoonoses monitoring

The European Union (EU) system for the monitoring and collection of information on zoonoses is based on Zoonoses Directive 2003/99/EC,[1] which obliges EU Member States (MSs) to collect relevant and, when applicable, comparable data on zoonoses, zoonotic agents, antimicrobial resistance and food-borne outbreaks (FBOs). In addition, MSs shall assess the trends and sources of these agents, as well as outbreaks in their territory, submitting an annual report each year by the end of May. The European Food Safety Authority (EFSA) is assigned the tasks of examining these data and publishing the EU Annual Summary Reports. In 2004, the European Commission entrusted EFSA with setting up an electronic reporting system and database for monitoring zoonoses (EFSA Mandate No 2004-0178, prolonged by M-2015-0231[2]).

Data collection on human diseases from MSs is conducted in accordance with Regulation (EU) 2022/2371[3] on serious cross-border threats to health. This Regulation, adopted in November 2022, repealed Decision No 1082/2013/EU and established a strengthened legal framework for health crisis preparedness, surveillance and response coordination at the EU level. The case definitions to be followed when reporting data on infectious diseases to the European Centre for Disease Prevention and Control (ECDC) are described in Commission Implementing Decision (EU) 2018/945[4] which specifies the diseases under surveillance and the criteria for case classification. ECDC has provided data on zoonotic infections in humans and their analysis for the EU Summary Reports since 2005. Since 2008, data on human cases have been submitted via The European Surveillance System (TESSy), which has now been integrated into EpiPulse Cases, the updated surveillance platform maintained by ECDC.

Reporting requirements

In accordance with List A, Annex I of Zoonoses Directive 2003/99/EC, data on animals, food and feed must be reported for the following eight zoonotic agents: *Salmonella*, *Campylobacter*, *Listeria monocytogenes*, Shiga toxin-producing *Escherichia coli* (STEC), *Mycobacterium bovis*,[5] *Brucella*, *Trichinella* and *Echinococcus*. In addition, and based on the epidemiological situation in each MS, data must be reported on the following agents and zoonoses (List B, Annex I of the Zoonoses Directive): (i) viral zoonoses: calicivirus, hepatitis A virus, influenza virus, rabies, viruses transmitted by arthropods; (ii) bacterial zoonoses: borreliosis and agents thereof, botulism and agents thereof, leptospirosis and agents thereof, psittacosis and agents thereof, tuberculosis due to agents other than *M. bovis*, vibriosis and agents thereof, yersiniosis and agents thereof; (iii) parasitic zoonoses: anisakiasis and agents thereof, cryptosporidiosis and agents thereof, cysticercosis and agents thereof, toxoplasmosis and agents thereof; and (iv) other zoonoses and zoonotic agents such as *Francisella* and *Sarcocystis*. Furthermore, MSs provide data on certain other microbiological contaminants in foods: histamine, staphylococcal enterotoxins and *Cronobacter sakazakii*, for which food safety criteria are set down in the EU legislation.

In accordance with Article 9 of the same Directive, MSs shall assess the trends and sources of zoonoses, zoonotic agents and antimicrobial resistance in their territories, and each MS shall send to the European Commission, every year by the end of May, a report on the trends in, and sources of, zoonoses, zoonotic agents and antimicrobial resistance. Reports, and any summaries of them, shall be made publicly available.

Terms of Reference

In accordance with Article 9 of Directive 2003/99/EC, EFSA shall examine the national reports and data submitted by the EU MSs regarding their zoonoses monitoring activities, as described above, and publish an annual EU Summary Report on the trends and sources of zoonoses, zoonotic agents and antimicrobial resistance in the EU.

Data sources and report production

The 2024 European Union One Health Zoonoses (EUOHZ) report was drafted and co-authored by EFSA and ECDC. In 2025, EFSA received support for production of the 2024 EUOHZ report by the ZOE (**Z**oonoses under a **O**ne health perspective in the **E**U) Consortium. The Consortium was composed of the French Agency for Food, Environmental and Occupational

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[1] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40.

[2] See mandate M-2015-0231 in Open EFSA Questions: https://open.efsa.europa.eu/questions/EFSA-Q-2020-00787.

[3] Regulation (EU) 2022/2371 of the European Parliament and of the Council of 23 November 2022 on serious cross-border threats to health and repealing Decision No 1082/2013/EU. OJ L 314, 6.12.2022, p. 26–63.

[4] Commission Implementing Decision 2018/945/EU on the communicable diseases and related special health issues to be covered by epidemiological surveillance as well as relevant case definitions. OJ L 170, 6.7.2018, p. 1–74.

[5] All cases of tuberculosis in cattle caused by the infectious *Mycobacterium tuberculosis* complex (MTBC) members (*M. bovis*, *M. caprae* or *M. tuberculosis*) were taken into account to summarise the EU situation on bovine tuberculosis.

Health & Safety (ANSES) (Maisons-Alfort, France), the *Istituto Superiore di Sanità* (Rome, Italy), the *Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise* (Teramo, Italy) and the *Istituto Zooprofilattico Sperimentale delle Venezie* (Padua, Italy), under the coordination of ANSES. The ZOE Consortium provided support for the scientific validation of the 2024 data reported to EFSA, data analysis and the evaluation of findings on animals, food and feed from a One-Health perspective.

This report focused on the most relevant information on zoonoses, food-borne outbreaks and food microbiological safety criteria for the EU in 2024. Where substantial differences with regard to the previous years were observed, they were highlighted.

On 1 February 2020, the United Kingdom withdrew from the EU and became a third country.[6] Data collection earlier than 2020 was therefore affected, since the number of EU MSs went from 28 to 27. In descriptive tables, the 2020 statistical data from the United Kingdom, when available for EFSA data, were assigned to the non-MS group. Starting in 2020, human data from the United Kingdom were not collected by ECDC. With regard to trend analyses for human data, only countries having contributed data for all the years of a considered period were taken into account. For trend analyses of the estimated prevalence at EU level of *Salmonella* in poultry populations covered by national control programmes, all data provided by the reporting MSs were taken into account. The United Kingdom data were only included when available for 2019 and earlier.

Since 2021, the only United Kingdom data reported to EFSA have been from Northern Ireland. **In accordance with the agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community, and in particular Article 5(4) of the Windsor Framework (see Joint Declaration No 1/2023 of the Union and the United Kingdom in the Joint Committee established by the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community of 24 March 2023**, OJ L 102, 17.4.2023, p. 87**) in conjunction with Section 24 of Annex 2 to that Framework, for the purposes of this Regulation, references to Member States include the United Kingdom in respect of Northern Ireland**. Therefore, for the purpose of this report, the European Union requirements on data sampling were also applicable to Northern Ireland (XI[7]) and data transmitted by the United Kingdom (Northern Ireland) have been assigned to the MSs group.

Regulation (EU) 2017/625[8] (known as the Official Controls Regulation (OCR)) specifies that the competent authorities (CAs) must only use methods complying with relevant internationally recognised rules or protocols (e.g. those accepted by the European Committee for Standardization (CEN)) for food testing. On 12 September 2024, however, the European Commission released Commission Implementing Regulation (EU) 2024/2463[9] laying down the analytical methods applicable to official controls performed for the verification of compliance of food business operators with Commission Regulation (EC) No 2073/2005.[10] This regulation states that 'the competent authorities may authorise designated official laboratories to use alternative analytical methods, including proprietary methods, provided these alternative analytical methods are validated against the analytical reference methods referred to in Annex I to Commission Regulation (EC) No 2073/2005 in accordance with the protocol set out in standard EN ISO 16140-2 and are validated either for the food category specified in the relevant microbiological criterion set in Annex I to Commission Regulation (EC) No 2073/2005 or for a broad range of foods as referred to in Standard EN ISO 16140-2'. Being released at the end of 2024, the implementation of Commission Implementing Regulation (EU) 2024/2463 shall not affect the comparison of the official food control samples taken in the context of Commission Regulation (EC) No 2073/2005 results with those of 2022 and 2023. Differences may still be present when the comparison is made with 2021 and earlier data and, for this reason, comparisons with previous years should be made with caution. Additionally, discrepancies between the current EUOHZ report and previously published reports may arise due to ongoing data updates made by countries over time.

Human data collection for 2024

In the 2024 EUOHZ report, the analysis of data from human diseases was prepared by the Food and Waterborne Diseases and Zoonoses (FWD) domain (brucellosis, campylobacteriosis, echinococcosis, listeriosis, salmonellosis, Shiga toxin-producing *Escherichia coli* (STEC) infection and trichinellosis) and the tuberculosis (TB) domain (infection with *Mycobacterium tuberculosis* complex, focusing on *M. bovis* and *M. caprae*) at ECDC. EpiPulse Cases (formerly TESSy) is a software platform in which data on communicable diseases and special health issues are collected. Both aggregated and case-based data are reported to EpiPulse cases by the MSs and other European countries. Although aggregated data did not include individual

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[6] Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community. OJ L 29, 31.1.2020, p. 7 ('withdrawal agreement').

[7] For the collection of data, EFSA has aligned itself with the guidelines of the European Commission concerning customs registration that lays down abbreviations and terminology, and which are available at https://taxation-customs.ec.europa.eu/system/files/2020-11/use_of_gb_and_xi_codes_guidance.pdf.

[8] Regulation (EU) 2017/625 of the European Parliament and of the Council of 15 March 2017 on official controls and other official activities performed to ensure the application of food and feed law, rules on animal health and welfare, plant health and plant protection products, amending Regulations (EC) No 999/2001, (EC) No 396/2005, (EC) No 1069/2009, (EC) No 1107/2009, (EU) No 1151/2012, (EU) No 652/2014, (EU) 2016/429 and (EU) 2016/2031 of the European Parliament and of the Council, Council Regulations (EC) No 1/2005 and (EC) No 1099/2009 and Council Directives 98/58/EC, 1999/74/EC, 2007/43/EC, 2008/119/EC and 2008/120/EC, and repealing Regulations (EC) No 854/2004 and (EC) No 882/2004 of the European Parliament and of the Council, Council Directives 89/608/EEC, 89/662/EEC, 90/425/EEC, 91/496/EEC, 96/23/EC, 96/93/EC and 97/78/EC and Council Decision 92/438/EEC (Official Controls Regulation). OJ L 095 7.4.2017, p. 1.

[9] Commission Implementing Regulation (EU) 2024/2463 of 12 September 2024 laying down analytical methods applicable to official controls performed for the verification of compliance of food business operators with Regulation (EC) No 2073/2005. OJ L, 13.9.2024, p. 1–2.

[10] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

case-based information, both reporting formats were included, when possible, to calculate the number of cases and country-specific case notification rates. **The human data used in this report were extracted from EpiPulse Cases as of 7 August 2025 for FWD and as of 3 October 2025 for TB due to *M. bovis* and *M. caprae***. The denominators used for calculating notification rates were based on the human population data from Eurostat on 1 January 2025.

The reporting of data to EpiPulse Cases is underpinned by specific standard definitions applicable to both the cases and surveillance systems in place in the MSs and in other European countries,[11] which are also used to summarise the data in this report. When interpreting statistics, data quality issues should be considered, as well as the differences between MS surveillance systems; comparisons between countries should therefore be undertaken with caution.

Data on human cases were received from the 27 MSs and from three non-MSs (Iceland, Liechtenstein and Norway). Switzerland reported its data on human cases directly to EFSA. In 2021, Liechtenstein resumed the reporting of human data independently for the first time since 2008; prior to this, they reported these data together with Switzerland.

Information provided in the EUOHZ 2024 report can be accessed via the interactive ECDC Surveillance Atlas of Infectious Diseases, although minor discrepancies may exist due to possible differences in the EpiPulse Cases data set at the time of data extraction and aggregation.

Data collection on food, animals, feed and food-borne outbreaks for 2024

For the year 2024, the 27 MSs and the United Kingdom (Northern Ireland) submitted data and national zoonoses reports on monitoring results in food, animals, feed and food-borne outbreaks. In addition, data and reports were submitted by four non-MSs which are also the four European Free Trade Association (EFTA) countries: Iceland, Norway, Switzerland and Liechtenstein.[12] For some food, animal and feed matrices, and for FBOs, EFSA received data and reports from the following pre-accession countries: Albania, Bosnia and Herzegovina, Montenegro, the Republic of North Macedonia and Serbia.

Data were submitted electronically to the EFSA zoonoses database through EFSA's Data Collection Framework (DCF). MSs were also able to update their data from previous years.

The deadline for data submission was 31 May 2025. Two data validation procedures were carried out, from 3 June to 13 June 2025 and from 1 July to 10 July 2025, respectively.

The final validated data on food, animals, feed and food-borne outbreaks used in the report were extracted from the EFSA zoonoses database on 22 July 2025.

A detailed description of the terms used in the report is available in EFSA's manuals for reporting on zoonoses (EFSA, 2025a, 2025b).

The national zoonoses reports submitted in accordance with Directive 2003/99/EC were published on the EFSA website together with the EU One Health Zoonoses Report. They are available online here.

To provide an overview of all the information reported by the MSs for the production of the EUOHZ 2024 report, EFSA created interactive story maps and dashboards for various food-borne outbreaks and zoonoses, providing detailed epidemiological data, monitoring activities and dynamic visualisations (link here). Moreover, for each zoonotic agent, additional information on related projects and internet sources were published for this report on the EFSA Knowledge Junction at Zenodo here.

Under the One Health surveillance grant agreements linked to EU4H-2022-DGA-MS-IBA3, 23 countries carried out surveillance activities for several pathogens, including West Nile Virus (WNV), *Coxiella burnetii* and *Echinococcus granulosus s.l.* This initiative of the EU4Health programme 2024 (CP-g-22-04.01) was co-funded by European Commission and aimed to reinforce coordinated surveillance systems for cross-border zoonotic pathogens in animals and the environment that pose a threat to public health across the EU. The 2024 animal and environmental data on WNV, *C. burnetii* and *E. granulosus* collected under the abovementioned grant agreements were aggregated by EFSA at the same level as the zoonoses data, for inclusion in the corresponding chapters of this report. Specifically, the 2024 One Health surveillance data were summarised in the report and discussed where notable decreases were observed in the 2024 zoonoses data for these pathogens as compared to 2023.

Finalisation of the EUOHZ 2024 report

The draft EUOHZ 2024 report was sent to the MSs for consultation on 3 October 2025 and comments were collected by 22 October 2025. The utmost effort was made to incorporate comments within the available time frame. In general, **data amended after the data correction deadline of 18 July 2025 were not considered in the summary calculations or other analyses**, and footnotes to tables and figures were added to account for these late data corrections. The report was finalised on 7 November 2025 and published online by EFSA and ECDC on 9 December 2025.

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[11] Current definitions are reported in Section 'Key definitions'.

[12] Based on the customs union treaty of the Principality of Liechtenstein with Switzerland, Liechtenstein is part of the Swiss customs territory. Due to the strong connection between the veterinary authorities of Liechtenstein and Switzerland, and Liechtenstein's integration into the Swiss system in the veterinary field, in principal, all legislation, rules and data on contagious diseases are identical for both Switzerland and Liechtenstein. If not mentioned otherwise, the Swiss data also include the data from Liechtenstein.

Data analysis and presentation

Data comparability and quality

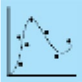
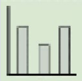
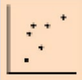
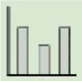
Humans

For data on human infections, please note that the numbers presented in this report may differ from those found in the national zoonoses reports due to differences in the case definitions used at the EU and national levels or because of differing dates of data submission and extraction. The latter may also result in some divergence between the case numbers and notification rates presented in the different ECDC reports and those in the reports produced in previous years. Results are not directly comparable among MSs or between different years. Data collection on human cases of food-borne diseases reported to ECDC through EpiPulse Cases and to EFSA through the European Union Food-borne Reporting System (EU-FORS, see chapter on Food-borne Outbreaks, section 2) is separate and independent. Comparability between the two systems is limited by the different contexts and purposes of case reporting and also by the adoption of different case definitions.

Food, animals, feed and food-borne outbreaks

The comparability of data obtained by the EFSA DCF can vary depending on data quality and harmonisation levels. The types of data analysis carried out for each zoonosis and matrix (food, animals, feed or food-borne outbreaks) strongly depended on this level of harmonisation and may be a descriptive summary of submitted data, trend watching (the monitoring of trends) or the quantitative analysis of trends. Data analyses were carried out in accordance with the quality criteria described in Table 1 as adapted from Boelaert et al. (2016). Food, animals, feed and food-borne outbreak data can be classified into three categories depending on the zoonotic agent monitored and the way the monitoring or surveillance was carried out. It follows that the type of data analyses that can be implemented is conditioned by these three distinct categories.

TABLE 1 Categorisation of the data used in the EU One Health Zoonoses 2024 Summary Report (adapted from Boelaert et al. (2016)).

Category	Type of analysis		Type/comparability between MSs	Examples
I	Descriptive summaries at the national and EU level EU trend watching (trend monitoring) Spatial and temporal trend analyses at the EU level	  	Programmed harmonised monitoring or surveillance Comparable between MSs Results are interpretable at the EU level	National *Salmonella* control programmes in poultry; tuberculosis caused by *M. bovis* or *M. caprae*; *Brucella abortus*, *B. melitensis* and *B. suis* in bovine, caprine and ovine animal populations; *Trichinella* in domestic pigs, farmed wild boar and solipeds at the slaughterhouse
II	Descriptive summaries at the national and EU level EU trend watching (trend monitoring) **No** EU trend analysis	 	Monitoring or surveillance not fully harmonised Not fully comparable between MSs Caution needed when interpreting results at the EU level	Food-borne outbreak data, official control samples related to process hygiene criteria for carcases at the slaughterhouse for *Salmonella* and *Campylobacter*, and to food safety criteria for *L. monocytogenes*, *Salmonella* and STEC in the context of Commission Regulation (EC) No 2073/2005, passive rabies surveillance, West Nile virus
III	Descriptive summaries at the national and EU level **No** EU trend watching (trend monitoring) **No** EU trend analysis		Non-harmonised monitoring or surveillance data with no (harmonised) reporting requirements Not comparable between MSs; extreme caution needed when interpreting results at the EU level	*Yersinia*, *Coxiella burnetii* (Q fever), *Francisella tularensis* (tularemia), *Tenia* spp., *Toxoplasma* and other zoonoses

Rationale of the table of contents

The following table of contents has been adopted for the 2024 EUOHZ report and takes account of the zoonoses listed in Annex I of Directive 2003/99/EC, of the mandatory reporting of food-borne outbreaks and of the above-mentioned categorisation of food, animal and feed data (Table 1).

A. Zoonoses and zoonotic agents included in compulsory annual monitoring (Directive 2003/99/EC[1] List A)

1. *Campylobacter*
2. *Salmonella*
3. *Listeria*
4. Shiga toxin-producing *Escherichia coli*
5. *Mycobacterium tuberculosis* complex, focussing on *M. bovis*[13]
6. *Brucella*
7. *Trichinella*
8. *Echinococcus*

B. Food-borne and water-borne outbreaks (in accordance with Directive 2003/99/EC)

C. Zoonoses and zoonotic agents monitored according to the epidemiological situation (Directive 2003/99/EC List B)

1. Rabies
2. Other bacterial zoonoses and zoonotic agents
3. Other viral zoonoses and zoonotic agents
4. Other parasitic zoonoses and zoonotic agents

D. Microbiological contaminants subject to food safety criteria (Commission Regulation (EC) No 2073/2005).

Chapter sections

The 2024 EUOHZ Report presents a harmonised structure for each chapter in 'Zoonoses and zoonotic agents included in compulsory annual monitoring' and 'Rabies' comprised of the following:

- 'Key facts'.
- 'Monitoring and surveillance' in the EU for each specific disease.
- 'Results', summarising the major findings of 2024 as regards trends and sources, starting with a table displaying summary statistics over the last 5 years (2020–2024) for human cases, food matrices and major animal species, followed by specific sections describing the main results in humans, food and/or animals.
- 'Discussion' section.

For food-borne outbreaks, the main findings are presented and discussed in a joint 'Results and discussion' section and key messages are summarised in the 'Conclusions' section.

For all zoonoses in the 'Other zoonoses' chapters, no structured format was used. A narrative text summarises the main results for the countries providing data. The main findings are described using key aggregate statistics in a succinct bullet point format. Concise observations and a critical review of the 2024 results and the historical trends are included.

When relevant for each chapter, overview tables present the data reported by each country. However, unless stated otherwise, the tables summarising MS-specific results and providing EU-level results for food, animals and feed exclude data from industry own-check programmes, hazard analysis and critical control point (HACCP) sampling, as well as data from suspect sampling, selective sampling and outbreak or clinical investigations. Moreover, regional data reported by countries for food, animals and feed, without statistics at the national level, were also excluded from these tables. For 'Zoonoses and zoonotic agents monitored according to the epidemiological situation (Directive 2003/99/EC List B)' and food-borne outbreaks, summary tables and figures can be found on the EFSA Knowledge Junction at Zenodo here.

Data analyses

Statistical trend analyses for humans were carried out to evaluate the significance of temporal variations in the EU over the 2020–2024 period. Further details can be found in the individual chapters. All countries that consistently reported cases with monthly information – or reported zero cases over the whole reporting period – were included. To visualise long-term trends in human case incidence across the European Union and its individual Member States from January 2014 to December 2024, we calculated the monthly case counts together with a moving average smoothing using the 'tssmoth ma' command in the Stata statistical software tool. Specifically, we calculated a 12-month moving average (the five previous months, the current month and the six subsequent months), providing clearer identification of underlying patterns by reducing short-term fluctuations. The p-value for a linear trend between 2020 and 2024 was calculated and the trend was considered significant if $p < 0.05$.

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[13] All cases of tuberculosis in cattle caused by the infectious MTBC members (*M. bovis*, *M. caprae* or *M. tuberculosis*) were taken into account to summarise the EU situation on bovine tuberculosis.

The notification rates were calculated considering the coverage of the human population under surveillance (percentage of national coverage). For countries where surveillance did not cover the whole population, the estimated coverage – if provided – was used to calculate the country-specific rate. Cases and populations of those countries not providing information on national coverage or reporting incomplete data were excluded from the EU notification rate.

ESRI ArcMap 10.8.2 was used to map the data. Choropleth maps with graduated colours over five class scales of values using the natural breaks function proposed by ArcGIS software were produced to map the proportion of positive sample units across the EU and other reporting countries. In the maps included in this report, EU MSs and the United Kingdom (Northern Ireland) were represented with a blue label, the EFTA/EEA countries were represented with a grey label, and all the candidate countries were represented with an orange label.

Statistical trend analysis of food-borne outbreaks was performed to evaluate the significance of temporal variations at the single MS level over the 2015–2024 period.

All country-specific data on food, animals, feed and food-borne outbreaks, summary data and the figures for food, animals, feed and food-borne outbreaks used to produce this report, as well as additional information on related projects and internet sources, are published at the EFSA Knowledge Junction in the Zenodo general-purpose open-access repository here.

Summary of human zoonoses data for 2024

The numbers of confirmed human cases of the zoonoses presented in this report are summarised in Table 2. In 2024, campylobacteriosis was confirmed as the most commonly reported zoonosis (as it has been since 2005). It accounted for 63.7% of all the reported and confirmed human cases of all diseases in 2024. Following campylobacteriosis, the next most frequently reported zoonoses were salmonellosis, STEC infections and listeriosis.

With regard to human cases involved in FBOs, *Salmonella* and norovirus and other caliciviruses accounted for the highest number of outbreaks and cases, respectively (Tables 2 and 52).

Severity of zoonoses in the EU

The severity of zoonotic diseases was descriptively analysed based on the number and proportion (%) of hospitalisations and the outcomes of reported cases, i.e. the number of deaths and the case fatality rate (%). Information for all zoonoses is shown in Table 2. According to the data submitted to ECDC by the MSs, listeriosis was the most severe disease in 2024, showing the highest case fatality and hospitalisation rates among reported cases. Nearly all listeriosis cases (97.3%) required hospitalisation. As in previous years, listeriosis accounted for the highest number of deaths ($N = 301$), followed by salmonellosis ($N = 116$) and campylobacteriosis ($N = 76$).

Among FBOs, *Salmonella* was the agent associated with the largest number of hospitalisations and *Salmonella* and *Listeria monocytogenes* with the largest number of deaths. Overall, the highest case fatality rates among outbreak cases were observed in outbreaks caused by *L. monocytogenes* (8.1%) (Table 2) followed by '*Clostridium botulinum* toxins' (4.3%) (statistics not displayed in Table 2 but available in Table 52).

TABLE 2 Reported hospitalisations and deaths due to zoonoses in confirmed human cases and food-borne outbreak cases in the EU, 2024.

	Surveillance data on human cases (source: ECDC)											Food-borne outbreaks (source: EFSA)					
		Hospitalisations					Deaths										
	Confirmed human cases	Status available		Reporting MSs[a]	Cases and proportion of hospitalised cases		Outcome available		Reporting MSs[a]	Deaths and case fatality rates		Outbreaks	Cases	Hospitalisations and proportion of hospitalised cases		Deaths and case fatality rates	
Disease	***N***	***N***	**%**	***N***	***N***	**%**	***N***	**%**	***N***	***N***	**%**	***N***	***N***	***N***	**%**	***N***	**%**
Campylobacteriosis	168,396	64,488	38.3	16	15,262	23.7	103,090	61.2	16	76	0.07	314	1420	101	7.1	0	–
Salmonellosis	79,703	37,567	47.1	16	16,337	43.5	47,870	60.1	18	116	0.24	1238	10,164	1823	18.3	17	0.17
STEC infections	11,738	3956	33.7	19	1411	35.7	8147	69.4	22	25	0.31	31	158	19	12.2	0	–
Listeriosis	3041	1762	57.9	17	1715	97.3	1929	63.4	19	301	15.6	38	210	149	72.3	17	8.1
Echinococcosis	984	425	43.2	14	193	45.4	604	61.4	16	3	0.50	0	0	0	–	0	–
Brucellosis	273	132	48.4	12	82	62.1	176	64.5	13	2	1.1	0	0	0	–	0	–
Tuberculosis caused by *M. bovis, M. caprae*	171	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0	0	–	0	–
Trichinellosis	102	50	49.0	7	19	38.0	52	51.0	8	0	–	6	67	35	52.2	0	–
Rabies	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Abbreviations: –, % not calculated; NA, not applicable, as information is not collected for this disease.

[a] Not all countries provided data for all diseases.

SECTION A – ZOONOSES AND ZOONOTIC AGENTS INCLUDED IN COMPULSORY ANNUAL MONITORING (DIRECTIVE 2003/99/EC LIST A)

A1 | *CAMPYLOBACTER*

Human cases [EU, 2024]

Notification rate *(per 100,000 population)* **55.3**

Trend *(2020-2024)* ⬆

⬆ *Increasing*
⬇ *Decreasing*
— *Stable*

168,396 **Cases of illness**

73,627 **Infections acquired in the EU**

15,262 **Hospitalisations** (23.7%)*

2538 **Infections acquired outside the EU**

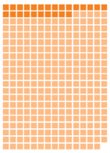
76 **Deaths** (0.07%)*

92,231 **Unknown travel status or unknown country of infection**

* *The percentages are calculated on the number of cases with information available (for further details see Table 2)*

🟩 *ECDC data*

Foodborne outbreaks & related cases [EU, 2024]



314 **Foodborne outbreaks**

25 **Strong-evidence outbreaks** 🟧

289 **Weak-evidence outbreaks** ▨

1420 **Cases of illness**

101 **Hospitalisations** (7.1%)*

* *The percentages are calculated on the number of cases with information available (for further details see Table 2)*

	N of outbreaks		N of outbreaks per 100,000 population **		N of outbreak cases per 100,000 population
Austria	7	AT	0.076	AT	0.175
Belgium	5	BE	0.042	BE	0.372
Bulgaria	0	BG	0	BG	0
Croatia	2	HR	0.052	HR	0.181
Cyprus	0	CY	0	CY	0
Czechia	0	CZ	0	CZ	0
Denmark	10	DK	0.168	DK	1.124
Estonia	0	EE	0	EE	0
Finland	2	FI	0.036	FI	1.802
France	70	FR	0.102	FR	0.764
Germany	69	DE	0.083	DE	0.198
Greece	6	EL	0.058	EL	0.154
Hungary	1	HU	0.010	HU	0.031
Ireland	0	IE	0	IE	0
Italy	16	IT	0.027	IT	0.112
Latvia	0	LV	0	LV	0
Lithuania	0	LT	0	LT	0
Luxembourg	0	LU	0	LU	0
Malta	35	MT	6.212	MT	14.376
Netherlands	1	NL	0.006	NL	0.011
Poland	2	PL	0.005	PL	0.011
Portugal	0	PT	0	PT	0
Romania	0	RO	0	RO	0
Slovakia	51	SK	0.940	SK	2.341
Slovenia	2	SI	0.094	SI	1.977
Spain	33	ES	0.068	ES	0.313
Sweden	2	SE	0.019	SE	0.038
UK (N. Ireland)	0	XI	0	XI	0

Implicated food vehicles
(Strong-evidence outbreaks)

Top food vehicles

Broiler meat (*Gallus gallus*) and products thereof
10 Outbreaks

Milk
4 Outbreaks

Mixed food
3 Outbreaks

Cheese
2 Outbreaks

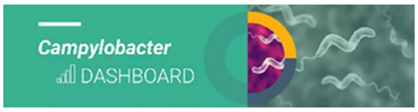
Pig meat and products thereof
Meat and meat products, unspecified
Vegetables and juices and other products thereof
Water
Eggs and egg products
Other or mixed red meat and products thereof
1 Outbreak (each)

** *Differences among countries shall be interpreted with caution as this indicator depends on several factors including the type of outbreaks under surveillance and does not necessarily reflect the level of food safety in each country.*

🟧 *EFSA data*

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about *Campylobacter* and for the consultation of data collected, the following interactive tools are available:



A1.1 | Key facts

- Campylobacteriosis was the most commonly reported food-borne gastrointestinal infection in humans in the European Union.
- In 2024, there were 168,396 confirmed cases of human campylobacteriosis, corresponding to a European Union notification rate of 55.3 cases per 100,000 population. This was an increase of 11.9% compared with the notification rate in 2023 (49.4 per 100,000 population).
- The overall trend for *Campylobacter* human infections showed a statistically significant increase over the 2020–2024 period.
- Twenty-six Member States and the United Kingdom (Northern Ireland) reported data for 2024 in the context of the *Campylobacter* process hygiene criterion, set out in Commission Regulation (EC) No 2073/2005. Seventeen Member States reported 15,431 test results from official controls, with 24.3% *Campylobacter*-positive samples exceeding the limit of 1000 CFU/g. Twenty Member States and the United Kingdom (Northern Ireland) reported 67,042 test results from the monitoring of food business operators, with 16.4% *Campylobacter*-positive samples exceeding the limit of 1000 CFU/g. Eleven Member States reported results from both samplers, showing that the number of samples exceeding the limit was significantly higher in official samples (26.0%) than in own-checks (14.7%).
- In 2024, 0.36% of 2517 ready-to-eat (RTE) food sampling units reported by 10 Member States were positive for *Campylobacter*, with positive samples originating from oysters (*N* = 3), pre-cut vegetables (*N* = 3) and three meat-based dishes (*N* = 3). Of 23,195 sampling units from non-RTE food categories reported by 17 Member States, 17.7% were positive, with the highest level of contamination (18.5%) found in 'meat and meat products', followed by 'fish and fishery products – non-RTE' (10.1%). *Campylobacter* was isolated from all fresh meat categories, with meat from broilers and turkeys showing the highest percentages of contamination, 22.8% and 26.0%, respectively.
- Data on *Campylobacter* spp. in different animal categories were reported by 15 Member States and the United Kingdom (Northern Ireland) and four non-Member States in 2024. The majority of units tested in the European Union were from broilers (*N* = 9303), cattle (bovine animals) (*N* = 4297) and small ruminants (*N* = 2337), with positive rates of 20.9%, 4.3% and 3.3%, respectively. Fewer samples were tested for turkeys (*N* = 1232) and pigs (*N* = 221), but higher proportions of positives were observed, at 70.5% and 57.5%, respectively.

A1.2 | Surveillance and monitoring of *Campylobacter* in the EU

A1.2.1 | Humans

In 2024, 26 EU MSs reported information on campylobacteriosis in humans. Surveillance of campylobacteriosis is mandatory in 22 EU MSs. In four MSs (Belgium, France, Italy and the Netherlands), notification is based on a voluntary system. The EU case definition was used by 22 MSs. Three MSs used a different case definition for reporting (France, Germany and Italy), and the Netherlands did not specify which case definition it used. All MSs, except three (Belgium, Italy and the Netherlands), had a comprehensive surveillance system.

The campylobacteriosis surveillance systems cover the whole population of all MSs except four (France, Italy, the Netherlands and Spain). The estimated coverage of the surveillance system was 20% in France, 64% in the Netherlands and 82% in Spain. These estimated proportions of population coverage were used in the calculation of notification rates for these three MSs. No estimated population coverage was provided for 2020 in Spain, so notification rates were not calculated. No estimate of population coverage in Italy was provided for any year, so no notification rate was calculated for this MS. All countries reported case-based data, except Belgium and Bulgaria, which reported aggregated data.

A1.2.2 | Food and animals

Campylobacter is monitored along the food chain during primary production (farm animals), harvest/slaughter, manufacturing and distribution.

Campylobacter **data in the context of Commission Regulation (EC) No 2073/2005**

A regulatory limit (microbiological process hygiene criterion (PHC)) of 1000 CFU/g of *Campylobacter* on the neck skins of chilled broiler carcases was set by Commission Regulation (EC) No 2073/2005[14] (Annex I, Chapter 2, point 2.1.9). This limit applies to a set of 50 pooled samples from 10 consecutive sampling sessions. As of 2020, a maximum number of 15 samples with values exceeding this limit is considered acceptable. Food business operators (FBOps) failing to comply with this limit are required to carry out corrective actions involving validation and verification of their food safety management procedures based on Hazard Analysis and Critical Control Point (HACCP) principles and good manufacturing practices (GMP). The PHC has been in force since 1 January 2018. On 14 December 2019, Commission Implementing Regulation (EU) 2019/627[15] came into force, harmonising sampling procedures for official controls. This legislation requires the Competent Authority (CA) to verify whether the FBOp is correctly implementing and checking the PHC on broiler carcases by choosing one of two approaches: implementing ad hoc official sampling[16] or collecting all the information from the samples taken by the FBOp. The results obtained in official controls enable improved trend watching and trend analyses (Table 1).

Other monitoring data for food and animals

Campylobacter monitoring data from food and animals submitted to EFSA in compliance with Chapter II 'Monitoring of zoonoses and zoonotic agents' of Directive 2003/99/EC[17] are collected without a harmonised procedure. These data allow descriptive summaries at the EU level, but they do not support EU-level trend analyses and trend watching and should be interpreted with caution (Table 1). In 2024, general data on food and animals reported to EFSA by MSs and non-MSs were obtained mainly from official sampling, industry HACCP sampling and own-checks, as part of national monitoring and surveillance and/or organised surveys. In addition, for animal data, other reported samples were obtained from clinical investigations by private veterinarians and industry (e.g. artificial insemination centres). The occurrence of *Campylobacter* reported in the main food categories for the year 2024 and for the 4-year period of 2020–2023 was descriptively summarised, making a distinction between RTE and non-RTE foods. Data sets were extracted using the 'objective sampling' strategy, meaning that the reporting MSs collected the samples as part of a planned strategy based on the selection of random samples that are statistically representative of the population to be analysed.

In 2024, other *Campylobacter* monitoring data from livestock primary production were obtained from broilers and fattening turkeys. These additional data were collected through antimicrobial resistance (AMR) monitoring, following the harmonised sampling scheme and protocol for isolation set out in Commission Implementing Decision (EU) 2020/1729[18] and focused on the species *Campylobacter jejuni* and *C. coli*. The results of AMR monitoring are published separately in an EU Summary Report.

The detection and confirmation of *Campylobacter* in food and animals are generally based on culture, with the use of international standards or equivalent validated methods. Species identification is carried out using biochemical and molecular methods (PCR-based), as well as matrix-assisted laser desorption/ionisation time-of flight mass spectrometry (MALDI–TOF MS).

A1.3 | Data analyses

A comparison of the proportions of *Campylobacter*-positive samples collected from the neck skins of broiler carcases after chilling that exceeded 1000 CFU/g was carried out, as obtained by the CAs and FBOps as part of the *Campylobacter* PHC, in compliance with Commission Regulation (EC) No 2073/2005. The significance of any differences was verified by a one-tailed Fisher's exact probability test in cases where the expected values of any of the cells in a contingency table were below 5; otherwise, the one-tailed z-test was used. The official control sampling results by the CA and the own-check results by the FBOps were expressed as prevalence ratios with an exact binomial confidence interval of 95%. A p-value of < 0.10 (Clayton

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[14] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

[15] Commission Implementing Regulation (EU) 2019/627 of 15 March 2019, laying down uniform practical arrangements for the performance of official controls on products of animal origin intended for human consumption in accordance with Regulation (EU) 2017/625 of the European Parliament and of the Council and amending commission Regulation (EC) No 2074/2005 as regards official controls. OJ L 131, 17.5.2019, p. 51–100.

[16] This means official sampling using the same method and sampling area as food business operators. At least 49 random samples shall be taken from each slaughterhouse each year. The number of samples may be reduced for small slaughterhouses and based on a risk evaluation.

[17] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40.

[18] Commission Implementing Decision (EU) 2020/1729 of 17 November 2020 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria and repealing Implementing Decision 2013/652/EU. OJ L387, 19.11.2020, p. 8–21.

& Hills, 2013) was considered significant, in order to highlight every possible indication of differences between the data collected by the FBOps and the CAs. R software (www.r-project.org, version 4.2.3) was used to conduct the above analyses.

A1.4 | Results

A1.4.1 | Overview of key statistics, EU, 2020–2024

Table 3 summarises EU statistics on human campylobacteriosis, and on the occurrence and percentage of positives for *Campylobacter* in food and animals for the period 2020–2024. In 2024, an increase was observed in the number of notified human cases and in the EU notification rate with respect to 2023.

The food data of interest in this report were classified into two major categories: 'meat and meat products' and 'milk and milk products', aggregated by year to obtain an annual overview of the volume of data submitted. In the last 5 years, the number of sampling units reported for 'meat and meat products' has increased, probably owing to Commission Implementing Regulation (EU) 2019/627 establishing compulsory reporting of *Campylobacter* PHC monitoring data (see above). The animal data collected at the primary production stage were mostly from broilers and cattle. Results showed year-to-year fluctuations, partially attributable to the number of reporting MSs, alongside a general decreasing trend in the reported sample sizes for broilers. More detailed descriptions of these statistics are provided in the subsections below and in the chapter on food-borne outbreaks.

TABLE 3 Summary of *Campylobacter* statistics relating to humans, major food categories and the main animal species, EU, 2020–2024.

	2024	2023	2022	2021	2020	Data source
Humans						
Total number of confirmed cases	168,396	147,622	139,225	140,666	121,752	ECDC
Total number of confirmed cases/100,000 population (notification rates)	55.3	49.4	47.7	47.8	43.5	ECDC
Number of reporting MSs	26	27	27	27	27	ECDC
Infection acquired in the EU	73,627	61,128	78,499	81,975	70,769	ECDC
Infection acquired outside the EU	2538	2768	3224	704	1586	ECDC
Unknown travel status or unknown country of infection	92,231	83,726	57,502	57,987	49,397	ECDC
Number of food-borne outbreak-related cases	1420	1262	1097	1051	1319	EFSA
Total number of food-borne outbreaks	314	266	255	249	317	EFSA
Food[a]						
Meat and meat products[b]						
Number of sampling units	109,790	107,300	107,177	87,808	66,101	EFSA
Number of reporting MSs	27	26	27	25	25	EFSA
Milk and milk products[c]						
Number of sampling units	1471	1802	2633	2125	2145	EFSA
Number of reporting MSs	11	13	14	11	11	EFSA
Animals[a]						
Cattle (bovine animals)						
Number of sampling units	4297	6305	5698	7529	4387	EFSA
Number of reporting MSs	8	13	7	11	7	EFSA
***Gallus gallus* (chickens)**						
Number of sampling units	9630	6732	9817	10,162	13,628	EFSA
Number of reporting MSs	13	5	14	6	15	EFSA
Pigs						
Number of sampling units	221	2428	1820	4502	2110	EFSA
Number of reporting MSs	4	12	5	14	4	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States.

[a] The number of sampling units was calculated by summing all reported sublevel entries for sampling units, stages, strategies and samplers, as listed in the EFSA Catalogue (EFSA, 2019). Animals from the sampling stage 'Artificial insemination stations' were not included.

[b] 'Meat and meat products' refers to carcases and fresh meat/ready-to-eat (RTE), cooked and fermented products.

[c] 'Milk and milk products' refers to raw and pasteurised milk and all dairy products including cheeses.

A1.4.2 | Human campylobacteriosis

In 2024, 168,396 confirmed cases of human campylobacteriosis were reported by 26 EU MSs, corresponding to an EU notification rate of 55.3 cases per 100,000 population (Table 3). This is an increase of 11.9% compared with the annual notification rate of 2023 (49.4 per 100,000 population). Cyprus, Estonia, Lithuania, Slovenia and Sweden reported lower rates in 2024 compared to the previous year. The highest country-specific notification rates in 2024 were observed in Luxembourg (172.9 cases per 100,000 population), Czechia (130.5), Slovakia (118.7) and Malta (96.2). The lowest rates in 2024 were observed in Bulgaria, Cyprus, Poland and Romania (≤ 6.6 per 100,000 population) (Table 4).

In 2024, almost half of the EU campylobacteriosis cases (46.0%; 77,447/168,396) were reported with data on importation status, 91.8% (71,087/77,447) of these cases were reported as domestically acquired, while 8.2% (6360/77,447) were imported.

Among cases with information on both importation status and place of infection (*N* = 76,165), the majority (73,627, 96.7%) were reported as acquired within the EU (either domestically acquired or acquired in another EU country), while 3.3% (2538) were reported as acquired in a country outside the EU. Among the 73,627 cases reported as acquired within the EU, the majority (96.6%; 71,087) were reported as domestically acquired, while 3.4% (2540 cases) were reported as acquired in another EU country. Among the latter, the most frequently reported countries of infection were Spain (35.6%; 904/2540), Greece (11.2%; 285/2540), Italy (8.0%; 204/2540), Portugal (6.2%; 158/2540) and France (5.6%; 150/2540). Among the 2538 imported cases reported as acquired in countries outside the EU, the most frequently reported countries of infection were Thailand (15.3%; 389/2538), Türkiye (12.8%; 325/2538), Indonesia (10.8%; 275/2538), Morocco (7.8%; 202/2538) and India (5.1%; 130/2538).

TABLE 4 Reported confirmed human cases of campylobacteriosis and notification rates per 100,000 population in EU MSs and non-MS countries, by country and year, 2020–2024.

	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	National Coverage[a]	Data format[a]	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	6848	74.8	6271	68.9	6293	70.1	6019	67.4	5406	60.7
Belgium	Y	A	7638	64.6	5597	47.7	5647	48.6	5083	44.0	5693	49.4
Bulgaria	Y	A	347	5.4	222	3.4	107	1.7	130	2.0	127	1.9
Croatia	Y	C	1835	47.5	1318	34.2	1467	38.0	1148	29.5	1054	26.8
Cyprus	Y	C	52	5.4	106	11.2	82	9.1	24	2.7	18	2.0
Czechia	Y	C	14,228	130.5	13,558	125.2	14,412	137.0	16,305	155.4	17,517	163.8
Denmark	Y	C	5546	93.0	5197	87.6	5143	87.6	3740	64.0	3742	64.3
Estonia	Y	C	268	19.5	270	19.8	211	15.8	185	13.9	265	19.9
Finland	Y	C	2698	48.1	2587	46.5	2462	44.4	1798	32.5	2074	37.5
France[b]	N	C	9652	70.5	9255	67.8	9095	66.8	8875	65.5	7920	58.7
Germany	Y	C	45,989	55.1	40,090	48.2	43,471	52.2	47,911	57.6	46,377	55.8
Greece	Y	C	908	8.7	635	6.1	302	2.9	260	2.4	218	2.0
Hungary	Y	C	5858	61.1	5488	57.2	5050	52.5	5088	52.7	4461	46.0
Ireland	Y	C	4015	75.0	3736	70.9	3617	70.2	3147	62.1	2419	48.3
Italy[c]	Y	C	2779	–	2363	–	1539	–	1541	–	1418	–
Latvia	Y	C	–	–	176	9.3	172	9.2	158	8.3	104	5.5
Lithuania	Y	C	610	21.1	643	22.5	497	17.7	357	12.7	684	24.3
Luxembourg	Y	C	1162	172.9	855	129.4	912	141.3	589	92.8	729	116.4
Malta	Y	C	542	96.2	485	89.5	372	71.5	378	73.2	206	40.0
Netherlands[d]	N	C	4737	41.3	4673	41.0	4758	42.3	4231	37.8	3758	37.2
Poland	Y	C	1264	3.5	843	2.3	527	1.4	616	1.7	414	1.1
Portugal	Y	C	1436	13.5	1057	10.1	868	8.3	973	9.4	790	7.6
Romania	Y	C	1253	6.6	1039	5.5	525	2.8	348	1.8	300	1.6
Slovakia	Y	C	6438	118.7	5665	104.4	4777	87.9	6099	111.7	4921	90.2
Slovenia	Y	C	856	40.3	995	47.0	938	44.5	856	40.6	811	38.7
Spain[e]	N	C	35,997	90.3	28,822	74.9	20,816	60.0	20,748	60.0	6891	–
Sweden	Y	C	5440	51.6	5676	53.9	5165	49.4	4059	39.1	3435	33.3

TABLE 4 (Continued)

Country	2024				2023		2022		2021		2020	
	National Coverage[a]	Data format[a]	Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
			Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
EU Total			**168,396**	**55.3**	**147,622**	**49.4**	**139,225**	**47.7**	**140,666**	**47.8**	**121,752**	**43.5**
Iceland	Y	C	132	34.4	155	40.0	104	27.6	58	15.7	95	26.1
Liechtenstein	Y	C	62	154.9	48	121.0	50	127.2	38	97.3	–	–
Norway	Y	C	3090	55.7	3034	55.3	2980	54.9	2049	38.0	2422	45.1
Switzerland[f]	Y	C	8220	91.7	6713	76.2	7551	86.4	6759	78.0	6157	71.5

Abbreviation: –, Data not reported.

[a] Y, yes; N, no; A, aggregated data; C, case-based data.

[b] Sentinel surveillance; notification rates calculated with estimated coverage of 20%.

[c] Sentinel surveillance: no information on estimated coverage. Notification rate cannot be estimated.

[d] Sentinel surveillance; notification rates calculated with estimated coverage of 64% in 2021–2024 and 58% in 2020.

[e] Sentinel surveillance; notification rates calculated with estimated population coverage of 82% in 2024, 80% in 2023 and 73% in 2021–2022. No information on estimated coverage in 2020, so notification rate cannot be estimated.

[f] Switzerland provided data directly to EFSA. The human data for Switzerland include data from Liechtenstein for 2020.

Between 2015 and 2024, the number of confirmed campylobacteriosis cases reported in the EU showed a clear seasonal trend, peaking in the summer months. Additionally, smaller but distinct annual increases were observed in January from 2015 to 2024, while the absolute number of cases during winter months consistently remained lower than the summer peaks. The overall campylobacteriosis trend in 2020–2024 showed a statistically significant ($p < 0.05$) increase between 2020 and 2024 (Figure 1). Twelve MSs observed a significantly increasing trend during the period 2020–2024. For most countries, however, the annual case numbers and notification rates reported during this period stayed at or below the levels recorded prior to the COVID-19 pandemic. No country recorded a significant decreasing trend.

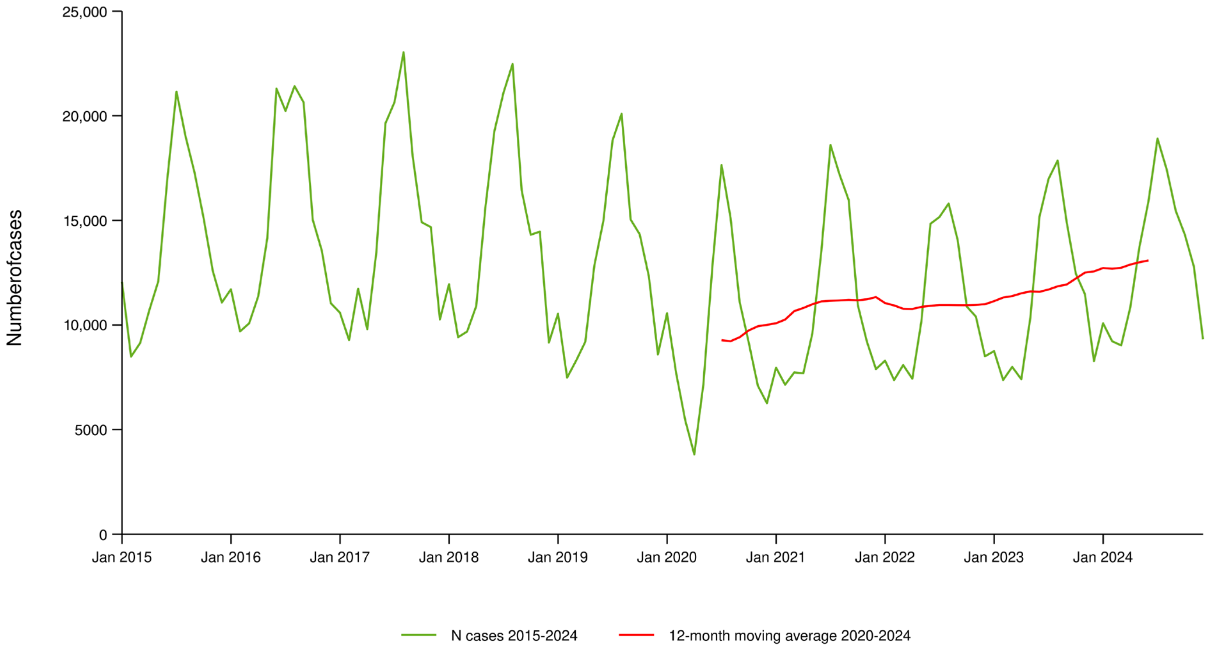

FIGURE 1 Trend in reported confirmed human cases of campylobacteriosis in the EU, by month, 2020–2024.
Source: Austria, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Hungary, Ireland, Italy, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden.

Campylobacter species information was provided by 24 MSs for 57.7% (97,231/168,396) of confirmed cases reported in the EU, representing an increase compared to 2023 (57.6%; 85,066/147,622). Of these cases, 87.5% were *Campylobacter jejuni*, 11.9% *C. coli*, 0.27% *C. fetus*, 0.26% *C. upsaliensis* and 0.1% *C. lari*.

A1.4.3 | *Campylobacter* in food

Campylobacter *data in the context of Commission Regulation (EC) No 2073/2005*

The *Campylobacter* PHC monitoring data are presented in Table 5. Twenty-six Member States and the United Kingdom (Northern Ireland) reported data for 2024 in the context of the *Campylobacter* PHC, set out in Commission Regulation (EC) No 2073/2005. Ad hoc official sampling results were reported by 17 MSs, while monitoring results from FBOps were reported by 20 MSs and the United Kingdom (Northern Ireland), and data from both samplers were provided by 11 MSs. Concerning official control samples (*N* = 15,431), 24.3% exceeded the limit of 1000 CFU/g, showing an increase from the 16.0% observed in 2023. Considerable variability was observed in the percentage of test results exceeding the limit, ranging from no positive samples in Luxembourg to 82.2% in Greece. Bulgaria and Romania showed 0.34% and 0.80% of samples exceeding the limit, respectively, while five MSs (Estonia, Germany, Hungary, the Netherlands and Poland) reported values between 7.7% and 9.5%. Conversely, eight MSs (Belgium, Cyprus, France, Ireland, Italy, Latvia, Lithuania and Spain) reported moderate and high proportions of samples exceeding the limit, ranging from 14.7% to 36.4%. Fifteen MSs reported *Campylobacter*-positive samples both below and above the limit, with 9560 positive samples (62.9%) out of 15,190 samples tested.[19] One non-MS (Montenegro) reported 38.9% of official samples exceeding the limit.

Concerning results from FBOps for neck skin samples from own-check sampling activities (*N* = 67,042), 16.4% exceeded the limit of 1000 CFU/g, showing an increase from 15.8% observed in 2023. No positive samples exceeding the limit were reported by Romania, while three MSs (Finland, Greece and Sweden) recorded less than 1.7% of samples exceeding the limit. The remaining 16 MSs and the United Kingdom (Northern Ireland) reported from low to high proportions of samples exceeding the limit, from 4.6% to 44.1%. Thirteen out of 20 MSs and the United Kingdom (Northern Ireland) reported *Campylobacter*-positive samples both below and above the limit, with 14,350 positive samples (42.1%) out of 34,105 samples tested.[20] Three non-MSs (Iceland, Montenegro and Switzerland) reported no positive, 36.4% and 15.9% samples from FBOps exceeding the limit, respectively.

Eleven MSs reported results from both samplers, showing that the overall percentage of samples exceeding the limit was significantly higher for official control samples (26.0%) than for own-checks (14.7%). A significantly higher percentage of samples above the limit was also observed in official samples compared to samples from FBOps in eight MSs.

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[19] Belgium, Bulgaria, Cyprus, Estonia, France, Greece, Hungary, Ireland, Italy, Latvia, Luxembourg, the Netherlands, Poland, Romania and Spain data from CAs were reported both below and above the threshold of 1000 CFU/g and were considered in the calculation of the percentage of positive samples and the total number of tested samples. Germany and Lithuania were excluded because they did not report positive units below the 1000 CFU/g limit, as verified during the data validation process.

[20] Austria, Croatia, Czechia, Denmark, Greece, Ireland, Italy, Latvia, Portugal, Romania, Slovakia, Slovenia and Spain data from FBOps were reported both below and above the threshold of 1000 CFU/g and were considered in the calculation of the percentage of positive samples and the total number of tested samples. Belgium, Finland, France, Germany, Poland, the Netherlands, Sweden and the United Kingdom (Northern Ireland) were excluded because they did not report positive units below the 1000 CFU/g limit, as verified during the data validation process.

TABLE 5 Comparison of proportions (%) of samples exceeding the *Campylobacter* PHC limit collected from the neck skins of chilled broiler carcases sampled at slaughterhouses in accordance with Commission Regulation (EC) No 2073/2005, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* samples tested**	***N* (%) samples above 1000 CFU/g**	**CI95 Samples above 1000 CFU/g**	***N* samples tested**	***N* (%) samples above 1000 CFU/g**	**CI95 Samples above 1000 CFU/g**	***p*-value**[a]	**Interpretation**[b]
Austria	–	–	–	1032	93 (9.0)	[7.3; 10.9]	–	–
Belgium	551	81 (14.7)	[11.8; 17.9]	2669	268 (10.0)	[8.9; 11.2]	< 0.001	CA > FBOp
Bulgaria	580	2 (0.34)	[0.04; 1.2]	–	–	–	–	–
Croatia	–	–	–	130	6 (4.6)	[1.7; 9.8]	–	–
Cyprus	170	61 (35.9)	[28.7; 43.6]	–	–	–	–	–
Czechia	–	–	–	3620	1218 (33.6)	[32.1; 35.2]	–	–
Denmark	–	–	–	1065	100 (9.4)	[7.7; 11.3]	–	–
Estonia	13	1 (7.7)	[0.19; 36.0]	–	–	–	–	–
Finland	–	–	–	495	3 (0.61)	[0.13; 1.8]	–	–
France	7705	2375 (30.8)	[29.8; 31.9]	17,935	4325 (24.1)	[23.5; 24.7]	< 0.001	CA > FBOp
Germany	11	1 (9.1)	[0.23; 41.3]	5570	437 (7.8)	[7.2; 8.6]	NS	
Greece	45	37 (82.2)	[67.9; 92.0]	5981	99 (1.7)	[1.3; 2.0]	< 0.001	CA > FBOp
Hungary	640	52 (8.1)	[6.1; 10.5]	–	–	–	–	–
Ireland	173	28 (16.2)	[11.0; 22.5]	1229	102 (8.3)	[6.8; 10.0]	< 0.001	CA > FBOp
Italy	1531	342 (22.3)	[20.3; 24.5]	6222	857 (13.8)	[12.9; 14.7]	< 0.001	CA > FBOp
Latvia	150	47 (31.3)	[24.0; 39.4]	792	292 (36.9)	[33.5; 40.3]	0.0976	CA < FBOp
Lithuania	230	54 (23.5)	[18.2; 29.5]	–	–	–	–	–
Luxembourg	5	0	[–]	–	–	–	–	–
Netherlands	282	23 (8.2)	[5.2; 12.0]	3368	195 (5.8)	[5.0; 6.6]	0.0536	CA > FBOp
Poland	1285	122 (9.5)	[7.9; 11.2]	1220	415 (34.0)	[31.4; 36.8]	< 0.001	CA < FBOp
Portugal	–	–	–	3912	1272 (32.5)	[31.0; 34.0]	–	–
Romania	625	5 (0.80)	[0.26; 1.9]	890	0	[0; 0.41][b]	0.01	CA > FBOp
Slovakia	–	–	–	828	53 (6.4)	[4.8; 8.3]	–	–
Slovenia	–	–	–	828	365 (44.1)	[40.7; 47.5]	–	–
Spain	1435	523 (36.4)	[34.0; 39.0]	7576	848 (11.2)	[10.5; 11.9]	< 0.001	CA > FBOp
Sweden	–	–	–	1030	11 (1.1)	[0.53; 1.9]	–	–
United Kingdom (Northern Ireland)	–	–	–	650	67 (10.3)	[8.1; 12.9]	–	–
EU Total (27 + XI)	**15,431**	**3754 (24.3)**	**[23.7; 25.0]**	**67,042**	**11,026 (16.4)**	**[16.2; 16.7]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**13,793**	**3584 (26.0)**	**[25.3; 26.7]**	**53,452**	**7838 (14.7)**	**[14.4; 15.0]**	**< 0.001**	**CA > FBOp**

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Other food monitoring data

In 2024, the occurrence of *Campylobacter* in sampling units from the main RTE and non-RTE food categories was 0.36% and 17.7%, respectively. In 2024, most of the 2517 RTE food sampling units reported by 10 MSs originated from 'fruit, vegetables and juices' (34.8%), followed by 'meat and meat products' (27.1%) and 'milk and milk products' (21.1%). In total, *Campylobacter* was detected in nine RTE food samples: three from live bivalve molluscs (oysters), three from RTE pre-cut vegetables and three from meat-based dishes. During the period 2020–2023, the percentage of *Campylobacter*-positive sampling units in RTE foods was very low, at 0.17% of the 12,265 sampling units tested, consistently remaining below 1.0% across the main RTE categories. However, despite the small number of units tested reported by three MSs (Germany, Italy and the Netherlands), the 'fish and fishery products – RTE' category showed the highest percentage of positive samples, at 4.4% (*N* = 203).

The results reported in 2024 by 17 MSs for non-RTE foods (*N* = 23,195) showed that 'meat and meat products' was the most contaminated food category (18.5%), followed by 'fish and fishery products – non-RTE' (10.1%). During the period 2020–2023, for the 62,259 sampling units tested, 'meat and meat products' was the most contaminated food category (14.8%), along with 'fish and fishery products – non-RTE' (15.0%), although fewer sampling units were tested (*N* = 619).

Fifteen MSs reported 21.0% of sampling units as positive for fresh meat categories. The percentage of *Campylobacter*-positive units was highest for meat from turkeys (26.0%), followed by broilers (22.8%) and 'other fresh meat' (7.2%). The percentages for fresh meat from pigs and bovine animals remained low and very low at 1.6% and 0.71%, respectively. In 2024, an increase was reported in the percentage of positive units compared with the period 2020–2023 for non-RTE foods (17.7% compared with 13.5%) and fresh meat (21.0% compared with 14.8%).

A1.4.4 | *Campylobacter* in animals

Table 6 shows the number of positive *Campylobacter* spp. samples detected during 2024 in the six main animal species, as well as in the 'other animals' category containing several different animal groups. In total, 15 MSs and the United Kingdom (Northern Ireland) and four non-MSs reported data, from broilers (*N* = 12,788), followed by bovine animals (*N* = 4443), small ruminants (*N* = 2394), cats and dogs (*N* = 1933), turkeys (*N* = 1264) and pigs (*N* = 247). The overall proportion of positive units in the EU was highest in turkeys (70.5%), followed by pigs (57.5%), broilers (20.9%), cats and dogs (9.3%), bovine animals (4.3%) and small ruminants (3.3%). For 'other animals', comprising around 40 animal categories, the proportion of positive samples was 19.6%, mostly coming from monkeys (27.3%) and land game mammals (20.9%). The four non-MSs confirmed the presence of *Campylobacter* spp. in most animal species, but reported different proportions of positive units, reflecting differences in sample size and representativeness.

TABLE 6 Summary of *Campylobacter* statistics relating to major animal species, reporting EU MSs and non-MS countries, 2024.

	EU MSs				**Non-MS countries**			
			Positive Sampling units				**Positive sampling units**	
Animals	***N* reporting countries**	***N* tested[a] sampling units**	***N***	**%**	***N* reporting countries**	***N* tested[a] sampling units**	***N***	**%**
Gallus gallus (broilers)	11	9303	1945	20.9	4	3485	354	10.2
Bovine animals[b]	8	4297	184	4.3	2	146	32	21.9
Pigs	4	221	127	57.5	3	26	0	0
Small ruminants	6	2337	76	3.3	2	57	10	17.5
Turkeys	5	1232	869	70.5	1	32	0	0
Cats and dogs	4	655	61	9.3	2	1278	170	13.3
Other animals[c]	7	2850	560	19.6	2	270	29	10.7
Total	**16**	**20,895**	**3822**	**18.3**	**4**	**5294**	**595**	**11.2**

Abbreviation: MSs, Member States.

[a] Summary statistics were obtained by totalling all sampling units (single samples, batch samples, animals, slaughter animal batches and herds or flocks).

[b] Animals from the sampling stage 'Artificial insemination stations' was not included in the count of the units tested.

[c] Alpacas, Badgers, Birds, Budgerigars, Buffalos, Camels, Cantabrian chamois, Capybaras, Chinchillas, Deer, Ducks, Ferrets, Foxes, *Gallus gallus* (fowl), Giraffes, Guinea pigs, Hares, Hedgehogs, Land game mammals, Lions, Lynxes, Marine mammals, Martens, Mice, Monkeys, Moose, Mouflons, Other animals – unspecified, Other carnivores, Other mustelids, Otters, Parrots, Peafowl, Pheasants, Pigeons, Poultry, unspecified, Rabbits, Raccoon dogs, Raccoons, Reptiles, Rhinoceroses, Rodents, Solipeds, Starlings, Tigers, Turtles, Wild boars, Wildcats (*Felis silvestris*), Wild ducks.

A1.4.5 | Occurrence of *Campylobacter* in animals based on data from harmonised monitoring of antimicrobial resistance (Commission Implementing Decision (EU) 2020/1729)

In 2024, AMR monitoring provided data on the prevalence of positive samples of *C. jejuni* and *C. coli* for broilers and fattening turkeys. Twenty-seven MSs, the United Kingdom (Northern Ireland) and three non-MSs (Iceland, Norway and Switzerland) reported data on 18,381 units from broilers tested for *Campylobacter*. The overall proportion of positive units for *C. jejuni* in the EU and the United Kingdom (Northern Ireland) was 25.6% (*N* = 3976). Five MSs (Latvia, Lithuania, Poland, Romania and Slovenia) and the United Kingdom (Northern Ireland) reported very high positivity levels (> 53%), while three MSs (Estonia, Finland and Sweden) reported low levels of positivity, below 8.5%. Among the three non-MSs reporting data (Iceland, Norway and Switzerland), the overall prevalence was 9.4% (*N* = 270), with marked inter-country variation. Meanwhile, a total of 1907 positive units for *C. coli* were reported in the EU and the United Kingdom (Northern Ireland), corresponding to a prevalence of 12.9%, with only Malta reporting extremely high positivity levels (73.5%). One non-MS (Switzerland) reported a low prevalence (6.6%) of positive samples.

Ten MSs reported information on 3701 units tested for *Campylobacter* from fattening turkeys. In the EU, 29.6% of samples were positive for *C. jejuni*. Conversely, *C. coli* was found at a high level of 42.3%, with two MSs (Ireland and Portugal) showing a very high prevalence of positive samples (> 65.0%).

A1.5 | Discussion

Campylobacteriosis has been the most frequently reported zoonosis in humans across the EU since the beginning of EU level surveillance in 2007. Despite comprehensive surveillance and national coverage in most MSs, the number of reported cases is underestimated in the EU (Teunis et al., 2013).

The EU notification rate increased between 2023 and 2024 from 49.4 to 55.3 cases per 100,000 population, representing an annual increase of 11.9%. Despite this increase, approximately half of EU MSs did not return to pre-pandemic notification rates in 2024. No definitive causes have been identified to explain this pattern within the EU.

The 5-year trend of confirmed cases of human campylobacteriosis in the EU showed a significant increase from 2020 to 2024. This is driven by several countries, including 12 that had statistically significant increasing trends nationally. Most countries showing an increasing trend between 2020 and 2024 continued to report case numbers and notification rates that were comparable to, or lower than, those reported before the COVID-19 pandemic. This increasing trend is likely an artefact of the pandemic's impact on surveillance data since 2020, rather than evidence of a genuine rise in case numbers. Since the trend analysis began in 2020, a year when surveillance for many diseases was heavily affected by the pandemic, it was expected that as countries returned to pre-pandemic reporting levels, an increasing trend would be observed between 2020 and 2024. The COVID-19 pandemic had a significant impact on surveillance systems, healthcare-seeking behaviour and reporting practices across the EU (Young et al., 2025).

Most of the reported campylobacteriosis cases were acquired in the reporting country in the EU, as in previous years. Nonetheless, the proportion of travel-associated campylobacteriosis cases has been steadily increasing since 2020, with a notable rise in 2022–2024 compared to 2020–2021, reflecting the gradual resumption of international travel following the COVID-19 pandemic (Young et al., 2025).

Campylobacter has characteristic seasonality, with cases increasing sharply in the summer. Campylobacteriosis cases have been positively associated with temperature and, to a lesser degree, with precipitation (Austhof et al., 2024; Lake et al., 2019). Recent studies have even shown a possible association between campylobacteriosis and global climate change (Kuhn et al., 2020).

A smaller but distinct winter peak in the EU has become apparent in the past 10 years, including in winter 2023–2024. Disease onset in cases notified during the winter peaks occurred predominantly in January. This indicates exposure around the Christmas/New Year period. Reports suggest that meat fondues or table-top grilling, which are popular during the festive season, could promote the transmission of *Campylobacter* in some countries, causing the winter peak (Bless et al., 2017; Rosner et al., 2021).

As in previous years, *C. jejuni* and *C. coli* were the main species notified by MSs in 2024, although a considerable proportion of campylobacteriosis cases (42.2%) had undetermined species, indicating that further improvements and efforts are warranted in species identification and reporting capacities. A One Health approach using whole genome sequencing (WGS) for typing *Campylobacter* isolates in humans, food and animals will contribute to better species characterisation and enhance the monitoring of zoonotic transmission, improving public health surveillance.

In 2024, all EU MSs reported information on the occurrence of *Campylobacter* in either animals or food. Data were also reported by Iceland, Montenegro, Norway, the Republic of North Macedonia, Serbia, Switzerland and the United Kingdom (Northern Ireland). As part of a food safety control strategy, most EU MSs (except Malta) and the United Kingdom (Northern Ireland) submitted *Campylobacter* PHC monitoring results, recording the highest number of samples tested in the last 5 years, with 11 MSs reporting both results from official control samples and own-check samples. PHC monitoring results continue to show that poultry is a significant source of campylobacteriosis in the EU. However, contamination levels varied across MSs, from very low to extremely high. These variations can be partially explained by differences in geographical contexts and/or the level of biosecurity farm management practices in individual MSs, but need to be interpreted with caution due to variability in the number of tested samples across countries.

Official control and FBOp monitoring data showed that about one in four samples and one in six samples, respectively, exceeded the limit of 1000 CFU/g. For the MSs that submitted data from both samplers, one in four samples from the CAs and one in seven samples from FBOps exceeded the limit, highlighting discrepancies between the two sampling strategies for the fifth consecutive year. In MSs reporting *Campylobacter*-positive samples both below and above the limit, the proportion of positives was higher in samples collected by CAs (62.9%) compared to those collected by FBOps (42.1%). These discrepancies require further investigation to understand the factors driving these differences, including verification of appropriate sample management in compliance with Commission Regulation (EC) No 2073/2005 (Annex 1, chapter 3, point 3.2).

The EU recorded an increase in the number of samples exceeding the limit compared to 2023, following a slight decrease from 2022, revealing fluctuations over time but no clear increasing or decreasing trend. The PHC aims to decrease *Campylobacter* counts on broiler carcases and to minimise human campylobacteriosis cases caused by consuming or handling contaminated chicken/broiler meat. However, interventions limited to the slaughterhouse may be insufficient, particularly in high-prevalence settings. At the EU level, additional surveillance strategies at primary production and/or at the retail stage are not present, with the exception of Scandinavian countries and Iceland (Olsen et al., 2024). Although epidemiological contexts differ across Europe, the implementation of integrated surveillance plans combined with on-farm measures could reduce caecal concentrations in animals. An EFSA scientific opinion on the update and review of control options for *Campylobacter* in broilers at primary production indicated that a 3-log10 reduction in broiler caecal concentrations would result in a 58% decrease in the risk of campylobacteriosis associated with broiler meat across the EU (EFSA BIOHAZ Panel, 2020).

Monitoring of other food in the EU showed overall percentages of *Campylobacter*-positive units in RTE and non-RTE foods of 0.36% and 17.7%, respectively. Although the presence of *Campylobacter* in RTE foods was very low and has remained stable over the years, these findings are of concern given that contaminated RTE products directly expose consumers to infection. Among RTE foods, three meat-based dishes, three pre-cut vegetables and three sample units of oysters were found to be contaminated with *Campylobacter*, the latter confirming the positive findings in bivalve molluscs for the fourth consecutive year. During the period 2020–2023, very low percentages of positivity were found for all RTE meat products, milk, fruit, vegetables, juices and other RTE foods. However, the percentage of positive sample units was higher, at around 4.4%, in fish and fishery products, particularly bivalve molluscs. Given the common practice of consuming raw shellfish in certain European sub-regions, the risk of campylobacteriosis from these sources is noteworthy (Teunis et al., 1997). It should also be noted that these data originated from three MSs, highlighting the need to increase the sampling frequency of food products consumed raw (such as scallops, mussels and oysters) across regions in the EU. The generally small number of units tested may have led to imprecise estimates concerning the occurrence of *Campylobacter* in RTE food samples.

Monitoring data for non-RTE foods showed positive results for one in five 'meat and meat products', while no positive results were observed for 'milk and milk products'. A moderate proportion of positive findings, specifically 10.1% ($N=327$), was reported in bivalve molluscs (mussels) by a single MS, similar to the scenario observed in RTE foods. *Campylobacter* contamination in fresh meat categories remained moderate in 2024, with meats from broilers and turkeys being far more contaminated than those from pigs and bovine animals. Although caution is required when interpreting trend results, due to non-harmonised monitoring, the data still consistently underline the significant role of these products in spreading campylobacteriosis. This may occur either through direct handling or by cross-contaminating other foods (Wagenaar et al., 2013).

In 2024, 15 MSs, the United Kingdom (Northern Ireland), and four non-MSs reported data from animals. *Campylobacter* spp. were detected mainly in poultry (broilers and turkeys) in the EU, reported by 11 MSs and four non-MSs. Although fewer MSs reported data and fewer samples were tested, *Campylobacter* spp. were also found with low, moderate and very high proportions in ruminants, pets (cats and dogs) and pigs, respectively, highlighting the potential role of several animal species beyond poultry as reservoirs.

In 2024, prevalence data from EU AMR monitoring of broilers and fattening turkeys were analysed. A high percentage of samples from broilers were positive for *C. jejuni* (23.1%), being detected twice as often as *C. coli*. In contrast, a high percentage of samples from fattening turkeys was positive for *C. coli* (42.3%), while a lower percentage of samples (29.6%) was positive for *C. jejuni*. These data confirm that *Campylobacter* is commonly present in broilers and turkeys and highlight the ability of *C. jejuni* to colonise broilers more effectively than *C. coli*, which was more common in turkeys. The data confirm that poultry is a potential source of human campylobacteriosis (Arning et al., 2021).

In conclusion, campylobacteriosis remains the most frequently reported zoonotic infection in the EU, with confirmed cases continuing to rise and high prevalence in poultry and poultry-derived meat products. Nevertheless, only 25 of 314 reported outbreaks were supported by strong evidence linking human cases and food vehicles, with broiler meat most frequently implicated as the primary source. Strengthening WGS-based genomic surveillance from a One Health perspective could be crucial for identifying hidden outbreaks, enabling timely outbreak detection and supporting effective public health interventions.

Human cases [EU, 2024]

Notification rate *(per 100,000 population)* 18.6

Trend *(2020-2024)* ↑

↑ Increasing
↓ Decreasing
— Stable

79,703 **Cases of illness**

49,984 **Infections acquired in the EU**

5473 **Infections acquired outside the EU**

24,246 **Unknown travel status or unknown country of infection**

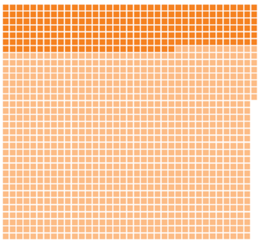
16,337 **Hospitalisations** (43.5%)*

116 **Deaths** (0.24%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

🟩 *ECDC data*

Foodborne outbreaks & related cases [EU, 2024]



1238 **Foodborne outbreaks**

247 **Strong-evidence outbreaks** 🟧

991 **Weak-evidence outbreaks** ▨

10,164 **Cases of illness**

1823 **Hospitalisations** (18.3%)*

17 **Deaths** (0.17%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

N of outbreaks			N of outbreaks per 100,000 population **		N of outbreak cases per 100,000 population
Austria	17	AT	0.186	AT	1.288
Belgium	8	BE	0.068	BE	0.838
Bulgaria	0	BG	0	BG	0
Croatia	11	HR	0.285	HR	1.709
Cyprus	1	CY	0.103	CY	0.310
Czechia	11	CZ	0.101	CZ	1.339
Denmark	10	DK	0.168	DK	3.456
Estonia	6	EE	0.436	EE	1.600
Finland	3	FI	0.054	FI	0.767
France	266	FR	0.389	FR	2.435
Germany	90	DE	0.108	DE	1.438
Greece	40	EL	0.385	EL	2.702
Hungary	6	HU	0.063	HU	1.982
Ireland	2	IE	0.037	IE	0.206
Italy	44	IT	0.075	IT	1.272
Latvia	16	LV	0.855	LV	2.618
Lithuania	13	LT	0.450	LT	2.634
Luxembourg	0	LU	0	LU	0
Malta	15	MT	2.662	MT	8.519
Netherlands	8	NL	0.045	NL	1.048
Poland	283	PL	0.773	PL	6.384
Portugal	7	PT	0.066	PT	1.156
Romania	1	RO	0.005	RO	0.241
Slovakia	132	SK	2.433	SK	8.535
Slovenia	3	SI	0.141	SI	2.966
Spain	240	ES	0.494	ES	3.760
Sweden	5	SE	0.047	SE	1.327
UK (N. Ireland)	0	XI	0	XI	0

Implicated food vehicles
(Strong-evidence outbreaks)

Top food vehicles

Eggs and eggs products
83 Outbreaks

Mixed food
36 Outbreaks

Bakery products
23 Outbreaks

Broiler meat (*Gallus gallus*) and products thereof
19 Outbreaks

Pig meat and products thereof
Vegetables and juices and other products thereof
16 Outbreaks (each)

*** Differences among countries shall be interpreted with caution as this indicator depends on several factors including the type of outbreaks under surveillance and does not necessarily reflect the level of food safety in each country.*

🟧 *EFSA data*

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about *Salmonella* and for the consultation of data collected, the following interactive tools are available:

A2.1 | Key facts

- Salmonellosis was the second most commonly reported food-borne gastrointestinal infection in humans in the European Union.
- In 2024, there were 79,703 confirmed cases of human salmonellosis, corresponding to a European Union notification rate of 18.6 cases per 100,000 population. This was a slight increase of 1.7% compared with the rate in 2023 (18.3 cases per 100,000 population).
- The overall trend for *Salmonella* infections showed a significant increase in the 2020–2024 period.
- The top five European Union-acquired *Salmonella* serovars involved in human infections were distributed as follows: *S*. Enteritidis (58.4%), S. Typhimurium (11.0%), monophasic *S*. Typhimurium (1,4,[5],12:i:-) (10.4%), *S*. Infantis (3.2%) and *S*. Derby (1.2%).
- In the context of Commission Regulation (EC) No 2073/2005 on food safety criteria, the prevalence of *Salmonella*-positive samples found at the manufacturing stage (4.9%) was twice as high as that at distribution (2.3%). The highest levels of contamination were found for 'meat products made from poultry meat intended to be eaten cooked' (13.2% at manufacturing and 5.0% at distribution), 'mechanically separated meat (MSM)' (12.8% at manufacturing and 3.6% at distribution), 'minced meat and meat preparations made from poultry meat intended to be eaten cooked' (9.9% at manufacturing and 5.8% at distribution) and 'fresh poultry meat' (7.7% at distribution and 6.3% at manufacturing).
- In the context of Commission Regulation (EC) No 2073/2005, Member States reported the highest proportions of *Salmonella*-positive samples during compliance checks for process hygiene criteria for carcases at slaughterhouses among those collected by the competent authorities for broilers (18.7%),[21] turkeys (17.4%) and pigs (3.8%). Lower prevalence was observed in official samples for cattle (1.5%) and sheep (1.2%). For samples collected by food business operators, the proportions of *Salmonella*-positive samples were significantly lower: 4.9% for broilers, 3.5% for turkeys, 0.95% for pigs, 0.39% for sheep and 0.29% for cattle. For horses and goats, the prevalence rates were very low (< 1%) for both official and own-check controls.
- In 2024, a very low proportion (0.23%) of *Salmonella*-positives was found in 'ready-to-eat' food sampling units ($N = 102,696$) reported by 24 Member States, with the highest levels of contamination found in 'meat and meat products from turkeys' (3.2%), 'sprouts (sprouted seeds)' (2.9%) and 'meat and meat products from broilers' (1.3%). Of 520,720 'non-ready-to-eat' sampling units reported by 28 Member States, 2.3% were *Salmonella* positive, with the highest levels of contamination found in 'meat and meat products from broilers' (5.1%), 'meat and meat products from turkeys' (4.7%), 'other meat and meat products' (2.5%), 'meat and meat products from pigs' (1.9%) and 'mixed meat products' (1.1%).
- Fourteen reporting Member States and the United Kingdom (Northern Ireland) met all *Salmonella* reduction targets for poultry populations in their control programmes. This compares with 15 MSs in 2023 and 19 in 2022. In 2024, four MSs failed to meet the targets for breeding *Gallus gallus*, seven for laying hens, one for broiler flocks and two for breeding and fattening turkeys.
- For broilers and fattening turkeys, the European Union-level prevalence of target *Salmonella* serovar-positive flocks reported by food business operators was significantly lower than that reported by competent authorities.
- Over the last 10 years (2015–2024), a significant increase in the European Union-level prevalence of *Salmonella* and target *Salmonella* serovar-positive flocks was observed in breeding *Gallus gallus* and breeding turkeys. For breeding turkeys, this significant upward trend was also confirmed in the most recent period (2020–2024). For the other poultry populations covered by the national control programmes, no significant trends (neither increasing nor decreasing) were detected.
- Considering the top-20 *Salmonella* serovars by food-animal source, *S*. Enteritidis was the most reported serovar in the laying hens–eggs source and the second most common in broilers–broiler meat. *Salmonella* Infantis was by far the dominant serovar in broilers–broiler meat. In pigs–pig meat, the most common serovars were monophasic *S*. Typhimurium and *S*. Derby, followed by *S*. Typhimurium. In 'bovine animals–bovine meat', *S*. Typhimurium was the most common serovar, followed by *S*. Dublin.

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[21] According to the footnote 'c', Table 11.

A2.2 | Surveillance and monitoring of *Salmonella* in the EU

A2.2.1 | Humans

For 2024, all 27 EU MSs reported information on non-typhoidal salmonellosis infections in humans. The notification of salmonellosis is mandatory in 24 EU MSs, whereas it is voluntary in three MSs (Belgium, France and the Netherlands). The EU case definition was used by 24 MSs, while three MSs (France, Germany and Italy) reported using other case definitions. All countries except Spain and the Netherlands had a comprehensive surveillance system. The surveillance systems for salmonellosis covered the whole population in all MSs except three: Belgium, the Netherlands and Spain. The estimated coverage of the surveillance system was 85% in Belgium, 64% in the Netherlands and 82% in Spain. These estimated proportions of population coverage were used in the calculation of notification rates for these MSs. No estimated population coverage was provided for 2020 in Spain, so notification rates were not calculated. All countries reported case-based data except Bulgaria, which reported aggregated data.

A2.2.2 | Food, animals and feed

Salmonella data in the context of Commission Regulation (EC) No 2073/2005

Commission Regulation (EC) No 2073/2005[22] lays down microbiological criteria, intended as food safety criteria (FSC) and process hygiene criteria (PHC), for *Salmonella* in specific food categories. Compliance with these criteria must be legally verified by the individual food business operator (FBOp) as part of their own Hazard Analysis and Critical Control Point (HACCP) programme according to Regulation (EC) No 852/2004.[23] In addition, the competent authority (CA), through official sampling or oversight of data, should verify compliance by the FBOp. The *Salmonella* FSC require that *Salmonella* species not be detected in different products during their shelf life with the exception of fresh poultry meat (from species covered by national control programmes (NCPs), whose FSC require the absence of target serovars (*S.* Enteritidis and *S.* Typhimurium including monophasic *S.* Typhimurium (1,4,[5],12:i:-) according to Commission Regulation (EU) No 1086/2011[24]). The *Salmonella* PHC are regulated for carcases of pigs, cattle, sheep, goats, horses, broilers and turkeys, as sampled by the FBOp. Moreover, in accordance with Commission Implementing Regulation (EU) 2019/627,[25] the CA has to verify whether the FBOp correctly implements and checks these PHC for carcases.

Data from national control programmes for *Salmonella* in poultry populations

Under Regulation (EC) No 2160/2003[26] and subsequent amendments, MSs are obligated to establish NCPs targeting *Salmonella* to reduce the prevalence of *Salmonella* serovars deemed relevant for public health (hereafter referred to as 'target serovars'). The Regulation requires the MSs to report combined results of *Salmonella*-positive flocks from official sampling and food business operators/industry sampling for all poultry populations, including rearing and adult flocks. For adult breeding *Gallus gallus*, laying hens and breeding turkeys, as well as for broilers and fattening turkeys, MSs must report combined results of target serovar *Salmonella*-positive flocks from official sampling and food business operators/industry sampling for the evaluation of target achievement. Additionally, for flocks of broilers, adult breeding turkeys and fattening turkeys, the separate reporting of target serovar *Salmonella*-positive flocks collected through official and food business operators/industry sampling is mandatory.

Other monitoring data for food, animals and feed including serovars

Food, animal and feed data other than those described above are not collected in a harmonised way, because there are no specific legal requirements. The reported occurrence of *Salmonella* in the main food categories was descriptively summarised, with a distinction being made between 'ready-to-eat (RTE)' and 'non-RTE food'. Data sets are extracted with 'objective sampling' being specified as the sampling strategy, which means that samples were representative of the population being analysed and were collected in accordance with a planned strategy.

The occurrence of *Salmonella* in animal populations is descriptively summarised considering all data collected in different sampling contexts and reported as different sampling units (e.g. 'holding', 'herd/flock', 'animal' and 'slaughter animal batch'), except for data related to poultry populations covered by NCPs, which have been discussed separately. Animal data

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[22] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

[23] Regulation (EC) No 852/2004 of the European Parliament and of the Council of 29 April 2004 on the hygiene of foodstuffs. OJ L 139, 30.4.2004, p. 1–54.

[24] Commission Regulation (EU) No 1086/2011 of 27 October 2011 amending Annex II to Regulation (EC) No 2160/2003 of the European Parliament and of the Council and Annex I to Commission Regulation (EC) No 2073/2005 as regards *Salmonella* in fresh poultry meat Text with EEA relevance. OJ L 281, 28.10.2011, p. 7–11.

[25] Commission Implementing Regulation (EU) 2019/627 of 15 March 2019 laying down uniform practical arrangements for the performance of official controls on products of animal origin intended for human consumption in accordance with Regulation (EU) 2017/625 of the European Parliament and of the Council and amending Commission Regulation (EC) No 2074/2005 as regards official controls. OJ L 131, 17.5.2019, p. 51–100.

[26] Regulation (EC) No 2160/2003 of the European Parliament and of the Council of 17 November 2003 on the control of Salmonella and other specified food-borne zoonotic agents. OJ L 325, 12.12.2003, p. 1–15.

have been aggregated into macro categories (birds, cattle/bovine animals, dogs, felids, land game mammals, pigs, poultry, small ruminants, solipeds and wild ungulates) to facilitate the interpretation of the collected results.

The reported data on *Salmonella* serovars are also descriptively summarised. For this purpose, only isolates with the complete antigenic formula and/or serovar name were considered. MSs are required to report the target serovars as part of their NCPs for poultry, whereas for samples collected in different contexts, serotyping is not mandatory. Also, for the food sector, serotyping is only mandatory for fresh poultry meat, since for this category, the FSC is the absence of target serovars. The compulsory reporting of target serovars in these contexts guarantees the consistency of such data over the years and among MSs but could result in the prevalence of these target serovars being overestimated compared with the other serovars.

A2.3 | Data analyses

A2.3.1 | Comparison between competent authority and food business operator sampling results

CA and FBOp *Salmonella* results in the context of NCPs for those poultry populations requiring separate reporting (i.e. broilers, fattening turkeys and adult breeding turkeys) were compared, as were *Salmonella* PHC monitoring data from carcases. The significance of differences was verified by the one-tailed Fisher's exact probability test, in cases where the expected values in any of the cells of a contingency table were below five; otherwise, the *z*-statistic one-tailed test was performed. CA control sampling results and the own-check results of the FBOp were expressed as prevalence and exact binomial confidence interval (95% level). A p-value < 0.10 (Clayton & Hills, 2013) was considered significant, to include all possible evidence of differences between data collected by the FBOp and CA. R software (www.r-project.org, version 4.2.3) was used to conduct the above-mentioned analyses.

A2.3.2 | Statistical trend analyses for poultry monitoring data

Statistical trend analyses were carried out with the objective of evaluating the significance of temporal variations in the EU-level flock prevalence of *Salmonella* spp., in general, and target *Salmonella* serovars, specifically, in poultry over the last 10 (2015–2024) and 5 (2020–2024) years of NCP implementation.

The tested flocks can be either positive or negative for *Salmonella* spp. and target *Salmonella* serovars, and so the status of the flocks is a dichotomous outcome variable. Therefore, the binomial probability distribution for the response variable was assumed and the logit link function was computed in the model for the trend analysis. The logit is defined as the logarithm of $p/(1-p)$, where $p/(1-p)$ is the odds of being positive for *Salmonella* spp.

Temporal flock prevalence trends in the MSs were analysed using both linear and B-spline models to estimate the probability of *Salmonella*-positive flocks across different poultry populations over the last 10 years of NCP implementation. In addition, a linear trend analysis was carried out with a special focus on the last 5 years to identify any significant increase in the flock prevalence of *Salmonella* spp. or target *Salmonella* serovars. The trend analysis was conducted using generalised linear mixed models for repeated measures, accounting for the variability among MSs (EFSA, 2009, 2011). To take into account the different levels of probability of MSs having positive flocks (baselines), yet with similar patterns over time, a random MS-specific intercept effect was included in the model. To evaluate the trend over time, the 'time' variable was included in the model as a fixed effect. The correlation between repeated observations in the same MS in subsequent years was considered using a first autoregressive or exchangeable structure of the correlation matrix for the residuals. To evaluate the significance of the overall effect of fixed factors specified in the model, Type III F-tests were applied, whereas the receiver operating characteristic (ROC) curve was used to assess the goodness of fit of the model. A p-value < 0.10 was considered to be significant for both random and fixed effects.

GLIMMIX and SGPLOT procedures in SAS 9.4 software were used to fit the models and produce the graphical outputs, respectively.

Details about the estimated parameters of the models, odds ratios, prevalence rates and graphical analyses (conditional and marginal) are reported in the supporting information for this report ('*Salmonella* poultry outcome trend analyses' Excel file, link here).

A2.3.3 | Descriptive analyses of *Salmonella* serovars

With the aims of evaluating the distribution of *Salmonella* serovars across the food chain and identifying potential sources of human infections, a Sankey diagram was provided to link the food and food-producing animal sources to the four most commonly reported *Salmonella* serovars from human cases acquired within the EU (domestically or during travel within the EU). For animal categories covered by NCPs, only serovar data reported in the context of these programmes were presented. For cattle, meat-producing animals were considered, whereas for pigs, data from fattening animals were used. In addition to possible reporting biases as regards serovars, reporting for animal or food categories may also have been unbalanced and specific sources (e.g. cattle) may have been underrepresented.

Moreover, using data from the NCPs for laying hens, the proportion of *S.* Enteritidis-positive flocks among total *Salmonella* spp.-positive laying hen flocks was compared with the proportion of *S.* Enteritidis human cases acquired in the EU among all human salmonellosis cases with serovar information, over the last 10 years (2015–2024). The same comparison was made for the proportion of monophasic *S.* Typhimurium among serotyped isolates from pig meat and the proportion of human monophasic *S.* Typhimurium cases among all cases with serovar information. Pearson's and Spearman's correlation coefficients were calculated to assess the linear or monotonic relationships between positive laying hen flocks and human cases for *S.* Enteritidis, as well as between positive pig meat isolates and human cases for monophasic *S.* Typhimurium.

A2.4 | Results

A2.4.1 | Overview of key statistics, EU, 2020–2024

Humans

In 2024, the number of reported human salmonellosis cases and the notification rate were higher than in 2023 (Table 7). The number of reported human salmonellosis cases acquired in the EU (i.e. by domestic infection and through travel within the EU), the number of outbreak-related cases and the total number of food-borne salmonellosis outbreaks were higher in 2024 than in 2023. More detailed descriptions of these statistics are provided in the subsections below and in the chapter on food-borne outbreaks.

TABLE 7 Summary of *Salmonella* statistics relating to humans, major food categories and the main animal species, EU, 2020–2024.

	2024	2023	2022	2021	2020	Data source
Humans						
Total number of confirmed cases	79,703	77,487	65,478	62,161	52,690	ECDC
Total number of confirmed cases/100,000 population (notification rate)	18.6	18.3	15.6	16.8	14.3	ECDC
Number of reporting MSs	27	27	27	27	27	ECDC
Infection acquired in the EU	49,984	46,946	40,643	44,000	38,247	ECDC
Infection acquired outside the EU	5473	4768	3219	925	973	ECDC
Unknown travel status or unknown country of infection	24,246	25,773	21,616	17,236	13,470	ECDC
Number of outbreak-related cases	10,164	9210	6632	6755	3686	EFSA
Total number of outbreaks	1238	1115	1014	773	694	EFSA
Food[a]						
Meat and meat products						
Number of sampling units	893,986	874,991	952,344	977,302	557,344	EFSA
Number of reporting MSs	28	28	28	28	26	EFSA
Milk and milk products						
Number of sampling units	61,492	62,529	68,740	43,907	38,492	EFSA
Number of reporting MSs	24	25	24	25	24	EFSA
Fish and fishery products						
Number of sampling units	20,210	20,201	22,797	14,882	16,486	EFSA
Number of reporting MSs	24	25	25	25	23	EFSA
Eggs and egg products						
Number of sampling units	19,918	20,260	19,105	14,696	11,579	EFSA
Number of reporting MSs	21	20	22	22	18	EFSA
Fruits and vegetables (and juices)						
Number of sampling units	17,619	20,817	18,658	12,641	17,222	EFSA
Number of reporting MSs	24	25	25	23	23	EFSA
Animals[a]						
***Gallus gallus* (chickens)**						
Number of sampling units	797,883	744,260	742,299	803,640	619,772	EFSA
Number of reporting MSs	27	28	28	28	26	EFSA
Turkeys						
Number of sampling units	63,983	63,269	65,637	70,872	63,473	EFSA
Number of reporting MSs	24	26	26	25	22	EFSA

(Continues)

TABLE 7 (Continued)

	2024	2023	2022	2021	2020	Data source
Ducks and geese						
Number of sampling units	1863	2138	1187	3751	412	EFSA
Number of reporting MSs	6	7	6	10	6	EFSA
Pigs						
Number of sampling units	20,075	24,133	15,283	16,689	17,234	EFSA
Number of reporting MSs	13	15	15	15	10	EFSA
Cattle (bovine animals)						
Number of sampling units	23,098	28,862	22,904	26,061	28,363	EFSA
Number of reporting MSs	13	15	13	14	11	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States.

[a] The total number of sampling units was calculated by summing all reported sub-level entries for sampling units, stages, strategies and samplers, as listed in the EFSA Catalogue (EFSA, 2019).

Food categories

In 2024, the number of sampling units reported decreased compared with 2023 for the food category 'fruits and vegetables (including juices)'; it also decreased slightly for 'milk and milk products' and 'eggs and egg products'. Conversely, a modest increase was observed for 'meat and meat products'. Across all categories, the number of reporting MSs remained unchanged (Table 7).

Animal categories

Across all animal categories, the number of reporting MSs decreased between 2023 and 2024. The number of sampling units also declined for 'ducks and geese', 'pigs' and 'cattle (bovine animals)'. In contrast, despite fewer reporting MSs, the number of sampling units for '*Gallus gallus*' and 'turkeys' increased compared with 2023 (Table 7). More detailed descriptions of the above statistics are provided in the subsections below and in the chapter on food-borne outbreaks.

A2.4.2 | Human salmonellosis

In total, 79,703 human salmonellosis cases were reported by 27 MSs in 2024, corresponding to an EU notification rate of 18.6 cases per 100,000 population (Table 8), which was slightly higher (1.7%) than the rate in 2023.

As in the previous year, the highest notification rates in 2024 were reported by Slovakia (72.2 cases per 100,000 population) and Czechia (64.2 cases per 100,000 population), while the lowest rates were reported by Estonia, Ireland and Italy (≤ 7.5 cases per 100,000 population).

In 2024, most of the EU salmonellosis cases (70.3%; 56,010/79,703) were reported with data on importation status; 86.7% (48,553/56,010) of cases were reported as domestically acquired, while 13.3% (7457/56,010) were imported.

Among cases with information on both importation status and place of infection ($N = 55,457$), the majority (90.1%; 49,984/55,457) were reported as acquired within the EU (either domestically acquired or acquired in another EU country), while 9.9% (5473/55,457) were reported as acquired outside the EU. Among 1431 imported cases reported as acquired within the EU, the most frequently reported countries of infection were Spain (21.7%; 311/1431), Italy (12.4%; 177/1431), Greece (11.6%; 166/1431), Croatia (8.5%; 121/1431) and Poland (8.3%; 119/1431). Among 5473 imported cases reported as acquired outside the EU, the most frequently reported countries of infection were Türkiye (25.5%; 1398/5473), Egypt (11.5%; 628/5473), Thailand (9.8%; 536/5473), Morocco (6.9%; 356/5473) and Indonesia (5.5%; 300/5473).

TABLE 8 Reported confirmed human cases of salmonellosis and notification rates per 100,000 population in EU MSs and non-MS countries, by country and year, 2020–2024.

	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	National coverage[a]	Data format[a]	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	1413	15.4	1279	14.0	1192	13.3	993	11.1	817	9.2
Belgium[b]	N	C	2440	24.3	2040	20.4	2375	24.1	2084	18.0	1595	13.8
Bulgaria	Y	A	947	14.7	516	8.0	310	4.8	241	3.7	187	2.8
Croatia	Y	C	1484	38.4	1270	33.0	1047	27.1	593	15.2	786	20.0

TABLE 8 (Continued)

	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	**National coverage**[a]	**Data format**[a]	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**
Cyprus	Y	C	80	8.3	64	6.7	66	7.3	41	4.6	70	7.8
Czechia	Y	C	7003	64.2	7482	69.1	7563	71.9	9894	94.3	10,516	98.3
Denmark	Y	C	1266	21.2	1206	20.3	898	15.3	692	11.8	614	10.5
Estonia	Y	C	103	7.5	168	12.3	134	10.1	112	8.4	91	6.8
Finland	Y	C	779	13.9	803	14.4	666	12.0	474	8.6	516	9.3
France[c]	Y	C	12,308	18.0	11,848	17.4	11,162	16.4	9315	28.7	7071	21.8
Germany	Y	C	12,316	14.8	10,599	12.8	9064	10.9	8144	9.8	8664	10.4
Greece	Y	C	1052	10.1	936	9.0	640	6.1	284	2.7	381	3.6
Hungary	Y	C	4525	47.2	4416	46.0	3249	33.8	3298	34.2	2964	30.6
Ireland	Y	C	393	7.3	402	7.6	340	6.6	173	3.4	214	4.3
Italy	Y	C	2637	4.5	3333	5.6	3572	6.1	3768	6.4	2713	4.5
Latvia	Y	C	211	11.3	101	5.4	90	4.8	218	11.5	296	15.5
Lithuania	Y	C	406	14.1	344	12.0	234	8.3	281	10.0	419	14.9
Luxembourg	Y	C	220	32.7	167	25.3	161	24.9	133	21.0	93	14.9
Malta	Y	C	164	29.1	169	31.2	199	38.3	249	48.2	176	34.2
Netherlands[d]	N	C	1614	14.1	1456	12.8	1027	9.1	862	7.7	695	6.2
Poland	Y	C	8028	21.9	9196	25.0	6054	16.4	7708	20.8	5192	13.7
Portugal	Y	C	983	9.2	535	5.1	412	4.0	361	3.5	262	2.5
Romania	Y	C	2133	11.2	1388	7.3	1010	5.3	518	2.7	408	2.1
Slovakia	Y	C	3915	72.2	3999	73.7	3669	67.5	4439	81.3	3385	62.0
Slovenia	Y	C	423	19.9	297	14.0	384	18.2	185	8.8	214	10.2
Spain[e]	N	C	11,248	28.2	12,161	31.6	8832	25.5	6168	17.8	3526	–
Sweden	Y	C	1612	15.3	1312	12.5	1128	10.8	933	9.0	825	8.0
EU Total			**79,703**	**18.6**	**77,487**	**18.3**	**65,478**	**15.6**	**62,161**	**16.8**	**52,690**	**14.3**
Iceland	Y	C	69	18.0	55	14.2	42	11.2	53	14.4	32	8.8
Liechtenstein	Y	C	7	17.5	8	20.2	5	12.7	7	17.9	–	–
Norway	Y	C	1199	21.6	757	13.8	712	13.1	389	7.2	441	8.2
Switzerland[f]	Y	C	2337	26.1	1815	20.6	1837	21.0	1476	17.0	1253	14.6

Abbreviation: –, Data not reported.

[a] Y, yes; N, no; A, aggregated data; C, case-based data.

[b] Since 2022, notification rates have been calculated with an estimated population coverage of 85%.

[c] Sentinel system until 2021; notification rates were calculated with an estimated population coverage of 48%. For 2022, voluntary system with population coverage of 100%.

[d] Sentinel system; notification rates were calculated with an estimated population coverage of 64%.

[e] Sentinel system; notification rates were calculated with an estimated population coverage of 82% in 2024, 80% in 2023 and 73% in 2021–2022. No information on estimated coverage in 2020, so notification rate cannot be estimated.

[f] Switzerland provided data directly to EFSA. The human data for Switzerland include data from Liechtenstein for 2020.

A seasonal trend was observed for confirmed salmonellosis cases acquired within the EU in 2015–2024, with more cases reported during summer months (Figure 2). The overall trend for salmonellosis in 2020–2024 showed a significant increase. Seventeen countries observed a significantly increasing trend ($p < 0.05$), while no countries reported a significantly decreasing trend during the same period. The majority of countries showing an increasing trend between 2020 and 2024 continued to report case numbers and notification rates that were comparable to, or lower than, those seen before the COVID-19 pandemic.

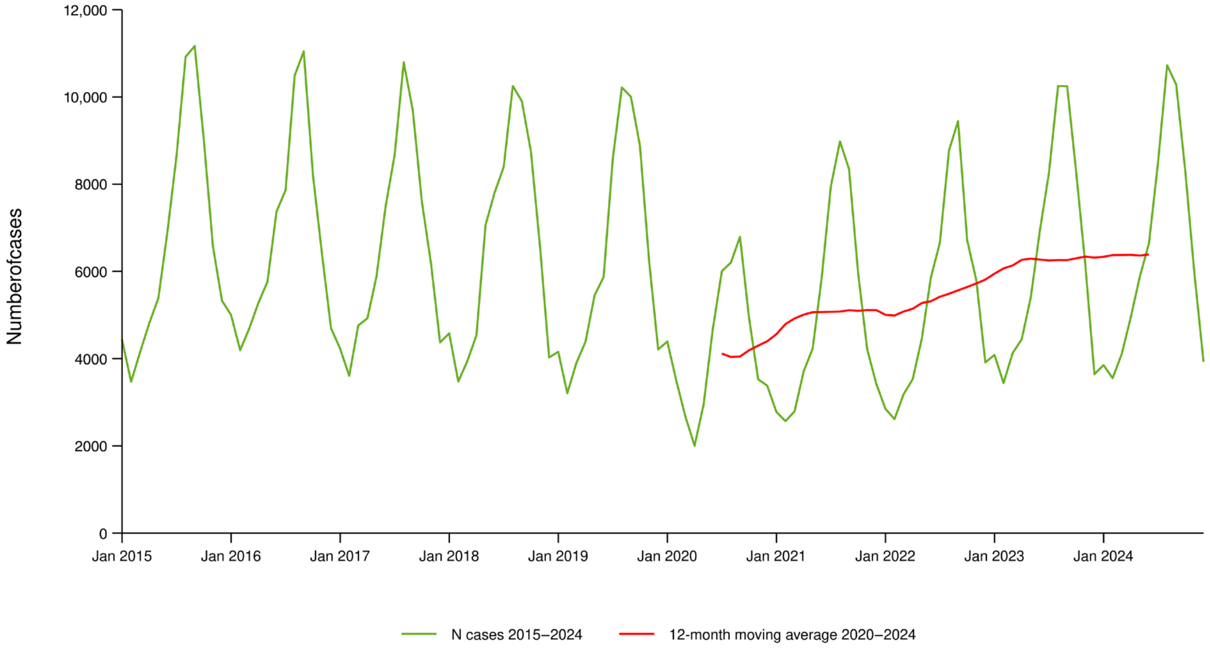

FIGURE 2 Trend in reported confirmed human cases of non-typhoidal salmonellosis in the EU by month, 2020–2024.
Source: Austria, Belgium, Denmark, Finland, France, Germany, Greece, Hungary, Ireland, Luxembourg, Netherlands, Poland, Portugal, Romania, Slovenia, Spain and Sweden.

A2.4.3 | *Salmonella* in food

Data collected in the context of Commission Regulation (EC) No 2073/2005 on microbiological criteria

Food safety criteria

The total number of official single samples collected at the distribution stage (*N* = 37,077; 21 MSs) was higher than at the manufacturing stage (*N* = 25,466; 18 MSs). However, the prevalence of *Salmonella*-positive samples was about twice as high at manufacturing (4.9%) as at distribution (2.3%) (Table 9). More than half (53.8%) of the single samples collected at manufacturing were 'fresh poultry meat'. Compared with 2023, both the number of reported 'fresh poultry meat' samples and the number of single samples increased at both stages. The rise was particularly notable at manufacturing, where 25,466 single samples were reported for 2024 – more than double the number reported in 2023 (10,313). The proportion of *Salmonella*-positive samples at distribution decreased slightly (2.3% in 2024 vs. 2.6% in 2023), whereas positivity at manufacturing nearly doubled (4.9% in 2024 vs. 2.5% in 2023).

Considering the food matrices, the highest levels of contamination were found for 'meat products made from poultry meat intended to be eaten cooked' (13.2% at the manufacturing stage and 5.0% at distribution), 'mechanically separated meat (MSM)' (12.8% at manufacturing and 3.6% at distribution), 'minced meat and meat preparations made from poultry meat intended to be eaten cooked' (9.9% at manufacturing and 5.8% at distribution) and 'fresh poultry meat' (7.7% at distribution and 6.3% at manufacturing). In particular, *Salmonella*-positive samples were also observed in 'live bivalve molluscs and live echinoderms, tunicates and gastropods' (6.4% at manufacturing), 'sprouted seeds (ready-to-eat)' (3.2% at distribution) and 'minced meat and meat preparations made from other species than poultry intended to be eaten cooked' (2.5% at manufacturing).

TABLE 9 Proportion (%) of *Salmonella*-positive samples from official sampling as part of the verification of *Salmonella* FSC in accordance with Commission Regulation (EC) No 2073/2005, by stage in the food chain, EU, 2024.

	Manufacturing stage (including processing)			**Distribution stage (including retail)**		
Food matrices	***N* MSs**	***N* tested samples**	***N* (%) positive**	***N* MSs**	***N* tested samples**	***N* (%) positive**
Cheeses, butter and cream made from raw milk or milk that has undergone a lower heat treatment than pasteurisation	9	1590	0	8	4603	20 (0.43)
Cooked crustaceans and molluscan shellfish	7	111	0	9	804	2 (0.25)
Dried follow-on formulae	1	2	0	8	958	0
Dried infant formulae and dried dietary foods for special medical purposes intended for infants below 6 months of age	1	90	0	6	1189	0

TABLE 9 (Continued)

Food matrices	Manufacturing stage (including processing)			Distribution stage (including retail)		
	N MSs	*N* tested samples	*N* (%) positive	*N* MSs	*N* tested samples	*N* (%) positive
Egg products, excluding products where the manufacturing process or the composition of the product will eliminate the *Salmonella* risk	8	143	0	6	170	0
Fresh poultry meat	11	13,710	863 (6.3)	17	4908	380 (7.7)
Gelatine and collagen	3	15	0	4	196	0
Ice cream, excluding products where the manufacturing process or the composition of the product will eliminate the *Salmonella* risk	9	239	0	9	1421	0
Live bivalve molluscs and live echinoderms, tunicates and gastropods	3	171	11 (6.4)	8	1576	9 (0.57)
Meat products intended to be eaten raw, excluding products where the manufacturing process or the composition of the product will eliminate the *Salmonella* risk	7	424	2 (0.47)	10	2362	19 (0.80)
Meat products made from poultry meat intended to be eaten cooked	5	204	27 (13.2)	8	721	36 (5.0)
Mechanically separated meat (MSM)	5	226	29 (12.8)	6	167	6 (3.6)
Milk powder and whey powder	8	719	0	7	350	0
Minced meat and meat preparations intended to be eaten raw	5	1347	24 (1.8)	7	419	5 (1.2)
Minced meat and meat preparations made from other species than poultry intended to be eaten cooked	12	4295	108 (2.5)	16	7654	128 (1.7)
Minced meat and meat preparations made from poultry meat intended to be eaten cooked	11	1870	185 (9.9)	16	3789	219 (5.8)
Precut fruit and vegetables (ready-to-eat)	5	247	2 (0.81)	13	3674	0
Ready-to-eat foods containing raw egg, excluding products where the manufacturing process or the composition of the product will eliminate the *Salmonella* risk	–	–	–	4	224	0
Sprouted seeds (ready-to-eat)	3	34	0	8	602	19 (3.2)
Unpasteurised fruit and vegetable juices (ready-to-eat)	3	29	0	12	1290	0
EU Total	**18**	**25,466**	**1251 (4.9)**	**21**	**37,077**	**843 (2.3)**

Abbreviation: MSs, Member States.

Five MSs (Belgium, Croatia, Ireland, Malta and Spain) reported sampling under the EU increased control programme on imported food, mandated by Commission Implementing Regulation (EU) 2019/1793,[27] which targets specific food categories imported from third countries. Out of 350 single samples tested, seven (2.0%) were positive for *Salmonella*: five in the category 'sesame seeds and similar' and two in 'peppers sweat', all reported by Spain. In addition, Belgium, Croatia and Ireland tested 271 batches. Nine (3.3%) of these were positive for *Salmonella*: three 'sesame paste (tahini)', three 'nuts-seeds based halva' and two 'seeds dried' samples from Belgium, as well as one 'nuts and nut products' sample from Croatia

Process hygiene criteria

Tables 10–16 present PHC monitoring statistics for carcases of various animal species, collected at slaughterhouses by both the CA and FBOp. The tables compare the proportions (%) of *Salmonella*-positive samples identified by each sampler, together with the corresponding *p*-values and interpretations. Moreover, the proportions reported by the countries with special guarantees in relation to *Salmonella* on carcases, as defined by Regulation (EC) No 853/2004,[28] are described.

For all species except goats and horses, the overall proportion of *Salmonella*-positive samples from official controls (CAs) was significantly higher than that from FBOp own checks. In addition, for both samplers, the proportions of *Salmonella*-positive neck skin samples from broilers and turkeys were markedly higher than those reported for carcase surface samples from pigs, ruminants (cattle, sheep and goats) and horses.

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[27] Commission Implementing Regulation (EU) 2019/1793 of 22 October 2019 on the temporary increase of official controls and emergency measures governing the entry into the Union of certain goods from certain third countries implementing Regulations (EU) 2017/625 and (EC) No 178/2002 of the European Parliament and of the Council and repealing Commission Regulations (EC) No 669/2009, (EU) No 884/2014, (EU) 2015/175, (EU) 2017/186 and (EU) 2018/1660. OJ L277, 29.10.2019, p. 89–129.

[28] Regulation (EC) No 853/2004 of the European Parliament and of the Council of 29 April 2004 laying down specific hygiene rules for on the hygiene of foodstuffs OJ L 139, 30.4.2004, p. 55.

Pig carcases

TABLE 10 Comparison of proportions (%) of *Salmonella*-positive single samples from pig carcases after dressing, but before chilling, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			**Food business operator (FBOp)**				
Country	***N* tested samples**	***N* (%) positive samples**	**CI$_{95}$**	***N* tested samples**	***N* (%) positive samples**	**CI$_{95}$**	***p*-value[a]**	**Interpretation**
Austria	–	–	–	3952	0	[0; 0.09][b]	–	–
Belgium	782	53 (6.8)	[5.1; 8.8]	3197	42 (1.3)	[0.95; 1.8]	< 0.001	CA > FBOp
Croatia	–	–	–	300	0	[0; 1.2][b]	–	–
Cyprus	16	1 (6.2)	[0.16; 30.2]	240	2 (0.83)	[0.10; 3.0]	NS	
Czechia	4438	35 (0.79)	[0.55; 1.1]	–	–	–	–	–
Denmark	–	–	–	9342	80 (0.86)	[0.68; 1.1]	–	–
Estonia	299	9 (3.0)	[1.4; 5.6]	1137	4 (0.35)	[0.10; 0.90]	< 0.001	CA > FBOp
France	–	–	–	11,148	542 (4.9)	[4.5; 5.3]	–	–
Germany	1083	63 (5.8)	[4.5; 7.4]	15,791	95 (0.60)	[0.49; 0.73]	< 0.001	CA > FBOp
Greece[c]	55	0	[0; 6.5][b]	625	0	[0; 0.59][b]	NS	
Hungary	1514	11 (0.73)	[0.36; 1.3]	–	–	–	–	–
Ireland	294	11 (3.7)	[1.9; 6.6]	2484	34 (1.4)	[0.95; 1.9]	0.0058	CA > FBOp
Italy	4812	191 (4.0)	[3.4; 4.6]	9409	139 (1.5)	[1.2; 1.7]	< 0.001	CA > FBOp
Latvia	605	6 (0.99)	[0.36; 2.1]	511	2 (0.39)	[0.05; 1.4]	NS	
Lithuania	700	28 (4.0)	[2.7; 5.7]	–	–	–	–	–
Luxembourg	40	1 (2.5)	[0.06; 13.2]	155	0	[0; 2.4][b]	NS	
Malta	60	11 (18.3)	[9.5; 30.4]	180	5 (2.8)	[0.91; 6.4]	< 0.001	CA > FBOp
Netherlands	183	18 (9.8)	[5.9; 15.1]	5930	171 (2.9)	[2.5; 3.3]	< 0.001	CA > FBOp
Poland	5667	83 (1.5)	[1.2; 1.8]	16,711	6 (0.04)	[0.01; 0.08]	< 0.001	CA > FBOp
Portugal	–	–	–	7622	94 (1.2)	[1.0; 1.5]	–	–
Romania	1524	0	[0; 0.24][b]	5117	6 (0.12)	[0.04; 0.26]	NS	
Slovakia	–	–	–	2295	0	[0; 0.16][b]	–	–
Slovenia	–	–	–	1027	5 (0.49)	[0.16; 1.1]	–	–
Spain	1945	207 (10.6)	[9.3; 12.1]	10,771	181 (1.7)	[1.4; 1.9]	< 0.001	CA > FBOp
United Kingdom (Northern Ireland)	–	–	–	590	3 (0.51)	[0.10; 1.5]	–	–
EU Total (27 + XI)	**24,017**	**728 (3.0)**	**[2.8; 3.3]**	**108,534**	**1411 (1.3)**	**[1.2; 1.4]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**17,365**	**654 (3.8)**	**[3.5; 4.1]**	**72,258**	**687 (0.95)**	**[0.88; 1.0]**	**< 0.001**	**CA > FBOp**

Abbreviation: –, Data not reported.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

[c] Greece informed during the last phase of the production of this report of a reporting error and that 60 samples had been taken by the competent authority, with 1 positive (1.7%). Based on the revised data from the competent authority, the 'EU Total (27+XI)' tested samples amount to 24,022, with 729 positives (3.0%), while the 'EU Total (27+XI) providing CA and FBOp data' tested samples amount to 17,370, with 655 positives (3.8%).

Finland, Iceland, Norway and Sweden – countries with special guarantees regarding *Salmonella* on pig carcases – reported the following monitoring results: 0 positive out of 2456 own-check samples in Finland; 42 positives out of 1814 official samples (2.3%) in Iceland; 0 positive out of 2969 official samples in Norway; and 0 positive out of 6453 official samples in Sweden. In addition, Switzerland reported 0 positive out of 1023 FBOp samples and Montenegro 0 positive out of five official samples.

Broiler carcases

TABLE 11 Comparison of proportions (%) of *Salmonella*-positive single samples from broiler carcases (neck skin samples) after chilling, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***p*-value[a]**	**Interpretation**
Austria	–	–	–	1065	241 (22.6)	[20.1; 25.3]	–	–
Belgium	551	59 (10.7)	[8.3; 13.6]	2694	148 (5.5)	[4.7; 6.4]	< 0.001	CA > FBOp
Croatia	–	–	–	130	15 (11.5)	[6.6; 18.3]	–	–
Cyprus	170	95 (55.9)	[48.1; 63.5]	651	18 (2.8)	[1.6; 4.3]	< 0.001	CA > FBOp
Czechia	760	78 (10.3)	[8.2; 12.6]	–	–	–	–	–
Denmark	–	–	–	233	0	[0; 1.6][b]	–	–
Estonia	–	–	–	330	0	[0; 1.1][b]	–	–
France	–	–	–	15,327	172 (1.1)	[0.96; 1.3]	–	–
Germany	–	–	–	15,187	422 (2.8)	[2.5; 3.1]	–	–
Greece[c]	70	0	[0; 5.1][b]	12,669	0	[0; 0.03][b]	NS	
Hungary	610	115 (18.9)	[15.8; 22.2]	–	–	–	–	–
Ireland	271	17 (6.3)	[3.7; 9.9]	1091	23 (2.1)	[1.3; 3.1]	< 0.001	CA > FBOp
Italy	1427	472 (33.1)	[30.6; 35.6]	5858	837 (14.3)	[13.4; 15.2]	< 0.001	CA > FBOp
Latvia	100	5 (5.0)	[1.6; 11.3]	659	11 (1.7)	[0.84; 3.0]	0.0476	CA > FBOp
Lithuania	640	58 (9.1)	[7.0; 11.6]	–	–	–	–	–
Luxembourg	5	0	[–]	–	–	–	–	–
Malta	34	22 (64.7)	[46.5; 80.3]	–	–	–	–	–
Netherlands	284	41 (14.4)	[10.6; 19.1]	3422	304 (8.9)	[8.0; 9.9]	0.001	CA > FBOp
Poland	–	–	–	1633	0	[0; 0.23][b]	–	–
Portugal	–	–	–	2781	8 (0.29)	[0.12; 0.57]	–	–
Romania	940	97 (10.3)	[8.4; 12.4]	4200	76 (1.8)	[1.4; 2.3]	< 0.001	CA > FBOp
Slovakia	–	–	–	533	0	[0; 0.69][b]	–	–
Slovenia	–	–	–	838	55 (6.6)	[5.0; 8.5]	–	–
Spain	1299	141 (10.9)	[9.2; 12.7]	5867	395 (6.7)	[6.1; 7.4]	< 0.001	CA > FBOp
United Kingdom (Northern Ireland)	–	–	–	366	1 (0.27)	[0.01; 1.5]	–	–
EU Total (27 + XI)	**7161**	**1200 (16.8)**	**[15.9; 17.6]**	**75,534**	**2726 (3.6)**	**[3.5; 3.7]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**5112**	**927 (18.1)**	**[17.1; 19.2]**	**37,111**	**1812 (4.9)**	**[4.7; 5.1]**	**< 0.001**	**CA > FBOp**

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

[c] Greece informed during the last phase of the production of this report of a reporting error and that 110 samples had been taken by the competent authority, with 34 positive (30.9%). Based on the revised data from the competent authority, the 'EU Total (27+XI)' tested samples amount to 7201, with 1234 positives (17.1%), while the 'EU Total (27+XI) providing CA and FBOp data' tested samples amount to 5152, with 961 positives (18.7%).

Finland, Iceland and Sweden – countries with special guarantees regarding *Salmonella* on broiler carcases – reported the following monitoring results: 0 out of 1060 FBOp samples in Finland; 7 positive out of 745 official samples (0.94%) in Iceland; and 0 out of 2117 CA samples in Sweden. In addition, Switzerland reported 1 positive out of 302 FBOp samples (0.33%) and Montenegro no positive out of either 55 FBOp samples or 90 CA samples.

Turkey carcases

TABLE 12 Comparison of proportions (%) of *Salmonella*-positive single samples from turkey carcases (neck skin samples) after chilling, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***p*-value[a]**	**Interpretation**
Austria	–	–	–	151	4 (2.6)	[0.73; 6.6]	–	–
Belgium	38	0	[0; 9.3][b]	140	5 (3.6)	[1.2; 8.1]	NS	
Croatia	–	–	–	60	0	[0; 6.0][b]	–	–
Cyprus	–	–	–	5	0	[–]	–	–
Czechia	265	3 (1.1)	[0.23; 3.3]	–	–	–	–	–
Germany	–	–	–	1454	191 (13.1)	[11.4; 15.0]	–	–
Greece	–	–	–	2699	0	[0; 0.14][b]	–	–
Hungary	553	28 (5.1)	[3.4; 7.2]	–	–	–	–	–
Ireland	30	0	[0; 11.6][b]	567	0	[0; 0.65][b]	NS	
Italy	229	69 (30.1)	[24.3; 36.5]	960	121 (12.6)	[10.6; 14.9]	< 0.001	CA > FBOp
Latvia	–	–	–	4	0	[–]	–	–
Poland	–	–	–	410	0	[0; 0.90][b]	–	–
Portugal	–	–	–	829	4 (0.48)	[0.13; 1.2]	–	–
Romania	50	0	[0; 7.1][b]	300	0	[0; 1.2][b]	NS	
Slovakia	–	–	–	55	0	[0; 6.5][b]	–	–
Slovenia[c]	–	–	–	4	4 (100)	[–]	–	–
Spain	130	14 (10.8)	[6.0; 17.4]	1632	0	[0; 0.23][b]	< 0.001	CA > FBOp
United Kingdom (Northern Ireland)	–	–	–	10	0	[0; 30.8][b]	–	–
EU Total (27 + XI)	**1295**	**114 (8.8)**	**[7.3; 10.5]**	**9280**	**329 (3.5)**	**[3.2; 3.9]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**477**	**83 (17.4)**	**[14.1; 21.1]**	**3599**	**126 (3.5)**	**[2.9; 4.2]**	**< 0.001**	**CA > FBOp**

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

[c] Slovenia informed during the last phase of the production of this report of a reporting error and that 115 samples had been taken by the food business operators, with 4 positives (3.5%). Based on the revised data from food business operators, the 'EU Total (27+XI)' tested samples are 9391, with 329 positive (3.5%).

Finland, Iceland and Sweden – countries with special guarantees regarding *Salmonella* on turkey carcases – reported no positive results: 0 out of 306 FBOp samples in Finland; 0 positive out of 71 CA samples in Iceland; and 0 out of 104 CA samples in Sweden. In addition, Switzerland reported 0 positive out of 130 FBOp samples.

Bovine carcases

TABLE 13 Comparison of proportions (%) of *Salmonella*-positive single samples from bovine carcases after dressing but before chilling, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***p*-value[a]**	**Interpretation**
Austria	–	–	–	2516	2 (0.08)	[0.01; 0.29]	–	–
Belgium	1083	7 (0.65)	[0.26; 1.3]	3349	11 (0.33)	[0.16; 0.59]	NS	
Croatia	–	–	–	291	0	[0; 1.3][b]	–	–
Cyprus	30	14 (46.7)	[28.3; 65.7]	120	5 (4.2)	[1.4; 9.5]	< 0.001	CA > FBOp
Czechia	3633	28 (0.77)	[0.51; 1.1]	–	–	–	–	–
Denmark	–	–	–	2264	4 (0.18)	[0.05; 0.45]	–	–

TABLE 13 (Continued)

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***p*-value[a]**	**Interpretation**
Estonia	189	4 (2.1)	[0.58; 5.3]	697	7 (1.0)	[0.40; 2.1]	NS	
France	–	–	–	17,330	118 (0.68)	[0.56; 0.81]	–	–
Germany	–	–	–	9690	13 (0.13)	[0.07; 0.23]	–	–
Greece[c]	38	0	[0; 9.3][b]	378	0	[0; 0.97][b]	NS	
Hungary	215	1 (0.47)	[0.01; 2.6]	–	–	–	–	–
Ireland	–	–	–	6653	0	[0; 0.06][b]	–	–
Italy	3298	40 (1.2)	[0.87; 1.6]	12,748	21 (0.16)	[0.10; 0.25]	< 0.001	CA > FBOp
Latvia	400	2 (0.50)	[0.06; 1.8]	2850	0	[0; 0.13][b]	0.0151	CA > FBOp
Lithuania	184	0	[0; 2.0][b]	–	–	–	–	–
Luxembourg	20	0	[0; 16.8][b]	130	0	[0; 2.8][b]	NS	
Malta	–	–	–	180	15 (8.3)	[4.7; 13.4]	–	–
Netherlands	248	7 (2.8)	[1.1; 5.7]	5403	21 (0.39)	[0.24; 0.59]	< 0.001	CA > FBOp
Poland	1153	13 (1.1)	[0.60; 1.9]	2952	19 (0.64)	[0.39; 1.0]	0.0566	CA > FBOp
Portugal	–	–	–	3657	5 (0.14)	[0.04; 0.32]	–	–
Romania	1486	0	[0; 0.25][b]	3622	0	[0; 0.10][b]	NS	
Slovakia	–	–	–	1775	0	[0; 0.21][b]	–	–
Slovenia	–	–	–	1930	0	[0; 0.19][b]	–	–
Spain	655	41 (6.3)	[4.5; 8.4]	4711	25 (0.53)	[0.34; 0.78]	< 0.001	CA > FBOp
United Kingdom (Northern Ireland)	–	–	–	1789	0	[0; 0.21][b]	–	–
EU Total (27 + XI)	**12,632**	**157 (1.2)**	**[1.1; 1.5]**	**85,035**	**266 (0.31)**	**[0.28; 0.35]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**8600**	**128 (1.5)**	**[1.2; 1.8]**	**36,960**	**109 (0.29)**	**[0.24; 0.36]**	**< 0.001**	**CA > FBOp**

Abbreviation: –, Data not reported.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

[c] Greece informed during the last phase of the production of this report of a reporting error and that 43 samples had been taken by the competent authority, with two positives (4.7%). Based on the revised data from the competent authority, the 'EU Total (27+XI)' tested samples amount to 12,637, with 159 positives (1.3%), while the 'EU Total (27+XI) providing CA and FBOp data' tested samples amount to 8605, with 130 positives (1.5%).

Finland, Iceland, Norway and Sweden – countries with special guarantees regarding *Salmonella* on bovine carcases – reported no positive results: 0 out of 2315 FBOp samples in Finland; 0 positive out of 200 FBOp samples in Iceland; 0 out of 3067 official samples in Norway; and 0 out of 3952 official controls in Sweden. In addition, Switzerland reported 0 out of 968 FBOp own-check samples and Montenegro 0 out of 121 FBOp samples and 0 out of 135 CA samples.

Sheep carcases

TABLE 14 Comparison of proportions (%) of *Salmonella*-positive single samples from sheep carcases after dressing but before chilling, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***N* tested samples**	***N* (%) positive samples**	**CI_{95}**	***p*-value[a]**	**Interpretation**
Austria	–	–	–	300	0	[0; 1.2][b]	–	–
Belgium	282	0	[0; 1.3][b]	779	9 (1.2)	[0.53; 2.2]	0.0612	CA < FBOp

(Continues)

TABLE 14 (Continued)

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI$_{95}$**	***N* tested samples**	***N* (%) positive samples**	**CI$_{95}$**	***p*-value[a]**	**Interpretation**
Croatia	–	–	–	55	0	[0; 6.5][b]	–	–
Cyprus	–	–	–	280	1 (0.36)	[0.01; 2.0]	–	–
Czechia	292	2 (0.68)	[0.08; 2.5]	–	–	–	–	–
Estonia	1	0	[–]	76	2 (2.6)	[0.32; 9.2]	–	–
Finland	–	–	–	113	3 (2.7)	[0.55; 7.6]	–	–
France	–	–	–	6449	57 (0.88)	[0.67; 1.1]	–	–
Germany	–	–	–	514	1 (0.19)	[0; 1.1]	–	–
Greece	70	0	[0; 5.1][b]	443	0	[0; 0.83][b]	NS	
Hungary	234	0	[0; 1.6][b]	–	–	–	–	–
Ireland	–	–	–	1512	0	[0; 0.24][b]	–	–
Italy	447	4 (0.89)	[0.24; 2.3]	1451	1 (0.07)	[0; 0.38]	0.0124	CA > FBOp
Latvia	–	–	–	122	0	[0; 3.0][b]	–	–
Luxembourg	–	–	–	9	0	[–]	–	–
Malta	–	–	–	142	8 (5.6)	[2.5; 10.8]	–	–
Netherlands	49	1 (2.0)	[0.05; 10.9]	267	0	[0; 1.4][b]	NS	
Poland	21	0	[0; 16.1][b]	135	0	[0; 2.7][b]	NS	
Portugal	–	–	–	2624	7 (0.27)	[0.11; 0.55]	–	–
Romania	597	0	[0; 0.62][b]	1350	0	[0; 0.27][b]	NS	
Slovakia	–	–	–	215	0	[0; 1.7][b]	–	–
Slovenia	–	–	–	136	0	[0; 2.7][b]	–	–
Spain	520	19 (3.7)	[2.2; 5.6]	5033	25 (0.50)	[0.32; 0.73]	< 0.001	CA > FBOp
United Kingdom (Northern Ireland)	–	–	–	626	0	[0; 0.59][b]	–	–
EU Total (27 + XI)	**2513**	**26 (1.0)**	**[0.68; 1.5]**	**22,631**	**114 (0.50)**	**[0.42; 0.60]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**1987**	**24 (1.2)**	**[0.78; 1.8]**	**9534**	**37 (0.39)**	**[0.27; 0.53]**	**< 0.001**	**CA > FBOp**

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Iceland reported 0 positive out of 65 FBOp samples, Switzerland 0 out of 235 sheep carcase samples collected by the FBOp and Montenegro 0 out of 66 CA samples and 0 out of 3 FBOp samples.

Goat carcases

TABLE 15 Comparison of proportions (%) of *Salmonella*-positive single samples from goat carcases after dressing but before chilling, by sampler and reporting MS, EU, 2024.

	Competent authority (CA)			Food business operator (FBOp)				
Country	***N* tested samples**	***N* (%) positive samples**	**CI$_{95}$**	***N* tested samples**	***N* (%) positive samples**	**CI$_{95}$**	***p*-value[a]**	**Interpretation**
Austria	–	–	–	16	0	[0; 20.6][b]	–	–
Belgium	118	0	[0; 3.1][b]	263	4 (1.5)	[0.42; 3.8]	NS	
Cyprus	–	–	–	340	2 (0.59)	[0.07; 2.1]	–	–
Czechia	31	0	[0; 11.2][b]	–	–	–	–	–
France	–	–	–	215	2 (0.93)	[0.11; 3.3]	–	–

TABLE 15 (Continued)

Country	Competent authority (CA)			Food business operator (FBOp)				
	N tested samples	*N* (%) positive samples	CI$_{95}$	*N* tested samples	*N* (%) positive samples	CI$_{95}$	*p*-value[a]	Interpretation
Germany	–	–	–	16	0	[0; 20.6][b]	–	–
Greece	5	0	[–]	77	0	[0; 4.7][b]	–	–
Italy	106	0	[0; 3.4][b]	249	0	[0; 1.5][b]	NS	
Latvia	–	–	–	34	0	[0; 10.3][b]	–	–
Luxembourg	–	–	–	3	0	[–]	–	–
Malta	–	–	–	38	2 (5.3)	[0.64; 17.7]	–	–
Netherlands	91	0	[0; 4.0][b]	281	0	[0; 1.3][b]	NS	
Poland	–	–	–	5	0	[–]	–	–
Portugal	–	–	–	903	1 (0.11)	[0; 0.62]	–	–
Romania	5	0	[–]	10	0	[0; 30.8][b]	–	–
Slovenia	–	–	–	35	0	[0; 10.0][b]	–	–
Spain	125	1 (0.80)	[0.02; 4.4]	24	0	[0; 14.2][b]	NS	
EU Total (27 + XI)	**481**	**1 (0.21)**	**[0.01; 1.2]**	**2509**	**11 (0.44)**	**[0.22; 0.78]**	**NS**	
EU Total (27 + XI) providing CA and FBOp data	**450**	**1 (0.22)**	**[0.01; 1.2]**	**904**	**4 (0.44)**	**[0.12; 1.1]**	**NS**	

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Horse carcases

TABLE 16 Comparison of proportions (%) of *Salmonella*-positive single samples from horse carcases before chilling, by sampler and reporting MS, EU, 2024.

Country	Competent authority (CA)			Food business operator (FBOp)				
	N tested samples	*N* (%) positive samples	CI$_{95}$	*N* tested samples	*N* (%) positive samples	CI$_{95}$	*p*-value[a]	Interpretation
Austria	–	–	–	4	0	[–]	–	–
Belgium	32	0	[0; 10.9][b]	113	2 (1.8)	[0.22; 6.2]	NS	
Czechia	3	0	[–]	–	–	–	–	–
France	–	–	–	65	0	[0; 5.5][b]	–	–
Finland	–	–	–	16	0	[0; 20.6][b]		
Germany	–	–	–	12	0	[0; 26.5][b]	–	–
Italy	200	3 (1.5)	[0.31; 4.3]	220	1 (0.45)	[0.01; 2.5]	NS	
Latvia	–	–	–	1	0	[–]	–	–
Netherlands	–	–	–	12	0	[0; 26.5][b]	–	–
Poland	61	0	[0; 5.9][b]	60	0	[0; 6.0][b]	NS	
Portugal	–	–	–	20	0	[0; 16.8][b]	–	–
Romania	61	0	[0; 5.9][b]	176	0	[0; 2.1][b]	NS	
Slovenia	–	–	–	31	0	[0; 11.2][b]	–	–
Spain	19	0	[0; 17.6][b]	85	1 (1.2)	[0.03; 6.4]	NS	
EU Total (27 + XI)	**376**	**3 (0.80)**	**[0.16; 2.3]**	**815**	**4 (0.49)**	**[0.13; 1.2]**	**NS**	
EU Total (27 + XI) providing CA and FBOp data	**373**	**3 (0.80)**	**[0.17; 2.3]**	**654**	**4 (0.61)**	**[0.17; 1.6]**	**NS**	

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Iceland reported 0 positive out of 80 horse carcase samples collected by the FBOp.

Occurrence in food

Monitoring data reported for food sampling units, which do not fit with the criteria described in the previous paragraphs, were described by merging investigations from all sampling stages (primary production, manufacturing, distribution and others), all samplers except 'HACCP and own checks' and 'private sampling', and all sampling units (single, batch and slaughter animal batch). Only sampling units collected through 'objective sampling' were considered in this context.

RTE food and non-RTE food

For 2024, 102,696 RTE and 520,720 non-RTE food sampling units were reported from 24 and 28 MSs with very low (0.23%) and low (2.3%) proportions of positive samples, respectively.

Within the category of RTE food, the vast majority of the sampled matrices had very low (< 1%) proportions of *Salmonella*-positive units, with the exception of 'meat and meat products from turkeys', 'sprouts (sprouted seeds)' and 'meat and meat products from broilers', for which the prevalence of positive sampling units was low (3.2%; *N* = 248; 2.9%; *N* = 694 and 1.3%; *N* = 715, respectively).

Within the category of non-RTE food, the highest percentages of positive sampling units were reported for 'meat and meat products from broilers' (5.1%; *N* = 104,662), 'meat and meat products from turkeys' (4.7%; *N* = 13,317), 'other meat and meat products' (2.5%; *N* = 89,308), 'meat and meat products from pigs' (1.9%; *N* = 153,001) and 'mixed meat products' (1.1%; *N* = 21,480). The lowest prevalence was found in 'meat and meat products from bovine animals' (0.65%; *N* = 99,944). 'other meat and meat products' includes meat from species different from those previously mentioned. For all the other food matrices different from meat and meat products, the proportion of *Salmonella*-positive units was very low (< 1%): it was 0.64% for 'fruits, vegetables and juices' (*N* = 2354), 0.47% for 'fish and fishery products' (*N* = 11,933), 0.31% for 'eggs and egg products' (*N* = 12,327), 0.17% for 'cereals, dried seeds' (*N* = 1193) and 0.01% for 'milk and milk products' (*N* = 7280).

Comparing the results for the year 2024 and the previous four-year period (2020–2023), the overall percentage of *Salmonella*-positive sampling units was rather stable, both for RTE food sampling units (0.23% in 2024 and 0.20% in the previous 4 years) and for non-RTE food (2.3% in 2024 and 2.1% previously).

Fresh meat

In 2024, 2.4% of fresh meat sampling units (*N* = 413,568) tested positive for *Salmonella*. The highest percentages of positive samples were reported for 'fresh meat from broilers' (*N* = 95,954; 4.9%) and 'fresh meat from turkeys' (*N* = 12,809; 4.7%). Compared to the previous four-year period (2020–2023), no notable changes in prevalence were detected. Lower percentages of positive samples were found for 'fresh meat from pigs' (*N* = 130,377; 1.6%) and 'fresh meat from bovine animals' (*N* = 96,782; 0.57%).

A2.4.4 | *Salmonella* in animals

Poultry monitoring data in accordance with the national control programmes for *Salmonella*

Achievement of Salmonella reduction targets

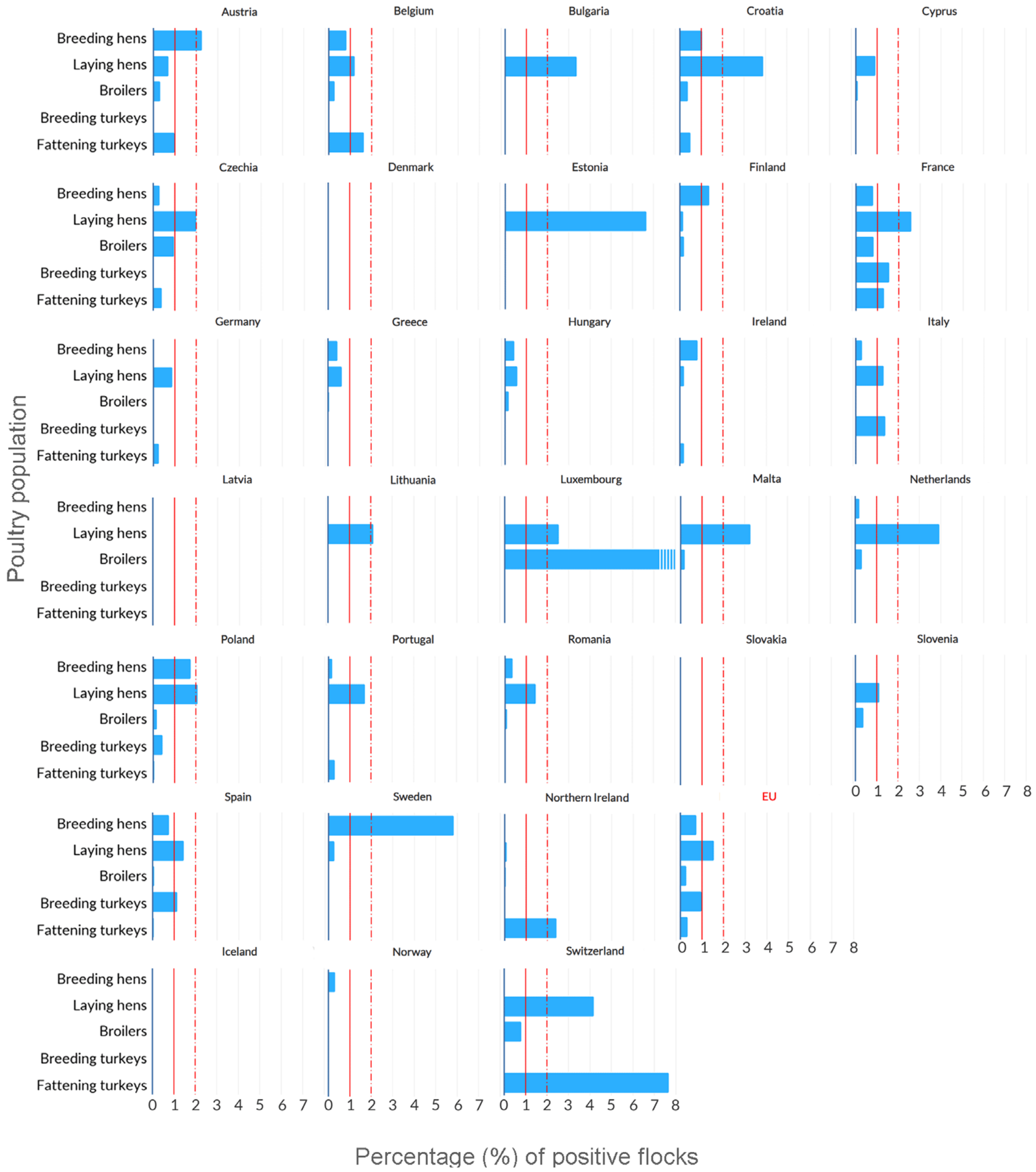

FIGURE 3 Prevalence of poultry flocks (breeding flocks of *Gallus gallus*, laying hens, broilers, breeding turkeys and fattening turkeys) positive for target *Salmonella* serovars, EU MSs and non-MS countries, 2024.
Vertical bars indicate the target to be reached, which was set at 1% for all poultry populations except for laying hens, for which it was 2%. The solid red vertical lines indicate the target for all poultry populations except laying hens, while the dotted vertical lines denote the target specifically for laying hens. For adult breeding *Gallus gallus*, in accordance with Commission Regulation (EU) No 200/2010,[28] Croatia reached the reduction target (Article 1.1: one adult flock can remain positive for target *Salmonella* serovars for MSs with less than 100 flocks). For laying hens, in accordance with Commission Regulation (EC) No 517/2011,[30] Estonia and Lithuania reached the reduction target (Article 1(b): one adult flock can remain positive for target *Salmonella* serovars for MSs with less than 50 flocks). Spain (for breeding turkeys) and the United Kingdom (Northern Ireland) (for fattening turkeys) reached the reduction target according to Commission Regulation (EU) No 1190/2012[31] (Article 1.1: one adult flock can remain positive for target *Salmonella* serovars for MSs with less than 100 flocks).

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[28] Commission Regulation (EU) No 200/2010 of 10 March 2010 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Union target for the reduction of the prevalence of *Salmonella* serotypes in adult breeding flocks of *Gallus gallus*. OJ L 61, 11.3.2010, p. 1–9.

[30] Commission Regulation (EU) No 517/2011 of 25 May 2011 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Union target for the reduction of the prevalence of certain *Salmonella* serotypes in laying hens of *Gallus gallus* and amending Regulation (EC) No 2160/2003 and Commission Regulation (EU) No 200/2010. OJ L 138, 26.5.2011, p. 45–51.

[31] Commission Regulation (EU) No 1190/2012 of 12 December 2012 concerning a Union target for the reduction of *Salmonella* Enteritidis and *Salmonella* Typhimurium in flocks of turkeys, as provided for in Regulation (EC) No 2160/2003 of the European Parliament and of the Council. OJ L 340, 13.12.2012, p. 29–34.

Breeding flocks of Gallus gallus

Rearing flocks

Fourteen MSs and the United Kingdom (Northern Ireland) reported merged data (official controls and food business operator checks) on *Salmonella* prevalence in rearing flocks of breeding *Gallus gallus*. Three of these countries also reported official and own-check data separately. Eight MSs (Bulgaria, Croatia, Estonia, Hungary, Lithuania, Luxembourg, Malta and Slovakia) did not provide data (Table 17). Based on the merged data and the FBOp data alone, the prevalence of *Salmonella*-positive rearing flocks was 1.1% and 1.0%, respectively.

TABLE 17 *Salmonella* in breeding flocks of *Gallus gallus* during the rearing period in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

	Merged		**Competent authority (CA)**		**Food business operator (FBOp)**	
Country	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**
Austria	90	2 (2.2)	9	0	89	2 (2.2)
Belgium	321	1 (0.31)	–	–	140	0
Cyprus	41	1 (2.4)	–	–	–	–
Czechia	–	–	–	–	607	0
Denmark	113	0	–	–	–	–
Finland	92	0	–	–	75	0
France	1149	20 (1.7)	125	0	1024	20 (2.0)
Germany	213	0	–	–	204	0
Greece[a]	203	0	–	–	324	0
Ireland	47	0	–	–	–	–
Italy	655	5 (0.76)	17	0	655	5 (0.76)
Latvia	24	0	–	–	20	0
Netherlands	864	4 (0.46)	–	–	–	–
Poland	–	–	–	–	1099	1 (0.09)
Portugal	–	–	–	–	258	0
Romania	–	–	–	–	365	9 (2.5)
Slovenia	–	–	–	–	55	1 (1.8)
Spain	939	22 (2.3)	–	–	939	22 (2.3)
Sweden	122	0	–	–	–	–
United Kingdom (Northern Ireland)	164	0	–	–	–	–
EU Total (27 + XI)	**5037**	**55 (1.1)**	**151**	**0**	**5854**	**60 (1.0)**
Iceland	–	–	–	–	31	0
Norway	55	0	–	–	–	–
Switzerland	–	–	–	–	62	0

Abbreviation: –, Data not reported.

[a] Greece informed during the last phase of the production of this report of a reporting error and that 203 flocks had been tested by the food business operators, with 0 positive (0%) for *Salmonella* spp. Based on the revised data from the food business operators, the 'EU Total (27+XI)' tested flocks amount to 5733, with 60 positives (1.0%) for *Salmonella* spp.

Adult flocks

All MSs and the United Kingdom (Northern Ireland), except Slovakia, reported *Salmonella* NCP data for adult breeding flocks of *Gallus gallus*. Luxembourg and Malta do not keep such flocks. In 2024, the EU *Salmonella* flock prevalence was 2.7%, compared with 2.3% in 2023 and 2.1% in 2022. The prevalence of flocks positive for any of the five target serovars (*S.* Enteritidis, *S.* Typhimurium including monophasic *S.* Typhimurium, *S.* Infantis, *S.* Virchow and *S.* Hadar) was 0.75%, compared with 0.58% in 2023 and 0.79% in 2022 (Table 18). All reporting countries met the flock prevalence reduction target of a maximum of 1%, except Austria, Finland, Poland and Sweden (Figure 3).

TABLE 18 *Salmonella* in breeding flocks of *Gallus gallus* during the production period (all types of breeding flocks, flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

Country	*N* tested flocks	*N* (%) positive for *Salmonella* spp.	*N* (%) positive for target serovars	*N* (%) positive samples for				
				S. Enteritidis	*S.* Typhimurium[a]	*S.* Hadar	*S.* Infantis	*S.* Virchow
Austria	**176**	**10 (5.7)**	**4 (2.3)**	**3 (1.7)**	**1 (0.57)**	**0**	**0**	**0**
Belgium	602	10 (1.7)	5 (0.83)	1 (0.17)	4 (0.66)	0	0	0
Bulgaria	6	0	0	0	0	0	0	0
Croatia	94	4 (4.3)	1 (1.1)[b]	0	0	1 (1.1)	0	0
Cyprus	39	1 (2.6)	0	0	0	0	0	0
Czechia	651	9 (1.4)	2 (0.31)	2 (0.31)	0	0	0	0
Denmark	183	0	0	0	0	0	0	0
Estonia	9	0	0	0	0	0	0	0
Finland	**144**	**2 (1.4)**	**2 (1.4)**	**0**	**2 (1.4)**	**0**	**0**	**0**
France	1235	17 (1.4)	10 (0.81)	9 (0.73)	1 (0.08)	0	0	0
Germany	787	2 (0.25)	0	0	0	0	0	0
Greece	220	11 (5.0)	1 (0.45)	1 (0.45)	0	0	0	0
Hungary	439	2 (0.46)	2 (0.46)	2 (0.46)	0	0	0	0
Ireland	119	1 (0.84)	1 (0.84)	0	1 (0.84)	0	0	0
Italy	1236	62 (5.0)	4 (0.32)	0	2 (0.16)	0	2 (0.16)	0
Latvia	36	0	0	0	0	0	0	0
Lithuania	42	1 (2.4)	0	0	0	0	0	0
Netherlands	1450	13 (0.90)	3 (0.21)	3 (0.21)	0	0	0	0
Poland	**2040**	**42 (2.1)**	**36 (1.8)**	**35 (1.7)**	**0**	**1 (0.05)**	**0**	**0**
Portugal	525	7 (1.3)	1 (0.19)	0	1 (0.19)	0	0	0
Romania	520	34 (6.5)	2 (0.38)	0	0	0	2 (0.38)	0
Slovenia	97	0	0	0	0	0	0	0
Spain	1663	99 (6.0)	13 (0.78)	3 (0.18)	3 (0.18)	0	6 (0.36)	1 (0.06)
Sweden	**137**	**8 (5.8)**	**8 (5.8)**	**8 (5.8)**	**0**	**0**	**0**	**0**
United Kingdom (Northern Ireland)	232	2 (0.86)	0	0	0	0	0	0
EU Total (27 + XI)	**12,682**	**337 (2.7)**	**95 (0.75)**	**67 (0.53)**	**15 (0.12)**	**2 (0.02)**	**10 (0.08)**	**1 (0.01)**
Iceland	45	0	0	0	0	0	0	0
Norway	297	1 (0.34)	1 (0.34)	1 (0.34)	0	0	0	0
Switzerland	122	0	0	0	0	0	0	0

Note: Countries not meeting the reduction target are highlighted in bold font.

[a] *Salmonella* Typhimurium, including monophasic *S.* Typhimurium (1,4,[5],12:i:-).

[b] In accordance with Commission Regulation (EU) No 200/2010, Article 1.1 'for Member States with less than 100 flocks of adult breeding *Gallus gallus*, the Union target shall be that annually no more than one flock of adult breeding *Gallus gallus* may remain positive', Croatia met the reduction target for breeding *Gallus gallus*.

Flocks of laying hens

Rearing flocks

Nineteen MSs and the United Kingdom (Northern Ireland) reported merged data (official controls and food business operator checks) on *Salmonella* spp. prevalence in rearing flocks of laying hens. Of these, eight also reported official and own-check data separately, three reported also FBOp data separately, and one provided also CA data separately. Five MSs (Croatia, Hungary, Lithuania, Luxembourg and Slovakia) did not provide data (Table 19). Based on the merged and FBOp data, the prevalence of *Salmonella*-positive rearing flocks was 2.1% and 2.2%, respectively, while the prevalence based on official samples was 6.0%.

TABLE 19 *Salmonella* in laying hen flocks of *Gallus gallus* during the rearing period in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

	Merged		**Competent authority (CA)**		**Food business operator (FBOp)**	
Country	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**
Austria	467	4 (0.86)	4	0	466	4 (0.86)
Belgium	–	–	–	–	410	1 (0.24)
Bulgaria	1	0	55	0	–	–
Cyprus	113	1 (0.88)	–	–	–	–
Czechia	230	4 (1.7)	–	–	–	–
Denmark	187	1 (0.53)	98	0	187	1 (0.53)
Estonia	13	0	–	–	–	–
Finland	185	0	–	–	136	0
France	2198	104 (4.7)	202	21 (10.4)	1996	81 (4.1)
Germany	672	5 (0.74)	47	0	672	5 (0.74)
Greece	122	1 (0.82)	1	1 (100)	122	1 (0.82)
Ireland	37	0	–	–	–	–
Italy	1453	46 (3.2)	51	5 (9.8)	1436	41 (2.9)
Latvia	25	0	–	–	17	1 (5.9)
Malta	17	1 (5.9)	2	0	15	1 (6.7)
Netherlands	983	9 (0.92)	–	–	–	–
Poland	1484	12 (0.81)	–	–	–	–
Portugal	–	–	–	–	222	0
Romania	238	8 (3.4)	–	–	238	8 (3.4)
Slovenia[a]	–	–	1	0	133	6 (4.5)
Spain	1418	16 (1.1)	7	1 (14.3)	1418	15 (1.1)
Sweden	161	0	–	–	–	–
United Kingdom (Northern Ireland)	225	0	–	–	–	–
EU Total (27 + XI)	**10,229**	**212 (2.1)**	**468**	**28 (6.0)**	**7468**	**165 (2.2)**
Iceland	–	–	–	–	78	0
Norway	82	0	109	0	–	–
Switzerland	–	–	–	–	107	0

Abbreviation: –, Data not reported.

[a] Slovenia informed during the last phase of the production of this report of a reporting error and that no flock had been tested by the competent authority. Based on the revised data from the competent authority, the 'EU Total (27+XI)' tested flocks amount to 467, with 28 positives (6.0%) for *Salmonella* spp.

Adult flocks

All MSs and the United Kingdom (Northern Ireland), except Slovakia, reported *Salmonella* NCP data for adult laying hen flocks (Table 20). In 2024, the EU *Salmonella* flock prevalence was 4.0%, compared with 3.9% in 2023 and 3.4% in 2022. The prevalence of flocks positive for either of the two target serovars (*S.* Enteritidis or *S.* Typhimurium, including monophasic *S.* Typhimurium) was 1.6%, similar to previous years (1.4% in 2023 and 1.2% in 2022).

Seven MSs (Bulgaria, Croatia, France, Luxembourg, Malta, the Netherlands and Poland) did not meet the reduction target of ≤ 2% (Figure 3). The number of MSs not meeting the target was also seven in 2023 and four in 2022.

TABLE 20 *Salmonella* in laying hen flocks of *Gallus gallus* during the production period (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

				***N* (%) positive samples for**	
Country	***N* tested flocks**	***N* (%) positive for *Salmonella* spp.**	***N* (%) positive for target serovars**	***S.* Enteritidis**	***S.* Typhimurium[a]**
Austria	3376	61 (1.8)	24 (0.71)	15 (0.44)	9 (0.27)
Belgium	816	18 (2.2)	10 (1.2)	10 (1.2)	0
Bulgaria	**59**	**1 (1.7)[b]**	**2 (3.4)[b]**	**1 (1.7)**	**1 (1.7)**

TABLE 20 (Continued)

Country	*N* tested flocks	*N* (%) positive for *Salmonella* spp.	*N* (%) positive for target serovars	*N* (%) positive samples for	
				***S.* Enteritidis**	***S.* Typhimurium**[a]
Croatia	**358**	**42 (11.7)**	**14 (3.9)**	**9 (2.5)**	**5 (1.4)**
Cyprus	107	13 (12.1)	1 (0.93)	1 (0.93)	0
Czechia	499	10 (2.0)	10 (2.0)	10 (2.0)	0
Denmark	364	2 (0.55)	0	0	0
Estonia	15	1 (6.7)	1 (6.7)[c]	0	1 (6.7)
Finland	555	1 (0.18)	1 (0.18)	0	1 (0.18)
France	**6878**	**303 (4.4)**	**178 (2.6)**	**124 (1.8)**	**54 (0.79)**
Germany	6605	99 (1.5)	59 (0.89)	41 (0.62)	18 (0.27)
Greece[d]	774	62 (8.0)	5 (0.65)	4 (0.52)	1 (0.13)
Hungary	1167	7 (0.60)	7 (0.60)	3 (0.26)	4 (0.34)
Ireland	464	2 (0.43)	1 (0.22)	0	1 (0.22)
Italy	4764	385 (8.1)	63 (1.3)	45 (0.94)	18 (0.38)
Latvia	60	0	0	0	0
Lithuania	47	1 (2.1)	1 (2.1)[c]	1 (2.1)	0
Luxembourg	**78**	**2 (2.6)**	**2 (2.6)**	**1 (1.3)**	**1 (1.3)**
Malta	**122**	**16 (13.1)**	**4 (3.3)**	**3 (2.5)**	**1 (0.82)**
Netherlands	**2529**	**123 (4.9)**	**100 (4.0)**	**96 (3.8)**	**4 (0.16)**
Poland	**2439**	**79 (3.2)**	**51 (2.1)**	**49 (2.0)**	**2 (0.08)**
Portugal	521	33 (6.3)	9 (1.7)	7 (1.3)	2 (0.38)
Romania	882	59 (6.7)	13 (1.5)	13 (1.5)	0
Slovenia	263	11 (4.2)	3 (1.1)	1 (0.38)	2 (0.76)
Spain	3325	213 (6.4)	49 (1.5)	36 (1.1)	13 (0.39)
Sweden	1032	3 (0.29)	3 (0.29)	2 (0.19)	1 (0.10)
United Kingdom (Northern Ireland)	819	4 (0.49)	1 (0.12)	1 (0.12)	0
EU Total (27 + XI)	**38,918**	**1551 (4.0)**	**612 (1.6)**	**473 (1.2)**	**139 (0.36)**
Iceland	48	0	0	0	0
Norway	1204	0	0	0	0
Switzerland	**740**	**40 (5.4)**	**31 (4.2)**	**21 (2.8)**	**10 (1.4)**

Note: Countries not meeting the reduction target are highlighted in bold font.

[a] *Salmonella* Typhimurium, including monophasic *S.* Typhimurium (1,4,[5],12:i:-).

[b] Bulgaria reported one *Salmonella*-positive laying hen flock, one positive for *S.* Enteritidis and one for *S.* Typhimurium.

[c] In accordance with Commission Regulation (EU) No 517/2011, Article 1.1(b) 'for Member States with less than 50 flocks of adult laying hens, the Union target shall be that annually no more than one flock of adult laying hens may remain positive', Estonia and Lithuania met the reduction target for laying hens.

[d] Greece informed during the last phase of the production of this report of a reporting error and that 774 flocks had been tested, of which 4 (0.52%) were positive for target serovars (3 flocks were positive for *S.* Enteritidis and 1 for *S.* Typhimurium). Based on the revised data, the 'EU Total (27+XI)' tested flocks amount to 38,918, with 611 positives for target serovars (1.6%).

Broiler flocks

All MSs and the United Kingdom (Northern Ireland), except Slovakia, reported *Salmonella* NCP data for broiler flocks (Table 21). In 2024, *Salmonella* was detected in 4.3% of tested flocks, compared with 3.9% in 2023 and 3.5% in 2022. The EU prevalence of flocks positive for either of the two target serovars (*S.* Enteritidis or *S.* Typhimurium, including monophasic *S.* Typhimurium) was 0.29%, similar to previous years (0.19% in 2023 and 0.25% in 2022). Luxembourg did not meet the reduction target of ≤ 1% (Figure 3).

TABLE 21 *Salmonella* in broiler flocks of *Gallus gallus* before slaughter (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

Country	*N* tested flocks	*N* (%) positive for *Salmonella* spp.	*N* (%) positive for target serovars	*N* (%) positive samples for	
				***S.* Enteritidis**	***S.* Typhimurium**[a]
Austria	6502	158 (2.4)	22 (0.34)	18 (0.28)	4 (0.06)
Belgium	11,723	268 (2.3)	35 (0.30)	4 (0.03)	31 (0.26)
Bulgaria	188	0	0	0	0
Croatia	3102	109 (3.5)	12 (0.39)	9 (0.29)	3 (0.10)
Cyprus	900	10 (1.1)	1 (0.11)	0	1 (0.11)
Czechia	4853	79 (1.6)	47 (0.97)	46 (0.95)	1 (0.02)
Denmark	4239	12 (0.28)	1 (0.02)	0	1 (0.02)
Estonia	685	7 (1.0)	0	0	0
Finland	3889	9 (0.23)	8 (0.21)	0	8 (0.21)
France	59,039	1458 (2.5)	488 (0.83)	260 (0.44)	228 (0.39)
Germany	20,393	271 (1.3)	12 (0.06)	3 (0.01)	9 (0.04)
Greece[b]	9101	51 (0.56)	6 (0.07)	6 (0.07)	0
Hungary	6784	13 (0.19)	13 (0.19)	7 (0.10)	6 (0.09)
Ireland	4339	6 (0.14)	1 (0.02)	0	1 (0.02)
Italy	28,570	8232 (28.8)	10 (0.04)	1 (0)	9 (0.03)
Latvia	723	10 (1.4)	0	0	0
Lithuania	228	5 (2.2)	0	0	0
Luxembourg	**28**	**5 (17.9)**[c]	**6 (21.4)**[c]	**2 (7.1)**	**4 (14.3)**
Malta	456	31 (6.8)	1 (0.22)	0	1 (0.22)
Netherlands	16,109	560 (3.5)	54 (0.34)	42 (0.26)	12 (0.07)
Poland	52,400	109 (0.21)	102 (0.19)	102 (0.19)	0
Portugal	10,979	37 (0.34)	7 (0.06)	5 (0.05)	2 (0.02)
Romania	15,923	341 (2.1)	19 (0.12)	16 (0.10)	3 (0.02)
Slovenia	2547	323 (12.7)	10 (0.39)	0	10 (0.39)
Spain	39,540	1234 (3.1)	35 (0.09)	8 (0.02)	27 (0.07)
Sweden	3621	0	0	0	0
United Kingdom (Northern Ireland)	7041	34 (0.48)	5 (0.07)	0	5 (0.07)
EU Total (27 + XI)	**313,902**	**13,372 (4.3)**	**895 (0.29)**	**529 (0.17)**	**366 (0.12)**
Iceland	675	2 (0.30)	0	0	0
Norway	4111	1 (0.02)	1 (0.02)	0	1 (0.02)
Switzerland	610	8 (1.3)	5 (0.82)	0	5 (0.82)

[a] *Salmonella* Typhimurium, including monophasic *S.* Typhimurium (1,4,[5],12:i:-).

[b] Greece informed during the last phase of the production of this report of a reporting error and that 9101 flocks had been tested, of which 50 (0.55%) were positive for *Salmonella* spp. Based on the revised data, the 'EU Total (27+XI)' tested flocks amount to 313,902, with 13,371 positives for *Salmonella* spp. (4.3%).

[c] Luxembourg reported five *Salmonella*-positive broiler flocks, with two positive for *S.* Enteritidis, four for *S.* Typhimurium and one for *S.* Paratyphi B.

According to Commission Regulation (EU) No 200/2012,[32] MSs must separately report results from FBOp checks and CA official controls for broiler flocks. Hungary provided data exclusively from CAs while Bulgaria, Lithuania, the Netherlands and Slovakia did not comply with this requirement, as they failed to differentiate results by sampler.

Table 22 presents a comparison of the prevalence of flocks positive for either of the two target serovars, based on CA and FBOp data, together with the *p*-values and their interpretation. At EU level, and in 11 MSs, the prevalence detected through official controls was significantly higher than that from FBOp own checks. In contrast, for eight MSs and the United Kingdom (Northern Ireland), no significant differences were observed. Considering official controls alone, nine MSs reported prevalence rates of flocks positive for target serovars above 1%, whereas based on FBOp data, only one MS exceeded this threshold.

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[32] Commission Regulation (EU) No 200/2012 of 8 March 2012 concerning a Union target for the reduction of *Salmonella* Enteritidis and *Salmonella* Typhimurium in flocks of broilers, as provided for in Regulation (EC) No 2160/2003 of the European Parliament and of the Council. OJ L 71, 09.3.2012, p. 31–36.

TABLE 22 Comparison of the prevalence of target *Salmonella* serovar-positive broiler flocks, by sampler and by reporting MS, EU, 2024.

	Competent authority (CA)			**Food business operator (FBOp)**				
Country	***N* tested flocks**	***N* (%) flocks positive for target serovars**	**CI$_{95}$**	***N* tested flocks**	***N* (%) flocks positive for target serovars**	**CI$_{95}$**	***p*-value**[a]	**Interpretation**
Austria	125	1 (0.80)	[0.02; 4.4]	6384	21 (0.33)	[0.20; 0.50]	NS	
Belgium	89	1 (1.1)	[0.03; 6.1]	11,710	34 (0.29)	[0.20; 0.41]	NS	
Cyprus	13	1 (7.7)	[0.19; 36.0]	900	0	[0; 0.41][b]	0.0142	CA > FBOp
Czechia	34	5 (14.7)	[5.0; 31.1]	4819	42 (0.87)	[0.63; 1.2]	< 0.001	CA > FBOp
Denmark	273	0	[0; 1.3][b]	4239	1 (0.02)	[0; 0.13]	NS	
Estonia	223	0	[0; 1.6][b]	482	0	[0; 0.76][b]	NS	
Finland	453	3 (0.66)	[0.14; 1.9]	3436	5 (0.15)	[0.05; 0.34]	0.0562	CA > FBOp
France	638	11 (1.7)	[0.86; 3.1]	58,401	477 (0.82)	[0.75; 0.89]	0.0059	CA > FBOp
Germany	340	1 (0.29)	[0.01; 1.6]	20,393	12 (0.06)	[0.03; 0.10]	NS	
Greece	113	4 (3.5)	[0.97; 8.8]	9101	2 (0.02)	[0; 0.08]	< 0.001	CA > FBOp
Hungary	6784	0	[0; 0.05][b]	–	–	–	–	–
Ireland	33	0	[0; 10.6][b]	4339	1 (0.02)	[0; 0.13]	NS	
Italy	458	4 (0.87)	[0.24; 2.2]	28,524	6 (0.02)	[0.01; 0.05]	< 0.001	CA > FBOp
Latvia	4	0	[–]	719	0	[0; 0.51][b]	–	–
Luxembourg	88	8 (9.1)	[4.0; 17.1]	155	6 (3.9)	[1.4; 8.2]	0.0466	CA > FBOp
Malta	5	0	[–]	451	1 (0.22)	[0.01; 1.2]	–	–
Poland	3334	84 (2.5)	[2.0; 3.1]	51,772	18 (0.03)	[0.02; 0.05]	< 0.001	CA > FBOp
Portugal	117	2 (1.7)	[0.21; 6.0]	10,979	5 (0.05)	[0.01; 0.11]	0.0022	CA > FBOp
Romania	343	12 (3.5)	[1.8; 6.0]	15,580	7 (0.04)	[0.02; 0.09]	< 0.001	CA > FBOp
Slovenia	31	0	[0; 11.2][b]	2516	10 (0.40)	[0.19; 0.73]	NS	
Spain	404	4 (0.99)	[0.27; 2.5]	39,499	31 (0.08)	[0.05; 0.11]	< 0.001	CA > FBOp
Sweden	164	0	[0; 2.2][b]	3621	0	[0; 0.10][b]	NS	
United Kingdom (Northern Ireland)	58	0	[0; 6.2][b]	6983	5 (0.07)	[0.02; 0.17]	NS	
EU Total (27 + XI)	**14,124**	**141 (1.0)**	**[0.84; 1.2]**	**285,003**	**684 (0.24)**	**[0.22; 0.26]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**7340**	**141 (1.9)**	**[1.6; 2.3]**	**285,003**	**684 (0.24)**	**[0.22; 0.26]**	**< 0.001**	**CA > FBOp**

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Breeding flocks of turkeys

Rearing flocks

Seven MSs and the United Kingdom (Northern Ireland) reported merged data (CA and FBOp controls) on *Salmonella* spp. prevalence in rearing flocks of breeding turkeys. Of these, three also reported official and own-check data separately, and one MS reported only own-check data. Bulgaria, Hungary and Slovakia did not provide *Salmonella* data for breeding turkey flocks at the rearing stage (Table 23). Based on the merged data and FBOp data alone, the prevalence of *Salmonella*-positive rearing flocks was 5.3% and 5.2%, respectively.

TABLE 23 *Salmonella* in breeding flocks of turkeys during the rearing period in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

Country	Merged		Competent authority (CA)		Food business operator (FBOp)	
	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**	***N* tested flocks**	***N* (%) flocks positive for *Salmonella* spp.**
Finland	6	0	–	–	4	0
France	416	6 (1.4)	43	0	373	6 (1.6)
Germany	30	1 (3.3)	1	0	30	1 (3.3)
Ireland	4	0	–	–	–	–
Italy	161	28 (17.4)	7	0	161	28 (17.4)
Poland	–	–	–	–	70	0
Spain	74	2 (2.7)	–	–	74	2 (2.7)
Sweden	4	0	–	–	–	–
United Kingdom (Northern Ireland)	1	0	–	–	–	–
EU Total (27 + XI)	**696**	**37 (5.3)**	**51**	**0**	**712**	**37 (5.2)**
Iceland	–	–	–	–	4	0
Norway	8	0	–	–	–	–

Abbreviation: –, Data not reported.

Adult flocks

For adult flocks of breeding turkeys, 10 MSs reported *Salmonella* NCP data, while Bulgaria and Slovakia did not. The overall EU *Salmonella* flock prevalence was 9.1%, compared with 6.4% in 2023 and 4.3% in 2022. The prevalence of flocks positive for either of the two target serovars (*S.* Enteritidis or *S.* Typhimurium, including monophasic *S.* Typhimurium) was 1.0%, up from 0.35% in 2023 and 0.32% in 2022. France and Italy did not meet the reduction target of ≤ 1% (Figure 3, Table 24).

TABLE 24 *Salmonella* in breeding flocks of turkeys during the production period (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

Country	***N* tested flocks**	***N* (%) positive for *Salmonella* spp.**	***N* (%) positive for target serovars**	***N* (%) positive samples for**	
				***S.* Enteritidis**	***S.* Typhimurium**[a]
Finland	7	0	0	0	0
France	**381**	**13 (3.4)**	**6 (1.6)**	**3 (0.79)**	**3 (0.79)**
Germany	96	2 (2.1)	0	0	0
Greece	4	0	0	0	0
Hungary	103	0	0	0	0
Ireland	5	0	0	0	0
Italy	**284**	**70 (24.6)**	**4 (1.4)**	**0**	**4 (1.4)**
Poland	223	1 (0.45)	1 (0.45)	1 (0.45)	0
Spain	86	23 (26.7)	1 (1.2)[b]	0	1 (1.2)
Sweden	4	0	0	0	0
EU Total (27 + XI)	**1193**	**109 (9.1)**	**12 (1.0)**	**4 (0.34)**	**8 (0.67)**
Iceland	4	0	0	0	0
Norway	18	0	0	0	0

[a] *Salmonella* Typhimurium, including monophasic *S.* Typhimurium (1,4,[5],12:i:-).

[b] In accordance with Commission Regulation (EU) No 1190/2012, Article 1.1 'for Member States with less than 100 flocks of adult breeding or fattening turkeys, the Union target shall be that annually no more than one flock of adult breeding or fattening turkeys may remain positive', Spain met the reduction target for breeding turkeys.

In accordance with Commission Regulation (EU) No 1190/2012, MSs are required to report breeding turkey flock results separately for CA and FBOp checks, in addition to providing overall merged data. Greece and Hungary submitted data exclusively from FBOp and CA controls, respectively, while Bulgaria and Slovakia did not comply with this requirement, as they failed to differentiate results by sampler.

Table 25 presents a comparison of the prevalence of flocks positive for either of the two target serovars, based on CA and FBOp data, together with the *p*-values and their interpretation. No significant differences were observed between official controls and own checks, either at EU level or within individual MSs.

TABLE 25 Comparison of the prevalence of target *Salmonella* serovar-positive flocks of breeding turkeys, by sampler and by reporting MS, EU, 2024.

Country	Competent authority (CA)			Food business operator (FBOp)				
	N **tested flocks**	***N*** **(%) flocks positive for target serovars**	CI_{95}	***N*** **tested flocks**	***N*** **(%) flocks positive for target serovars**	CI_{95}	***p*-value**[a]	**Interpretation**
Finland	7	0	[–]	7	0	[–]	–	–
France	115	1 (0.87)	[0.02; 4.7]	266	5 (1.9)	[0.61; 4.3]	NS	
Germany	77	0	[0; 4.7][b]	92	0	[0; 3.9][b]	NS	
Greece	–	–	–	4	0	[–]	–	–
Hungary	103	0	[0; 3.5][b]	–	–	–	–	–
Ireland	5	0	[–]	5	0	[–]	–	–
Italy	168	1 (0.60)	[0.02; 3.3]	284	3 (1.1)	[0.22; 3.1]	NS	
Poland	143	1 (0.70)	[0.02; 3.8]	223	0	[0; 1.6][b]	NS	
Spain	50	0	[0; 7.1][b]	82	1 (1.2)	[0.03; 6.6]	NS	
Sweden	4	0	[–]	4	0	[–]	–	–
EU Total (27 + XI)	**672**	**3 (0.45)**	**[0.09; 1.3]**	**967**	**9 (0.93)**	**[0.43; 1.8]**	**NS**	
EU Total (27 + XI) providing CA and FBOp data	**569**	**3 (0.53)**	**[0.11; 1.5]**	**963**	**9 (0.93)**	**[0.43; 1.8]**	**NS**	

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Flocks of fattening turkeys

For fattening turkey flocks, 21 MSs and the United Kingdom (Northern Ireland) reported data (Table 26), while Bulgaria and Slovakia did not. The overall EU *Salmonella* flock prevalence was 7.7%, slightly lower than in 2023 (8.0%) and 2022 (9.2%). The EU prevalence of flocks positive for either of the two target serovars (*S.* Enteritidis or *S.* Typhimurium, including monophasic *S.* Typhimurium) was 0.35%, compared with 0.28% in 2023 and 0.32% in 2022. Belgium and France did not meet the reduction target of ≤ 1%.

TABLE 26 *Salmonella* in fattening flocks of turkeys before slaughter during the production period (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2024.

Country	***N*** **tested flocks**	***N*** **(%) positive for *Salmonella* spp.**	***N*** **(%) positive for target serovars**	***N*** **(%) positive samples for**	
				***S.* Enteritidis**	***S.* Typhimurium**[a]
Austria	505	30 (5.9)	5 (0.99)	3 (0.59)	2 (0.40)
Belgium	**183**	**4 (2.2)**	**3 (1.6)**	**2 (1.1)**	**1 (0.55)**
Croatia	389	13 (3.3)	2 (0.51)	2 (0.51)	0
Cyprus	4	0	0	0	0
Czechia	246	2 (0.81)	1 (0.41)	0	1 (0.41)
Denmark	92	1 (1.1)	0	0	0
Finland	271	0	0	0	0
France	**4826**	**164 (3.4)**	**64 (1.3)**	**39 (0.81)**	**25 (0.52)**
Germany	4220	23 (0.55)	12 (0.28)	4 (0.09)	8 (0.19)
Greece	53	4 (7.5)	0	0	0
Hungary	1405	0	0	0	0
Ireland	455	3 (0.66)	1 (0.22)	0	1 (0.22)
Italy	4803	1830 (38.1)	3 (0.06)	0	3 (0.06)

(Continues)

TABLE 26 (Continued)

Country	*N* tested flocks	*N* (%) positive for *Salmonella* spp.	*N* (%) positive for target serovars	*N* (%) positive samples for	
				S. Enteritidis	*S.* Typhimurium[a]
Lithuania	11	0	0	0	0
Netherlands	418	1 (0.24)	0	0	0
Poland	6126	25 (0.41)	4 (0.07)	2 (0.03)	2 (0.03)
Portugal	1303	39 (3.0)	4 (0.31)	0	4 (0.31)
Romania	283	1 (0.35)	0	0	0
Slovenia	103	14 (13.6)	0	0	0
Spain	3829	124 (3.2)	3 (0.08)	1 (0.03)	2 (0.05)
Sweden	118	1 (0.85)	0	0	0
United Kingdom (Northern Ireland)	41	1 (2.4)	1 (2.4)[b]	0	1 (2.4)
EU Total (27 + XI)	**29,684**	**2280 (7.7)**	**103 (0.35)**	**53 (0.18)**	**50 (0.17)**
Iceland	33	0	0	0	0
Norway	127	0	0	0	0
Switzerland	**26**	**13 (50.0)**	**2 (7.7)**	**2 (7.7)**	**0**

[a] *Salmonella* Typhimurium, including monophasic *S.* Typhimurium (1,4,[5],12:i:-).

[b] In accordance with Commission Regulation (EU) No 1190/2012, Article 1.1 'for Member States with less than 100 flocks of adult breeding or fattening turkeys, the Union target shall be that annually no more than one flock of adult breeding or fattening turkeys may remain positive', the United Kingdom (Northern Ireland) met the reduction target for fattening turkeys.

In accordance with Commission Regulation (EU) No 1190/2012, MSs are required to report fattening turkey flock results separately for CA and FBOp checks, in addition to providing overall merged data. Seventeen MSs and the United Kingdom (Northern Ireland) complied with this requirement. Bulgaria, Lithuania, the Netherlands and Slovakia did not provide separate results, while Hungary reported only CA data.

Table 27 compares the prevalence of flocks positive for either of the two target serovars, based on CA and FBOp data, together with the *p*-values and their interpretation. At EU level, and in four MSs, prevalence estimates from official controls were significantly higher than those from FBOp own checks. In contrast, in eight MSs, no significant differences were observed between the two data sources.

TABLE 27 Comparison of the prevalence of target *Salmonella* serovar-positive flocks of fattening turkeys, by sampler and by reporting MS, EU, 2024.

Country	Competent authority (CA)			Food business operator (FBOp)				
	N tested flocks	*N* (%) flocks positive for target serovars	CI_{95}	*N* tested flocks	*N* (%) flocks positive for target serovars	CI_{95}	*p*-value[a]	Interpretation
Austria	21	1 (4.8)	[0.12; 23.8]	495	5 (1.0)	[0.33; 2.3]	NS	
Belgium	4	1 (25.0)	[–]	182	2 (1.1)	[0.13; 3.9]	–	–
Cyprus	1	0	[–]	4	0	[–]	–	–
Czechia	8	0	[–]	238	1 (0.42)	[0.01; 2.3]	–	–
Denmark	45	0	[0; 7.9][b]	92	0	[0; 3.9][b]	NS	
Finland	44	0	[0; 8.0][b]	227	0	[0; 1.6][b]	NS	
France	104	2 (1.9)	[0.23; 6.8]	4722	62 (1.3)	[1.0; 1.7]	NS	
Germany	151	3 (2.0)	[0.41; 5.7]	4219	11 (0.26)	[0.13; 0.47]	0.0111	CA > FBOp
Greece	9	0	[–]	53	0	[0; 6.7][b]	–	–
Hungary	1405	0	[0; 0.26][b]	–	–	–	–	–
Ireland	10	0	[0; 30.8][b]	455	1 (0.22)	[0.01; 1.2]	NS	
Italy	109	1 (0.92)	[0.02; 5.0]	4796	2 (0.04)	[0.01; 0.15]	0.0652	CA > FBOp
Poland	230	12 (5.2)	[2.7; 8.9]	6048	0	[0; 0.06][b]	< 0.001	CA > FBOp
Portugal	19	0	[0; 17.6][b]	1303	4 (0.31)	[0.08; 0.78]	NS	
Romania	19	0	[0; 17.6][b]	283	0	[0; 1.3][b]	NS	

TABLE 27 (Continued)

Country	Competent authority (CA)			Food business operator (FBOp)				
	N tested flocks	*N* (%) flocks positive for target serovars	CI_{95}	*N* tested flocks	*N* (%) flocks positive for target serovars	CI_{95}	*p*-value[a]	Interpretation
Slovenia	8	0	[–]	95	0	[0; 3.8][b]	–	–
Spain	75	2 (2.7)	[0.32; 9.3]	3823	1 (0.03)	[0; 0.15]	0.0011	CA > FBOp
Sweden	14	0	[0; 23.2][b]	118	0	[0; 3.1][b]	NS	
United Kingdom (Northern Ireland)	4	0	[–]	37	1 (2.7)	[0.07; 14.2]	–	–
EU Total (27 + XI)	**2280**	**22 (0.96)**	**[0.61; 1.5]**	**27,190**	**90 (0.33)**	**[0.27; 0.41]**	**< 0.001**	**CA > FBOp**
EU Total (27 + XI) providing CA and FBOp data	**875**	**22 (2.5)**	**[1.6; 3.8]**	**27,190**	**90 (0.33)**	**[0.27; 0.41]**	**< 0.001**	**CA > FBOp**

Abbreviations: –, Data not reported; [–], the confidence interval is not provided because of the small sample size.

[a] *p*-value: NS, not significant.

[b] One-sided, 97.5% confidence interval.

Achievement of final Salmonella reduction targets since the start of the NCPs

Salmonella reduction targets have been applied since 2010 for breeding *Gallus gallus*, since 2011 for laying hens, since 2012 for broilers and since 2013 for breeding and fattening turkeys. From 2010 to 2019, the United Kingdom was included in the EU-level assessment, while from 2021 onwards, only Northern Ireland was considered.

For breeding *Gallus gallus* (2010–2024), the number of reporting MSs ranged from 24 to 26. Compliance was lowest in 2012 (76.0%; 6 of 25 MSs not meeting the target) and highest in 2015 and 2016 (92.0%; 2 of 25 MSs not compliant). In the last 3 years, compliance rates were 84.6% (2022), 88.0% (2023) and 84.0% (2024).

For laying hens (2011–2024), 26 to 28 countries reported data. The lowest compliance rates were observed in 2021 (71.4%), followed by 2020 (73.1%), 2024 (74.1%), 2023 (75.0%) and 2018 (77.8%), when six to eight MSs failed to meet the target. In contrast, in 2013, all reporting MSs met the target. Overall, compliance has been lower in recent years than in earlier ones.

For broilers (2012–2024), 26 to 28 countries submitted reports. Annual compliance rates consistently exceeded 88.5%. All MSs met the target in 2022, while in 2013, 2017, 2018, 2019 and 2024, only one MS failed to comply. The highest number of non-compliant countries (three) was observed in 2012, 2014, 2020 and 2021.

For breeding turkeys (2013–2024), 10 to 15 countries reported data. Non-compliance peaked in 2017, when three MSs failed to meet the target. In 6 years (2013, 2014, 2015, 2019, 2022 and 2023), all reporting MSs complied.

For fattening turkeys (2013–2024), 21 to 24 MSs submitted data. The greatest number of non-compliant MSs (three) was recorded in 2018 and 2020, while in 2023, all reporting MSs successfully met the target.

The results for all poultry populations, reporting MSs and years are available at Zenodo here.

Salmonella prevalence trends in poultry flocks

Trends in the estimated EU prevalence of poultry flocks positive for *Salmonella* spp. and for the target *Salmonella* serovars across different poultry populations over the past 10 years of NCP implementation are shown in Figure 4.

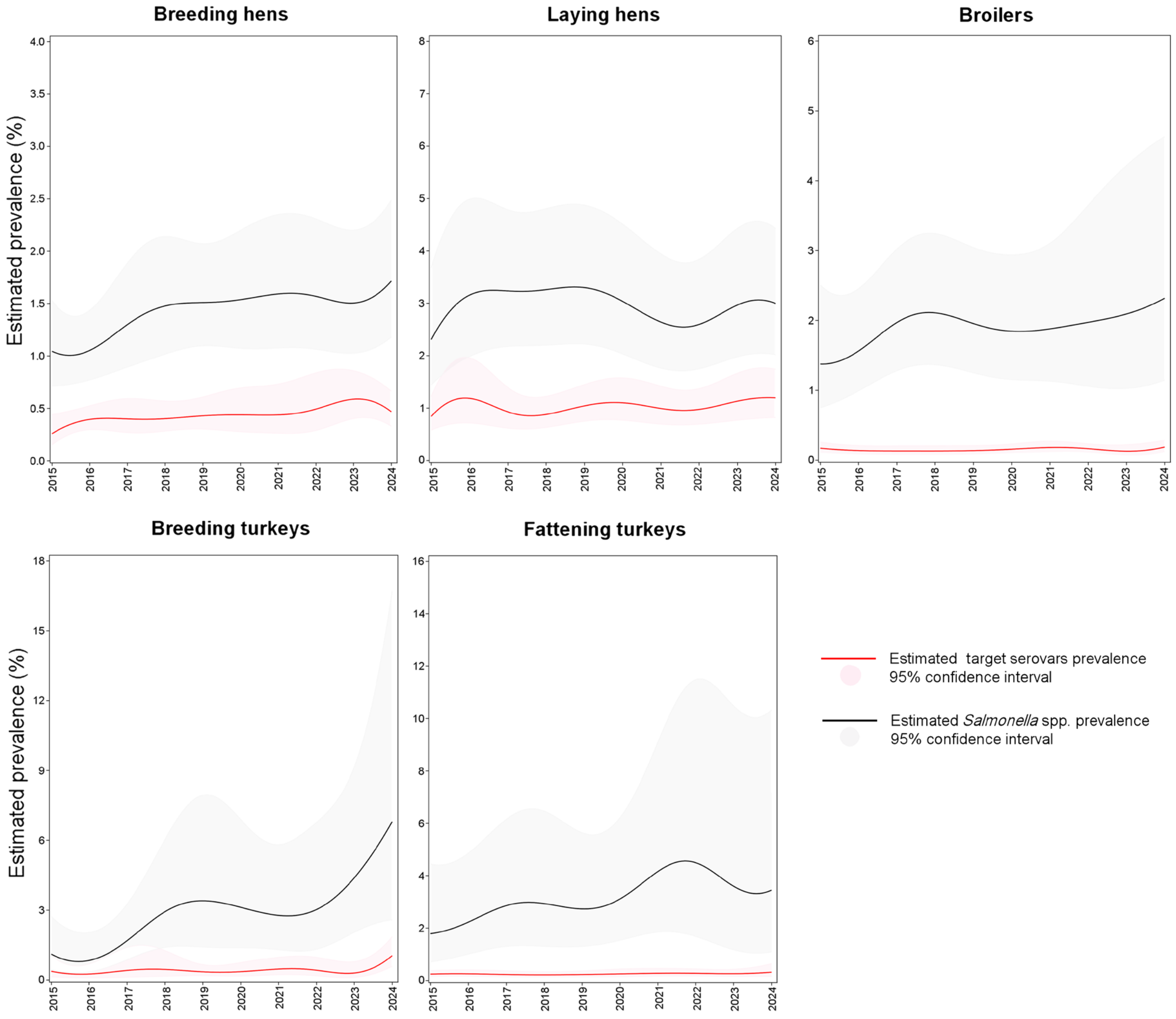


FIGURE 4 Trend in the estimated prevalence of poultry flocks positive for *Salmonella* spp. and target *Salmonella* serovars, at EU level for different poultry populations, 2015–2024.
The apparent discrepancy between the proportion of positive flocks (both for target *Salmonella* serovars and for *Salmonella* spp., as described in the previous paragraphs) and the estimated prevalence shown above is due to the fact that the first value is the overall EU ratio of all positive to all tested flocks for each poultry population, whereas the estimated EU prevalence is obtained by modelling the ratio of positive to all tested flocks in each reporting country, taking into account inter-country variability and the correlation between years.

The supporting information for this report (‘*Salmonella* poultry outcome trend analyses’, available at Zenodo here) presents EU-level trends in the percentage of flocks positive for *Salmonella* – both target and non-target serovars, as well as *S.* Enteritidis – across the poultry populations covered by the NCPs. The figures also show modelling results for trends in the prevalence of *Salmonella* spp. and target serovars in poultry flocks, with detailed outputs provided at both subject and population levels.

Figure 5 summarises the EU-wide prevalence of flocks positive for target *Salmonella* serovars and for *Salmonella* spp. across different poultry populations over the last 10 years (2015–2024) and the last 5 years (2020–2024). Over the past 10 years, a significant increase in the prevalence of both target *Salmonella* serovars and *Salmonella* spp.-positive flocks was observed in breeding *Gallus gallus*. This upward trend was largely driven by the endpoint years (2015 and 2024), as confirmed by spline model estimates for those years (Figure 4). In 2024, the estimated EU prevalence of target serovar-positive flocks was 0.47%, significantly higher than 0.26% in 2015 ($p = 0.026$), which coincided with the highest compliance rate (92.0% of reporting MSs). Similarly, the prevalence of *Salmonella* spp.-positive flocks rose to 1.7% in 2024, compared with 1.0% in 2015 ($p = 0.039$). However, over the last 5 years, no significant increases were observed for either target serovars or *Salmonella* spp.

For breeding turkeys, the prevalence of both target serovars and *Salmonella* spp.-positive flocks increased significantly over the last 10 years and also over the last 5 years (Figure 5). For target serovars, this trend was mainly driven by the high prevalence in 2024: the EU estimate was 1.0% (Figure 4), significantly higher than in 2023 (0.30%, $p = 0.013$) and 2022 (0.41%, $p = 0.036$).

In contrast, no significant trends were detected in laying hens, broilers or fattening turkeys during either observation period, for either target serovars or *Salmonella* spp.-positive flocks.

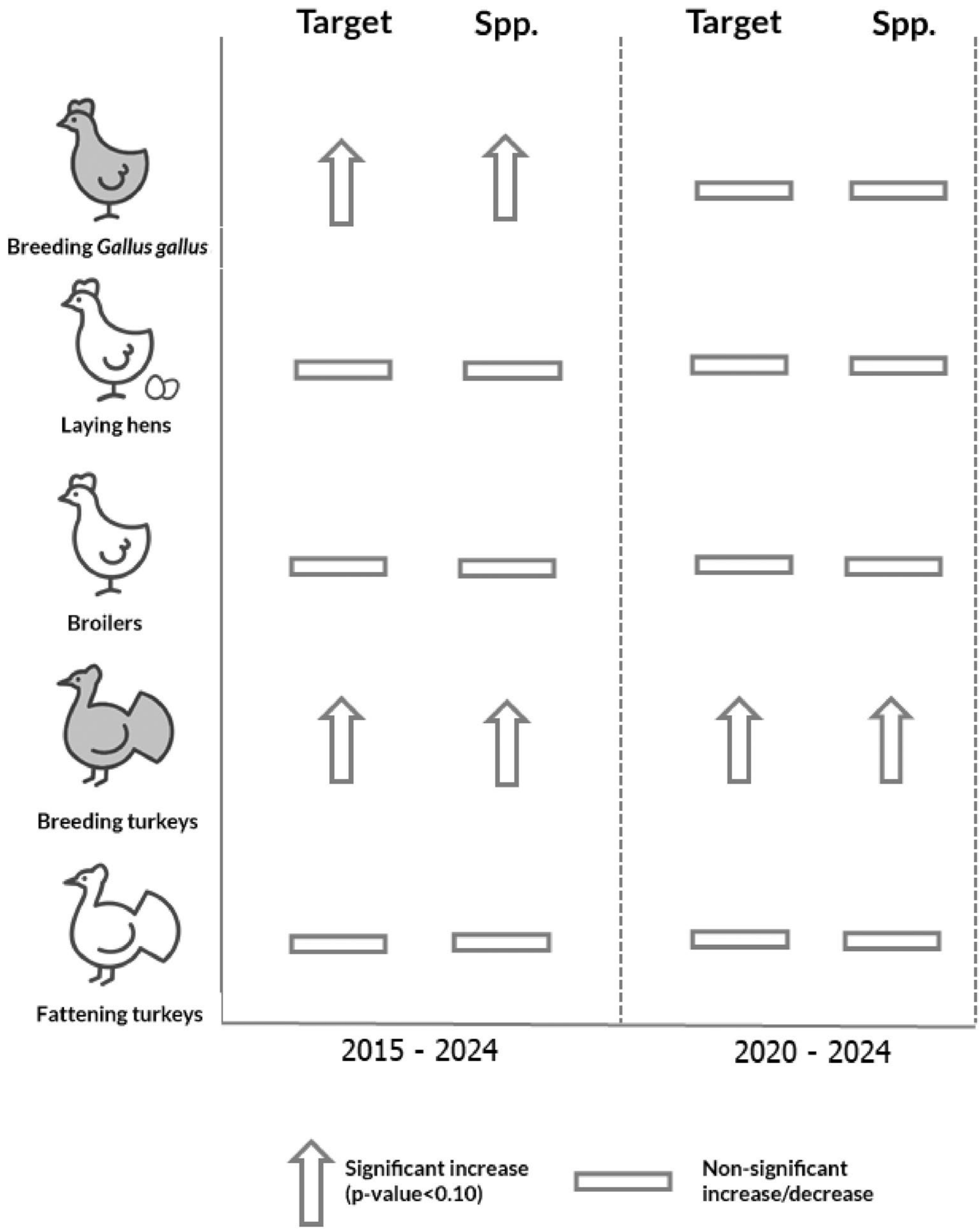


FIGURE 5 Trend in the EU-level prevalence of target *Salmonella* serovar (Target)-positive or *Salmonella* spp. (Spp.)-positive flocks of poultry populations (2015–2024 and 2020–2024).

Salmonella data for other animals

Excluding NCP poultry data, 117,863 samples for *Salmonella* detection from various animal species were reported by 14 MSs. Overall, 7.3% of these samples tested positive for *Salmonella*. The largest proportion came from pigs (*N* = 71,508; 60.7% of all animal samples, reported by 12 MSs), with a positivity rate of 7.6%. The second largest source was cattle/bovine animals (*N* = 23,049; 19.6%, reported by 12 MSs), of which 3.9% were positive. Felids, reported by eight MSs, showed the highest proportion of positive results (50.7%), although 99.0% of these originated from suspect cat/pet samples reported by Sweden. Solipeds also showed a notable prevalence rate, with 13.2% of samples testing positive (seven MSs). For wild ungulates, 6.4% of samples were positive (seven MSs). These results should be interpreted with caution, as prevalence estimates can be affected by the sampling context and scope.

A2.4.5 | *Salmonella* in feed

In 2024, the overall EU-level occurrence of *Salmonella*-positive sampling units in 'animal and vegetable-derived feed' was 0.68% (*N* = 78,281). For compound feed (finished feed for animals), the prevalence of positive units was 0.34% in cattle feed (*N* = 3195), 0.61% in poultry feed (*N* = 19,942) and 0.35% in pig feed (*N* = 3959). No notable isolates were detected in 2024. For pet food, the prevalence of *Salmonella*-positive sampling units was 0.76% (*N* = 8136).

A2.4.6 | *Salmonella* serovars in humans, food and animals

Humans

Serovars acquired in the EU

To estimate the impact of *Salmonella* infections acquired in the EU, serovar data (*N* = 56,412) from all cases were analysed for both domestic and travel-associated cases where the probable country of infection was an EU MS. Information on *Salmonella* serovars combined with travel data (importation status and/or probable country of infection) was available from 23 MSs. Bulgaria, Croatia, Cyprus and Portugal did not provide such combined data. The 23 reporting countries accounted for 73.1% (41,241/56,412) of salmonellosis cases with known serovar and travel information in 2024. Since 2022, the Netherlands has not reported serovar data for domestic cases. Among cases with both serovar and travel information, 90.4% (37,284/41,241) were acquired within the EU. Overall, 74.6% (37,284/49,984) of human salmonellosis cases acquired in the EU – either domestically or in another EU country – had accompanying serovar data.

Among reported human salmonellosis cases acquired in the EU, *S.* Enteritidis was predominant, accounting for 58.4% of cases. Together, *S.* Enteritidis, *S.* Typhimurium and monophasic *S.* Typhimurium (1,4,[5],12:i:-) represented 79.7% of confirmed EU-acquired cases in 2024 (Table 28), a proportion similar to that observed in 2022–2023.

More specifically, the proportion of EU-acquired cases due to *S.* Enteritidis decreased in 2024, while the proportion due to *S.* Typhimurium increased compared with 2023 (Table 28). Twelve serovars (monophasic *S.* Typhimurium (1,4,[5],12:i:-), *S.* Infantis, *S.* Derby, *S.* Coeln, *S.* Napoli, *S.* Bovimorbificans, *S.* Mikawasima, *S.* Strathcona, *S.* Umbilo, *S.* Brandenburg, *S.* Kentucky and *S.* Kottbus) increased in 2024 compared to both 2023 and 2022. In addition, *S.* Newport and *S.* Agona increased in 2024 compared to 2023, while *S.* Chester, *S.* Virchow, *S.* Thompson and *S.* Poona decreased.

TABLE 28 Distribution of reported cases of human salmonellosis acquired in the EU, 2022–2024, for the 20 most frequently reported serovars in 2024.

	2024			2023			2022		
Serovar	**Cases**	**MSs**	**%**	**Cases**	**MSs**	**%**	**Cases**	**MSs**	**%**
Enteritidis	21,762	22	58.4	24,198	25	70.8	19,752	25	65.0
Typhimurium	4093	22	11.0	3068	25	9.0	3793	24	12.5
Monophasic Typhimurium 1,4,[5],12:i:-	3860	16	10.4	1738	16	5.1	1684	15	5.5
Infantis	1192	22	3.2	681	22	2.0	717	22	2.4
Derby	448	20	1.2	239	17	0.70	281	18	0.92
Coeln	378	19	1.0	267	19	0.78	206	17	0.68
Napoli	280	13	0.75	62	13	0.18	92	11	0.30
Newport	263	18	0.71	151	17	0.44	245	20	0.81
Agona	208	18	0.56	123	16	0.36	177	16	0.58
Bovismorbificans	205	18	0.55	148	20	0.43	162	16	0.53
Mikawasima	199	15	0.53	97	10	0.28	101	12	0.33
Strathcona	190	13	0.51	104	12	0.30	36	8	0.12
Chester	157	19	0.42	259	15	0.76	135	13	0.44
Umbilo	155	12	0.42	10	6	0.03	15	6	0.05
Brandenburg	149	16	0.40	66	13	0.19	66	14	0.22
Kentucky	125	18	0.34	105	16	0.31	104	15	0.34
Kottbus	122	16	0.33	89	18	0.26	86	14	0.28
Virchow	108	16	0.29	154	15	0.45	132	12	0.43
Thompson	105	15	0.28	198	14	0.58	55	14	0.18
Poona	97	12	0.26	125	11	0.37	67	11	0.22
Other	3188	–	8.55	2296	–	6.72	2500	–	8.22
Total[a,b]	**37,284**	**22**	**100**	**34,178**	**25**	**100**	**30,406**	**25**	**100**

Abbreviations: MSs, Member States; –, Data not reported.

[a] Source(s): 2024–22 MSs: Austria, Belgium, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Poland, Romania, Slovakia, Slovenia, Spain and Sweden. 2023–25 MSs: Austria, Belgium, Croatia, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden. 2022–25 MSs: Austria, Belgium, Croatia, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden.

[b] Only isolates with the complete antigenic formula and/or serovar name have been considered.

A clear seasonal trend was observed for confirmed *S.* Enteritidis infections acquired in the EU during 2015–2024, with more cases reported during summer months. A decrease in the total number of cases was observed in 2020, due to the COVID-19 pandemic, followed by an increase in subsequent years; however, pre-pandemic levels were not reached until

2024. Overall, the trend for *S*. Enteritidis infections acquired in the EU during 2020–2024 showed no significant increase or decrease (Figure 6). At country level, a significant increasing trend was observed in 13 MSs. Most countries showing an increasing trend between 2020 and 2024 continued to report case numbers and notifications that were comparable to, or lower than, those seen before the COVID-19 pandemic.

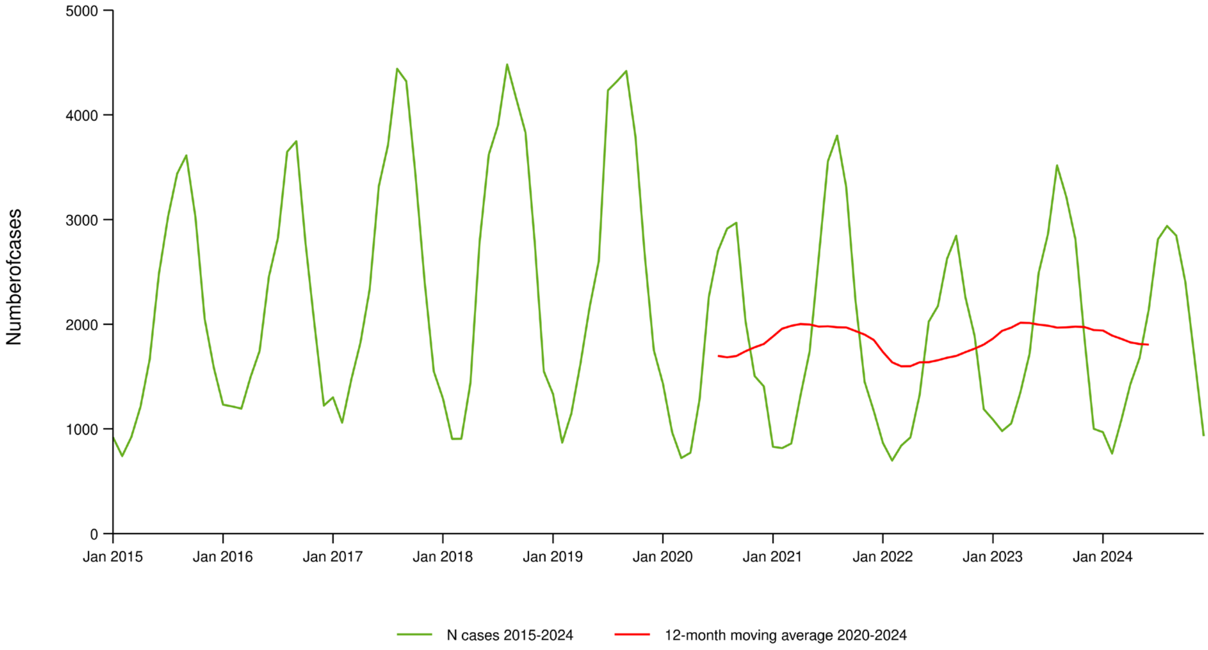


FIGURE 6 Trend in reported confirmed human cases of *Salmonella* Enteritidis infections acquired in the EU, by month, 2020–2024.
Source: Austria, Belgium, Czechia, Denmark, Estonia, Greece, Spain, Finland, France, Germany, Hungary, Ireland, Italy, Lithuania, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia and Sweden.

Food and animals

Descriptive analyses were undertaken using serotyped isolates (isolates with the complete antigenic formula and/or serovar name) from food and animals. In this context, only isolates related to the most common food-producing animal species and food matrices thereof were considered and were aggregated into the following categories for further analysis: broiler flocks – broiler meat, laying hen flocks – eggs, fattening turkey flocks – turkey meat, fattening pigs – pig meat and cattle – bovine meat. Overall, a total of 20,740 serotyped *Salmonella* isolates meeting the inclusion criteria were retained (Table 29).

TABLE 29 Distribution of *Salmonella* isolates with and without serovar identification among the different selected sources (food and animals), EU, 2024.

	***Salmonella*-positive sampling units without serotyped isolates**		***Salmonella*-positive sampling units with serotyped isolates**	
Source	***N***	**%**	***N***	**%**
Broilers	1735	20.2	11,771	56.8
Broiler meat	3072	35.7	3946	19.0
Cattle	3	0.03	46	0.22
Cattle meat	449	5.2	233	1.1
Pigs	12	0.14	41	0.20
Pig meat	2446	28.4	933	4.5
Turkeys	77	0.89	2204	10.6
Turkey meat	469	5.4	310	1.5
Layers	329	3.8	1230	5.9
Eggs and egg products	16	0.19	26	0.13
Total	**8608**	**100**	**20,740**	**100**

Most serotyped isolates originated from 'broilers' – both animals (56.8%) and food (19.0%). 'Turkey' sources (animals and food) accounted for 12.1% of isolates, while 'pig' and 'laying hen' sources represented 4.7% and 6.0%, respectively. Serotyped isolates from 'cattle' sources made up 1.3% of the total.

For further analysis, isolates belonging to the four serovars most frequently associated with human salmonellosis cases acquired in the EU in 2024 (Table 28) – *S*. Enteritidis, *S*. Typhimurium, monophasic *S*. Typhimurium (1,4,[5],12:i:-) and *S*. Infantis – were considered. Across the main food-animal sources, 12,040 serotyped isolates were reported, of which *S*. Infantis accounted for 78.3%, *S*. Enteritidis 11.9%, *S*. Typhimurium 5.5% and monophasic *S*. Typhimurium (1,4,[5],12:i:-) 4.2%. A marked increase in *S*. Infantis isolates was observed in 2024 (9428), compared with 2023 (7665) and 2022 (6840); these were mainly reported by a single MS (Italy).

A Sankey diagram (Figure 7) illustrates the links between these four major *Salmonella* serovars and their food-animal sources. *Salmonella* Enteritidis isolates were primarily from 'broiler' sources (61.2%; flocks and meat) and from 'layers and eggs' (33.6%). *Salmonella* Typhimurium isolates were more widely distributed but were mainly from 'broiler' (51.4%), 'pig' (18.4%) and 'laying hen' (18.3%) sources, with smaller proportions from 'bovine' (6.3%) and 'turkey' (5.5%) sources. Monophasic *S*. Typhimurium (1,4,[5],12:i:-) was mainly linked to 'pig' (54.7%), followed by 'broiler' (30.2%) and 'turkey' (8.8%) sources. *Salmonella* Infantis was almost exclusively associated with the 'broiler' source (96.5%). These findings should be interpreted with caution, as the distribution of serotyped isolates among sources is highly unbalanced. Most serotyped isolates considered in this analysis came from poultry populations covered by NCPs, especially broilers, whereas for pigs, 71.6% of reported strains were not serotyped.

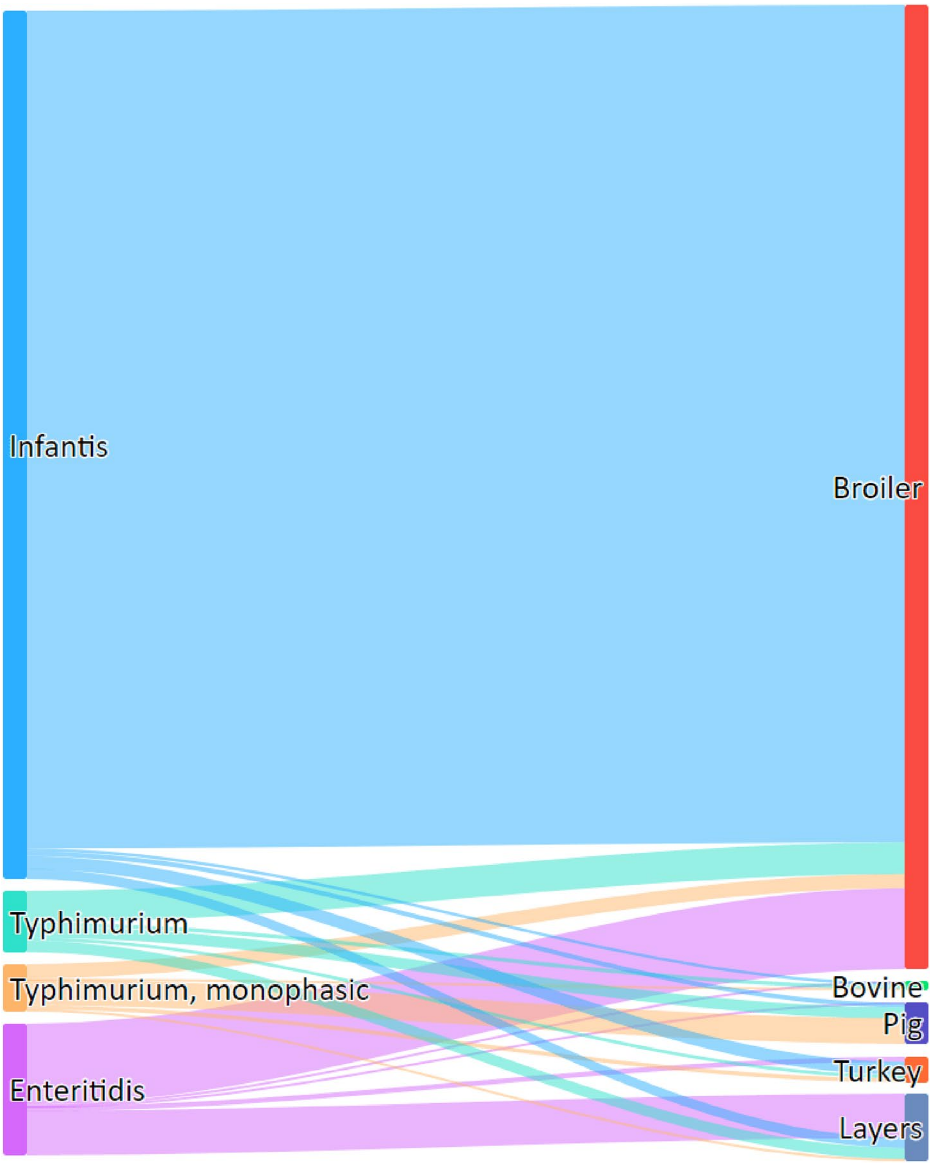


FIGURE 7 Sankey diagram of the distribution of the top four EU-level *Salmonella* serovars involved in human salmonellosis cases acquired in the EU, reported from specified food-animal categories, by food-animal source, EU, 2024.

Sankey diagram of the distribution of the top four EU-level *Salmonella* serovars involved in human salmonellosis cases acquired in the EU, reported from specified food-animal categories, by food-animal source, EU, 2024. The left side of the diagram shows the four most reported *Salmonella* serovars involved in human salmonellosis cases acquired in the EU: *S*. Infantis (light blue), *S*. Typhimurium (green), monophasic *S*. Typhimurium (light orange) and *S*. Enteritidis (violet). Animal and food data from the same source were merged: 'broiler' includes isolates from broiler flocks and broiler meat, 'bovine' includes isolates from bovine animals for meat production and from bovine meat, 'pig' includes isolates from fattening pigs and pig meat, 'turkey' includes isolates from fattening turkey flocks and turkey meat and 'layers' includes isolates from laying hen flocks and eggs. The right side shows the five sources considered (broiler (red), bovine (green), pig (blue), turkey (orange) and layer (indigo) sources). The width of the coloured bands linking the sources and serovars is proportional to the percentage of isolates of each serovar from each source.

Table 30 presents the top-20 *Salmonella* serovars reported from all serotyped isolates originating from food and animal sources, including laying hens, broilers, turkeys, pigs and bovine animals. This aggregation applied different criteria from those used in Table 29: while Table 30 includes all serotyped isolates, Table 29 was limited to a predefined selection of isolates. Among the isolates from the laying hens-eggs source (*N* = 1413), 47.4% were identified as one of the three target serovars: *S*. Enteritidis, *S*. Typhimurium, including monophasic *S*. Typhimurium (1,4,[5],12:i:-). *Salmonella* Kentucky and *S*. Infantis remained the second and fourth main serovars from this source (as in 2023). *Salmonella* Kentucky was reported by six MSs, with most isolates coming from a single country, whereas *S*. Infantis was reported by 13 MSs, with a more balanced distribution of isolates across the reporting countries. In the broiler source (*N* = 15,717), three serovars (*S*. Infantis, *S*. Enteritidis and *S*. Mbandaka) represented 69% of the serotyped isolates, with *S*. Infantis accounting for more than one out of two isolates reported (57.9%) and *S*. Enteritidis surpassing *S*. Mbandaka (5.6 and 5.5% respectively). In the turkey source, two serovars (*S*. Agona and *S*. Anatum) were by far the most common ones, accounting for 61.1% of the serotyped isolates reported and confirming the scenario already described in 2023, with *S*. Agona as the most prevalent serovar (46.1%). *Salmonella* Infantis was the third main serovar reported from turkey sources (5.4%). In the pig sources, monophasic *S*. Typhimurium (1,4,[5],12:i:-), *S*. Derby and *S*. Typhimurium represented 67.5% of the serotyped strains, with *S*. Rissen (8.1%) and *S*. Infantis (4.9%) being other frequently reported serovars. In the bovine source, *S*. Typhimurium and *S*. Dublin were by far the most common ones, followed by *S*. Infantis, *S*. Derby and *S*. Enteritidis. The distribution of serovars among the different species reported for 2024 was comparable to that reported in 2023. This scenario is strongly affected by what the MSs decide to report each year in terms of serotyped isolates since the reporting of such data is mandatory only for target serovars in the context of NCPs.

TABLE 30 Distribution of the top-20 *Salmonella* serovars by food-animal source (laying hens, broilers, turkeys, pigs and bovine animals), EU, 2024.

Poultry population											
	Serovar	***N* (%) positive samples**	***N* MSs**		**Serovar**	***N* (%) positive samples**	***N* MSs**		**Serovar**	***N* (%) positive samples**	***N* MSs**
Laying hens	Enteritidis	481 (38.5)	22	**Broilers**	Infantis	9094 (57.9)	24	**Turkeys**	Agona	1204 (46.1)	9
	Kentucky	145 (11.6)	5		Enteritidis	878 (5.6)	17		Anatum	389 (14.9)	4
	Typhimurium	122 (9.8)	17		Mbandaka	860 (5.5)	15		Infantis	142 (5.4)	9
	Infantis	108 (8.6)	13		Paratyphi B[a]	520 (3.3)	8		Lagos	125 (4.8)	1
	Corvallis	38 (3.0)	5		Give	500 (3.2)	2		Newport	112 (4.3)	6
	Mbandaka	31 (2.5)	9		Thompson	455 (2.9)	3		Enteritidis	58 (2.2)	7
	Coeln	19 (1.5)	6		Livingstone	454 (2.9)	6		Bredeney	47 (1.8)	5
	Typhimurium, monophasic	19 (1.5)	7		Typhimurium	343 (2.2)	21		Typhimurium	47 (1.8)	9
	Agona	17 (1.4)	7		Kedougou	261 (1.7)	5		Typhimurium, monophasic	47 (1.8)	10
	Thompson	16 (1.3)	6		Virchow	215 (1.4)	6		Saintpaul	38 (1.4)	3
	Braenderup	14 (1.1)	3		Newport	183 (1.2)	13		Thompson	35 (1.3)	2
	Montevideo	14 (1.1)	4		Typhimurium, monophasic	154 (0.98)	13		Derby	33 (1.3)	4
	Senftenberg	14 (1.1)	5		Montevideo	151 (0.96)	8		Give	33 (1.3)	3
	Livingstone	13 (1.0)	5		Senftenberg	150 (0.95)	12		Chester	29 (1.1)	3
	Ohio	10 (0.80)	2		Agona	139 (0.88)	11		Kentucky	29 (1.1)	4
	Mikawasima	9 (0.72)	2		Napoli	97 (0.62)	2		Uganda	25 (0.96)	1
	Newport	9 (0.72)	4		Bredeney	65 (0.41)	5		Senftenberg	24 (0.92)	5
	Altona	7 (0.56)	2		Anatum	59 (0.38)	7		Napoli	19 (0.73)	1
	Kottbus	7 (0.56)	6		Grumpensis	56 (0.36)	1		Goldcoast	13 (0.50)	2
	Napoli, Veneziana	7 (0.56)	2, 2		Kentucky	43 (0.27)	6		Mbandaka	13 (0.50)	3
	Other serovars	143 (11.4)	26		Other serovars	1040 (6.6)	27		Other serovars	150 (5.7)	20
	Total	**1250**			**Total**	**15,717**			**Total**	**2612**	

TABLE 30 (Continued)

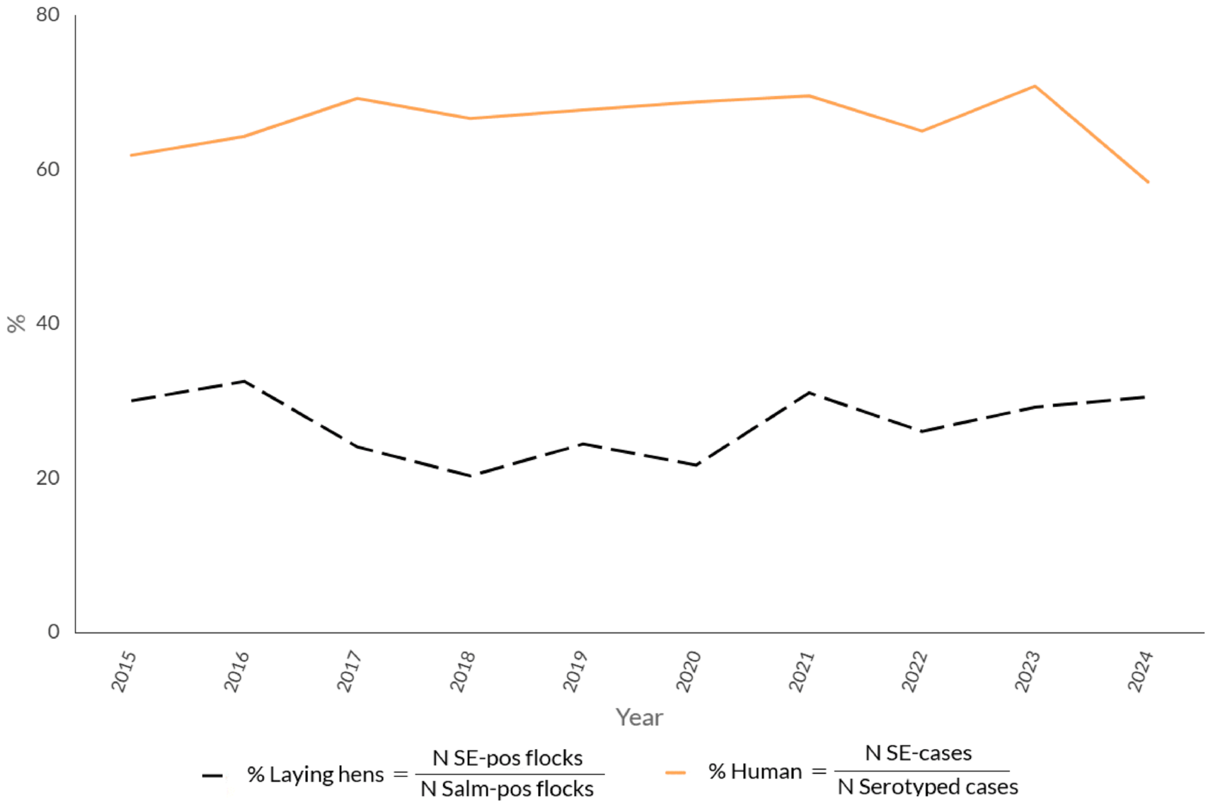
Pigs and cattle (bovine animals)							
	Serovar	***N* (%) positive samples**	***N* MSs**		**Serovar**	***N* (%) positive samples**	***N* MSs**
Pigs	Typhimurium, monophasic	290 (27.9)	16	**Bovine animals**	Typhimurium	254 (36.4)	14
	Derby	243 (23.4)	16		Dublin	222 (31.9)	12
	Typhimurium	168 (16.2)	18		Infantis	33 (4.7)	3
	Rissen	84 (8.1)	7		Derby	30 (4.3)	6
	Infantis	51 (4.9)	11		Enteritidis	30 (4.3)	11
	Brandenburg	25 (2.4)	7		Typhimurium, monophasic	14 (2.0)	5
	Bredeney	19 (1.8)	3		Bredeney	12 (1.7)	1
	Livingstone	13 (1.2)	3		Montevideo	9 (1.3)	3
	Choleraesuis	12 (1.1)	1		Indiana	8 (1.1)	1
	London	12 (1.1)	3		Muenster	6 (0.86)	3
	Wien	9 (0.87)	1		Agona	5 (0.72)	2
	Give	8 (0.77)	2		Bovismorbificans	5 (0.72)	3
	Indiana	8 (0.77)	1		Anatum	4 (0.57)	2
	Bovismorbificans	7 (0.67)	3		Chester	4 (0.57)	1
	Enteritidis	7 (0.67)	5		Hayindogo	4 (0.57)	1
	Goldcoast	6 (0.58)	4		Mbandaka	4 (0.57)	3
	Panama	6 (0.58)	3		Mishmarhaemek	4 (0.57)	1
	Pasing	6 (0.58)	1		Szentes	4 (0.57)	1
	Amsterdam	5 (0.48)	1		Apeyeme	3 (0.43)	1
	Tumodi	5 (0.48)	1		Duesseldorf, Konstanz, Muenchen, Newport	3 (0.43)	1, 1, 2, 2
	Other serovars	55 (5.3)	23		Other serovars	30 (4.3)	22
	Total	**1039**			**Total**	**697**	

Abbreviation: MSs, Member States.

[a] *Salmonella* Paratyphi B is tartrate negative and causes typhoidal disease, except for *S*. Paratyphi B var. Java, which is tartrate positive and non-typhoidal. Since the isolates reported were from food and animal sources, we can suppose that these isolates were *S*. Paratyphi B var. Java.

Trends in *S.* Enteritidis in laying hen flocks and human cases, EU 2015–2024

Figure 8 presents the percentage of *S.* Enteritidis-positive flocks among all *Salmonella*-positive laying hen flocks, alongside the percentage of human *S.* Enteritidis cases acquired in the EU among all serotyped isolates acquired in the EU over the past 10 years. No significant correlation was observed between trends in human cases and positive laying hen flocks for this serovar.

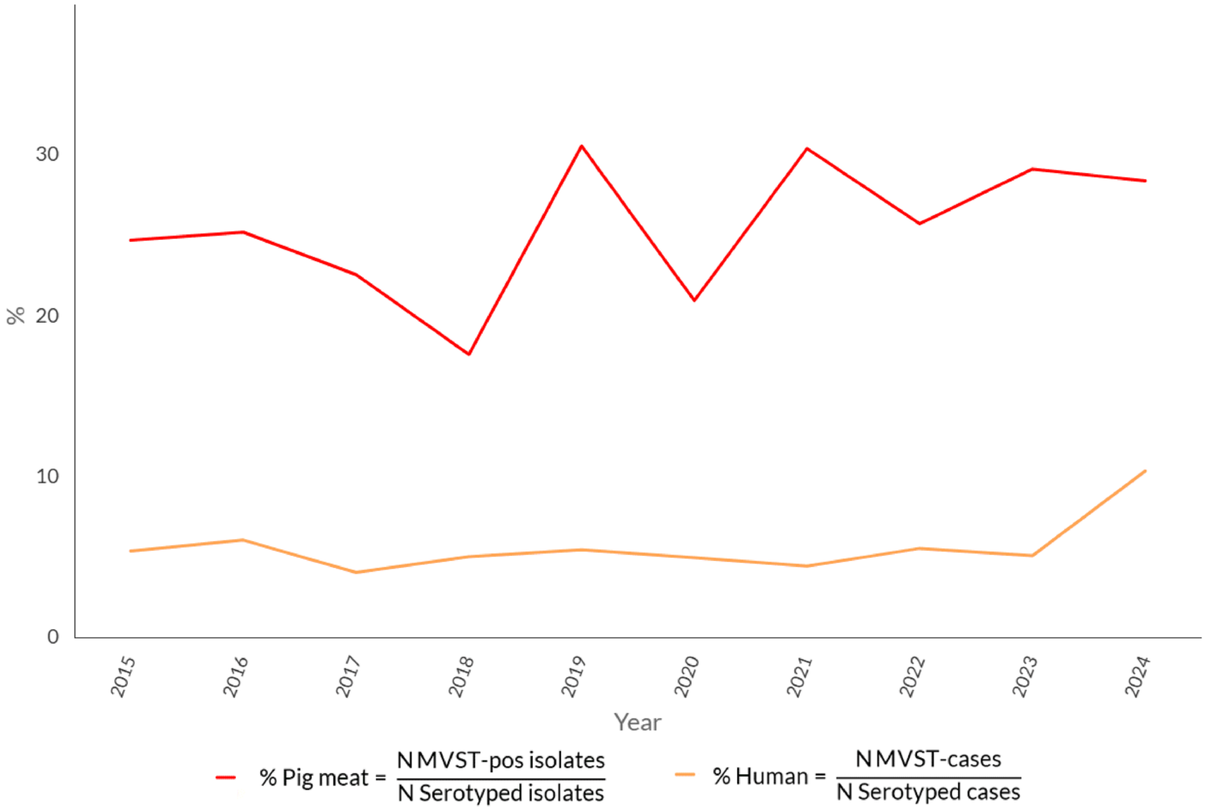


		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Laying hens	*N* SE-pos flocks	279	434	327	312	373	301	411	340	424	473
	N MSs	18	19	20	20	18	20	22	19	23	22
Human	*N* SE-cases	24,910	25,909	31,362	31,910	31,201	21,203	23,932	19,752	24,198	21,762
	N MSs	21	22	24	23	23	23	24	25	25	22

FIGURE 8 Percentage of *Salmonella* Enteritidis-positive flocks out of total *Salmonella*-positive flocks in laying hens, percentage of human *S.* Enteritidis cases acquired in the EU out of total cases with *Salmonella* serovar information available, EU, 2015–2024.

Trends in monophasic *S.* Typhimurium (MVST) in pig meat and human cases, EU 2015–2024

Figure 9 shows the percentage of monophasic *S.* Typhimurium among all *Salmonella* isolates from pig meat, alongside the percentage of human cases caused by monophasic *S.* Typhimurium acquired in the EU among all serotyped isolates acquired in the EU over the past 10 years. No significant correlation was observed between trends in human cases and pig meat isolates for this serovar.



		2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
Pig meat	*N* MVST-pos isolates	184	218	132	148	420	174	290	257	330	265
	N MSs	15	12	14	15	17	15	14	17	16	13
Human	*N* MVST-cases	2169	2437	1833	2411	6432	4697	1529	1684	1738	3860
	N MSs	13	15	15	16	16	16	15	15	16	16

FIGURE 9 Percentage of monophasic variant *Salmonella* Typhimurium (MVST) out of serotyped *Salmonella* isolates from pig meat, percentage of human MVST cases acquired in the EU out of total cases with *Salmonella* serovar information available, EU, 2015–2024.

A.2.5. | Discussion

Salmonellosis remained the second most common food-borne zoonosis in humans in the EU in 2024, after campylobacteriosis. The overall notification rate of salmonellosis in the EU increased slightly by 1.7% in 2024 compared to 2023, reaching 18.6 cases per 100,000 population, with Slovakia and Czechia continuing to report the highest rates. In 2024, for the first time since 2020, the number of human salmonellosis cases slightly exceeded those reported in 2019, the last year before a decline in cases reported during the COVID-19 pandemic, suggesting that case numbers at the EU level are returning to pre-pandemic levels. The overall EU trend for salmonellosis cases in the EU in 2020–2024 showed a significant increase. Similarly, 17 MSs also had an increasing trend, while no countries had a significant decreasing trend. Most countries showing an increasing trend between 2020 and 2024 continued to report case numbers and notification rates that were comparable to, or lower than, those reported before the COVID-19 pandemic. This apparent increasing trend is likely an artefact of the pandemic's impact on surveillance data since 2020, rather than evidence of a genuine rise in case numbers. Since the trend analysis begins in 2020, a year when surveillance for many diseases was heavily affected by the pandemic, it is expected that, as countries return to pre-pandemic reporting levels, an increasing trend will be observed between 2020 and 2024. The COVID-19 pandemic had a significant impact on surveillance systems, healthcare-seeking behaviour and reporting practices across the EU (Young et al., 2025).

To assess the impact of *Salmonella* infections acquired within the EU, serovar data combined with travel information were available from 23 MSs covering nearly three-quarters of salmonellosis cases with known serovar and travel status in 2024. The majority (over 90%) of these cases were infected within the EU, with Spain, Italy, Greece, Croatia and Poland being the most common travel destinations for EU-acquired cases.

Similar to previous years, the three most commonly reported EU acquired human serovars (*S.* Enteritidis, *S.* Typhimurium and its monophasic variant (1,4,[5],12:i:-)) remained predominant, accounting for 79.7% of human cases in 2024. *Salmonella* Enteritidis remained the most frequently reported serovar, although its proportion declined slightly compared to 2023, while the proportion of *S.* Typhimurium increased. *Salmonella* Infantis has consistently remained the fourth most frequently reported serovar from humans. Additionally, several less frequently reported serovars showed increasing numbers in 2024. The increase in *S.* Strathcona since 2023 may at least partly be attributable to a prolonged multi-country outbreak of *S.* Strathcona ST2559 linked to the consumption of tomatoes in 16 EU/EEA countries and the UK (ECDC and EFSA, 2024b). Similarly, the increase in *S.* Typhimurium cases since 2023 may be partly explained by a prolonged cross-border outbreak involving multiple *Salmonella* serovars, associated with the consumption of sprouted seeds in nine EU/EEA countries and the UK (ECDC and EFSA, 2025).

The leading food sources of salmonellosis outbreaks in the EU are eggs, pork and meat products (Chanamé Pinedo et al., 2022; EFSA and ECDC, 2024). In recent year, outbreaks associated with non-animal-derived foods have been also documented (ECDC and EFSA, 2024b, 2025; Rosner et al., 2024). Interestingly, in some cases, the outbreaks related to non-animal-derived foods involved serovars historically considered 'rare', and the exact origin of the contamination was not fully understood, highlighting the complexity of the bacteria's circulation routes along these productive chains. Indeed, foods of non-animal origin are generally produced outdoors in an environment that is challenging to control. Contamination can be associated with many different sources, such as irrigation and washing water, contaminated manure, wild birds and other animals. Moreover, fresh products are often consumed without any further heat treatment, have a short shelf-life, requiring prompt investigations and are subject to seasonal variation (Hoban et al., 2025). The identification of positive food batches is hampered by the low concentrations of the pathogens and their heterogeneous distribution, which require highly sensitive sampling to ensure pathogen identification. A One Health approach, based on the interconnection between human, animal and environmental health, is a cornerstone for managing these challenging food safety incidents associated with this type of food.

All MSs and EEA and EFTA countries reported *Salmonella* data from food and/or animal sources, confirming that the information presented here provides a comprehensive overview of the pathogen's distribution along the EU food production chain. To effectively control *Salmonella*, its presence is monitored throughout the food chain: preharvest (e.g. farm animals at primary production and feed), processing (e.g. slaughterhouses, cutting plants, manufacturing) and post-harvest (e.g. distribution, households, restaurants).

In 2024, as in previous years, meat and meat products were confirmed as the food categories with the highest levels of *Salmonella* contamination, particularly from poultry sources. The increasing occurrence of human isolates associated with *S.* Typhimurium and its monophasic variant (1,4,[5],12:i:-), which are generally linked to pig and bovine sources, also highlights the potential relevance of these reservoirs in terms of human infections. Although no harmonised *Salmonella* control programmes in pigs and bovine animals have been implemented in many Member States, the data suggest that special attention should be paid to the spread of *Salmonella* in these species.

Poultry samples in particular showed high prevalence, whether collected under the EU regulation to verify compliance with microbiological criteria (process hygiene criteria on carcases at slaughterhouses and food safety criteria on meat at manufacturing and distribution) or in other monitoring contexts. Poultry meat was most frequently positive at the early stages of processing – in particular carcase samples at slaughterhouses and meat samples at processing plants – but contamination was also observed at market level, including in RTE products. *Salmonella* contamination for meat is generally due to contact with intestinal contents/faeces during processing, or with contaminated water, equipment or the hands of workers along the slaughter line (Rodríguez et al., 2023). At this stage, hygiene practices are central to controlling the pathogen, while the *Salmonella* status of flocks entering the slaughterhouse is also a critical factor (Marin et al., 2022). Animals can acquire *Salmonella* through contaminated feed, environmental sources or contact with infected animals. The strong ability of *Salmonella* to survive under adverse conditions and develop antimicrobial resistance contributes to its persistence throughout the food chain and facilitates its transmission (Kumar et al., 2025).

The current EU *Salmonella* control system for poultry production is the result of nearly two decades of development. Despite long-standing surveillance and consolidated national control programmes in EU poultry populations, the epidemiological situation has not shown notable improvements in recent years. In fact, some deterioration has been observed in certain categories, such as breeding *Gallus gallus* and breeding turkeys over the past 10 years, and also breeding turkeys over the last 5 years. A further descriptive analysis of NCP data was carried out to assess the achievement of final *Salmonella* reduction targets by MSs across different poultry populations, covering the full implementation period, ranging from 12 years for turkeys to 15 years for breeding *Gallus gallus*. This assessment revealed that, in recent years, a considerable number of MSs failed to reach the targets in some poultry populations compared with the early years of NCP implementation. The trend was particularly evident for breeding *Gallus gallus* and laying hens. Moreover, even in countries with long-standing, comprehensive surveillance programmes based on a zero-tolerance approach aimed at eradication, unexpected *Salmonella* outbreaks were reported in breeders during the last year (according to data provided by MSs in the national text forms). Analyses comparing *S.* Enteritidis isolates from laying hens with human cases of the same serovar over the past 10 years showed no significant correlation. The same outcome was observed when comparing monophasic *S.* Typhimurium isolates from pig meat with human cases. However, these findings must be interpreted with caution, as they are strongly influenced by variability in the data reported by MSs over the years. This is particularly relevant for contexts such as pig meat, where serovar reporting is not mandatory and has lacked consistency across MSs and time.

Although disentangling the mechanisms behind this apparent stagnation of the *Salmonella* situation remains challenging, several hypotheses have been proposed. Current control programmes generally provide only a snapshot of prevalence rather than a holistic picture, limiting the understanding of transmission pathways – a prerequisite for implementing timely and effective corrective measures (Cargnel et al., 2023). In addition, inadequacies in sampling programmes and premature relaxation of control measures have been suggested as potential drivers of the recent increase in *S.* Enteritidis infections in some countries. Targeted interventions focusing on poultry health and production may help reverse this trend. These include stricter biosecurity measures, improved sampling strategies (Huneau-Salaün et al., 2025) and, where necessary, enhanced vaccination campaigns, particularly for laying hens with extended productive lifespans (Van Den Berg et al., 2025). Such interventions, if applied in synergy, may create the turning point needed to regain progress (Chanamé Pinedo et al., 2023). Ultimately, addressing the persistence of *Salmonella* in specific contexts requires coordinated, cross-sectoral control strategies and integrated surveillance to fully unravel the underlying causes and effectively curb transmission.

A3 | *LISTERIA MONOCYTOGENES*

Human cases [EU, 2024]

Notification rate *(per 100,000 population)* **0.69**

Trend *(2020-2024)* ↑

↑ *Increasing* ↓ *Decreasing* — *Stable*

3041 **Cases of illness**

2062 **Infections acquired in the EU**

14 **Infections acquired outside the EU**

965 **Unknown travel status or unknown country of infection**

1715 **Hospitalisations** (97.3%)*

301 **Deaths** (15.6%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

🟩 *ECDC data*

Foodborne outbreaks & related cases [EU, 2024]

38 **Foodborne outbreaks**

14 **Strong-evidence outbreaks** 🟧

24 **Weak-evidence outbreaks** ▨

210 **Cases of illness**

149 **Hospitalisations** (72.3%)*

17 **Deaths** (8.1%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

N of outbreaks		**N of outbreaks per 100,000 population ****		**N of outbreak cases per 100,000 population**	
Austria	1	AT	0.011	AT	0.044
Belgium	8	BE	0.068	BE	0.228
Bulgaria	0	BG	0	BG	0
Croatia	0	HR	0	HR	0
Cyprus	0	CY	0	CY	0
Czechia	1	CZ	0.009	CZ	0.092
Denmark	6	DK	0.101	DK	0.403
Estonia	0	EE	0	EE	0
Finland	3	FI	0.054	FI	0.625
France	1	FR	0.001	FR	0.038
Germany	5	DE	0.006	DE	0.013
Greece	0	EL	0	EL	0
Hungary	0	HU	0	HU	0
Ireland	1	IE	0.019	IE	0.056
Italy	8	IT	0.014	IT	0.095
Latvia	0	LV	0	LV	0
Lithuania	0	LT	0	LT	0
Luxembourg	0	LU	0	LU	0
Malta	0	MT	0	MT	0
Netherlands	1	NL	0.006	NL	0.022
Poland	1	PL	0.003	PL	0.011
Portugal	0	PT	0	PT	0
Romania	0	RO	0	RO	0
Slovakia	0	SK	0	SK	0
Slovenia	0	SI	0	SI	0
Spain	1	ES	0.002	ES	0.004
Sweden	1	SE	0.009	SE	0.038
UK (N. Ireland)	0	XI	0	XI	0

Implicated food vehicles
(Strong-evidence outbreaks)

Top food vehicles

Vegetables and juices and other products thereof
3 Outbreaks

Mixed food
3 Outbreaks

Fish and fish products
3 Outbreaks

Pig meat and products thereof
2 Outbreaks

Cheese
Dairy products other than cheeses
Meat and meat products, unspecified
1 Outbreak (each)

*** Differences among countries shall be interpreted with caution as this indicator depends on several factors including the type of outbreaks under surveillance and does not necessarily reflect the level of food safety in each country.*

🟧 *EFSA data*

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about *Listeria monocytogenes* and for the consultation of data collected, the following interactive tools are available:

A3.1 | Key facts

- In 2024, 3041 confirmed invasive human cases of *Listeria monocytogenes*, corresponding to a European Union notification rate of 0.69 cases per 100,000 population. This was an increase of 3.0% compared with the rate in 2023 (0.67 cases per 100,000 population) and the highest rate and number of cases reported since 2007.
- The overall trend for *L. monocytogenes* infections showed a significant increase over the 2020–2024 period.
- A total of 353,691 sampling units from different 'ready-to-eat' (RTE) food categories, collected at the distribution or manufacturing stages, were reported by 26 Member States and the United Kingdom (Northern Ireland). The number of samples returned to a comparable level to that observed in 2022; in 2023, non-reporting of data from Poland had significantly decreased numbers.
- At distribution, the proportions of single samples testing positive for *L. monocytogenes*, based either on enumeration or detection tests conducted by competent authorities as part of verification of the food safety criteria listed in Commission Regulation (EC) No 2073/2005 on microbiological criteria, were either zero or remained rare (< 0.1%) to very low (0.1%–1.0%) in 6 out of 11 targeted 'ready-to-eat' food categories. The highest proportion of positive samples (6.6%) was found in 'products of meat origin, fermented sausages'. For 'fish', 'products of meat origin other than fermented sausages', 'hard cheeses' and 'other products', the proportions of positive samples were relatively low (2.9%, 2.2%, 1.6% and 1.6%, respectively). Statistics on positive samples indicated further that the proportion of samples exceeding 100 CFU/g was either zero or consistently rare to very low across all 'ready-to-eat' food categories, except for 'products of meat origin, fermented sausages' with a proportion of 3.0%. No *L. monocytogenes* was detected in 'food for infants'.
- At manufacturing, in the context of Commission Regulation (EC) No 2073/2005, the proportions of single samples testing positive for *L. monocytogenes*, based on detection tests conducted by competent authorities, were either zero or remained rare (< 0.1%) to very low (0.1%–1.0%) in 4 out of 8 targeted 'ready-to-eat' food categories. The highest proportion of positive samples (2.5%) was found in 'products of meat origin, other than fermented sausages'. For 'fish' and 'cheese unspecified', the proportions of positive samples were low (2.4% and 2.3, respectively). These proportions were higher or equivalent at the manufacturing stage versus the distribution stage, except for 'fish', 'other dairy products' and 'other RTE products', where the proportion was lower (2.4%/2.9%, 0.14%/0.16% and 1.1%/1.6%, respectively for manufacturing/distribution).
- Results varied according to the 'ready-to-eat' food category, sampling stage, number of tested samples and number of reporting countries. In the framework of objective sampling, all samplers and sampling units included, overall occurrences remained generally low (1%–10%) to very low (0.1%–1%) in these categories: 4.6% for 'bovine meat products', 2.7% for 'pork meat products', 2.3% for 'fruits, vegetables and juices', 1.3% for 'poultry meat products' and 0.40% for 'milk and milk products'. Moderate overall occurrences were observed for 'fish and fishery products' (14.6%).
- At primary production, the percentage of positive units was rare in pigs (0.05%), and low in small ruminants (sheep and goats) and cattle (3.6% and 2.3%, respectively). The low number of Member States reporting data reflects the absence of minimum legal requirements for harmonised sampling and reporting at primary production.

A3.2 | Surveillance and monitoring of *Listeria monocytogenes* in the EU

A3.2.1 | Humans

Surveillance of listeriosis in humans in the EU focuses on invasive forms of *L. monocytogenes* infection, mostly manifesting as septicaemia, influenza-like symptoms, meningitis or spontaneous abortion.

Surveillance of listeriosis is mandatory in all MSs, except in one country (Belgium). The EU case definition was used by 25 countries. Germany reported using another case definition, and France did not specify which case definition was used.

All countries have comprehensive surveillance systems. The surveillance systems for listeriosis cover the whole population in all MSs, except in one country (Belgium), where the estimated coverage of the surveillance system was 80%. The estimated coverage of the surveillance system was 97% in Spain for 2021–2023. These estimated proportions of population coverage were used in the calculation of notification rates for these two countries. No estimated population coverage was provided for Spain prior to 2021, so notification rates were not calculated. Bulgaria reported aggregated data, while the other 25 countries reported case-based data.

A3.2.2 | Food, animals and feed

Monitoring of *L. monocytogenes* is carried out along the food chain, at primary production, manufacturing and distribution.

The public health risk associated with 'ready-to-eat' (RTE) foods depends mainly on the effectiveness of control measures implemented by food business operators (FBOps), including:

- Good agricultural practices (GAP) at primary production,
- Good manufacturing practices (GMP) and Hazard Analysis and Critical Control Point (HACCP) programmes at manufacturing and distribution,
- Microbiological criteria for RTE foods, as defined in Commission Regulation (EC) No 2073/2005.[33]

Listeria monocytogenes **data in the context of Commission Regulation (EC) No 2073/2005**

Official sampling is scheduled by national competent authorities (CAs) to verify whether FBOps correctly implement the legal framework of their own-check programmes. Official control samples are thus part of the verification of *L. monocytogenes* food safety criteria (FSC) of Commission Regulation (EC) No 2073/2005. Data provided to EFSA within this context enable a descriptive summary of contamination levels, especially of RTE foods, at the EU level.

Listeria monocytogenes **monitoring data for food, animals and feed**

All the food testing data were provided through Member State reporting obligations under Directive 2003/99/EC.[34] The rationale for surveillance and monitoring of *L. monocytogenes* in animals, feed and food at the different stages along the food chain and the number of samples provided to EFSA are shown in Figure 10. Most of the reported data in animals and feed are generated by non-harmonised monitoring schemes across MSs, and for which mandatory reporting requirements are not in place. Data on the occurrence of *L. monocytogenes* in feed are only collected as part of clinical investigations in farm animals. Hence, monitoring data on *L. monocytogenes* in animal feed are rarely available.

A3.3 | Data analyses

A3.3.1 | Data on RTE foods in the context of Commission Regulation (EC) No 2073/2005 on microbiological criteria

These data are based on single samples collected by CAs as part of verification of *L. monocytogenes* FSC listed in Commission Regulation (EC) No 2073/2005, which are to be complied by FBOps. These FSC are specified by RTE food category and by sampling stage and are underpinned by the results of either detection or enumeration analytical methods (Table 31). These data were extracted from the database using the criteria 'official sampling' for the sampler, 'single units' for the sampling unit and 'objective sampling' for the sampling strategy (Table 34).

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[33] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

[34] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40.

TABLE 31 *Listeria monocytogenes* FSC as described in Commission Regulation (EC) No 2073/2005 for the different RTE categories across the food chain, 2024.

Sampling stage	RTE foods intended for infants and RTE foods for special medical purposes	Other RTE foods	
		Able to support growth of *L. monocytogenes*	Unable to support growth of *L. monocytogenes*
Manufacturing[a]	NA	Based on detection method: *L. monocytogenes* not detected in 25 g of sample ($n=5$, $c=0$)[b]	NA
Distribution[c]	Based on detection method: *L. monocytogenes* not detected in 25 g of sample ($n=10$, $c=0$)	Based on enumeration method: limit of 100 CFU/g ($n=5$, $c=0$)[d]	Based on enumeration method: limit of 100 CFU/g ($n=5$, $c=0$)

Abbreviations: NA, not applicable; RTE, ready-to-eat.

[a] Before the food has left the immediate control of the food business operator that has produced it.

[b] This criterion shall apply if the food business operator has not been able to demonstrate, to the satisfaction of the CA, that the product will not exceed the limit of 100 CFU/g throughout the shelf-life.

[c] Products placed on the market during their shelf-life.

[d] This criterion shall apply if the food business operator has been able to demonstrate, to the satisfaction of the CA, that the level of *L. monocytogenes* will not exceed the limit of 100 CFU/g throughout the shelf-life. The operator may fix intermediate limits during the process that must be low enough to guarantee that the limit of 100 CFU/g is not exceeded at the end of the shelf-life of the food.

Data reported by MSs were classified into the different categories of RTE food/sampling stages based on the assumptions described in the EU Summary zoonoses and food-borne outbreaks report of 2016 (EFSA and ECDC, 2017). Briefly, these assumptions are: all sampling units that were collected from 'cutting plants' and 'processing plants' were considered units collected at the manufacturing stage, while sampling units that were obtained from 'catering', 'hospital or medical care facility', 'retail', 'wholesale', 'restaurant or cafe or pub or bar or hotel or catering service', 'border inspection activities', 'packing centre' and 'automatic distribution system for raw milk' were considered units collected at distribution. When the stage was 'not available' or 'unspecified', data were also considered part of the distribution stage. Other assumptions concerning the RTE categories are presented in the footnotes of Table 34.

A3.3.2 | Monitoring data assessing *Listeria monocytogenes* occurrence in RTE foods

The overall occurrence of *L. monocytogenes* in different RTE food categories, regardless of the stage, was assessed from detection results reported by MSs. All levels of sampling unit (single and batches), sampling stages, sampler and sampling contexts ('surveillance', 'monitoring' and 'surveillance based on Commission Regulation (EC) No 2073/2005') were considered. Only data obtained from the sampling strategies 'objective sampling' and 'census sampling' were used, excluding data reported from 'convenient sampling', 'suspect sampling', 'selective sampling' and 'other' contexts. Since data were mostly reported by a limited number of MSs and are of a heterogeneous nature, results may not be representative of the EU level nor directly comparable across years.

A3.3.3 | Monitoring data for *Listeria monocytogenes* in animals and feed

For animals and feed, all sampling strategies were included, even data reported for 'suspect sampling' and 'selective sampling'.

A3.4 | Results

A3.4.1 | Overview of key statistics, EU, 2020–2024

Table 32 summarises EU-level statistics on human listeriosis and on sampling units from RTE foods tested for *L. monocytogenes* during the period 2020–2024. Food data of interest reported were classified into the major categories and aggregated by year to obtain an annual overview of the volume of data submitted. More detailed descriptions of these statistics are provided in the below subsections and in the chapter on food-borne outbreaks.

Following the decrease of 36% observed in 2023 due to the absence of data from Poland, the number of sampling units reported in 2024 surpassed that of 2022 by 21%. It is important to note that 75% of the 2024 increase is explained by the number of units from Poland. A more noticeable increase in the reported number of sampling units from major RTE food categories has been observed for 'fish and fishery products' and 'meat and meat products', with an increase of 392% and 108%, respectively, compared with 2023. The only decrease in the number of reported sampling units has been observed for 'RTE foods intended for infants and for special medical purposes' (–7.7%). On the other hand, notable reductions in reported sampling units were observed for Denmark (1055 units in 2023 vs. 219 in 2024) and for Germany (25,677 units in 2023 vs. 9987 in 2024).

TABLE 32 Summary of *Listeria monocytogenes* statistics relating to invasive human infections and major RTE food categories, EU, 2020–2024.

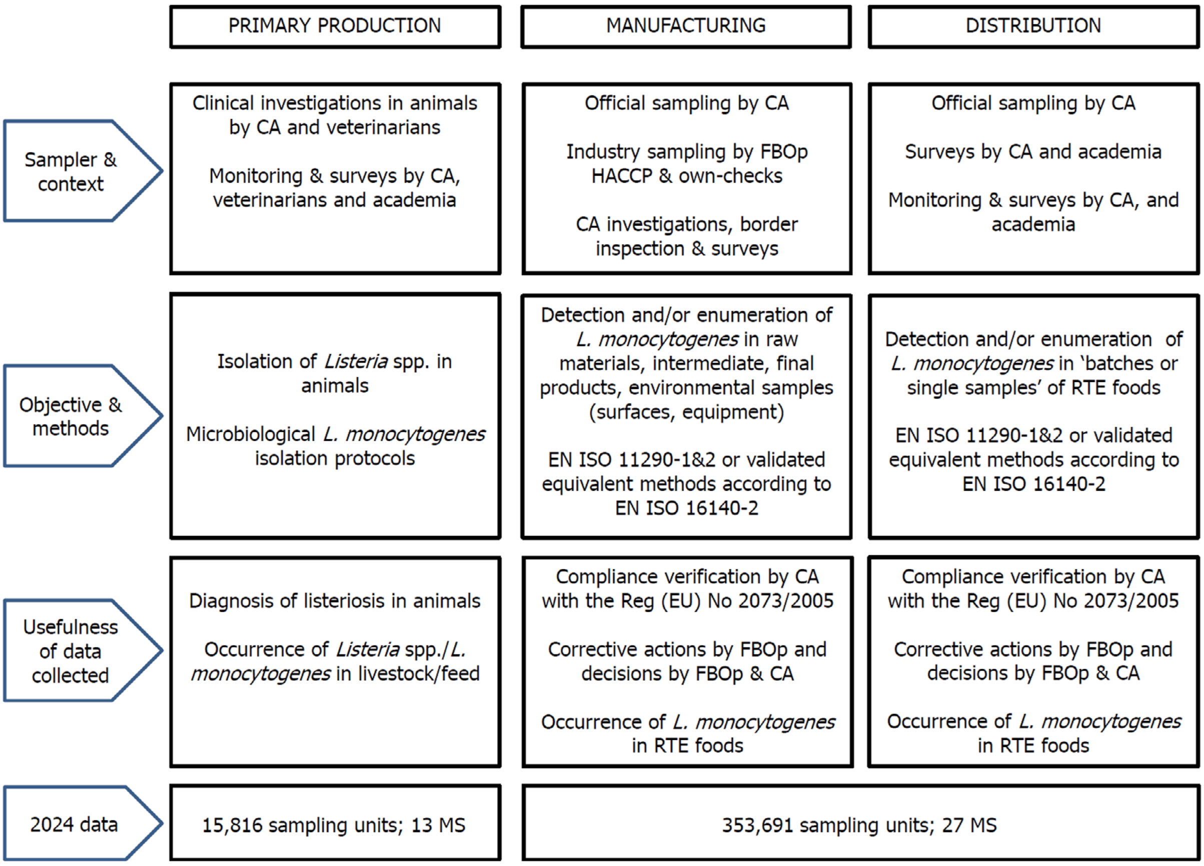
	2024	2023	2022	2021	2020	Data source
Humans						
Total number of confirmed cases	3041	2952	2780	2363	1887	ECDC
Total number of confirmed cases/100,000 population (notification rates)	0.69	0.67	0.63	0.54	0.43	ECDC
Number of reporting MSs	26	27	27	27	27	ECDC
Infection acquired in the EU	2062	1697	1508	1255	1286	ECDC
Infection acquired outside the EU	14	8	10	5	5	ECDC
Unknown travel status or unknown country of infection	965	1247	1262	1103	596	ECDC
Number of outbreak-related cases	210	133	296	106	123	EFSA
Total number of outbreaks	38	19	35	24	17	EFSA
Sampled major RTE food categories[a]						
Meat and meat products						
Number of sampling units	130,699	62,839	135,005	106,802	39,923	EFSA
Number of reporting MSs	26	23	24	23	22	EFSA
Fish and fishery products						
Number of sampling units	68,198	13,872	24,995	29,767	11,197	EFSA
Number of reporting MSs	25	22	24	24	23	EFSA
Milk and milk products						
Number of sampling units	89,434	60,026	97,113	66,521	48,940	EFSA
Number of reporting MSs	25	24	24	23	23	EFSA
Products intended for infants or special medical purposes						
Number of sampling units	3763	4079	2672	2764	2394	EFSA
Number of reporting MSs	19	19	19	19	19	EFSA
Other products[b]						
Number of sampling units	167,258	103,964	120,471	94,613	81,399	EFSA
Number of reporting MSs	27	25	25	26	24	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States; RTE, ready-to-eat.

[a] Number of sampling units tested by detection or enumeration method.

[b] Includes RTE products other than those detailed in the table.

Figure 10 shows that in 2024, 26 MSs and the United Kingdom (Northern Ireland) reported a total of 353,691 sampling units tested for *L. monocytogenes* across various RTE food categories at the manufacturing and distribution stages. Finland did not provide data in 2024. Ireland and Sweden did not provide any data from objective sampling. Compared with 2023, there was a slight increase in the number of reporting MSs (25 in 2023) and a 90% increase in the number of sampling units tested at these stages (186,997 in 2023 and 312,849 samples in 2022). The 2024 increase was primarily due to the contribution of data from Poland which did not report any in 2023. Poland contributed 35% ($N = 125{,}005$) of the samples in 2024, similar figures compared with 2022 at 36% ($N = 113{,}766$). At the primary production level, the volume of reported data is similar to that of 2023, with an additional MS contributing, Spain for 4.3% ($N = 678$). In 2024, 12 MSs and the United Kingdom (Northern Ireland) reported 15,816 samples, comparable to 2023 figures at 15,422 samples.



	PRIMARY PRODUCTION	MANUFACTURING	DISTRIBUTION
Sampler & context	Clinical investigations in animals by CA and veterinarians Monitoring & surveys by CA, veterinarians and academia	Official sampling by CA Industry sampling by FBOp HACCP & own-checks CA investigations, border inspection & surveys	Official sampling by CA Surveys by CA and academia Monitoring & surveys by CA, and academia
Objective & methods	Isolation of *Listeria* spp. in animals Microbiological *L. monocytogenes* isolation protocols	Detection and/or enumeration of *L. monocytogenes* in raw materials, intermediate, final products, environmental samples (surfaces, equipment) EN ISO 11290-1&2 or validated equivalent methods according to EN ISO 16140-2	Detection and/or enumeration of *L. monocytogenes* in 'batches or single samples' of RTE foods EN ISO 11290-1&2 or validated equivalent methods according to EN ISO 16140-2
Usefulness of data collected	Diagnosis of listeriosis in animals Occurrence of *Listeria* spp./*L. monocytogenes* in livestock/feed	Compliance verification by CA with the Reg (EU) No 2073/2005 Corrective actions by FBOp and decisions by FBOp & CA Occurrence of *L. monocytogenes* in RTE foods	Compliance verification by CA with the Reg (EU) No 2073/2005 Corrective actions by FBOp and decisions by FBOp & CA Occurrence of *L. monocytogenes* in RTE foods
2024 data	15,816 sampling units; 13 MS	353,691 sampling units; 27 MS	

FIGURE 10 Overview of *Listeria monocytogenes* testing of 'ready-to-eat' food along the food chain according to the sampling stage, the sampler and the objective of the sampling, EU, 2024.

A3.4.2 | Human listeriosis

In 2024, 26 MSs reported 3041 confirmed cases of invasive listeriosis in humans (Tables 32 and 33). The EU notification rate was 0.69 cases per 100,000 population, 3.0% higher than in 2023 (0.67 per 100,000 population). The highest notification rates were observed for Luxembourg, Sweden, Denmark, Spain and Belgium, with 1.2, 1.1, 1.0, 0.96 and 0.98 cases per 100,000 population, respectively. The lowest notification rates were reported by Bulgaria and Romania (≤ 0.20 per 100,000 population). Malta reported no cases of listeriosis.

For most (99.3%) of the reported listeriosis cases of known origin, the infection was acquired in the EU (including both domestic and travel-associated cases within the EU) (Table 32). This figure is slightly lower than in 2023 (99.5%). The proportion of domestic cases among the cases of known origin was 93%–100% in all reporting countries. Nine MSs reported imported cases, and the proportion of travel-related cases among cases with information on importation status in these countries ranged from 0.43% to 6.3%.

Similar to previous years, nearly all listeriosis cases in 2024 (97.3%; 1715/1762) required hospitalisation. There were 301 reported deaths, with the majority (81.7%; 246/301) occurring among individuals aged over 65 years).

TABLE 33 Reported confirmed human cases of invasive listeriosis and notification rates per 100,000 population in EU MS and non-MS countries, by country and year, 2020–2024.

	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	National coverage[a]	Data format[a]	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	44	0.48	37	0.41	47	0.52	38	0.43	41	0.46
Belgium[b]	N	C	93	0.98	84	0.89	87	0.94	68	0.74	54	0.59
Bulgaria	Y	A	13	0.20	15	0.23	5	0.08	3	0.05	4	0.06
Croatia	Y	C	10	0.26	6	0.16	5	0.13	8	0.21	5	0.13
Cyprus	Y	C	2	0.21	0	0	1	0.11	1	0.11	2	0.22

TABLE 27 (Continued)

Country	2024				2023		2022		2021		2020	
	National coverage[a]	Data format[a]	Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
			Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Czechia	Y	C	61	0.56	44	0.41	48	0.46	24	0.23	16	0.15
Denmark	Y	C	61	1.0	53	0.89	86	1.5	62	1.06	43	0.74
Estonia	Y	C	7	0.51	5	0.37	11	0.83	5	0.38	3	0.23
Finland	Y	C	50	0.89	92	1.7	69	1.2	70	1.3	94	1.7
France	Y	C	619	0.90	538	0.79	451	0.66	435	0.64	334	0.50
Germany	Y	C	646	0.77	664	0.80	551	0.66	560	0.67	546	0.66
Greece	Y	C	26	0.25	31	0.30	7	0.07	21	0.20	20	0.19
Hungary	Y	C	46	0.48	46	0.48	64	0.67	35	0.36	32	0.33
Ireland	Y	C	22	0.41	18	0.34	17	0.33	14	0.28	6	0.12
Italy	Y	C	238	0.40	231	0.39	385	0.65	230	0.39	155	0.26
Latvia	Y	C	–	–	11	0.58	8	0.43	10	0.53	8	0.42
Lithuania	Y	C	17	0.59	20	0.70	13	0.46	7	0.25	7	0.25
Luxembourg	Y	C	8	1.2	4	0.61	4	0.62	4	0.63	4	0.64
Malta	Y	C	0	0	2	0.37	1	0.19	0	0	5	0.97
Netherlands	Y	C	117	0.65	95	0.53	94	0.53	86	0.49	90	0.52
Poland	Y	C	240	0.66	240	0.65	142	0.38	120	0.32	57	0.15
Portugal	Y	C	95	0.89	99	0.94	63	0.60	57	0.55	47	0.45
Romania	Y	C	24	0.13	21	0.11	14	0.07	11	0.06	2	0.01
Slovakia	Y	C	11	0.20	21	0.39	25	0.46	13	0.24	7	0.13
Slovenia	Y	C	12	0.56	16	0.76	20	0.95	19	0.90	26	1.2
Spain[c]	Y	C	465	0.96	428	0.92	437	0.95	355	0.77	191	–
Sweden	Y	C	114	1.1	131	1.2	125	1.2	107	1.0	88	0.85
EU Total			**3041**	**0.69**	**2952**	**0.67**	**2780**	**0.63**	**2363**	**0.54**	**1887**	**0.43**
Iceland	Y	C	7	1.8	3	0.77	2	0.53	5	1.4	4	1.1
Liechtenstein	Y	C	0	0	0	0	0	0	0	0	–	–
Norway	Y	C	29	0.52	39	0.71	30	0.55	20	0.37	37	0.69
Switzerland[d]	Y	C	51	0.57	74	0.84	78	0.89	33	0.38	58	0.67

Abbreviation: –, Data not reported.

[a] Y, yes; N, no; A, aggregated data; C, case-based data.

[b] Sentinel system; notification rates calculated with an estimated population coverage of 80%.

[c] Notification rates calculated with an estimated population coverage of 100% in 2024 and 97% in 2021–2023. No information on estimated coverage in 2020, so notification rate cannot be estimated.

[d] Switzerland provided data directly to EFSA. The human data for Switzerland include data from Liechtenstein for 2020.

The distribution of cases by month in the last 5 years (2020–2024) shows a rise in case reports in the second half of the year, with a peak in the summer (Figure 11). The overall EU trend for listeriosis cases in the period 2020–2024 showed a significant increase. At the country level, a statistically significant increasing trend ($p < 0.05$) was observed in 10 countries (Belgium, Czechia, France, Hungary, Ireland, Poland, Portugal, Romania, Spain and Sweden), while Slovenia had a significant decreasing trend.

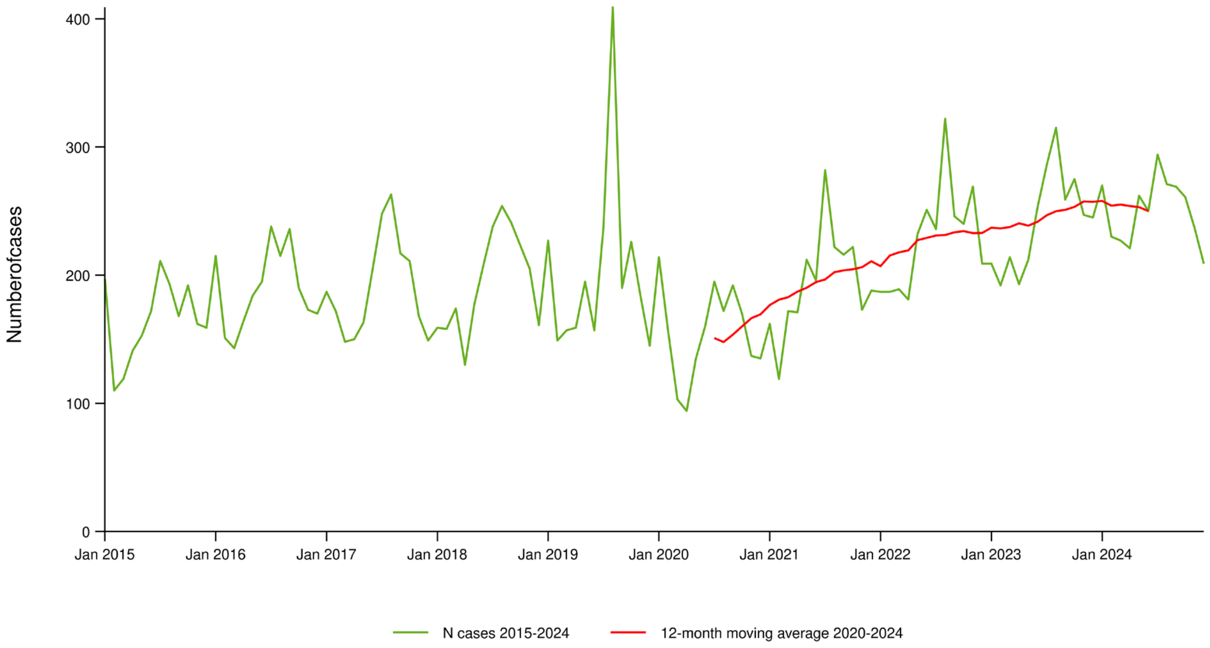


FIGURE 11 Trend in reported confirmed human cases of listeriosis in the EU by month, 2020–2024.
Source: Austria, Belgium, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden.

A3.4.3 | *Listeria monocytogenes* in RTE food

Data collected in the context of Commission Regulation (EC) No 2073/2005

In total, 23 MSs reported data in the context of the FSC according to the specifications mentioned above (Section 3.3.1) for 11 RTE food categories (Table 34).

Overall, *L. monocytogenes* occurrences reported from official sampling were rare to low, both at manufacturing and distribution (from 0% to 6.6%).

At distribution, the highest occurrences were reported for ‘products of meat origin, fermented sausages’ (6.6%), ‘fish’ (2.9%), ‘products of meat origin, other than fermented sausages’ (2.2%), ‘hard cheeses’ (1.6%) and ‘other RTE products’ (1.6%). The proportion of samples exceeding 100 CFU/g was either zero or consistently rare to very low across all RTE food categories, except for fermented sausages (3.0%). This last result is, however, driven only by data reported by Lithuania.

At manufacturing, the highest occurrences were reported for ‘products of meat origin other than fermented sausages’ (2.5%), ‘fish’ (2.4%) and ‘cheeses, unspecified’ (2.3%).

TABLE 34 Proportions (%) of *Listeria monocytogenes* positive single samples at the manufacturing and distribution stages from official sampling by CAs in the context of verification of implementation by FBOps of the *Listeria monocytogenes* FSC in accordance with Commission Regulation (EC) No 2073/2005, EU, 2024.

	Manufacturing[b]	**Distribution**[c]		
	Analytical method[d]			
	Detection (EN ISO 11290-1)	**Detection (EN ISO 11290-1)**	**Enumeration (EN ISO 11290-2)**	
RTE food category[a]	**% positive Samples (*N* samples tested, *N* reporting MSs)**[d]	**% positive samples (*N* samples tested, *N* reporting MSs)**[d]	**% positive samples (*N* samples tested, *N* reporting MSs)**[d]	**% of samples exceeding 100 CFU/g**[e]
Foods intended for infants and for medical purposes: data reported from BE, BG, CY, CZ, ES, GR, HU, IT, SI, SK		0 (*N* = 2292; 10 MSs)		
Fish: data reported from AT, BE, BG, CY, CZ, DE, DK, EE, ES, FR, GR, HR, HU, IT, LU, PT, PL, SI, SK	2.4 (*N* = 2169; 10 MSs)		2.9 (*N* = 1361; 16 MSs)	0.37
Fishery products: data reported from AT, BE, BG, CY, CZ, DK, EE, ES, FR, HR, IT, LU, PL, RO, SI, SK, XI	0.99 (*N* = 1310; 10 MSs)		0.87 (*N* = 1261; 12 MSs)	0.32

TABLE 34 (Continued)

	Manufacturing[b]	Distribution[c]		
	Analytical method[d]			
	Detection (EN ISO 11290-1)	Detection (EN ISO 11290-1)	Enumeration (EN ISO 11290-2)	
RTE food category[a]	% positive Samples (*N* samples tested, *N* reporting MSs)[d]	% positive samples (*N* samples tested, *N* reporting MSs)[d]	% positive samples (*N* samples tested, *N* reporting MSs)[d]	% of samples exceeding 100 CFU/g[e]
Cheeses, soft and semi-soft: data reported from AT, BE, BG, CY, CZ, EE, ES, GR, HR, HU, IT, LT, LU, PT, PL, RO, SK, XI	0.73 (*N* = 5930; 13 MSs)		0.53 (*N* = 1325; 13 MSs)	0.23
Cheeses, hard: data reported from BG, ES, IT, LU, PT, SK			1.6 (*N* = 308; 6 MSs)	0
Cheeses, unspecified: data reported from AT, BE, CY, DE, ES, GR, IT, PL, RO, SI, SK, XI	2.3 (*N* = 1009; 8 MSs)		0.29 (*N* = 348; 7 MSs)	0.29
Other dairy products (excluding cheeses) – entire category: data reported from AT, BE, BG, CY, CZ, DE, DK, EE, ES, GR, HU, IT, LU, PL, RO, SI, SK, XI	0.14 (*N* = 4141; 13 MSs)		0.16 (*N* = 1283; 13 MSs)	0
Milk: data reported from AT, BG, CY, CZ, EE, ES, GR, HR, IT, LU, PL, RO, SK	0.20 (*N* = 488; 9 MSs)		0 (*N* = 154; 6 MSs)	0
Products of meat origin, fermented sausages: data reported from BE, CZ, ES, GR, HR, HU, LT, LU, PT, SK			6.6 (*N* = 634; 10 MSs)	3.0
Products of meat origin, other than fermented sausages: data reported from AT, BE, BG, CY, CZ, DK, EE, ES, FR, GR, HR, HU, IT, LU, PT, PL, RO, SI, SK, XI	2.5 (*N* = 20,800; 13 MSs)		2.2 (*N* = 3592; 16 MSs)	0.86
Other products: data reported from AT, BE, BG, CY, CZ, DK, EE, ES, FR, GR, HR, HU, IT, LU, PL, PT, RO, SI, SK, XI	1.1 (*N* = 1582; 14 MSs)		1.6 (*N* = 9133; 17 MSs)	0.02

Note: Grey boxes are not applicable in relation to the analytical method for the specific food category and sampling stage in the context of Commission Regulation (EC) No 2073/2005.

Abbreviations: CFU, colony forming units; MSs, Member States; *N*, number of single samples tested; RTE, ready-to-eat.

[a] In the absence of relevant physicochemical data (pH, aw), EFSA assumes that foods listed under ‘fish and fishery products’, ‘soft and semi-soft cheeses’, ‘unspecified cheeses’, ‘milk’, ‘products of meat origin other than fermented sausages’, ‘other dairy products’ and ‘other products’ belong to the category of foods that are able to support the growth of *L. monocytogenes*. EFSA assumes that ‘fermented sausages’ and ‘hard cheeses’ belong to the category of foods that are unable to support the growth of *L. monocytogenes*, because foods classified under these two categories of RTE products undergo ripening/fermentation and are expected to have low pH and moderate aw values. For ‘other dairy products’, EFSA presents the results in a conservative way, by considering all foods included in this category as capable of supporting the growth of *L. monocytogenes*.

[b] Includes samples collected from ‘cutting plants’ and ‘processing plants’.

[c] Includes samples collected from ‘catering’, ‘hospital or medical care facility’, ‘retail’, ‘wholesale’, ‘not available’, ‘unspecified’, ‘restaurant or cafe or pub or bar or hotel or catering service’, ‘automatic distribution system for raw milk’, ‘border inspection’ and ‘packing centre’.

[d] Proportion (%) of positive samples (detection of *L. monocytogenes* in 25 g of sample for qualitative analyses, or number of *L. monocytogenes* > or ≤ 100 CFU/g for enumeration analyses); in parentheses, the number of tested samples and the number of reporting MSs.

[e] Proportion (%) of samples exceeding 100 CFU/g for enumeration analyses.

The below text summarises occurrence data for the major food categories according to the criteria described in Section 3.3.2.

Monitoring data assessing *L. monocytogenes* occurrence in RTE foods

Fish and fishery products, RTE

In 2024, 21 MSs and the United Kingdom (Northern Ireland) reported detection data for fish or fishery products from objective sampling (*N* = 13,940). Three non-MSs (Albania, Iceland and Serbia) also reported data (*N* = 54).

Seven MSs (Bulgaria, France, Italy, the Netherlands, Poland, Romania and Spain) accounted for 92.5% of the reported data for these categories in the EU.

In the EU, as in previous years, the overall occurrence of *L. monocytogenes* in fish or fishery products remained among the highest across all RTE food categories. In 2024, the overall mean occurrence was moderate at 14.6%, ranging from 0%

to 60.0% depending on the MS, food category and sample size. Compared with previous years, the general occurrence for fish and fishery products was driven by high occurrence reported by Poland for smoked fish (25.0%, *N* = 7411).

Meat and meat products, RTE

In 2024, 20 MSs and the United Kingdom (Northern Ireland) reported detection data for meat and meat products from objective sampling (*N* = 40,863). Four non-MSs (Albania, Iceland, Republic of North Macedonia and Serbia) also reported data (*N* = 417).

In the EU, five MSs accounted for 86.3% of the reported data (Bulgaria, Czechia, Poland, Romania and Spain). The overall mean occurrence of *L. monocytogenes* in meat and meat products was 2.4% with occurrence depending on the MS, food category and sample size. Details for the main categories are shown below. A total of 72.8% of tested units were associated with the main animal species (pigs, cattle and poultry), while the remaining units came from other, mixed or unspecified animals. RTE meat and meat products specifically from pigs were the most frequently tested (64.1%). RTE meat and meat products from cattle and poultry (poultry unspecified, broiler or turkey) represented 4.7% and 4.1% of the tested sampling units, respectively.

Pork products

Seventeen MSs and the United Kingdom (Northern Ireland) reported data for pork meat products (*N* = 26,186). Four non-MSs (Albania, Iceland, Republic of North Macedonia and Serbia) reported 213 units tested in this meat category.

In the EU, the overall occurrence was low and comparable to previous years: 2.7% in 2024 (*N* = 26,186), 3.1% in 2023 (*N* = 11,976) and 1.9% in 2022 (*N* = 32,068). As in previous years, five MSs accounted for 91.7% of the reported data on pork meat products (Bulgaria, Czechia, Poland, Romania and Spain).

Poultry meat products (broilers and turkeys)

Sixteen MSs reported data for RTE poultry meat products (*N* = 1660): broilers, turkey or unspecified poultry. No data were reported by non-MSs for this category.

In the EU, the overall mean occurrence of *L. monocytogenes* in RTE poultry meat products was 1.3%. This occurrence was comparable to previous years: 0.44% (*N* = 455) in 2023, 0.64% (*N* = 1248) in 2022 and 1.3% (*N* = 895) in 2021. In 2024, five positive sampling units were detected in RTE meats from broilers (*N* = 883) and four from turkeys (*N* = 189). In 2024, four MSs (Bulgaria, Czechia, Hungary and Poland) accounted for 72.2% of the reported data on poultry meat products.

Bovine meat products

Sixteen MSs and the United Kingdom (Northern Ireland) reported data for RTE bovine meat products (*N* = 1912). One non-MSs (Serbia) reported data for this category (*N* = 150).

In the EU, the overall mean occurrence of *L. monocytogenes* reported in RTE bovine meat products was 4.6% (*N* = 1912). Three MSs (Italy, the Netherlands and Poland) accounted for 79.6% of the reported data on bovine meat products. For comparison, occurrences were 9.9% (*N* = 679) in 2023, 4.9% in 2022 (*N* = 2712) and 3.9% in 2021 (*N* = 2217).

Milk and milk products, RTE

In 2024, twenty MSs and the United Kingdom (Northern Ireland) reported detection data for RTE milk and milk products from objective sampling (*N* = 38,128). Four non-MSs (Albania, Montenegro, Republic of North Macedonia and Serbia) reported data for this category (*N* = 5065).

In the EU, seven MSs (Bulgaria, Cyprus, Czechia, Italy, Poland, Romania and Spain) provided 88.6% of the reported data. The overall mean occurrence of *L. monocytogenes* in RTE milk products was very low regardless of the sampling stage, at 0.40%. The occurrence was 0.39% in cheeses made from pasteurised milk (*N* = 10,444), 1.6% in cheeses made from raw milk or low heat-treated milk (*N* = 3763) and 0.18% in milk (*N* = 1087). Among the tested sampling units, 77.6% of cheeses (*N* = 22,323) and 83.4% of milks (*N* = 1087) were specifically of bovine origin.

Fruits, vegetables and juices, RTE

Nineteen MSs and the United Kingdom (Northern Ireland) reported detection data for RTE fruits, vegetables and juices from objective sampling (*N* = 3194). Two units were reported by one non-MS (Albania).

In the EU, the overall occurrence was 2.3% (*N* = 3194), ranging from 0% to 18.6% depending on the food category and sample size.

A total of 88.6% of the data were reported by eight MSs (Austria, Bulgaria, France, Germany, Hungary, Italy, Malta and Spain).

A3.4.4 | *Listeria* spp. in animals

In 2024, 12 MSs together with the United Kingdom (Northern Ireland) and three non-MSs (Norway, Republic of North Macedonia and Switzerland) reported 15,816 and 79 samples, respectively, across various animal categories, including food-producing, wild, zoo and pet animals, as well as birds, from different species.

In the EU, the majority of the data (Table 35) were derived from individual animals (94.4%, *N* = 14,934) compared to other samples such as herd/flock or holdings.

Cattle accounted for the largest proportion of animals tested for *Listeria* (49.1% of the total units tested), followed by small ruminants (28.8%) and pigs (12.8%). The percentages of positive units for *Listeria* spp. were 2.3% in cattle, 3.6% in small ruminants and 0.05% in pigs. The sample size, sampling strategies and proportion of positive findings varied considerably among the reporting countries and animal species. Notably, 81.5% of the EU data were reported by two MSs: the Netherlands (42.2%) and Ireland (39.3%).

Among the 356 positive samples for *Listeria* spp., 66.3% were reported as *L. monocytogenes*. Limited positive findings were attributed to *L. ivanovii* (3.9%) and *L. innocua* (2.8%). As in previous years, a relatively large proportion of positive findings (27.0%) were classified as other or unspecified *Listeria* species.

TABLE 35 Summary of *Listeria* species statistics relating to major animal species, MSs, 2024.

Animal species	*N* reporting MSs	*N* tested units	% positive units	*N* positive units for *L. monocytogenes*	*N* positive units for *L. ivanovii*	*N* positive units for *L. innocua*	*N* positive units for other *Listeria* species
Cattle	12	7770	2.3	153	0	8	18
Sheep and goats	13	4548	3.6	80	11	1	71
Pigs	5	2020	0.05	0	0	1	0
Others	13	1478	0.88	3	3	0	7
Total EU	13	15,816	2.2	236	14	10	96

A3.5 | Discussion

Listeriosis was the fifth most commonly reported zoonosis in humans in the EU in 2024. It is one of the most serious foodborne diseases under EU surveillance due to the high proportion of hospitalisations, and elevated morbidity and mortality, particularly among elderly people (ECDC, 2025a, 2025b; Quereda et al., 2021). Consistent with previous years, nearly all listeriosis cases (97.3%) in 2024 required hospitalisation, and there were 301 reported deaths, with the majority (81.7%) occurring in people over 65 years of age.

The EU notification rate increased slightly between 2023 and 2024 from 0.67 to 0.69 cases per 100,000 population, representing an annual increase of 3.0%. This was the highest notification rate and number of cases reported in the EU since the beginning of EU level surveillance in 2007. The 5-year trend of confirmed cases of human listeriosis in the EU showed a significant increase from 2020 to 2024. This is driven by several countries, including 10 that had statistically significant increasing trends nationally. There was also a drop in EU case numbers reported in 2020 due to the COVID-19 pandemic, but cases returned to pre-pandemic numbers in 2022 and have been rising since. Slovenia had a significant decreasing trend; it is important to note that Slovenia recorded their highest case numbers in 2020, followed by a decline in subsequent years.

In the food sector, we observed an overall increase of the number of tested units in RTE products compared with 2023 – when no data were reported by Poland, leading to a comparable level with 2022. The sampling effort at manufacturing and distribution remained focused on RTE products of animal origin. The occurrence of *L. monocytogenes* as assessed from detection results reported by MSs varied according to the food category and sample size. Occurrences remained generally rare to low in RTE foods, except for ‘fish and fishery products’, which reached a moderate level (14.6%). Excluding ‘fish and fishery products’, the highest values were observed from ‘bovine meat products’ (4.6%), ‘pork meat products’ (2.7%), ‘fruits, vegetables and juices’ (2.3%) and ‘poultry meat products’ (1.3%). The highest proportions of positive official control samples, as part of verification of *L. monocytogenes* FSC, were observed at manufacturing compared with distribution for five out of eight of the main RTE categories. No *L. monocytogenes* was detected in ‘food intended for infants and medical purposes’ at any stage, and in ‘milk’ at the distribution stage. Results from official sampling at distribution showed that the proportion of samples exceeding 100 CFU/g was either zero or consistently rare to very low across all RTE food categories, except for ‘products of meat origin, fermented sausages’, associated with a low proportion. In primary production, cattle were the most frequently sampled animal species, followed by small ruminants, both presented a low proportion of positive units (2.3% and 3.6%, respectively).

The weight of occurrence data from Poland concerning smoked fish and three multi-country outbreaks leading to a Rapid Outbreak Assessment from EFSA and ECDC (ECDC and EFSA, 2023, 2024a, 2024c) show that smoked fish remains a matter of concern at the EU level. This key focus is further underscored by the number of notifications reported through the Rapid Alert System for Food and Feed (RASFF[35]) in 2024, where 'fish and fishery products', 'meat and meat products' and 'milk and milk products' were the most frequently notified food categories.

National data and trends for the occurrence of *L. monocytogenes* in food or animals over time must be interpreted with caution. Currently, surveillance data come from systems that are not fully harmonised and that vary in nature and effectiveness, depending on the MS. Moreover, data may be reported by a limited number of MSs depending on each food/animal category. The data currently collected do not allow to assess the possible correlation between trends in food contamination and the occurrence of human cases, the latter showing a significant increase since 2020.

Invasive listeriosis (fever, meningitis and septicaemia) affects mainly susceptible populations (elderly people over 65, pregnant women, newborns and immunocompromised people) (ECDC, 2025a, 2025b; EFSA BIOHAZ Panel, 2018; Quereda et al., 2021; Radoshevich & Cossart, 2018; Vázquez et al., 2024). With the ageing of the European population (21.6% of the European population is over 65) (Eurostat, 2024) and the increase in chronic age-related diseases (EFSA BIOHAZ Panel, 2020), more people are at risk of severe symptoms. Other risk factors have been identified, including contamination of the food processing environment, occurrence and level of contamination of *L. monocytogenes* in RTE foods, dietary practices, adherence to food expiration dates and practices related to food storage and handling (EFSA BIOHAZ Panel, 2018). Active communication should be strengthened towards food business operators and consumers to raise awareness of the risks associated with *L. monocytogenes*.

The use of whole genome sequencing (WGS) for the molecular characterisation of clinical isolates of *Listeria* has significantly enhanced sensitivity in identifying clusters of cases that would otherwise appear to be sporadic (ECDC, 2019; Moura et al., 2016; Nielsen et al., 2017; Ruppitsch et al., 2015). For this reason, WGS is now considered the reference method for bacterial typing and the investigation of listeriosis outbreaks (Fagerlund et al., 2022; Lee et al., 2023; Pietzka et al., 2019). At the EU level, the EFSA-ECDC One Health WGS System, launched in 2022 (EFSA and ECDC, 2022b), has improved *Listeria* genomic surveillance by integrating genome sequencing data from human, food, animal and environmental sources across Europe, enabling earlier detection and more precise identification of multi-country outbreak and clusters through continuous cross-sectoral data sharing. Application of WGS has also been recommended to strengthen strategic hygiene measures and environmental monitoring in food and feed production (EFSA, 2018; EFSA BIOHAZ Panel, 2024).

Further to the recording of high rates of *Listeria* infections in Europe in 2023 (Anonymous, 2025; ECDC, 2025a; EFSA, 2024b; EFSA and ECDC, 2024), the EU has taken steps to tackle food-borne outbreaks linked to *L. monocytogenes* by reinforcing the food safety criteria (Commission Regulation (EU) 2024/2895[36]) and by making it mandatory to collect and sequence *L. monocytogenes* isolates linked to food-borne outbreaks, with subsequent transmission of data to EFSA – ECDC One Health WGS system (Commission Implementing Regulation (EU) 2025/179[37]). An additional step was the recent designation of the European Reference Laboratory for public health on food- and water-borne bacteria, with *L. monocytogenes* in the scope of its activities (Commission Implementing Regulation (EU) 2024/2959[38]).

In this context, international recommendations and risk assessment models from the Joint FAO/WHO Expert Committee have led to a revision of the *Codex Alimentarius* Guidelines on the Application of General Principles of Food Hygiene to the Control of *Listeria monocytogenes* in Foods (CXG 61–2007) (FAO and WHO, 2007). These new draft guidelines will be presented at the 55th session of the Codex Committee on Food Hygiene (CCFH55) to be held in December 2025.

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[35] European Commission: Rapid Alert System for Food and Feed (RASFF) Window: https://webgate.ec.europa.eu/rasff-window/screen/search. Findings related to the most frequently notified food items in RASFF were based on a query dated 17/09/2025, covering notifications from 01/01/2024 to 31/12/2024 that included the word '*Listeria*' in the subject.

[36] Commission Regulation (EU) 2024/2895 of 20 November 2024 amending Regulation (EC) No 2073/2005 as regards *Listeria monocytogenes*. OJ L, 21.11.2024, p. 1–3.

[37] Commission Implementing Regulation (EU) 2025/179 of 31 January 2025 on the collection and transmission of molecular analytical data within the frame of epidemiological investigations of food-borne outbreaks in accordance with Directive 2003/99/EC of the European Parliament and of the Council. OJ L, 3.2.2025, p. 1–3.

[38] Commission Implementing Regulation (EU) 2024/2959 of 29 November 2024 designating European Union reference laboratories for public health on food- and water-borne bacteria; on food-, water- and vector-borne helminths and protozoa; and on food- and water-borne viruses. OJ L, 2.12.2024, p. 1–8.

A4 | SHIGA TOXIN-PRODUCING *ESCHERICHIA COLI* (STEC)

Human cases [EU, 2024]

Notification rate *(per 100,000 population)* **3.5**

Trend *(2020-2024)* ↑

↑ *Increasing*
↓ *Decreasing*
— *Stable*

11,738 **Cases of illness**

7221 **Infections acquired in the EU**

684 **Infections acquired outside the EU**

3833 **Unknown travel status or unknown country of infection**

1411 **Hospitalisations** (35.7%)*

25 **Deaths** (0.31%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

🟩 *ECDC data*

Foodborne outbreaks & related cases [EU, 2024]

31 **Foodborne outbreaks**

4 **Strong-evidence outbreaks** ■

27 **Weak-evidence outbreaks** ■

158 **Cases of illness**

19 **Hospitalisations** (12.2%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

N of outbreaks			N of outbreaks per 100,000 population **		N of outbreak cases per 100,000 population
Austria	0	AT	0	AT	0
Belgium	4	BE	0.034	BE	0.118
Bulgaria	0	BG	0	BG	0
Croatia	0	HR	0	HR	0
Cyprus	0	CY	0	CY	0
Czechia	0	CZ	0	CZ	0
Denmark	3	DK	0.050	DK	0.302
Estonia	0	EE	0	EE	0
Finland	1	FI	0.018	FI	0.071
France	3	FR	0.004	FR	0.019
Germany	7	DE	0.008	DE	0.020
Greece	1	EL	0.010	EL	0.019
Hungary	0	HU	0	HU	0
Ireland	3	IE	0.056	IE	0.336
Italy	1	IT	0.002	IT	0.005
Latvia	0	LV	0	LV	0
Lithuania	0	LT	0	LT	0
Luxembourg	0	LU	0	LU	0
Malta	4	MT	0.710	MT	1.420
Netherlands	1	NL	0.006	NL	0.028
Poland	2	PL	0.005	PL	0.147
Portugal	0	PT	0	PT	0
Romania	0	RO	0	RO	0
Slovakia	0	SK	0	SK	0
Slovenia	0	SI	0	SI	0
Spain	0	ES	0	ES	0
Sweden	0	SE	0	SE	0
UK (N. Ireland)	1	XI	0.052	XI	0.104

Implicated food vehicles
(Strong-evidence outbreaks)

Top food vehicles

Water
2 Outbreaks

Bovine meat and products thereof
1 Outbreak

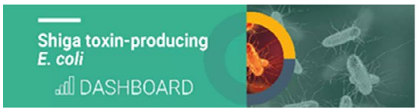
Milk
1 Outbreak

*** Differences among countries shall be interpreted with caution as this indicator depends on several factors including the type of outbreaks under surveillance and does not necessarily reflect the level of food safety in each country.*

🟧 *EFSA data*

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here, Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about Shiga toxin-producing *Escherichia coli* (STEC) and for the consultation of data collected, the following interactive tools are available:



A4.1 | Key facts

- Shiga toxin-producing *Escherichia coli* (STEC) infections were the third most commonly reported gastrointestinal foodborne illness in humans in the European Union.
- The overall trend for STEC infections showed a significant increase during the 2020–2024 period.
- In 2024, there were 11,738 confirmed cases of human STEC infections, corresponding to an European Union notification rate of 3.5 cases per 100,000 population. This was an increase of 12.9% compared with 2023 (3.1 cases per 100,000 population).
- In 2024, a total of 417 Haemolytic Uremic Syndrome cases were reported from 23 Member States.
- In 2024, STEC were isolated from 365 food sample units (2.3%) of the 16,031 specimens sampled with 'objective sampling' as sampling strategy and tested with methods detecting any STEC.[39]
- The 'ready-to-eat' food category included 5535 sampling units reported by 17 MSs and 0.63% were positive for STEC, with similar figures of positive samples observed across the different food categories.
- Testing of RTE-salads samples ($N=292$) revealed six STEC-positive units (2.1%).
- Official control of 'sprouted seeds' in the context of Commission Regulation (EC) No 2073/2005 included the testing of only 709 samples taken by 10 MSs at retail and processing plants, with no positive results.
- In 2024, STEC testing was carried out by four MSs on animal samples belonging to different categories. The most tested animal category in the EU was 'cattle' ($N=831$), with 6.3% positives. The highest proportions of positive samples were obtained from the 'deer' animal category with 29.8% of the 430 animal samples tested being contaminated with STEC.

A4.2 | Surveillance and monitoring of STEC infections in the EU

A4.2.1 | Humans

In 2024, 27 MSs reported information on STEC infections in humans. STEC surveillance is mandatory in 24 MSs, voluntary in two MSs (Belgium, France) and based on another system in Italy.

The EU case definition was used by 24 MSs. Three MSs (France, Germany and the Netherlands) reported using a different case definition.

All MSs, except Italy, indicated that the surveillance system is comprehensive. The surveillance systems for STEC infections cover the whole population in all EU MSs except for two MSs (France and Italy). The notification rates were not calculated in France and Italy, countries for which STEC surveillance is sentinel and primarily based on haemolytic-uraemic syndrome (HUS) cases.

All MSs reported case-based data.

A4.2.2 | Food and animals

STEC data in the context of Commission Regulation (EC) No 2073/2005, STEC food safety criterion for sprouts and seeds at the distribution level

A food safety criterion has been in place for STEC in sprouts since 2013 (Commission Regulation (EC) No 2073/2005[40]). The regulation specifies that sprouts placed on the market shall not contain detectable STEC O157, O26, O111, O103, O145 or O104:H4 in 25 g of product during their shelf life. The legal basis indicates that the ISO TS 13136:2012 method (ISO, 2012)

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[39] The methods considered here are those not restricted to the detection of specific STEC serogroups e.g. ISO 16654 for O157. It should be noted that ISO TS 13136:2012 detects all the known *stx* subtypes, with the only exception of *stx2f*.

[40] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

with the adaptation developed by the EURL for *E. coli* for detecting O104:H4 is the reference testing methodology. However, FBOps are allowed to use alternative methods validated according to the requirements of ISO 16140-4 (ISO, 2020).

As the sampling objectives and frequency are not indicated, these activities vary or are interpreted differently among MSs, resulting in non-harmonised data.

Other STEC monitoring data from food and animals

All the food and animal testing data, except for those on sprouts and seeds, originate from the reporting obligations of MSs under Directive 2003/99/EC[41] (i.e. the Zoonoses Directive). Due to the absence of explicitly indicated sampling strategies in this directive, the data generated by MSs are based on investigations with non-harmonised sampling programmes. Therefore, STEC monitoring data according to Directive 2003/99/EC are not comparable among MSs and preclude assessing temporal and spatial trends at the EU level. Different sampling designs and inaccuracies due to limited numbers of samples tested also preclude an accurate estimation of prevalence.

Nevertheless, descriptive summaries of sample statistics at the EU level can be used to indicate the circulation of certain STEC types in food and animals. This information may be used to design sampling strategies within the MSs, provided that the above-mentioned relevant limitations of the data set are taken into consideration.

The analysis of the data available suggests that the isolated STEC strains should be characterised. Indeed, typing and subtyping data (e.g. virulotyping and *stx* gene subtyping) are considered to be the most valuable source of information for inferring the circulation of the various STEC types and their possible association with the severity of human disease (EFSA BIOHAZ Panel, 2020; FAO and WHO, 2018; NACMCF, 2019).

A4.3 | Data analyses

A4.3.1 | Occurrence in food and animals

The monitoring data on sprouts as part of Commission Regulation (EC) No 2073/2005 were aggregated and summarised for trend watching according to the following 'filters': Sampling context: 'surveillance, based on Commission Regulation No 2073/2005'; Sampling unit type: 'single'; Sampling stage: 'distribution'; Sampling strategy: 'objective sampling' and Sampler: 'official sampling'.

For the description of the occurrence of STEC-positive samples in the different food categories, the subset of the monitoring data with 'objective sampling' specified as sampling strategy was used ($N = 16{,}031$), meaning that the reporting MSs collected the samples according to a planned strategy based on the selection of random samples statistically representative of the population to be analysed.

A4.3.2 | Serogroups and virulence features in food and animals

In 2024, the methods targeting any STEC were based on *stx* gene polymerase chain reaction (PCR) and included the ISO TS 13136:2012 method (ISO, 2012) and other PCR-based methods and commercial kits using the same principle. The ISO 16654:2001 method designed to detect only *E. coli* O157 (ISO, 2001), adapted for testing animal samples (WOAH, 2023), was used for testing animal samples only.

For the descriptive analyses of STEC strains from food and animals (primarily those on virulence gene types and on their frequency distribution), the full data set — regardless of the sampling strategy, but excluding the samples assayed with methods detecting *E. coli* O157 only — was used ($N = 18{,}352$ for food and $N = 1698$ for animals).

A4.4 | Results

A4.4.1 | Overview of key statistics, EU, 2020–2024

Table 36 summarises EU-level statistics on human STEC infections and on samples tested for STEC from food and animals during 2020–2024. Food and animal data were classified into major categories and aggregated by year to obtain an annual overview of the volume of data submitted. The number of food-borne outbreaks caused by STEC in 2024 ($N = 31$) was reduced by half compared to that reported in 2023 ($N = 66$). More detailed descriptions of these statistics are provided in the subsections below and in the chapter on food-borne outbreaks (see also the dashboard referenced at the start of the chapter).

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[41] Directive 2003/99/EC of The European Parliament And Of The Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40.

TABLE 36 Summary of STEC statistics relating to humans, major food categories and the main animal species, EU, 2020–2024.

	2024	2023	2022	2021	2020	Data source
Humans						
Total number of confirmed cases	11,738	10,220	8031	6405	4489	ECDC
Total number of confirmed cases/100,000 population (notification rates)	3.5	3.1	2.4	1.9	1.5	ECDC
Number of reporting MSs	27	27	26	27	27	ECDC
Infection acquired in the EU	7221	7200	5272	4364	3370	ECDC
Infection acquired outside the EU	684	895	564	117	148	ECDC
Unknown travel status or unknown country of infection	3833	2125	2195	1924	971	ECDC
Number of food-borne outbreak-related cases	158	270	408	275	208	EFSA
Total number of food-borne outbreaks	31	66	71	31	34	EFSA
Food[a]						
Meat and meat products						
Number of sampling units	8990	10,108	9932	12,160	10,866	EFSA
Number of reporting MSs	20	21	21	19	17	EFSA
Milk and milk products						
Number of sampling units	4097	3582	5957	4094	4665	EFSA
Number of reporting MSs	12	15	14	11	10	EFSA
Fruits and vegetables (and juices)						
Number of sampling units	2143	4501	3402	4151	3398	EFSA
Number of reporting MSs	12	16	16	17	15	EFSA
Animals[a]						
Cattle (bovine animals)						
Number of sampling units	831	937	282	2077	868	EFSA
Number of reporting MSs	2	3	3	5	3	EFSA
Small ruminants (sheep, goats) and deer						
Number of sampling units	495	421	822	151	227	EFSA
Number of reporting MSs	3	4	3	2	2	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States; STEC, Shiga toxin-producing *Escherichia coli*.

[a] The total number of sampling units was calculated by summing all reported sub-level entries for sampling units, stages, strategies and samplers, as listed in the EFSA Catalogue (EFSA, 2019).

A4.4.2 | STEC infections in humans

In 2024, 11,738 confirmed cases of STEC infections were reported in the EU (Table 37). Twenty-six MSs reported at least one confirmed STEC case, only Cyprus reported zero cases. The EU notification rate was 3.5 cases per 100,000 population in 2024, representing an increase of 12.9% compared with year 2023 (3.1 cases per 100,000 population).

The highest country-specific notification rates among the EU MSs were observed in Denmark, Malta, Ireland and Austria (21.3, 15.1, 13.7 and 9.3 cases per 100,000 population, respectively) (Table 37). Two countries (Lithuania and Portugal) reported ≤ 0.1 cases per 100,000 population.

In 2024, almost three quarters of the EU STEC cases (73.4%; 8619/11,738) were reported with data on importation status; of these, 80.7% (6955/8619) of cases were reported as domestically acquired, while 19.3% (1664/8619) were imported.

Among cases with information on both importation status and place of infection ($N = 7905$) the majority (91.4%; 7221/7905) were reported as acquired within the EU (either domestically acquired or acquired in another EU country), while 8.7% (684/7905) were reported as acquired outside the EU (Table 36). Among the 266 imported cases reported as acquired within the EU, the most frequently reported probable countries of infection were Spain (25.9%; 69/266), Greece (11.3%; 30/266), France (8.7%; 23/266), Italy (8.7%; 23/266) and Germany (7.9%; 21/266). Among the 684 imported cases reported as acquired outside the EU, the most probable countries of infection were Egypt (20.5%; 140/684) and Türkiye (18.4%; 126/684).

TABLE 37 Reported confirmed human cases of STEC and notification rates per 100,000 population in EU MSs and non-MS countries, by country and year, 2020–2024.

	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	**National Coverage[a]**	**Data format[a]**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**
Austria	Y	C	853	9.3	584	6.4	469	5.2	383	4.3	288	3.2
Belgium	Y	C	637	5.4	336	2.9	187	1.6	124	1.1	84	0.73
Bulgaria	Y	C	11	0.17	1	0.02	0	0	0	0	0	0
Croatia	Y	C	32	0.83	23	0.60	16	0.41	12	0.31	8	0.20
Cyprus	Y	C	0	0	0	0	0	0	0	0	0	0
Czechia	Y	C	75	0.69	52	0.48	58	0.55	36	0.34	32	0.30
Denmark	Y	C	1270	21.3	1431	24.1	1329	22.6	928	15.9	445	7.6
Estonia	Y	C	10	0.73	21	1.5	11	0.83	7	0.53	10	0.75
Finland	Y	C	362	6.5	306	5.5	283	5.1	288	5.2	175	3.2
France[b]	N	C	303	–	342	–	473	–	298	–	262	–
Germany	Y	C	4580	5.5	3485	4.2	1873	2.3	1635	2.0	1409	1.7
Greece	Y	C	28	0.27	22	0.21	14	0.13	10	0.09	3	0.03
Hungary	Y	C	45	0.47	41	0.43	26	0.27	24	0.25	8	0.08
Ireland	Y	C	733	13.7	833	15.8	892	17.3	878	17.3	734	14.6
Italy[b]	N	C	84	–	96	–	118	–	64	–	45	–
Latvia	Y	C	2	0.11	31	1.6	–	–	13	0.69	2	0.10
Lithuania	Y	C	1	0.03	2	0.07	0	0	0	0	0	0
Luxembourg	Y	C	31	4.6	16	2.4	9	1.4	10	1.6	0	0
Malta	Y	C	85	15.1	66	12.2	78	15.0	68	13.2	43	8.4
Netherlands	Y	C	645	3.6	576	3.2	585	3.3	484	2.8	323	1.9
Poland	Y	C	145	0.40	79	0.21	34	0.09	7	0.02	3	0.01
Portugal	Y	C	11	0.10	11	0.10	6	0.06	2	0.02	5	0.05
Romania	Y	C	41	0.22	41	0.22	28	0.15	6	0.03	14	0.07
Slovakia	Y	C	10	0.18	4	0.07	4	0.07	5	0.09	1	0.02
Slovenia	Y	C	52	2.4	58	2.7	58	2.8	48	2.3	30	1.4
Spain[c,d]	Y	C	844	1.7	824	1.8	623	1.4	422	0.92	74	–
Sweden	Y	C	848	8.0	939	8.9	857	8.2	653	6.3	491	4.8
EU Total			**11,738**	**3.5**	**10,220**	**3.1**	**8031**	**2.4**	**6405**	**1.9**	**4489**	**1.5**
Iceland	Y	C	79	20.6	14	3.6	4	1.1	7	1.9	4	1.1
Liechtenstein	Y	C	7	17.5	8	20.2	4	10.2	7	17.9	–	–
Norway	Y	C	655	11.8	662	12.1	518	9.5	437	8.1	331	6.2
Switzerland[e]	Y	C	1356	15.1	1216	13.8	1203	13.8	932	10.7	710	8.3

Abbreviations: –, Data not reported.

[a] Y, yes; N, no; A, aggregated data; C, case-based data.

[b] Sentinel surveillance; mainly haemolytic-uraemic syndrome (HUS) cases are notified. Notification rate not calculated.

[c] Notification rates calculated with an estimated population coverage of 100% in 2024 and 97% in 2021–2023.

[d] No information on estimated coverage in 2020, so notification rate cannot be estimated.

[e] Switzerland provided the data directly to EFSA. The human data for Switzerland includes data from Liechtenstein for 2020.

The confirmed STEC cases maintained a stable marked seasonal trend, with most cases being reported during the summer months (Figure 12). The observed STEC infection seasonality is in line with that reported in the literature (Sapountzis et al., 2020). The overall trend for STEC in 2020–2024 showed a significant increasing trend ($p < 0.05$) (Figure 12). At the MS level, a significant increasing trend ($p < 0.05$) was observed over the same time period in 14 MSs, while no country reported a significant decreasing trend. Most countries with an increasing trend between 2020 and 2024 reported case numbers and notification rates higher than pre-COVID-19 levels.

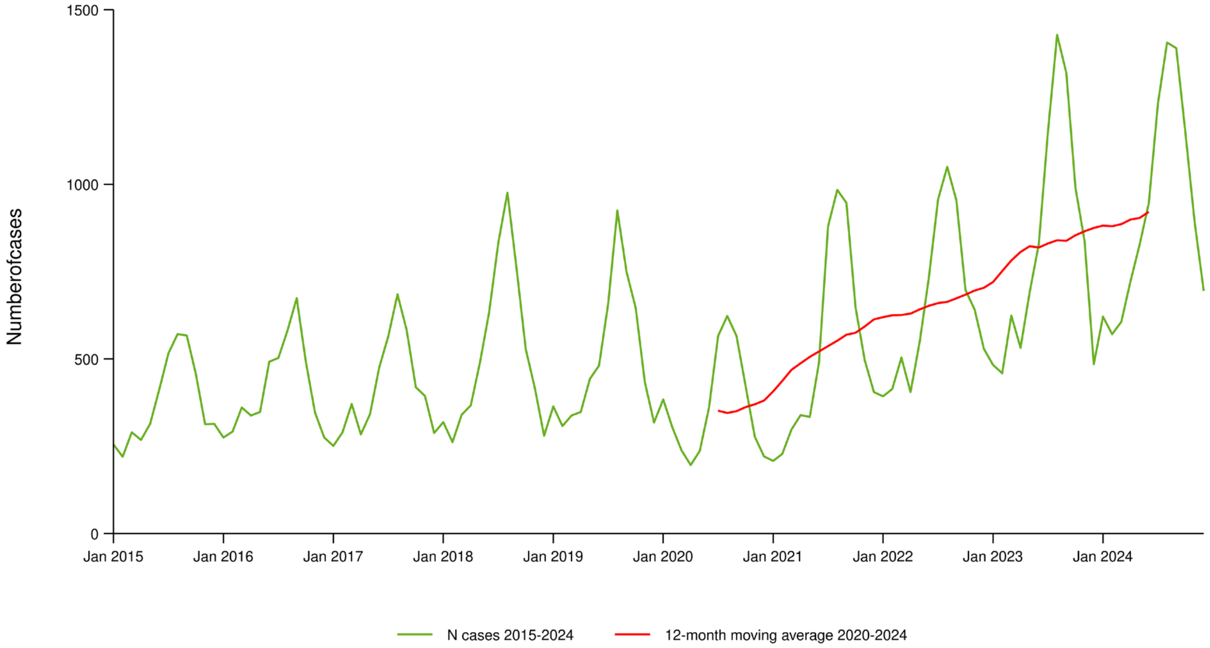

FIGURE 12 Trend in reported confirmed human cases of Shiga toxin-producing *Escherichia coli* (STEC) infection in the EU by month, 2020–2024. *Source:* Austria, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Lithuania, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden.

In 2024, 417 HUS cases were reported by 23 MSs, including 12 fatalities. Consistent with 2023, the most frequently reported STEC serogroup among HUS cases in 2024 was O26, representing 40.7% of HUS cases with serogroup information (92/226), followed by O157 (18.6%; 42/226), O145 (8.0%; 18/226) and O111 (6.2%; 14/226).

A4.4.3 | STEC in food

In 2024, 23 MSs provided results from analyses of 18,352 food units (batches or single samples) regardless of the sampling strategy adopted, all assayed with methods detecting any STEC. The most tested food categories were 'bovine meat and products thereof', 'milk and milk products' and 'vegetables and products thereof' (Table 36).

Data collected in the context of Commission Regulation (EC) No 2073/2005

Regarding 2024 data for STEC on sprouted seeds in the context of Commission Regulation (EC) No 2073/2005, 654 samples taken at the distribution level and 55 at processing plants were tested by 10 MSs with no positive batches (see the dashboard referenced at the start of the chapter).

Other STEC monitoring data from food

Overall, 2.3% (*N* = 365) of the 16,031 food sample units collected using an objective sampling strategy and tested by 22 EU MSs were positive for STEC. An additional 985 food samples were tested by two non-MS countries with one of these reporting two positive units out of the 169 samples tested.

RTE food

As regards 'ready-to-eat' (RTE) food, the testing of 5535 samples was reported by 17 MSs, with 0.63% found positive. The food category with the highest number of sample units tested was 'milk and milk products' with 2153 samples assayed, of which 84.9% were cheese samples, followed by 'meat and meat products' (*N* = 1126) and 'fruits, vegetables and juices'[42] (*N* = 1032). In total, 35 RTE food samples were positive for STEC: 0.53% (*N* = 6) in 'meat and meat products', 0.84% (*N* = 18) in 'milk and milk products' and eight positive samples were identified among the fruits, vegetables, juices and similar products (0.78%). Notably, six out of the eight positive samples detected in RTE vegetables commodities, were found in RTE salads (*N* = 292, 2.1%). Finally, 1.8% (N = 2) and 1.4% (N = 1) positive samples were detected in the 'other processed food products and prepared dishes' and 'bakery products' food categories.

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[42] For the scope of this analysis the categories 'fruit, vegetable and juice', 'fruit, vegetable and juice (fresh)' and RTE salads are merged in a single category 'fruit, vegetable and juice'.

RTE and non-RTE food

To provide overall statistics, the following descriptive analyses are based on merged data from RTE food and non-RTE food.

Meat and meat products

Bovine meat

In 2024, 4060 units of fresh and unprocessed bovine meat were tested by 15 MSs with 2.5% testing positive. At the distribution level, 613 units were sampled by 10 MSs with 2.3% of positives. Samples taken at the manufacturing level (*N* = 3171, 11 MS) resulted in 2.8% of contaminated samples. Most specimens sampled at the manufacturing level were taken at the slaughterhouse (77.2%, *N* = 2448) and 3.0% tested positive for STEC.

Sheep and goat meat

In 2024, six MSs (Austria, Belgium, Bulgaria, Italy, the Netherlands and Spain) reported the results of the investigation on 464 sample units of fresh sheep meat with 8.2% of these being STEC-positive, confirming the importance of these animals as reservoirs of STEC (Persad & LeJeune, 2014).

The sampling stage that yielded the highest proportion of positive fresh sheep meat samples was the distribution level, with 11.5% of samples producing a STEC isolate, while the samples taken at the slaughterhouse (*N* = 272), accounting for 97.5% of the manufacturing level samples, showed a lower STEC contamination rate (6.2%).

Goat meat samples were not taken with an objective sampling strategy in 2024.

Meat from other ruminants

In 2024, three MSs (Austria, Germany and the Netherlands) provided information on the presence of STEC in 335 fresh deer meat samples with 93 (27.8%) positive sample units. The samples taken at the distribution and manufacturing levels showed STEC contamination rates of 28.2% and 21.7%, respectively. Only 23 samples were taken at the manufacturing level, of which 16 were from processing plants and seven from game-handling establishments.

Meat from other animal species

In 2024, six MSs (Austria, Czechia, Italy, the Netherlands, Portugal and Spain) tested fresh pig meat and reported data on 514 samples, with 15 (2.9%) of these being positive for STEC. The proportion of pig meat positive samples was slightly higher than that observed in 2023 (2.0%).

Fresh meat from animal species other than bovine, ovine, goat, pig and deer species was tested in 2024 by five MSs (Austria, Hungary, Italy, the Netherlands and Spain) that reported on analyses carried out on 164 sample units and seven (4.3%) samples were reported as STEC-positive (five positive samples from horse meat, one from wild boar meat and one in meat from a non-specified species).

Meat products and meat preparations

Meat products and meat preparations other than fresh meat, were sampled in 2024 by 11 MSs, which tested 2329 samples, resulting in 32 (2.7%%) positive sample units ffrom 1203 samples of non-RTE meat and meat products and 6 (0.53%) positive sample units detected in RTE meat and meat products (*N* = 1126).

Milk and milk products

Overall, STEC were found in 18 (0.84%) out of 2153 samples of RTE milk and milk products reported by seven MSs (Austria, Belgium, Hungary, Italy, the Netherlands, Portugal and Spain) and in 22 (4.3%) out of 516 samples of non-RTE milk and milk products reported by six MSs (Austria, Belgium, Hungary, Italy, Latvia and Slovenia).

In 2024, five MSs (Austria, Belgium, Hungary, Italy and Slovenia) reported on the testing of 443 sample units of raw cows' milk with 21 positive units (4.7%). The proportion of positive units more than doubled with respect to the same figure observed in 2023, while the number of samples tested was comparable (*N* = 567 and 1.8% positive samples). Notably, the highest proportion of contaminated samples (10.2%, *N* = 108) was taken at the retail or wholesale sampling stage in four MSs (Austria, Hungary, Italy and Slovenia).

Only one MS (Italy) reported monitoring results on 19 sample units of raw goats' milk, and two MSs (Austria and Italy) reported 11 samples of raw sheep milk. Neither category revealed positive samples.

The testing for STEC in RTE milk products other than milk and cheeses was reported by three MSs (Austria, Belgium and Italy), which tested 200 sample units of butter, cream, ice cream, yoghurt, whey and fermented dairy products. No positive samples were detected in these food categories.

For the cheese samples, 1828 samples were tested in 2024 for the presence of STEC by seven MSs (Austria, Belgium, Hungary, Italy, the Netherlands, Portugal and Spain), with 18 (0.98%) positive units.

Fruits, vegetables and juices

STEC were found in 2 out of 1725 samples of fruits, vegetables and juices (0.12%). Only RTE products were positive.

In total, 1300 sample units of herbs and spices, salads and sprouted seeds were tested, and six STEC-positive units were reported (0.46%), all from the 292 RTE salad samples (2.1%).

Other foodstuffs

This category contains miscellaneous food commodities not comprised in the above-mentioned categories, and included 'cereals and meals', 'bakery products', 'fish and fishery products' and other. For the whole category, 2322 samples were analysed by 11 MSs with 23 (0.99%) positive samples reported from the 'cereals and meals' (16), other processed food categories (3), 'other food of non-animal origin' (2), 'fish and fishery products' (1) and 'bakery products' (1) (see the dashboard referenced at the start of the chapter).

A4.4.4 | STEC in animals

In 2024, in EU 1727 sampling units (single heads or herds or flocks) from animals, regardless of the sampling strategy and the method adopted, were assayed and reported by four MSs (Germany, Italy, Sweden and the United Kingdom (Northern Ireland)) with 11.2% positive samples. The number of tested animals was comparable to that reported in 2023 (*N* = 2129), which produced 23.0% of positive samples.

The most tested animal category in 2024 was cattle, followed by deer and pigs, with 831, 430 and 133 sample units tested, respectively, which yielded 6.3%, 29.8% and 3.8% positive units, respectively (see dashboard referenced at the start of the chapter). In particular, all pig samples were assayed by a single MS (Italy) and most of them (80.5%) consisted of tissue/organ specimens collected with clinical investigation as sampling context and only 26 were taken from faeces or caecal contents.

A4.4.5 | Focus on STEC strain features: virulence genes and serogroups

Humans

In 2024, serogroup information was reported for 24.3% of confirmed STEC cases (2855 cases out of 11,738 cases). In addition to these 2855 cases with serogroup data, an additional 94 strains were reported as non-O157 serogroups and 246 were reported as non-typable ('NT'); these 340 cases were not included among isolates reported with known serogroup information. The most common human STEC serogroups reported in the EU were O157 (19.9%; 569/2855) and O26 (17.2%; 492/2855), together representing 37.2% (1061/2855) of the total number of confirmed human cases with known serogroups in 2024, excluding the NT isolates and those categorised as non-O157. Overall, the six most frequent serogroups of STEC from human infections were O157, O26, O103, O146, O145 and O91, representing 59.8% (1707/2855) of the human isolates with serogroup information.

Data on virulotypes (based on the Shiga toxin genes *stx1*, *stx2* and the intimin-coding gene *eae*) were reported for 17.9% (2103/11,738) of confirmed STEC infections in 2024 (Table 38). Among these, the most frequently reported virulence gene combinations were *stx2/eae+*, representing 28.4% (*N* = 597) of cases, followed by *stx2/eae-* (19.1%; *N* = 401) and *stx1/stx2–/eae* + (15.7%; *N* = 331) (Table 38). Data for shiga toxin genes were reported for 4526 cases, among which subtyping of the *stx* gene was reported for 2222 (49.1%; 2222/4526) isolates. The most common *stx* gene subtypes identified in strains from all human infections were *stx1a* (28.9%; 641/2222 isolates with reported *stx* gene subtyping data), *stx2b* (20.0%; 444/2222), *stx2a* (17.8%; 396/2222) and *stx1c* (11.3%; 252/2222).

In 2024, a total of 2467 cases of severe infection (HUS, bloody diarrhoea and/or hospitalised cases) were reported. Data on virulotypes (based on the presence of Shiga toxin genes *stx1*, *stx2* and the intimin-coding gene *eae*) were reported for 24.9% (614/2467) of severe cases. Among these, the most frequently reported virulence gene combinations were *stx2/eae+*, representing 38.4% (*N* = 236) of cases, followed by the *stx1/stx2/eae* + (19.7%; *N* = 121) (Table 38). Data for shiga toxin genes were reported for 419 isolates. The most common *stx* gene subtypes identified in strains from severe human infections were *stx2a* (35.1%; 147/419), *stx1a* (25.5%; 107/419), *stx2c* (11.5%; 48/419) and *stx2b* (11.2%; 47/419).

Food

The information on the serogroups of STEC strains from food was reported for 54.3% of the isolates (236 strains out of the 435 strains in total). The six serogroups most reported in food isolates were O146, O157, O113, O26, O103 and O111, together accounting for 37.7% of the strains with serogroup information.

Information on the presence of *stx1* and/or *stx2* and *eae* genes was provided or inferred by other strain features for 335 (77.0%) of the 435 isolated STEC strains (Table 38), without further *stx* gene typing, while 211 isolates were provided with this information (48.5%). Finally, the presence of enteroaggregative adhesion determinants was assessed for 117 strains, all negative.

Regarding the *stx* gene subtypes, the most frequently identified in STEC food isolates in 2024 was *stx2b* (27.0% of the 211 strains with this information available), followed by *stx1a* and *stx2a* with 16.6% and 13.3% of the subtyped isolates, respectively. The remaining subtypes were each represented in less than 10% of the STEC isolates provided with this information (see dashboard referenced at the start of the chapter).

Animals

This section includes the analysis of the data relating to the 1698 animal sample units tested with methods detecting any STEC, of which 11.4% (*N* = 193) were positive for the presence of STEC.

For the analysis of the distribution of STEC serogroups and virulotypes, 199 STEC strains isolated from the 193 animal positive samples were considered. Of these, 50 strains (25.1%) were provided with serogroup information, belonging to three distinct O-groups: O157, O26 and O103. The most prevalent was O157, representing 64.0% of all strains with a known serogroup. O26 accounted for 31.0% (*N* = 16), while O103 was the least common serogroup, comprising 4.0% (*N* = 2).

For the analysis of the virulence genes, 172 STEC animal isolates (86.4%) were provided with their virulotype based on the identification of the *stx1*, *stx2* and *eae* genes (Table 38) and 72 were also provided with information on the *stx* subtype (36.2%). As in the food isolates, the most represented *stx* subtype was *stx2b* (*N* = 38, 52.8% of the strains with a known *stx* subtype).

TABLE 38 Virulotypes (*stx* type and presence of *eae*) identified in food, animal and human STEC isolates in all cases and in cases with severe infection (haemolytic-uraemic syndrome (HUS), hospitalisation and bloody diarrhoea) in 2024.

Virulence gene profile	*N* of animal isolates in 2024[a,b]	*N* of food isolates in 2024[a,b]	*N* of human isolates in severe infections 2024 (%)	*N* of human isolates in all cases 2024 (%)
stx2; eae+	37	33	236 (38.4)	597 (28.4)
stx1; stx2; eae+	18	11	121 (19.7)	273 (13.0)
stx2; eae-	73	161	102 (16.6)	401 (19.1)
stx1; eae+	7	56	71 (11.6)	331 (15.7)
stx1; eae-	31	40	43 (7.0)	254 (12.1)
stx1; stx2; eae-	6	34	41 (6.7)	247 (11.8)
Total	**172**	**335**	**614 (100)**	**2103 (100)**

Abbreviations: STEC, Shiga toxin-producing *Escherichia coli*. The *stx* genes were characterised at the type level (*stx1* and *stx2*).

[a] Due to the low number of isolates virulotyped for food and animals, only the number of isolates is shown.

[b] Includes strains for which the status of the presence of the *eae* gene was not directly provided by the reporting country, but could be inferred thorough expert interpretation of isolate features (e.g. serotypes known to be associated presence/absence of *eae* gene).

A4.5 | Discussion

During the 2020–2024 period, a statistically significant increasing trend in STEC infections was observed in the EU. Similarly, the annual notification rate in 2024 increased by 12.9% relative to 2023.

The increasing EU trend was driven by several countries, including 14 that had statistically significant increasing trends nationally. This trend may be attributed in part to the adoption of PCR tests that are more sensitive than traditional testing methods and which allow for broader testing beyond specific patient groups or symptom types (ECDC, 2025a).

Although serogroup is not a virulence feature, it provides valuable information for tracking the spread and sources of infections, thereby enhancing the understanding of STEC epidemiology in human populations. The serogroups O157 and O26 have been well documented to be isolated from severe disease, including HUS (Joseph et al., 2020; Misselwitz et al., 2003; Tarr et al., 2005). In 2024, one quarter of the confirmed human cases reported by EU MSs had information on the serogroup with the most frequently reported being O157, followed by O26. However, for HUS cases, the figures of these two serogroups were reversed, with O26 reported in almost twice as many HUS cases as O157.

The proportion of non-typeable STEC isolates declined to 7.7% in 2024, compared to 29.3% in 2023. Nevertheless, non-typeable isolates remained the third most frequently reported STEC serogroup in 2024. The number of isolates without serogroup identification may result from phenotyping/genotyping methods focusing on a limited range of serogroups or from laboratories omitting the serotyping process entirely.

In 2024, virulotype data based on Shiga toxin genes (*stx1*, *stx2*) and the intimin gene (*eae*) were available for approximately 17.9% of confirmed STEC infections and 24.9% of severe cases. Among all reported cases, the *stx2/eae* + combination was the most frequent, followed by *stx2/eae-* and *stx1/stx2–/eae+*. This pattern was even more pronounced in severe infections, where *stx2/eae* + accounted for 38% of cases, highlighting its association with increased disease severity. Subtyping of the *stx* genes provided further resolution, revealing *stx1a* and *stx2b* as the dominant subtypes overall, while severe cases showed a higher proportion of *stx2a*, followed by *stx1a*. These findings are consistent with the observation that certain virulence gene profiles are linked to more severe clinical outcomes (EFSA BIOHAZ Panel, 2020). However, the incomplete reporting of virulotype data limits the ability to fully understand the distribution of STEC strains, highlighting the need for whole-genome sequencing (WGS)-based surveillance to improve risk assessment and public health response.

In 2024 in EU, 23 MSs reported monitoring results of STEC in 18,352 food samples. The most frequently tested food categories, representing the majority of all food samples assayed, were 'meat and meat products', 'milk and milk products' and 'vegetables and products thereof', which are known to be the food vehicles most often implicated in STEC infections (EFSA BIOHAZ Panel, 2020; FAO and WHO, 2018). In 2024 four EU MSs (Denmark, Greece, Malta and Poland) and three EFTA Countries (Iceland, Liechtenstein and Switzerland) did not report data on food testing for STEC. Overall, 2.3% of the total food samples collected using an objective sampling strategy ($N = 16{,}031$) tested positive for STEC. This figure falls in the range of the fluctuations observed in the last four-year period (2020–2023) (2.2%, 1.8%, 3.6% and 2.4%).

STEC were isolated in 0.63% of the RTE products; within this food group, 'milk and milk products' — particularly cheese — was the most frequently tested and contaminated matrix (0.84% of positive samples). These data confirm the importance of testing RTE food commodities for the presence of STEC, because these foods are generally consumed without any treatment to reduce or eliminate the possible presence of the pathogen, posing a direct risk to the consumer. Testing of RTE salad samples ($N = 292$) revealed six STEC-positive units (2.1%). This is noteworthy, given the increasing importance of vegetables as vehicles of STEC outbreaks and the increasing consumption of RTE salads worldwide (Łepecka et al., 2022).

Fresh meat from small ruminants, with 335 samples of deer and 464 of sheep samples tested in 2024, was confirmed to be among the most contaminated meat categories, underlining the importance of these animal reservoirs.

Fresh bovine meat samples showed a contamination rate of 2.5%. Most samples were taken at the manufacturing level (78.1% of the total bovine meat samples) and revealed 2.8% of contaminated samples, approximately half of those reported in 2023 for bovine meat taken at this sampling stage (5.3%).

The low testing rate of sprouts and seeds appears to be entrenched. In 2024, 10 MSs tested 709 official control single samples taken in the context of Commission Regulation (EC) No 2073/2005, with no positive results. This low sampling effort was observed notwithstanding the existence of a microbiological criterion for this food commodity in Commission Regulation (EC) No 2073/2005 since 2013 and seems to be due to a poor perception of the risks associated with sprouts despite the German outbreak of O104:H4 STEC infections.

Similarly, in 2024, the number of animal samples assayed continued to be low. The total number of these specimens was 1727, with 11.2% positives. The highest percentage of positive STEC samples was detected in deer, reflecting the comparably high percentage of positives found in deer meat. Indeed, deer are generally hunted (not raised), suggesting that the perforation of intestine tract may occur more frequently than in animals conventionally slaughtered.

Although the total number of animal samples tested was similar to that sampled in 2023 (EFSA and ECDC, 2024), the number of positive units was much lower in 2024. This discrepancy may be due to the differences in the animal species sampled and in the non-harmonised sampling strategies. In particular, the number of pig samples was much higher in 2023 ($N = 405$, with 46.9% positives) (EFSA and ECDC, 2024) and these were mostly taken at the slaughterhouse. In contrast, in 2024, all samples were taken at the farm level, with clinical investigation instigating sampling. Furthermore, samples consisted mainly of organs/tissues (107 out of the total 133 samples tested for this species), with the remaining 26 samples being faeces or caecal contents, matrices more likely to harbour STEC, if present.

Strain characterisation is pivotal to understanding the epidemiology of human STEC disease and the dynamics of STEC circulation in vehicles of infection. In 2024, 54.3% of food isolates were provided with information on the O-group. The six serogroups most reported in food isolates were O146, O157, O113, O26, O103 and O111, all known to be frequent in human disease, including severe HUS, in accordance with the zoonotic and food-borne origin of infection. In detail, among these, the O157, O26, O103 and O146 serogroups ranked highest in the STEC isolates from human infections in 2024.

Regarding STEC isolate characterisation, the determination of the presence of the *stx* and *eae* virulence genes (virulotyping) and of the *stx* gene subtypes, represents the most informative strategy for assessing the association of certain STEC with the most severe forms of human infection (EFSA BIOHAZ Panel, 2020). In 2024, 77.0% of the food isolates, 86.4% of animal isolates and 17.9% of the human isolates could be characterised for virulotype (presence and type of *stx* genes and presence of the *eae* gene). Information on *stx* subtyping was available only for 48.5% of the food isolates, 36.2% of animal strains and 49.1% of human strains. The *stx* gene subtype *stx2a* is recognised as being the most frequently associated with the severe forms of human infection (EFSA BIOHAZ Panel, 2020). This *stx* subtype was identified as the unique *stx* subtype in 13.3% of STEC from food samples in 2024. In general, typing data for STEC isolates from food and animals remain limited, although a slight increase in *stx* subtyping data for both sources has been observed. Despite the growing use of WGS across the EU, producing and sharing detailed characterisation data of STEC isolates still shows slow progress. As a result, *stx* typing and subtyping continue to lack broad application.

In 2026, the Commission Implementing Regulation (EU) 2025/179[43] will enter into force, requiring MSs to share WGS data generated during official outbreak investigations. This obligation is expected to catalyse broader adoption of WGS across sectors, supporting a One Health approach. Its implementation should enhance the availability of STEC typing and subtyping data, thereby strengthening the capacity to detect, investigate and manage STEC outbreaks.

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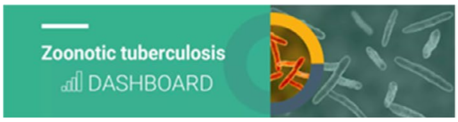
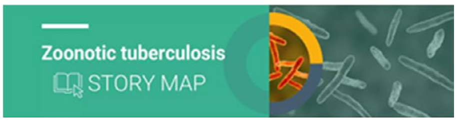
[43] Commission Implementing Regulation (EU) 2025/179 of 31 January 2025 on the collection and transmission of molecular analytical data within the frame of epidemiological investigations of food-borne outbreaks in accordance with Directive 2003/99/EC of the European Parliament and of the Council. OJ L, 3.2.2025, p. 1–3.

A5 | INFECTION WITH *MYCOBACTERIUM TUBERCULOSIS* COMPLEX (FOCUSING ON *MYCOBACTERIUM BOVIS* AND *MYCOBACTERIUM CAPRAE*)

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about zoonotic tuberculosis focusing on *Mycobacterium bovis* and *M. caprae*, and for the consultation of data collected, the following interactive tools are available:





A5.1 | Key facts

- In 2024, the percentage of zoonotic tuberculosis cases among the total number of tuberculosis cases in humans in European Union countries was 0.50%. A total of 171 confirmed cases of human tuberculosis due to *Mycobacterium bovis* or *Mycobacterium caprae* were reported, corresponding to an European Union notification rate of 0.04 cases per 100,000 population and a 22.6% increase in notification in the European Union compared with 2023.
- From 2022 to 2024, the number of cases of human tuberculosis due to *M. bovis* or *M. caprae* reported in the European Union continued to be higher than during the pandemic years 2020 and 2021. In 2024, the number of human cases among the 26 Member States exceeded the yearly number of cases reported between 2020 and 2023.
- In 2024, the *M. bovis* and *M. caprae* case notification rate was 0.03 cases per 100,000 among European Union Member States with disease-free status regarding infection with *Mycobacterium tuberculosis* complex in bovine animal populations and 0.06 cases per 100,000 in European Union Member States with non-disease-free status.
- Almost half of *M. bovis* and *M. caprae* cases in humans (49.7%) originated from outside of the European Union.
- In 2024, the prevalence of tuberculosis-positive cattle herds in the EU and the United Kingdom (Northern Ireland) was 0.72%, attributable to *M. bovis* or *M. caprae*. This is a slight increase compared with 2023 (0.58%). The total number of positive herds rose by 16.4%, from 8985 in 2023 to 10,463 in 2024.
- As in previous years, the distribution of positive herds was heterogeneous and spatially clustered, with national herd-level prevalence ranging from 0.01% or below (Austria, Belgium, Germany, Poland and Romania) to 9.0% in the United Kingdom (Northern Ireland).
- In 2024, 17 Member States had disease-free status of which one did not report data to EFSA. Ten Member States and the United Kingdom (Northern Ireland) remained under an eradication programme, of which one Member State did not report data to EFSA. Among these, Italy, Portugal and Spain had disease-free status zones.
- In disease-free status zones, 187 cattle herds (0.02%) were reported as positive for the *M. tuberculosis* complex, 25 more than in 2023, confirming that infection remains very rare in these areas.
- In zones under an eradication programme, 10,276 cattle herds (1.9% of the total) tested positive in 2024 for *M. tuberculosis* complex, which is a 16.5% increase compared with the 8823 herds reported in 2023. The highest prevalences were observed in the United Kingdom (Northern Ireland, 9.0%), Ireland (5.9%), Spain (1.5%) and Greece (1.3%). No positive herds were reported by Cyprus or Malta. Over the last decade (2015–2024), the total number of positive cattle herds in zones under an eradication programme has decreased by 41.2%, mainly due to the United Kingdom's withdrawal from the European Union in 2020. However, an upward trend of 42.4% has been observed in the last 5 years.

A5.2 | Surveillance and monitoring of tuberculosis due to *Mycobacterium bovis* or *Mycobacterium caprae* in the EU

A5.2.1 | Humans

The notification of tuberculosis in humans is mandatory in all Member States (MS) and covers the whole population. Countries can update their data retroactively, hence reported numbers are therefore subject to change in the future or may vary from numbers reported in previous reports. The European Union (EU) *Mycobacterium bovis* or *Mycobacterium caprae* notification rate is calculated using the combined population of the EU MSs that reported data in 2024. The proportion of tuberculosis cases caused by *M. bovis* or *M. caprae* was calculated using the preliminary estimate of the total number of confirmed tuberculosis cases in 2024 among reporting EU MS species-specific data.

In 2024, no human data on *M. bovis* or *M. caprae* cases were available for France because this MS did not report species-specific data within the *M. tuberculosis complex* (MTBC) for human tuberculosis cases. France has not reported species-specific data in any previous years. Because tuberculosis is a chronic disease with a long incubation period, it is not possible to assess travel-associated cases in the same way as for diseases with acute onset. Instead, a distinction is made between individuals with the disease originating from an EU MS (cases of EU origin) and those originating from outside the EU (case originating outside of the EU). In the analysis, origin is mainly based on the reported birthplace, except for cases from Austria, Belgium, Greece, Hungary and Poland, whose origin is based on reported nationality.

A5.2.2 | Animals

Bovine tuberculosis surveillance data

Article 2 of Regulation (EU) 2016/429[44] states that its scope applies to transmissible diseases, including zoonoses, without prejudice to the provisions laid down in Directive 2003/99/EC.[45] Therefore, the annual zoonoses data reporting requirements for MSs, as stipulated in Directive 2003/99/EC and implemented by EFSA through specific tools, manuals and guidance, remain unaffected by the entry into force of Commission Implementing Regulation (EU) 2020/2002.[46] This latter Commission Implementing Regulation outlines the compulsory notification and annual reporting obligations that MSs must fulfil with respect to ADIS[47]: EU MSs need to report to ADIS outbreaks of infection with MTBC in bovine species (cattle, buffalo and bison), even-toed ungulates (*Artiodactyla*) and other terrestrial mammals. Summaries of these reports are regularly made available online.

In accordance with Directive 2003/99/EC MSs must report annual surveillance data for bovine tuberculosis. These data are derived from compulsory national eradication and surveillance programmes implemented in compliance with EU legislation, including the Animal Health Law (AHL). The reports submitted by MSs are harmonised and enable the assessment of the epidemiological situation and the analysis of trends across MSs and their zones.

Article 36 of Regulation (EU) 2016/429 provides for European Commission approval of disease-free status (DFS) of MSs or specific zones within them, with respect to MTBC infections. Due to the differing levels of infection risk between DFS zones and zones under an eradication programme (UEP), these zones have been treated separately in this chapter.

All cases of bovine tuberculosis caused by MTBC members (*M. bovis*, *M. caprae* or *M. tuberculosis*) were considered in summarising the EU situation on the disease in cattle. Whenever possible, reporting MSs provided detailed distinctions between these MTBC species.

***Mycobacterium* surveillance data from food and from animals other than bovine animals**

Mycobacterium spp. monitoring data from food and from animals other than bovine animals are submitted to EFSA in accordance with Directive 2003/99/EC. Data collected allow for descriptive summaries to be compiled at the EU level, but do not allow trend watching or trend analyses (Table 1).

In accordance with Commission Implementing Regulation (EU) 2020/2002, notification to ADIS and surveillance rules apply to *Artiodactyla* mammals other than bovine animals (such as camelids, cervids, suids, ovine and caprine animals) and other terrestrial mammals susceptible to infection with MTBC.

A5.3 | Results

A5.3.1 | Overview of key statistics, EU, 2020–2024

Table 39 summarises the EU-level statistics on human tuberculosis due to *M. bovis* or *M. caprae* and on bovine tuberculosis during 2020–2024. More detailed descriptions of these statistics are provided in the subsections below.

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[44] Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016 on transmissible animal diseases and amending and repealing certain acts in the area of animal health ('Animal Health Law'). OJ L 84, 31.3.2016, p. 1–208.

[45] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40.

[46] Commission Implementing Regulation (EU) 2020/2002 of 7 December 2020 laying down rules for the application of Regulation (EU) 2016/429 of the European Parliament and of the Council with regard to Union notification and Union reporting of listed diseases, to formats and procedures for submission and reporting of Union surveillance programmes and of eradication programmes and for application for recognition of disease-free status, and to the computerised information system, OJ L 412, 8.12.2020, p. 1–28.

[47] EU Animal Diseases Information System (ADIS). More information is available at: https://food.ec.europa.eu/animals/animal-diseases/animal-disease-informationsystem-adis_en.

TABLE 39 Summary of tuberculosis due to *Mycobacterium bovis* and *Mycobacterium caprae* statistics relating to humans and bovine animals (stratified by disease status of MSs/MS zones), EU, 2020–2024.

	2024[a]	2023[a]	2022[a]	2021[a]	2020	Data source
Humans						
Number of confirmed *M. bovis* cases	160	126	140	108	95	ECDC
Number of confirmed *M. caprae* cases	11	11	7	10	4	ECDC
Total number of confirmed cases	171	137	147	118	99	ECDC
Total number of confirmed cases/100,000 population (notification rates)	0.04	0.03	0.03	0.03	0.02	ECDC
Number of EU MSs that reported data on *M. bovis* or *M. caprae* cases	26	26	26	26	26	ECDC
M. bovis or *M. caprae* cases in individuals of EU origin	80	72	93	63	60	ECDC
M. bovis or *M. caprae* cases in individuals originating from outside the EU	85	61	50	49	35	ECDC
M. bovis or *M. caprae* cases in individuals of unknown origin	6	4	4	6	4	ECDC
Total number of food-borne outbreaks[b]	0	1	0	0	0	EFSA
Number of outbreak-related cases	0	3	0	0	0	EFSA
Bovine animals						
Number of positive herds in disease-free status zones[c]	187	162	150	155	154	EFSA
Number of reporting disease-free status MSs[c]	16[d]	17	17	17	17	EFSA
Number of positive herds in zones under an eradication programme[e]	10,276	8823	9695	9235	7218	EFSA
Number of reporting MSs with zones under an eradication programme[e]	10[f]	11	11	11	9[f]	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States.

[a] Data reported to EFSA from the United Kingdom (Northern Ireland) were taken into account for 2021–2024. In accordance with the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community, and in particular Article 5(4) of the Windsor Framework (see Joint Declaration No 1/2023 of the Union and the United Kingdom in the Joint Committee established by the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community of 24 March 2023, OJ L 102, 17.4.2023, p.87) in conjunction with section 24 of Annex 2 to that Framework, for the purposes of this Regulation, references to Member States include the United Kingdom in respect of Northern Ireland.

[b] No information on the species was available for the *Mycobacterium* outbreak reported in 2023.

[c] Member States, or zones thereof, with disease-free status regarding infection with the *Mycobacterium tuberculosis* complex (*M. bovis, M. caprae, M. tuberculosis*) (MTBC).

[d] No data reported by Slovakia.

[e] Member States or zones thereof with an approved eradication programme for infection with MTBC. In addition, United Kingdom (Northern Ireland) has an approved eradication programme for infection with MTBC.

[f] No data reported by Bulgaria.

A5.3.2 | Tuberculosis due to *Mycobacterium bovis* or *Mycobacterium caprae* in humans

In 2024, 171 confirmed human cases of tuberculosis due to *M. bovis* or *M. caprae* were reported from 12 MSs (Austria, Belgium, Czechia, Germany, Greece, Hungary, Ireland, Italy, the Netherlands, Romania, Spain and Sweden) (Table 40). Tuberculosis cases due to *M. bovis* (160 cases) were reported from all the above-mentioned MSs except Czechia, which only reported cases caused by *M. caprae*. Germany and Spain also reported cases due to *M. caprae*, which accounted altogether for nine cases in the EU. In 2024, tuberculosis cases due to *M. bovis* or *M. caprae* accounted for a small proportion (0.50%) of total tuberculosis cases reported in the EU, Iceland, Norway, Liechtenstein and Switzerland. Overall, 26 MSs reported species-specific data on MTBC and 14 MSs did not report any cases. Reported cases of human tuberculosis due to *M. bovis* or *M. caprae* in the EU increased in 2024 compared with 2023 and showed the highest number reported since the 2020–2021 COVID-19 pandemic years. The EU notification rate in 2024 was 0.038 cases per 100,000 population, which is an increase of 22.6% compared with 2023, when the notification rate was 0.031 per 100,000 population. In 2024, the highest notification rate was reported by Ireland (0.19 per 100,000), followed by Spain (0.16 per 100,000). Among the 17 MSs with DFS regarding infection with MTBC in bovine animal populations in 2024, 16 MSs reported on MTBC species. *M. bovis* and *M. caprae* human cases were reported in seven MSs. The notification rate in these MSs reporting on MTBC species was 0.03 cases per 100,000 population. The notification rate for *M. bovis* and *M. caprae* human cases reported in the 10 non-DFS MSs in 2024 was 0.06 cases per 100,000 population.

The majority of *M. bovis* and *M. caprae* human cases reported in 2024 (*N* = 85/171; 49.7%) originated from outside of the EU. The other cases were of EU origin (*N* = 80; 46.8%; native cases and/or cases originating from other MSs) or had unknown origin (*N* = 6; 3.5%) (Table 39). Notification rates of *M. bovis* and *M. caprae* human cases of EU origin were lower in MSs with DFS (*N* = 26; 32.5%) than in non-DFS MSs (*N* = 54; 67.5%).

TABLE 40 Reported confirmed human cases of tuberculosis due to *Mycobacterium bovis* or *Mycobacterium caprae* and notification rates per 100,000 population in EU MS and non-MS countries, by country and year, 2020–2024.

	2024					**2023**		**2022**		**2021**		**2020**	
				Confirmed cases and rates		**Confirmed cases and rates**		**Confirmed cases and rates**		**Confirmed cases and rates**		**Confirmed cases and rates**	
Country	**Status**	**National coverage**[a]	**Data format**[a]	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**
Austria	DFS	Y	C	2	0.02	3	0.03	5	0.06	4	0.04	0	0
Belgium	DFS	Y	C	8	0.07	3	0.03	9	0.08	10	0.09	6	0.05
Bulgaria	■	Y	C	0	0	0	0	0	0	0	0	0	0
Croatia	■	Y	C	0	0	0	0	0	0	0	0	0	0
Cyprus	■	Y	C	0	0	0	0	0	0	0	0	0	0
Czechia	DFS	Y	C	2	0.02	0	0	0	0	0	0	0	0
Denmark	DFS	Y	C	0	0	1	0.02	0	0	0	0	0	0
Estonia	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Finland	DFS	Y	C	0	0	1	0.02	0	0	0	0	1	0.02
France[b]	DFS	–	–	–	–	–	–	–	–	–	–	–	–
Germany	DFS	Y	C	42	0.05	45	0.05	38	0.05	44	0.05	37	0.04
Greece	■	Y	C	1	0.01	1	0.01	1	0.01	0	0	2	0.02
Hungary	DFS	Y	C	1	0.01	1	0.01	0	0	0	0	0	0
Ireland	■	Y	C	10	0.19	8	0.15	9	0.17	2	0.04	4	0.08
Italy	▨	Y	C	15	0.03	8	0.01	15	0.03	12	0.02	6	0.01
Latvia	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Lithuania	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Luxembourg	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Malta	■	Y	C	0	0	0	0	0	0	0	0	0	0
Netherlands	DFS	Y	C	7	0.04	7	0.04	5	0.03	5	0.03	6	0.03
Poland	DFS	Y	C	0	0	0	0	1	< 0.01	0	0	0	0
Portugal	▨	Y	C	0	0	0	0	0	0	0	0	0	0
Romania	■	Y	C	1	0.01	3	0.02	1	0.01	0	0	1	0.01
Slovakia	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Slovenia	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Spain	▨	Y	C	76	0.16	55	0.11	57	0.12	37	0.08	30	0.06
Sweden	DFS	Y	C	6	0.06	1	0.01	6	0.06	4	0.04	6	0.06
EU Total				**171**	**0.04**	**137**	**0.03**	**147**	**0.03**	**118**	**0.03**	**99**	**0.02**
Iceland[c]		Y	C	0	0	0	0	0	0	0	0	0	0
Liechtenstein	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Norway	DFS	Y	C	0	0	1	0.02	0	0	0	0	0	0
Switzerland[d]	DFS	Y	C	8	0.09	10	0.11	1	0.01	4	0.05	3	0.03

Abbreviations: –, Data not reported; DFS, Disease-free status, i.e. free of infection with *M. bovis*, *M. caprae* or *M. tuberculosis* in the bovine animal population.

[a] Y: yes; N: no; A: aggregated data; C: case-based data.

[b] No surveillance system.

[c] In Iceland, which has no special agreement concerning animal health (status) with the EU, the last outbreak of bovine tuberculosis was in 1959.

[d] Switzerland provided data directly to EFSA. The human data for Switzerland include data from Liechtenstein for the year 2020.

DFS	All zones of the MS have disease-free status.
▨	Not all zones of the MS have disease-free status.
■	No zones of the MS have disease-free status.

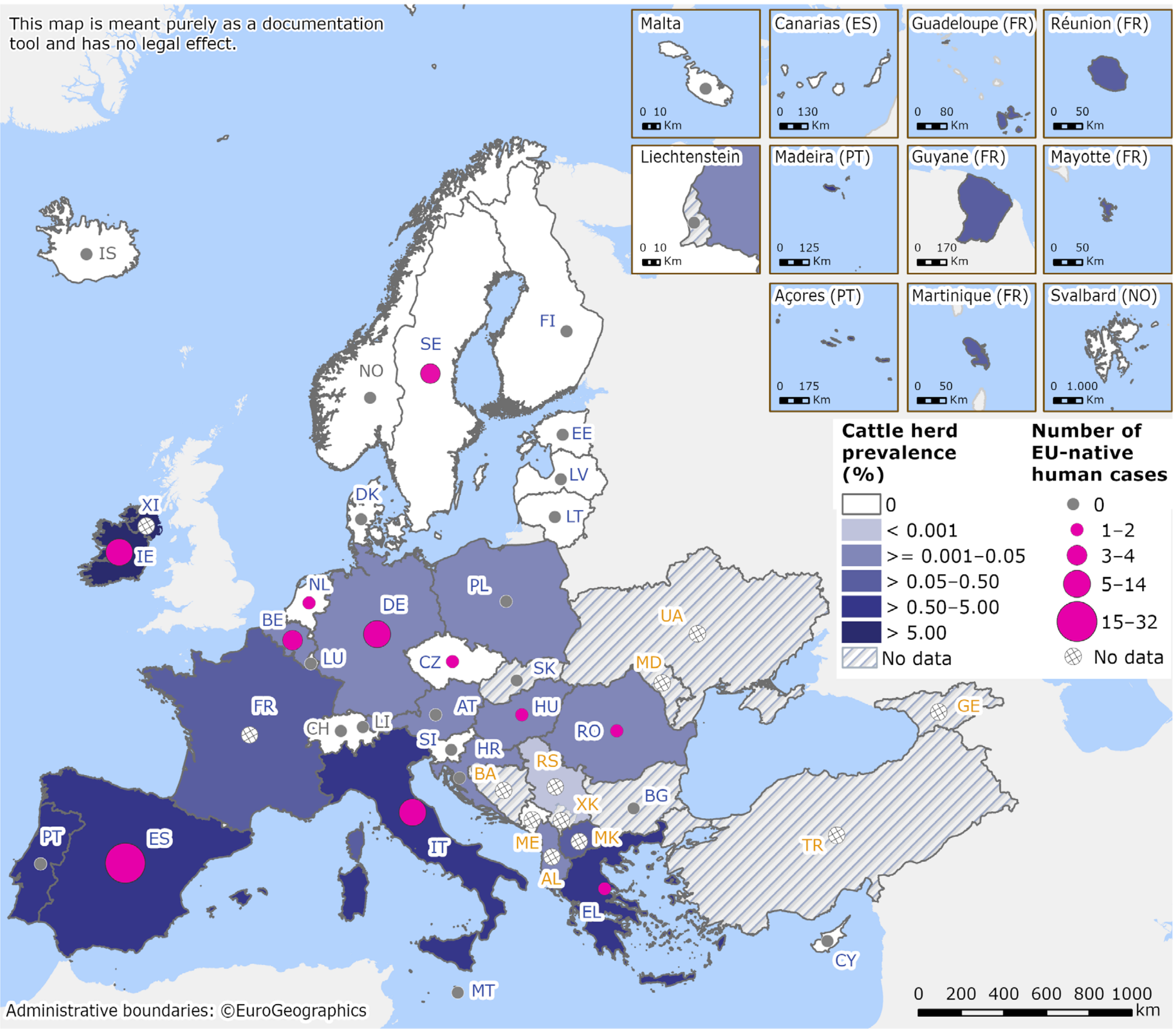


FIGURE 13 Map of the number of confirmed human tuberculosis cases due to *Mycobacterium bovis* or *Mycobacterium caprae* in individuals of EU origin, and national herd prevalence of tuberculosis in the bovine animal population in EU MS and non-MS countries, 2024.
Member States that reported data at the national level without specifying the specific zones or overseas territories where the bovine tuberculosis-positive cattle herds were detected were assigned the same colour for all their zones, including overseas territories. The two-letter country codes are shown in blue for the EU MSs and the United Kingdom (Northern Ireland), in grey for the EFTA/EEA countries and in orange for the candidate countries. For Albania, Kosovo and Serbia, prevalence data are at the animal level. The designation of Kosovo is without prejudice to positions on status and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.
Among cases reported from Switzerland, four cases with known origin were of non-EU origin, and four cases were of unknown origin.

A5.3.3 | *Mycobacterium* in food

No *Mycobacterium* species monitoring data from food were submitted for the year 2024.

A5.3.4 | Tuberculosis in bovine animals

Sixteen reporting MSs had DFS regarding MTBC during 2024 (Table 39). Of the remaining 10 reporting countries, i.e. nine MSs and the United Kingdom (Northern Ireland), three MSs had DFS zones or provinces:

- Italy: 13 regions and 16 provinces;
- Portugal: two regions (Algarve and Azores, except the island of São Miguel);
- Spain: seven autonomous communities and three provinces.

Six reporting MSs and the United Kingdom (Northern Ireland) had no zones with DFS regarding MTBC. No data were reported by Bulgaria and Slovakia.

Norway, Switzerland and Liechtenstein had DFS, in accordance with the EU legislation. In Iceland, which has no special agreement with the EU on animal health status, the last outbreak of bovine tuberculosis was reported in 1959.

In 2024, the overall proportion of MTBC-positive cattle herds in the EU was very low: 0.72%, a slight increase from 0.58% in 2023. The total number of positive bovine herds in the EU also increased by 16.4% from 8985 in 2023 to 10,463 in 2024.

Twelve MSs (10 DFS and two UEP countries) reported no cases of bovine tuberculosis. Thirteen MSs (6 DFS and 7 UEP) and the United Kingdom (Northern Ireland) reported cases of bovine tuberculosis. The distribution of positive herds was heterogeneous and spatially clustered, with national herd-level prevalence of positive herds ranging from 0.01% or below (Austria, Belgium, Germany, Poland and Romania) to 9.0% (the United Kingdom (Northern Ireland)). MTBC infections were primarily concentrated in UEP zones, where the overall proportion of positive herds (1.9%) was 95 times higher than in DFS zones (0.02%).

Six MSs reported MTBC infections in cattle without specifying the *Mycobacterium* species. *M. bovis* was specifically detected in France, Germany, Ireland, Italy, Poland, Romania and the United Kingdom (Northern Ireland), while *M. caprae* was specifically reported in Austria, Germany and Romania. No cases of *M. tuberculosis* infection in cattle herds were reported.

MSs and MS zones with disease-free status regarding *Mycobacterium* tuberculosis complex infection

The majority of the reported EU's cattle population (63.1%) is located in the DFS zones across 19 reporting MSs. However, the number of cattle herds in these zones has steadily declined, with a 30.7% decrease over the last decade (2015–2024). Over this 10-year period, there has been a slight, but steady increase in the number of MTBC-positive herds (Figure 14).

The total number of DFS zones in the EU increased during 2024 and in these zones eight MSs reported a total of 187 MTBC-positive bovine herds, confirming that the detection of bovine tuberculosis in DFS zones is rare. When comparing 2024 with 2023, the number of positive cattle herds increased by 25, while the proportion of positive herds remained unchanged at 0.02%. The total number of cattle herds decreased by 3.3%.

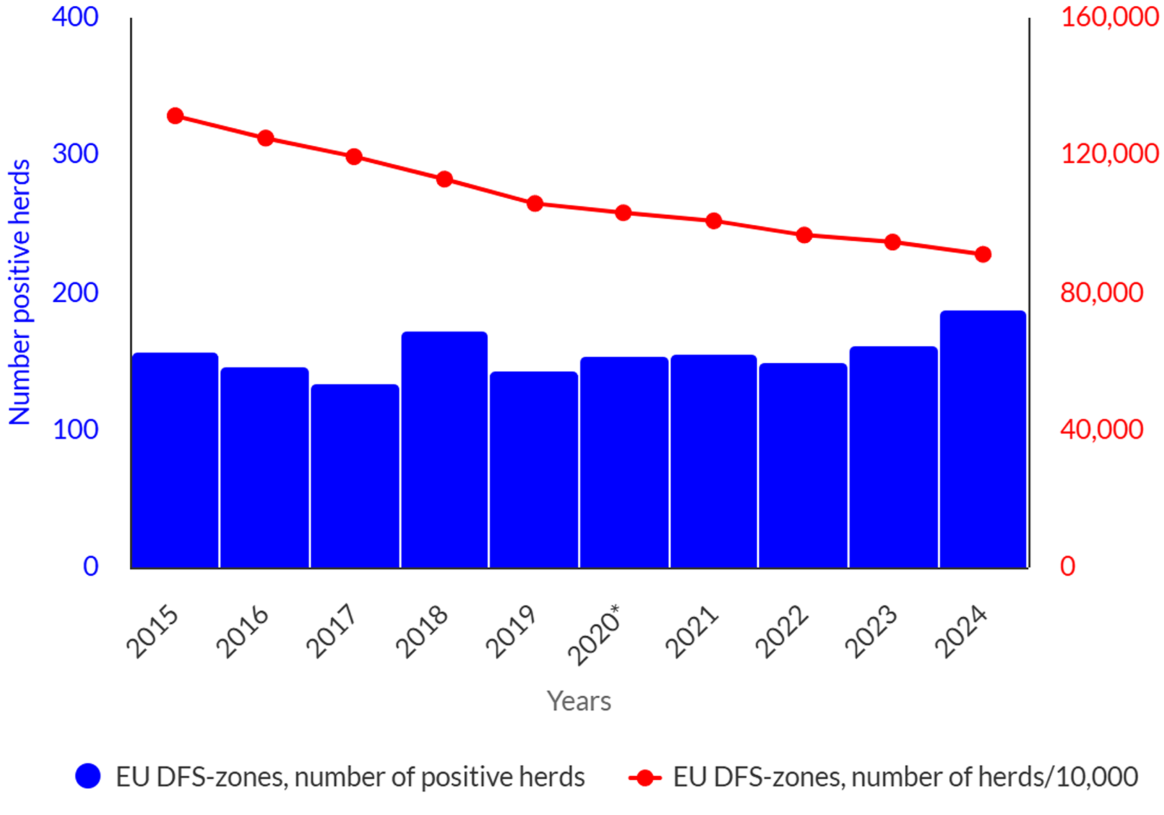


FIGURE 14 Number of cattle herds positive for the *Mycobacterium tuberculosis* complex in disease-free status (DFS) zones, EU, 2015–2024.
*In contrast to years 2015–2019, year 2020 does not include the United Kingdom (Scotland) data. Since 1 February 2020, the United Kingdom has withdrawn from the EU and has become a third country.
No 2024 data were reported by Slovakia.

MSs and MS zones with an approved eradication programme for infection with *Mycobacterium tuberculosis* complex

In 2024, cattle herds from UEP zones across nine reporting MSs and the United Kingdom (Northern Ireland) represented 36.9% of the total reported EU cattle herd population. This population has been steadily declining, with a 53.8% decrease compared with 2015 (Figure 15). From 2015 to 2019, data included the EU-28 MSs. However, the sharp decrease in 2020 can be attributed to the withdrawal of the United Kingdom from the EU and to the absence of data from Bulgaria in that year. Starting from 2021, the increase in the number of reported cattle herds can be mainly explained by the resumption of data from Bulgaria after its 2020 hiatus and by the inclusion of data from the United Kingdom (Northern Ireland). Over the last decade (2015–2024), the total number of positive cattle herds in UEP zones decreased by 41.2%, largely due to the withdrawal of the United Kingdom from the European Union in 2020 (Figure 15). However, there has been a 42.4% increase in the number of positive herds in the last 5 years.

Seven MSs and the United Kingdom (Northern Ireland) reported a total of 10,276 herds positive for bovine tuberculosis in 2024, a 16.5% increase from the 8823 positive herds in 2023. This increase was largely driven by Ireland, which reported 1082 more positive herds in 2024 than in 2023; Italy, which reported 164 additional positive herds in its UEP zones, with a marked rise in Sicily; and the United Kingdom (Northern Ireland), which reported 150 more positive herds than in 2023. The United Kingdom (Northern Ireland) (9.0%), Ireland (5.9%), Spain (1.5%) and Greece (1.3%) were the countries with a prevalence higher than 1%. No positive herds were reported by Cyprus or Malta. Compared with 2023, the overall proportion of positive herds in UEP zones increased from 1.5% in 2023 to 1.9% in 2024.

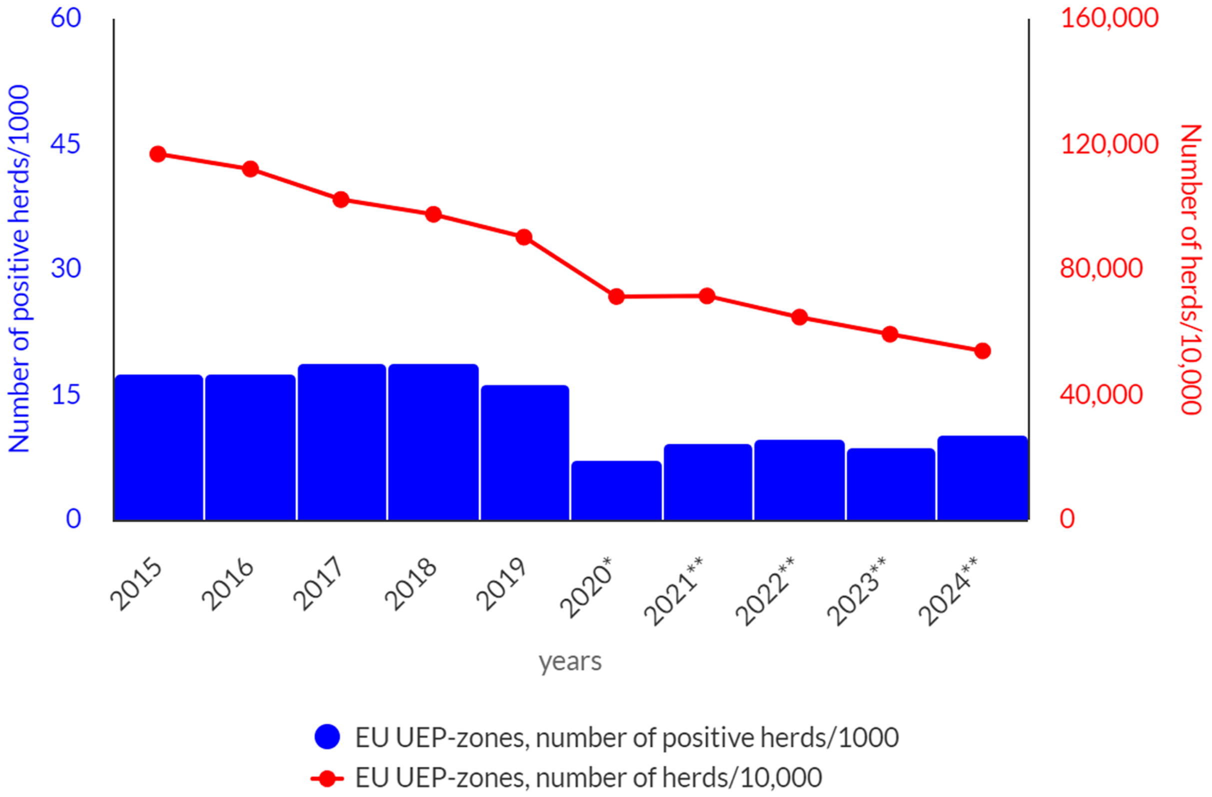


FIGURE 15 Number of cattle herds positive for bovine tuberculosis in zones under an eradication programme (UEP), EU, 2015–2024.
*In contrast to the years 2015–2019, the year 2020 does not include the United Kingdom data. Since 1 February 2020, the United Kingdom has withdrawn from the EU and has become a third country.
**Data from the United Kingdom (Northern Ireland) were taken into account for 2021–2024. In accordance with the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community, and in particular Article 5(4) of the Windsor Framework (see Joint Declaration No 1/2023 of the Union and the United Kingdom in the Joint Committee established by the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community of 24 March 2023, OJ L 102, 17.4.2023, p. 87) in conjunction with Section 24 of Annex 2 to that Framework, for the purposes of this Regulation, references to MSs include the United Kingdom in respect of Northern Ireland.
No data were reported from Bulgaria in 2020 and 2024.

Non-MSs and pre-accession countries

Bovine tuberculosis was not detected in 2024 in Norway, Iceland, Liechtenstein or Switzerland. Among the pre-accession countries, Montenegro, as in the previous 3 years, reported no positive herds; the Republic of North Macedonia reported eight positive herds (0.07%), whereas Albania reported 5 positive herds (less than 0.01%). Serbia reported five bovine animals with a positive intradermal tuberculin skin test (less than 0.01%).

A5.3.5 | *Mycobacterium tuberculosis* complex surveillance data from animals other than bovine animals

In 2024, two MSs (Finland and Sweden), the United Kingdom (Northern Ireland) and one non-MS (Norway) reported surveillance data on MTBC infection in farmed deer. Sweden specifically provided data from a control programme in farmed deer. A single case of MTBC infection in farmed deer was reported by the United Kingdom (Northern Ireland).

MSs also reported cases of MTBC infection in other mammal species. In particular, *M. bovis* was detected in farmed alpacas (Ireland), goats (Albania, Spain), pigs (France, Ireland, Italy), sheep (France, Ireland), cats (Ireland, Italy, the United Kingdom (Northern Ireland)), an otter (the United Kingdom (Northern Ireland)), wild deer (Ireland, the United Kingdom (Northern Ireland)), wild boar (France, Italy), foxes (France) and badgers (France, Ireland, Spain, the United Kingdom (Northern Ireland)). *M. caprae* was detected in wild deer (Hungary), wild boar (Hungary) and laboratory monkeys (Hungary).

A5.4 | Discussion

In 2024, a total of 171 human cases of tuberculosis due to *M. bovis* and *M. caprae* were reported in the EU, an increase compared with the year 2023. The increase in the disease notification rate was 22.6% in 2024 (0.038 cases per 100,000) compared with 2023 (0.031 per 100,000 population). The increase was driven by *M. bovis* cases, which represent by far the most frequent infection compared with *M. caprae* cases. The total number of *M. caprae* cases appears to remain relatively stable over recent years. It is important to highlight that, when analysing the trend in the last 5 years, notification rates remained higher from 2022 to 2024 than during the COVID-19 pandemic years (2020–2021). This should be interpreted with caution due to the impact the COVID-19 pandemic had on the healthcare systems across the EU. Overall, this upward trend is mainly driven by the increased number of cases reported in Spain. This observed increase in *M. bovis* and *M. caprae* cases in recent years by Spain may reflect the ongoing efforts of enhanced genomic surveillance, improved molecular diagnostics and growing recognition of transmission risks at the human-to-livestock interface (Martínez-Lirola et al., 2023; Pérez De Val et al., 2025; Roy et al., 2025).

Overall, the other countries observe a relatively stable epidemiological situation over the last five-year period, suggesting a recovery in notifications after the effect of the COVID-19 pandemic. An analysis by country showed that 14 MSs reported no cases. In addition, notification of total cases noticeably decreased in Austria, Denmark, Finland and Romania. In contrast, some countries showed an increase in total cases, particularly Belgium, Czechia, Ireland, Italy, Spain and Sweden. The total number of cases reported was highest in Germany and Spain, but when the data accounted for population distribution, the highest notification rates were observed in Ireland and Spain, which are countries that do not hold DFS at the national level for tuberculosis in their bovine populations. The increase in notifications continues to highlight the importance of targeted surveillance, effective control measures and timely diagnostic interventions.

For one EU country, France, MTBC data continue to be unreported in 2024 as no surveillance system in place, as in previous years.

With regard to where the disease was acquired, the ratio of foreign-to-native origin changed for the first time in the five-year window analysis, with the total foreign-acquired cases surpassing native-origin disease notification. A contributing factor to these changes is likely due to the resumption of population movement after the COVID-19 pandemic restrictions (McAuliffe & Oucho, 2024).

Tuberculosis cases of zoonotic origin (due to *M. bovis* or *M. caprae*) and notification rates are highly likely to have been underestimated. Bias is introduced by EU MSs that do not regularly perform routine tests to distinguish *M. bovis* and *M. caprae* in the MTBC. This bias results in under-notification at the EU level, due to all cases being reported as *M. tuberculosis* in these MSs, thereby undermining the possibility of tracing the origin of infections (Fujiwara & Olea-Popelka, 2016). Additionally, a lower notification rate was observed in EU MSs with DFS compared with non-DFS MSs, supporting the effectiveness of the surveillance programmes.

In 2024, the distribution of MTBC infection in bovine animals was heterogeneous and spatially clustered in the EU, with a national herd prevalence ranging from 0.01% or below (Austria, Belgium, Germany, Poland, Romania) to 9.0% in the United Kingdom (Northern Ireland). Sixteen MSs that reported data to EFSA had DFS. Of the remaining nine MSs that reported data to EFSA and the United Kingdom (Northern Ireland), three had DFS zones or provinces. The total number of DFS zones in the EU increased slightly in 2024, due to changes in Italy. Eight of these UEP MSs continued to detect bovine tuberculosis, consistent with the situation over the past decade (2015–2024). Seven of the nine UEP MSs that reported data to EFSA, together with the United Kingdom (Northern Ireland), reported a 16.5% increase in the number of positive herds compared with 2023. This overall rise was largely driven by Ireland, Italy (particularly Sicily) and the United Kingdom (Northern Ireland). Ireland attributed part of the increase to large decreases in dairy herds, animal movements and residual infections within herds. Italy reported a slight increase in disease incidence over the past 3 years, which is likely linked to the expanded use of the gamma-interferon assay in high-risk herds and improved MTBC detection capacity in non-DFS provinces. The disease remains geographically concentrated, with clusters mainly in Sicily and several southern provinces, including Salerno, Cosenza, Crotone and Foggia. The United Kingdom (Northern Ireland) reported a general upward trend in disease levels in recent years. MS-specific evaluations of status, trends and the relevance of bovine tuberculosis as a source of disease for humans can be found in the 2024 Annual National Zoonoses Country Reports available online here.

Over the last 5 years (2020–2024), the total number of positive cattle herds in UEP increased by 42.4%, while the number of total herds continued to decrease. This increase in prevalence may have multiple explanations, including a self-sustaining multi-host cycle in wildlife and livestock, imperfect testing, cattle movements that spread undetected infections to new areas and inconsistent resource allocation, coordination and implementation of control policies that undermine programme effectiveness. Improved surveillance can reveal more cases, while reduced monitoring hides the true extent of infection (Byrne et al., 2024; More, 2024).

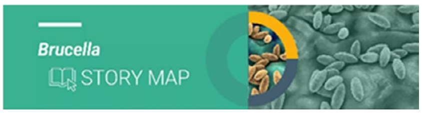
In 2024, *M. bovis* was reported from a wide range of domestic and wild mammal species (other than bovine animals), which reflects the broad host range of this pathogen. *M. caprae* was reported in cattle, goats, wild boar, deer and laboratory monkeys, clearly illustrating the broad host range capacity of this MTBC species. Effective control of bovine tuberculosis also requires consideration of the wildlife component of this multi-host disease (Santos et al., 2020).

In conclusion, tuberculosis cases in humans due to *M. bovis* and *M. caprae* remain rare in the EU, but underdiagnosis continues to be a concern. Reinforcing surveillance that allows active detection of cases and integrating a One Health perspective is essential (De Macedo Couto et al., 2022). The coordinated One Health approach linking human, animal and environmental health can enhance early detection and support targeted public health action. More MTBC-positive cattle herds were reported in 2024 than in 2023. This increase was notably due to the increased incidence in Ireland, in certain UEP zones of Italy and in the United Kingdom (Northern Ireland). Whether the observed increase in human cases reflects improved detection and reporting of zoonotic transmission, or a true rise in animal cases, remains to be clarified through continued surveillance in the coming years. These trends should encourage authorities to strengthen and refine control measures to better address this complex and persistent disease.

A6 | *BRUCELLA*

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about *Brucella* the following interactive tool is available:



A6.1 | Key facts

- In 2024, 273 confirmed cases of human brucellosis were reported in the EU, corresponding to a notification rate of 0.06 cases per 100,000 population, the same rate as in 2023.
- The overall trend for *Brucella* infections showed a significant increase during 2020–2024.
- Among cases with known information, 22.5% acquired infection in a country outside the EU.
- Most human infections were caused by *Brucella melitensis* 90.7% (88/97 cases).
- No food-borne outbreaks of brucellosis were reported for the year 2024.
- In cattle, 22 Member States and the United Kingdom (Northern Ireland) held disease-free status for brucellosis in 2024, of which one Member State did not report any data to EFSA. Five Member States (Bulgaria, Greece, Hungary, Italy and Portugal) remained under eradication programmes, with Italy and Portugal having disease-free zones.
- Within disease-free status zones for brucellosis in cattle, six positive herds were reported in 2024, all of which were in Italy, confirming the rare occurrence of the disease (prevalence < 0.001%). In four Member States with zones under eradication programmes (Greece, Hungary, Italy and Portugal), the number of positive herds increased slightly from 281 in 2023 to 304 in 2024.
- In sheep and goats, 21 Member States and the United Kingdom (Northern Ireland) were disease-free in 2024, of which one Member State did not report any data to EFSA. Five Member States (Bulgaria, Croatia, Greece, Italy and Portugal) remained under eradication programmes, with Italy and Portugal having disease-free zones. Malta had no official disease status for brucellosis in sheep and goats in 2024.
- Within the disease-free status zones for brucellosis in sheep and goats, four positive flocks were reported in 2024 (Germany: one; Italy: three), corresponding to a rare prevalence (< 0.001%). In zones under eradication programmes of reporting MS, the prevalence of *Brucella*-positive sheep and goat flocks continued to decrease, with 43 affected flocks (0.04%) in 2024.
- Brucellosis remains an animal health concern with public health relevance in southern European and Balkan countries that are not disease-free for brucellosis.

A6.2 | Surveillance and monitoring of *Brucella* in the EU

A6.2.1 | Humans

For 2024, 26 Member States (MSs) reported information on brucellosis in humans. Surveillance is mandatory in 25 MSs. Belgium has another (unspecified) system. Denmark has no surveillance system in place for brucellosis, and the disease is not notifiable or reported at the EU level. The EU case definition was used by 23 countries, while three countries (France, Germany and Italy) reported using another case definition. All countries had a comprehensive surveillance system, with full national coverage in all MSs reporting brucellosis data. All countries reported case-based data with the exception of Bulgaria, which reported aggregated data.

A6.2.2 | Food and animals

Surveillance data for bovine brucellosis and ovine and caprine brucellosis

Regulation (EU) 2016/429[48] applies to transmissible diseases, including zoonoses, without prejudice to the provisions laid down in Directive 2003/99/EC.[49] Therefore, the annual zoonosis data reporting requirements for MSs, as stipulated in Directive 2003/99/EC and implemented by EFSA through specific tools, manuals and guidance, remain unaffected by the entry into force of Commission Implementing Regulation (EU) 2020/2002.[50] The Commission Implementing Regulation (EU) 2020/2002 outlines the compulsory notification and annual reporting requirements that MSs must fulfil with respect to ADIS[51]: EU MSs are required to report to the EU ADIS outbreaks of infection with *Brucella abortus*, *B. melitensis* and *B. suis* in cattle and in sheep and goat populations, in other even-toed ungulates (*Artiodactyla*) and in other terrestrial animals. Summaries of these reports are regularly made available online. In accordance with Directive 2003/99/EC, MSs must report annual surveillance data for bovine brucellosis. These data are derived from compulsory national eradication and surveillance programmes implemented in compliance with EU legislation, including Regulation (EU) 2016/429. The reports submitted by MSs are harmonised and enable the assessment of the epidemiological status and the analysis of trends across MSs and MS zones.

Regulation (EU) 2016/429 provides for the European Commission's approval of the disease-free status (DFS) of MSs or specific zones within them, with respect to infection with *B. abortus*, *B. melitensis* and *B. suis* in cattle and in sheep and goat populations, and of the non-vaccination status of MSs or MS zones or compartments. Due to the differing levels of infection risk between DFS zones and zones under an eradication programme (UEP), these zones have been treated separately in this chapter. Commission Implementing Regulation (EU) 2018/1882[52] includes *Bos* ssp., *Bubalus* ssp., *Bison* ssp., *Ovis* ssp. and *Capra* ssp. as species for notification, surveillance, prevention, certification and compulsory eradication. Commission Delegated Regulation (EU) 2020/689[53] (Annex IV) describes the conditions required to grant, maintain or suspend the status of free from infection with *B. abortus*, *B. melitensis* and *B. suis* for an establishment keeping cattle or sheep and goats.

Annual surveillance programmes are carried out in DFS zones to confirm the absence of infection with *B. abortus*, *B. melitensis* and *B. suis* in cattle, and in sheep and goats. In UEP zones, control and eradication programmes are in place for brucellosis in cattle and in sheep and goats. These data are comparable across MSs because the monitoring schemes are harmonised, and the data collected and reported to EFSA originate from the census-as-sampling framework or a randomised design. These data can be used to carry out trend analyses both at the EU and MS levels, to perform trend watching and produce descriptive summaries, and to assess the impact of control and eradication programmes (Table 1).

Surveillance data for *Brucella* from food and from animals other than cattle, sheep and goats

Monitoring data for *Brucella* from food and from animals other than cattle, or sheep and goats are submitted to EFSA in accordance with Directive 2003/99/EC. Data collected allow for descriptive summaries to be compiled at the EU level, but do not enable trend watching or trend analyses (Table 1). In accordance with Commission Implementing Regulation (EU)

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[48] Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016 on transmissible animal diseases and amending and repealing certain acts in the area of animal health (‘Animal Health Law’). OJ L 84, 31.3.2016, pp. 1–208.

[49] Directive 2003/99/EC of The European Parliament and of The Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, pp. 31–40.

[50] Commission Implementing Regulation (EU) 2020/2002 of 7 December 2020 laying down rules for the application of Regulation (EU) 2016/429 of the European Parliament and of the Council with regard to Union notification and Union reporting of listed diseases, to formats and procedures for submission and reporting of Union surveillance programmes and of eradication programmes and for application for recognition of disease-free status, and to the computerised information system, OJ L 412, 8.12.2020, pp. 1–28.

[51] EU Animal Disease Information System (ADIS). More information is available on the EU ADIS website at: https://food.ec.europa.eu/animals/animal-diseases/animal-disease-information-system-adis_en.

[52] Commission Implementing Regulation (EU) 2018/1882 of 3 December 2018 on the application of certain disease prevention and control rules to categories of listed diseases and establishing a list of species and groups of species posing a considerable risk for the spread of those listed diseases. OJ L 308, 4.12.208, pp. 21–29.

[53] Commission Delegated Regulation (EU) 2020/689 of 17 December 2019 supplementing Regulation (EU) 2016/429 of the European Parliament and of the Council as regards rules for surveillance, eradication programmes and disease-free status for certain listed and emerging diseases. OJ L 174, 3.6.2020, pp. 211–340.

2020/2002, notification to ADIS and surveillance rules apply to other *Artiodactyla* species (such as camelids or cervids) as they are susceptible species for brucellosis.

A6.3 | Results

A6.3.1 | Overview of key statistics, EU, 2020–2024

Table 41 displays statistics at the EU level on human and animal brucellosis, along with data on detection of *Brucella* in food, between 2020 and 2024. More detailed descriptions of these statistics are provided in the subsections below and in the chapter on food-borne outbreaks.

TABLE 41 Summary of *Brucella* statistics relating to humans, major food categories and animal species (stratified by status of disease of MSs/MS zones), EU, 2020–2024.

	2024[a]	2023[a]	2022[a]	2021[a]	2020	Data source
Humans						
Total number of confirmed cases	273	259	226	162	132	ECDC
Total number of confirmed cases/100,000 population (notification rates)	0.06	0.06	0.05	0.03	0.03	ECDC
Number of reporting MSs	26	26	26	26	26	ECDC
Infection acquired in the EU	127	71	58	71	68	ECDC
Infection acquired outside the EU	37	37	22	18	14	ECDC
Unknown travel status or unknown country of infection	109	151	146	73	50	ECDC
Total number of food-borne outbreaks	0	0	0	2	2	EFSA
Number of outbreak-related cases	0	0	0	1	1	EFSA
Food						
Milk and milk products						
Number of sampling units	187	200	182	320	275	EFSA
Number of reporting MSs	2	3	3	3	3	EFSA
Animals						
Cattle (bovine animals)						
Number of positive herds in disease-free status zones[b]	6	8	12	7	6	EFSA
Number of reporting disease-free status MSs[b]	22[c]	23	23	22	20	EFSA
Number of positive herds in zones under an eradication programme[d]	682	281	412	547	603	EFSA
Number of reporting MSs with zones under an eradication programme[d]	5	5	5	6	6[e]	EFSA
Sheep and goats						
Number of positive flocks in disease-free zones[f]	4	4	2	11	3	EFSA
Number of reporting disease-free status MSs[f]	21[c]	22	21	21	19	EFSA
Number of positive herds in zones under an eradication programme[g]	43	141	234	335	349	EFSA
Number of reporting MSs with zones under an eradication programme[g]	5[e,h]	5[e,h]	7[i]	7	7[e]	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States.

[a] Data from the United Kingdom (Northern Ireland) were taken into account for 2021–2024. In accordance with the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community, and in particular Article 5(4) of the Windsor Framework (see Joint Declaration No 1/2023 of the Union and the United Kingdom in the Joint Committee established by the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community of 24 March 2023, OJ L 102, 17.4.2023, p. 87) in conjunction with section 24 of Annex 2 to that Framework, for the purposes of this Regulation, references to Member States include the United Kingdom in respect of Northern Ireland.

[b] Member States, or zones thereof, with DFS regarding infection with *B. abortus*, *B. melitensis* and *B. suis* in their bovine animal populations. In addition, the United Kingdom (Northern Ireland) has DFS from infection with *B. abortus*, *B. melitensis* and *B. suis* in its bovine animal population.

[c] No data were reported by Slovakia.

[d] Member States or zones thereof with an approved eradication programme for *B. abortus*, *B. melitensis* and *B. suis* in bovine animal populations.

[e] No data were reported by Bulgaria.

[f] Member States, or zones thereof, with DFS regarding infection with *B. abortus*, *B. melitensis* and *B. suis* in their sheep and goat populations. In addition, the United Kingdom (Northern Ireland) has DFS with regard to *B. abortus*, *B. melitensis* and *B. suis* in its sheep and goat populations.

[g] Member States or zones thereof with an approved eradication programme for *B. abortus*, *B. melitensis* and *B. suis* in ovine and caprine animal populations.

[h] Including Malta, which had no official disease status as regards infection with *B. abortus*, *B. melitensis* and *B. suis* in ovine and caprine animal populations, in 2024 and 2023.

[i] Including France, in which the whole of metropolitan France obtained DFS in 2022 whereas overseas French regions did not have this status.

A6.3.2 | Human brucellosis

In 2024, 273 cases of confirmed human brucellosis were reported in the EU, which represents a slight increase in the number of cases reported compared to 2023. Despite this, the notification rate remained stable at 0.06 cases per 100,000 population between 2023 and 2024. In 2024, 26 MSs provided data and information on brucellosis in humans (Table 41). Greece, Malta and Portugal reported the highest notification rates (0.4, 0.18 and 0.17 cases per 100,000 population, respectively) (Table 42). Eight MSs (Croatia, Cyprus, Estonia, Finland, Hungary, Latvia, Lithuania and Luxembourg) reported zero cases (Table 42).

In 2024, most cases (68.5%; 187/273) were reported with data on importation status; 65.8% (123/187) of cases were reported as domestically acquired, while 34.2% (64/187) were reported as imported (Figure 17).

A total of 164 cases were reported with known information on both importation status and place of infection, the majority of which (77.4%; 127/164) were reported as acquired within the EU (either domestically or in another MS) (Table 41). This corresponds to an approximately 90% increase in the number of EU-acquired cases in 2024 compared to the average of 67 cases reported between 2020 and 2023; this is driven by a few countries. In particular, Italy reported importation information for their cases in 2024 for the first time, while Greece, Portugal and Spain also reported a slight increase in the number of domestic cases compared to previous years. Of the four imported cases acquired within the EU in 2024, the probable countries of infection were Spain (two cases), Czechia (one case) and Italy (one case). Consistent with 2023, 37 cases (22.6%; 37/164) were reported as acquired outside the EU (Table 41). Among the 37 imported cases acquired outside the EU, the most probable countries of infection were Iraq (29.7%; 11/37), Bosnia and Herzegovina (10.8%; 4/37) and Türkiye (10.8%; 4/37).

TABLE 42 Reported confirmed human cases of brucellosis and notification rates per 100,000 population in EU MSs and non-MSs, by country and year, 2020–2024.

	2024						2023		2022		2021		2020	
	Status				Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	**Bv[a]**	**Ov, Cp[b]**	**National coverage[c]**	**Data format[c]**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**	**Cases**	**Rate**
Austria	DFS	DFS	Y	C	11	0.12	8	0.09	7	0.08	6	0.07	8	0.09
Belgium[d]	DFS	DFS	Y	C	4	0.03	5	0.04	3	0.03	7	0.06	4	0.03
Bulgaria	■	■	Y	A	5	0.08	1	0.02	2	0.03	0	0	1	0.02
Croatia	DFS	■	Y	C	0	0	2	0.05	2	0.05	2	0.05	1	0.03
Cyprus	DFS	DFS	Y	C	0	0	0	0	0	0	1	0.11	0	0
Czechia	DFS	DFS	Y	C	1	0.01	1	0.01	0	0	1	0.01	0	0
Denmark[e]	DFS	DFS	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	DFS	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Finland	DFS	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
France	DFS	DFS	Y	C	22	0.03	22	0.03	37	0.05	21	0.03	19	0.03
Germany	DFS	DFS	Y	C	54	0.06	36	0.04	35	0.04	13	0.02	19	0.02
Greece	■	■	Y	C	42	0.40	29	0.28	35	0.33	24	0.22	30	0.28
Hungary	■	DFS	Y	C	0	0	0	0	0	0	0	0	0	0
Ireland	DFS	DFS	Y	C	1	0.02	5	0.09	1	0.02	0	0	0	0
Italy	░	░	Y	C	33	0.06	74	0.13	48	0.08	32	0.05	18	0.03
Latvia	DFS	DFS	Y	C	0	0	0	0	0	0	0	0	1	0.05
Lithuania	DFS	DFS	Y	C	0	0	2	0.07	0	0	0	0	0	0
Luxembourg	DFS	DFS	Y	C	0	0	0	0	1	0.15	1	0.16	0	0
Malta[f]	DFS	▨	Y	C	1	0.18	0	0	0	0	0	0	0	0
Netherlands	DFS	DFS	Y	C	14	0.08	4	0.02	5	0.03	2	0.01	2	0.01
Poland	DFS	DFS	Y	C	4	0.01	4	0.01	1	< 0.01	1	< 0.01	0	0
Portugal	░	░	Y	C	18	0.17	14	0.13	13	0.12	10	0.10	9	0.09
Romania	DFS	DFS	Y	C	9	0.05	1	0.01	0	0	0	0	0	0
Slovakia	DFS	DFS	Y	C	7	0.13	10	0.18	3	0.06	6	0.11	2	0.04
Slovenia	DFS	DFS	Y	C	1	0.05	3	0.14	1	0.05	0	0	1	0.05
Spain[g]	DFS	DFS	Y	C	32	0.07	28	0.06	22	0.05	25	–	10	–
Sweden	DFS	DFS	Y	C	14	0.13	10	0.10	10	0.10	10	0.10	7	0.07
EU Total			–	–	**273**	**0.06**	**259**	**0.06**	**226**	**0.05**	**162**	**0.03**	**132**	**0.03**

TABLE 42 (Continued)

	2024						2023		2022		2021		2020	
	Status				Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	Bv[a]	Ov, Cp[b]	National coverage[c]	Data format[c]	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Iceland			Y	C	0	0	0	0	0	0	0	0	0	0
Liechtenstein	DFS	DFS	Y	C	0	0	0	0	0	0	0	0	–	–
Norway	DFS	DFS	Y	C	3	0.05	1	0.02	1	0.02	3	0.06	2	0.04
Switzerland[h]	DFS	DFS	Y	C	4	0.04	9	0.10	6	0.07	6	0.07	3	0.03

Abbreviations: –, data not reported; DFS, disease-free status with regard to infection with *B. abortus*, *B. melitensis* and *B. suis* in cattle populations and/or in sheep and goat populations.

[a] Cattle populations.

[b] Sheep and goat populations.

[c] Y: yes; N: no; A: aggregated data; C: case-based data.

[d] During the final report phase of production, Belgium updated their data to correct a data entry error in EpiPulse cases: four cases were initially reported, but due to duplicate records, the correct number is two.

[e] No surveillance system.

[f] Malta had no official disease status as regards infection with *B. abortus*, *B. melitensis* and *B. suis* in ovine and caprine animal populations, in 2024.

[g] Data incomplete for 2020–2021, rate not estimated.

[h] Switzerland provided data directly to EFSA. The human data for Switzerland include data from Liechtenstein for 2020.

DFS	All zones of the MS have disease-free status.
▒	Not all zones of the MS have disease-free status.
■	No zone of the MS has disease-free status.
▨	No status.

In 2024, the number of confirmed brucellosis cases in the EU showed a clear seasonal pattern, with most cases reported between May and August (Figure 16). Over the period 2020–2024, a significant increasing trend was observed at the EU level. Despite this, the annual number of cases and notification rates reported during this period remained at or below the levels reported before the COVID-19 pandemic. At the MS level, a significant increasing trend was observed in three countries – Germany, the Netherlands and Portugal – while no country showed a decreasing trend. Germany and the Netherlands reported their highest number of brucellosis cases and notification rates in 2024 compared to previous years, whereas the number of cases and the notification rate reported in Portugal in 2024 remained consistent with those reported prior to the COVID-19 pandemic.

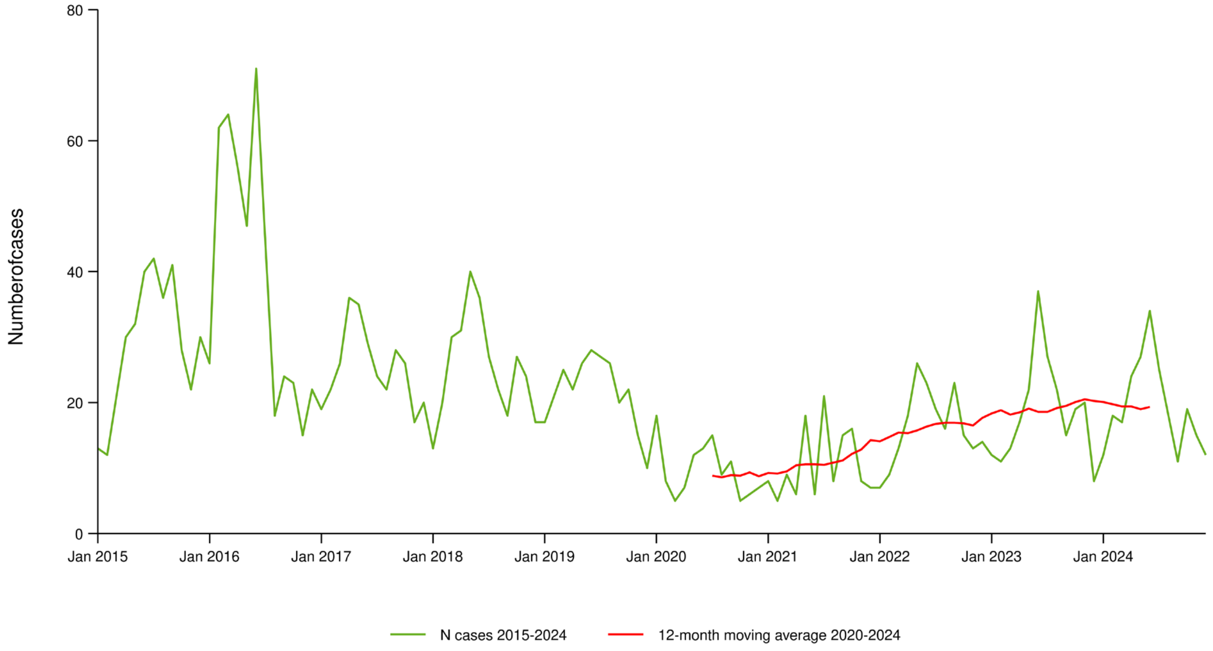

FIGURE 16 Trend in reported confirmed human cases of brucellosis in the EU, by month, 2020–2024.
Source: Austria, Cyprus, Czechia, Germany, Estonia, Greece, Finland, France, Ireland, Italy, Latvia, Lithuania, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia and Sweden.

Of the 273 human cases reported in 2024, 97 (35.5%) included information on the *Brucella* species, provided by 14 MSs. Among these, 13 countries reported 88 cases (90.7%; 88/97) caused by infection with *Brucella melitensis*, with the majority reported by France (21.6%; 19/88), Germany (19.3%; 17/88) and Greece, the Netherlands and Sweden, each with 10 cases (11.4% 10/88). Four countries (Germany, the Netherlands, Portugal and Slovakia) reported nine cases (9.3%; 9/97), which were caused by *B. abortus*.

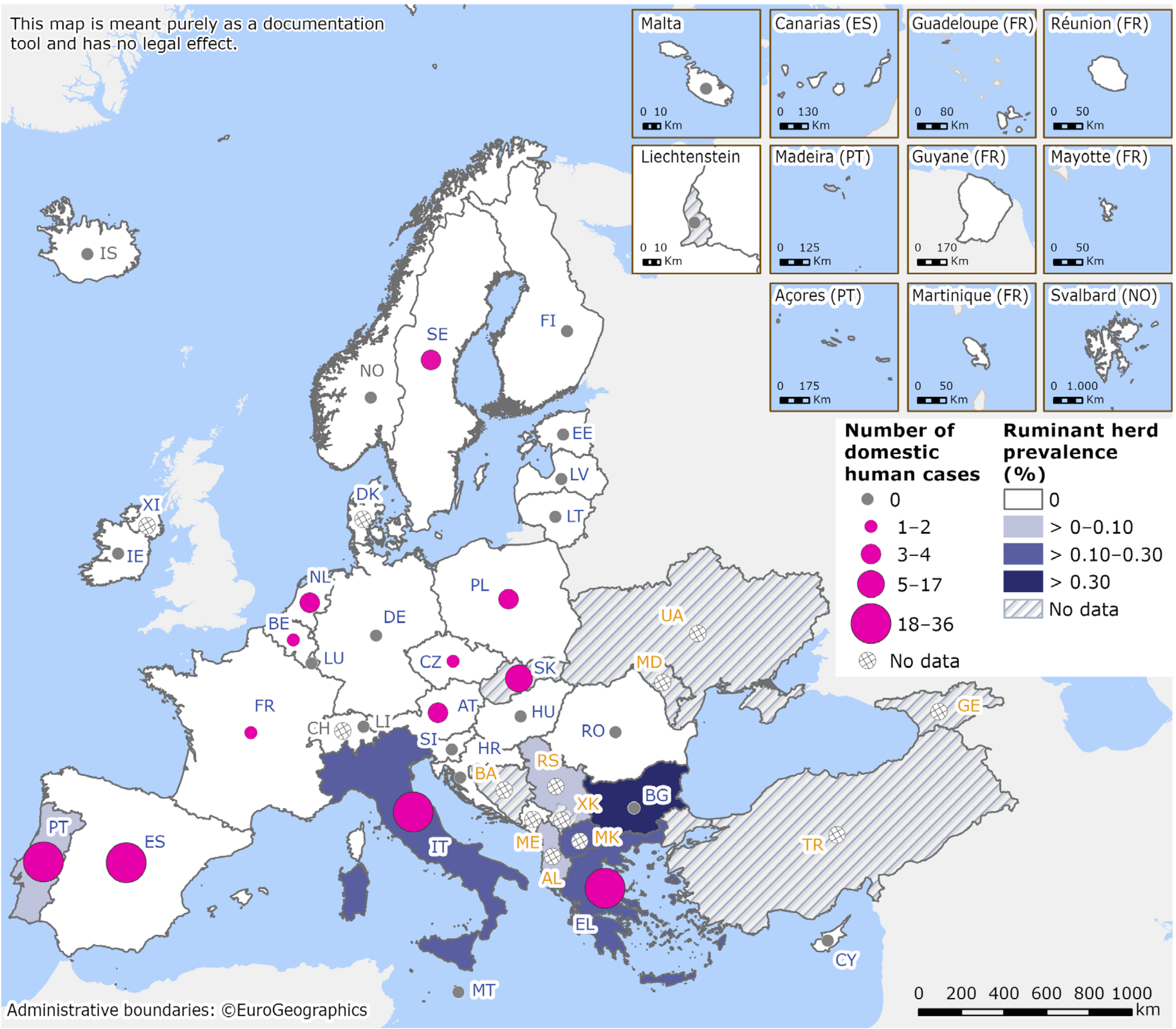

FIGURE 17 Number of confirmed, domestically acquired brucellosis cases in humans and national prevalence of *Brucella*-positive cattle herds and sheep and goat flocks, in EU MSs and non-MSs, 2024.
Member States that reported data at the national level without specifying the specific zones or overseas territories where the *Brucella*-positive animal herds were detected, were assigned the same colour for all their zones, including overseas territories. EU MSs and the United Kingdom (Northern Ireland) were represented with a blue label, the EFTA/EEA countries were represented with a grey label, and all the candidate countries were represented with an orange label. For Albania, the Republic of North Macedonia and Serbia, prevalence data are at the animal level.
The confirmed case acquired domestically in Belgium involves a chronic infection in an individual likely infected prior to the country attaining official brucellosis disease-free status.

A6.3.3 | *Brucella* in food

Very few monitoring data for *Brucella* were submitted in 2024, as was the case in previous years. In total, 187 single samples of milk and cheese were collected from primary production, and from the manufacturing and distribution stages, by two MSs (Portugal and Spain). No positive samples were reported.

A6.3.4 | *Brucella* in animals

Surveillance data for bovine brucellosis, and ovine and caprine brucellosis

Cattle

The status of countries for brucellosis in cattle was stable in 2024 compared with 2023, with 22 MSs and the United Kingdom (Northern Ireland) having DFS in 2024. Out of the five MSs with UEP zones (Bulgaria, Greece, Hungary, Italy and Portugal), two countries had DFS zones or provinces for cattle:

- Italy: 13 regions and 13 provinces (the Agrigento province having acquired DFS in 2024); and
- Portugal: eight of the nine islands of the autonomous region of the Azores and nine districts (Aveiro, Castelo Branco, Coimbra, Faro, Guarda, Leiria, Santarem, Setubal and Viseu).

Italy was the only MS to report an increased number of DFS zones. Bulgaria, Greece and Hungary did not have any DFS zones. Slovakia did not report any data for cattle brucellosis for the year 2024.

Liechtenstein, Norway and Switzerland have DFS in accordance with EU legislation. Iceland, which does not have any special agreement on animal health (status) with the EU, has never reported any brucellosis cases caused by *B. abortus*, *B. melitensis* or *B. suis*.

In 2024, brucellosis in cattle herds remained rare in the EU (< 0.01%; 688 out of 1,459,457 herds). Twenty-two MSs and the United Kingdom (Northern Ireland) reported no cases. The highest numbers of positive herds were observed in Bulgaria, Greece and Italy, while Portugal reported only a few cases.

Within the DFS zones, no positive cattle herds were reported in 2024, except in Italy, where six herds tested positive. The overall prevalence in DFS zones remained below 0.001%.

In 2024, within the UEP zones, Bulgaria reported a sharp rise in bovine brucellosis cases, with 378 positive cattle herds, compared with 11 in 2023 and two in 2022. This substantial increase drove up the overall number of positive herds in UEP zones. However, these figures should be interpreted with caution, as the data submitted by Bulgaria show considerable year-to-year variation, which may reflect changes in surveillance or reporting practices rather than a consistent trend. In the other four MSs with UEP zones (Greece, Hungary, Italy and Portugal), the number of positive herds remained relatively stable but showed a slight increase overall, from 281 in 2023 to 304 in 2024. Compared with 2020, however, these countries reported a notable 50% reduction in positive herds, from 603 in 2020 to 304 in 2024. By country, Italy reported 258 positive herds (up from 217 in 2023), Greece 40 (up from 35 in 2023) and Portugal six. Over the last decade (2015–2024), the total number of positive cattle herds in UEP zones (excluding Bulgaria) decreased by 67.6%, from 938 in 2015 to 304 in 2024 (Figure 18).

In 2024, no cases of bovine brucellosis were detected in the four non-MSs (Iceland, Liechtenstein, Norway and Switzerland). Among EU candidate countries, Albania reported nine positive herds, Montenegro reported none and the Republic of North Macedonia reported 11 positive herds. Serological surveillance also yielded positive results in several candidate countries: Albania detected 31 seropositive animals out of 1538 tested, the Republic of North Macedonia detected 88 seropositive animals out of 100,533 tested and Serbia detected 18 positive animals out of 425,275 tested.

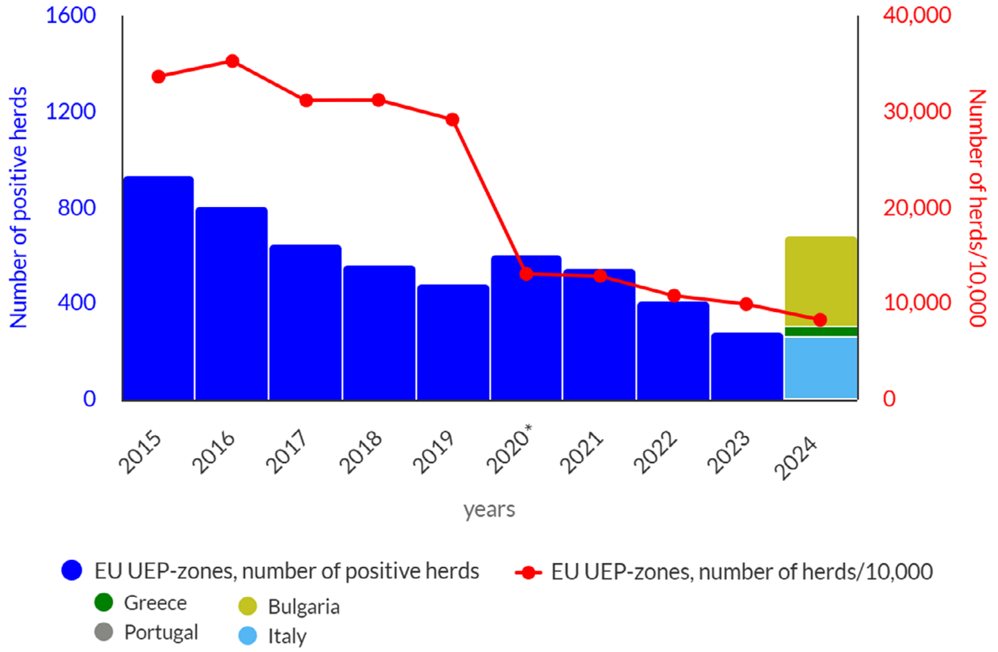

FIGURE 18 Number of *Brucella*-positive cattle herds in zones under an eradication programme (UEP), EU, 2015–2024.

Sheep and goats

In 2024, 21 MSs and the United Kingdom (Northern Ireland) had DFS regarding ovine and caprine brucellosis, while five MSs had UEP zones (Bulgaria, Croatia, Greece, Italy and Portugal). Malta had no official disease status as regards infection with *B. abortus*, *B. melitensis* and *B. suis* in sheep and goats. Bulgaria and Slovakia did not report any data for sheep and goats brucellosis for the year 2024. Two of the five MSs with UEP zones had DFS zones or provinces for sheep and goats:

- Italy: 15 regions and 11 provinces (the Matera province having acquired DFS in 2024, Italy was the only MS reporting an increased number of DFS zones),
- Portugal: one region (the autonomous region of the Azores).

In 2024, the overall proportion of sheep and goat flocks positive for *B. abortus*, *B. melitensis* and *B. suis* remained rare in the EU (0.005%; 47 out of 947,509 flocks).

Within the DFS zones, no positive sheep or goat flocks were reported in 2024, except in Germany (one flock) and Italy (three flocks). The overall prevalence in DFS zones remained below 0.001%.

In the UEP zones of the four reporting non-DFS MSs and Malta, the prevalence of *Brucella*-positive flocks continued to decline, with 43 affected flocks (0.04%) in 2024, down from 141 flocks (0.11%) in 2023 (Figure 19). By country, Italy reported 29 positive flocks (down from 34 in 2023), Greece five (up from three in 2023) and Portugal nine. Croatia and Malta reported no positive flocks.

Over the last decade (2015–2024), the number of positive sheep and goat flocks in UEP zones fell by 96.1%, from 1094 in 2015 to 43 in 2024 (Figure 19), while prevalence decreased by 86.7%, from 0.30% in 2015 to 0.04% in 2024.

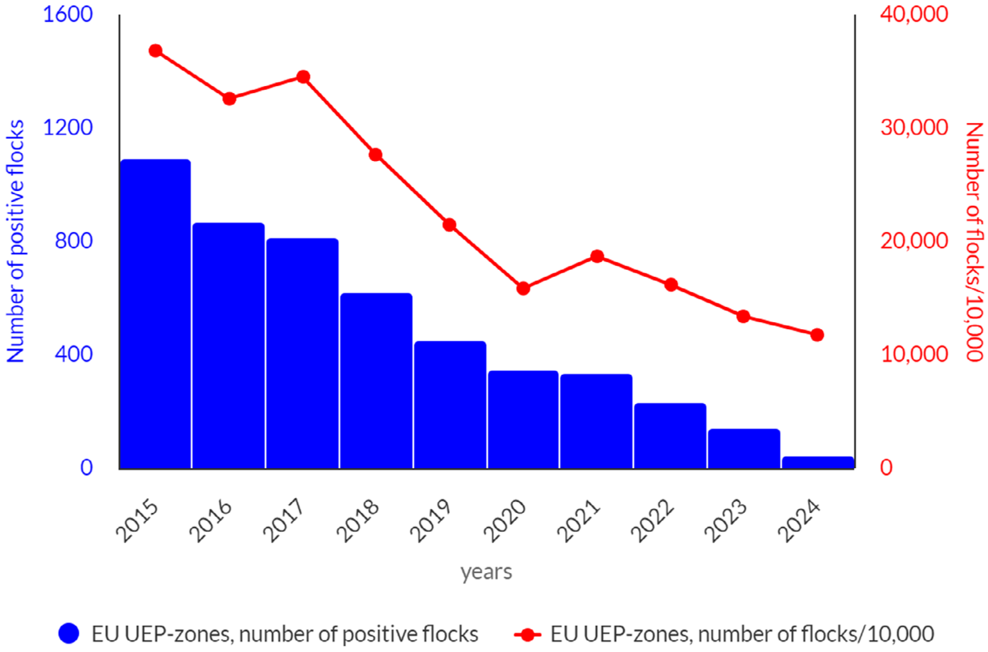

FIGURE 19 Number of *Brucella*-positive sheep and goat flocks, in zones under an eradication programme (UEP), EU, 2015–2024. No data were reported from Bulgaria in 2020, 2023 and 2024. In 2023 and 2024, no disease status was attributed to Malta.

In 2024, no cases of brucellosis were detected in sheep and goat flocks in the following non-MS countries: Iceland, Liechtenstein, Norway and Switzerland. Among EU candidate countries, Albania reported two positive flocks, Montenegro reported none and the Republic of North Macedonia reported 23 positive flocks. In addition, serological monitoring data for ovine and caprine brucellosis showed 3058 seropositive small ruminants out of 493,104 tested in the Republic of North Macedonia and six positive animals out of 1,182,761 tested in Serbia.

Surveillance data for *Brucella* from animals other than cattle, sheep and goats

In 2024, 12 MSs, the United Kingdom (Northern Ireland) and two non-MSs reported a total of 119,909 *Brucella* test results from animal species other than cattle, or sheep and goats. This total also includes records where the analytical testing method was not specified. The majority of tests were performed on pigs (85.7%; *N* = 102,771) and wild boars (12.8%; *N* = 15,351), with smaller numbers reported for deer (0.41%; *N* = 496), dogs (0.36%; *N* = 433) and hares (0.11%; *N* = 135).

In dogs, direct tests (microbiological isolation or polymerase chain reaction methods) did not detect *Brucella* in 247 samples collected from four MSs (Finland, Ireland, Italy and Sweden). Three MSs (Finland, Italy and Sweden) reported 3, 8 and 11 serologically positive dogs, respectively, out of 162 tested animals (13.6%). In pigs, in six MSs (Finland, Germany, Italy, Romania, Sweden and the Netherlands), 5995 direct tests were reported in 2024, with no evidence of the presence of *Brucella* spp. in the different matrices tested. Serological tests (*N* = 81,915) were reported from Bulgaria, Finland, Germany, Italy, Romania and the United Kingdom (Northern Ireland), yielding 19 positive results in samples collected in Germany. In wild boars, in four MSs (Germany, Italy, Romania and Spain), 3580 direct tests were reported in 2024, with evidence of the presence of *Brucella* spp. in Germany (*N* = 1), Italy (*N* = 26) and Spain (*N* = 57) in the different matrices tested. Serological tests (*N* = 11,756) were reported from Finland, Germany, Italy and Romania, yielding five positive results in samples collected from wild boars in Finland and 1529 collected in Germany. *Brucella* spp. was also identified by direct methods from other wildlife, such as three marine mammals and one hare in Italy, and one roe-deer in Spain, out of 971 tested.

A6.4 | Discussion

The notification rates of brucellosis in the EU remained stable at 0.03 cases per 100,000 population in 2020 and 2021 before rising to 0.05 in 2022 and peaking at 0.06 in both 2023 and 2024, indicating a gradual upward trend over the 5-year period considered. Similarly, confirmed human cases in the EU increased significantly from 2020 to 2024. However, the number of cases and notification rates remained at or below the pre-pandemic levels observed in 2019. This apparent increasing trend is likely an artefact of the pandemic's impact on surveillance data since 2020, rather than evidence of a genuine rise in case numbers. Since the trend analysis was initiated in 2020, when surveillance for many diseases was heavily affected by the pandemic, an increasing trend is expected to be observed between 2020 and 2024, as countries resumed standard surveillance practices post-pandemic. The observed upward trend may thus reflect a normalisation of data collection rather than an actual increase in disease incidence.

Portugal, which reported the second highest notification rate, conformed to this pattern, with reported cases and notification rates in 2024 remaining stable or below 2019 levels despite a 5-year upward trend. This aligns with the EU-wide context, where COVID-19-related surveillance limitations likely influenced the perceived increase. Nonetheless, brucellosis remains a public health concern in Portugal, where the 2024 notification rate (0.17 per 100,000 population) was nearly threefold the EU average.

Similar to previous years, Greece reported the highest notification rate in 2024, which was more than six times higher than the EU/EEA average. Germany, Italy, Spain and Greece collectively accounted for most EU cases, with Greece, Italy and Portugal yet to achieve DFS for brucellosis in their bovine, and ovine and caprine populations. Despite ongoing animal control efforts, the disease remains endemic in these countries or persists in their non-disease-free zones.

Notably, Germany and the Netherlands recorded their highest notification rates and number of brucellosis cases since EU-wide surveillance began. Most cases in these countries were reported to be travel related, which was also the case in Slovakia and Sweden, which jointly reported the fourth highest notification rate in the EU in 2024. When travel destinations were documented for cases in these countries, most infections were linked to travel outside the EU. Indeed, among all imported brucellosis cases reported among all countries in the EU in 2024, almost half were acquired in Iraq, Türkiye and Bosnia and Herzegovina. Disease incidence may be higher among migrants who have recently arrived from regions where brucellosis is endemic, including the Middle East, parts of Africa, Asia and Central and South America (Georgi et al., 2017).

The number of infections reported as having been acquired within the EU increased in 2024 to 127 cases, representing a rise of around 90% relative to the annual average of 67 cases reported between 2020 and 2023. This increase was driven by a few countries; Italy provided information on the importation status of their 2024 cases for the first time, while Greece, Portugal and Spain reported higher numbers of domestic cases than in previous years. In Spain, improved brucellosis surveillance may partly explain the increase in reported domestic cases, along with more complete data distinguishing whether cases were domestic or travel-related. Spain achieved eradication of brucellosis in sheep and goats and in bovine animals respectively in 2021 and 2022 (EFSA and ECDC, 2022a, 2023) Food-borne exposure remains a potential source of infection. This mainly affects individuals consuming unpasteurized milk or dairy products from countries where brucellosis is endemic (BfR, 2023; Ramos et al., 2008). Indeed, bovine, ovine and caprine brucellosis have been largely eradicated in most EU MSs. Consequently, brucellosis is now rare in northern and western Europe, where most cases are linked to travel outside the EU (ECDC, 2024).

Human brucellosis cases also show a seasonal trend, with case numbers typically peaking between May and August. This pattern is likely related to increased human exposure to infected animals and animal products during the warmer months. This coincides with livestock birthing seasons and related farming activities. Consumption of unpasteurized milk and dairy products, which are known transmission routes of brucellosis, also tend to rise during spring and early summer. Travel may also contribute to this seasonal pattern as many cases, in northern and western Europe in particular, are linked to travel outside the EU to regions where brucellosis is endemic.

As in previous years, species information was available for only 35.5% of human brucellosis cases reported in 2024, representing a relatively low proportion of the total. Among the cases with species identified, the vast majority (90.7%) were attributed to *B. melitensis*. Since 2020, *B. melitensis* has consistently accounted for at least 90% of identified cases each year. This finding is relevant for risk management, as *B. melitensis* is primarily associated with infections in sheep and goats. Expanding species identification for human cases would significantly enhance the understanding of brucellosis epidemiology and support more targeted control measures.

From an animal health perspective, most EU MSs have eradicated bovine, ovine and caprine brucellosis. In DFS areas, only a few infected herds or flocks were reported in 2024: six infected cattle herds and four infected sheep and goat flocks.

Nevertheless, some MSs—most notably Bulgaria and Greece—and certain UEP areas in Italy and Portugal have not yet achieved official DFS status, with infections persisting in both cattle and small ruminants. Surveillance intensity varied substantially between countries, making direct comparisons of infection prevalence challenging. For example, Greece conducted only limited testing of herds and flocks, which may reduce the reliability of its surveillance data. Bulgaria reported a sharp increase in the number of *Brucella*-positive cattle herds and did not submit data for sheep and goats, limiting the ability to fully assess disease dynamics. This increase should be interpreted with caution, as the Bulgarian data show marked year-to-year variability, which may reflect changes in surveillance or reporting practices rather than a consistent epidemiological trend.

In Italy, infections remained concentrated in the southern regions, particularly in water buffalo populations in the Caserta province (Ottaiano et al., 2024), where the prevalence and incidence of infection have remained high in recent years, with a low genetic diversity among *B. abortus* isolates from this species (Orrù et al., 2024). Importantly, in UEP zones, brucellosis transmission to humans can still occur through direct contact with infected animals rather than only through food-borne routes. Individuals working with livestock – such as farmers, breeders, butchers, slaughterhouse workers and veterinarians – therefore still remain at elevated occupational risk in endemic regions, as reported in the past (De Massis et al., 2005).

Despite limited testing, several Balkan EU candidate countries, including Albania, the Republic of North Macedonia and Serbia, continue to report brucellosis cases in cattle, and in sheep and goats, indicating the persistence of the disease in parts of south-eastern Europe. Reports of human cases imported from these areas (Schaeffer et al., 2021) highlight the need to strengthen animal brucellosis surveillance and control programmes.

In 2024, over 119,000 *Brucella* tests from non-traditional livestock species were reported across the EU, the United Kingdom (Northern Ireland), and five non-MSs. Most samples came from pigs and wild boars, with rare occurrence in pigs and moderate occurrence in wild boars. Limited positivity was also detected in isolated wildlife, suggesting a possible low but ongoing circulation of *Brucella* spp. outside cattle, sheep and goats.

Despite limited reporting on testing for canine brucellosis, there are still concerns about the emerging zoonotic potential of the disease in dogs (Djokic et al., 2023). Such cases highlight the importance of enhancing canine brucellosis diagnostics and of strengthening importation controls to prevent disease introduction.

In conclusion, the observed increase in the reported incidence of brucellosis in humans in the EU may reflect a normalisation of data collection following the pandemic. In livestock, brucellosis continues to decline, but the disease remains an animal health concern with public health relevance in southern European and Balkan countries that have not yet achieved DFS. Strengthening surveillance, expanding testing coverage and implementing targeted control measures in ruminants will be essential to further reduce transmission risks and progress towards eradication within a One Health framework. In addition, many human cases reported in the EU continue to be linked to travel or exposure outside the EU in regions where brucellosis remains endemic.

A7 | *TRICHINELLA*

Human cases [EU, 2024]

Notification rate *(per 100,000 population)* **0.02**

102 **Cases of illness**

23 **Infections acquired in the EU**

1 **Infection acquired outside the EU**

78 **Unknown travel status or unknown country of infection**

19 **Hospitalisations** (38.0%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

🟩 *ECDC data*

Foodborne outbreaks & related cases [EU, 2024]

6 **Foodborne outbreaks**

5 **Strong-evidence outbreaks** 🟧

1 **Weak-evidence outbreaks** 🟧

67 **Cases of illness**

35 **Hospitalisations** (52.2%)*

** The percentages are calculated on the number of cases with information available (for further details see Table 2)*

N of outbreaks		N of outbreaks per 100,000 population **		N of outbreak cases per 100,000 population	
Austria	0	AT	0	AT	0
Belgium	0	BE	0	BE	0
Bulgaria	0	BG	0	BG	0
Croatia	0	HR	0	HR	0
Cyprus	0	CY	0	CY	0
Czechia	0	CZ	0	CZ	0
Denmark	0	DK	0	DK	0
Estonia	0	EE	0	EE	0
Finland	0	FI	0	FI	0
France	0	FR	0	FR	0
Germany	0	DE	0	DE	0
Greece	0	EL	0	EL	0
Hungary	0	HU	0	HU	0
Ireland	0	IE	0	IE	0
Italy	1	IT	0.002	IT	0.007
Latvia	0	LV	0	LV	0
Lithuania	0	LT	0	LT	0
Luxembourg	0	LU	0	LU	0
Malta	0	MT	0	MT	0
Netherlands	0	NL	0	NL	0
Poland	0	PL	0	PL	0
Portugal	0	PT	0	PT	0
Romania	3	RO	0.016	RO	0.226
Slovakia	0	SK	0	SK	0
Slovenia	0	SI	0	SI	0
Spain	2	ES	0.004	ES	0.041
Sweden	0	SE	0	SE	0
UK (N. Ireland)	0	XI	0	XI	0

Implicated food vehicles
(Strong-evidence outbreaks)

Top food vehicles

Pig meat and products thereof
3 Outbreaks

Meat and meat products, unspecified
1 Outbreak

Other or mixed red meat and products thereof
1 Outbreak

*** Differences among countries shall be interpreted with caution as this indicator depends on several factors including the type of outbreaks under surveillance and does not necessarily reflect the level of food safety in each country.*

🟧 *EFSA data*

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about *Trichinella* and for the consultation of data collected, the following interactive tools are available:

A7.1 | Key facts

- In 2024, there were 102 confirmed cases of human trichinellosis, corresponding to a European Union notification rate of 0.02 cases per 100,000 population, the same notification rate as in 2023.
- The overall notification rate for trichinellosis did not exceed 0.03 cases per 100,000 population in 2020–2024.
- In 2024, one MS (Croatia) reported *Trichinella* presence in two pork-based fermented sausages. *Trichinella spiralis* was identified in both samples.
- No *Trichinella* infections were reported in over 26 million domestic pigs raised under controlled housing conditions recognised by the competent authorities in the EU. Similarly, no positive cases were detected among approximately 70 million pigs raised under controlled housing conditions not officially recognised.
- Among domestic pigs not raised under controlled housing conditions and tested in the European Union in 2024, 30 out of more than 41 million (0.00007%) were positive for *Trichinella*. Positive findings were reported by Bulgaria (one case), France (four cases) and Romania (25 cases).
- Of the nine reporting MSs, two (Finland and Spain) detected *Trichinella* in farmed wild boar, with 2 positive cases among 4920 animals tested (0.04%).
- No *Trichinella* infections were reported among the 215,835 domestic solipeds tested in the EU in 2024.
- In 2024, the proportions of *Trichinella*-positive hunted wild boar and foxes (used as indicator animals) were 0.08% and 0.81%, respectively, compared to 0.07% and 1.8% in 2023.

A7.2 | Surveillance and monitoring of *Trichinella* in the EU

A7.2.1 | Humans

For 2024, 26 EU MSs reported information on trichinellosis in humans. The surveillance of *Trichinella* infections is mandatory in all reporting MSs, except in Belgium and France, where the surveillance systems are voluntary. Denmark has no surveillance system for trichinellosis, and the disease is not notifiable or reported at the EU level. Twenty-three MSs used the EU case definition, while other case definitions were used by three MSs. The surveillance systems cover the whole population in all MSs reporting trichinellosis data. All countries reported case-based data except Bulgaria, which reported aggregated data.

A7.2.2 | Animals

Trichinella monitoring data for domestic pigs, farmed wild boar and solipeds

In accordance with Commission Implementing Regulation (EU) 2015/1375,[54] all *Trichinella*-susceptible animals intended for human consumption in the EU, i.e. domestic pigs (both fattening and breeding animals), farmed wild boar and solipeds, should be tested for the presence of *Trichinella* larvae in the muscles, unless carcases have undergone a freezing treatment to inactivate the parasite. ISO 18743:2015/Amd 1:2023 (ISO, 2023) or an equivalent method should be used (Commission Implementing Regulation (EU) 2015/1375 and Commission Implementing Regulation (EU) 2025/506[55]). Therefore, data on *Trichinella* infections in these animals are comparable across MSs because the monitoring schemes are harmonised and the data collected and reported to EFSA originate from census sampling (EFSA BIOHAZ Panel, 2013a, 2013b) (Table 1).

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[54] Commission Implementing Regulation (EU) 2015/1375 of 10 August 2015 laying down specific rules on official controls for *Trichinella* in meat. OJ L 212, 11.8.2015, p. 7–34.

[55] Commission Implementing Regulation (EU) 2025/506 of 19 March 2025 amending Annex I to Implementing Regulation (EU) 2015/1375 as regards the reference method and the authorisation of lumiVAST *Trichinella* as an equivalent method for detection of *Trichinella* in meat of domestic swine. OJ L, 20.3.2025, p. 1–3.

Domestic pigs, farmed and hunted wild boar and other wild animals (e.g. bears) that are not processed to be placed on the EU market (e.g. those intended for own consumption) are exempted from Commission Implementing Regulation (EU) 2015/1375, and their control falls under national legislation. Commission Implementing Regulation (EU) 2015/1375 states that the reporting of data for domestic pigs shall, at least, provide specific information related both to the number of animals tested that were raised under controlled housing conditions and to the number of breeding sows, boar and fattening pigs tested. Furthermore, the regulation states that negligible risk status for a country or region is no longer recognised.

Since 2022, when reporting *Trichinella* monitoring results for domestic pigs, MSs have been required to indicate whether the animals were raised under controlled housing conditions recognised by the CA or not. In addition, MSs may voluntarily specify whether the pigs were raised under controlled housing conditions not recognised by the CA or whether they were not raised under controlled housing conditions. If *Trichinella*-positive results are reported, it is mandatory to indicate whether the pigs were raised indoors or outdoors.

***Trichinella* monitoring data for animals other than domestic pigs, farmed wild boar and solipeds**

MSs should monitor the circulation of *Trichinella* in the main natural reservoir hosts (carnivorous and omnivorous animals) to gather information on the risk of transmission to domestic animals, and subsequently to humans, as well as on the potential introduction of new *Trichinella* species from non-MSs. However, the monitoring data provided by MSs to EFSA are generated through non-harmonised schemes and are not subject to mandatory reporting requirements. Wild animals are the primary reservoir hosts of *Trichinella*, but their biology and ecology vary significantly between MSs and even within regions or habitats of the same MS, due to human and environmental impacts on ecosystems. These variations result in differing transmission patterns and infection prevalence rates. Consequently, data on *Trichinella* in wild animals are not fully comparable across MSs. The absence of harmonised monitoring schemes and mandatory reporting requirements means that findings must be interpreted with caution. While these data support the creation of descriptive summaries at the EU level, they do not allow for robust analyses such as assessments of temporal or spatial trends (Table 1).

A7.3 | Results

A7.3.1 | Overview of key statistics, EU, 2020–2024

Table 43 summarises EU-level statistics on human trichinellosis and *Trichinella* in animals for 2020–2024. More detailed descriptions of these statistics are provided in the subsections below and in the chapter on food-borne outbreaks.

TABLE 43 Summary of *Trichinella* statistics relating to humans (2020–2024), domestic pigs (2023–2024) and other main animal species (2020–2024), EU.

	2024	2023	2022	2021	2020	Data source
Humans						
Total number of confirmed cases	102	80	39	77	117	ECDC
Total number of confirmed cases/100,000 population (notification rate)	0.02	0.02	0.01	0.02	0.03	ECDC
Number of reporting MSs	26	26	26	26	26	ECDC
Infections acquired in the EU	23	72	25	29	99	ECDC
Infections acquired outside the EU	1	4	1	2	2	ECDC
Unknown travel status or unknown country of infection	78	4	13	46	16	ECDC
Number of outbreak-related cases	67	31	68	2	119	EFSA
Total number of outbreaks	6	3	7	1	6	EFSA
Animals[a]						
Domestic pigs raised under controlled housing conditions, recognised by the competent authorities						
Number of units tested	26,239,611	30,653,165	34,183,655	–	–	EFSA
% of positive units	0	0	0		–	EFSA
Number of reporting MSs	9	10	7			EFSA
Domestic pigs (other)						
Controlled housing conditions not recognised by the competent authorities						
Number of units tested	69,848,383	17,806,783	15,644,310		–	EFSA
% of positive units	0	0	0		–	EFSA
Number of reporting MSs	8	7	8	–	–	EFSA
Not controlled housing conditions						
Number of units tested	41,718,136	133,449,395	96,748,782	–	–	EFSA

(Continues)

TABLE 43 (Continued)

	2024	2023	2022	2021	2020	Data source
% of positive units	0.00007	0.00003	0.00007	–	–	EFSA
Number of reporting MSs	19	20	20	–	–	EFSA
Unspecified						
Number of units tested	62,691,540	17,365,718	63,084,065	–	–	EFSA
% of positive units	0	0	0	–	–	EFSA
Number of reporting MSs	6	4	5	–	–	EFSA
Farmed wild boar						
Number of units tested	4920	4726	5372	5755	3922	EFSA
% of positive units	0.04	0	0	0	0	EFSA
Number of reporting MSs	9	8	8	8	6	EFSA
Hunted wild boar						
Number of units tested	1,678,433	1,692,182	1,514,255	1,786,892	1,470,830	EFSA
% of positive units	0.08	0.07	0.08	0.07	0.05	EFSA
Number of reporting MSs	22	21	21	20	21	EFSA
Foxes						
Number of units tested	3442	3731	6652	6776	5764	EFSA
% of positive units	0.81	1.8	0.95	1.6	0.85	EFSA
Number of reporting MSs	7	10	11	11	9	EFSA

Abbreviations: –, Data not reported; ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States.

[a] Units: animals and/or slaughter animal batches.

A7.3.2 | Human trichinellosis

In 2024, 102 confirmed cases of trichinellosis were reported by 11 MSs, which was an increase of 22 cases compared with 2023 (Table 44). The notification rate remained unchanged at 0.02 cases per 100,000 population in both 2023 and 2024, representing an increase from the rate of 0.01 cases per 100,000 population in 2022. Fifteen MSs reported zero cases in both 2024 and 2023 (Table 44).

In 2024, Bulgaria and Romania had the highest notification rates in the EU (0.64 and 0.14 cases per 100,000, respectively), followed by Austria and Latvia (both reported 0.05 cases per 100,000) (Table 42). Bulgaria, Romania and Spain together accounted for more than three-quarters (79.4%) of all confirmed EU cases in 2024.

In 2024, 23 out of 24 cases of trichinellosis with known travel status and known country of infection were reported as having been acquired in the EU. One travel-associated trichinellosis case was reported with a history of travel to China. Most cases had unknown travel status or unknown country of infection (76.5%) (Table 43).

TABLE 44 Reported confirmed human cases of trichinellosis and notification rates per 100,000 population in EU MSs and non-MS countries, by country and year, 2020–2024.

Country	2024				2023		2022		2021		2020	
	National coverage[a]	Data format[a]	Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
			Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	5	0.05	6	0.07	2	0.02	10	0.11	6	0.07
Belgium	Y	C	0	0	0	0	0	0	0	0	–	–
Bulgaria	Y	A	41	0.64	1	0.02	9	0.14	29	0.44	13	0.20
Croatia	Y	C	0	0	1	0.03	0	0	17	0.44	0	0
Cyprus	Y	C	0	0	0	0	0	0	0	0	0	0
Czechia	Y	C	0	0	0	0	0	0	0	0	0	0
Denmark[b]	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	0	0	0	0	1	0.08	0	0	0	0
Finland	Y	C	1	0.02	0	0	0	0	0	0	0	0
France	Y	C	0	0	2	< 0.01	15	0.02	2	< 0.01	1	< 0.01
Germany	Y	C	3	< 0.01	3	< 0.01	0	0	2	< 0.01	1	< 0.01
Greece	Y	C	0	0	0	0	0	0	0	0	0	0

TABLE 44 (Continued)

	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
Country	National coverage[a]	Data format[a]	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Hungary	Y	C	0	0	0	0	0	0	0	0	0	0
Ireland	Y	C	0	0	0	0	0	0	0	0	0	0
Italy	Y	C	5	0.01	12	0.02	4	0.01	0	0	79	0.13
Latvia	Y	C	1	0.05	8	0.42	3	0.16	7	0.37	1	0.05
Lithuania	Y	C	1	0.03	1	0.03	0	0	1	0.04	0	0
Luxembourg	Y	C	0	0	0	0	0	0	0	0	0	0
Malta	Y	C	0	0	0	0	0	0	0	0	0	0
Netherlands	Y	C	0	0	0	0	0	0	0	0	0	0
Poland	Y	C	3	0.01	5	0.01	1	< 0.01	2	0.01	11	0.03
Portugal	Y	C	0	0	0	0	0	0	0	0	0	0
Romania	Y	C	26	0.14	23	0.12	4	0.02	6	0.03	4	0.02
Slovakia	Y	C	2	0.04	0	0	0	0	0	0	0	0
Slovenia	Y	C	0	0	0	0	0	0	0	0	0	0
Spain[c]	Y	C	14	0.03	18	0.04	0	0	1	–	1	–
Sweden	Y	C	0	0	0	0	0	0	0	0	0	0
EU Total			**102**	**0.02**	**80**	**0.02**	**39**	**0.01**	**77**	**0.02**	**117**	**0.03**
Iceland	Y	C	0	0	0	0	0	0	0	0	0	0
Liechtenstein	Y	C	0	0	0	0	0	0	0	0	–	–
Norway	Y	C	0	0	0	0	0	0	0	0	0	0
Switzerland[d]	Y	C	0	0	2	0.02	4	0.05	0	0	4	0.05

Abbreviation: –, Data not reported.

[a] Y: yes; N: no; A: aggregated data; C: case-based data.

[b] No surveillance system.

[c] Data incomplete for 2020–2021, rate not estimated.

[d] Switzerland provided data directly to EFSA. The human data for Switzerland include data from Liechtenstein for 2020.

Between 2015 and 2024, the number of confirmed trichinellosis cases in the EU increased during the winter months (Figure 20).

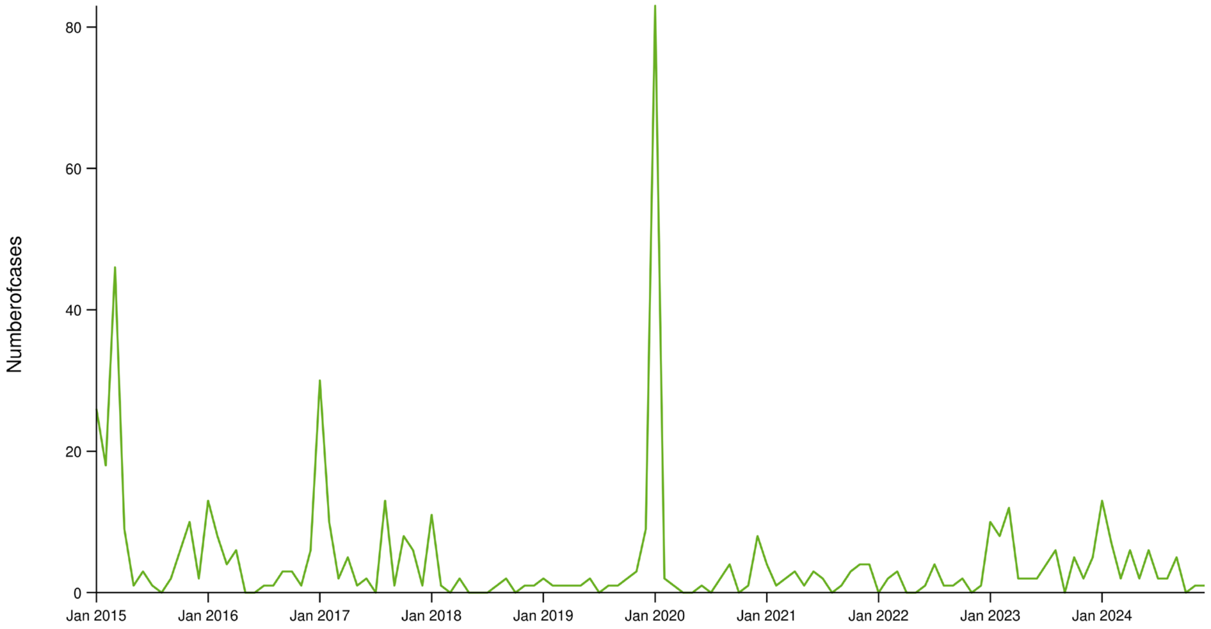


FIGURE 20 Number of confirmed human cases of trichinellosis in the EU by month and year, 2015–2024.
Source: Austria, Germany, Estonia, Greece, Finland, Hungary, Italy, Latvia, Lithuania, Poland, Portugal, Romania, Slovakia, Sweden and Slovenia.

Trichinella spiralis was identified as the causative agent in 28 of 102 confirmed human cases (27.5%) reported by six MSs.

In 2024, 67 human cases of trichinellosis linked to six food-borne outbreaks (FBOs) were reported to EFSA by three MSs: Italy (1), Romania (3) and Spain (2). Of these, four outbreaks were attributed to *T. spiralis*, while for two outbreaks, the species was not specified. In five strong-evidence outbreaks, 'meat and meat products' were identified as the implicated food vehicles. The three largest outbreaks, all caused by *T. spiralis*, were reported by Romania (two FBOs with 21 and 15 cases, respectively) and Spain (one FBO with 13 cases).

A7.3.3 | *Trichinella* infection in food and animals

In 2024, one MS (Croatia) reported *Trichinella* presence in two pork-based fermented sausages. *Trichinella spiralis* was identified in both samples.

During the same reporting year, 30 countries, including 26 MSs, the United Kingdom (Northern Ireland) and three non-MSs (Iceland, Norway and Switzerland), submitted data on *Trichinella* in domestic animals (pigs and/or farmed wild boar) (Table 43). Eight MSs (Belgium, Bulgaria, Denmark, Estonia, Finland, France, Italy and Lithuania) and the United Kingdom (Northern Ireland) reported data on pigs raised under controlled housing conditions recognised by the CA ($N = 26{,}239{,}611$); no positive cases were detected. Eight MSs (Bulgaria, Czechia, Estonia, Ireland, Italy, Portugal, Romania and Spain) and one non-MS (Iceland) provided data on pigs raised under controlled housing conditions not recognised by the CA ($N = 69{,}848{,}383$ and 76,715, respectively); no positive findings were reported. Data on pigs not raised under controlled housing conditions were provided by 18 MSs and the United Kingdom (Northern Ireland), covering a total of 41,718,136 animals (Table 43). This included 34,258,646 fattening pigs, 7,234,838 breeding pigs and 224,652 mixed herds. In addition, two non-MSs (Norway and Switzerland) reported testing 3,822,970 animals belonging to the same housing category. A total of 30 positive cases (0.00007%) were reported by three MSs (Bulgaria, France and Romania). Bulgaria reported one positive outdoor pig from a mixed herd, France reported four positive outdoor pigs from mixed herds, and Romania reported 25 positive fattening indoor pigs (Table 45). No positive findings were reported from breeding pigs. Species identification was successfully performed for 26 out of 30 pigs (86.6%). Among these, *T. spiralis* was detected in 11 cases (42.3%) and *T. britovi* in 15 cases (57.7%). Consistent with previous years, *Trichinella* infections were observed exclusively in pigs not raised under controlled housing conditions.

Data on farmed wild boar were reported by nine MSs (Austria, Denmark, Finland, France, Germany, Greece, Italy, the Netherlands and Spain) (Table 43). Two positive findings out of 4920 animals tested (0.04%) were reported by two MSs (Finland and Spain). *Trichinella nativa* was identified in one of the two animals, while species identification was not reported for the other.

TABLE 45 Positive *Trichinella* monitoring results for domestic pigs not raised under controlled housing conditions, in reporting EU MSs and non-MS countries, 2024.

	***N* positive/tested (% positive)**	
	Not controlled housing conditions (NCHC)	
Country	**Fattening pigs**	**Mixed herd pigs**
Bulgaria[a]	–	1/735 (0.1)
France[a]	–	4/22,914 (0.02)
Romania[b]	25/184,929 (0.01)	–
EU Total (27 + XI)	**25/34,258,646 (0.00007)**[c]	**5/224,652 (0.002)**[c]
Total non-MSs	**0/1,600,001 (0)**[c]	**0/2,222,969 (0)**[c]
Total EU (27+ XI) + non-MSs	**25/35,858,647 (0.00007)**[c]	**5/2,447,621 (0.0002)**[c]

Note: Grey shaded cell indicates no positive results.

[a] Outdoor pigs.

[b] Indoor pigs.

[c] Total *N* tested includes samples from countries not reported in the table where no positive monitoring results were documented (*N* positive) but where they still contributed to the total animals sampled (*N* tested).

In 2024, no *Trichinella* infections were reported among the 215,835 domestic solipeds tested in 20 MSs, nor among the 7489 tested in three non-MSs (Iceland, Norway and Switzerland). This confirmed the trend observed over the 2013–2023 period.

TABLE 46 Positive *Trichinella* monitoring results for hunted wild boar, wild boar with unspecified habitat and foxes, in reporting EU MSs and non-MS countries, 2024.

	***N* positive/tested (% positive)**	
Country	**Hunted or unspecified wild boar**	**Foxes**
Austria	–	2/52 (3.8)
Bulgaria	137/8515 (1.6)	–
Croatia	69/45,502 (0.15)	–
Estonia	42/4866 (0.86)	–
Finland	1/962 (0.10)	23/84 (27.4)
France	2/46,062 (0.004)	–
Germany	6/464,134 (0.001)	–
Italy	20/227,027 (0.01)	2/2189 (0.09)
Latvia	10/6899 (0.14)	–
Poland	274/233,246 (0.12)	–
Romania	36/6611 (0.54)	–
Slovenia	–	1/282 (0.35)
Spain	680/182,549 (0.37)	–
Sweden	3/125,022 (0.002)	–
EU Total (27 + XI)	**1280/1,678,433 (0.08)**[a]	**28/3442 (0.81)**[a]
Republic of North Macedonia	11/3199 (0.34)	–
Total non-MSs	**11/11,411 (0.1)**[a]	**0/1 (0)**[a]
Total EU (27+ XI) + non-MSs	**1291/1,689,844 (0.08)**[a]	**28/3443 (0.81)**[a]

Note: Grey shaded cell indicates no positive results.

[a] Total *N* tested includes samples from countries not reported in the table where no positive monitoring results were documented (*N* positive) but where they still contributed to the total animals sampled (*N* tested).

Trichinella monitoring data on hunted or unspecified wild boar were reported by 22 MSs and three non-MSs (Norway, Republic of North Macedonia and Switzerland). Positive findings were reported only by 12 MSs and the Republic of North Macedonia, for a total of 1291 positive out of 1,689,844 animals tested (0.08%) (Table 46). Species identification was provided for 106 wild boar (8.2%), revealing *T. spiralis* in 29 animals (27.3%) and *T. britovi* in 77 (72.6%). For the remaining 1185 animals (91.7%), species identification was not reported.

A total of 3443 fox (*Vulpes vulpes*) specimens were tested in six MSs (Austria, Finland, Germany, Italy, Luxembourg and Slovenia) and the United Kingdom (Northern Ireland) and in one non-MS (Switzerland) (Table 43). *Trichinella* infections were reported only by four MSs (Austria, Finland, Italy and Slovenia) with a total of 28 positive results (0.81%) (Table 46). Among the 28 positive foxes, *T. britovi* was identified in five cases (17.8%) and *T. nativa* in one case (3.5%). Species identification was not provided for the remaining 22 animals (78.5%).

Among other sentinel wildlife species, the highest proportions of *Trichinella*-positive cases were found in raccoon dogs (25.9%), lynxes (15.5%) and wolves (13.6%). In Finland and Italy, 170 raccoon dogs were tested, with 44 positive results. In the same countries, 610 wolves were tested, of which 83 were positive. In Finland and Switzerland, 116 lynxes were tested, with 18 positive results. However, these species have relatively small populations and limited geographical ranges, mostly confined to a few European countries, which may affect the representativeness of the findings.

A7.4 | Discussion

Trichinellosis is a severe but rare human disease reported by 11 EU MSs in 2024. One hundred and two human cases were reported in 2024. The notification rate remained unchanged at 0.02 cases per 100,000 population in both 2023 and 2024, representing an increase from the rate of 0.01 cases per 100,000 population in 2022. In 2024, 15 of 26 MSs reported zero cases, including three MSs (Cyprus, Luxembourg and Malta) that have never reported any trichinellosis cases to EpiPulse Cases (formerly TESSy).

Between 2020 and 2024, the EU notification rate of trichinellosis did not exceed 0.03 cases per 100,000 population. The highest rate (0.03) was reported in 2020, linked to a food-borne outbreak in Italy caused by *T. britovi* (Stroffolini et al., 2022). The lowest rate (0.01) was reported in 2022. Similar to previous years, Romania and Spain accounted for a large proportion of cases in 2024, and together with Bulgaria, these countries represented more than three-quarters (79.4%) of all confirmed EU cases in 2024. As in previous years, *T. spiralis* was the most frequently identified causative species (27.5% of confirmed human cases).

In general, *Trichinella* infections in humans are often linked to FBOs; therefore, the number and size of FBOs have affected the number of trichinellosis cases reported in the EU each year. In 2024, six *Trichinella* FBOs were reported by three

MSs: Italy, Romania and Spain. Romania accounted for half of these (three FBOs), where *Trichinella* was the most frequently reported causative agent of FBOs. Discrepancies between the number of FBO-related human cases reported to EFSA and the confirmed human cases of trichinellosis reported to EpiPulse arise from differences in case classification between the two reporting systems.

In 2024, nearly 200 million pigs were tested for the presence of *Trichinella* spp. across MSs, out of over 220 million pigs slaughtered (European Commission, 2025). Only 30 animals tested positive, corresponding to approximately 0.15 cases per million slaughtered pigs, and an overall prevalence of just 0.000015%. Positive findings were limited to three MSs (Bulgaria, France and Romania), and all occurred in pigs not raised under controlled housing conditions. Specifically, Bulgaria and France reported one and four positive outdoor pigs, respectively, while Romania documented 25 positive indoor pigs from backyard farms. Eight MSs and the United Kingdom (Northern Ireland) submitted data for pigs raised under controlled housing conditions recognised by the CA, and eight reported data on pigs raised under controlled housing conditions not recognised by the CA. In both groups, no positive cases were detected, confirming that controlled housing conditions continue to be an effective preventive measure against this zoonosis. In the EU, *Trichinella*-infected pigs are predominantly found in MSs with a high prevalence of backyard and free-range pig farming systems, although sporadic cases have been reported in other regions as well (Pozio, 2014). In 2024, species-level identification of *Trichinella* larvae isolated from the positive pigs showed a prevalence for *T. britovi* (57.7%) higher than for *T. spiralis* (42.3%). This finding deviates from the commonly observed epidemiological pattern, in which the prevalence of *T. spiralis* in pigs typically exceeds that of *T. britovi* (Marucci et al., 2022; Pozio et al., 2009). No cases of infection with *T. pseudospiralis* were reported in 2024, in accordance with the low prevalence of this species in Europe, especially in pigs (Pozio, 2016). In particular, 2024 also included the detection of *Trichinella*-positive farmed wild boar (0.04%). This positive finding highlights the importance of continued monitoring of farmed wild boar, as recommended by the EFSA BIOHAZ Panel (EFSA BIOHAZ Panel, 2013b).

Since 2015, hunted wild boar meat has become the principal source of trichinellosis in the EU, according to data reported to EpiPulse Cases (formerly TESSy), replacing domestic pig meat. Human infection is primarily linked to the consumption of undercooked or untested wild boar meat, and the risk increases when hunters and consumers are unaware of safe meat-handling practices, including inspection and proper cooking. Wild boar represent a key reservoir for *Trichinella* spp. in the sylvatic cycle. Other wildlife species, such as foxes and scavengers, may also become infected by feeding on contaminated carcases. Human behaviour plays a pivotal role in the parasite's transmission dynamics: for instance, carcases left in forests by hunters or animals killed in road accidents can be scavenged by wildlife, perpetuating the parasite in natural ecosystems. Improper disposal of animal remains therefore contributes to environmental contamination. Addressing these risks requires sustainable hunting practices, responsible carcase management and coordinated surveillance efforts. In addition to wild boar and pigs, continued monitoring of other animal species remains essential. No positive cases of *Trichinella* spp. infection were reported in solipeds in 2024. Over the past 12 years, not a single infected horse has been detected among more than 1.7 million animals tested in the EU (EFSA and ECDC, 2015, 2016, 2017, 2018, 2019, 2021a, 2021b, 2022a, 2023, 2024). Nevertheless, sustained vigilance is warranted due to the lack of robust traceability systems (EFSA BIOHAZ Panel, 2013a), particularly since horse meat is consumed raw in some EU countries.

Trichinella spp. circulate widely among European wildlife, though prevalence varies with region and sampling intensity. Negative results may reflect limited survey coverage, small sample sizes or environmental conditions that do not favour transmission. In addition to horses, herbivores such as beavers and moose can serve as accidental hosts (Kärssin et al., 2021; Różycki et al., 2020). In 2024, five of 72 beavers sampled in Latvia tested positive, although the *Trichinella* species could not be identified. Surveillance in these species is particularly relevant in areas of high sylvatic endemicity or when convenience sampling is applied. Foxes, widely used as indicator species, remain the main natural reservoir of *Trichinella* in Europe. In 2024, 0.81% of tested foxes were positive, representing a clear decrease from 1.8% in 2023.

For domestic pigs, the number of MSs reporting data on animals raised under controlled housing conditions recognised by the CA increased from seven in 2022 to nine in 2024. Enhanced slaughterhouse controls for pigs not raised under such conditions, together with improved farmer education and awareness, have likely contributed to reducing parasite biomass in domestic settings and, consequently, the risk of human infection. Nevertheless, high-risk farming practices – such as outdoor, backyard or free-range pig rearing – continue to occur, particularly in rural or less developed areas where veterinary services may be insufficient or absent, and in some cases, veterinary oversight is circumvented (Pozio, 2014; Pozio et al., 2021).

Historical experience shows that socioeconomic disruptions can undermine previously effective control systems, leading to a resurgence of trichinellosis as a public health concern (Cuperlovic et al., 2005; Djordjevic et al., 2003). In addition, growing populations of wild boar and foxes, together with the westward spread of raccoon dogs from eastern Europe and the northward expansion of jackals from south-eastern Europe, may further facilitate *Trichinella* circulation in wildlife reservoirs (Alban et al., 2011; Széll et al., 2013).

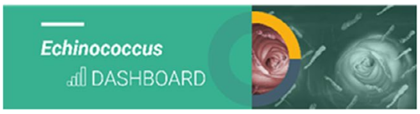
In conclusion, controlling *Trichinella* transmission and safeguarding public health requires a coordinated, sustainable strategy that integrates wildlife ecology, animal husbandry, human behaviour and environmental management. A One Health approach enables such integration by bringing together public health authorities, veterinarians, wildlife experts and environmental agencies to reduce circulation in wildlife, prevent human infections and support safer human–wildlife interactions.

A8 | *ECHINOCOCCUS*

The summary data which make up this chapter, and additional information on related projects and internet sources as well as summary statistics on One-Health Surveillance, are published for this report on the EFSA Knowledge Junction at Zenodo here.

Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases here.

For additional information about *Echinococcus* and for the consultation of data collected, the following interactive tools are available:



A8.1 | Key facts

- In 2024, there were 984 confirmed cases of human echinococcosis, corresponding to a European Union notification rate of 0.22 cases per 100,000 population and an increase of 19.1% compared with 2023 (0.21 cases per 100,000 population).
- In 2024, *Echinococcus granulosus* sensu lato causing cystic echinococcosis accounted for 65.0% of human cases reported with species information, while *E. multilocularis* causing alveolar echinococcosis accounted for 35.0% of cases.
- In 2024, *Echinococcus multilocularis* was detected by 10 Member States and one non-Member State in three different animal categories (i.e. foxes, dogs and wild animals). The animal species most frequently found positive in the European Union were foxes, with 6480 samples collected, and a positivity rate of 14.3%. Czechia, Germany, the Netherlands, Luxembourg, Slovenia and Austria reported the largest proportions of infected foxes among those tested, accounting for 28.3%, 20.8%, 20.0%, 18.9%, 14.6% and 13.5% of positive individuals, respectively.
- In 2024, *Echinococcus granulosus* sensu lato was detected by 11 Member States and one non-Member State in seven different animal categories. Most of the samples tested in the European Union were from sheep and goats (12,134,767), cattle (7,376,568) and pigs (59,233,296), and the proportion of positives was 0.49%, 0.20% and 0.01%, respectively. Italy and Spain accounted for the largest proportions of sheep and goats (2.9% and 0.30%), cattle (0.26% and 0.39%) and pigs (0.04% and 0.01%) that tested positive, respectively.
- Data from Finland, Ireland, Malta, the United Kingdom (Northern Ireland) and mainland Norway confirmed the free status of these countries for *E. multilocularis* in 2024 in accordance with Commission Delegated Regulation (EU) 2018/772.

A8.2 | Surveillance and monitoring of cystic and alveolar echinococcosis in humans and animals in the EU

A8.2.1 | Humans

For 2024, 26 Member States (MSs) reported information on echinococcosis infections in humans. Surveillance is mandatory in 23 MSs and voluntary in three (Belgium, France and the Netherlands). Denmark does not have a surveillance system for echinococcosis. The EU case definition was used by 23 countries; Germany and Italy reported cases using a different case definition, and France did not specify which case definition was used. All MSs except Belgium have comprehensive surveillance systems. The surveillance systems for echinococcosis cover the whole population in all MSs where surveillance systems are in place. All countries reported case-based data except Bulgaria and the Netherlands, which reported aggregated data.

Alveolar echinococcosis (AE) caused by the tapeworm *Echinococcus multilocularis* and cystic echinococcosis (CE) caused by *Echinococcus granulosus* sensu lato (*s.l.*) are listed under the common disease name 'echinococcosis' in the EU case definition, thus making no distinction between the two diseases. Alveolar and cystic echinococcosis can be reported by species and, as of 2019 (2018 data), by clinical presentation of the disease in the ECDC EpiPulse Cases (formerly TESSy) database.

A8.2.2 | Animals

Surveillance of *E. multilocularis* in Europe is usually carried out voluntarily, except in the reporting countries claiming to be free of this parasite per Commission Delegated Regulation (EU) 2018/772.[56] Surveillance is mainly carried out in red foxes,

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[56] Commission Delegated Regulation (EU) 2018/772 of 21 November 2017 supplementing Regulation (EU) 576/2013 of the European Parliament and of the Council with regard to preventive health measures for the control of *Echinococcus multilocularis* infection in dogs and repealing Delegated Regulation (EU) 1152/2011 C/2017/7619 OJ L130, 28.5.2018, pp. 1–10.

Europe's main definitive host. In 2024, Finland, Ireland, mainland Norway (Svalbard archipelago excluded) and the United Kingdom (Northern Ireland) demonstrated the absence of *E. multilocularis* through the implementation of an annual surveillance programme in compliance with Commission Delegated Regulation (EU) 2018/772 (EFSA, 2024a). In accordance with this regulation, Malta is not required to implement a surveillance programme due to the absence of the definitive host (red fox) on its territory.

In all other MSs, data on *E. multilocularis* depend on whether findings are notifiable, monitoring is in place or studies on *E. multilocularis* are performed. Data on *E. multilocularis* in animals vary geographically across and within countries and over time, depending on the sampling effort, and it is therefore challenging to compare reported cases of *E. multilocularis* within and between countries. In accordance with Commission Implementing Regulation (EU) 2020/2002,[57] disease-free EU MSs must notify outbreaks of infection with *E. multilocularis* in canidae to the EU ADIS.[58] Human AE country-based incidences in Europe during 1997–2023 were reported recently (Casulli et al., 2025).

Surveillance of *E. granulosus s.l.* is carried out in livestock intermediate hosts during slaughterhouse inspections. Necropsies on sheep livers and lungs are performed to detect the presence of parasitic cysts. In contrast, methods based on polymerase chain reaction (PCR) methods are used to confirm and identify genotype/species belonging to the *Echinococcus* genus (Siles-Lucas et al., 2017). Although Commission Delegated Regulation (EU) 2018/772 is in force for *E. multilocularis*, no specific EU regulation is in place for detecting *E. granulosus s.l.* in animals or humans. Surveillance of the latter parasite, therefore, depends on national regulations. Approximate geographical distribution of *E. granulosus s.l.* species causing human CE as well as country-based incidences during 1997–2021 in Europe were reported recently (Casulli et al., 2022; Casulli et al., 2023).

One-Health Surveillance

Under the One-Health grant agreements linked to EU4H-2022-DGA-MS-IBA3, three MSs (Croatia, Italy and Poland) carry out surveillance activities for *E. granulosus s.l.* The 2024 animal data on *E. granulosus s.l.*, collected under the above-mentioned grant agreements, have been aggregated by EFSA at the same level as the zoonoses data. Specifically, the 2024 One-Health surveillance data were summarised into the report and discussed where notable decreases were observed in the 2024 zoonoses data for these pathogens compared to previous years.

A8.3 | Results

A8.3.1 | Overview of key statistics, EU, 2020–2024

Table 47 summarises EU-level statistics aggregated by year for echinococcosis (CE and AE) in humans and *E. granulosus s.l.* and *E. multilocularis* in their most relevant definitive and intermediate animal hosts in 2020–2024. More detailed descriptions of these statistics are provided in the subsections below. In the analysis of the data from animals, samples reported positive for *Echinococcus* spp. without species-level identification were interpreted using a contextual strategy based on host specificity and geographic endemicity. For animal species that are known to be infected exclusively by a single *Echinococcus* species, samples reported as *Echinococcus* spp. were directly attributed to that species. For animal species that can be infected with either *E. multilocularis* or *E. granulosus s.l.*, the interpretation relied on the endemic presence of the parasite in the reporting country. However, in countries where both species are known to circulate, data reported as *Echinococcus* spp. were excluded from the analysis to avoid misclassification. Specifically, within the EU, a total of three MSs (Italy, the Netherlands and Slovakia) reported 10 positive animal samples as *Echinococcus* spp., originating from four different animal species. Of these, three samples from pigs, reported by Slovakia, and one sample from domestic solipeds, reported by Italy, were excluded from species-level attribution due to the confirmed circulation of both *Echinococcus* species.

In calculating the total number of animals tested, samples from all countries were included, irrespective of the known endemicity of *Echinococcus* species, provided that the animal species in question was known to be infected by either *Echinococcus* species.

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[57] Commission Implementing Regulation (EU) 2020/2002 of 7 December 2020 laying down rules for the application of Regulation (EU) 2016/429 of the European Parliament and of the Council with regard to Union notification and Union reporting of listed diseases, to formats and procedures for submission and reporting of Union surveillance programmes and of eradication programmes and for application for recognition of disease-free status, and to the computerised information system. OJ L 412, 8.12.2020, pp. 1–28.

[58] EU Animal Disease Information System (ADIS). More information is available at: https://food.ec.europa.eu/animals/animal-diseases/animal-disease-information-system-adis_en.

TABLE 47 Summary statistics on echinococcosis caused by *Echinococcus multilocularis* and *Echinococcus granulosus s.l.* in humans and the most relevant definitive and intermediate animal hosts, EU, 2020–2024.

	2024	2023	2022	2021	2020	Data source
Humans						
Total number of confirmed cases	984	946	741	592	547	ECDC
Total number of confirmed cases/100,000 population (notification rates)	0.22	0.21	0.19	0.17	0.16	ECDC
Number of reporting MSs	26	26	25	25	25	ECDC
Infection acquired in the EU	418	370	223	112	132	ECDC
Infection acquired outside the EU	64	48	45	37	77	ECDC
Unknown travel status or unknown country of infection	502	528	473	443	338	ECDC
Animals						
***Echinococcus multilocularis* in foxes**						
Number of animals tested	6480	6399	6331	6318	5506	EFSA
positive animals	14.3	15.2	13.2	17.0	16.1	EFSA
Number of reporting MSs	14	14	14	14	10	EFSA
***Echinococcus* spp. in dogs**						
Number of animals tested	2670	2619	2502	2942	2515	EFSA
positive animals	0.07	0.73	0.08	0.07	0.08	EFSA
Number of reporting MSs	6	6	7	5	5	EFSA
***Echinococcus granulosus s.l.* in cattle (bovine animals)**						
Number of animals tested	7,376,568	6,794,791	7,185,526	7,065,934	7,035,066	EFSA
positive animals	0.20	0.28	0.32	0.21	0.21	EFSA
Number of reporting MSs	17	17	16	16	15	EFSA
***Echinococcus granulosus s.l.* in sheep and goats**						
Number of animals tested	12,134,767	11,543,410	12,337,176	10,806,419	11,089,043	EFSA
positive animals	0.49	0.66	0.81	0.38	0.96	EFSA
Number of reporting MSs	13	14	13	14	12	EFSA

Abbreviations: ECDC, European Centre for Disease Prevention and Control; EFSA, European Food Safety Authority; MSs, Member States.

Croatia, Italy and Poland reported additional data on *Echinococcus granulosus* not included in this table within the One-Health Surveillance data collection.

A8.3.2 | Human echinococcosis

In 2024, 984 confirmed echinococcosis cases were recorded by 26 MSs, corresponding to an EU notification rate of 0.22 cases per 100,000 population (Table 48) and an increase of 19.1% compared with 2023 (0.21 per 100,000 population). A mean notification rate of 0.18 per 100,000 population was reported over 2020–2024. In 2024, 23 MSs reported at least one confirmed case; three MSs reported zero cases (Cyprus, Luxembourg and Malta); and Denmark did not report any data. In 2024, the highest notification rates were observed in Lithuania and Bulgaria, with 3.4 and 1.7 cases per 100,000 population, respectively, followed by Slovenia and Austria with 0.80 and 0.59 cases per 100,000 population, respectively.

In 2024, half of the EU echinococcosis cases (50.1%; 493/984) were reported with data on importation status; 83.2% (410/493) of cases were reported as domestically acquired, while 16.8% (83/493) were imported.

Among cases with information on importation status and place of infection (*N* = 482), most (86.7%; 418/482) were reported as having been acquired within the EU (either domestically acquired or acquired in another EU country), while 13.3% (64/482) were reported as having been acquired outside the EU. Among eight imported cases reported as acquired within the EU, the most probable countries of infection were Romania (four cases), Spain (three cases) and Lithuania (one case). Among 64 imported cases reported as having been acquired outside the EU, the most probable countries of infection were Morocco (23.4%; 15/64), Syria (18.8%; 12/64), Iraq (9.4%; 6/64) and Türkiye (9.4%; 6/64).

TABLE 48 Reported confirmed human cases of cystic and alveolar echinococcosis and notification rates per 100,000 population in EU MSs and non-MSs, by country and year, 2020–2024.

Country	2024				2023		2022		2021		2020	
			Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate		Confirmed cases and rate	
	National coverage[a]	Data format[a]	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	54	0.59	54	0.59	54	0.60	42	0.47	34	0.38
Belgium	Y	C	31	0.26	28	0.24	23	0.20	17	0.15	19	0.16
Bulgaria	Y	A	112	1.7	117	1.8	89	1.4	89	1.4	95	1.4
Croatia	Y	C	8	0.21	8	0.21	5	0.13	3	0.08	3	0.08
Cyprus	Y	C	0	0	2	0.21	0	0	0	0	1	0.11
Czechia	Y	C	18	0.17	13	0.12	10	0.10	1	0.01	4	0.04
Denmark[b]	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	3	0.22	0	0	1	0.08	4	0.30	1	0.08
Finland	Y	C	5	0.09	0	0	2	0.04	6	0.11	4	0.07
France	Y	C	94	0.14	94	0.14	79	0.12	75	0.11	55	0.08
Germany	Y	C	182	0.22	200	0.24	182	0.22	163	0.20	171	0.21
Greece	Y	C	6	0.06	10	0.10	5	0.05	4	0.04	7	0.07
Hungary	Y	C	20	0.21	19	0.20	9	0.09	7	0.07	4	0.04
Ireland	Y	C	3	0.06	0	0	1	0.02	1	0.02	0	0
Italy[c]	Y	C	17	0.03	15	0.03	–	–	–	–	–	–
Latvia	Y	C	14	0.75	7	0.37	4	0.21	6	0.32	5	0.26
Lithuania	Y	C	97	3.4	89	3.1	74	2.6	20	0.71	37	1.3
Luxembourg	Y	C	0	0	3	0.45	1	0.15	1	0.16	3	0.48
Malta	Y	C	0	0	0	0	0	0	0	0	0	0
Netherlands	Y	A	55	0.31	46	0.26	45	0.26	53	0.30	48	0.28
Poland	Y	C	73	0.20	66	0.18	46	0.12	26	0.07	18	0.05
Portugal	Y	C	4	0.04	2	0.02	2	0.02	2	0.02	1	0.01
Romania	Y	C	34	0.18	38	0.20	4	0.02	1	0.01	0	0
Slovakia	Y	C	18	0.33	10	0.18	6	0.11	2	0.04	3	0.05
Slovenia	Y	C	17	0.80	16	0.76	5	0.24	11	0.52	3	0.14
Spain[d]	Y	C	98	0.20	90	0.19	72	0.15	33	–	8	–
Sweden	Y	C	21	0.20	19	0.18	22	0.21	25	0.24	23	0.22
EU Total			**984**	**0.22**	**946**	**0.21**	**741**	**0.19**	**592**	**0.17**	**547**	**0.16**
Iceland	Y	C	0	0	0	0	0	0	0	0	0	0
Liechtenstein[b]	–	–	–	–	–	–	–	–	–	–	–	–
Norway	Y	C	12	0.22	12	0.22	9	0.17	11	0.20	6	0.11
Switzerland[b]	–	–	–	–	–	–	–	–	–	–	–	–

Abbreviation: –, data not reported.

[a] Y: yes; N: no; A: aggregated data; C: case-based data.

[b] No surveillance system.

[c] No surveillance system before 2023.

[d] Data incomplete for 2020 and 2021, rate not calculated.

In 2024, *Echinococcus* species information was provided for 760 out of 984 (77.3%) confirmed echinococcosis cases reported by 19 MSs. In 2024, human infections caused by *E. multilocularis* accounted for 282 cases (37.1% of cases with known species information). Lithuania, France, Germany and Poland reported the highest numbers of human cases caused by *E. multilocularis*, accounting for 23.1%, 20.6%, 18.8% and 12.4% of all reported AE cases, respectively. Human infections caused by *E. granulosus s.l.* accounted for 478 cases (62.9%) out of the cases with species information available. Bulgaria, Spain and Germany reported the highest numbers of human cases caused by *E. granulosus s.l.*, accounting for 23.4%, 20.5% and 18.4% of all reported CE cases, respectively.

A8.3.3 | *Echinococcus* spp. in animals and food

Monitoring data for *Echinococcus multilocularis*

Table 49 shows *Echinococcus multilocularis* positive monitoring results in wild and domestic animals in reporting EU MSs and non-MSs in 2024. In 2024, a total of 14 MSs, the United Kingdom (Northern Ireland) and two non-MSs (Norway and Switzerland) reported monitoring data from 6480 and 539 foxes examined for *E. multilocularis*, respectively. Nine MSs (Austria, Czechia, Denmark, France, Germany, Luxembourg, the Netherland, Slovenia and Sweden) and one non-MS (Switzerland) reported overall 13.2% positive samples. Czechia, Germany and Slovenia reported the largest numbers of infected foxes in Europe, accounting for 28.3%, 20.8%, 14.6% of positive individuals, respectively.

In addition to its presence in foxes, *E. multilocularis* was reported in two dogs (France and Germany), three pigs (Germany) and 13 other wild species (two wolves and one wild board in France; one beaver, six wild boar and two coypu in Germany; and one wild boar in Slovakia).

TABLE 49 *Echinococcus multilocularis*-positive monitoring results in wild and domestic animals in reporting EU MSs and non-MSs, 2024.

		***N* positive/*N* tested (% positive)**		
Country	**Presence of *Em/Eg*[a]**	**Dogs**	**Foxes**	**Other wild species[b]**
Austria	*Em*	–	7/52 (13.5)	–
Czechia	*Em/Eg*	–	693/2446 (28.3)	–
Denmark	*Em*	–	7/313 (2.2)	–
France	*Em/Eg*	1/18 (5.6)	5/224 (2.2)	3/31 (9.7)
Germany	*Em*	1/30 (3.3)	164/787 (20.8)	9/90 (10.0)
Luxembourg	*Em*	–	7/37 (18.9)	–
Netherlands	*Em*	–	6/30 (20.0)[c]	–
Slovakia	*Em/Eg*	–	–	1/2 (50.0)
Slovenia	*Em/Eg*	–	23/157 (14.6)	–
Sweden	*Em/Eg*	–	14/1029 (1.4)	–
EU total (27 + XI)		2/2670 (0.07)[d,e]	926/6480 (14.3)[d]	13/18,210 (0.07)[d,e]
Switzerland		10/22 (45.5)	1/2 (50.0)	6/16 (37.5)
Total non-MSs		10/22 (45.5)	1/539 (0.19)[d]	6/16 (37.5)[d]
Total EU (27+ XI) + non-MSs		12/2692 (0.45)[d,e]	927/7019 (13.2)[d]	19/18,226 (0.10)[d,e]

Note: Grey shaded cell indicates no positive results.

Abbreviations: –, data not reported; *Em*, *Echinococcus multilocularis*; *Eg*, *Echinococcus granulosus* sensu lato.

[a] Presence in the country of *Echinococcus multilocularis* (*Em*) and/or *Echinococcus granulosus* sensu lato (*Eg*).

[b] Includes beavers, coypu, wild felidae, jackals, leporidae, mustalidae, raccoons, raccoon dogs, squirrels, wolves and wild boar, with only beavers, coypu, wolves and wild boar found positive, while land mammals, other carnivores, farmed and zoo animals were excluded from the total number of animals tested (e.g. *N* tested).

[c] Positive samples reported without *Echinococcus* species information were mentioned in the table given the known circulation of *E. multilocularis* in the reporting country.

[d] Total N tested includes samples from additional countries not listed in the table, as no positive monitoring results (N positive) were reported for those countries. However, their data contribute to the overall total number of animals sampled and tested (N tested).

[e] The percentage of positive cases was calculated based on the total number of samples (i.e. *N* tested) from suitable hosts.

Monitoring data for *Echinococcus granulosus sensu lato*

Table 50 shows *Echinococcus granulosus s.l.* positive monitoring results in relevant definitive and intermediate hosts in reporting EU MSs and non-MSs in 2024. In 2024, 18 MSs, the United Kingdom (Northern Ireland) and two non-MSs (Norway and Switzerland) reported monitoring data for *E. granulosus s.l.*. The data reported were from approximately 79 million domestic and wild animals tested for *E. granulosus s.l.*, more than 99% of which were domestic animals (sheep, cattle, goats, pigs, horses, water buffalos and dogs). Most of these data were obtained from livestock during meat inspections at the slaughterhouse. Wild animals tested included Cantabrian chamois, deer, jackals, moose, mouflons, reindeers, wild boar and wolves. Specifically, regarding pigs (with a total of 73,706,460 samples collected in the EU), the number of animals considered in the analysis was restricted to those originating from countries where *E. granulosus s.l.* is known to circulate, resulting in a total of 59,233,296 samples included in the final count.

A total of 80,856 (0.10%) positive samples were reported by 11 MSs and one non-MS, mainly from domestic animals. These positive samples came primarily from small ruminants (sheep and goats; *N* = 59,564), accounting for 73.7% of positive results. Positive tests in small ruminants were mainly reported by Italy and Spain, accounting for 60.6% and 37.3% of positive animals, respectively, followed by Greece and Slovakia. A total of 14,508 cattle tested positive (17.9% of animals positive for *E. granulosus s.l.*), mainly reported by Spain (63.0%) and Italy (35.2%). A total of 6671 pigs tested positive (8.3% of animals positive for *E. granulosus s.l.*), mainly reported by Spain (55.3%) and Italy (44.6%).

During the last 5 years (2020–2024), small ruminants accounted for 76.6% of all positive samples for *E. granulosus s.l.* and were mainly reported by a small number of countries (Italy, Spain, Greece and Bulgaria) with large animal populations. During the same period, cattle and pigs accounted for 17.2% and 6.1% of all positive samples for *E. granulosus s.l.*, respectively, and were mainly reported by a small number of countries (Italy and Spain for cattle; Poland and Spain for pigs).

TABLE 50 *Echinococcus granulosus* sensu lato-positive monitoring results in wild and domestic animals in reporting EU MSs and non-MSs, 2024.

Country	Presence of *Em/Eg*[a]	***N* positive/*N* tested (% positive)**						
		Buffalos	**Cattle (bovine animals)**	**Pigs**	**Goats**	**Sheep**	**Solipeds, domestic**	**Wild species**[b]
Belgium	*Em*	–	–	–	–	3/66,896 (0.004)	–	–
Finland	*Eg*	–	–	–	–	–	–	30/48,955 (0.06)
France	*Em/Eg*	–	–	–	–	–	–	1/19 (5.3)
Greece	*Eg*	–	239/37,531 (0.64)	–	78/1,755,555 (0.004)	1073/601,625 (0.18)	–	–
Hungary	*Em/Eg*	–	2/2 (100)	–	–	–	–	–
Italy	*Em/Eg*	8/6526 (0.12)	5104/1,978,209 (0.26)	2978/7,909,661 (0.04)	1203/56,010 (2.1)	34,873/1,208,223 (2.9)	–	8/48,117 (0.02)
Portugal	*Eg*	–	6/325,260 (0.002)	–	–	2/629,417 (0.0003)	–	–
Romania	*Em/Eg*	–	13/16 (81.3)	1/13 (7.7)	–	2/37 (5.4)	–	–
Slovakia	*Em/Eg*	–	8/29,923 (0.03)	–	–	128/32,829 (0.39)	–	–
Spain	*Eg*	–	9136/2,354,770 (0.39)	3689/38,499,581 (0.01)	3752/863,166 (0.43)	18,450/6,558,053 (0.28)	2/18,861 (0.01)	62/386,612 (0.02)
Sweden	*Em/Eg*	–	–	–	–	–	1/1220 (0.08)	–
EU total (27 + XI)		8/6526 (0.12)[d]	14,508/7,376,568 (0.20)[c]	6668/59,233,296 (0.01)[c]	5033/2,755,037 (0.18)[c]	54,531/9,367,487 (0.58)[c]	3/34,759 (0.01)[d]	101/552,093 (0.02)[c,d]
Norway	*Eg*	–	–	–	–	–	–	1/6 (16.7)
Total non-MSs countries		0/0 (0)	0/310,002 (0)[c]	0/1,600,000 (0)[c]	0/28,000 (0)[c]	0/110,001 (0)[c]	0/34 (0)[c]	1/6 (16.7)[c]
Total EU (27+ XI) + non-MSs		8/6526 (0.12)[c]	14,508/7,686,570 (0.19)[c]	6668/60,833,296 (0.01)[c]	5033/2,783,037 (0.18)[c]	54,531/9,477,488 (0.58)[c]	3/34,793 (0.01)[c]	102/552,099 (0.02)[c,d]

Note: Grey shaded cell indicates no positive results.

Abbreviations: –, data not reported; *Em*, *Echinococcus multilocularis*; *Eg*, *Echinococcus granulosus* sensu lato.

Croatia, Italy and Poland (also) reported data on *Echinococcus granulosus* within the One-Health Surveillance data collection.

[a] Presence in the country of *E. multilocularis* (*Em*) and/or *E. granulosus* sensu lato (*Eg*).

[b] Includes cantabrian chamois, deer, jackals, moose, mouflons, racoon dogs, reindeers, voles, wolves and wild boar, with land game mammals, other carnivores, farmed or zoo animals excluded from the total number of animals tested (e.g. *N* tested).

[c] Total *N* tested includes samples from additional countries not listed in the table, as no positive monitoring results (*N* positive) were reported for those countries. However, their data contribute to the overall total number of animals sampled and tested (*N* tested).

[d] The percentage of positive cases was calculated based on the total number of samples (i.e. *N* tested) from suitable hosts.

Echinococcus granulosus *sensu lato in animals through the One-Health Surveillance data*. Croatia, Italy and Poland reported data on One-Health Surveillance on *E. granulosus s.l.* in dogs and wild animals including jackals and wolves, for a total of 927 animals tested.

Croatia tested 677 domestic and wild animals, and the overall proportion of positive was 2.7% with positive findings only in dogs (2.6%) and jackals (6.4%). Italy tested 50 wild animals with no positive findings. Poland tested 200 wild animals, and the overall proportion of positive was 3.5% with positive findings only in wolves (7.0%).

A8.4 | Discussion

In 2024, the EU notification rate of confirmed human echinococcosis cases increased when compared with previous data reported from 2020 to 2023. This increase, corresponding to the highest number of confirmed human cases ($N = 984$) since the beginning of EU-level surveillance in 2007, may be explained by increased human surveillance activities and improved notification systems for these diseases. For instance, Italy notified cases to the ECDC EpiPulse Cases database for the first time in 2023, reporting 15 and 17 cases of echinococcosis in 2023 and 2024, respectively. Increased awareness about the diseases among clinicians, as well as immigration from endemic countries, may also have influenced the numbers of CE and AE diagnosed cases in some non-endemic countries in Northern Europe (Scandinavia) and Western Europe (Casulli et al., 2022; Casulli et al., 2023; Richter et al., 2019).

In 2024, species information was available for the majority of confirmed echinococcosis cases reported by 19 MSs. Among these, alveolar echinococcosis (AE; infections caused by *E. multilocularis*) accounted for just over one-third of cases, with Lithuania, France, Germany and Poland reporting the highest numbers. In contrast, cystic echinococcosis (CE; infections caused by *E. granulosus* sensu lato) caused nearly two-thirds of the cases, predominantly reported by Bulgaria, Spain and Germany. These findings reflect the distinct geographic distributions of the two main *Echinococcus* species responsible for human infection in Europe, with *E. multilocularis* more common in central and northern countries and *E. granulosus s.l.* prevalent in southern and south-eastern regions.

The recent discovery of AE in other countries such as Croatia, Italy and Serbia points to a geographical spread of the parasite (Balen Topić et al., 2023; Cafiero et al., 2025; Casulli et al., 2025; Lalošević et al., 2023; Tamarozzi et al., 2024). It should be emphasised that the true proportion of positive samples of these diseases is extremely difficult to estimate due to the long incubation period (years), high proportion of asymptomatic or paucisymptomatic carriers who never seek medical attention, non-specific symptoms and under-reported or misdiagnosed CE and AE cases. The factors mentioned above contribute to an underestimation of the burden of these diseases (Casulli, 2020). For these reasons, the patchy data reported by MSs on the number of people with echinococcosis currently represent the 'tip of the iceberg' for infections, with asymptomatic carriers and misdiagnosed cases of CE and AE making up the invisible portion. For instance, it has been estimated that the official figures from hospital records should be far higher, with true values 10 and 700 times greater for Bulgaria and Romania in 2015–2016, respectively (Tamarozzi et al., 2018). More recently, a multicentered retrospective study to lower uncertainty limits on the impact of human CE identified around 65,000 human cases in Europe in 1997–2021 (Casulli et al., 2023). Using different data sources, this study also identified a total number of CE cases fourfold greater than ECDC data in 2017–2019 (Casulli et al., 2023).

In 2024, 21 MSs, the United Kingdom (Northern Ireland) and two non-MSs (Norway and Switzerland) reported monitoring data on *E. granulosus s.l.* and *E. multilocularis* in animals. No data were reported by Bulgaria, Croatia, Estonia, Iceland, Ireland, Lithuania, Liechtenstein or Poland. As for 2023, in 2024, the highest numbers of animals infected with *E. granulosus s.l.* were reported in Italy and Spain, followed by Greece. Infections were mainly observed in sheep intermediate hosts and, to a lesser extent, in cattle, pigs and goats. Regarding *E. multilocularis*, similar to data reported in 2023, in 2024, most of the infected animals (primarily red foxes) were reported by Czechia, followed by Germany. The surveillance of *E. multilocularis* in foxes is important for assessing the proportion of positive samples of AE in Europe, given that its geographical distribution seems to have widened in recent decades. It is difficult to establish whether the increased geographical distribution of *E. multilocularis* is due to a growing fox population in Europe (Deplazes et al., 2004) or whether it reflects greater surveillance efforts, as there is a general lack of baseline data and standardised detection methods. One growing concern is the detection in recent years of *E. multilocularis* in golden jackals, which are extending their geographical range from south-eastern to north-western Europe and therefore contributing to the dispersion of this parasite over long distances (Balog et al., 2021; Dušek et al., 2020). In this context, this parasite has also been recently found in golden jackals and foxes from Bosnia and Herzegovina, Croatia, Hungary, Serbia, Slovenia and central Italy (Balog et al., 2021; Cafiero et al., 2025; Dušek et al., 2020; Kapo et al., 2025; Miljević et al., 2021; Omeragić et al., 2022; Sindičić et al., 2018). Moreover, in animals, notification is necessary to obtain reliable data, and information on parasite speciation is essential to risk management efforts, since *E. granulosus s.l.* and *E. multilocularis* have different epidemiologies and pose different health risks for humans (Conraths et al., 2017; Possenti et al., 2016).

In line with the monitoring obligations set out in Directive 2003/99/EC, MSs must collect and report data on animal species entering the food chain where the presence of *Echinococcus* spp. is suspected. For *E. granulosus s.l.*, notification ensures that comparable data are obtained across MSs from meat inspections of food-producing animals. For *E. multilocularis*, notification is mandatory in countries free from this parasite, in accordance with Commission Delegated Regulation (EU) 2018/772.[59]

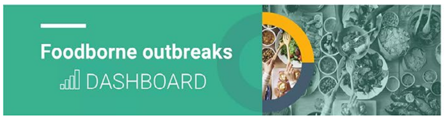
The 2024 One-Health surveillance data on *E. granulosus s.l.* in wildlife suggests that, irrespective of the low prevalence detected in wild canids, these animals may play an important role in the spillover of this zoonotic parasite from wildlife to livestock, with consequences for its surveillance and control.

Data reported in this chapter should be used to support national surveillance planning for *E. multilocularis* and *E. granulosus s.l.* in animals and humans in Europe, within a One Health approach.

SECTION B – FOOD-BORNE OUTBREAKS (IN ACCORDANCE WITH DIRECTIVE 2003/99/EC)

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here.

For additional information about food-borne outbreaks and for the consultation of data collected, the following interactive tools are available:



B1 | KEY FACTS

- In 2024, 27 European Union Member States and the United Kingdom (Northern Ireland) reported 6558 food-borne outbreaks, 62,481 human cases, 3336 hospitalisations and 53 deaths. The number of deaths in 2024 was lower than in 2023 (12 fewer deaths in 2024). A total of 102 food-borne outbreaks, 1583 cases of illness, 185 hospitalisations and two deaths were reported by eight non-Member States.
- Food-borne outbreaks in the European Union increased by 14.5% in 2024 compared with the previous year (5728 in 2023). The number of human cases and hospitalisations also increased, by 19.7% (52,215 cases in 2023) and 15.2% (2896 hospitalisations in 2023), respectively. Conversely, the number of deaths decreased in 2024, by 18.5% (65 deaths in 2023).
- The food-borne outbreak reporting rate was 1.5 per 100,000 population, a relative increase of 40.3% compared with the mean annual rate for the period 2020–2023 (1.0 per 100,000 population). The case reporting rate rose to 13.8 cases per 100,000 population, a relative increase of 62.0% compared with the mean annual rate for the 2020–2023 period (8.5 per 100,000 population).
- *Salmonella* was identified in the most food-borne outbreaks with known causative agents ($N = 1238$) and was associated with the highest number of hospitalisations ($N = 1823$) and deaths ($N = 17$, the same as for *Listeria monocytogenes*). *S.* Enteritidis was the most frequently reported *Salmonella* serovar (512 food-borne outbreaks; 74.1% of *Salmonella* outbreaks with serovar information available). *Salmonella* was also the causative agent most frequently reported in multi-country food-borne outbreaks in 2024.
- Norovirus and other caliciviruses were responsible for the highest number of human cases ($N = 14,297$).
- *Listeria monocytogenes* caused 17 deaths, which is a high number given that this agent caused only a small number of food-borne outbreaks ($N = 38$), confirming its high health impact in terms of case fatality rate (8.1% of cases) and proportion of hospitalisations (72.3% of cases).
- The proportion of food-borne outbreaks of unknown aetiology accounted for 42.2% of all reported outbreaks in the EU. The Netherlands and Belgium contributed the most to this reporting.
- A total of 65 very large food-borne outbreaks (≥ 100 cases each) were reported. They were caused by norovirus and other caliciviruses, bacterial toxins (i.e. *Bacillus cereus*, *Clostridium perfringens* and *Staphylococcus aureus* toxins and bacterial toxins, unspecified), *Salmonella* followed by *Escherichia coli* other than Shiga toxin-producing *E. coli* including enteropathogenic *E. coli* (EPEC), *Yersinia*, *Campylobacter*, *Cryptosporidium* and Hepatitis E virus.
- A total of 533 strong-evidence outbreaks were reported in 2024 (8.1% of all food-borne outbreaks), causing 10,786 human cases, 1081 hospitalisations and 25 deaths.
- Foodstuffs belonging to the group 'composite foods, multi-ingredient foods and other foods' were implicated in most of these food-borne outbreaks (174 strong-evidence food-borne outbreaks; 32.6% of strong-evidence food-borne outbreaks), similarly to 2023 (179 strong-evidence outbreaks in 2023), causing most cases (4466 cases, 41.4% of cases in strong-evidence outbreaks).
- Foods of animal origin had a major impact. 'Meat and meat products' was the second most frequently reported food vehicle group in strong-evidence food-borne outbreaks (112 strong-evidence outbreaks) and caused the highest number of hospitalisations ($N = 363$). 'Broiler meat (*Gallus gallus*) and products thereof' and 'pig meat and products thereof' contributed mainly to this food group causing 35 and 28 strong-evidence outbreaks, respectively. 'Eggs and egg products' was the third most frequently reported food vehicle group in strong-evidence food-borne outbreaks (89 strong-evidence outbreaks).

- 'Foods of non-animal origin', and in particular 'vegetables and juices and other products thereof' caused the highest number of deaths in strong-evidence outbreaks ($N = 10$). This was the highest number of deaths reported for this food vehicle group since 2011.
- Most strong-evidence food-borne outbreaks took place in a 'restaurant or cafe or pub or bar or hotel or catering service' (170 outbreaks; 31.9% of all strong-evidence outbreaks). Approximately one in four cases and one in four hospitalisations were also associated with this place (2539 cases; 23.5% of all strong-evidence outbreak-related cases and 253 hospitalisations; 23.4% of all hospitalisations in strong-evidence outbreaks). The numbers of strong-evidence food-borne outbreaks, cases and hospitalisations were rather stable compared with 2023 (181 outbreaks, 2608 cases and 270 hospitalisations).
- 'Infected food handler' and 'cross-contamination' ranked first among the contributory factors for outbreaks taking place in a 'restaurant, pub, street vendor, take-away, etc.' (22 outbreaks, 31.0% of all strong-evidence outbreaks with information on risk factors available). The most frequent factor contributing to strong-evidence outbreaks occurring in 'domestic premises' was 'inadequate heat treatment' (14 outbreaks, 40.0% of all strong-evidence outbreaks with information on risk factors available).

B2 | SURVEILLANCE AND MONITORING OF FOOD-BORNE OUTBREAKS IN THE EU

Every year, EU Member States (MSs) and non-MSs report to EFSA data concerning the food-borne outbreaks (FBOs) occurring in their country, in compliance with Directive 2003/99/EC.[59] This reporting of FBO data is mandatory for EU MSs and is based on the standard set out in the guidance document, published annually by EFSA (EFSA, 2025a). The key findings are summarised in this report.

EFSA is assigned the task of describing the causative agents and foodstuffs implicated in FBOs, the places of exposure and contributing factors, along with their time trends. The aim is to assess the health impact of FBOs in Europe and to characterise the food vehicles most frequently implicated. Outbreaks are categorised as 'strong-evidence' or 'weak-evidence' based on the strength of evidence implicating a suspected food vehicle as the cause of the outbreak (EFSA, 2014).

The analysis takes account of uncertainty around the evidence implicating a given food as the vehicle of the outbreak, by limiting the description of certain findings (i.e. implicated food vehicles, place of exposure and contributory factors) to strong-evidence outbreaks.

In strong-evidence FBOs, the link with human cases involved in the outbreak and the same food source is assessed with more certainty than in weak-evidence FBOs, i.e. in strong-evidence FBOs, it is highly probable that cases had consumed the same contaminated food or contaminated ingredient. The evaluation of the strength of evidence should be based on a carefully considered assessment of all relevant categories of evidence, including evidence provided by analytical epidemiological studies, compelling descriptive data, identification of the same causative agent in both human cases and food or its environment, and comprehensive product-tracing investigations.

The current data reporting system is known as the European Union Foodborne Outbreak Reporting System (EU-FORS) (EFSA, 2014). It applies to FBOs caused by bacteria, viruses, parasites, fungi and their products, such as toxins and biological amines (e.g. histamine), whether typical food-borne agents or agents for which food-borne transmission is usually accidental.

Outbreaks caused by the ingestion of drinking water are also considered in FBO reporting, since drinking water is defined as a food in Regulation (EC) No 178/2002.[60]

A description of the national systems in place for FBO surveillance and reporting can be found in the national zoonoses reports submitted in accordance with Directive 2003/99/EC and published on the EFSA website, together with the EU One Health Zoonoses Report, both available online here.

Information on the surveillance and monitoring of food-borne outbreaks in the EU is also summarised in the EFSA story map (here see story map sections on 'What food-borne outbreaks are and how they are classified', 'Who investigates food-borne outbreaks' and 'EU regulatory framework and the role of EFSA').

B3 | DATA ANALYSES

Key statistics on FBOs described in this chapter refer to the EU level for 2024, unless specified otherwise. Basic indicators used to describe the impact of FBOs on human health include the total number of outbreaks, human cases, the number and proportion of cases (%) leading to hospitalisations or deaths, the mean outbreak size (N cases per outbreak) and its range (minimum and maximum). Outbreak size was categorised as very small (< 10 cases), small (≥ 10 and < 25 cases), medium (≥ 25 and < 50 cases), large (≥ 50 and < 100 cases) and very large ($100 \geq$ cases). Outbreak and case reporting rates (per 100,000 population) are used as relative measures of occurrence in the population, allowing a direct comparison among

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[59] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40.

[60] Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority and laying down procedures in matters of food safety. OJ L 31, 1.2.2002, p. 1–24.

MSs, independently of the size of the population and its variation over time. However, due to the lack of full harmonisation of FBO surveillance among MSs, any direct comparison of findings between countries should be interpreted with caution. Counts of hospitalisations and deaths and the proportion (%) of hospitalisations and deaths among outbreak cases are used as indicators for outbreak severity, considering only outbreaks for which this information was available.

The causative agents in FBOs in 2024 have been grouped in accordance with the following criteria (see also Section 1 of the FBO addendum for further details on the EFSA Knowledge Junction at Zenodo here):

- '*E. coli* other than STEC' includes any pathogenic *Escherichia coli* other than 'Shiga Toxin-producing *E. coli* (STEC)'. In 2024, this group included 'enteroaggregative *E. coli* (EAEC)', 'enteroinvasive *E. coli* (EIEC)', 'enteropathogenic *E. coli* (EPEC)', 'enterotoxigenic *E. coli* (ETEC)' and '*E. coli*, unspecified'.
- '*Bacillus cereus* toxins' includes '*B. cereus*', '*B. cereus* enterotoxins' and 'toxins – *B. cereus* toxin – *B. cereus* emetic toxin'.
- '*Staphylococcus aureus* toxins' includes '*S. aureus*', '*Staphylococcus*, unspecified' and 'staphylococcal enterotoxins'.
- 'Norovirus (and other caliciviruses)' includes 'caliciviruses, unspecified', 'norovirus' (Norwalk-like virus) and 'sapovirus' (Sapporo-like virus).

Food vehicles have been grouped according to the general criteria (see Section 2 of the FBO addendum for further details on the EFSA Knowledge Junction at Zenodo here) set out in the EFSA data guidance (EFSA, 2025a). Places of exposure have been grouped according to the general characteristics and level of risk associated with the setting, as well as the process behind food preparation (see Section 3 of the FBO addendum for further details on the EFSA Knowledge Junction at Zenodo here).

Eurostat data on the resident population (on 1 January 2025) were used to calculate reporting rates at national and EU level. Data from the NISRA[61] from 2021 to 2023 were used for the United Kingdom (Northern Ireland).

Short-term variations over time were described using the same metrics (annual mean) by comparison with 2023 and 2020–2023. Long-term variations were also described, taking 2015–2024 as the reference time period, unless specified otherwise. Frequency distributions are shown at EU level. Trends were analysed only at MS level, according to the rationale described in Boelaert et al. (2016) for data quality. Time trends were tested for statistical significance over the period 2015–2024 using the Cox-Stuart sign test, a non-parametric test appropriate for limited numbers of observations. A p-value of < 0.05 was considered to identify a statistically significant trend, beyond chance. Significant long-term trends 2015–2024 may not fully reflect short-term trend fluctuations. No trend analysis was performed at the overall EU level due to the heterogeneity of national surveillance and reporting systems. Time series with missing values were also excluded from the 10-year trend analyses. Key statistics on FBOs for 2023 and previous years may differ from those published in the European Union One Health 2023 Zoonoses Report, as MSs may have updated their historical data.

B4 | RESULTS AND DISCUSSION

B4.1 | Overview of countries reporting food-borne outbreak data, in 2024

In 2024, 27 MSs and the United Kingdom (Northern Ireland) reported a total of 6558 food-borne outbreaks (FBOs), with 62,481 human cases, 3336 hospitalisations and 53 deaths. In addition, eight non-MSs reported 102 FBOs, 1583 cases, 185 hospitalisations and two deaths (Table 51).

The number of FBOs and cases reported by each MS varied considerably across countries. Most outbreaks (5308 outbreaks; 80.9%) and cases (47,304 cases; 75.7%) were limited to a few countries (Belgium, France, the Netherlands, Poland and Spain). France was the main contributor, accounting for 31.5% of all FBOs and 32.6% of all cases reported in 2024, which is consistent with observations from previous years.

Five MSs (France, Germany, Italy, Poland and Spain) reported most hospitalisations (2370 hospitalisations; 71.0%) and six MSs (Belgium, Finland, France, Germany, Italy and Spain) reported most deaths (45 deaths; 84.9%). Deaths were mainly caused by *Salmonella* and *Listeria monocytogenes*, both of which combined caused 34 deaths (64.2% of all deaths, i.e. roughly one in three caused by either one of the two causative agents). Other causative agents causing deadly cases included, in descending order, *Bacillus cereus* toxins, *Clostridium botulinum* toxins, *Clostridium perfringens* toxins, 'bacterial toxins, unspecified', 'norovirus and other caliciviruses', *Shigella* and unknown agents. For Belgium, Finland and Spain, the number of deaths from FBOs reported in 2024 was the highest over the last 10 years.

The outbreak reporting rates and case reporting rates (Table 51) show how frequently FBOs and cases were reported, regardless of the country's population size. In 2024, there was a relative increase of 40.3% in the outbreak reporting rate and of 62.0% in the case reporting rate compared with the respective mean annual rates for the 2020–2023 period. There was enormous variation in these values among MSs. Among the 27 MSs and the United Kingdom (Northern Ireland), the median 'outbreak reporting rate' was 0.44 outbreaks per 100,000 and ranged from 0.03 (Bulgaria) to 12.2 (Malta), while the median 'case reporting rate' was 9.2 cases per 100,000 and ranged from 0.10 (United Kingdom (Northern Ireland)) to 39.5

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[61] Northern Ireland Statistics and Research Agency (NISRA). https://www.nisra.gov.uk/.

(Latvia). Considerable variations among MSs were also observed in the 'mean outbreak size' (Table 51). All these indicators provide evidence on the large variability in the sensitivity of the surveillance and the types of FBOs monitored across MSs.

Although an increase was observed in 2024 in the numbers of FBOs (830 more FBOs, 14.5% increase compared with 2023), cases (10,266 more cases, 19.7% increase) and hospitalisations (440 more hospitalisations, 15.2% increase), the number of deaths decreased (12 fewer deaths), with 18.5% fewer deaths in 2024 than in 2023 (65 deaths were reported in 2023).

At the country level, the relative variation in the number of FBOs, and the outbreak-related cases reported in 2024 compared with 2023, are shown in Figure 21 (left panel and right panel, respectively). An increase in the number of FBOs was observed for 18 MSs, while for seven MSs (Austria, Croatia, Denmark, Estonia, Hungary, Ireland and Romania) and the United Kingdom (Northern Ireland) the number of FBOs decreased. For Bulgaria and Cyprus, the number of FBOs reported in 2024 was stable. A similar pattern was observed for outbreak-related cases, with 22 MSs reporting more cases in 2024, and five MSs (Austria, Cyprus, Denmark, Estonia and Hungary) and the United Kingdom (Northern Ireland) fewer cases.

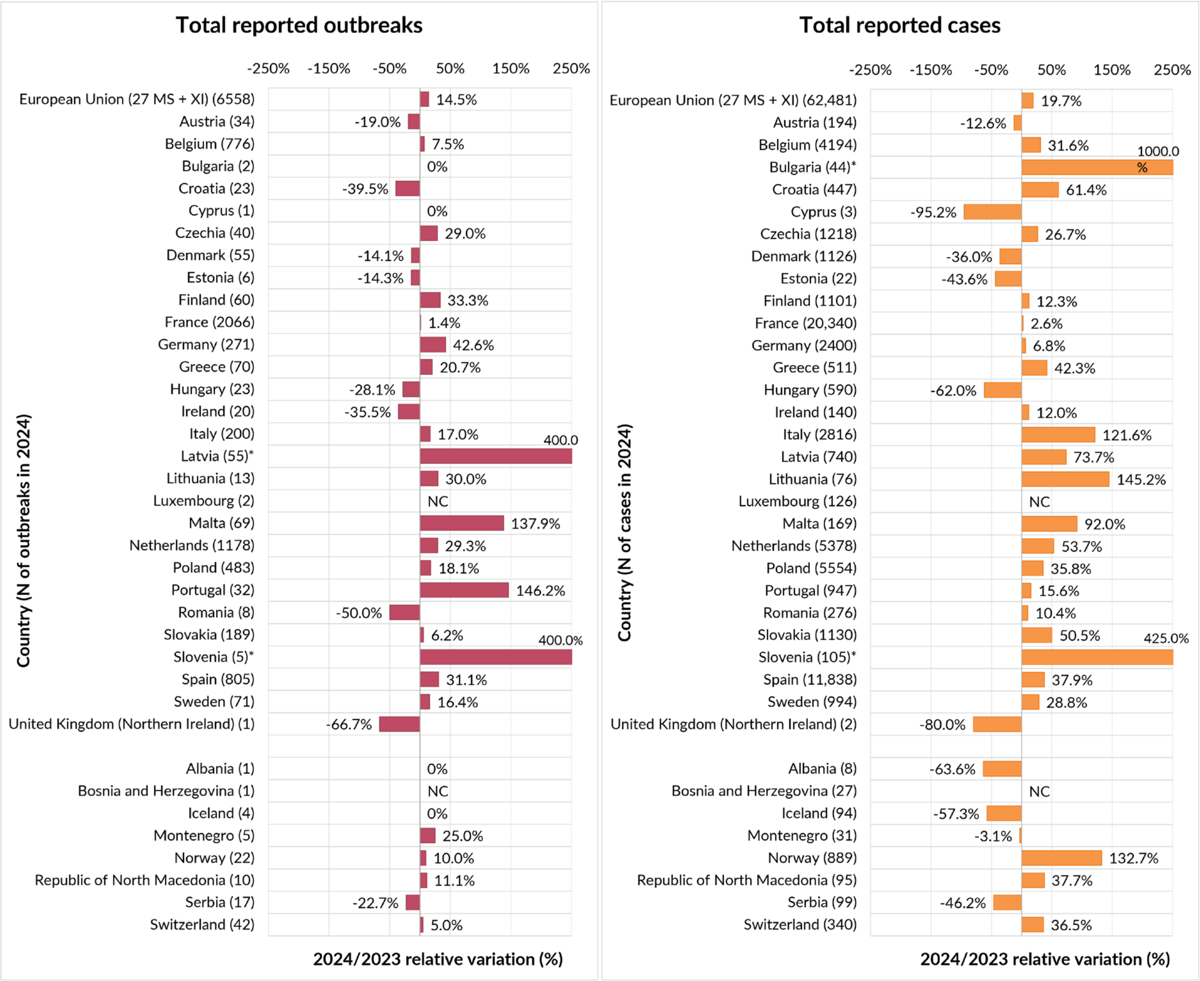

FIGURE 21 Relative variation (%) in food-borne outbreaks and outbreak-related cases reported in 2024 compared with 2023, by reporting country.

Note: NC, Not Calculable. Countries with values exceeding the range of representation are marked with an asterisk. The exact value is reported at the scale border of the bar.

In 2024, information on the type of outbreak was reported for 4318 FBOs (65.8%) by all MSs except Bulgaria (Figure 22). 'General' outbreaks involve human cases from more than one household, while 'household' outbreaks, which are usually smaller, are outbreaks where all cases live in a single household. All MSs but Cyprus, and the United Kingdom (Northern Ireland), reported 'general' outbreaks (3056 FBOs). For three MSs (Hungary, Luxembourg and Portugal) and the United Kingdom (Northern Ireland), this was the only type of outbreak reported in 2024. Twenty MSs provided information on 'household' outbreaks (1229 FBOs), and this was the most frequently reported type of outbreak for eight MSs (Croatia, Cyprus, Estonia, Greece, Lithuania, Malta, Poland and Slovakia). No 'household' outbreaks were reported by Denmark, Finland, Hungary, Luxembourg, the Netherlands, Portugal and the United Kingdom (Northern Ireland). The mean size of 'general' and 'household' outbreaks was 15.8 and 3.5 cases, respectively. In non-MSs, most outbreaks (45 FBOs) were reported as 'general' outbreaks by all non-MSs but Albania, followed by 'household' outbreaks (17 FBOs). No 'household' outbreaks were reported by Iceland, Norway and Bosnia and Herzegovina.

Ten MSs (Austria, Belgium, Czechia, Denmark, Finland, Germany, Italy, the Netherlands, Slovenia and Sweden) reported 22 general FBOs as part of multi-country outbreaks in 2024, resulting in 849 cases (574 more cases than in 2023, 208.7% increase), 52 hospitalisations and one death. Most FBOs reported as part of multi-country outbreaks by EU MSs were caused by *Salmonella* (20 FBOs) including *S.* Agona, *S.* Enteritidis, *S.* Mikawasima, *S.* Strathcona, *S.* Typhimurium and *S.* Umbilo. Hepatitis A and *Yersinia enterocolitica* were each responsible for one FBO reported by Belgium as part of a multi-country outbreak in 2024. In addition, two FBOs caused by *Salmonella* and involving a total of 315 cases were reported by Norway as part of multi-country outbreaks. The serovars involved were *S.* Newport and *S.* Muenster. Rapid information exchange systems, such as the Early Warning Response System (EWRS), EpiPulse and the Rapid Alert System for Food and Feed (RASFF), play a crucial role in real-time alert dissemination across European countries, significantly supporting the investigation of multi-country FBOs.

In 2024, MSs and non-MSs reported a total of 65 and three very large FBOs (≥ 100 cases each), respectively. Overall, the numbers of cases included in these outbreaks were 10,983 and 478, respectively.

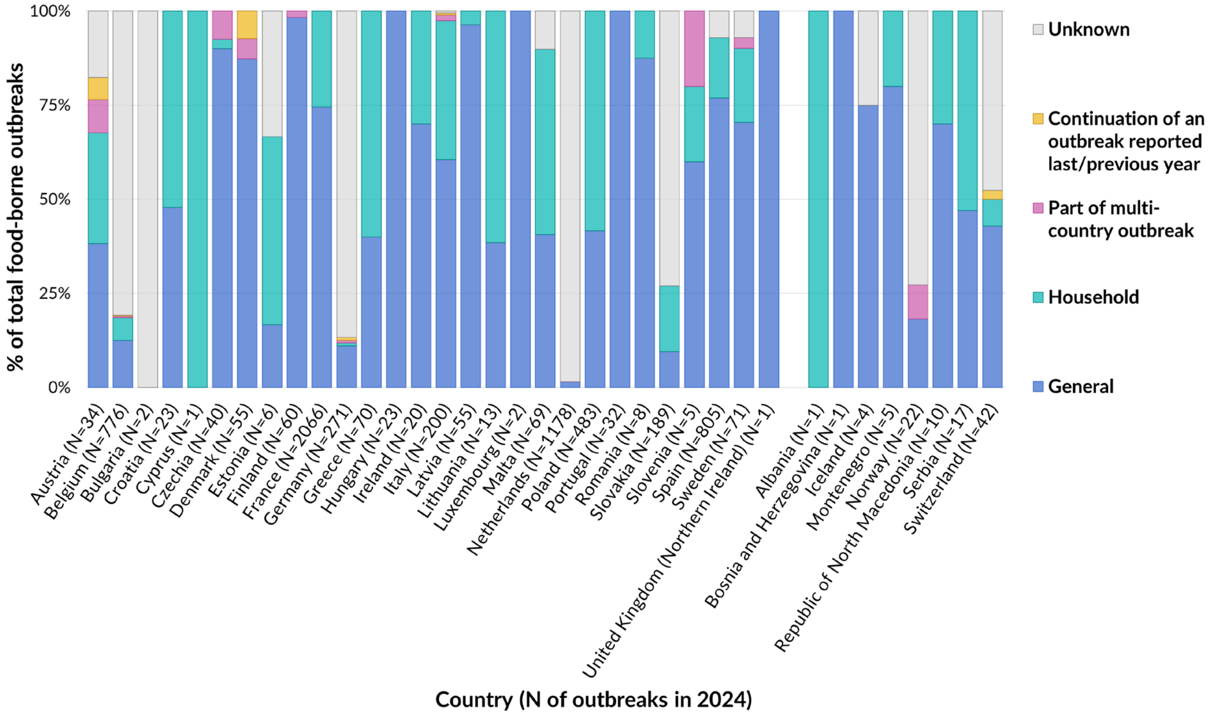

FIGURE 22 Frequency distribution (%) of food-borne outbreaks, by type of outbreak and country, in reporting EU MSs and non-MS countries, 2024.

TABLE 51 Number of food-borne outbreaks, human cases, hospitalisations and deaths, in reporting EU MSs and non-MS countries, 2024.

	Outbreaks				Cases					Hospitalised		Deaths	
	Total (strong-evidence)		Outbreaks per 100,000 population					Cases per 100,000 population					
Country	*N*	% of total	2024	2020–2023	*N*	% of total	Mean outbreak size (*N*) and range (min-max)	2024	2020–2023	*N*	% of total	*N*	% of total
Austria	34 (11)	0.52	0.37	0.31	194	0.31	5.7 (2–28)	2.1	1.4	77	2.3	2	3.8
Belgium	776 (7)	11.8	6.6	5.2	4194	6.7	5.4 (2–90)	35.5	23.1	115	3.4	6	11.3
Bulgaria	2 (2)	0.03	0.03	0.03	44	0.07	22.0 (6–38)	0.68	0.56	14	0.42	0	0
Croatia	23 (0)	0.35	0.60	0.56	447	0.72	19.4 (2–101)	11.6	9.2	11	0.33	0	0
Cyprus	1 (0)	0.02	0.10	0.08	3	< 0.01	3.0 (–)	0.31	2.5	3	0.09	0	0
Czechia	40 (9)	0.61	0.37	0.33	1218	1.9	30.5 (4–160)	11.2	12.7	39	1.2	1	1.9
Denmark	55 (19)	0.84	0.92	0.96	1126	1.8	20.5 (2–95)	18.9	24.5	44	1.3	0	0
Estonia	6 (1)	0.09	0.44	0.65	22	0.04	3.7 (2–8)	1.6	2.0	7	0.21	0	0
Finland	60 (17)	0.91	1.1	0.83	1101	1.8	18.4 (2–160)	19.6	16.1	99	3.0	6	11.3
France	2066 (81)	31.5	3.0	2.3	20,340	32.6	9.8 (2–335)	29.7	19.7	569	17.1	6	11.3
Germany	271 (36)	4.1	0.32	0.23	2400	3.8	8.9 (2–191)	2.9	1.8	451	13.5	8	15.1
Greece	70 (3)	1.1	0.67	0.24	511	0.82	7.3 (2–144)	4.9	2.3	138	4.1	2	3.8
Hungary	23 (12)	0.35	0.24	0.20	590	0.94	25.7 (3–70)	6.2	7.0	110	3.3	0	0
Ireland	20 (2)	0.30	0.37	0.41	140	0.22	7.0 (2–34)	2.6	1.7	16	0.48	0	0
Italy	200 (40)	3.0	0.34	0.22	2816	4.5	14.1 (2–385)	4.8	1.9	338	10.1	4	7.5
Latvia	55 (0)	0.84	2.9	0.59	740	1.2	13.5 (2–29)	39.5	15.2	0	0	0	0
Lithuania	13 (13)	0.20	0.45	0.27	76	0.12	5.8 (2–25)	2.6	1.3	44	1.3	0	0
Luxembourg	2 (1)	0.03	0.30	0.16	126	0.20	63.0 (26–100)	18.7	2.6	1	0.03	0	0
Malta	69 (1)	1.1	12.2	5.2	169	0.27	2.4 (2–9)	30.0	20.8	26	0.78	0	0
Netherlands	1178 (7)	18.0	6.6	4.9	5378	8.6	4.6 (2–717)	30.0	19.0	15	0.45	0	0
Poland	483 (83)	7.4	1.3	0.81	5554	8.9	11.5 (2–237)	15.2	8.4	660	19.8	2	3.8
Portugal	32 (13)	0.49	0.30	0.11	947	1.5	29.6 (2–91)	8.9	7.2	27	0.81	0	0
Romania	8 (7)	0.12	0.04	0.04	276	0.44	34.5 (7–118)	1.4	0.67	49	1.5	0	0
Slovakia	189 (18)	2.9	3.5	3.9	1130	1.8	6.0 (2–498)	20.8	12.9	119	3.6	1	1.9
Slovenia	5 (2)	0.08	0.24	0.08	105	0.17	21.0 (4–38)	4.9	3.7	7	0.21	0	0
Spain	805 (134)	12.3	1.7	0.83	11,838	18.9	14.7 (2–851)	24.3	10.0	352	10.6	15	28.3
Sweden	71 (14)	1.1	0.67	0.60	994	1.6	14.0 (2–121)	9.4	9.5	4	0.12	0	0
United Kingdom (Northern Ireland)	1 (0)	0.02	0.05	0.09	2	< 0.01	2.0 (–)	0.10	0.60	1	0.03	0	0

TABLE 51 (Continued)

	Outbreaks				**Cases**					**Hospitalised**		**Deaths**	
	Total (strong-evidence)		**Outbreaks per 100,000 population**					**Cases per 100,000 population**					
Country	***N***	**% of total**	**2024**	**2020–2023**	***N***	**% of total**	**Mean outbreak size (*N*) and range (min-max)**	**2024**	**2020–2023**	***N***	**% of total**	***N***	**% of total**
EU Total (27 + XI)	**6558 (533)**	**100**	**1.5**	**1.0**	**62,481**	**100**	**9.5 (2–851)**	**13.8**	**8.5**	**3336**	**100**	**53**	**100**
Albania	1 (0)	-	0.04	0.01	8	-	8.0 (–)	0.29	0.20	2	–	0	–
Bosnia and Herzegovina	1 (0)	–	0.03	0.04	27	-	27.0 (–)	0.85	1.2	10	–	0	–
Iceland	4 (2)	–	1.0	0.87	94	-	23.5 (11–49)	24.5	26.6	19	–	0	–
Montenegro	5 (0)	–	0.80	0.69	31	-	6.2 (2–10)	5.0	9.1	4	–	0	–
Norway	22 (6)	–	0.40	0.48	889	-	40.4 (4–238)	16.0	8.5	80	–	0	–
Republic of North Macedonia	10 (6)	–	0.55	0.21	95	-	9.5 (3–18)	5.2	4.7	25	–	0	–
Serbia	17 (9)	–	0.26	0.20	99	-	5.8 (2–16)	1.5	2.5	33	–	0	–
Switzerland[a]	42 (6)	–	0.47	0.37	340	-	8.3 (2–49)	3.8	5.0	12	–	2	–

[a] For one outbreak, information on cases was not available. This outbreak was excluded from the calculation of the mean outbreak size.

FIGURE 23 Trends in the number of strong-evidence and weak-evidence outbreaks (left axis) and outbreak reporting rate (per 100,000 population) (right axis) in the EU and reporting EU MSs and non-MSs, 2015–2024.

Note: Dark red and light red represent strong- and weak-evidence outbreaks, respectively. Black dots and lines represent FBO reporting rates. Countries with a statistically significant trend ($p < 0.05$) in the total number of FBOs per year over the period are marked with an asterisk. The dotted line and the secondary *Y*-axis in blue have been used for Belgium, Malta, the Netherlands and Slovakia, in order to draw attention to a scale that is different to that of the other countries. Missing points and lines correspond to years with no data reported.

FIGURE 23 (Continued)

A total of 533 strong-evidence FBOs were identified by 24 MSs (all MSs except Croatia, Cyprus and Latvia). This reporting accounted for 8.1% of all FBOs, which is a lower proportion compared to 2023 when strong-evidence outbreaks accounted for 10.1% (579 outbreaks) of total reported FBOs. Most strong-evidence FBOs were reported by five MSs (France, Germany, Italy, Poland and Spain), which alone accounted for 70.2% of the reporting (374 strong-evidence FBOs).

For the period 2015–2024, the country-level distribution of FBOs by strength of evidence and outbreak reporting rate (per 100,000 population) in the EU MSs and non-MSs is presented in Figure 23. Overall, the number of FBOs observed over the last 10 years has decreased significantly for 10 MSs (Austria, Bulgaria, Croatia, Germany, Hungary, Latvia, Lithuania, Romania, Slovakia and Sweden), although in five of these MSs (Germany, Latvia, Lithuania, Slovakia and Sweden) the number of FBOs reported in 2024 was higher than that of 2023. Due to possible under-reporting, these trends do not necessarily reflect a change in the true occurrence of FBOs. They should be interpreted with caution since annual variations are strongly influenced by changes in FBO surveillance by MSs, including changes in the procedures for outbreak detection and investigation (see also Section B.5).

In 2024, there were 12 FBOs involving 59 travel-associated cases, including 20 hospitalisations and one death. The death was associated with an outbreak caused by *S.* Enteritidis. No previous deaths have been reported from outbreaks associated with cases travelling abroad since EFSA started to collect data on FBOs in 2007. Among the travel-related outbreaks, *Salmonella* was the most frequently reported causative agent (eight FBOs), followed by *Shigella* (two FBOs) and *Campylobacter* (two FBOs). In particular, *S.* Enteritidis caused six FBOs and *S.* Mikawasima and *S.* Typhimurium one outbreak each.

For a more interactive look at FBO data by reporting countries, visit the dedicated page in EFSA's dashboard on FBOs (here).

B4.2 | Overview of causative agents in food-borne outbreaks in 2024

In 2024, a causative agent was identified in 3793 FBOs (57.8% of all FBOs reported in the EU). These outbreaks were responsible for 43,284 cases, 2946 hospitalisations and 50 deaths. Figure 24 and Table 52 provide a detailed overview of the causative agents responsible for FBOs in the EU in 2024.

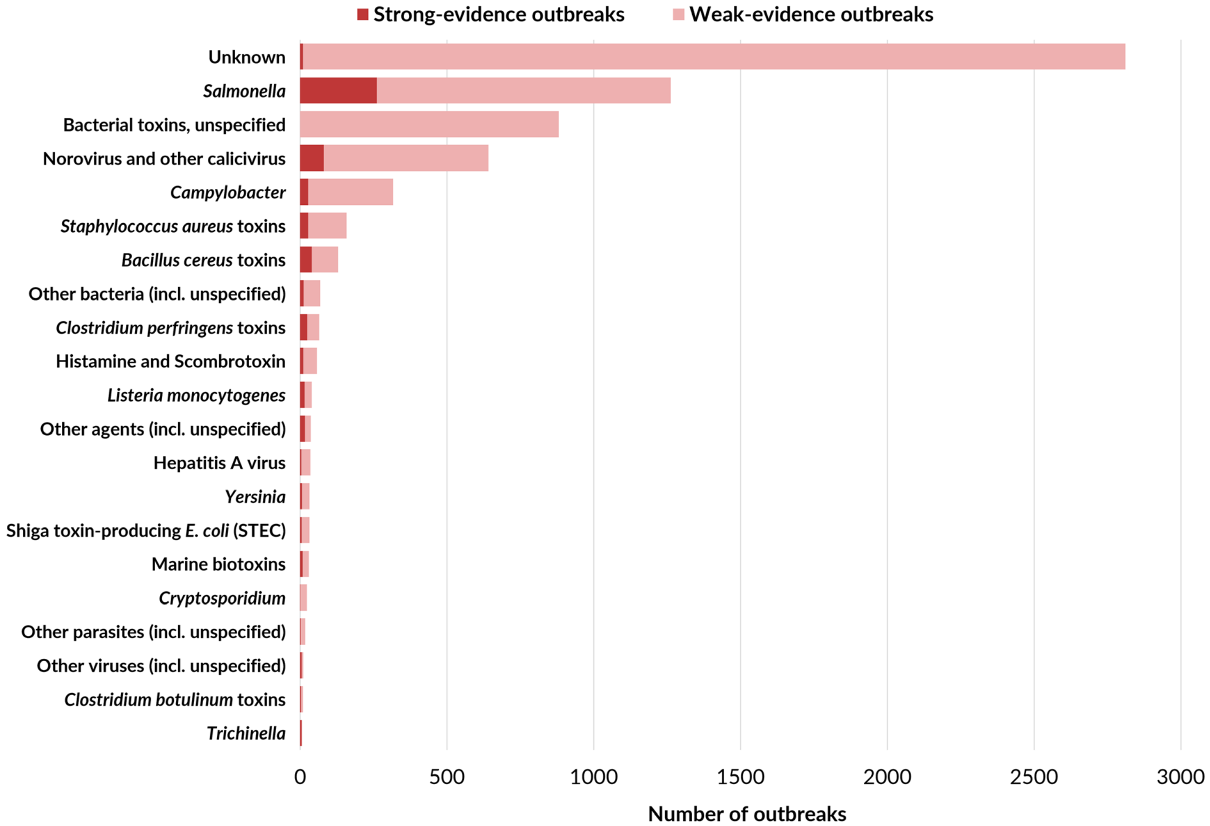

FIGURE 24 Number of strong-evidence and weak-evidence outbreaks, by causative agent, EU, 2024.
Note: 'Norovirus and other calicivirus' includes 'norovirus', 'sapporo virus' and unspecified caliciviruses.
'Other bacteria (incl. unspecified)' includes '*Aeromonas*', '*Enterococcus*', '*Escherichia coli* other than STEC', '*Shigella*' and '*Vibrio parahaemolyticus*'.
'Other agents (incl. unspecified)' includes 'mushroom toxins', 'atropine' and 'lectins'.
'Marine biotoxins' includes 'ciguatoxin' and unspecified marine biotoxins.
'Other parasites (incl. unspecified)' includes '*Giardia*' and unspecified parasites.
'Other viruses (incl. unspecified)' includes 'adenovirus', 'enterovirus', 'hepatitis E virus' and 'rotavirus'.
During the final phase of report production, the Netherlands informed that adenovirus (here included among 'other viruses') was mistakenly reported as the causative agent of one strong-evidence outbreak.
The correct causative agent was Hepatitis A virus.

The proportion of FBOs of unknown aetiology (42.2%) was lower than that observed in 2023 (48.1%). Altogether, the Netherlands (1147 FBOs), Belgium (711 FBOs), Spain (294 FBOs) and France (290 FBOs) contributed the most to the reporting of FBOs of unknown aetiology (2442 FBOs; 88.3%). Fifty-six FBOs with known causative agents (54.9%) and 46 with unknown aetiology (45.1%) were also reported by eight and five non-MSs, respectively. The majority of FBOs with unknown causative agents were reported by Switzerland (29 outbreaks).

Among outbreaks with known causative agents reported by MSs, bacteria were reported to have caused a high proportion of FBOs, followed by bacterial toxins, viruses, 'other causative agents' and parasites. Bacteria, and in particular, *Salmonella*, were also responsible for the highest number of hospitalisations and deaths. The same number of total deaths was reported for FBOs caused by *L. monocytogenes*. No deaths were reported in FBOs caused by parasites or 'other causative agents'. Viruses, in particular norovirus (and other caliciviruses), and bacterial toxins caused more human cases than bacteria. FBOs caused by *Clostridium botulinum* toxins and *L. monocytogenes* had the most severe health impact in relative terms, i.e. as regards the percentage of hospitalisations and case fatality rate, respectively (Table 52).

The range of causative agents reported in FBOs by MSs and non-MSs was very variable in 2024. This finding likely reflects differences in the monitoring of FBOs across European countries. A high number of causative agents (10 or more agents) was reported by eight MSs (Belgium, Finland, France, Germany, Italy, Poland, Spain and Sweden) while seven MSs (Bulgaria, Cyprus, Estonia, Latvia, Lithuania, Luxembourg and Slovenia) and the United Kingdom (Northern Ireland) reported three or fewer causative agents.

In the very large outbreaks (≥ 100 cases each) reported by MSs in 2024, norovirus prevailed (19 FBOs), followed by bacterial toxins (i.e. *Bacillus cereus* toxins, *Clostridium perfringens* toxins, *Staphylococcus aureus* toxins and bacterial toxins, unspecified) (altogether 17 FBOs), *Salmonella* (12 FBOs), *Yersinia enterocolitica* (two FBOs) and *Escherichia coli* other than STEC, including *E. coli* 'unspecified' and enteropathogenic *E. coli* (EPEC) (two and one FBOs, respectively). *Campylobacter, Cryptosporidium* and Hepatitis E virus each caused one single very large FBO. Nine very large FBOs had an unknown aetiology. In non-MSs, two very large FBOs were associated with norovirus, as well as one with *S.* Newport and one with unknown aetiology.

For a more interactive look at FBO data by causative agents, visit the dedicated page in EFSA's dashboard on FBOs (here).

B4.2.1 | Bacteria

Except for Bulgaria and Luxembourg, all MSs and the United Kingdom (Northern Ireland) and all non-MSs reported FBOs caused by bacteria. Key statistics on FBOs associated with this agent group are available in Table 52.

Salmonella

In 2024, FBOs caused by ***Salmonella*** (1238 FBOs) were reported by most MSs (all except Bulgaria and Luxembourg) as well as by all eight non-MSs (24 FBOs). Details on FBOs caused by *Salmonella* are shown in Table 52. *Salmonella* was associated with a major health impact in the EU, with one in two hospitalisations and almost one in three deaths reported in FBOs being caused by this agent.

Most FBOs associated with this causative agent were reported by four MSs, i.e. Poland (283 FBOs), France (266 FBOs), Spain (240 FBOs) and Slovakia (132 FBOs), accounting altogether for 74.4% of all *Salmonella* outbreaks in the EU. In 13 MSs and six non-MSs, *Salmonella* was the leading cause of FBOs.

FBOs caused by *Salmonella* increased in 2024 with 123 more FBOs counted than in 2023 (1238 outbreaks in 2023, 11.0% increase). This fourth consecutive annual progressive increase since 2020 (i.e. the first year of the COVID-19 pandemic) has brought the total number of *Salmonella* FBOs back to pre-pandemic levels, although slightly lower compared with 2018 and 2019. Likewise, human cases, hospitalisations and deaths also saw a low or moderate increase in 2024. A total of 954 more cases (10.4% increase), 97 more hospitalisations (5.6% increase) and one more death (6.3% increase) were reported than in 2023.

FBOs reported in 2024 were mainly reported as 'household' outbreaks (*N* = 536) or 'general' outbreaks (*N* = 468). Twenty FBOs were instead reported as being 'part of a multi-country outbreak' while three FBOs were a 'continuation of an outbreak reported in the last/previous year'.

At the individual country level, Poland was the MS reporting the most *Salmonella* FBOs (*N* = 283), cases (*N* = 2338) and hospitalisations (*N* = 493), and Germany the most deaths (*N* = 7). Five MSs (Finland, France, Latvia, Lithuania and Slovenia) experienced in 2024 a relative increase of more than 50% in the number of *Salmonella* FBOs compared to the previous year. France had the sharpest increase in terms of absolute number of outbreaks (123 more outbreaks than in 2023, 86.0% increase). These FBOs involved a total of 503 more cases (43.2% increase), 124 more hospitalisations (112.7% increase) and one more death (100% increase). Germany had the sharpest increase in terms of absolute number of cases (560 more cases, 87.5% increase), hospitalisations (169 more hospitalisations, 75.4% increase) and deaths (two more deaths, 40.0% increase) reported in 2024 compared to 2023. The main reason for the higher health impact in this MS was the occurrence of five very large *Salmonella* FBOs. Two of these FBOs were strong-evidence outbreaks, with the former being caused by *S.* Infantis (191 cases) and linked to the consumption of raw minced pork meat contaminated at the slaughterhouse, and the latter being part of a multi-country outbreak caused by *S.* Umbilo implicating the consumption of imported green leafy vegetables. Italy also reported many more human cases in *Salmonella* FBOs than in 2023 (412 more cases, 121.9% increase), although the highest relative increase in the number of cases was observed for Slovenia, Lithuania and Belgium (215.0%, 181.5% and 160.5% increase in 2024 compared with 2023, respectively). Among non-MSs, the number of cases and hospitalisations increased sharply in Norway. There were 361 cases and 80 hospitalisations in 2024 compared with 17 cases and four hospitalisations in 2023 (an increase of 2023.5% and 1900.0%, respectively). The increase was due to a single very large outbreak caused by *S.* Newport, which was part of a multi-country outbreak linked to imported sprouts (see also Section B.4.8).

Information on the serovar was available for 55.8% of the FBOs caused by *Salmonella* in the EU (691 FBOs). A total of 32 *Salmonella* serovars were reported in outbreaks. *S.* Enteritidis was the most frequently reported (512 FBOs), followed by ***S.* Typhimurium** (84 FBOs) and **monophasic *S.* Typhimurium** (34 FBOs). Altogether, these three serovars accounted for 91.2% of all *Salmonella* FBOs with known serovars.

The health impact of FBOs caused by ***S.* Enteritidis** was less severe compared with 2023 (see Section 4 of the FBO addendum for further details on the EFSA Knowledge Junction at Zenodo here). Despite only a small decrease in outbreaks, i.e. 5.5% (30 fewer FBOs than in 2023), the number of cases, hospitalisations and deaths dropped sharply by 27.5% (1464 fewer cases), 30.0% (312 fewer hospitalisations) and 66.6% (six fewer deaths), respectively. These downward variations appear to offset the pattern observed in 2023, suggesting that a certain degree of annual variability exists, which cannot be explained by any specific reason but rather corresponds to a general trend at the country level. *S.* Enteritidis outbreaks were mostly associated with consumption of 'eggs and egg products' (i.e. 'eggs', 'eggs – table eggs – mixed whole', unspecified 'eggs and egg products') and 'composite foods, multi-ingredient foods and other foods' (i.e. 'bakery products', including 'cake – containing raw cream', 'desserts – containing raw eggs', 'dessert' and 'pastry'; 'buffet meals'; 'mixed food', including 'meat-based dishes', 'egg-based dishes', 'sandwiches – with meat', 'fish and seafood-based dishes' and unspecified 'mixed food'; 'sweets and chocolate'). Foods belonging to these groups were identified in 75.0% (i.e. more than three in four FBOs) of the strong-evidence outbreaks caused by *S.* Enteritidis (*N* = 100). Details on food vehicles implicated in strong-evidence outbreaks caused by *S.* Enteritidis in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-a, of the FBO Addendum (here). The food vehicles implicated in *S.* Enteritidis strong-evidence FBOs reported by non-MSs were 'eggs and egg products' (*N* = 5), 'meat and meat products' (*N* = 2) (i.e. 'bovine meat and products thereof' and unspecified 'meat and meat products') and 'bakery products' (*N* = 2). Outbreaks caused by *S.* Enteritidis in the EU were very small in size (7.5 cases on average) and were reported mostly in 'domestic premises' and a 'restaurant or cafe or pub or bar or hotel or catering service' (39.0% and 31.0% of strong-evidence outbreaks caused by this serovar, respectively). Regarding FBOs with fewer than 10 cases (i.e. very small), there were 427 (83.4%) in 2024, while only four very large outbreaks (≥ 100 cases) were reported (all from Poland), of which three were strong-evidence FBOs. The foods implicated in the largest strong-evidence *S.* Enteritidis outbreaks were 'mixed food', 'other or mixed red meat and products thereof' and 'fruit, berries and juices and other products thereof'.

The number of FBOs caused by ***S.* Typhimurium** increased by 68.0% (34 more FBOs), and those caused by **monophasic *S.* Typhimurium** increased by 78.9% (15 more FBOs), compared to 2023. Human cases increased even more than the number of FBOs. *S.* Typhimurium was associated with 512 more human cases (159.5% increase), while monophasic *S.* Typhimurium caused 383 more cases (216.4% increase). Hospitalisations also rose for both serovars, with 64 more for *S.* Typhimurium (68.1% increase) and 71 more for monophasic *S.* Typhimurium (173.2% increase). FBOs caused by *S.* Typhimurium and monophasic *S.* Typhimurium had a mean size of 9.9 and 16.5 cases, respectively. *S.* Typhimurium was responsible for 19 strong-evidence FBOs and 349 cases, respectively. For monophasic *S.* Typhimurium the numbers were 11 and 262, respectively. Both outbreaks and cases associated with *S.* Typhimurium and monophasic *S.* Typhimurium were much less frequently reported in 'domestic premises' than *S.* Enteritidis. Only 15.8% of strong-evidence FBOs and 2.6% of total cases due to *S.* Typhimurium occurred in this setting, whereas for monophasic *S.* Typhimurium the corresponding percentages were 9.1% and 0.76%, respectively. Strong-evidence *S.* Typhimurium FBOs were mostly reported in a 'school or kindergarten' and monophasic *S.* Typhimurium in 'multiple places of exposure in one country' as well as in a 'restaurant, pub, street vendor, take-away, etc.' 'Meat and meat products' (i.e. 'pig meat and products thereof', 'bovine meat and products thereof', 'unspecified meat and meat products', 'broiler meat (*Gallus gallus*) and products thereof' and 'other or mixed red meat and products thereof') ranked first among the implicated food group in strong-evidence FBOs caused by *S.* Typhimurium and monophasic *S.* Typhimurium, as this food group was reported in eight and 10 outbreaks, respectively. A more detailed description of the implicated 'meat and meat products' in strong-evidence FBOs due to monophasic *S.* Typhimurium was available for six FBOs. Specifically, these were linked to the consumption of 'meat specialities from pig', 'meat preparation from pig – intended to be eaten raw', 'minced meat from bovine animals', 'fresh meat from bovine animals', 'meat preparation from bovine animals, intended to be eaten cooked' and 'mixed meat – meat preparation'. Other implicated foods were 'milk and milk products' for both serovars (i.e. 'cheese' for *S.* Typhimurium and 'dairy products (other than cheeses)' for monophasic *S.* Typhimurium), while 'eggs and egg products', 'composite foods, multi-ingredient foods and other foods' (i.e. 'buffet meals' and 'desserts, containing raw eggs') and 'food of non-animal origin' (i.e. 'vegetables and juices and other products thereof' including 'alfaalfa sprouts', 'watermelon' and 'onion') were only reported for *S.* Typhimurium. In particular, sprouts were the food item implicated in the only very large strong-evidence FBO caused by *S.* Typhimurium. This outbreak was reported from Sweden as 'part of multi-country outbreak'. One non-MS (Iceland) reported one strong-evidence FBO caused by monophasic *S.* Typhimurium linked to 'other, mixed or unspecified poultry meat and products thereof'. Details on food vehicles implicated in strong-evidence outbreaks caused by *S.* Typhimurium and monophasic *S.* Typhimurium in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-b and S7-c of the FBO Addendum (here).

Among non-typhoidal *Salmonella*, the other serovars identified in FBOs in 2024 accounted overall for 8.8% (61 FBOs) of the total number of *Salmonella* outbreaks with known serovars. They included ***S.* Infantis** and ***S.* Strathcona**, which each caused seven FBOs (all outbreaks but one caused by *S.* Strathcona were classified as 'part of multi-country outbreak' or 'continuation of an outbreak reported last/previous year'). ***S.* Coeln** was reported in six FBOs, and ***S.* Umbilo** in five FBOs (all reported as 'part of multi-country outbreak'). Four FBOs were caused by ***S.* Derby** and ***S.* Mikawasima**, respectively (two FBOs caused by *S.* Mikawasima were reported as 'part of multi-country outbreak'). Another 23 *Salmonella* serovars were identified in 28 FBOs, i.e. ***S.* Agona, *S.* Bareilly**, ***S.* Blockley, *S.* Bovismorbificans, *S.* Braenderup, *S.* Brandenburg, *S.* Bredeney, *S.* Chester, *S.* Choleraesuis, *S.* Dublin, *S.* Eastbourne, *S.* Glostrup, *S.* Hessarek, *S.* Hvittingfoss, *S.* Liverpool, *S.* London, *S.* Muenster, *S.* Newport, *S.* Saintpaul, *S.* Senftenberg, *S.* Szentes, *S.* Virchow and *S.* Worthington**. Altogether, these outbreaks involved 1435 human cases, 242 hospitalisations and seven deaths. *S.* Umbilo, *S.* Bovismorbificans, *S.* Infantis and *S.* Strathcona were associated with four single very large FBOs each including ≥ 100 cases reported by Germany (*S.* Umbilo and *S.* Infantis), Greece (*S.* Bovismorbificans) and Italy (*S.* Strathcona).

Twenty-eight strong-evidence FBOs caused by *Salmonella* serovars other than *S.* Enteritidis, *S.* Typhimurium and monophasic *S.* Typhimurium were reported in 2024. These outbreaks were attributed to various types of food including, in descending order, 'food of non-animal origin' (mainly 'vegetables and juices and other products thereof', including 'tomato', 'vegetables – leaves', 'rocket, rucola', 'cherry tomato', 'alfaalfa sprouts' and unspecified 'vegetables, juices and other products thereof'), 'composite foods, multi-ingredient foods and other foods' (mainly 'mixed food', including 'meat-based dishes', 'paste-based dishes', 'fish and sea food-based dishes', 'other processed food products and prepared dishes' and unspecified 'mixed food'), 'eggs and egg products', 'meat and meat products' (i.e. 'minced meat from pig, intended to be eaten raw', 'broiler meat (*Gallus gallus*) and products thereof'), 'fish and fishery products' (i.e. 'raw fish') and 'water (and other beverages)' (i.e. 'tap water, including well water'). One non-MS (Norway) reported two strong-evidence outbreaks caused by *S.* Muenster and *S.* Newport. The implicated food vehicles were 'cereal products including rice and seeds/pulses (nuts, almonds)' and 'alfaalfa sprouts', respectively.

Details on food vehicles implicated in strong-evidence outbreaks caused by other *Salmonella* serovars in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-d, of the FBO Addendum (here).

Three weak-evidence outbreaks associated with paratyphoid *Salmonella* were reported by two MSs in 2024. One outbreak was reported by Croatia and was caused by *S.* Paratyphi B variant Java. *S.* Paratyphi A, a human-host restricted agent that may accidentally be transmitted through water or food, was reported in two FBOs from Poland.

For additional information about *Salmonella* outbreaks, see the infographic at the front of chapter A2 – *Salmonella*.

Campylobacter

Campylobacter ranked second in 2024 among bacterial causative agents and fourth among all known causative agents in the EU. Compared with 2023, in 2024 the number of FBOs caused by *Campylobacter* (314 FBOs) increased by 18.0% (48 more FBOs). In parallel, cases and hospitalisations also increased, with 158 more cases and nine more hospitalisations than in 2023.

Seventeen MSs reported FBOs caused by *Campylobacter*. France, Germany and Slovakia contributed the most to *Campylobacter* reporting in the EU (190 FBOs; 60.5%). Malta was the MS with the highest number of *Campylobacter* FBOs reported in relation to the (small) population size. In this country, *Campylobacter* was the main causative agent reported in FBOs, similarly to 2023. The number of outbreaks increased to 35 FBOs, an increase of 133.3% compared with 2023 (20 more FBOs than in 2023). *Campylobacter* outbreaks were very small in size, on average (Table 52), although one very large FBO reported by France involved 113 cases, with no hospitalisations or deaths.

The type of outbreak caused by *Campylobacter* was fairly evenly distributed, with 114 classified as 'general' outbreaks and 99 as 'household' outbreaks.

In the majority of FBOs, the *Campylobacter* species involved was unspecified (192 FBOs; 61.1% of FBOs caused by *Campylobacter*). Among the FBOs with known species, ***C. jejuni*** and ***C. coli*** were identified in 110 and 12 outbreaks, respectively.

The most frequently reported place of exposure identified among the 25 strong-evidence *Campylobacter* FBOs was a 'restaurant, pub, street vendor, take-away, etc.' ($N = 10$) and 'multiple places of exposure' ($N = 7$). 'Meat and meat products' was the food group most often implicated (13 FBOs) in these strong-evidence outbreaks. In particular 'broiler meat (*Gallus gallus*) and products thereof' caused 10 FBOs, followed by 'other or mixed red meat and products thereof', 'pig meat and products thereof' (i.e. 'meat preparation from pig, intended to be eaten raw') and 'unspecified meat and meat products' (one FBO each). The other food categories implicated in FBOs were in descending order 'milk and milk products' (six FBOs), 'mixed food' (three FBOs), 'eggs', 'vegetables and juices and other products thereof' and 'potable water' (one FBO each). Among the six strong-evidence FBOs linked to the consumption of 'milk and milk products', 'raw milk from sheep' and 'unspecified milk' were each associated with one outbreak, reported by Italy and Poland, respectively. In contrast, raw cows' milk was linked to two FBOs reported by Germany. Additionally, two FBOs associated with the consumption of cheese were reported by Italy and Spain (one each). The FBO linked to the consumption of 'potable water' (i.e. well water) was reported by Finland and caused a total of 96 cases and four hospitalisations. Details on food vehicles implicated in strong-evidence outbreaks caused by *Campylobacter* in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-e, of the FBO Addendum (here). Two non-MSs (Switzerland and Serbia) reported two strong-evidence outbreaks linked to raw cows' milk and 'meat from broilers (*Gallus gallus*)', respectively.

For additional information about *Campylobacter*, see also the infographic at the front of chapter A1 – *Campylobacter*.

Listeria monocytogenes

In 2024, *Listeria monocytogenes* was reported as the causative agent of 38 FBOs in the EU. This agent was responsible for the largest number of deaths (*N* = 17, the same as *Salmonella*), and ranked third among causative agents causing the most hospitalisations in FBOs. The health impact of FBOs caused by *L. monocytogenes* rose significantly in 2024 as the numbers of FBOs, cases, hospitalisations and deaths were all higher than in 2023 (19 more outbreaks, 100% increase; 77 more cases, 57.9% increase; 65 more hospitalisations, 77.4% increase; six more deaths, 54.5% increase). *L. monocytogenes* was the causative agent associated with the highest case fatality rate among all agents reported in FBOs in 2024 (Table 52). However, the value resulting for 2024 was the lowest since 2020.

Overall, 13 MSs, i.e. five more MSs than in 2023, and one non-MS reported FBOs caused by *L. monocytogenes*. *L. monocytogenes* subtyping information reported by MSs indicated that strains involved in FBOs belonged to serovar 1/2a (ST1, ST2, ST3, ST37, ST155) (eight FBOs), serovar 4b (ST4, ST2408) (two FBOs) and molecular serogroup IIa (ST101) (one FBO). For most listeriosis outbreaks (*N* = 27), information on the serovar was not available, even though a *L. monocytogenes* strain associated with one outbreak from Belgium was reported to belong to ST10.

FBOs reported in 2024 were mainly classified as 'general' outbreaks (*N* = 25) or 'continuation of an outbreak reported last/previous year' (*N* = 8). Only two 'household' outbreaks were reported.

Food vehicles reported in strong-evidence FBOs caused by *L. monocytogenes* (*N* = 14) belonged to a wide variety of food groups: 'composite foods, multi-ingredient foods and other foods' (i.e. 'fish and seafood-based dishes', 'meat-based dishes' and 'other processed food products and prepared dishes'), 'fish and fishery products' (i.e. 'smoked fish' and unspecified 'fish and fish products'), 'vegetables and juices and other products thereof' (i.e. 'table olives' and 'vegetable protein preparation (RTE)'), 'meat and meat products' (i.e. 'meat preparation from pig intended to be eaten raw', 'pig meat and products thereof' and unspecified 'meat and meat products'), 'milk and milk products' (i.e. 'cheese' and 'infant formula'). No single food group prevailed over the others. Details on food vehicles implicated in strong-evidence outbreaks caused by *Listeria monocytogenes* in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-f, of the FBO Addendum (here).

One non-MS (Switzerland) reported one strong-evidence outbreak linked to 'bakery products'.

For additional information about *Listeria monocytogenes*, see also the infographic available at the front of chapter A3 – *Listeria monocytogenes*.

Shiga toxin-producing *E. coli* (STEC)

In 2024, the number of FBOs caused by Shiga toxin-producing *E. coli* (STEC) halved in the EU compared to the previous year, with 31 outbreaks reported against 66 in 2023, corresponding to a decrease of 53.0%. In line with this, the numbers of cases, hospitalisations and deaths also decreased. STEC outbreaks were reported in 2024 by 11 MSs and the United Kingdom (Northern Ireland). France and Belgium were the MSs with the sharpest falls, as they reported three and four FBOs in 2024, against 18 and 14 FBOs in 2023, respectively. No deaths were reported in STEC FBOs. One FBO was also reported by Iceland, involving 49 cases and 12 hospitalisations. In the EU, FBOs reported in 2024 were mainly classified as 'general' outbreaks (*N* = 18). Only five 'household' outbreaks were reported. Information on the STEC serogroup was available for 13 outbreaks in MSs and Iceland. STEC O157 was identified in four FBOs. Among non-O157 STEC FBOs, serogroups O26 and O145 caused two outbreaks each and prevailed over STEC O103, O111, O114, O132 and O153, which each caused one FBO. Interestingly, STEC O114 associated with one FBO in Denmark causing four cases was positive for the *stx2f* subtype. Implicated food vehicles described in the four strong-evidence FBOs reported by MSs included 'tap water, including well water' (two FBOs), 'meat preparation intended to be eaten cooked' and 'raw cow's milk' (one FBO each). The implicated food vehicle in the FBO reported by the non-MS (Iceland) was 'minced meat – intended to be eaten cooked'. Details on food vehicles implicated in strong-evidence outbreaks caused by STEC in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-g, of the FBO Addendum (here). For additional information about STEC, see also the infographic available at the front of chapter A4 – Shiga toxin-producing *Escherichia coli* (STEC).

Other bacteria

Thirty-two FBOs caused by ***Yersinia*** were reported from nine MSs (Austria, Belgium, Croatia, Finland, France, Germany, Poland, Spain and Sweden). This is a rise of 88.2% compared with 2023 (15 more FBOs than in 2023) and was accompanied by a huge increase in the number of cases (464 more cases than in 2023, 635.6% increase), mainly due to more FBOs and cases reported by France. The FBOs reported in 2024 were classified as 'household' and 'general' outbreaks, in equal numbers (13 FBOs each). Only one FBO was reported as 'part of multi-country outbreak'. *Y. enterocolitica* was identified in 30 FBOs. In 2024, France reported a total of 14 FBOs and 374 cases, which were mostly part of two very large strong-evidence FBOs associated with the consumption of cheese made from either goats' or cows' milk in multiple places of exposure in the country. The outbreaks involved 177 cases (one hospitalisation) and 154 cases (two hospitalisations), respectively. They were the second and third largest outbreaks caused by *Y. enterocolitica* infection reported to EFSA since the start of FBO data collection at the EU level in 2007. Five cases attributable to *Y. enterocolitica* (serotype O:9) linked to the former French outbreak implicating 'cheese made from goats' milk' were also reported by Belgium as 'part of a multi-country outbreak'. Another very small strong-evidence FBO caused by *Y. enterocolitica* associated with the consumption of 'dairy products (other than cheeses)' was reported by France. Interestingly, no strong-evidence yersiniosis outbreaks caused by 'milk and milk products' have ever previously been reported to EFSA. Foods belonging to the group 'composite foods, multi-ingredient foods and other foods' were implicated in the other two strong-evidence FBOs reported in 2024. One FBO caused by *Yersinia* was also reported by one non-MS (Switzerland). Details on food vehicles implicated in strong-evidence outbreaks caused by *Yersinia* in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-h, of the FBO Addendum (here).

Thirty FBOs caused by ***Shigella*** were reported by 10 MSs (Austria, Belgium, France, Germany, Greece, Italy, Malta, Slovakia, Spain and Sweden), which was a slightly higher number than in 2023 (24 FBOs). In 2024, similar numbers of FBOs were reported as 'household' outbreaks ($N=8$) and 'general' outbreaks ($N=7$). However, one death occurred in 2024 in a household FBO reported by Spain caused by ***S. flexneri*** and involving two cases. Three other FBOs caused by ***S. flexneri*** were reported in 2024, while ***S. sonnei*** was reported in seven FBOs. No information was provided on the *Shigella* species for the other 19 FBOs.

***Escherichia coli* other than STEC** were identified in 26 FBOs reported by six MSs (Austria, France, Hungary, Italy, Romania and Spain). These FBOs were mainly classified as 'general' outbreaks ($N=20$). Only four 'household' outbreaks were reported.

Pathogroups involved in these FBOs were **enteropathogenic *E. coli*** (EPEC) ($N=8$), **enteroinvasive *E. coli*** (EIEC) ($N=3$), **enteroaggregative *E. coli*** (EAEC) ($N=1$) and **enterotoxigenic *E. coli*** (ETEC) ($N=1$). Spain reported two large strong-evidence FBOs caused by EPEC involving 64 and 119 human cases associated with consumption of 'eggs and egg products' and 'meat and meat products', respectively. A third smaller FBO associated with EPEC and the consumption of 'tap water (including well water)' was also reported by Spain. Food vehicles implicated in two strong-evidence EIEC outbreaks reported by France and Spain included 'drinks, including bottled water' and 'pig meat and products thereof', respectively.

The *E. coli* pathogroup was unknown for 13 FBOs, including two very large weak-evidence FBOs reported by Spain causing a total of 248 cases with no hospitalisation or deaths. Foodstuff groups associated with strong-evidence FBOs caused by unspecified *E. coli* included 'composite foods, multi-ingredient foods and other foods' (three strong-evidence FBOs) (i.e. 'meat-based dishes' and unspecified 'mixed food'), 'vegetables and juices and other products thereof', 'milk and milk products' (i.e. 'yoghurt, made from raw or low heat-treated milk') and 'water (and other beverages)' (i.e. 'tap water (including well water)'), which altogether were reported in three strong-evidence outbreaks.

Vibrio parahaemolyticus was identified in eight FBOs reported by three MSs (Belgium, France and Spain). Five and three outbreaks were classified as 'general' and 'household' outbreaks, respectively. 'Crustaceans, shellfish, molluscs and products thereof' (i.e. 'live bivalve molluscs – mussels') were implicated in the only strong-evidence FBO reported to EFSA.

In 2024, a large FBO causing 80 human cases of ***Aeromonas*** infection was reported by Belgium with no hospitalisations or deaths. Another smaller *Aeromonas caviae* outbreak was reported by Spain involving nine human cases (one hospitalisation). Both FBOs were 'general' outbreaks.

B4.2.2 | Bacterial toxins

In 2024, FBOs caused by bacterial toxins were reported by 19 MSs (1231 FBOs) and four non-MSs (12 FBOs). France was the main contributor, alone accounting for 88.5% (1090 FBOs) of the reporting in the EU. More information on the outbreaks caused by bacterial toxins in the EU is available in Table 52.

Staphylococcus aureus toxins were the most frequently reported agents in this group, followed by *Bacillus cereus* toxins, *Clostridium perfringens* toxins and *Clostridium botulinum* toxins. Outbreaks caused by *S. aureus* toxins saw a relative decrease of 28.5% (59 fewer FBOs than in 2023), likewise *B. cereus* toxins fell by 73.2% (347 fewer FBOs) and *C. perfringens* toxins by 53.6% (75 fewer FBOs), respectively. Conversely, the number of FBOs due to unspecified bacterial toxins saw a 12-fold relative increase compared with 2023 (812 more FBOs). FBOs caused by unspecified bacterial toxins were reported by two MSs (Finland and France), with France being the main contributor (880 out of 881 FBOs due to unspecified bacterial toxins).

The vast majority of FBOs caused by bacterial toxins (except *C. botulinum* toxins) were reported as 'general' outbreaks. Overall, there were 1058 'general' outbreaks, accounting for 85.9% of all outbreaks caused by bacterial toxins.

More than 70.0% of the strong-evidence outbreaks caused by bacterial toxins were reported to have occurred after food consumption in either a 'restaurant, pub, street vendor, take-away, etc.' ($N=23$; 26.7%), 'health care and residential facilities' ($N=21$; 24.4%) or 'canteen or catering at workplace, school, etc.' ($N=18$; 20.9%). Implicated food vehicles in these FBOs included foodstuffs belonging to the group 'composite foods, multi-ingredient foods and other foods' (48 FBOs; 55.8%) (mainly 'mixed food'), followed by the groups 'meat and meat products' ($N=22$; 25.6%) (mainly unspecified 'meat and meat products' and 'broiler meat and products thereof'), 'foods of non-animal origin' ($N=12$; 14.0%) (including 'vegetables and juices and other products thereof' and 'cereal products including rice and seeds/pulses (nuts, almonds)'), 'milk and milk products' (i.e. 'cheese') ($N=2$; 2.3%), 'eggs and egg products' ($N=1$; 1.2%) and 'fish and fishery products' (i.e. 'fish and fish products') ($N=1$; 1.2%). Specific differences and peculiarities were observed in the implicated foodstuffs, by type of bacterial toxins causing the outbreak. 'Composite foods, multi-ingredient foods and other foods' predominated in strong-evidence FBOs caused by *B. cereus* toxins and *S. aureus* toxins ($N=26$ and $N=11$, respectively), while 'meat and meat products' were in the majority in FBOs caused by *C. perfringens* toxins ($N=13$). 'Milk and milk products' (i.e. 'cheese') and 'eggs and egg products' were only implicated in strong-evidence FBOs caused by *S. aureus* toxins. Three non-MSs (Norway, Republic of North Macedonia and Switzerland) reported eight strong-evidence outbreaks caused by bacterial toxins. The implicated food vehicles belonged to the food groups 'composite foods, multi-ingredient foods and other foods' (i.e. 'other processed food products and prepared dishes – meat-based dishes', 'other processed food products and prepared dishes, unspecified', 'bakery products – cakes), 'cereal products including rice and seeds/pulses (nuts, almonds)' (i.e. 'rice' and 'cereal products including rice and seeds/pulses (nuts, almonds), unspecified'), 'meat and meat products' and 'fish and fish products' (i.e. 'raw fish').

More specific details are reported below.

***Staphylococcus aureus* toxins**, reported in 148 FBOs, caused the highest number of hospitalisations in FBOs for which the type of bacterial toxin was known. Fourteen MSs and three non-MSs reported FBOs linked to *S. aureus* toxins. *S. aureus* toxins were the only causative agents of FBOs reported by Bulgaria. Three very large FBOs (including two strong-evidence FBOs) caused by *S. aureus* toxins were reported by France, Spain and Romania. In two outbreaks involving 224 and 118 cases, respectively, the place of exposure was a canteen at 'school or kindergarten' while the other one (105 cases) occurred in a 'restaurant, pub, street vendor, take-away, etc.'. 'Mixed food' was implicated in both strong-evidence FBOs. Ten *S. aureus* toxin outbreaks were also reported by non-MSs, and six of them were strong-evidence FBOs. The implicated food vehicles in the strong-evidence FBOs in non-MSs were 'mixed food', 'meat and meat products', 'bakery products' and 'fish and fish products' (i.e. 'raw fish'). Details on food vehicles implicated in strong-evidence outbreaks caused by *S. aureus* toxins in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-i, of the FBO Addendum (here).

***Bacillus cereus* toxins** ranked second among FBOs by bacterial toxins with known causative agents in 2024, totalling 127 FBOs. Nine MSs (Belgium, Czechia, Denmark, France, Germany, Italy, Portugal, Spain and Sweden) contributed to this reporting. *B. cereus* toxins were the leading causative agent of FBOs reported by Portugal. The *B. cereus* toxins had a major health impact, with nine deaths reported in 2024, which is the highest number reported for this agent since the start of FBO data collection. Eight deaths were reported among cases involved in three FBOs occurring in 'health care and residential facilities'. In particular, there were seven deaths in two different FBOs that occurred in Spain in 'nursing homes', while one fatality was reported by France in an outbreak in a 'residential institution (prison or boarding school)'. An additional FBO causing one death was linked to a 'restaurant or cafe or pub or bar or hotel or catering service' in Germany. 'Vegetables and juices and other products thereof' and 'mixed food' were the implicated foods in these FBOs, which were all strong-evidence outbreaks. Five very large FBOs involving altogether a total of 945 cases and all linked to a canteen at 'school or kindergarten' were reported from France, Germany and Czechia. Two of them were strong-evidence FBOs and were also associated with the same items described above, i.e. 'vegetables and juices and other products thereof' and 'mixed food'. Two non-MSs (Norway and Switzerland) also reported two strong-evidence FBOs caused by *B. cereus* toxins, with 'cereal products including rice and seeds/pulses (nuts, almonds)' and 'rice' as the implicated food vehicles. Details on food vehicles implicated in strong-evidence outbreaks caused by *Bacillus cereus* toxins in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-j, of the FBO Addendum (here).

***Clostridium perfringens* toxins** were reported in 65 FBOs by 10 MSs (Belgium, Denmark, Finland, France, Germany, Ireland, Italy, Luxembourg, Portugal and Spain). One death was associated with *C. perfringens* toxins and was reported in an FBO occurring in a 'health care and residential facility' (i.e. 'nursing home') in Spain. Four very large FBOs involving altogether a total of 538 cases were reported from France, Italy and Spain. The place of exposure was a 'health care and residential facilities' (i.e. 'residential institution (prison or boarding school)') in two FBOs (one weak-evidence and one strong-evidence FBO). In the other two FBOs (one weak-evidence and one strong-evidence FBO), a canteen at 'school or kindergarten' and an 'other places of exposure' (i.e. 'temporary mass catering (fairs or festivals)') were implicated. In the 24 strong-evidence FBOs the implicated food vehicles belonged to the groups 'meat and meat products' (i.e. various meat and meat products from bovine, pig, poultry and sheep meat), 'composite foods, multi-ingredient foods and other foods' (mainly 'mixed food') and 'vegetables and juices and other products thereof'. Details on food vehicles implicated in strong-evidence outbreaks caused by *Clostridium perfringens* toxins in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-k, of the FBO Addendum (here).

In 2024, the number of FBOs caused by ***Clostridium botulinum* toxins** was twice as high as in 2023 (five more FBOs for a total of 10 FBOs). However, the health impact associated with these FBOs did not differ substantially compared with the last 4 years. One death was reported from Italy in a household FBO implicating a 'processed food product and prepared dish – vegetable-based dish'. 'Household' outbreaks predominated in *C. botulinum* toxin FBOs (seven FBOs; 70.0%). Other implicated foods in strong-evidence FBOs were 'meat and meat products' and 'vegetables and juices and other products thereof' (i.e. 'mushrooms'). Details on food vehicles implicated in strong-evidence outbreaks caused by *Clostridium botulinum* toxins in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-l, of the FBO Addendum (here).

TABLE 52 Number of food-borne outbreaks, human cases, hospitalisations and deaths, by causative agent, in reporting EU MSs, 2024.

		Outbreaks				**Cases of illness**						
		Total (strong-evidence)		**Reporting rate per 100,000 population**		**Human cases**		**Mean outbreak size (cases) and range (min-max)**	**Hospitalisations**		**Deaths**	
Type of agent		***N***	**% of total[a]**	**2024**	**2020–2023**	***N***	**% of total[a]**		***N***	**% of cases[b]**	***N***	**% of cases[b]**
Bacteria	*Aeromonas*	2 (0)	0.03	< 0.01	< 0.01	89	0.14	44.5 (9–80)	1	1.1	0	0
	Campylobacter	314 (25)	4.8	0.07	0.06	1420	2.3	4.5 (2–113)	101	7.1	0	0
	Escherichia coli other than STEC[c]	26 (11)	0.40	0.01	< 0.01	965	1.5	37.1 (2–125)	24	2.5	0	0
	Listeria monocytogenes	38 (14)	0.58	0.01	0.01	210	0.34	5.5 (2–26)	149	72.3	17	8.1
	Salmonella	1238 (247)	18.9	0.27	0.20	10,164	16.3	8.2 (2–237)	1823	18.3	17	0.17
	Shiga toxin-producing *E. coli* (STEC)	31 (4)	0.47	0.01	0.01	158	0.25	5.1 (2–29)	19	12.2	0	0
	Shigella	30 (0)	0.46	0.01	< 0.01	93	0.15	3.1 (2–17)	19	25.0	1	1.1
	Vibrio parahaemolyticus	8 (1)	0.12	< 0.01	< 0.01	24	0.04	3.0 (2–5)	1	4.2	0	0
	Yersinia	32 (6)	0.49	0.01	< 0.01	537	0.86	16.8 (2–177)	21	4.0	0	0
	Subtotal	**1719 (308)**	**26.2**	**0.38**	**0.29**	**13,660**	**21.9**	**7.9 (2–237)**	**2158**	**16.1**	**35**	**0.26**
Bacterial toxins	*Bacillus cereus* toxins	127 (38)	1.9	0.03	0.05	3315	5.3	26.1 (2–335)	49	1.5	9	0.27
	Clostridium botulinum toxins	10 (3)	0.15	< 0.01	< 0.01	23	0.04	2.3 (2–3)	18	78.3	1	4.3
	Clostridium perfringens toxins	65 (24)	0.99	0.01	0.01	2104	3.4	32.4 (2–163)	9	0.43	1	0.05
	Staphylococcus aureus toxins	148 (21)	2.3	0.03	0.02	1934	3.1	13.1 (2–224)	84	4.4	0	0
	Bacterial toxins, unspecified	881 (0)	13.4	0.20	0.09	6660	10.7	7.6 (2–160)	121	1.8	1	0.02
	Subtotal	**1231 (86)**	**18.8**	**0.27**	**0.18**	**14,036**	**22.5**	**11.4 (2–335)**	**281**	**2.0**	**12**	**0.09**
Viruses	Adenovirus[d]	3 (1)	0.05	< 0.01	< 0.01	38	0.06	12.7 (7–24)	8	33.3	0	0
	Enterovirus	1 (1)	0.02	< 0.01	0	45	0.07	45.0 (–)	0	0	0	0
	Hepatitis A virus[d]	35 (4)	0.53	0.01	< 0.01	117	0.19	3.3 (2–10)	69	60.0	0	0
	Hepatitis E virus	3 (1)	0.05	< 0.01	< 0.01	131	0.21	43.7 (2–127)	50	38.2	0	0
	Norovirus and other calicivirus[e]	631 (78)	9.6	0.14	0.06	14,297	22.9	22.7 (2–851)	237	1.8	3	0.02
	Rotavirus	4 (2)	0.06	< 0.01	< 0.01	95	0.15	23.8 (3–69)	3	3.2	0	0
	Subtotal	**677 (87)**	**10.3**	**0.15**	**0.06**	**14,723**	**23.6**	**21.7 (2–851)**	**367**	**2.6**	**3**	**0.02**

(Continues)

TABLE 52 (Continued)

		Outbreaks				**Cases of illness**						
		Total (strong-evidence)		**Reporting rate per 100,000 population**		**Human cases**		**Mean outbreak size (cases) and range (min-max)**	**Hospitalisations**		**Deaths**	
Type of agent		***N***	**% of total**[a]	**2024**	**2020–2023**	***N***	**% of total**[a]		***N***	**% of cases**[b]	***N***	**% of cases**[b]
Parasites	*Cryptosporidium*	22 (1)	0.34	< 0.01	< 0.01	231	0.37	10.5 (2–160)	6	3.0	0	0
	Giardia	15 (2)	0.23	< 0.01	< 0.01	35	0.06	2.3 (2–5)	3	8.6	0	0
	Trichinella	6 (5)	0.09	< 0.01	< 0.01	67	0.11	11.2 (4–21)	35	52.2	0	0
	Parasites, unspecified	2 (0)	0.03	< 0.01	0	12	0.02	6.0 (4–8)	0	0	0	0
	Subtotal	**45 (8)**	**0.69**	**0.01**	**< 0.01**	**345**	**0.55**	**7.7 (2–160)**	**44**	**14.0**	**0**	**0**
Other causative agents	Histamine and Scombrotoxin	56 (10)	0.85	0.01	0.01	264	0.42	4.7 (2–48)	17	6.4	0	0
	Marine biotoxins[f]	29 (8)	0.44	0.01	0.01	90	0.14	3.1 (2–8)	1	1.1	0	0
	Mushroom toxins	26 (13)	0.40	0.01	< 0.01	112	0.18	4.3 (2–25)	75	67.0	0	0
	Other agents (incl. unspecified)[g]	10 (3)	0.15	< 0.01	< 0.01	54	0.09	5.4 (2–15)	3	7.7	0	0
	Subtotal	**121 (34)**	**1.8**	**0.03**	**0.02**	**520**	**0.83**	**4.3 (2–48)**	**96**	**19.0**	**0**	**0**
Unknown	Unknown	2765 (10)	42.2	0.61	0.47	19,197	30.7	6.9 (2–385)	390	2.0	3	0.02
EU Total		**6558 (533)**	**100**	**1.5**	**1.0**	**62,481**	**100**	**9.5 (2–851)**	**3336**	**5.4**	**53**	**0.09**

[a] Percentage based on the total number of outbreaks or cases reported in the EU.

[b] Percentage based on the total number of cases reported in the EU, by causative agent; outbreaks with an unknown number of cases and/or hospitalisations were excluded from the calculation of the hospitalisation rate; outbreaks with an unknown number of cases and/or deaths were excluded from the calculation of the fatality rate.

[c] '*Escherichia coli* other than STEC' includes 'enteropathogenic *E. coli* (EPEC)' (8), 'enteroinvasive *E. coli* (EIEC)' (3), 'enteroaggregative *E. coli* (EAEC)' (1), 'enterotoxigenic *E. coli* (ETEC)' (1) and other unspecified *Escherichia coli* (13).

[d] During the final phase of report production, the Netherlands informed that adenovirus was mistakenly reported as the causative agent of one strong-evidence outbreak, which involved 24 cases and caused eight hospitalisations. The causative agent was hepatitis A virus.

[e] 'Norovirus and other calicivirus' includes 'norovirus' (570), 'Sapporo virus' (1) and other unspecified caliciviruses (60).

[f] 'Marine biotoxins' includes 'ciguatoxin' (6) and other unspecified toxins (23).

[g] 'Other agents (incl. unspecified)' includes 'atropine' (8) and 'lectins' (2).

B4.2.3 | Viruses

During 2024, 20 MSs reported 677 FBOs caused by viruses. Eleven FBOs involving viruses were also reported by three non-MSs. Key statistics on FBOs associated with viruses are available in Table 52.

Norovirus (and other caliciviruses)

Outbreaks caused by **norovirus (and other caliciviruses)** were reported by 19 MSs and three non-MSs.

Norovirus (and other caliciviruses) caused the most cases involved in FBOs in 2024 (*N* = 14,297) and were the third most frequently implicated agent in terms of number of outbreaks (631 FBOs). In eight MSs (Belgium, Czechia, Denmark, Finland, Latvia, Luxembourg, the Netherlands and Sweden) and two non-MSs (Norway and Switzerland), norovirus (and other caliciviruses) was the leading causative agent of FBOs.

Among this group of causative agents, norovirus (Norwalk-like virus) was identified in 570 FBOs and sapovirus (Sapporo virus) in one outbreak, while for 60 FBOs the information was not available.

Overall, the health impact in the EU of FBOs caused by norovirus (and other caliciviruses) was considerably higher than in 2023. The number of FBOs and human cases increased by 75.8% and 75.4%, respectively (272 more FBOs and 6148 more cases), compared with 2023. Hospitalisations rose by 139.4% (138 more hospitalisations than in 2023) and two more deaths were also reported (in 2023 one death was reported). Ten MSs (Austria, Czechia, Ireland, Italy, Latvia, the Netherlands, Poland, Portugal, Spain and Sweden) and one non-MS (Switzerland) had a ≥ 50% relative increase in the number of FBO caused by these agents. In France, 72 more FBOs than in 2023 (37.7% increase) were observed.

Most outbreaks caused by norovirus (and other caliciviruses) were 'general' outbreaks (*N* = 475; 75.3%). The mean size of outbreaks associated with this agent group was among the largest observed in 2024 and many outbreaks were large (34 outbreaks included ≥ 50 and < 100 cases each) or very large in size (19 outbreaks included ≥ 100 cases each). Two outbreaks involved more than 700 cases each and were reported by Spain and the Netherlands. They were both weak-evidence outbreaks with water suspected to be the implicated source. Two very large FBOs caused by these agents were also reported by Norway. One of them was a strong-evidence FBO typically associated with 'crustaceans, shellfish, molluscs and products thereof' as the implicated food vehicle.

The most frequent place of exposure documented in strong-evidence FBOs was a 'restaurant, pub, street vendor, take-away, etc.' (36 FBOs; 46.2%), followed by 'domestic premises' (18 FBOs; 23.1%). 'Fish and fishery products' (29 FBOs) and 'composite foods, multi-ingredient foods and other foods' (29 FBOs) were mostly implicated in strong-evidence FBOs. Among the former group, 'crustaceans, shellfish, molluscs and products thereof' (i.e. 'oysters', 'mussels' and 'unspecified crustaceans, shellfish, molluscs and products thereof') caused 28 outbreaks (35.9% of all strong-evidence FBOs caused by norovirus (and other caliciviruses)) while in the latter group, 'mixed food' and 'buffet meals' were reported in 21 FBOs (26.9%) and six FBOs (7.7%), respectively. Other implicated vehicles were 'foods of non-animal origin' (nine FBOs) (i.e. 'vegetables and juices and other products thereof', 'fruit, berries and juices and other products thereof' and 'cereal products including rice and seeds/pulses (nuts, almonds)'), 'water (and other beverages)' (i.e. 'tap water, including well water') (five outbreaks), 'meat and meat products' (i.e. 'fresh meat from pig', 'other or mixed red meat and products thereof' and 'unspecified meat and meat products') (three FBOs), 'eggs and egg products' (two FBOs) and 'milk and milk products' (i.e. 'dairy products (other than cheeses)') (one FBO). Details on food vehicles implicated in strong-evidence outbreaks caused by 'norovirus (and other caliciviruses)' in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-m, of the FBO Addendum (here).

One non-MS (Norway) reported two strong-evidence outbreaks caused by norovirus, both linked to 'crustaceans, shellfish, molluscs and products thereof'.

Hepatitis A

Outbreaks caused by **hepatitis A virus** were reported by 11 MSs, resulting in 36 FBOs, 141 cases and 77 hospitalisations (respectively 25 FBOs, 95 cases and 41 hospitalisations more than in 2023). Five strong-evidence FBOs were reported by the Netherlands and Poland. The implicated foods were 'foods of non-animal origin' (i.e. 'fruit, berries and juices and other products thereof') in four FBOs and 'fish and fishery products' (i.e. 'oysters') in one FBO. Most FBOs were classified as 'household' outbreaks (*N* = 16), followed by 'general' outbreaks (*N* = 12). One FBO was classified as 'part of multi-country outbreak'. For seven FBOs, the type of outbreak was unknown.

Other viruses

Four FBOs caused by **rotavirus** were reported by three MSs (Germany, Poland and Spain). Two of them were strong-evidence outbreaks and were associated with 'fruit, berries and juices and other products thereof' and 'water' (i.e. 'tap water, including well water'). No substantial difference was observed in the type of outbreak (two 'general' and one 'household' outbreak).

Germany and Finland reported three **Hepatitis E** outbreaks (including one strong-evidence FBO). The largest one was a 'general' outbreak reported by Finland and was associated with paslahepevirus balayani (formerly Hepatitis E virus) G3f.

It involved 127 human cases and 48 hospitalisations. This FBO was the largest Hepatitis E outbreak reported to EFSA since the start of data collection. Mettwurst (salami-type sausage) from pork and horse meat, consumed in multiple places in the country, was the implicated vehicle.

Two FBOs caused by **adenovirus** were notified in 2024 by Latvia. Both were classified as weak-evidence 'general' outbreaks.

Enterovirus caused 45 cases of illness in a single strong-evidence outbreak reported by Spain in a 'hospital or medical care facility' associated with consumption of 'pig meat and products thereof'. This FBO was classified as a 'general' outbreak.

B4.2.4 | Parasites

Outbreaks caused by parasites were reported by 11 MSs and by one non-MS. In the EU, no substantial difference in numbers was observed in the type of outbreak reported for these FBOs (i.e. 18 'general' outbreaks and 15 'household' outbreaks). For 12 FBOs, the type of outbreak was unknown. Details on the FBOs caused by parasites are available in Table 52.

Cryptosporidium

Among parasites, ***Cryptosporidium*** was the leading causative agent of FBOs and cases in the EU in 2024, responsible for 22 FBOs (four more FBOs than in 2023). A total of seven MSs (Finland, Germany, Greece, Ireland, Malta, Spain and Sweden) contributed to this reporting. Ireland contributed the most to the reported outbreaks (six FBOs; 27.3%). In this country, ***Cryptosporidium*** was the most frequently reported causative agent of FBOs in 2024. Another outbreak was reported by one non-MS (Norway).

C. parvum was involved in four FBOs while ***C. hominis*** was reported in Finland in one very large FBO causing 160 cases and five hospitalisations. For 17 outbreaks, information on the *Cryptosporidium* species was not available. Only one single FBO caused by *C. parvum* was reported by Sweden as a strong-evidence outbreak. A vegetable (i.e. kale) was the implicated food, which was consumed in a 'restaurant, pub, street vendor, take-away, etc.'.

Trichinella

Six outbreaks caused by ***Trichinella*** were reported by three MSs (Italy, Romania and Spain). Romania contributed to half of the reported outbreaks (three FBOs) and in this country, ***Trichinella*** was the most frequently reported causative agent of FBOs in 2024.

T. spiralis was involved in four FBOs, while for two FBOs information on the species was not reported. In all five strong-evidence outbreaks, 'meat and meat products' were the implicated food vehicles (i.e. 'meat and meat products from pig', 'meat preparation from wild boar, intended to be eaten cooked', 'unspecified meat and meat products'). The three largest outbreaks were caused by *T. spiralis* and were reported by Romania (two FBOs involving 21 and 15 cases, respectively) and Spain (one FBO involving 13 cases). Details on food vehicles implicated in strong-evidence outbreaks caused by *Trichinella* in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-n, of the FBO Addendum (here).

For additional information about *Trichinella*, see also the infographic available at the front of chapter A7 – *Trichinella*.

Other parasites

Giardia was reported in 15 FBOs from four MSs (Germany, Malta, Poland and Spain). ***G. intestinalis*** was implicated in six FBOs, while no information on the species was reported for the other nine FBOs. All outbreaks were very small in size. Two strong-evidence FBOs were reported with 'mixed food' and 'fruit, berries and juices and other products thereof' as implicated vehicles.

Two FBOs caused by an unspecified parasite were reported by France.

B4.2.5 | Other causative agents

Nine MSs (Belgium, Croatia, France, Hungary, Italy, Malta, Portugal, Spain and Sweden) reported a total of 121 FBOs caused by causative agents other than the ones mentioned above. One FBO was reported by one non-MS (Norway). These causative agents are not routinely monitored by national surveillance programmes. As a result, the total number of such FBOs reported in the EU may be underestimated and direct comparison among MSs, even when using population-based indicators (e.g. FBO reporting rate), is likely highly biased. Key statistics on FBOs associated with other causative agents are available in Table 52.

'Histamine and scombrotoxin' were the most frequent agents reported in this group (46.3%) with eight MSs (Belgium, Croatia, France, Italy, Malta, Portugal, Spain and Sweden) providing information on such outbreaks. In 2024, the number of FBOs (56 FBOs) saw a relative decrease of 15.2% (10 fewer FBOs) compared with the number of outbreaks reported in 2023. Almost all these FBOs were due to **histamine** (55 FBOs; 98.2%), while only one outbreak was caused by **scombrotoxin**. A single outbreak caused by histamine was also reported by one non-MS (Norway).

FBOs reported in 2024 in the EU were mainly classified as 'general' outbreaks ($N=40$), followed by 'household' outbreaks ($N=15$). For one FBO the type of outbreak was unknown.

'Histamine and scombrotoxin' poisoning outbreaks were mostly very small in size, involving fewer than 10 human cases, and occurred mainly in a 'restaurant, pub, street vendor, take-away, etc.' (three strong-evidence FBOs) and in 'domestic premises' (three strong-evidence FBOs). All but one of the reported strong-evidence FBOs caused by histamine were linked to the consumption of 'fish and fishery products' (nine FBOs). One outbreak reported by France was linked to the consumption of 'foods of non-animal origin' (i.e. 'vegetables and juices and other products thereof') in a 'school or kindergarten' canteen, with 48 cases involved. Details on food vehicles implicated in strong-evidence outbreaks caused by 'histamine and scombrotoxin' in the EU are available in the EFSA Knowledge Junction at Zenodo, Section 7, Table S7-o, of the FBO Addendum (here).

One non-MS (Norway) reported one strong-evidence outbreak caused by histamine and linked to 'fish and fish products'.

Marine biotoxins were responsible for 29 FBOs reported by three MSs (France, Spain and Sweden), with nine fewer outbreaks than in 2023 (a decrease of 23.7%). France accounted for most of these FBOs (15 FBOs; 51.7%). Most FBOs were classified as 'general' outbreaks ($N=20$; 69.0%). Ciguatoxins were implicated in six FBOs while in the other FBOs the specific marine biotoxins were not mentioned. 'Fish and fishery products', including 'fish and fish products' (seven FBOs) and 'crustaceans, shellfish, molluscs and products thereof' (i.e. 'mussels') (one FBO), were the implicated foods in strong-evidence FBOs.

Four MSs (France, Hungary, Italy and Spain) reported 26 FBOs caused by **mushroom toxins** (eight more FBOs than in 2023). Italy contributed the most to this reporting (21 FBOs; 80.8%). Overall, mushroom toxins were associated with very small outbreaks, mainly classified as 'household' outbreaks ($N=24$; 92.3%), and the place of consumption was mostly 'domestic premises'. However, a medium-size outbreak (25 cases, 15 hospitalisations) was reported by Hungary in a 'restaurant, pub, street vendor, take-away, etc.'. The implicated food vehicles in the 13 strong-evidence outbreaks belonged to the food groups 'composite foods, multi-ingredient foods and other foods' (i.e. 'mushroom-based dishes') and 'food of non-animal origin' (i.e. 'mushroom').

Atropine and lectin were associated with eight and two FBOs in 2024 reported by France and Sweden, respectively. All FBOs caused by atropine were classified as 'household' outbreaks, while those due to lectin were 'general' outbreaks. The implicated food vehicles were 'vegetables and juices and other products thereof' for atropine (one strong-evidence FBO), and 'mixed food' (i.e. 'sandwiches – non-meat') and 'vegetables and juices and other products thereof' (i.e. 'legumes') for lectin (one strong-evidence FBO each).

B4.2.6 | Outbreaks caused by unknown/unspecified agents

In 2024, the number of FBOs with unknown aetiology or unspecified causative agents accounted for just eight more FBOs than in 2023 for a total of 2765 FBOs. Key statistics on FBOs caused by unknown causative agents are available in Table 52.

Seventeen MSs contributed to reporting this data. Forty-six outbreaks with unknown causative agents were also reported by five non-MSs. Countries with the most reported outbreaks with an unknown or unspecified causative agent were Belgium, France, the Netherlands, Poland and Spain. In Belgium and the Netherlands, the reporting of FBOs with unknown aetiology accounted for more than 90.0% of all reported FBOs.

Most outbreaks were very small (< 10 cases) in size (2471 FBOs; 89.4%). This finding suggests that in very small outbreaks, occurring in a confined environment, it is relatively easier to find a link among cases, although identification of the causative agent may be challenging. However, in 2024, five MSs (Czechia, France, Italy, Poland and Spain) reported nine very large outbreaks, all weak-evidence outbreaks. The total number of cases and hospitalisations involved in these FBOs were 1486 and 11, respectively.

B4.2.7 | Top-10 agent/food pairs in strong-evidence outbreaks associated with the highest impact on health in the EU

FBOs with the highest health impact in 2024 in the EU, in terms of number of FBOs, cases, hospitalisations and deaths, are shown in Tables 53–56. These tables include details on the number of MSs reporting FBOs for the related food/agent pair in 2024, as well as for the period 2020–2024, for trend watching purposes. Regarding food vehicles, details are provided in the table footnotes, if available.

Overall, *Salmonella* paired with either 'pig meat and products thereof' 'or 'vegetables and juices and other products thereof' ranked among the top 10 pairs in all the classifications. *Salmonella* in combination with 'eggs and egg products' was the pair causing the most number of outbreaks and hospitalisations, and ranked fourth for cases. *Salmonella* and 'mixed food' was also among the most frequently reported pairs for total number of outbreaks, cases and hospitalisations. Other relevant combinations for *Salmonella* included 'broiler meat (*Gallus gallus*) and products thereof' or 'bakery products'. These pairs ranked among the top 10 pairs for total number of outbreaks, hospitalisations and deaths. Other relevant pairs involving *Salmonella* in combination with other food types are reported in Tables 53–56. These findings confirm the high health burden of this food-borne pathogen in the EU in 2024, not only in combination with typical foods from the poultry production chain and products thereof but also with other relevant animal and non-animal primary production chains, i.e. pig meat and vegetables, respectively.

Another critical pair included *Bacillus cereus* toxins in combination with either 'mixed food' or 'vegetables and juices and other products thereof'. The former pair was among the most frequently reported pairs for total number of outbreaks, cases and deaths, while the latter caused the highest number of deaths in 2024 and was also among the top pairs causing the highest number of cases.

Norovirus (and other caliciviruses) and 'mixed food' was the pair causing the highest number of cases and ranked six for total number of outbreaks. These agents in combination with 'crustaceans, shellfish, molluscs and products thereof' were also among the most frequently reported pairs for total number of outbreaks.

Listeria monocytogenes in combination with various types of food of either animal or non-animal origin was included in four pairs associated with the highest number of deaths (Table 56).

Other agent/food combinations of particular interest reported in strong-evidence FBOs include *Yersinia* in 'cheese' (see also Section B.4.2.1) and Hepatitis E in 'other or mixed red meat and products thereof' (see also Section B.4.2.3). The first pair was never previously reported to EFSA (as also described in Section B.4.2.1 'other bacteria') and as such represents a signal calling attention to a potential relevant new risk related to the raw milk cheese production chain (Table 53).

TABLE 53 Top 10 pathogen/food vehicle pairs causing the highest number of strong-evidence outbreaks in reporting EU MSs, in 2024.

2024					**2020–2023**			**Evaluation**
Rank[a]	**Causative agent**	**Food vehicle**	**Outbreaks (*N*)**	**Reporting MS (*N* outbreaks)**	**Rank**[a]	**Outbreaks (*N*/year) (range)**	**Reporting MS (*N*/year)**	**2024 vs. 2020–2023**[b]
1	*Salmonella*	Eggs and egg products[c]	83	Poland (31), Spain (26), France (13), Lithuania (3), Belgium (2), Portugal (2), Austria (1), Czechia (1), Hungary (1), Ireland (1), Netherlands (1), Sweden (1)	1	61.3 (37–86)	8.3	↑
2	*Salmonella*	Mixed food[d]	36	Spain (13), Germany (5), Hungary (4), Slovakia (4), Czechia (3), Poland (3), France (2), Italy (2)	2	29.0 (3–65)	7.3	≈
3	Norovirus and other calicivirus	Crustaceans, shellfish, molluscs and products thereof[e]	28	France (12), Finland (6), Spain (5), Italy (2), Denmark (1), Netherlands (1), Portugal (1)	3	21.8 (10–30)	5.0	↑
4	*Bacillus cereus* toxins	Mixed food[f]	24	France (6), Spain (6), Germany (5), Portugal (5), Italy (2)	13	6.5 (5–9)	3.8	↑↑
5	*Salmonella*	Bakery products[g]	23	Poland (11), Slovakia (5), Spain (3), Austria (2), Germany (1), Romania (1)	6	13.0 (9–17)	4.5	↑↑
6	Norovirus and other calicivirus	Mixed food[h]	21	Spain (6), Germany (4), Finland (2), France (2), Hungary (2), Italy (2), Belgium (1), Slovakia (1), Sweden (1)	8	11.8 (5–16)	5.0	↑↑
7	*Salmonella*	Broiler meat (*Gallus gallus*) and products thereof[i]	19	Spain (7), Lithuania (5), France (3), Slovakia (3), Hungary (1)	7	12.5 (2–30)	6.3	↑↑
8	*Salmonella*	Pig meat and products thereof[j]	16	Italy (6), Germany (4), Lithuania (2), Poland (2), Slovakia (1), Sweden (1)	5	13.3 (10–18)	5.3	≈
8	*Salmonella*	Vegetables and juices and other products thereof[k]	16	Germany (5), Austria (2), Spain (2), Sweden (2), Czechia (1), Denmark (1), France (1), Italy (1), Slovakia (1)	14	5.8 (1–11)	4.3	↑↑
9	Mushroom toxins	Mixed food[l]	11	Italy (11)	18	3.5 (0–14)	0.25	↑↑
10	*Campylobacter*	Broiler meat (*Gallus gallus*) and products thereof[m]	10	Denmark (7), Germany (1), Hungary (1), Spain (1)	9	8.8 (4–15)	3.8	≈
10	*Clostridium perfringens* toxins	Mixed food[n]	10	France (6), Denmark (1), Germany (1), Portugal (1), Spain (1)	11	7.5 (5–10)	5.0	↑
10	*Salmonella*	Meat and meat products, unspecified	10	Spain (5), Poland (3), France (2)	12	6.8 (4–10)	3.3	↑

Abbreviation: NA, Not Applicable.

[a] Ranking of the causative agent/food vehicle combinations based on the number of strong-evidence FBOs in which the combinations were implicated (rank 1 is the highest rank meaning the most commonly implicated). Strong-evidence outbreaks with unknown causative agents are not included.

[b] Double arrows indicate variations < −50% (↓↓) or > 50% (↑↑) in the number of outbreaks; a single arrow indicates variations ≥ − 50% and < −25% (↓) or variations > 25% and ≤ 50% (↑); a double tilde (≈) indicates variations ≥ − 25% and ≤ 25%.

[c] In 2024, 'eggs and egg products' includes 'eggs and egg products' (72), 'eggs' (10), 'eggs – table eggs – mixed whole' (1).

[d] In 2024, 'mixed food' includes 'mixed food' (18), 'other processed food products and prepared dishes – meat-based dishes' (7), 'other processed food products and prepared dishes – egg-based dishes' (3), 'other processed food products and prepared dishes – fish and seafood-based dishes' (2), 'other processed food products and prepared dishes – pasta-based dishes' (2), 'other processed food products and prepared dishes' (1), 'other processed food products and prepared dishes – noodles' (1), 'other processed food products and prepared dishes – sandwiches – with meat' (1), 'sauce and dressings – mayonnaise' (1).

[e] In 2024, 'crustaceans, shellfish, molluscs and products thereof' includes 'live bivalve molluscs – oysters' (18), 'crustaceans, shellfish, molluscs and products thereof' (7), 'live bivalve molluscs – oysters – depurated' (2), 'live bivalve molluscs – mussels' (1).

(Continues)

TABLE 53 (Continued)

[f] In 2024, 'mixed food' includes 'mixed food' (6), 'other processed food products and prepared dishes – pasta – simple pasta' (3), 'other processed food products and prepared dishes' (2), 'other processed food products and prepared dishes – legumes-based dishes' (2), 'other processed food products and prepared dishes – noodles' (2), 'other processed food products and prepared dishes – meat-based dishes' (1), 'other processed food products and prepared dishes – pasta – filled pasta' (1), 'other processed food products and prepared dishes – pasta/rice salad' (1), 'other processed food products and prepared dishes – rice-based dishes' (1), 'other processed food products and prepared dishes – sandwiches' (1), 'other processed food products and prepared dishes – sandwiches – with meat' (1), 'other processed food products and prepared dishes – vegetable-based dishes' (1), 'soups' (1), 'soups – ready-to-eat' (1).

[g] In 2024, 'bakery products' includes 'bakery products – cakes – containing raw cream' (8), 'bakery products – desserts – containing raw eggs' (6), 'bakery products – cakes – containing heat-treated cream' (3), 'bakery products' (2), 'bakery products – desserts' (2), 'bakery products – cakes' (1), 'bakery products – pastry' (1).

[h] In 2024, 'mixed food' includes 'mixed food' (11), 'other processed food products and prepared dishes – sushi' (3), 'other processed food products and prepared dishes' (1), 'other processed food products and prepared dishes – meat-based dishes' (1), 'other processed food products and prepared dishes – pasta – simple pasta' (1), 'other processed food products and prepared dishes – potato-based dishes' (1), 'other processed food products and prepared dishes – sandwiches' (1), 'ready-to-eat salads' (1), 'tzatziki' (1).

[i] In 2024, 'broiler meat (*Gallus gallus*) and products thereof' includes 'broiler meat (*Gallus gallus*) and products thereof' (16), 'meat from broilers (*Gallus gallus*)' (3).

[j] In 2024, 'pig meat and products thereof' includes 'pig meat and products thereof' (9), 'meat from pig – meat preparation – intended to be eaten raw' (2), 'meat from pig – meat products' (2), 'meat from pig' (1), 'meat from pig – meat products – meat specialities' (1), 'meat from pig – minced meat – intended to be eaten raw' (1).

[k] In 2024, 'vegetables and juices and other products thereof' includes 'vegetables and juices and other products thereof' (4), 'tomato' (3), 'alfalfa sprouts' (2), 'rocket, rucola' (2), 'vegetables – leaves' (2), 'cherry tomato' (1), 'onion' (1), 'watermelon' (1).

[l] In 2024, 'mixed food' includes 'other processed food products and prepared dishes – mushroom-based dishes' (11).

[m] In 2024, 'broiler meat (*Gallus gallus*) and products thereof' includes 'meat from broilers (*Gallus gallus*)' (7), 'broiler meat (*Gallus gallus*) and products thereof' (2), 'meat from broilers (*Gallus gallus*) – fresh' (1).

[n] In 2024, 'mixed food' includes 'other processed food products and prepared dishes – meat-based dishes' (6), 'other processed food products and prepared dishes – pasta – simple pasta' (2), 'mixed food' (1), 'other processed food products and prepared dishes' (1).

TABLE 54 Top-10 pathogen/food vehicle pairs causing the highest number of cases in strong-evidence outbreaks in reporting EU MSs, in 2024.

2024					**2020–2023**			**Evaluation**
Rank[a]	**Causative agent**	**Food vehicle**	**Cases (*N*)**	**Reporting MS (*N* cases)**	**Rank**[a]	**Cases (*N*/year) (range)**	**Reporting MS (*N*/year)**	**2024 versus 2020–2023**[b]
1	Norovirus and other calicivirus	Mixed food[c]	1180	Slovakia (498), Spain (256), Germany (141), Sweden (90), Finland (79), Hungary (48), France (45), Italy (21), Belgium (2)	3	382.8 (233–487)	5.0	↑↑
2	*Salmonella*	Mixed food[d]	887	Italy (337), Poland (209), Hungary (117), Germany (105), Slovakia (45), Spain (43), Czechia (26), France (5)	2	415.5 (91–839)	7.3	↑↑
3	*Bacillus cereus* toxins	Mixed food[e]	773	Germany (229), Portugal (180), France (158), Spain (153), Italy (53)	23	74.8 (26–120)	3.8	↑↑
4	*Salmonella*	Eggs and egg products[f]	748	Spain (240), Poland (163), Netherlands (79), Hungary (70), France (64), Belgium (62), Portugal (30), Lithuania (12), Ireland (9), Sweden (8), Czechia (7), Austria (4)	1	578.8 (303–1101)	8.3	↑
5	*Salmonella*	Vegetables and juices and other products thereof[g]	486	Germany (225), Sweden (124), Austria (46), Spain (34), Denmark (22), Italy (16), Slovakia (10), Czechia (7), France (2)	4	359.0 (7–1103)	4.3	↑
6	Norovirus and other calicivirus	Water	444	Spain (340), Italy (104)	6	296.8 (8–751)	2.5	↑
7	*Clostridium perfringens* toxins	Mixed food[h]	443	France (354), Portugal (50), Denmark (20), Spain (11), Germany (8)	9	203.5 (105–292)	5.0	↑↑
8	*Bacillus cereus* toxins	Vegetables and juices and other products thereof[i]	340	Czechia (160), France (154), Spain (26)	21	81.8 (18–189)	1.3	↑↑
9	*Yersinia*	Cheese[j]	336	France (331), Belgium (5)	NA	0	0	NA

TABLE 55 (Continued)

2024					2020–2023			Evaluation
Rank[a]	**Causative agent**	**Food vehicle**	**Cases (*N*)**	**Reporting MS (*N* cases)**	**Rank**[a]	**Cases (*N*/year) (range)**	**Reporting MS (*N*/year)**	**2024 versus 2020–2023**[b]
10	*Salmonella*	Pig meat and products thereof[k]	334	Germany (218), Italy (60), Lithuania (27), Poland (23), Slovakia (4), Sweden (2)	10	196.8 (69–294)	5.3	↑↑

Abbreviation: NA, Not Applicable.

[a] Ranking of the causative agent/food vehicle combinations based on the number of cases of illness in strong-evidence FBOs in which the combinations were implicated (rank 1 is the highest rank meaning the most commonly implicated). Strong-evidence outbreaks with unknown causative agents are not included.

[b] Double arrows indicate variations < –50% (↓↓) or > 50% (↑↑) in the number of cases; a single arrow indicates variations ≥ – 50% and < –25% (↓) or variations > 25% and ≤ 50% (↑); a double tilde (≈) indicates variations ≥ – 25% and ≤ 25%.

[c] In 2024, 'mixed food' includes 'mixed food' (881), 'other processed food products and prepared dishes – sushi' (111), 'other processed food products and prepared dishes' (99), 'other processed food products and prepared dishes – pasta – simple pasta' (30), 'ready-to-eat salads' (20), 'tzatziki' (20), 'other processed food products and prepared dishes – potato-based dishes' (15), 'other processed food products and prepared dishes – meat-based dishes' (2), 'other processed food products and prepared dishes – sandwiches' (2).

[d] In 2024, 'mixed food' includes 'other processed food products and prepared dishes – pasta-based dishes' (337), 'mixed food' (259), 'other processed food products and prepared dishes – meat-based dishes' (118), 'other processed food products and prepared dishes – noodles' (79), 'other processed food products and prepared dishes' (45), 'other processed food products and prepared dishes – egg-based dishes' (25), 'other processed food products and prepared dishes – fish and seafood-based dishes' (19), 'other processed food products and prepared dishes – sandwiches – with meat' (3), 'sauce and dressings – mayonnaise' (2).

[e] In 2024, 'mixed food' includes 'mixed food' (153), 'other processed food products and prepared dishes – noodles' (138), 'other processed food products and prepared dishes – pasta – simple pasta' (103), 'other processed food products and prepared dishes – meat-based dishes' (77), 'other processed food products and prepared dishes – legume-based dishes' (76), 'other processed food products and prepared dishes – sandwiches – with meat' (60), 'other processed food products and prepared dishes – rice-based dishes' (50), 'other processed food products and prepared dishes – vegetable-based dishes' (34), 'soups – ready-to-eat' (30), 'other processed food products and prepared dishes' (21), 'soups' (13), 'other processed food products and prepared dishes – pasta – filled pasta' (11), 'other processed food products and prepared dishes – sandwiches' (4), 'other processed food products and prepared dishes – pasta/rice salad' (3).

[f] In 2024, 'eggs and egg products' includes 'eggs and egg products' (594), 'eggs' (147), 'eggs – table eggs – mixed whole' (7).

[g] In 2024, 'vegetables and juices and other products thereof' includes 'alfalfa sprouts' (142), 'rocket, rucola' (139), 'tomato' (73), 'vegetables and juices and other products thereof' (56), 'vegetables – leaves' (36), 'cherry tomato' (26), 'watermelon' (10), 'onion' (4).

[h] In 2024, 'mixed food' includes 'other processed food products and prepared dishes – pasta – simple pasta' (193), 'other processed food products and prepared dishes – meat-based dishes' (189), 'other processed food products and prepared dishes' (50), 'mixed food' (11).

[i] In 2024, 'vegetables and juices and other products thereof' includes 'vegetables and juices and other products thereof' (180), 'common bean' (160).

[j] In 2024, 'cheese' includes 'cheeses made from goats' milk' (177), 'cheeses made from cows' milk' (154), 'cheese' (5).

[k] In 2024, 'pig meat and products thereof' includes 'meat from pig – minced meat – intended to be eaten raw' (191), 'pig meat and products thereof' (105), 'meat from pig – meat preparation – intended to be eaten raw' (24), 'meat from pig – meat products' (7), 'meat from pig' (4), 'meat from pig – meat products – meat specialities' (3).

TABLE 55 Top 10 pathogen/food vehicle pairs causing the highest number of hospitalisations in strong-evidence outbreaks in reporting EU MSs, in 2024.

2024					2020–2023			Evaluation
Rank[a]	**Causative agent**	**Food vehicle**	**Hospitalisations (*N*)**	**Reporting MS (*N* hospitalisations)**	**Rank**[a]	**Hospitalisations (*N*/year) (range)**	**Reporting MS (*N*/year)**	**2024 versus 2020–2023**[b]
1	*Salmonella*	Eggs and egg products[c]	138	Poland (61), Spain (36), France (13), Lithuania (10), Belgium (5), Ireland (4), Hungary (3), Portugal (3), Czechia (2), Austria (1)	1	93.0 (46–124)	6.5	↑
2	*Salmonella*	Pig meat and products thereof[d]	106	Germany (73), Lithuania (13), Italy (12), Poland (6), Slovakia (2)	3	54.3 (22–94)	4.3	↑↑
3	*Salmonella*	Vegetables and juices and other products thereof[e]	96	Germany (65), Spain (14), Austria (11), Czechia (2), Slovakia (2), France (1), Italy (1)	5	32.5 (2–75)	2.5	↑↑
4	*Salmonella*	Mixed food[f]	85	Germany (25), Hungary (18), Poland (16), Slovakia (16), Spain (4), Czechia (3), France (3)	2	75.8 (11–149)	6.8	≈
5	*Salmonella*	Bakery products[g]	75	Poland (37), Romania (14), Spain (8), Austria (7), Slovakia (7), Germany (2)	4	52.8 (21–82)	4.3	↑
6	*Salmonella*	Bovine meat and products thereof[h]	56	Denmark (24), Germany (24), Italy (4), Slovenia (4)	12	13.3 (0–37)	1.8	↑↑
7	Hepatitis E virus	Other or mixed red meat and products thereof[i]	48	Finland (48)	NA	0	0	NA
8	*Staphylococcus aureus* toxins	Mixed food[j]	33	Spain (22), Romania (10), Greece (1)	6	30.0 (0–58)	2.3	≈
9	*Salmonella*	Broiler meat (*Gallus gallus*) and products thereof[k]	32	Spain (12), Lithuania (9), Slovakia (7), Hungary (3), France (1)	7	24.8 (3–79)	4.5	↑
10	*Salmonella*	Other or mixed red meat and products thereof[l]	28	Germany (15), Poland (13)	28	2.8 (0–8)	1.0	↑↑

Abbreviation: NA, Not Applicable.

[a] Ranking of the causative agent/food vehicle combinations based on the number of hospitalisations in strong-evidence FBOs in which the combinations were implicated (rank 1 is the highest rank meaning the most commonly implicated). Strong-evidence outbreaks with unknown causative agents are not included.

[b] Double arrows indicate variations < –50% (↓↓) or > 50% (↑↑) in the number of hospitalisations; a single arrow indicates variations ≥ – 50% and < –25% (↓) or variations > 25% and ≤ 50% (↑); a double tilde (≈) indicates variations ≥ – 25% and ≤ 25%.

[c] In 2024, 'eggs and egg products' includes 'eggs and egg products' (126), 'eggs' (10), 'eggs – table eggs – mixed whole' (2).

[d] In 2024, 'pig meat and products thereof' includes 'meat from pig – minced meat – intended to be eaten raw' (64), 'pig meat and products thereof' (29), 'meat from pig – meat preparation – intended to be eaten raw' (6), 'meat from pig – meat products – meat specialities' (3), 'meat from pig' (2), 'meat from pig – meat products' (2).

[e] In 2024, 'vegetables and juices and other products thereof' includes 'rocket, rucola' (37), 'tomato' (25), 'vegetables and juices and other products thereof' (17), 'cherry tomato' (9), 'alfalfa sprouts' (6), 'watermelon' (2).

[f] In 2024, 'mixed food' includes 'other processed food products and prepared dishes – meat-based dishes' (39), 'mixed food' (26), 'other processed food products and prepared dishes' (10), 'other processed food products and prepared dishes – fish and seafood-based dishes' (4), 'other processed food products and prepared dishes – noodles' (2), 'sauce and dressings – mayonnaise' (2), 'other processed food products and prepared dishes – egg-based dishes' (1), 'other processed food products and prepared dishes – sandwiches – with meat' (1).

[g] In 2024, 'bakery products' includes 'bakery products – cakes – containing raw cream' (32), 'bakery products – cakes – containing heat-treated cream' (18), 'bakery products – desserts – containing raw eggs' (9), 'bakery products' (7), 'bakery products – desserts' (7), 'bakery products – cakes' (1), 'bakery products – pastry' (1).

[h] In 2024, 'bovine meat and products thereof' includes 'meat from bovine animals – meat preparation – intended to be eaten cooked' (24), 'meat from bovine animals – minced meat' (24), 'meat from bovine animals – fresh' (4), 'meat from bovine animals – meat preparation – intended to be eaten raw' (4).

[i] In 2024, 'other or mixed red meat and products thereof' includes 'meat, mixed meat – meat products – ready-to-eat' (48).

[j] In 2024, 'mixed food' includes 'mixed food' (22), 'other processed food products and prepared dishes' (10), 'other processed food products and prepared dishes – meat-based dishes' (1).

[k] In 2024, 'broiler meat (*Gallus gallus*) and products thereof' includes 'broiler meat (*Gallus gallus*) and products thereof' (25), 'meat from broilers (*Gallus gallus*)' (7).

[l] In 2024, 'other or mixed red meat and products thereof' includes 'meat, mixed meat – meat preparation' (15), 'other or mixed red meat and products thereof' (13).

TABLE 56 Top-10 pathogen/food vehicle pairs causing the highest number of deaths in strong-evidence outbreaks in reporting EU MSs, in 2024.

2024					2020–2023			Evaluation
Rank[a]	**Causative agent**	**Food vehicle**	**Deaths (*N*)**	**Reporting MS (*N* deaths)**	**Rank**[a]	**Deaths (*N*/year) (range)**	**Reporting MS (*N*/year)**	**2024 versus 2020–2023**[b]
1	*Bacillus cereus* toxins	Vegetables and juices and other products thereof	6	Spain (5), France (1)	NA	0	0	NA
2	*Bacillus cereus* toxins	Mixed food[c]	3	Spain (2), Germany (1)	NA	0	0	NA
2	*Salmonella*	Pig meat and products thereof[d]	3	Germany (3)	3	0.50 (0–1)	0.5	↑↑
3	*Listeria monocytogenes*	Vegetables and juices and other products thereof[e]	2	Finland (1), Italy (1)	1	1.8 (0–5)	0.5	≈
3	*Salmonella*	Water	2	Greece (2)	NA	0	0	NA
4	*Clostridium botulinum* toxins	Mixed food[f]	1	Italy (1)	NA	0	0	NA
4	*Listeria monocytogenes*	Cheese	1	Belgium (1)	NA	0	0	NA
4	*Listeria monocytogenes*	Meat and meat products, unspecified	1	Austria (1)	3	0.50 (0–2)	0.25	↑↑
4	*Listeria monocytogenes*	Pig meat and products thereof	1	Belgium (1)	2	1.3 (0–3)	1	≈
4	Norovirus and other calicivirus	Vegetables and juices and other products thereof	1	France (1)	NA	0	0	NA
4	*Salmonella*	Bakery products[g]	1	Poland (1)	NA	0	0	NA
4	*Salmonella*	Broiler meat (*Gallus gallus*) and products thereof	1	Slovakia (1)	4	0.25 (0–1)	0.25	↑↑
4	*Salmonella*	Buffet meals	1	Austria (1)	NA	0	0	NA
4	*Salmonella*	Vegetables and juices and other products thereof[h]	1	Germany (1)	NA	0	0	NA

Abbreviation: NA, Not Applicable.

[a] Ranking of the causative agent/food vehicle combinations based on the number of deaths in strong-evidence FBOs in which the combinations were implicated (rank 1 is the highest rank meaning the most commonly implicated). Strong-evidence outbreaks with unknown causative agents are not included.

[b] Double arrows indicate variations < –50% (↓↓) or > 50% (↑↑) in the number of deaths; a single arrow indicates variations ≥ – 50% and < –25% (↓) or variations > 25% and ≤ 50% (↑); a double tilde (≈) indicates variations ≥ – 25% and ≤ 25%.

[c] In 2024, 'mixed food' includes 'mixed food' (2), 'other processed food products and prepared dishes – pasta – filled pasta' (1).

[d] In 2024, 'pig meat and products thereof' includes 'meat from pig – minced meat – intended to be eaten raw' (3).

[e] In 2024, 'vegetables and juices and other products thereof' includes 'table olives' (1), 'vegetables – products' (1).

[f] In 2024, 'mixed food' includes 'other processed food products and prepared dishes – vegetable-based dishes' (1).

[g] In 2024, 'bakery products' includes 'bakery products – cakes – containing raw cream' (1).

[h] In 2024, 'vegetables and juices and other products thereof' includes 'rocket, rucola' (1).

B4.3 | Overview of food vehicles implicated in food-borne outbreaks in 2024

The following sections provide information on the food vehicles implicated in FBOs in 2024. Only strong-evidence outbreaks are considered for this purpose since the body of evidence (i.e. the proof) linking a food vehicle and the human cases means that the association is highly likely and the level of uncertainty around this association is low.

For a more interactive look at FBO data by food vehicles, visit the dedicated page in EFSA's dashboard on FBOs (here).

B4.3.1 | Food vehicles in strong-evidence outbreaks

Twenty-four MSs (all MSs except Croatia, Cyprus and Latvia) provided information on 533 strong-evidence FBOs (8.1% of all FBOs reported in the EU in 2024), a relative decrease of 7.9% over 2023 (46 fewer FBOs than in 2023). Spain was by far the main contributor of strong-evidence FBOs (25.1%), followed by Poland (15.6%) and France (15.2%). Table 57 describes the food vehicles implicated in strong-evidence FBOs in 2024 in the EU. In addition, information on a total of 29 strong-evidence FBOs was also reported by five non-MSs (Iceland, Norway, Republic of North Macedonia, Serbia and Switzerland).

Composite foods, multi-ingredient foods and other foods

In 2024, foodstuffs belonging to the group '**composite foods, multi-ingredient foods and other foods'** ranked first among the food vehicles implicated in strong-evidence FBOs, similarly to the last 3 years. Nineteen MSs and three non-MSs reported a total of 174 and six strong-evidence FBOs linked to this food group, respectively (Table 57). At the EU level the reporting of this food group was stable compared with 2023 (five fewer FBOs than in 2023). A complete description of the food vehicles included in this category is available as a footnote to Table 57.

Within this large group, the foodstuffs classified under the **'mixed food'** category caused the highest number of strong-evidence FBOs, cases and hospitalisations among all foods implicated in strong-evidence FBOs in 2024. Approximately one in four strong-evidence FBOs and one in three cases were due to the consumption of 'mixed food'. Sixteen MSs and one non-MS reported strong-evidence FBOs caused by this type of food. Strong-evidence outbreaks associated with 'mixed food' were mainly 'general' outbreaks ($N=102$; 78.5%). Most cases (60.0%) had consumed 'mixed food' either in a 'canteen or catering at workplace, school, etc.' (1310 cases) or in a 'restaurant, pub, street vendor, take-away, etc.' (1003 cases). Mixed food includes a huge combination of ingredients and preparations. This foodstuff can potentially be contaminated with any type of agent, since contamination may occur at any point throughout the food chain, from the primary level through to the final preparation of the dishes by the consumer. This is the reason why strong-evidence FBOs associated with 'mixed food' were associated with a wide variety of causative agents in 2024: either bacteria (i.e. *Salmonella*, *Campylobacter*, *Escherichia coli* other than STEC, *Listeria monocytogenes* and *Yersinia* altogether accounting for 47 FBOs, 36.2%), bacterial toxins (44 FBOs, 33.8%), norovirus (21 FBOs, 16.2%), other causative agents (i.e. mushroom toxins and lectin – 12 FBOs, 9.2%) or parasites (i.e. *Giardia*, one FBO). Mixed foods in combination with various causative agents were reported among the top 10 pairs causing the highest number of outbreaks, cases, hospitalisations and deaths (see also Section B.4.2.7). **'Bakery products'** were reported as the implicated food in FBOs from 10 MSs and three non-MSs, a similar number compared with 2023. This foodstuff was mainly implicated in FBOs caused by *Salmonella* (23 FBOs, 85.2%) and in particular *S*. Enteritidis (15 FBOs), and in a few outbreaks with *Bacillus cereus* toxins and norovirus (two outbreaks each). '**Buffet meals**' were mainly implicated in FBOs caused by norovirus (six FBOs, including one large outbreak with 94 cases), followed by *S*. Enteritidis (five FBOs). Other *Salmonella* serovars included *S*. Mikawasima and *S*. Typhimurium (one FBO each). Buffet meals featured more in 2024 than in 2023, with more FBOs, cases and hospitalisations. One fatality was also reported in 2024 while no death had resulted from FBOs associated with buffet meals in the years 2020–2023.

The importance of **sweets and chocolate** was limited in 2024 as these foods were only implicated in two strong-evidence FBOs, both caused by *S*. Enteritidis and reported by Poland.

Foods of animal origin

Foods of animal origin include '**eggs and egg products'**, '**meat and meat products'**, '**fish and fishery products'** and '**milk and milk products'**. Altogether, these food vehicles caused 289 strong-evidence FBOs (54.2% of all strong-evidence FBOs), 3966 cases (36.8% of all cases in strong-evidence FBOs), 552 hospitalisations (51.1% of all hospitalisations in strong-evidence FBOs) and seven deaths (28.0% of all deaths in strong-evidence FBOs). Twenty-two MSs, as well as five non-MSs, provided information on FBOs associated with foods of animal origin.

'Meat and meat products' was the group reported most frequently by MSs even if fewer strong-evidence FBOs were reported than in 2023. In total, 19 MSs and three non-MSs reported 112 and eight strong-evidence FBOs, respectively. In the EU, 'meat and meat products' were implicated in one third of all hospitalisations and a quarter of deaths reported in strong-evidence outbreaks. Cases had consumed 'meat and meat products' mainly in a 'restaurant, pub, street vendor, take-away, etc.' (803 cases, 37.1%) and 'multiple places of exposure' (657 cases, 30.3%). Among products in this food group, '**pig meat and products thereof'** were associated with the highest health impact as they caused 636 cases, 140 hospitalisations and four deaths. The burden was moderately higher than in 2023 (454 cases, 118 hospitalisations and three deaths). 'Pig meat and products thereof' were implicated in strong-evidence FBOs caused by a large range of causative agents: *Salmonella* (16 FBOs), *Trichinella* and *Clostridium perfringens* toxins (three FBOs each), *Listeria monocytogenes* (two FBOs), norovirus, enterovirus, *Campylobacter* and enteropathogenic *Escherichia coli* (EPEC) (one FBO each).

'Eggs and egg products' were implicated in 89 and five strong-evidence FBOs reported by 12 MSs and two non-MSs, respectively. The overall impact on health in the EU was rather stable compared to last year. The vast majority of FBOs implicating this foodstuff were caused by *Salmonella* (83 FBOs, 93.3%) and this food/agent combination was one of the pairs with the highest impact on health in the EU (see Section B.4.2.7). Other known causative agents associated with this food group included norovirus, *Staphylococcus aureus* toxins, *Campylobacter* and EPEC.

Ten MSs and two non-MSs reported 57 and four strong-evidence FBOs linked to consumption of contaminated '**fish and fishery products'**, respectively. The burden of these products in 2024 decreased by 31.3% compared to 2023 (26 fewer FBOs) and was accompanied by a 61.2% reduction in the number of human cases (506 fewer cases) and a 65.5% reduction in hospitalisations (38 fewer hospitalisations). Deaths also decreased sharply, as they were zero in 2024 compared to seven in 2023. FBOs implicating '**crustaceans, shellfish, molluscs and products thereof'** were typically associated with norovirus infection (28 strong-evidence FBOs). Cases had consumed this foodstuff mainly at a 'restaurant, pub, street vendor, take-away, etc.' but also in domestic premises. Other causative agents of strong-evidence FBOs implicating this foodstuff were *Vibrio parahaemolyticus*, *Salmonella*, marine biotoxins and Hepatitis A virus (one outbreak each). '**Fish and fish products'** were associated with a larger range of agents compared with the previous group, i.e. (in decreasing order) 'histamine and scombrotoxin', marine biotoxins, *Salmonella*, *Listeria monocytogenes, Staphylococcus aureus* toxins and norovirus. A 'restaurant, pub, street vendor, take-away, etc.' and 'domestic premises' were the most commonly reported places of consumption of 'fish and fish products'.

'**Milk and milk products**' were reported in 31 and two strong-evidence FBOs by nine MSs (Belgium, Denmark, France, Germany, Italy, Poland, Romania, Slovakia and Spain) and two non-MSs (Serbia and Switzerland), respectively. In the EU, fewer outbreaks, cases and hospitalisations were attributed to this food group in 2024 than in 2023. One death was also documented in 2024 in an outbreak from Belgium due to consumption of cheese contaminated with *Listeria monocytogenes*. The most unexpected finding from the analysis of 2024 data was the reporting of *Yersinia* in cheeses made from cows' milk and goats' milk and in 'dairy products (other than cheeses)' (see Section B.4.2.1 'Other bacteria', and Section B.4.2.7 for details). In 'milk and milk products', *Yersinia* ranked third among causative agents for total number of strong-evidence FBOs ($N=4$, 12.9%) but it was first for total number of cases involved (340 cases, 58.4%). Other FBOs implicating 'milk and milk products' were caused (in decreasing order) by *Salmonella*, *Campylobacter*, *Staphylococcus aureus* toxins, *L. monocytogenes*, norovirus, STEC and *Escherichia coli* other than STEC.

Foods of non-animal origin

Strong-evidence FBOs linked to foods of non-animal origin were reported by 14 MSs. Two non-MSs also reported four strong-evidence FBOs. In total, 57 FBOs were reported in the EU, which is the highest number since 2018. In terms of numbers of hospitalisations and deaths, the health impact of foods of non-animal origin was much higher compared to both 2023 and any other year since 2011, when the major outbreak of STEC O104:H4 in sprouted seeds caused more than 53 deaths. The higher hospitalisations and death toll were attributable to the rise of strong-evidence FBOs implicating 'vegetables and juices and other products thereof'.

Overall, 16 more FBOs (61.5% relative increase), 777 more cases (161.2%), 62 more hospitalisations (80.5%) and eight more deaths (400.0%) resulted for '**vegetables and juices and other products thereof**' compared with 2023. Strikingly, most strong-evidence outbreaks ($N=11$, i.e. one in four FBOs) and deaths ($N=8$) attributable to this food group were reported from 'health care and residential facilities', while cases ($N=409$) and hospitalisations ($N=74$) were mostly reported from 'multiple places of exposure'. Deaths attributable to consumption of 'vegetables and juices and other products thereof' in 'health care and residential facilities' were caused by *Bacillus cereus* toxins ($N=6$), *L. monocytogenes* and norovirus (one death each). Eleven strong-evidence FBOs associated with the consumption of 'vegetables and juices and other products thereof' were reported by MSs as 'part of a multi-country outbreak' or 'continuation of an outbreak reported in the last/previous year'. *S.* Umbilo was reported by five countries in 'rocket, rucola' and spinach, which were part of the same multi-country outbreak. Four MSs reported various types of tomatoes or mixed foods containing tomatoes associated with FBOs caused by *S.* Strathcona (see Section B.4.8). Sweden and Germany reported alfaalfa sprouts in two strong-evidence FBOs, which were both 'part of multi-country outbreak' associated with multiple *Salmonella* serovars. A further very large strong-evidence FBO reported by Norway was also linked to the same multi-country outbreak (see also Section B.4.8). Consumption of table olives was reported by Italy to have caused one death in a strong-evidence listeriosis outbreak, which was a 'continuation of an outbreak reported in the last/previous year' (EFSA and ECDC, 2024). Causative agents reported in strong-evidence FBOs implicating '**fruit, berries and juices and other products thereof'** were mainly viruses (Hepatitis A virus, norovirus and rotavirus). The largest outbreak caused by *S.* Enteritidis was reported by Poland and involved 113 cases and 21 hospitalisations in a 'school or kindergarten'. '**Cereal products including rice and seeds/pulses (nuts, almonds)'** were also reported in 2024 by three MSs (Estonia, Germany and Spain) and two non-MSs (Norway and Switzerland).

TABLE 57 Frequency distribution of strong-evidence food-borne outbreaks, by food vehicle, in reporting EU MSs, in 2024.

	Strong-evidence outbreaks								Reporting rate per 100,000 population		Rank	
	Outbreaks		Cases		Hospitalisations		Deaths					
Type of vehicle	***N***	**% of total**	***N***	**% of total**	***N***	**% of total**	***N***	**% of total**	**2024**	**2020–2023**	**2024**	**2020–2023**
Composite foods, multi-ingredient foods and other foods												
Mixed foods[a]	130	24.4	3853	35.7	205	19.0	4	16.0	0.029	0.019	1	1
Bakery products[b]	27	5.1	349	3.2	75	6.9	1	4.0	0.006	0.004	7	8
Buffet meals	15	2.8	251	2.3	34	3.1	1	4.0	0.003	0.001	10	14
Sweets and chocolate	2	0.38	13	0.12	2	0.19	0	0	< 0.001	0.001	17	15
Subtotal	**174**	**32.6**	**4466**	**41.4**	**316**	**29.2**	**6**	**24.0**	**0.039**	**0.027**	**–**	**–**
Meat and meat products												
Broiler meat (*Gallus gallus*) and products thereof[c]	35	6.6	341	3.2	35	3.2	1	4.0	0.008	0.006	4	5
Pig meat and products thereof[d]	28	5.3	636	5.9	140	13.0	4	16.0	0.006	0.005	6	7
Meat and meat products, unspecified	23	4.3	299	2.8	30	2.8	1	4.0	0.005	0.004	9	9
Bovine meat and products thereof[e]	11	2.1	337	3.1	57	5.3	0	0	0.002	0.002	13	11
Other or mixed red meat and products thereof[f]	7	1.3	388	3.6	90	8.3	0	0	0.002	0.002	15	13
Other, mixed or unspecified poultry meat and products thereof[g]	7	1.3	161	1.5	11	1.0	0	0	0.002	0.001	15	16
Sheep meat and products thereof[h]	1	0.19	4	0.04	0	0	0	0	< 0.001	< 0.001	18	18
Subtotal	**112**	**21.0**	**2166**	**20.1**	**363**	**33.6**	**6**	**24.0**	**0.025**	**0.020**	**–**	**–**
Eggs and egg products[i]	**89**	**16.7**	**897**	**8.3**	**139**	**12.9**	**0**	**0**	**0.020**	**0.016**	**2**	**2**
Fish and fishery products												
Crustaceans, shellfish, molluscs and products thereof[j]	32	6.0	216	2.0	5	0.46	0	0	0.007	0.007	5	4
Fish and fish products[k]	25	4.7	105	0.97	15	1.4	0	0	0.006	0.008	8	3
Subtotal	**57**	**10.7**	**321**	**3.0**	**20**	**1.9**	**0**	**0**	**0.013**	**0.015**	**–**	**–**
Foods of non-animal origin												
Vegetables and juices and other products thereof[l]	42	7.9	1259	11.7	139	12.9	10	40.0	0.009	0.005	3	6
Fruit, berries and juices and other products thereof[m]	10	1.9	170	1.6	42	3.9	0	0	0.002	0.001	14	17
Cereal products including rice and seeds/pulses (nuts, almonds)[n]	5	0.94	93	0.86	9	0.83	0	0	0.001	0.001	16	15
Subtotal	**57**	**10.7**	**1522**	**14.1**	**190**	**17.6**	**10**	**40.0**	**0.013**	**0.008**	**–**	**–**
Milk and milk products												
Cheese[o]	14	2.6	443	4.1	19	1.8	1	4.0	0.003	0.003	11	10
Dairy products (other than cheeses)[p]	12	2.3	119	1.1	8	0.74	0	0	0.003	0.002	12	11
Milk[q]	5	0.94	20	0.19	3	0.28	0	0	0.001	0.001	16	16

TABLE 57 (Continued)

	Strong-evidence outbreaks								Reporting rate per 100,000 population		Rank	
	Outbreaks		Cases		Hospitalisations		Deaths					
Type of vehicle	*N*	% of total	*N*	% of total	*N*	% of total	*N*	% of total	2024	2020–2023	2024	2020–2023
Subtotal	**31**	**5.8**	**582**	**5.4**	**30**	**2.8**	**1**	**4.0**	**0.007**	**0.006**	**–**	**–**
Water (and other beverages)												
Water	12	2.3	794	7.4	23	2.1	2	8.0	0.003	0.002	12	12
Drinks, including bottled water	1	0.19	38	0.35	0	0	0	0	< 0.001	< 0.001	18	18
Subtotal	**13**	**2.4**	**832**	**7.7**	**23**	**2.1**	**2**	**8.0**	**0.003**	**0.002**	**-**	**-**
EU Total	**533**	**100**	**10,786**	**100**	**1081**	**100**	**25**	**100**	**0.118**	**0.006**	**0**	**0**

Note: Single food items are consolidated into major groups according to their origin. The ‘outbreak reporting rate’ columns include the mean outbreak reporting rate per 100,000 population for 2024 and for the previous years (2020–2023) for trend watching. The ranking of each food item provides a visual demonstration of its relative importance, among all food vehicles implicated in food-borne outbreaks, for the same year and period.

[a]‘Mixed food’ includes ‘mixed food’ (45), ‘other processed food products and prepared dishes – meat-based dishes’ (20), ‘other processed food products and prepared dishes – mushroom-based dishes’ (11), ‘other processed food products and prepared dishes’ (8), ‘other processed food products and prepared dishes – pasta – simple pasta’ (6), ‘other processed food products and prepared dishes – fish and seafood-based dishes’ (4), ‘other processed food products and prepared dishes – sushi’ (4), ‘other processed food products and prepared dishes – egg-based dishes’ (3), ‘other processed food products and prepared dishes – noodles’ (3), ‘other processed food products and prepared dishes – sandwiches’ (3), ‘other processed food products and prepared dishes – sandwiches – with meat’ (3), ‘other processed food products and prepared dishes – legumes-based dishes’ (2), ‘other processed food products and prepared dishes – pasta-based dishes’ (2), ‘other processed food products and prepared dishes – pasta/rice salad’ (2), ‘other processed food products and prepared dishes – vegetable-based dishes’ (2), ‘other processed food products and prepared dishes – pasta’ (1), ‘other processed food products and prepared dishes – pasta – filled pasta’ (1), ‘other processed food products and prepared dishes – pizza and pizza-like dishes’ (1), ‘other processed food products and prepared dishes – potato-based dishes’ (1), ‘other processed food products and prepared dishes – rice-based dishes’ (1), ‘other processed food products and prepared dishes – sandwiches – non-meat’ (1), ‘ready-to-eat salads’ (1), ‘sauce and dressings’ (1), ‘sauce and dressings – mayonnaise’ (1), ‘soups’ (1), ‘soups – ready-to-eat’ (1), ‘tzatziki’ (1).

[b]‘Bakery products’ includes ‘bakery products – cakes – containing raw cream’ (8), ‘bakery products – desserts – containing raw eggs’ (6), ‘bakery products’ (3), ‘bakery products – cakes – containing heat-treated cream’ (3), ‘bakery products – desserts’ (3), ‘bakery products – cakes’ (2), ‘bakery products – bread’ (1), ‘bakery products – pastry’ (1).

[c]‘Broiler meat (*Gallus gallus*) and products thereof’ includes ‘broiler meat (*Gallus gallus*) and products thereof’ (24), ‘meat from broilers (*Gallus gallus*)’ (10), ‘meat from broilers (*Gallus gallus*) – fresh’ (1).

[d]‘Pig meat and products thereof’ includes ‘pig meat and products thereof’ (12), ‘meat from pig – meat products’ (5), ‘meat from pig – meat preparation – intended to be eaten raw’ (4), ‘meat from pig – fresh’ (3), ‘meat from pig – meat products – meat specialities’ (2), ‘meat from pig’ (1), ‘meat from pig – minced meat – intended to be eaten raw’ (1).

[e]‘Bovine meat and products thereof’ includes ‘bovine meat and products thereof’ (2), ‘meat from bovine animals – fresh’ (2), ‘meat from bovine animals – meat preparation – intended to be eaten cooked’ (2), ‘meat from bovine animals – meat products’ (2), ‘cooked cured (or seasoned) bovine meat’ (1), ‘meat from bovine animals – meat preparation – intended to be eaten raw’ (1), ‘meat from bovine animals – minced meat’ (1).

[f]‘Other or mixed red meat and products thereof’ includes ‘other or mixed red meat and products thereof’ (3), ‘meat from wild boar – meat preparation – intended to be eaten cooked’ (1), ‘meat, mixed meat – meat preparation’ (1), ‘meat, mixed meat – meat products’ (1), ‘meat, mixed meat – meat products – ready-to-eat’ (1).

[g]‘Other, mixed or unspecified poultry meat and products thereof’ includes ‘meat from duck’ (2), ‘other, mixed or unspecified poultry meat and products thereof’ (2), ‘cooked cured (or seasoned) poultry meat’ (1), ‘meat from duck – fresh – frozen’ (1), ‘meat from poultry, unspecified’ (1).

[h]‘Sheep meat and products thereof’ includes ‘sheep meat and products thereof’ (1).

[i]‘Eggs and egg products’ includes ‘eggs and egg products’ (77), ‘eggs’ (11), ‘eggs – table eggs – mixed whole’ (1).

[j]‘Crustaceans, shellfish, molluscs and products thereof’ includes ‘live bivalve molluscs – oysters’ (19), ‘crustaceans, shellfish, molluscs and products thereof’ (7), ‘live bivalve molluscs – mussels’ (3), ‘live bivalve molluscs – oysters – depurated’ (2), ‘molluscan shellfish’ (1).

[k]‘Fish and fish products’ includes ‘fish and fish products’ (20), ‘fish – cooked’ (2), ‘fish – fishery products from fish species associated with a high amount of histidine – not enzyme maturated’ (1), ‘fish – raw’ (1), ‘fish – smoked’ (1).

[l]‘Vegetables and juices and other products thereof’ includes ‘vegetables and juices and other products thereof’ (20), ‘tomato’ (3), ‘alfalfa sprouts’ (2), ‘mushrooms’ (2), ‘rocket, rucola’ (2), ‘table olives’ (2), ‘vegetables – leaves’ (2), ‘watermelon’ (2), ‘cherry tomato’ (1), ‘common bean’ (1), ‘Kale’ (1), ‘onion’ (1), ‘vegetables’ (1), ‘vegetables – legumes’ (1), ‘vegetables – products’ (1).

[m]‘Fruit, berries and juices and other products thereof’ includes ‘fruit, berries and juices and other products thereof’ (8), ‘blueberries’ (1), ‘raspberries and raspberry-like’ (1).

[n]‘Cereal products including rice and seeds/pulses (nuts, almonds)’ includes ‘cereal products including rice and seeds/pulses (nuts, almonds)’ (3), ‘cereals and meals’ (1), ‘pumpkin seeds and similar’ (1).

[o]‘Cheese’ includes ‘cheese’ (12), ‘cheeses made from cows’ milk’ (1), ‘cheeses made from goats' milk’ (1).

[p]‘Dairy products other than cheeses’ includes ‘dairy products (other than cheeses)’ (10), ‘dairy products (excluding cheeses) – yoghurt – made from raw or low heat-treated milk’ (1), ‘Infant formula’ (1).

[q]‘Milk’ includes ‘milk, cows’ – raw milk’ (3), ‘milk’ (1), ‘milk, sheep's – raw milk’ (1).

B4.3.2 | Suspect foods in weak-evidence outbreaks

In 2024, 22 MSs and six non-MSs described the suspect foods in weak-evidence FBOs. The information was available for a total of 3315 weak-evidence FBOs reported in the EU (55.0% of all weak-evidence FBOs) and 37 outbreaks in non-MSs.

The pattern of food groups reported for weak-evidence FBOs was consistent with that observed in strong-evidence outbreaks, except for 'fish and fishery products', which ranked third in weak-evidence FBOs (13.4% of weak-evidence FBOs with information available) and fourth in strong-evidence FBOs (10.7% of strong-evidence FBOs), as well as 'eggs and egg products', which on the contrary ranked fourth in weak-evidence FBOs (8.4% of weak evidence FBOs with information available) and third in strong-evidence FBOs (16.7% of strong evidence FBOs).

There were other remarkable surprising discrepancies at a more detailed level of description of the food vehicle for a series of food items. Among 'composite foods, multi-ingredient foods and other foods', the proportion of weak-evidence FBOs reporting 'mixed food' as the suspect food (42.1% of weak-evidence FBOs with information available) was twice as high as in strong-evidence FBOs (Table 57) while 'bakery products' were reported in a lower proportion in weak-evidence FBOs (1.9%). In the 'meat and meat products' group, 'broiler meat (*Gallus gallus*) and products thereof' and 'meat and meat products, unspecified' were more frequently suspected in weak-evidence outbreaks (9.3% and 7.8% of weak-evidence FBOs, respectively) than in strong-evidence FBOs (Table 57). The opposite pattern was seen for 'pig meat and products thereof' (2.7% in weak-evidence FBOs). Among 'foods of non-animal origin', 'vegetables and juices and other products thereof' were more frequently reported in strong-evidence FBOs (Table 57) than in weak-evidence FBOs (4.4%). In the 'milk and milk products' group, cheese was less frequently suspected in weak-evidence FBOs (0.30%) than in strong-evidence FBOs (Table 57).

B4.4 | Overview of the places of exposure in strong-evidence outbreaks in 2024

A place of exposure in strong-evidence FBOs was reported for 485 FBOs (91.0% of all strong-evidence FBOs) by 23 MSs (all MSs reporting strong-evidence FBOs in 2024 except Bulgaria). Key statistics on the place of exposure are shown in Table 58. Four non-MSs also provided EFSA with this information for 23 strong-evidence FBOs.

In detail, 'restaurants or cafe or pubs or bars or hotels or catering services', 'multiple places of exposure in one country', 'school or kindergarten' and 'canteen or workplace catering' were the sites associated with a larger number of cases compared with FBOs occurring in 'domestic premises'. Overall, in these settings, a total of 6449 cases were exposed to contaminated food (59.8% of total cases involved in strong-evidence FBOs). These statistics did not substantially change compared with last year (6341 cases, 56.6% of total cases in strong-evidence FBOs in 2023). Similarly, the number of cases exposed in 'domestic premises' was very similar to 2023 (866 cases, 7.7% of total cases in strong-evidence FBOs in 2023). However, caution should be exercised when drawing conclusions on the relative importance of the different place of exposure since the reporting of cases potentially exposed in 'domestic premises' is likely underestimated in those countries not reporting 'household' outbreaks (see Section B.4.1). In fact, no cases exposed in 'domestic premises' resulted for Denmark, Finland, Luxembourg and the Netherlands, which did not report any 'household' outbreaks in 2024.

In terms of the health impact, one finding of particular concern from the analysis of data on the place of exposure was the high number of deaths among cases exposed to contaminated foods in 'health care and residential facilities' ($N=11$). Fatal cases were mostly reported in a 'nursing home'. Eight deaths resulted in 2024 in this setting, accounting for a 3.6% of deaths among cases exposed in strong-evidence FBOs in this place. In a 'hospital or medical care facility' and in 'residential institutions (prison or boarding school)', this percentage was 0.99% and 0.34%, respectively, which is also higher than any other place of exposure except for 'domestic premises' (0.35%). Causative agents associated with deaths in 'health care and residential facilities' included *Bacillus cereus* toxins (eight deaths), *Listeria monocytogenes* (two deaths) and norovirus (one death). These findings stress the importance of ensuring very high food safety standards in settings hosting fragile people. Age and underlying conditions affecting persons living in these places, even temporarily, can contribute to make the impact of food-borne diseases more severe than in most other population subgroups.

In the various places of exposure, the analysis of which causative agents were most frequently detected in strong-evidence FBOs provides interesting information which can be used to guide the food safety control programmes of food business operators and public catering companies, as well as education campaigns to consumers. The top three causative agents in strong-evidence outbreaks occurring in the various places of exposure are listed below:

- ***Salmonella*** was among the top three agents reported in strong-evidence FBOs in six different places of exposure, i.e. 'canteen or catering at workplace, school, etc.', 'domestic premises', 'health care and residential facilities', 'multiple places of exposure', 'other places of exposure' and 'restaurant, pub, street vendor, take-away, etc.'.
- ***Bacillus cereus*** toxins were among the top three agents reported in strong-evidence FBOs in three different places of exposure, i.e. 'canteen or catering at workplace, school, etc.', 'health care and residential facilities' and 'other places of exposure'.
- ***Campylobacter*** was among the top three agents reported in strong-evidence FBOs in two different places of exposure, i.e. 'multiple places of exposure' and 'restaurant, pub, street vendor, take-away, etc.'

- ***Clostridium perfringens*** toxins were among the top three agents in two different places of exposure, i.e. 'canteen or catering at workplace, school, etc.' and 'health care and residential facilities'.
- **Norovirus** was among the top three agents reported in strong-evidence FBOs in two different places of exposure, i.e. 'domestic premises' and 'restaurant, pub, street vendor, take-away, etc.'.
- ***Listeria monocytogenes*** was among the top three agents in 'multiple places of exposure'.
- ***Escherichia coli*** other than STEC were among the top three agents in 'other places of exposure'.
- ***Staphylococcus aureus*** toxins were among the top three agents in 'restaurant, pub, street vendor, take-away, etc.'.
- **Mushroom toxins** were among the top three agents in 'domestic premises'.

TABLE 58 Frequency distribution of strong-evidence food-borne outbreaks by place of exposure (setting), in reporting EU MSs, 2024.

	Strong-evidence outbreaks								Outbreak reporting rate per 100,000 population	
	Outbreaks		Cases		Hospitalisation		Deaths			
Place of exposure	***N***	**% of total**	***N***	**% of total**	***N***	**% of total**	***N***	**% of total**	**2024**	**2020–2023**
Restaurant, pub, street vendor, take-away, etc.										
Restaurant or cafe or pub or bar or hotel or catering service	170	31.9	2539	23.5	253	23.4	4	16.0	0.038	0.025
Take-away or fast-food outlet	7	1.3	206	1.9	32	3.0	0	0	0.002	0.001
Mobile retailer or market/street vendor	5	0.94	80	0.74	13	1.2	0	0	0.001	0.001
Domestic premises	144	27.0	847	7.9	216	20.0	3	12.0	0.032	0.031
Multiple places of exposure										
Multiple places of exposure in one country	35	6.6	1556	14.4	213	19.7	5	20.0	0.008	0.005
Multiple places of exposure in more than one country	15	2.8	672	6.2	72	6.7	1	4.0	0.003	0.001
Canteen or catering at workplace, school, etc.										
School or kindergarten	31	5.8	1326	12.3	97	9.0	0	0	0.007	0.006
Canteen or workplace catering	18	3.4	1028	9.5	24	2.2	0	0	0.004	0.002
Health care and residential facilities										
Residential institution (prison or boarding school)	17	3.2	588	5.5	7	0.65	2	8.0	0.004	0.003[a]
Nursing home	13	2.4	225	2.1	27	2.5	8	32.0	0.003	0.003[a]
Hospital and medical care facility	6	1.1	101	0.94	15	1.4	1	4.0	0.001	0.001
Other place of exposure										
Camp or picnic	11	2.1	256	2.4	13	1.2	0	0	0.002	0.002
Temporary mass catering (fairs or festivals)	7	1.3	316	2.9	9	0.83	0	0	0.002	0.001
Farm	3	0.56	16	0.15	3	0.28	0	0	0.001	< 0.001
Primary production	3	0.56	32	0.30	13	1.2	0	0	0.001	< 0.001
Unknown	48	9.0	998	9.3	74	6.8	1	4.0	0.011	0.007
EU Total	**533**	**100**	**10,786**	**100**	**1081**	**100**	**25**	**100**	**0.118**	**0.006**

[a] Since 2024, food-borne outbreaks occurring in nursing homes can be reported specifically within the 'nursing home' setting. Previously, this setting was grouped under 'residential institution (nursing home, prison or boarding school)'. As no information on FBOs occurring specifically in nursing homes in 2020–2022 was available, these outbreak reporting rates refer only to 2023.

B4.5 | Contributing factors in strong-evidence food-borne outbreaks in 2024

Information on factors contributing to strong-evidence FBOs was available for 180 FBOs (33.8% of all strong-evidence FBOs).

'Cross-contamination' and **'unprocessed contaminated ingredient'** were the most commonly reported contributory factors in strong-evidence FBOs and were reported in 47 and 44 FBOs, respectively. In particular, in strong-evidence FBOs caused by *Listeria monocytogenes* and *Salmonella* with information on factors available (seven and 61 FBOs, respectively), **'cross-contamination'** was the contributory factor reported most often (six and 25 FBOs, respectively). It was also the most commonly reported factor in strong-evidence FBOs attributable to 'egg and eggs products' (six outbreaks; 50.0%). Cross-contamination was also important in FBOs in a 'restaurant, pub, street vendor, take-away, etc. ' (22 outbreaks; 31.0%) and 'canteen or catering at workplace, school, etc.' (nine outbreaks; 39.1%).

'Unprocessed contaminated ingredient' made a major contribution to FBOs due to *Campylobacter* (eight outbreaks, 47.1%) and norovirus (and other caliciviruses) (11 outbreaks, 35.5%). This contributory factor was reported in more than a third of strong-evidence FBOs attributable to 'fish and fishery products' (12 outbreaks), 'food of non-animal origin' (six outbreaks) and 'meat and meat products' (17 outbreaks). Thirteen FBOs in 'multiple places of exposure' reported 'unprocessed contaminated ingredient' as the main contributory factor (13 outbreaks, 61.9%).

'Inadequate heat treatment' was reported in 37 strong-evidence FBOs and was among the factors that contributed the most to FBOs caused by *Salmonella* (22 outbreaks, 36.1%). Outbreaks in 'domestic premises' were mostly associated with 'inadequate heat treatment' (14 outbreaks, 40.0%).

'Infected food handler' was identified in 30 strong-evidence FBOs and ranked first among factors contributing to FBOs caused by norovirus (and other caliciviruses) (15 outbreaks, 48.4%). This factor was mainly reported in FBOs implicating 'composite foods, multi-ingredient foods and other foods' (24 outbreaks; 29.6%) and it contributed considerably to FBOs occurring in a 'restaurant, pub, street vendor, take-away, etc.' (22 outbreaks; 31.0%).

'Storage time/temperature abuse' and **'inadequate chilling'** were reported in 26 and 17 strong-evidence FBOs, respectively, mainly in FBOs caused by bacterial toxins (21 and eight FBOs, respectively). In particular, 'storage time/temperature abuse' was the top contributory factor for *Bacillus cereus* toxins and *Clostridium perfringens* toxins. FBOs occurring in 'health care and residential facilities' were mainly associated with 'storage time/temperature abuse' (six outbreaks; 50.0%) and 'inadequate chilling' (four outbreaks; 33.3%). Many outbreaks associated with 'composite foods, multi-ingredient foods and other foods' were linked to 'storage time/temperature abuse' (17 outbreaks, 21.0%).

'Water treatment failure' and **'untreated drinking water'** were reported in five and one strong-evidence waterborne outbreaks, respectively. These contributory factors were reported in all strong-evidence FBOs implicating 'water (and other beverages)' (five outbreaks). See the EFSA story map on FBOs (here), section on 'How, why and where food contamination may occur'.

B4.6 | Temporal trends by causative agents, 2015–2024

B4.6.1 | Temporal trends at EU level

The number of FBOs reported by MSs over 2015–2024, by causative agent, is illustrated in Figure 25. Since the collection of FBO data is not fully harmonised across the EU, the annual fluctuations in the distribution of causative agents reported in this figure might not accurately represent the true epidemiological pattern of occurrence of causative agents implicated in FBOs at the EU level. The underlying reasons are that the trend mainly reflects the reporting of MSs contributing the most to the EU total, and that changes in FBO surveillance in individual MSs directly affect the estimates at the EU level over the years. These major limitations are the main reason why a statistical trend analysis is performed not at the EU level (see Section B.3), but only at the individual country level.

For a more interactive look at time trends in FBO data, visit the dedicated page in EFSA's dashboard on FBOs (here).

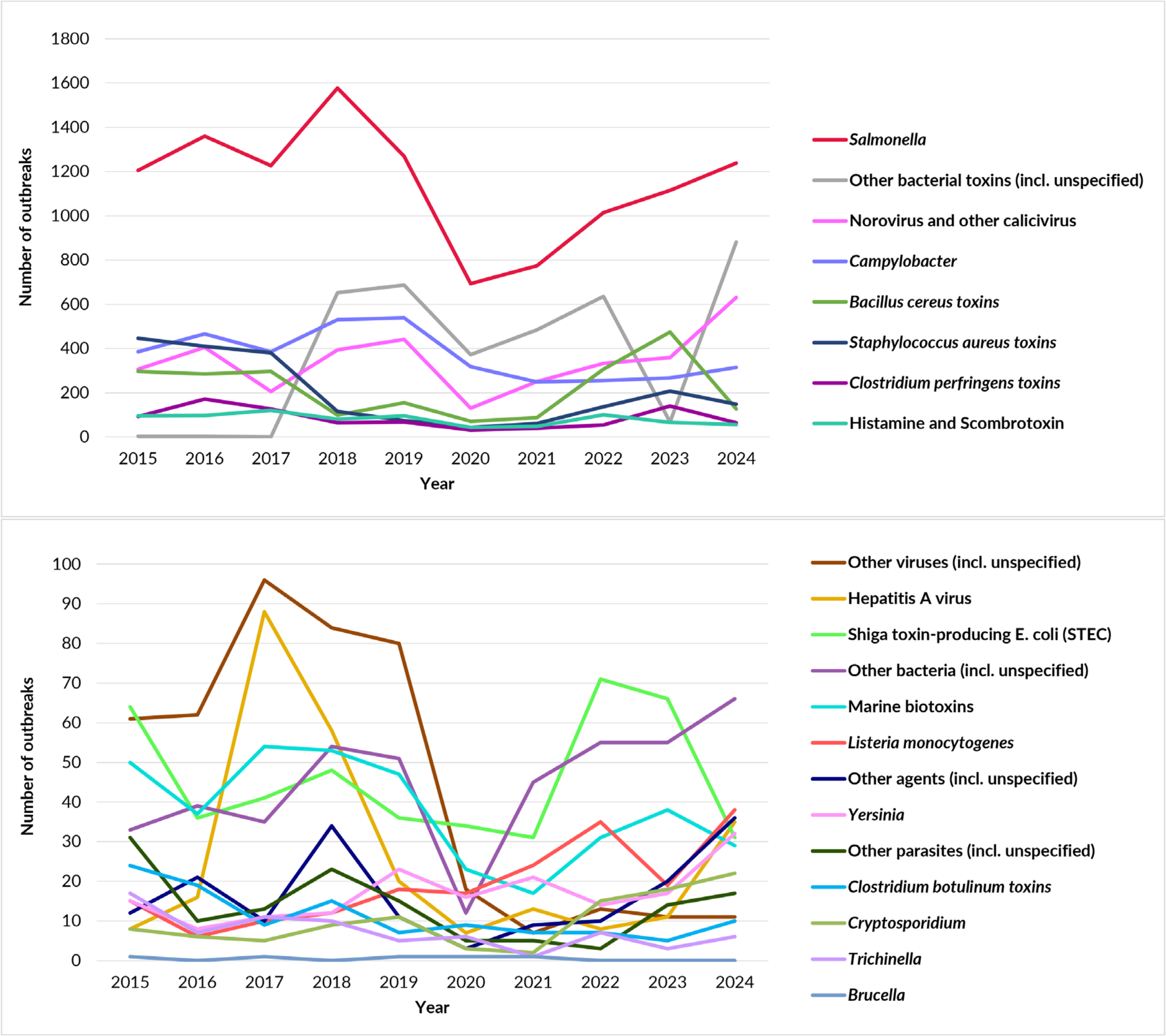

FIGURE 25 Number of food-borne outbreaks by causative agent, reported to the EU by MSs, 2015–2024.

Note: The term 'other bacterial toxins (incl. unspecified)' includes *Clostridium difficile* and unspecified bacterial toxins.
The term 'norovirus and other calicivirus' includes norovirus, sapporo virus and unspecified caliciviruses.
The term 'other viruses (incl. unspecified)' includes adenovirus, enterovirus, flavivirus (incl. Tick-borne Encephalitis virus), hepatitis E virus, hepatitis virus, unspecified, rotavirus and other unspecified viruses. During the final phase of report production, the Netherlands informed that adenovirus (here included among 'other viruses') was mistakenly reported as the causative agent of one strong-evidence outbreak. The correct causative agent was Hepatitis A virus.
The term 'other bacteria (incl. unspecified)' includes *Brucella*, *Aeromonas*, *Arcobacter*, *Cronobacter*, *Enterococcus*, *Escherichia coli* other than STEC, *Francisella*, *Leptospira*, *Mycobacterium* spp., *Shigella*, *Streptococcus*, *Vibrio cholerae* (non-toxigenic), *Vibrio cholerae* (toxigenic), *Vibrio parahaemolyticus* and unspecified bacteria.
The term 'marine biotoxins' includes ciguatoxin and unspecified marine biotoxins.
'Other agents (incl. unspecified)' includes mushroom toxins, mycotoxins, atropine, chemical agents, lectins, monosodium glutamate, wax esters (from fish) and unspecified toxins.
'Other parasites (incl. unspecified)' includes *Anisakis*, cysticerci (metacestode of *Taenia* spp.), *Enterocytozoon bieneusi*, *Giardia* and unspecified parasites.

B4.6.2 | Temporal country-specific trends by causative agent

Only statistically significant trends in the number of FBOs, by causative agent and country, are described in this section. More information on the methodology used for trend analyses is provided in the section on data analyses of this chapter (Section 3 on 'Data analyses'). Figures on statistically significant country-specific temporal trends by causative agent, over the 2015–2024 period, are available in the 'Addendum on food-borne outbreaks, complementing the European Union One Health Zoonoses Report 2024', Section 5, published on the EFSA Knowledge Junction at Zenodo (here). Various statistically significant increasing or decreasing trends, by causative agent and reporting EU MS, were observed over the period 2015–2024.

The trend analysis for *Salmonella* highlighted a significant decreasing trend in the number of reported FBOs for seven MSs (Austria, Croatia, Germany, Hungary, Latvia, Lithuania and Slovakia), i.e. three more countries than in 2023. In all these countries except Hungary and Latvia, this decrease was primarily due to a significant decrease in the number of outbreaks caused by *S.* Enteritidis.

The second bacterial agent with statistically significant trends was *Campylobacter*. A significant decreasing trend over 2015–2024 was observed in three MSs, i.e. Austria and Germany (similarly to last year) and Slovakia. Conversely, the trend increased significantly in France.

Other statistically significant decreasing trends resulted in France (for both *Staphylococcus aureus* toxins and *Clostridium perfringens* toxins, as well as marine biotoxins), Poland (for norovirus and other caliciviruses) and Spain (for histamine and scombrotoxin). French findings on bacterial toxins (e.g. *Staphylococcus aureus* and *Clostridium perfringens* toxins) should be interpreted with caution, as the data submitted by France show considerable year-to-year variation.

Lastly, in the EU, a statistically significant decrease in the number of FBOs with an unknown agent was observed in Finland, Slovakia and Sweden, while Czechia experienced a significant increase. In non-MSs, a decreasing trend was also observed in Norway. The differences in trends across these countries may be attributed to variations in outbreak surveillance sensitivity, as well as changes in laboratory testing and subtyping methods.

B4.6.3 | Temporal trends by implicated food vehicle

Only strong-evidence FBOs were considered for the trend analysis by implicated food vehicle at country level. Few statistically significant trends were detected for food vehicles over the 2015–2024 period. Decreasing trends were identified for strong-evidence FBOs associated with the consumption of 'bakery products' and 'meat and meat products, unspecified' in Poland and 'fish and fish products' in Spain.

Figures describing statistically significant temporal trends in the number of outbreaks, both by causative agent and MS and by food vehicle and MS, are available as downloadable files from the EFSA knowledge junction at Zenodo here.

B4.7 | Water-borne outbreaks

In 2024, 48 water-borne outbreaks were reported by 11 MSs and two by two non-MSs. In the EU, water-borne outbreaks involved a total of 2181 human cases causing 61 hospitalisations. This corresponds to an increase compared with 2023 in the number of FBOs (six more FBOs; 14.3% increase), cases (227 more cases; 11.6% increase) and hospitalisations (52 more hospitalisations; 577.8% increase). In addition, for the first time since EFSA began collecting data on FBOs, two deaths were reported in water-borne outbreaks.

Among the FBOs observed in the EU, 12 outbreaks were considered strong-evidence FBOs and included outbreaks caused by **'tap water, including well water'** (*N* = 11) and **'potable water'** (*N* = 1).

The causative agents involved in strong and weak-evidence FBOs in the EU were norovirus and other caliciviruses (*N* = 10), *Cryptosporidium* (*N* = 6), *Salmonella* (*N* = 4), *E. coli* other than STEC (i.e. EPEC and unspecified *E. coli*) (*N* = 3), Shiga toxin-producing *E. coli* (STEC) (*N* = 3), *Campylobacter* (*N* = 2), Hepatitis A virus (*N* = 2), *Shigella* (*N* = 1) and Rotavirus (*N* = 1). In 16 outbreaks, the aetiology remained unknown.

Water-borne outbreaks often include a large or very large number of cases. In 2024, the mean size of water-borne outbreaks in the EU was 45.4 cases per outbreak (range 2–851 cases).

Six very large outbreaks (≥ 100 cases each) were reported to EFSA from three MSs (Greece, Italy and Spain). Four of them were caused by norovirus, including one of the largest water-borne FBOs, reported by Spain, which accounted for 851 cases. *Salmonella* Bovismorbificans was responsible for a very large strong-evidence outbreak reported by Greece, including 144 human cases, 15 hospitalisations and two deaths. Place of exposure was 'domestic premises'.

The two water-borne outbreaks reported by non-MSs were caused by norovirus and *Enterococcus*, respectively.

B4.8 | ECDC and EFSA rapid outbreak assessment (ROA)

ECDC and EFSA work in close and constant collaboration to assess significant multi-country FBOs occurring in Europe and to publish Rapid Outbreak Assessments (ROA) promptly to support outbreak investigation. In all these assessments, the sharing of information on epidemiology, traceability and Whole Genome Sequencing (WGS) across countries is essential in assessing and managing the outbreaks.

The first ROA referred to a multi-country FBO caused by *Salmonella* Strathcona ST2559, which involved 232 cases in 16 EU/EEA countries between January 2023 and November 2024. A total of 29 cases were also observed in the United Kingdom. Case interviews and microbiological and traceability investigations indicated small tomatoes as the likely source of infection. WGS analysis suggested that the outbreak strain in the affected countries shared a recent common origin. However, further traceability and microbiological investigations were needed to confirm small tomatoes as the source of infections and to investigate the role of the environment in the contamination, as other food products may also have been implicated in transmission (ECDC and EFSA, 2024b).

A second large outbreak was caused by various serovars of *Salmonella* enterica (*S.* Adelaide, *S.* Enteritidis, *S.* Hvittingfoss, *S.* Kinondoni, *S.* Kisarawe, *S.* Newport, *S.* Richmond and *S.* Typhimurium) involving nine EU/EEA countries (Belgium, Denmark, Estonia, Finland, France, Germany, the Netherlands, Norway and Sweden) and the United Kingdom, over the period 2023–2025. A total of 510 cases were reported, including one from the United Kingdom. Epidemiological, microbiological and WGS data, and food traceability investigations identified sprouted seeds as the probable vehicle of human infection. The traceability investigation pointed to primary producers and seed suppliers located in Italy. Several control measures were adopted, including the withdrawal and recall of positive and suspected-positive contaminated batches, which led to a considerable decrease in case notifications. However, a few cases were still detected after the implementation of the control measures, highlighting the need for further investigations to identify the source/s of contamination of the seeds (ECDC and EFSA, 2025).

Two other assessments were published in 2024, both referring to multi-country outbreaks caused by *Listeria monocytogenes* in fish and fish products.

The first assessment described an FBO associated with *L. monocytogenes* ST173, with fish and fish products as the suspected food vehicle. A total of 73 cases and 14 deaths were reported by six EU countries (Belgium, Czechia, Germany, Finland, Italy and the Netherlands) and the United Kingdom, over the period 2012–2024. Only one human case was observed in 2024 (ECDC and EFSA, 2024a).

Lastly, the other multi-country outbreak was linked to *Listeria monocytogenes* ST1607 in smoked salmon products. In total, 20 human cases and five deaths were observed in Denmark, Germany and Italy, between 2019 and 2024 (ECDC and EFSA, 2024c). A brief description of this ROA is also available in the section on 'ECDC and EFSA rapid outbreak assessment (ROA)' of the European Union One Health 2023 Zoonoses report (EFSA and ECDC, 2024).

B5 | CONCLUSIONS

B5.1 | Health impact, causative agents and trends

In 2024, the health impact of FBOs in the EU was greater compared with 2023 in terms of total outbreaks, cases and hospitalisations, but not in terms of deaths. The increase in the number of FBOs and cases has been a widespread trend across all MSs, particularly affecting those countries that contribute most significantly to the overall European reporting. Indeed, it should be noted that certain countries have a greater impact in shaping the EU trend. Considerable variability at the national level was observed in the epidemiological indicators used to describe FBOs, including reporting rates, average outbreak size, types of outbreaks and severity. Such variability reflects both methodological differences and disparities in the organisation, criteria and sensitivity of FBO surveillance systems across countries. In this context, even a slight improvement in detection efficiency compared with the last few years may have resulted in a general increase in the national and EU-level numbers of outbreaks and outbreak reporting rates. This is particularly relevant for countries where the outbreak reporting rate remains considerably lower than the EU rate and where a high or very high level of FBO under-detection is suspected. Differences in outbreak rates are primarily influenced by the types of outbreaks reported to EFSA, as not all MSs communicate all types of outbreaks, especially 'household' outbreaks. In some countries such as Belgium and the Netherlands, systems allow citizens to directly report outbreaks to the authorities, whereas in others, only events notified by medical doctors or identified by health authorities are recorded in the official systems. Even when accounting for these differences, the substantial variability among countries suggests that under-detection and under-reporting of FBOs remain likely in several national contexts.

Technical innovation, such as the application of epidemic intelligence systems, combined with the extensive implementation of advanced pathogen subtyping methods, particularly whole genome sequencing (WGS) at national level and across multiple countries, has significantly improved the detection of food-borne outbreaks. It has substantially enhanced the early identification of links among infection cases, including those that span national borders (Gomes et al., 2025; Laisnez et al., 2025) and strengthened the cross-sectoral approach to the investigation and management of such events (Knijn et al., 2023). In 2026, Commission Implementing Regulation (EU) 2025/179[62] will enter into force, formally introducing WGS within regulated outbreak investigations. This development has the potential to catalyse broader adoption across sectors, supporting a One Health approach. Its implementation is expected to enhance the availability of typing and subtyping data for major food-borne pathogens, such as *Salmonella, Listeria*, STEC and *Campylobacter*, thereby strengthening the capacity to detect, investigate and manage outbreaks more effectively.

Over the extended period from 2015 to 2024, the outbreak reporting rate in 2024 reached its highest level since the dip observed during the COVID-19 pandemic years (2020–2021) and even surpassed pre-pandemic levels. This trend may be attributed to multiple factors, including annual variability in reporting, as well as potential increases in population exposure to contaminated food or enhanced sensitivity of FBO surveillance systems.

The consumption of contaminated food at the consumer level may result from a combination of factors, such as the inadequate mitigation of pre-existing contaminated ingredients derived from primary production (e.g. agricultural or livestock stages), and/or new contamination occurring during food handling or preparation. While the general principles and pillars of the EU's 'farm to fork' food safety framework remained unchanged in 2024, several contextual factors may have contributed to the observed rise in FBO reporting. Household food safety practices may also play a role, as changes in consumption patterns (e.g. increased intake of RTE foods and take-away meals) and reduced vigilance during home food preparation, could elevate exposure risks. Additionally, travel-related behaviours, such as consuming unfamiliar or undercooked foods, may also increase the risk of consuming contaminated food.

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[62] Commission Implementing Regulation (EU) 2025/179 of 31 January 2025 on the collection and transmission of molecular analytical data within the frame of epidemiological investigations of food-borne outbreaks in accordance with Directive 2003/99/EC of the European Parliament and of the Council. OJ L, 3.2.2025, p. 1–3.

At the primary production level, climate change-driven stressors (e.g. flooding, extreme weather events) and enhanced pathogen circulation in livestock, agricultural ecosystems and water sources may contribute to increased bacterial contamination and proliferation in both plant- and animal-based foods.

Salmonella remains the leading causative agent of FBOs in Europe. Despite an overall increase in the *Salmonella* outbreak reporting rate in 2024, a greater number of MSs than in previous years reported a significant decreasing trend in *Salmonella* outbreaks, suggesting an uneven distribution of the epidemic risk across the EU. The increase in outbreak reporting rate and food vehicles implicated in *Salmonella* outbreaks suggests that aside from the poultry population, which continues to represent the primary source of *Salmonella* entering the food-production chain, the role of other sources and, in particular, pig meat and vegetables is growing. While 'eggs and egg products' continued to represent the predominant source of *Salmonella* outbreaks in the EU in 2024, the number of outbreaks, associated cases and hospitalisations linked to pig meat and vegetables increased notably compared to 2023 in strong-evidence FBOs. Vegetables, in particular, were implicated in major long-lasting multi-country outbreaks associated with *Salmonella* serovars rarely or very rarely reported in livestock. This finding highlights the public health impact of specialised, geographically concentrated intensive production systems, combined with extensive distribution networks. Such systems amplify the risk of cross-border contamination and underscore the urgent need for targeted epidemiological investigations into reservoirs and contamination mechanisms in vegetable production chains.

B5.2 | Food vehicles and places of exposure

Directive 2003/99/EC highlights the importance of gathering information on FBOs across Europe. This data source is unique in enabling the simultaneous collection of information on both food vehicles and associated human disease cases. Assessing the degree of uncertainty related to the evidence linking outbreak cases to specific food vehicles and places of exposure, while focusing primarily on strong-evidence outbreaks, allows for a more accurate interpretation of findings within the epidemic framework, even though such FBOs represent only a small proportion of the total reported.

In addition to well-established causative agent/vehicle combinations having a major impact in 2024 (e.g. *Salmonella* in various types of food; norovirus in either crustaceans, shellfish, molluscs or mixed foods; bacterial toxins in mixed foods; *Listeria* monocytogenes in various types of food), other combinations warranting specific attention included Hepatitis E in '*Mettwurst'* (a salami-type sausage made from pork and horse meat) and *Yersinia* in raw milk cheese. While the association between consumption of pork meat and Hepatitis E infection has long been documented (Pavio et al., 2015), in 2024 for the first time Hepatitis E ranked among the top pairs responsible for the highest number of hospitalisations in strong-evidence FBOs in the EU. The high number of cases and hospitalisations was linked to a single general outbreak attributed to *Mettwurst*. This event highlights the risk of contamination when pork meat (potentially contaminated at the primary production stage) is mixed with other types of meat during industrial processing and subsequently distributed widely across markets. Cross-border outbreaks caused by *Yersinia* in raw milk cheese also necessitated a dedicated reporting focus for several reasons. While cattle and goats are known sources of *Yersinia enterocolitica* with potential for contaminating milk, cheese and dairy products (Ackers et al., 2000), no *Yersinia* outbreaks attributable to these foods had previously been reported in Europe. Between 2019 and 2022 in Europe, milk and milk products represented the food category most frequently contaminated with *Yersinia enterocolitica*, accounting for 11.0% of tested samples (EFSA and ECDC, 2024), and a high proportion of positive samples in milk and milk products was also reported in 2024 (31.0%) (See chapter C2.1). Although milk and milk products were sampled and tested for *Yersinia* in only a few countries, these findings highlight the potential risk of human infection through the consumption of dairy products. In this epidemiological context, the occurrence of outbreaks was not surprising, but the large spread of cases was unexpected. Interestingly, Savin et al. (2025), while commenting on the French *Yersinia enterocolitica* outbreak associated with soft unpasteurised milk cheese, underlined the problem posed by food specialities produced in confined regional areas having nationwide distribution, a pattern akin to that mentioned above for vegetables. There is considerable debate in Europe about the risks associated with consuming cheese made from raw or unpasteurised milk, particularly concerning STEC, *Listeria*, *Salmonella, Staphylococcus aureus* and *Campylobacter.* In recent years, many countries have enhanced specific risk communication campaigns especially for highly vulnerable population subgroups such as children, pregnant women and the elderly. Results of a recent survey showed that the consumption of raw milk products was widespread within the EU and the perception of the risk was low (Belluco et al., 2025).

Although yersiniosis was the fourth most frequently reported zoonosis in the EU in 2023, with a significant increasing trend (EFSA and ECDC, 2024), *Yersinia* is not always considered in risk assessment studies focusing on raw milk and unpasteurised products obtained from cattle and goats (ANSES, 2022; EFSA BIOHAZ Panel, 2015). Even data collected by EFSA within the mandate of Directive 2003/99/EC are limited and sparse, highlighting the need to better investigate the risk posed by this pathogen in this food production chain.

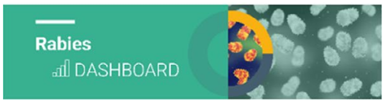
Similar to recent years, *Listeria monocytogenes* remained the causative agent with the highest case fatality rate, with many fatal cases reported among patients in health care and residential facilities. In 2024, a high number of deaths caused by *Bacillus cereus* toxins were also reported in these settings. Overall analysis of data on strong-evidence FBOs indicates that the proportion of deaths among patients in a 'nursing home' and 'hospital or medical care facility' was notably higher than in any other place of exposure. It cannot be ruled out that outbreaks involving fatal cases in these settings may have been more likely to be reported than less severe outbreaks, which often go unnoticed or under-reported, thereby inflating the observed death rate among cases. Regardless of this potential bias, this finding is a cause for concern and highlights the severe health consequences of food-borne exposure for vulnerable subpopulations. Patients in nursing homes and hospitals include elderly individuals and immunocompromised persons, and those with chronic conditions, cancer and various other comorbidities and/or medical treatments, all of which increase the risk of severe or even life-threatening outcomes from food-borne illness. Catering companies and food business operators (FBOps) operating in this context should strictly enforce high hygiene and food safety standards and ensure rigorous adherence to these practices. Such measures are not only critical but also a regulatory requirement in all public catering contexts within the EU, including workplace and school canteens, restaurants, pubs and other food service establishments. Even in domestic settings, where consumers control the final steps of food preparation or consumption, individuals preparing food for household members, especially parents and caregivers, should always be aware of their responsibility to make safe food choices. This emphasises the importance of targeted education campaigns to raise awareness of food safety practices. EFSA's 2024 data on FBO food vehicles and consumption settings reinforce the trends observed between 2020 and 2023. The food groups most frequently involved in strong-evidence outbreaks were composite or multi-ingredient foods, followed by various types of foods of animal origin. Contamination at the plate level often arises from ingredients contaminated at the primary production stage or along the food production chain, which are then improperly prepared, treated or preserved (i.e. through poor hygiene conditions or insufficient cooking). Errors can occur at multiple stages, both at home and in external settings such as restaurants, workplaces, schools and health care or social facilities. Key contributing factors include poor hygiene, cross-contamination and improper food handling, particularly in public catering environments. Vegetables were responsible for the highest number of deaths in strong-evidence outbreaks, mainly in health care facilities. The role of vegetables in food-borne illness is becoming increasingly relevant as dietary patterns across Europe shift towards plant-based diets. A 2023 survey in Europe highlighted that more consumers are reducing their meat intake in favour of plant-based foods (Smart Protein, 2023). This is in line with the EU agricultural outlook report (European Commission, 2024), which forecasts growth in the consumption of plant proteins, alongside stable or increased intake of fresh vegetables and fruit, by 2035. These findings underscore the critical challenge of contamination at the pre-harvest level of foodstuffs intended to be eaten raw (i.e. with no other effective control points), emphasising the need for farmers to be fully engaged in the responsibility of delivering safe food to the food production chain.

SECTION C – ZOONOSES AND ZOONOTIC AGENTS MONITORED ACCORDING TO THE EPIDEMIOLOGICAL SITUATION (DIRECTIVE 2003/99/EC LIST B)

C1 | RABIES

The summary data which make up this chapter, as well as additional information on related projects and internet sources, are published for this report on the EFSA Knowledge Junction at Zenodo here. Summary statistics on human surveillance data with downloadable files are retrievable using the ECDC Surveillance Atlas of Infectious Diseases available here.

For additional information about rabies and for the consultation of data collected, the following interactive tools are available:



C1.1 | Key facts

- In 2024, no autochthonous human cases of rabies were reported in the European Union.
- In animals excluding bats, surveillance data on rabies were reported by 24 European Union Member States. A total of 87 cases of autochthonous origin due to the rabies virus (RABV) strain were reported by four Member States: 43 cases in Poland (30 foxes, 4 cats, 3 cattle, 2 raccoon dogs, 2 dogs, 1 marten and 1 roe deer), 25 cases in Romania (11 cattle, 8 dogs and 6 foxes), 18 cases in Hungary (11 foxes, 3 dogs, 2 cats, 1 cattle and 1 jackal) and one case in Slovakia (one fox). The total number of reported indigenous rabies cases in non-flying animals in the European Union has increased in 2024 compared to 2023 and 2022 (both with 70 cases) but remains lower than in 2021 (114 cases) and higher than in 2020 (15 cases).
- A case of rabies was reported by France during passive surveillance in an illegally imported dog infected with a rabies virus lineage of RABV (Africa 1 lineage) from North Africa.
- In 2024, Romania reported three positive foxes sampled during oral rabies vaccination monitoring.
- Surveillance data on lyssavirus in bats were reported by 20 European Union Member States. Seven Member States (Czechia, France, Germany, Hungary, the Netherlands, Poland and Spain) reported 44 positive results for lyssavirus, 43

European bat 1 lyssavirus (EBLV-1) and one Bokeloh bat lyssavirus (BBLV). One non-Member State (Switzerland) reported a positive result in a bat for European bat lyssavirus 2 (EBLV-2).

- A case of rabies was reported by the Netherlands during passive surveillance in an indigenous cat infected with EBLV-1.

C1.2 | Surveillance and monitoring of rabies in the EU

C1.2.1 | Humans

Data concerning humans are included only in the event that autochthonous cases are reported within the EU.

C1.2.2 | Animals

The objective of passive rabies surveillance is to detect the presence and assess the geographic distribution of the virus over time, to allow timely dissemination of information for immediate integrated control actions among different sectors, such as the public health and veterinary sectors. For rabies-free countries, surveillance aims to confirm absence of the disease. In accordance with Regulation (EU) No 652/2014[63] and Commission Delegated Regulation (EU) No 2020/689,[64] multiannual control programmes and surveillance programmes for rabies, as well as oral rabies vaccination (ORV) campaigns were conducted in 11 MSs (Bulgaria, Croatia, Estonia, Finland, Greece, Hungary, Latvia, Lithuania, Poland, Romania and Slovakia), as well as in some EU-bordering countries. Surveillance of rabies is carried out by sampling and testing 'indicator animals'; these are wild or domestic animals (foxes, raccoon dogs, jackals, badgers, dogs, cattle, cats, sheep, equines, goats, etc.) that are found dead (including road-killed) and/or suspect animals, i.e. animals showing neurological clinical signs or abnormal behaviour compatible with rabies, like biting, licking a wound or scratching a human in the absence of clear neurological signs (European Commission, 2015).

To monitor the efficacy of ORV campaigns, apparently healthy individuals of the wild animal species targeted by oral vaccination (i.e. foxes, raccoon dogs and golden jackals) are hunted and the animal carcasses are used to determine rabies immunity and oral vaccine bait uptake (EFSA AHAW Panel, 2015). This specific active rabies surveillance is traditionally designated as 'ORV monitoring' or 'monitoring' or 'active rabies surveillance' when rabies diagnosis is performed on such sampling. These hunted animals can also be tested for rabies and very few of them (below 5%) are usually found to be positive for the disease.

Imported or travel-related companion animals (mainly dogs and cats) from territories and non-MSs not included in Annex II of Commission Implementing Regulation (EU) No 577/2013[65] are currently tested for rabies virus neutralising antibodies.

In accordance with Commission Implementing Regulation (EU) 2020/2002,[66] EU MSs must notify outbreaks of infection with rabies virus in non-flying animals to the EU Animal Disease Information System, ADIS[67]; these are the animal species and groups of species: *Carnivora*, *Bovidae*, *Suidae*, *Equidae*, *Cervidae* and *Camelidae*, but not *Chiroptera* (bats).

The data reported here include all animals tested for rabies, i.e. those collected for disease surveillance (passive surveillance) as well as those for ORV monitoring (active surveillance) purposes.

C1.3 | Results

C1.3.1 | Overview of key statistics, EU, 2020–2024

A summary of EU-level rabies statistics in wild and domestic animals is shown in Table 59. For animals, the total number of samples analysed for passive surveillance from foxes, raccoon dogs, golden jackals, dogs, cats and bats, as well as the

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[63] Regulation (EU) No 652/2014 of the European Parliament and of the Council of 15 May 2014 laying down provisions for the management of expenditure relating to the food chain, animal health and animal welfare, and relating to plant health and plant reproductive material, amending Council Directives 98/56/EC, 2000/29/EC and 2008/90/EC, Regulations (EC) No 178/2002, (EC) No 882/2004 and (EC) No 396/2005 of the European Parliament and of the Council, Directive 2009/128/EC of the European Parliament and of the Council and Regulation (EC) No 1107/2009 of the European Parliament and of the Council and repealing Council Decisions 66/399/EEC, 76/894/EEC and 2009/470/EC. OJ L 189, 27.6.2014, pp. 1–32.

[64] Commission Delegated Regulation (EU) 2020/689 of 17 December 2019 supplementing Regulation (EU) 2016/429 of the European Parliament and of the Council as regards rules for surveillance, eradication programmes and disease-free status for certain listed and emerging diseases. OJ L 174, 3.6.2020, p. 211–340.

[65] Commission Implementing Regulation (EU) No 577/2013 of 28 June 2013 on the model identification documents for the non-commercial movement of dogs, cats and ferrets, the establishment of lists of territories and third countries and the format, layout and language requirements of the declarations attesting compliance with certain conditions provided for in Regulation (EU) No 576/2013 of the European Parliament and of the Council. OJ L 178, 28.6.2013, pp. 109–148.

[66] Commission Implementing Regulation (EU) 2020/2002 of 7 December 2020 laying down rules for the application of Regulation (EU) 2016/429 of the European Parliament and of the Council with regard to Union notification and Union reporting of listed diseases, to formats and procedures for submission and reporting of Union surveillance programmes and of eradication programmes and for application for recognition of disease-free status, and to the computerised information system, OJ L 412, 8.12.2020, p. 1–28.

[67] EU Animal Disease Information System (ADIS). More information is available at: Animal Disease Information System (ADIS) - European Commission.

number of MSs from which these samples originated, are shown. A slight decrease was observed in the number of tested samples from foxes, which are the main reservoir of the virus in Europe, compared with 2023. The number of tested raccoon dogs increased compared with 2023, while the tested samples of jackals decreased in 2024 compared with 2023. In 2024, the number of tested bats considerably increased as compared with 2023. For cats and dogs, the number of samples reported increased slightly compared with the 2020–2023 period. The number of samples tested from domestic farmed mammals decreased in 2024 compared with 2023. Compared with previous years, the number of positive cases in 2024 increased in dogs, cats and bats, while it remained stable in cattle, red foxes and raccoon dogs. The case reported in 2024 in a jackal was the first in the period 2020–2024.

Table 59 also displays the active surveillance (ORV monitoring) statistics for ORV target species (foxes, raccoon dogs and golden jackals). In the context of ORV monitoring, the number of tested foxes increased slightly in 2024 compared with 2023. The number of tested raccoon dogs remained stable, while the number of tested jackals in two MSs decreased considerably compared with numbers for the 2020–2023 period.

TABLE 59 Summary of rabies lyssavirus statistics (RABV in non-flying animals; EBLV-1 and BBLV in bats) relating to the main animal reservoirs, EU, 2020–2024.

	2024	2023	2022	2021	2020	Data source
Animals under passive surveillance						
Dogs (*Canis lupus familiaris*)						
Number of tested animals	2214	2167	2137	1823	1730	EFSA
Number of positive animals	14[a]	8	11	3	4	EFSA
Number of reporting MSs	24	21	23	21	22	EFSA
Cats (*Felis catus*)						
Number of tested animals	2967	2723	2957	2335	2440	EFSA
Number of positive animals	7[b]	1	1	8	2	EFSA
Number of reporting MSs	24	25	22	20	21	EFSA
Farmed mammals[c]						
Number of tested animals	422[d]	540	374	410	392	EFSA
Number of positive animals	15	30	15	4	3	EFSA
Number of reporting MSs	17	16	16	17	17	EFSA
Wild animals – Red foxes (*Vulpes vulpes*)						
Number of tested animals	10,518	11,445	18,486	12,907	9805	EFSA
Number of positive animals	48	31	43	97	6	EFSA
Number of reporting MSs	21	20	18	17	18	EFSA
Wild animals – Raccoon dogs (*Nyctereutes procyonoides*)						
Number of tested animals	1400	1176	1096	1339	1214	EFSA
Number of positive animals	2	–	–	2	–	EFSA
Number of reporting MSs	7	7	7	6	6	EFSA
Wild animals – Jackals (*Canis aureus*)						
Number of tested animals	560	913	241	230	102	EFSA
Number of positive animals	1	–	–	–	–	EFSA
Number of reporting MSs	8	7	7	5	6	EFSA
Wild animals – Bats (order Chiroptera)						
Number of tested animals	1840[e]	1658	1622	1316	1308	EFSA
Number of positive animals	44	23	26	29	31	EFSA
Number of reporting MSs	20	18	16	16	15	EFSA
Animals under active surveillance (ORV monitoring)[f]						
Red foxes (*Vulpes vulpes*)						
Number of tested animals	14,074	13,399	1801	10,581	14,416	EFSA
Number of positive animals	3	4	–	–	–	EFSA
Number of reporting MSs	10	8	6	9	10	EFSA
Raccoon dogs (*Nyctereutes procyonoides*)						
Number of tested animals	359	331	221	369	324	EFSA
Number of positive animals	–	–	–	–	–	EFSA
Number of reporting MSs	3	3	3	4	4	EFSA

TABLE 59 (Continued)

	2024	2023	2022	2021	2020	Data source
Jackals (*Canis aureus*)						
Number of tested animals	48	115	1100	1499	1319	EFSA
Number of positive animals	–	–	–	–	–	EFSA
Number of reporting MSs	2	2	1	3	3	EFSA

Note: Sampling context items for historical data: Passive surveillance: clinical investigations, monitoring–passive, surveillance, control and eradication programmes; Active surveillance: monitoring–active and unspecified. Sampling context items from 2023 data onward: Passive surveillance: clinical investigations and monitoring–passive; Active surveillance: monitoring–active.

Abbreviations: EFSA, European Food Safety Authority; MSs, Member States; ORV, oral rabies vaccination.

[a] One imported case included.

[b] One case positive for EBLV-1 included.

[c] Includes cattle (bovine animals), foxes, horses, sheep, goats, pigs, alpacas and donkeys.

[d] Includes 51 farmed foxes from Germany, all negative.

[e] During the final phase of report production, France reported a correction stating that the number of tested bats was 983 (instead of 536). Based on the new data the total samples tested at the EU level was 2287.

[f] Samples collected in the framework of oral rabies vaccination monitoring (ORV).

C1.3.2 | Humans

In 2024, no autochthonous human cases of rabies were reported in the European Union.

C1.3.3 | Animals

Rabies cases in wildlife

In 2024, 10,518 foxes (*Vulpes vulpes*) were tested using passive surveillance by 21 MSs. In total, 48 cases of rabies were detected in foxes in the EU: 30 cases in Poland, 11 in Hungary, 6 in Romania and 1 in Slovakia. The geographical distribution and number of cases in foxes per NUTS 3 (Nomenclature of territorial units for statistics),[68] as well as a choropleth map of the total number of foxes sampled per MS for passive surveillance, are shown in Figure 26. Three foxes tested positive for rabies (RABV) in Romania in animals sampled during active surveillance.

Four non-MSs (Republic of North Macedonia, Norway, Serbia and Switzerland) reported a total of 18 foxes tested under passive surveillance schemes and found none to be positive. One arctic fox tested positive for rabies (RABV) in Norway in an animal sampled during active surveillance.

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[68] The NUTS are a hierarchical system divided into three levels. NUTS 1: major socio-economic regions, NUTS 2: basic regions for the application of regional policies, NUTS 3: small regions for specific diagnoses. (https://ec.europa.eu/eurostat/web/gisco/geodata/statistical-units/territorial-units-statistics).

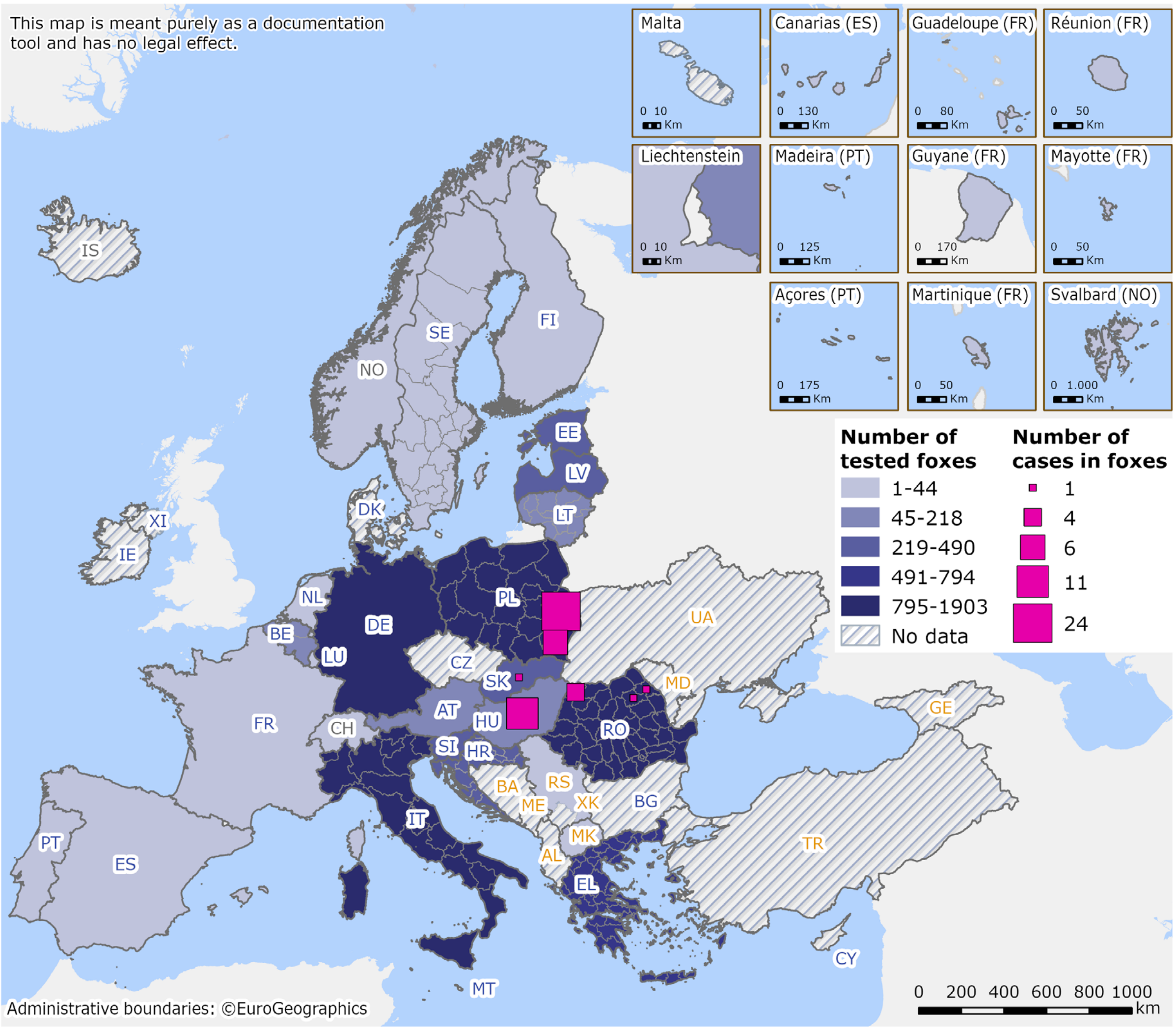

FIGURE 26 Number of tested and positive foxes in the framework of passive surveillance, and the geographical distribution of the rabies cases reported in foxes in EU MSs and non-MSs, 2024.
EU MSs and the United Kingdom (Northern Ireland) are represented with a blue label, EFTA/EEA countries are represented with a grey label, and all candidate countries are represented with an orange label. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

In 2024, 1400 raccoon dogs (*Nyctereutes procyonoides*) were tested for rabies by seven MSs (Estonia, Finland, Italy, Latvia, Lithuania, Poland and Slovakia) and two were found to be positive in Poland. Most (88.0%) of these samples came from raccoon dogs originating from two MSs (Estonia and Latvia).

In 2024, 560 jackals (*Canis aureus*) were tested for rabies by eight MSs (Croatia, Germany, Greece, Hungary, Italy, Romania, Slovakia and Slovenia) and one was found to be positive in Hungary.

Nineteen MSs reported data from passive surveillance for 4264 non-flying wild animals other than foxes, raccoon dogs or golden jackals. The other most widely tested wild animal species were raccoons ($N=1065$), badgers ($N=1062$), martens ($N=623$), deer and reindeer, red and roe deer ($N=515$) and wolves ($N=416$). One roe deer and one marten tested positive for rabies (RABV) in Poland. Other species tested included mice, lynxes, otters, squirrels, hedgehogs, rats, wild boars, bears, ferrets, dormice, wild cats, wolverines, minks, beavers, polecats, alpine chamois, alpacas, guinea pigs, voles, hamsters, buffalos, land game mammals, seals, coypus, hares, rodents, kangaroos, mouflons, fur animals and moose. All the animals tested negative for rabies. One non-MS (Serbia) analysed one marten and the sample tested negative.

In 2024, 20 MSs reported surveillance data on bats. In total, 2287[69] bats were investigated in the EU (Figure 27). Of these, 44 samples tested positive in seven MSs: France (15 EBLV-1), Germany (13 EBLV-1 and 1 Bokeloh bat lyssavirus), the Netherlands (5 EBLV-1), Poland (4 EBLV-1), Hungary (3 EBLV-1), Spain (2 EBLV-1) and Czechia (1 EBLV-1). Two non-MSs analysed 37 bats (Norway, 1 sample and Switzerland, 36 samples) and one bat tested positive (EBLV-2) in Switzerland.

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[69] According to the footnote 'e', Table 59.

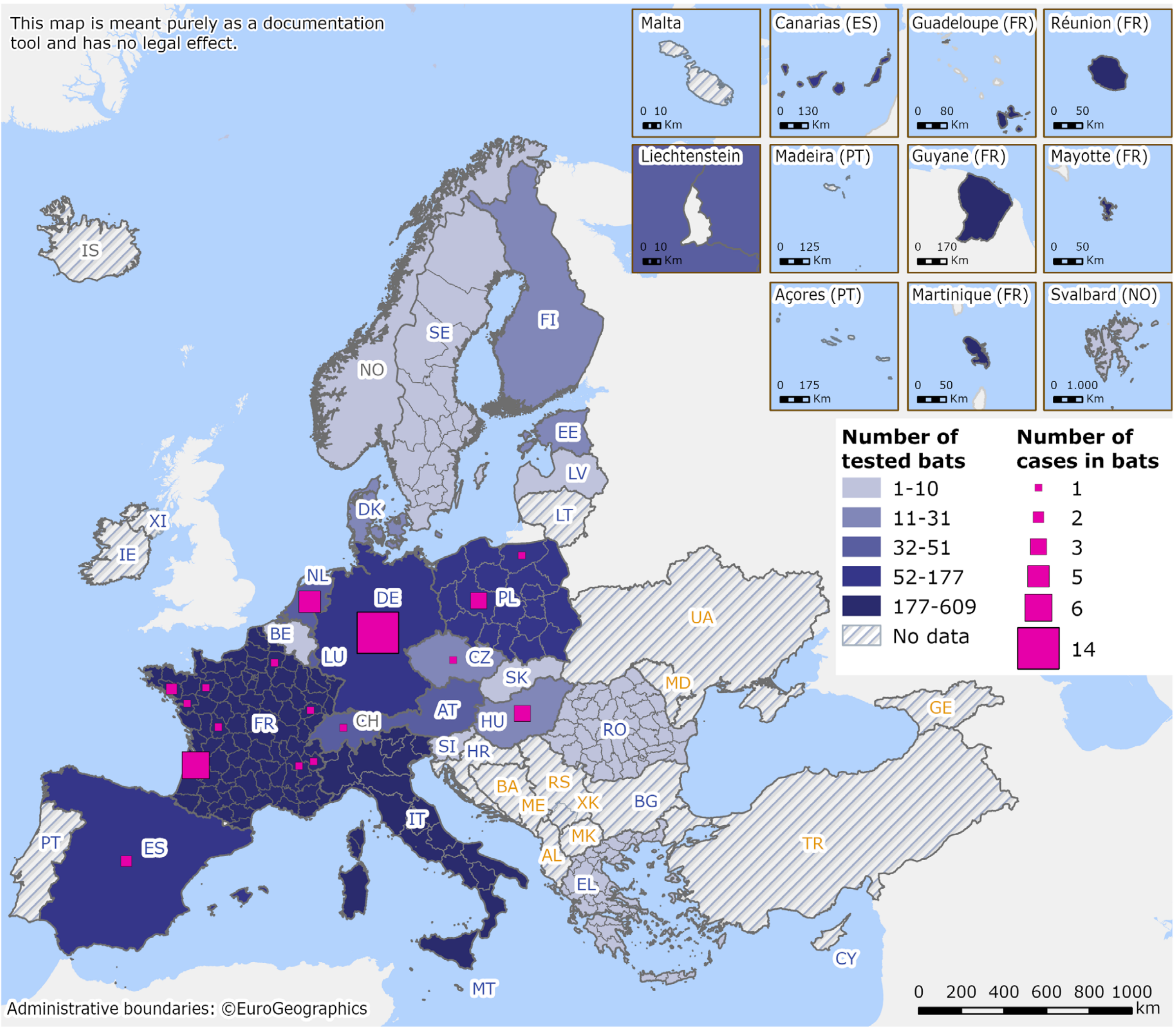

FIGURE 27 Number of tested and positive bats, and the geographical distribution of the rabies cases reported in bats in EU MSs and non-MSs, 2024.
EU MSs and the United Kingdom (Northern Ireland) are represented with a blue label, EFTA/EEA countries are represented with a grey label, and all candidate countries are represented with an orange label. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.
During the final phase of report production, France reported a correction stating that the number of tested bats was 983 (instead of 536). Based on the new data the total samples tested at the EU level was 2287.

Rabies cases in domestic animals

In 2024, 35 autochthonous domestic animals tested positive for rabies (RABV). Twenty-four MSs tested in total 5181 samples for dogs and cats: 2214 dogs (from 24 MSs) and 2967 cats (from 24 MSs). A total of 14 dogs tested positive for rabies (RABV): in Romania, eight cases; in Hungary, three cases; and in Poland, two cases. In France, one dog was reported to be positive for rabies (RABV, Africa 1 lineage from North Africa). The animal had been imported from Morocco, a country where canine rabies is endemic.

Six cases (RABV) were reported in cats: by Poland (four cases) and Hungary (two cases). In addition, an indigenous cat was detected positive for EBLV-1 in the Netherlands. Three non-MSs (Republic of North Macedonia, Serbia and Switzerland) reported in total results for 45 dogs and 26 cats, with no rabies positives. The geographical distribution and number of tested and reported cases in pets (dogs and cats) are shown in Figure 28.

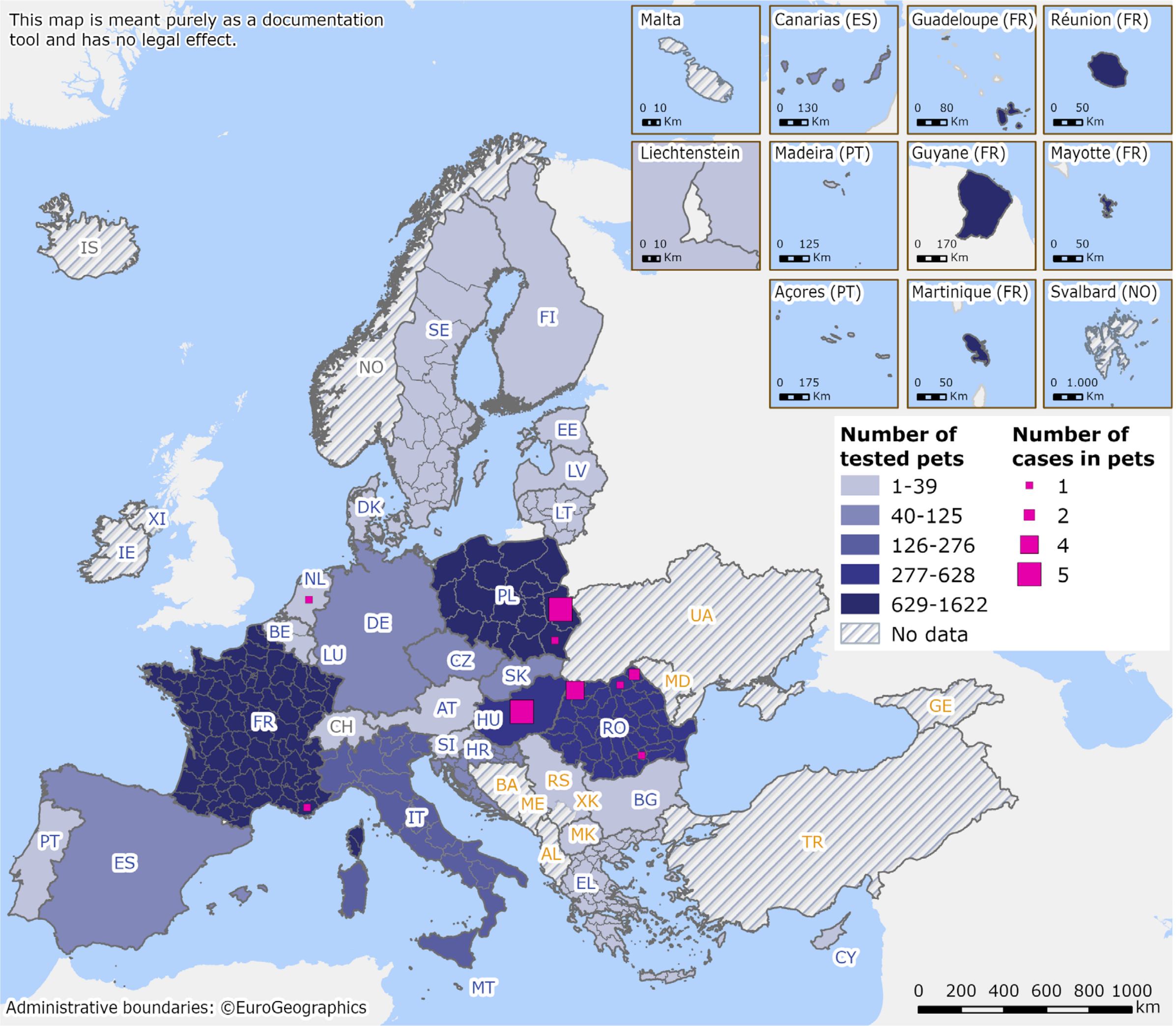

FIGURE 28 Number of tested and positive pets, and the geographical distribution of the rabies cases reported in pets in EU MSs and non-MSs, 2024.
EU MSs and the United Kingdom (Northern Ireland) are represented with a blue label, EFTA/EEA countries are represented with a grey label, and all candidate countries are represented with an orange label. The designation of Kosovo is without prejudice to positions on status and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.
The case reported in the Netherlands involved a cat infected with EBLV-1.
The case reported in France concerned a dog imported from North Africa.

A total of 422 samples from farmed mammals (Figure 29) were tested by 17 MSs (reports included mainly cattle, small ruminants and domestic solipeds). Of these, 15 samples from cattle tested positive (RABV): 11 cases in Romania, 3 cases in Poland and 1 case in Hungary. One non-MS, Switzerland, reported one sample tested from a bovine animal, which returned a negative result.

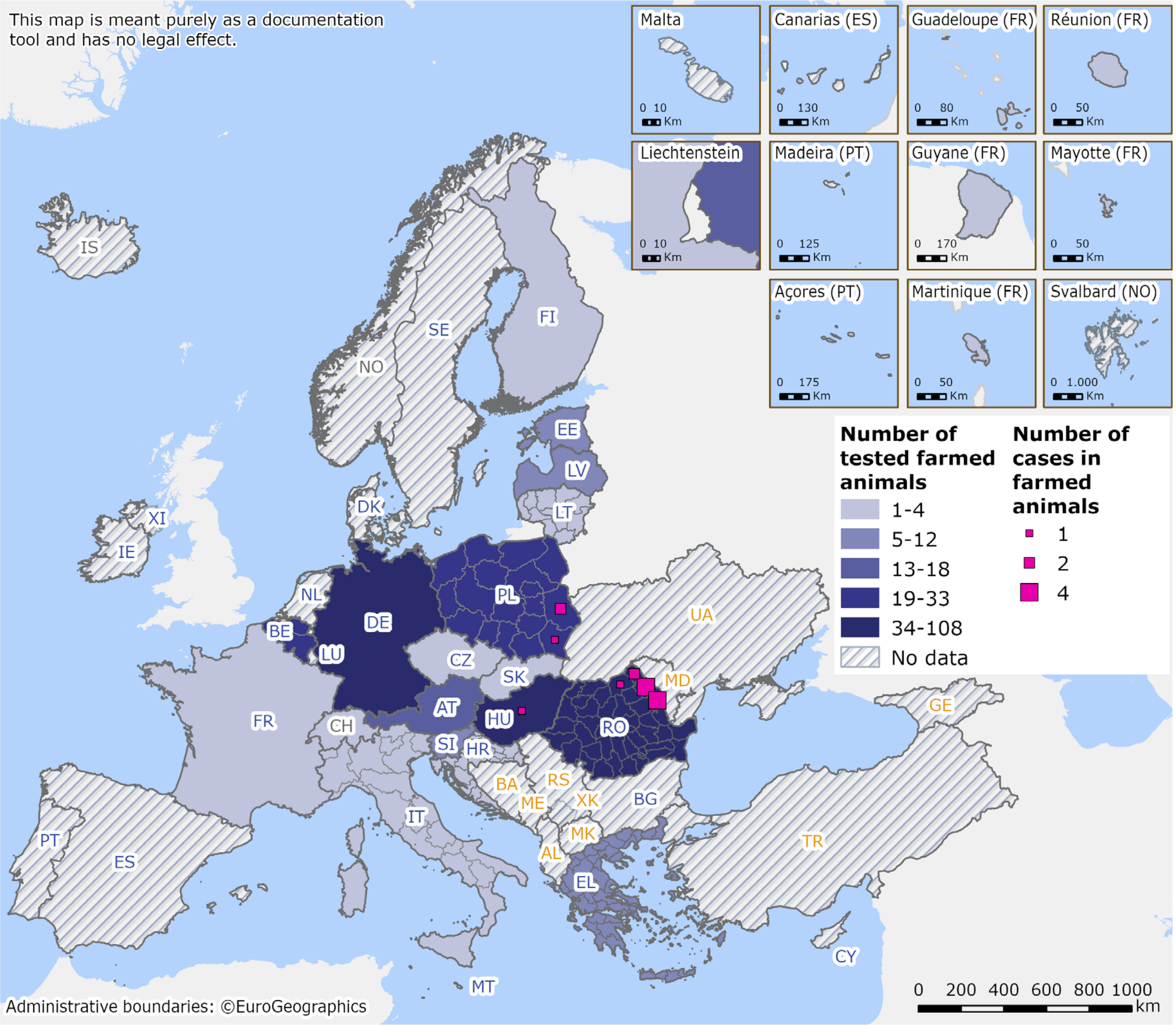

FIGURE 29 Number of tested and positive farmed animals, and the geographical distribution of the rabies cases reported in farmed animals in EU MSs and non-MSs, 2024.
EU MSs and the United Kingdom (Northern Ireland) are represented with a blue label, EFTA/EEA countries are represented with a grey label, and all candidate countries are represented with an orange label. The designation of Kosovo is without prejudice to positions on status and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

C1.4 | Discussion

No autochthonous human cases were reported in the EU in 2024.

The EU programmes for rabies eradication include disease surveillance, oral vaccination campaigns, monitoring of ORV and awareness activities (European Commission, 2015; EFSA AHAW Panel, 2015). Data relating to passive surveillance in wildlife, mainly in foxes and raccoon dogs, show relative stability in the number of samples tested over the 2020–2024 period, due to surveillance efforts maintained by most rabies-free and infected MSs for controlling the last foci. Results in 2024 (total of 89 rabies cases reported from passive surveillance, including the case of imported RABV in a dog and the case on a cat infected with EBLV-1) show maintenance of the infection in Poland (in total 43 cases, including 34 wild and 9 domestic animals, compared with 7 cases in 2023) and in Romania (in total 25 cases, including 6 foxes and 19 domestic animals, of which 11 cattle, compared with 49 cases in 2023). The disease is also maintained in Hungary, with 18 cases reported in 2024 (compared with 15 cases in 2023). After a period without reported cases since 2017, the country experienced re-emergence in 2022, when four cases were recorded. The epidemiological data localised these cases in administrative units close to the borders with Ukraine and Romania. One case was reported in 2024 in Slovakia, compared with no cases in 2023 and three cases in 2022, following a seven-year absence period since the last reported cases in 2015. In Poland, the data showed a markedly increased number of cases, with most cases being detected in bordering areas with Ukraine. Epidemiological data from Romania showed a decrease in reported cases through passive surveillance, but an increase through active surveillance, resulting in contradictory outcomes. This discrepancy may suggest that cases are being missed within the passive surveillance system.

In 2024, positive cases were reported in Hungary in a jackal and in Poland in a roe deer and a marten. These types of animal species, which are sensitive to rabies, are not commonly detected. Data relative to passive surveillance in pets showed a marked increase in 2024 in the number of positive cases (14 dogs and 7 cats in 2024 compared with 8 dogs and 1 cat in

2023), while a slight increase was observed in the number of samples tested over the 2020–2024 period. These two findings could reveal efforts in several countries aimed at improving passive surveillance to collect suspect wild mammal samples aside from samples from foxes, which are the main transmitters of rabies virus in Europe along with companion animals.

In 2024, a case of imported rabies in a dog was reported by France. Imported cases of this type may pose a threat of rabies reintroduction into rabies-free areas, and the rabies importation risk must not be neglected.

The overall picture in the EU shows how fragile the epidemiological situation of a country is, given how it is linked to that of neighbouring countries. The cases still being reported over several years in the few remaining MSs with infections, or re-emergence of rabies, highlight the importance of a sustainable surveillance programme for wild and domestic animals, and of awareness campaigns for the general public and professionals, to ensure the early detection of any potential cases (Rupprecht et al., 2025).

The epidemiological data also stress the importance of implementing ORV programmes in all infected areas on a biannual basis (in spring and in autumn) and over sufficiently large areas to cover reservoir movements. Data relating to active surveillance (ORV monitoring) are reported for foxes, raccoon dogs and jackals, and a sample size linked to the area covered by vaccination is recommended. This opportunistic surveillance is conducted by hunting apparently healthy animals to assess the efficacy of vaccination campaigns in countries involved in eradication programmes. In 2024, the data revealed relative stability in the number of analysed foxes and raccoon dogs compared with the 2020–2023 period (except in 2022), reflecting a relatively stable number of MSs still involved in eradication programmes. In 2024, Romania reported three positive foxes sampled during ORV monitoring.

Regarding rabies surveillance in bats, the number of tests considerably increased in 2024 compared with the 2020–2023 period, as well as the number of positive cases: 44 cases in 2024, while the previous highest level was recorded in 2020 with 31 cases. The number of reporting MSs has also increased regularly over the 2020–2024 period (20 countries in 2024 compared with 15 countries in 2020). Positive results obtained in 2024 are in line with the findings of the previous years and confirm that European bats act as reservoirs for lyssaviruses other than rabies virus. The public health hazard of bat lyssavirus in Europe should not be underestimated, reaffirming the public recommendation to handle bats with the utmost caution, if at all.

In 2024, an indigenous cat from the Netherlands was found to be infected with EBLV-1, indicating spillover transmission of these viruses from bats to non-flying mammals, and a rare but possible risk of exposure of humans to a lyssavirus via their pets (Eblé et al., 2025).

As rabies is still endemic in countries bordering the EU, in areas not far from the borders, several MSs are involved in collaborations with these countries for the implementation of vaccination and testing schemes in buffer zones. The Global Framework for the Progressive Control of Transboundary Animal Diseases (GF-TADs) created a Standing Group of Experts on Rabies (SGE RAB) in 2019, and the sixth meeting was held in 2024, with the goal of coordinating rabies control and improving surveillance activities, primarily in the Balkan sub-region, where the last case was detected in a dog in 2020.

Maintaining appropriate surveillance is of paramount importance for all MSs, due to the persistence of active foci in Hungary, Poland and Romania and more globally due to the risk of re-introduction, given that rabies is still endemic in many countries outside the EU. Apparent disappearance of the virus was almost achieved in the EU in 2019 (Robardet et al., 2019), but subsequent resurgence (Robardet et al., 2023) has been a warning that maintaining adequate surveillance efforts (mainly at borders with infected areas), cross-border collaborations and relevant regular ORV implementation remain important strategies for rabies elimination in the EU.

C2 | OTHER BACTERIAL ZOONOSES AND ZOONOTIC AGENTS

The summary data which make up this chapter, as well as additional information on related projects, internet sources and summary statistics on One Health Surveillance, are published for this report on the EFSA Knowledge Junction at Zenodo here. In 2024, data on *Yersinia*, *Coxiella burnetii* (Q fever), *Francisella tularensis* (tularemia), *Bacillus*, *Chlamydia*, *Clostridium*, pathogenic *Escherichia coli* other than STEC, *Klebsiella*, *Proteus*, *Staphylococcus*, *Streptococcus* and *Vibrio* were reported to EFSA. The monitoring and surveillance efforts provide insight into the occurrence of these bacterial zoonoses in food categories and relevant animal species, highlighting the importance of continued vigilance and research on these diseases

C2.1 | *Yersinia* spp.

Data on *Yersinia* spp. were reported by nine Member States (Belgium, Germany, Ireland, Italy, Latvia, the Netherlands, Slovakia, Slovenia and Spain) and one non-MS (Norway). The occurrence of *Yersinia* spp. was reported in different food categories, ranging from ready-to-eat (RTE) foods, non-RTE foods and fresh meat, and in eight animal categories, including cattle, pigs and small ruminants. Reporting *Yersinia* spp. in food and animals is not mandatory, but MSs may voluntarily submit monitoring data to EFSA under Directive 2003/99/EC (Annex I, List B), based on the epidemiological situation. There is currently no harmonised EU monitoring programme for *Yersinia* spp. in food or animals. Therefore, only data obtained from food samples collected and tested for *Yersinia* spp. under an objective sampling strategy were considered to reduce selection bias. Both conventional microbiological methods (ISO 10273:2017) and molecular methods (ISO/TS 18867) are commonly used to investigate *Yersinia* spp. in food and animals (ISO, 2015, 2017).

Summary tables showing the occurrence of *Yersinia* spp. in food and animals are available on the EFSA Knowledge Junction at Zenodo here. In 2024, fewer RTE food samples were reported compared to the previous 5 years (a decrease of 12.9%), while non-RTE sample numbers increased (by 16.2%). The number of samples for the fresh meat category remained stable.

- 384 RTE food units were reported by five MSs, with 0.26% testing positive for *Yersinia enterocolitica*. Most units were from 'meat and meat products' (56.5%, *N* = 217) and 'fruits and vegetables' (40.1%, *N* = 154); this latter category was the only one including samples that tested positive ('vegetables – pre-cut'). A difference was observed compared with the 2020–2023 period, when eight MSs analysed 1763 RTE food units, of which 2.4% (*N* = 43) tested positive. Notably, the only category among RTE food that tested positive was 'meat and meat products' reported by five MSs, with 3.4% (*N* = 43) positive samples for *Y. enterocolitica* of the 1281 RTE units tested during the same period.
- 923 non-RTE food units were reported by six MSs, with 7.2% testing positive for Y. *enterocolitica*. Most units were from 'meat and meat products' (96.4%, *N* = 890), with 6.4% (*N* = 57) testing positive, followed by 'milk and milk products' (3.1%, *N* = 29; reported by one MS), with 31.0% (*N* = 9) testing positive.
- 615 fresh meat units were reported by six MSs, with 8.1% testing positive for *Y. enterocolitica*. Most units were from 'fresh meat from pigs' (55.1%, *N* = 339), with 11.2% (*N* = 38) testing positive. Among samples from 'other fresh meat' (*N* = 266) 12 tested positive for *Yersinia* (4.5%). Positive samples were all from 'fresh meat from deer (venison)' and were reported by one MS (Germany), which tested a total of 234 samples from 'fresh meat from deer (venison)' (88.0% of total samples from 'other fresh meat' category).
- 16,966 individual animals were sampled and reported by five MSs, with 0.24% (*N* = 41) testing positive for *Y. enterocolitica* and 0.21% (*N* = 35) for *Yersinia pseudotuberculosis*. Most animal samples were from cattle (40.9%, *N* = 6938), pet animals (18.5%, *N* = 3136), small ruminants (16.6%, *N* = 2822) or pigs (11.8%, *N* = 2005). In these four animal categories, the highest proportion of positive samples for *Y. enterocolitica* was in cattle (0.39%), followed by small ruminants (0.11%) and pet animals (0.10%). For *Y. pseudotuberculosis*, the highest proportion of positive samples was in small ruminants (0.25%), followed by cattle (0.17%) and pet animals (0.13%). No positive samples were detected in pigs either for *Y. enterocolitica* or for *Y. pseudotuberculosis*, in contrast with year 2023 in which the proportion of positive samples in pigs (for *Y. enterocolitica*) was 1.5%.
- 'Wild animals' represented 2.4% (*N* = 413) of all animals sampled, with percentages of *Y. enterocolitica*- and *Y. pseudotuberculosis*-positive samples of 0.48% and 1.5%, respectively.

Overall, the data indicate that *Yersinia* was more prevalent in non-RTE foods and fresh meat than in RTE foods in 2024. These findings were consistent with 2020–2023, when the percentage of positive samples was higher for non-RTE foods and fresh meat than for RTE foods. In the RTE food category, the percentage of positive samples was lower in 2024 than in previous years. These findings suggest that improving the monitoring of non-RTE food and fresh meat should be considered, emphasising the need for data collection efforts.

In particular, the 'milk and dairy products' food category showed a high number of positive samples, despite the low number of samples analysed. Enhancing the monitoring and sampling of this food category may improve the understanding of its relevance for public health in light of two large *Y. enterocolitica* outbreaks in 2024 related to the consumption of raw bovine milk and raw goat milk (Savin et al., 2025).

Furthermore, a particularly high percentage of positive samples reported in 'fresh meat from deer (venison)' in 2024, originating from a single MS, highlights the potential relevance of this food category in *Y. enterocolitica* transmission and suggests that broader monitoring activities may be beneficial.

C2.2 | *Coxiella burnetii* (Q fever)

Data on *Coxiella burnetii* were reported by 18 MSs (17 in 2023; Cyprus and Romania reported data in 2024, but not in 2023, and Bulgaria reported data in 2023, but not in 2024) and, like in 2023, five non-MSs (Iceland, Norway, Republic of North Macedonia, Serbia and Switzerland). The occurrence of *C. burnetii* was monitored in 25 animal species, mostly in cattle and small ruminants. The samples from cattle and small ruminants (97.4%; *N* = 22,810) were primarily taken from blood, foetuses and stillborn animals, placentas and vaginal swabs from animals suspected of being infected with *C. burnetii*, along with bulk milk samples used for screening purposes. Testing was conducted either using serological methods (to detect antibodies indicating past or recent exposure to *C. burnetii*) or direct detection methods (to identify active carriage). In most MSs, detection of *C. burnetii* in this species was based on clinical investigation and passive monitoring. Only a few countries implemented planned surveillance or active monitoring in cattle and small ruminants. In the mentioned active monitoring, most tests relied on direct detection by PCR in various sample types: blood (Poland, *N* = 4859 herds/flocks), organ or tissue (Ireland, *N* = 1437 animals), milk (the Netherlands, *N* = 426 herds/flocks; Belgium, *N* = 236 holdings) and vaginal swabs (Spain, *N* = 130 herds/flocks). Some countries reported only local surveys or selective tests not representative of the situation in the entire country. In addition to cattle and small ruminants, samples were also collected from other farmed or domestic animals (in particular, water buffalos in Italy) as well as from wild animal species, either in zoos or from natural habitats. Summary tables showing the occurrence of *C. burnetii* in animals are available on the EFSA Knowledge Junction at Zenodo here.

- For cattle, serological tests on 4331 animals and 41 herds were reported by nine MSs, with respectively 14.2% and 22.0% positivity. Most animals were from Hungary (*N* = 1347 animals, 25.9% positivity), Austria (*N* = 980 animals, 10.7% positivity), Italy (*N* = 837 animals, 13.3% positivity) and Slovakia (*N* = 824 animals, 1.5% positivity).
- Serological tests on 625 sheep and 189 goats were reported by respectively six and five MSs, with respectively 20.2% and 25.9% positivity. Most units were from Italy (*N* = 467 sheep, 25.9% positivity; *N* = 113 goats, 30.1% positivity).
- For cattle, direct detection tests on 4410 animals and 2570 herds were reported by respectively nine and six MSs, with respectively 3.5% and 2.3% positivity. Most units were from Poland (*N* = 2390 herds, 1.2% positivity), Belgium (*N* = 2201 animals, 2.4% positivity) and Ireland (*N* = 1147 animals, 2.7% positivity). Switzerland also reported 3728 direct detection tests at the individual animal level with 12.0% positivity.
- Direct detection tests on 1343 sheep and 2644 flocks, were reported by respectively seven and six MSs, with respectively 5.3% and 3.0% positivity. Most units were from the Netherlands (*N* = 516 sheep, 0% positivity; *N* = 32 flocks, 3.1% positivity) and Poland (2217 flocks, 0% positivity). Positive units were also reported by Austria, Belgium, Hungary, Ireland, Italy and Spain. Switzerland also reported 226 direct detections tests on sheep with 9.3% positivity.
- Direct detection tests on 729 goats and 1524 goat herds were reported by respectively seven and five MSs, with respectively 6.2% and 3.3% positivity. Most units were from the Netherlands (*N* = 537 goats and *N* = 394 goat herds, 0% positivity for both) and Poland (*N* = 854 goat herds, 0% positivity). Positive units were reported by Austria, Belgium, Italy and Spain. Switzerland also reported 152 direct detections tests on goats, with 11.8% positivity.
- Data on animals other than cattle and small ruminants were reported by nine MSs and two non-MSs. Among the other farmed, domestic or wild animals tested (*N* = 602 animals, *N* = 2 herds), positivity was reported mainly in buffalos by Italy (8.7%, *N* = 253 animals) and by Romania (8.3%, *N* = 12 animals). Positivity was also reported by Italy in bears (100%, *N* = 1 animal), in dogs (5.9%, *N* = 17 animals) and in deer (2.1%, *N* = 48 animals). Austria reported one positive alpaca (14.3% positive, *N* = 7 animals).
- In 2024, eight MSs and one non-MS reported data on ruminants and environment in the context of EFSA One-Health surveillance (OHS) data collection, of which five MSs (Germany, Estonia, Croatia, Lithuania and Portugal) have not reported data in the context of Zoonoses Directive 2003/99/EC in the last 5 years. Most tests were ELISA tests performed on milk by Norway (*N* = 1743 cattle herds, 0.06% positivity) and Sweden (*N* = 1733 cattle herds, 24.7% positivity) or on blood by Estonia (*N* = 1747 sheep, 0.4% positivity) and Germany (*N* = 75 goats, 0% positivity).

Overall, the data indicate that in 2024, compared with year 2023, the total number of samples submitted by EU MSs in the context of Zoonoses Directive 2003/99/EC decreased for all ruminants, independently of the data collected within the context of OHS. The number of animal (individual) samples was stable for cattle (+0.09%, *N* = 8741), decreased for sheep (−32.9%, *N* = 1968) and increased for goats (+15.3%, *N* = 918). Concomitantly, the number of sampled herds decreased by 38.0% for cattle (*N* = 2611 in 2024), by 37.3% for sheep (*N* = 2644 in 2024) and by 30.0% for goats (*N* = 1525 in 2024). The monitoring and surveillance efforts provide valuable insight into the occurrence and distribution of *C. burnetii* in domestic ruminants. However, persistent heterogeneity in Q fever surveillance across Europe (particularly in case definitions and diagnostic approaches) continues to hinder effective risk assessment and coordinated response strategies (van den Brom et al., 2025). This highlights the need for continued research and monitoring of *C. burnetii*. Despite the growing emphasis on the One Health concept, the findings suggest a decline in testing of animals and herds in recent years. This trend highlights the importance of developing other surveillance tools for monitoring the presence of *C. burnetii* in various environmental matrices (e.g. farm dust and manure) using validated methodologies, to prevent animal and human exposure to this zoonotic pathogen. Furthermore, given the variability in virulence among C. *burnetii* strains, integrating strain-level surveillance may help to promote more effective and preventive strategies, within the One-Health concept (Abou Abdallah et al., 2022; Gil-Zamorano et al., 2025).

C2.3 | *Francisella tularensis* (tularemia)

Data on *Francisella tularensis* were reported by four MSs (Austria, Finland, Germany and Sweden) and one non-MS (Switzerland). The occurrence of *F. tularensis* was monitored in 41 animal species, as well as in felids, rodents, solipeds and zoo animals. Wild hares (61.3%; *N* = 1365) and farmed animals (17.1%; *N* = 381) were the most frequently tested. Samples were collected in natural habitats, zoos and farms for passive monitoring and clinical investigations.

In EU a total of 2204 samples distributed in six different animal categories (1355 wild hares, 21 other wild animals, 381 farmed animals, 293 unspecified animals, 104 pets and 50 zoo animals) were reported, with 15.3% (*N* = 337) testing positive. Switzerland reported 23 samples, with 21.7% (*N* = 5) positive.

- Wild animals (99.3% were hares), tested with PCR-based, microbiological or immunological methods, were reported by Austria, Finland, Germany, Sweden and Switzerland, with 23.7% (*N* = 329) testing positive.
- Farmed animals were reported only by Germany, with no positives out of 381 tested samples.
- Pets were reported by Austria, Germany and Sweden, with 0.96% (*N* = 1) testing positive. Switzerland reported no positives out of 10 tested pets. Most units were dogs.
- Zoo animals were reported by Austria and Germany, with 4.0% (*N* = 2) testing positive. Most units were monkeys tested using microbiological and PCR-based methods.

- Most of the animals tested were reported by Germany (92.4%; *N* = 2058), with 14.7% of animals being positive (303 hares, 1 rabbit and 1 wild boar). Austria registered the highest positivity rate with 30.8% (*N* = 16 out of 52 samples tested), followed by Sweden, with 22% (*N* = 9 out of 41 samples tested) and Finland, with 17.0% (*N* = 9 out of 53 samples tested). Switzerland reported data for pets, wild animals and zoo animals, with 21.7% of the samples testing positive (*N* = 5 out of 23 samples tested).

Overall, the data indicate that the number of samples collected in 2024 significantly increased in comparison with those taken and tested in 2023 (2204 vs. 188). This increase is mainly due to the number of animals monitored by Germany. In Germany, during the 2017–2022 period, animal surveillance data for *F. tularensis* showed an increase from 16.0% to 33.0%, in particular in the Baden-Württemberg region (Nothdurfter et al., 2025). In the last 5 years, among the reporting MSs, the number of hares tested has increased (from 222 to 1355), but positivity has decreased from 36.5% to 23.9%. The monitoring and surveillance efforts provide valuable insight into the occurrence and distribution of *F. tularensis* in wild animals, especially hares, which play a key role in the maintenance of *F. tularensis* within the ecological cycle (Maurin & Gyuranecz, 2016; WHO, 2007). The detection of *F. tularensis* in wildlife, with hares serving as effective indicators, is crucial for the early identification of potential risks for human health, emphasising the need for continuous cooperation between both the veterinarian and public health sectors. This collaboration is essential for comprehensive and timely epidemiological, laboratory and clinical investigations, particularly during the early stages of tularemia outbreaks.

C2.4 | *Bacillus* spp.

Data on *Bacillus* spp. were reported by four MSs (Bulgaria, Greece, Italy and Luxembourg). The occurrence of *Bacillus* spp. was monitored by two MSs (Italy and Luxembourg) in the following 18 food categories: 'bakery products', 'cereals and meals', 'cheeses made from cows' milk', 'cheeses made from sheep's milk', 'crustaceans', 'fish', 'fishery products', 'herbs and spices', 'meat from bovine animals', 'meat from poultry', 'meat from pigs', 'meat – mixed meat', 'molluscan and shellfish', 'other processed food products and prepared dishes', 'ready-to-eat salads', 'sauces and dressings', 'soups' and 'vegetables'.

Out of 1075 single samples, only 0.93% (*N* = 10) tested positive. Seven positive units were from 'other processed food products and prepared dishes', two from 'vegetable-based cooked sauce' and one from 'meat from broilers' collected at the distribution level, particularly at 'restaurant or café or pub or bar or hotel or catering services' and 'hospital or medical care facility'. One positive sample was collected at a processing plant. In all positive samples, *Bacillus cereus* was identified.

The occurrence of *Bacillus* spp. was monitored in four animal species by two MSs (Bulgaria and Greece), particularly in bovine animals, goats, pigs and sheep, collected for clinical investigations related to the detection of *Bacillus anthracis*.

Overall, the data indicate that the occurrence of *Bacillus* spp. in the tested samples is very low. It would be advisable to extend the monitoring and sampling efforts of *Bacillus* spp. in foods, especially in the categories 'other processed food products and prepared dishes' and in 'sauces and dressings', particularly in those MSs that report a high number of food-borne outbreaks due to bacterial toxins.

C2.5 | *Chlamydia* spp.

Data on *Chlamydia* spp. were reported by two MSs (Austria and Denmark) and one non-MS (Republic of North Macedonia). The occurrence of *Chlamydia* spp. was monitored in eight animal species, such as alpacas, birds (including pigeons and Psittacidae), bovine animals, pigs and small ruminants. Blood, organs or tissues were collected as part of official or industry sampling, mainly on farmed animals.

Austria collected 1198 samples, with 21.7% (*N* = 260) testing positive. Most positive units were bovine animals and pigs. Denmark collected 13 pharyngeal swabs from birds during clinical investigations, with 7.7% (*N* = 1) testing positive. The Republic of North Macedonia tested 15 samples collected from bovine animals and sheep, with 13.3% (*N* = 2) testing positive.

Overall, the data indicate that this pathogen is poorly monitored at the European level. Increasing the diagnostic capability for better identification of *Chlamydia* at the species level and expanding monitoring would help to better understand the occurrence and distribution of these pathogens in the veterinary sector at the EU level.

C2.6 | *Clostridium* spp.

Data on *Clostridium* spp. were reported by five MSs (Italy, Greece, Lithuania, Romania and Slovenia) and one non-MS (Republic of North Macedonia). The occurrence of *Clostridium* spp. was monitored in 16 food categories, i.e. 'cheeses made from cows' milk', eggs – table' eggs', 'fish – cooked', 'fish – marinated', 'fish – raw', 'fruits – products', 'meat from bovine animals', 'meat from poultry', 'meat from pigs', 'meat from turkey', 'mixed meat', 'molluscan shellfish', 'other processed food products and prepared dishes', 'sauce and dressings', 'soups' and 'vegetables'. Out of 328 samples, no positive samples were detected.

The occurrence of *Clostridium* spp. was also monitored in four animal species, i.e. bovine animals, goats, sheep and rabbits, collected in Greece during clinical investigations. Out of 43 tested samples, 67.4% (*N* = 29) were positive. The most recognised microbial species was *Clostridium perfringens*.

C2.7 | Pathogenic *Escherichia coli* other than STEC

Data on pathogenic *Escherichia coli* other than STEC were not reported in 2024.

Overall, the lack of data indicates that these microorganisms are not tested in food and animal samples in the EU. Some MSs have reported data produced on *E. coli* indicators of hygiene process or produced in the framework of the categorisation of live bivalve mollusc production areas, which are not related to any pathogenic group of bacteria belonging to the *E. coli* species.

In particular, the monitoring of pathogenic *E. coli* other than STEC would provide valuable insight into the occurrence and distribution of these microorganisms in food and animals. However, the infections caused by pathogenic groups of *E. coli* other than STEC are not actively monitored in most EU MSs, limiting the knowledge available on the burden of these infections and thus demonstrating that these pathogens are overlooked in food vehicles.

C2.8 | *Klebsiella* spp.

Greece reported data on *Klebsiella* spp., collecting 173 milk samples from bovine animals, goats and sheep during clinical investigations. No positive samples were found.

C2.9 | *Leptospira* spp.

Data on *Leptospira* spp. were reported by two MSs (Bulgaria and Slovenia). The occurrence of *Leptospira* spp. was monitored in three animal species (pigs, bovine animals and dogs) through the collection of 120 samples during official sampling. The only two positive samples (1.7%) were detected by Slovenia, testing nine pigs.

C2.10 | *Proteus* spp.

Data on *Proteus* spp. were reported by Greece testing milk samples collected from bovine animals, goats and sheep during clinical investigations. Out of 173 samples, 9.2% (*N* = 16) tested positive.

C2.11 | *Staphylococcus* spp.

Data on *Staphylococcus* spp. were reported by five MSs (Bulgaria, Germany, Greece, Italy and Poland). The occurrence of *Staphylococcus* spp. was monitored in nearly all food categories.

- Bulgaria collected 25 cheeses from cows' milk samples at wholesale, with 8.0% (*N* = 2) testing positive for *Staphylococcus aureus*.
- Poland collected 767 cheese and dairy product samples at processing plants, with 1.0% (*N* = 8) testing positive for *S. aureus*.
- Germany reported data on 1673 cheeses, dairy products, milk and poultry meat samples, mainly from retail, with 19.2% (*N* = 322) testing positive for *S. aureus*.
- Italy reported data on 4778 food samples including bakery products and desserts, bivalve molluscs, cheeses, dairy products, fish, fishery products, fruit and vegetables, herbs and spices, sauces and dressing, milk, meat, other processed food products and prepared dishes and foodstuffs intended for special nutritional uses, with 8.0% (*N* = 584) testing positive.

Greece and Italy also monitored the occurrence of *Staphylococcus* spp. in nine animal species, specifically in bovine animals, small ruminants, birds, wild bears, wild deer, solipeds, dogs and turtles. Out of 6595 animal samples collected from farms, natural habitats and during veterinary activities, 14.8% (*N* = 978) tested positive.

Crustaceans, poultry meat, cheeses, bakery products and other processed food products and prepared dishes were the food categories most contaminated. Overall, data on *Staphylococcus* spp. highlighted the importance of continued vigilance and research in this area for improving the diagnostic capability to be able to identify all *Staphylococcus* spp. at the species level.

C2.12 | *Vibrio* spp.

Data on *Vibrio* spp. were reported by four MSs (Germany, Greece, the Netherlands and Portugal). The occurrence of *Vibrio* spp. was monitored in five food categories, including 'crustaceans – shrimps', 'crustaceans – unspecified', 'fish – raw',' fishery products' and 'live bivalve molluscs'.

- Germany collected 312 samples at primary production and distribution (retail, wholesale and border control posts) with 46.1% (*N* = 144) testing positive. Most units were from crustaceans collected at the retail level. *Vibrio parahaemolyticus* was the most commonly isolated species.
- Greece collected four shrimp samples at 'restaurant or café or pub or bar or hotel or catering service' during a clinical investigation,[70] with one positive, and fishery products at 'border control posts' with no positives.
- The Netherlands collected shrimp and raw fish at border control posts and live bivalve molluscs at wholesale and processing plants. Of the 485 tested samples, 6.8% (*N* = 33) tested positive. *V. parahaemolyticus* and *V. cholerae* were the most commonly isolated species.
- Portugal collected 60 samples of shrimp and live bivalve molluscs at processing plants, with 15.0% (*N* = 9) testing positive for *V. cholerae*.

Overall, the data show that out of 922 samples tested, 20.8% (*N* = 192) were positive. This highlights the presence of *Vibrio* spp. in crustaceans, live bivalve molluscs and fresh fish, underlining the need for continued attention to potential risks associated with these products.

C3 | OTHER VIRAL ZOONOSES AND ZOONOTIC AGENTS

The summary data which make up this chapter, as well as additional information on related projects, internet sources and summary statistics on One Health Surveillance, are published for this report on the EFSA Knowledge Junction at Zenodo here. In 2024, data on West Nile Virus (WNV) and other flaviviruses, caliciviruses, Hepatitis A virus and Paslahepevirus balayani (formerly Hepatitis E virus), were collected. The monitoring and surveillance efforts provide insights into the occurrence of these viral zoonoses in food categories and relevant animal species, highlighting the importance of continued vigilance and research on these diseases.

C3.1 | West Nile Virus

Data on West Nile virus infections in animals were reported to EFSA by 19 Member States (MSs) and one non-MS. In the European Union (EU), the occurrence of WNV was monitored in 31,383 birds (in particular in strigiforms and corvids) and 2755 equids. WNV surveillance in animals is mainly passive, focusing on neuro-invasive cases in equids. However, some MSs conduct active surveillance in equids and/or birds to detect both symptomatic and asymptomatic cases, improving understanding of WNV circulation and ecology. Summary tables showing the occurrence of West Nile virus in animals are available on the EFSA Knowledge Junction at Zenodo here.

- A total of 547 infected birds were reported by 11 MSs, with 1.7% testing positive by real time-reverse transcription PCR (RT-qPCR). Most units were from crows, magpies and strigiforms identified by Italy performing RT-qPCR. Italy, the Netherlands and Spain performed more active surveillance of WNV in birds. Although the number of individuals tested remained stable compared to 2023 (*N* = 32,200), the number of birds infected with WNV increased from 320 in 2023 to 547 in 2024 (Table 65). This represents an increase of approximately 71%.
- A total of 557 equid cases were reported by nine MSs (Austria, France, Germany, Spain, Greece, Hungary, Italy, Poland and Portugal), with 21.2% testing positive by IgM capture ELISA and competition ELISA and/or RT-qPCR. Most units were from Germany (30.3%), France (20.7%), Spain (12.7%) and Austria (7.9%) performing IgM ELISA. This represents a significant increase (302.2%) in the number of equine cases reported in 2024 compared to 2023 (*N* = 182 cases) (Table available in Zenodo here). This is the highest number of reported equine cases since 2020.
- In addition, 10 MSs (Belgium, Croatia, Estonia, Germany, Italy, Latvia, Lithuania, Luxembourg, Netherlands and Portugal) collected EFSA One Health surveillance data on WNV, covering 5496 bird samples. Of these, five MSs (Croatia, Estonia, Latvia, Lithuania and Portugal) also reported WNV infection data from 487 equid samples. Thirty WNV-positive bird samples were reported by Croatia (2), Estonia (1), Germany (22), Italy (1), Latvia (2) and Portugal (2). In contrast, no equid samples tested positive for WNV using IgM-capture ELISA or PCR-like methods.

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[70] During the final phase of the production of the report the sampling context was corrected since Greece informed that the original value ('outbreak investigation') had been mistakenly reported.

- In 2024, a total of 429 bird and 503 equine outbreaks were reported to the Animal Disease Information System (ADIS) by 13 and 12 MSs, respectively, in accordance with Commission Implementing Regulation (EU) 2020/2002.[71] In 2024, Estonia, Latvia and Poland reported for the first time ever outbreaks in birds and/or equids to ADIS.
- As part of their 'One Health' activities, ECDC and EFSA conduct joint surveillance of WNV infections in humans, equids and birds, while also assessing the epidemiological situation in Europe. This collaborative initiative supports public health and veterinary authorities by providing insights for the implementation of prevention and control measures. Starting in 2025, joint ECDC-EFSA online reports on WNV surveillance in humans and animals are being published monthly from July to December. For 2024, the overview of WNV transmission in humans, equids and birds in Europe is provided in the December report (available online), which includes data submitted up to 4 December 2024.

Overall, the data indicate that WNV actively circulated among equids in the western, central and southern MSs and among birds in southern and central MSs, as well as in one northern EU country, in 2024. As asymptomatic or mildly symptomatic cases in animals often go undetected or unreported, the reported data likely underestimate the true extent of WNV infections in animals in the EU. In addition, animal testing is mostly limited to clinically suspect cases in the majority of MSs. Animal surveillance practices vary across MSs, potentially highlighting or masking virus circulation in certain regions. These limitations highlight the importance of interpreting animal surveillance data, as monitoring systems are not harmonised across the EU. The monitoring and surveillance efforts provide important knowledge about the presence and spread of West Nile virus in birds reported by MSs performing active surveillance such as Italy (16,250 birds tested, 430 WNV-positive birds) or the Netherlands (7120 birds tested, 1 WNV-positive bird). Although the number of equine cases reported to EFSA in 2024 tripled compared to the previous year, the total number of animals tested (2755 equids) was among the lowest in the 5-year period. A key point is that Germany and France experienced unprecedented transmission seasons, reporting 177 and 121 equine cases and 41 and 6 bird cases, respectively, to EFSA. WNV infections were detected in both mainland France and its overseas territories, including Guadeloupe and Martinique, highlighting the importance of continued West Nile virus surveillance in this area. These findings suggest a higher level of WNV circulation than in previous years. It may have been more intense in some MSs such as Germany or France. Many cases may have gone undetected, especially subclinical ones, highlighting gaps in surveillance sensitivity and emphasising the need to strengthen WNV preparedness across the EU. There is an urgent need to scale up and harmonise animal surveillance to better detect and compare outbreaks. A coordinated One Health approach—integrating animal, human and vector surveillance—is essential to improve early detection, risk assessment and response.

C3.2 | Flaviviruses other than West Nile virus

Data on orthoflaviviruses other than West Nile virus were reported by three MSs (Cyprus, Denmark and Italy) and one non-MS (Switzerland). A total of 852 samples (including blood and organs) were collected during official sampling activities and analysed by RT-qPCR and ELISA. These samples originated from birds (84.4%; $N = 716$) such as swans, parrots, geese and ducks, as well as from domestic solipeds (15.8%; $N = 135$) such as horses and mules, and one bear. Most of the total units tested were submitted by Cyprus (45.8%).

A total of 65 units tested positive: 27 out of 135 domestic solipeds from Cyprus (20.0%) and 38 out of 716 birds from Cyprus and Denmark (5.3%). Specifically, Cyprus reported a positivity rate of 7.7% among sampled birds, while Denmark reported 3.1%. No positive cases were reported by Italy or Switzerland.

Overall, the data indicate that orthoflaviviruses other than West Nile virus are circulating in Cyprus and Denmark. These findings suggest that West Nile virus and other orthoflaviviruses are co-circulating in Europe, which complicates their specific identification, emphasising the need to implement more sensitive and specific diagnostic tests.

C3.3 | Caliciviruses

Data on caliciviruses (including norovirus) were reported by six MSs (Bulgaria, Croatia, France, Germany, Romania and Slovenia). The occurrence of caliciviruses was monitored in four food categories: fruits, vegetables, ready-to-eat salads and other processed food products and prepared dishes. In total, two batches and 823 individual sampling units were tested, with just one (0.12%) fruit sample from Slovenia testing positive.

C3.4 | Hepatitis A virus

Data on hepatitis A virus were reported by six MSs (Bulgaria, France, Germany, Romania, Slovenia and the Netherlands). The occurrence of hepatitis A virus was monitored in five food categories: fruits, vegetables, ready-to-eat salads, live bivalve

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[71] Commission Implementing Regulation (EU) 2020/2002 of 7 December 2020 laying down rules for the application of Regulation (EU) 2016/429 of the European Parliament and of the Council with regard to Union notification and Union reporting of listed diseases, to formats and procedures for submission and reporting of Union surveillance programmes and of eradication programmes and for application for recognition of disease-free status, and to the computerised information system.

molluscs and spices/herbs. A total of 61 batches and 1164 individual sampling units were tested. Three samples (0.24%) of live bivalve molluscs sampled by the Netherlands were detected positive.

C3.5 | *Paslahepevirus balayani* (formerly Hepatitis E virus)

Data on *Paslahepevirus balayani* were reported by one MS (the Netherlands) that tested 427 sampling units, including live bivalve molluscs, pig liver and other meat products, and found 32 (7.5%) positive samples, most of which were associated with the meat product and pig liver samples.

C4 | OTHER PARASITIC ZOONOSES AND ZOONOTIC AGENTS

The summary data which make up this chapter are published as supporting information for this report on the EFSA Knowledge Junction at Zenodo here. In 2024, data on *Toxoplasma*, *Leishmania* spp., zoonotic *Taenia* spp. and *Sarcocystis* spp. were reported to EFSA. The monitoring and surveillance efforts provide an outlook into the occurrence of these parasitic zoonoses in food categories and relevant animal species, highlighting the importance of continued vigilance and research on these diseases.

C4.1 | *Toxoplasma gondii*

Data on *Toxoplasma gondii* were reported by 11 Member States (MSs) and three non-Member States (non-MSs) (Norway, Republic of North Macedonia and Switzerland). Occurrence of the protozoa was monitored in 33 animal species and 4 broader groups of species: livestock (small ruminants, cattle and pigs), pets, zoo animals and wildlife. Most samples from individual animals (80.8%; 5324 out of 6589) with sampling context provided were collected during clinical investigations. Summary tables showing the occurrence of *T. gondii* in animals are available on the EFSA Knowledge Junction at Zenodo here.

In small ruminants, 4135 individual animal samples were reported by 10 MSs, with 507 samples (12.3%) testing positive. Moreover, two MSs (Italy and Spain) reported 362 herd/flock samples tested, 75 of which (28.8%) were positive. Three non-MSs (Norway, Republic of North Macedonia and Switzerland) reported 22 individual animal samples tested, with six positive (27.2%).

- In cattle, 936 individual animal samples were reported by seven MSs (Austria, Germany, Greece, Ireland, Italy, Latvia and Slovakia), with 105 samples (11.2%) testing positive. Moreover, Italy reported 19 herd/flock sample data, all negative. One non-MS (Norway) reported information on one tested animal, which was negative. Most of the samples were reported to be analysed with indirect methods (40.5%; $N = 379$).
- In pigs, 367 samples were reported by three MSs (Germany, Ireland and Italy), with 3 samples (0.82%) testing positive.
- For other livestock (alpacas, buffalos, deer, horses, fowl and turkeys), 686 individual animal samples were reported by three MSs (Austria, Italy and Slovakia), with two samples positive for alpacas (40.0%), 14 for turkeys (9.6%), 28 for fowl (11.9%) and 72 for horses (23.9%). One non-MS (Switzerland) reported information on two animals tested, which were negative.
- In pet animals, 1996 individual animal samples from cats, 879 samples from dogs and 19 samples from rabbits were reported by eight MSs (Finland, Germany, Greece, Hungary, Italy, Latvia, the Netherlands and Slovakia), with 92 samples (4.6%) positive for cats, 134 (15.2%) positive for dogs and no samples positive for rabbits. One non-MS (Switzerland) reported 306 individual animal samples from cats, 58 samples from dogs and one sample from a rabbit, with 54 samples (17.6%) for cats and 12 samples (20.6%) for dogs testing positive, while the rabbit sample was negative.
- In zoo animals, 85 individual animal samples were reported by four MSs (Germany, Italy, the Netherlands and Slovakia), with no positive samples identified. Two non-MSs (Republic of North Macedonia and Switzerland) reported four samples tested and one sample (25%) was positive.
- In wild animals, 638 individual animal samples were reported by five MSs (Austria, Finland, Germany, Ireland and Italy), with 36 positive samples (5.6%). One non-MS (Switzerland) reported data on four samples, with one positive sample (25.0%).

Overall, the data indicate that *Toxoplasma gondii* is present in all species or groups of species investigated across the EU except in bears, buffalos, hedgehogs, kangaroos, monkeys, mouflons, reindeers, seals, squirrels and wild boars. However, it is impossible to accurately estimate the prevalence of *T. gondii* infections in animals due to different diagnostic methods, sampling schemes in Member States and lack of information on the animals' ages and rearing conditions. Furthermore, there is no relationship between the presence of anti-*T. gondii* antibodies and infecting parasites in cattle and horses (Aroussi et al., 2015; Blaga et al., 2019; Opsteegh et al., 2019). For pigs, poultry and small ruminants, serological methods could be useful for the detection of high-risk animals or herds, but serology is not an indicator of infection in individual animals, as the agreement between direct and indirect methods was estimated to be low to moderate (Opsteegh et al., 2019).

These data provide key information regarding the occurrence and distribution of *T. gondii* in food-producing animal species (small ruminants, cattle and pigs), as well as in the definitive host, the cat, suggesting noticeable fluctuations in animal *T. gondii* occurrence over the past 5 years and emphasising the need for a harmonised monitoring and surveillance system across the EU.

C4.2 | *Leishmania* spp.

Data on *Leishmania* spp. were reported by one MSs (Greece) and one non-MS (Republic of North Macedonia). The occurrence of *Leishmania* spp. was monitored in the dog animal category for a total of 6563 animals tested. A total of 647 (9.9%) dogs tested positive for *Leishmania* spp. Greece reported 15.5% positive dogs, while the Republic of North Macedonia reported 4.1% positive dogs.

C4.3 | Zoonotic *Taenia* spp.

Data on the zoonotic cysticercus larval stage (metacestode of *Taenia* spp.) were reported by eight MSs (Belgium, Finland, Luxembourg, Malta, Slovakia, Slovenia, Spain and Sweden). The occurrence of zoonotic *Taenia* spp. was monitored in organs/tissues in five animal species, mainly cattle and pigs (99.5%), but also sheep, dogs and wild boars, for a total of 52,839,330 animals tested. Positive findings for zoonotic *Taenia* spp. were reported by six MSs (Belgium, Finland, Luxembourg, Slovakia, Slovenia and Spain) for a total of 0.008%. The highest prevalence rates were found in Luxembourg (0.14%) and Belgium (0.062%).

C4.4 | *Sarcocystis* spp.

Belgium reported data from 812,834 bovine animals collected at the slaughterhouse, with 107 samples (0.0001%) testing positive for *Sarcocystis* spp.

SECTION D – MICROBIOLOGICAL CONTAMINANTS SUBJECT TO FOOD SAFETY CRITERIA (COMMISSION REGULATION (EC) NO 2073/2005)

This chapter summarises the 2024 data and information provided by reporting countries on microbiological contaminants in food for which food safety criteria (FSC) have been set down in EU legislation (Commission Regulation (EC) No 2073/2005[72]): histamine, staphylococcal enterotoxins and *Cronobacter sakazakii*.

D1 | HISTAMINE

D1.1 | Histamine data in the context of Commission Regulation (EC) No 2073/2005

Histamine is a thermostable biogenic amine occurring naturally in the human body that plays a role in key physiological functions. However, when ingested in high concentrations through food, histamine can cause health disorders such as scombroid poisoning. Scombroid, which resembles an allergy, remains a relevant concern in seafood safety.

The amino acid histidine is decarboxylated to histamine by bacterial or tissue enzymes.

In histidine-rich foods, such as some fish species, high amounts of histamine can be found due to microbial contamination or inadequate conditions during food processing or storage, so its concentration can be used as a parameter of process hygiene and food spoilage/quality.

EU legislation has therefore set maximum limits for histamine in fish and fish products.

Commission Regulation (EC) No 2073/2005 on microbiological criteria for foodstuffs sets FSC for histamine in three categories at the retail level:

- 'Fishery products from fish species associated with a high amount of histidine' (food category 1.26).
- 'Fishery products which have undergone enzyme maturation treatment in brine, manufactured from fish species associated with a high amount of histidine' (food category 1.27).
- 'Fish sauce produced by fermentation of fishery products' (food category 1.27a).

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[72] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

At the manufacturing level, information is collected to ensure the proper application of good manufacturing practices (GMPs) and the maintenance of the cold chain, which are crucial for preventing the development or increase of histamine in fish and fish products.

Histamine data for the abovementioned three categories were reported by 15 MSs and one non-MS (Albania).

Fishery products from fish species associated with a high amount of histidine (food category 1.26)

Among 4198 official control samples for histamine in food category 1.26 at the distribution level, 0.36% exceeded 200 mg/kg of histamine, 0.10% had histamine levels between 100 and 200 mg/kg and 2.5% had detectable levels above the limit of detection, up to 100 mg/kg. Of the total samples, 38.8% originated from EU countries (including Italy, Latvia, Lithuania, Poland, Portugal, Romania and Spain), 18.2% were from 19 non-EU countries, while origin information was unavailable for 42.9%. In total, 32.9%, 16.9%, 12.1%, 10.6% and 0.60% of samples were taken from retail, cold storage, wholesale, border control posts and a 'restaurant or cafe or pub or bar or hotel or catering service', respectively. For 26.9% of the samples, no specific source information was provided.

In terms of product type, 15.8% of samples were from canned fish and 9.0% from raw fish, while 75.2% lacked detailed product information.

At the manufacturing level, 93 official control sampling units were collected from processing plants. Of these, 1.1% had a histamine content that exceeded 200 mg/kg, 1.1% had histamine levels between 100 and 200 mg/kg, and 2.2% had histamine levels above the limit of detection, but less than or equal to 100 mg/kg. Of the total samples, 51.6% were from an EU country (Italy), while for 48.4%, origin information was unavailable. Regarding product types, 10.8% of the samples came from canned fish, 30.1% from raw fish and for 59.1%, no product details were reported.

Fishery products which have undergone enzyme maturation treatment in brine, manufactured from fish species associated with a high amount of histidine (food category 1.27)

For food category 1.27, a total of 750 official control samples were collected at the distribution level and 18 at the manufacturing level. At the distribution level, 3.87% of samples had a histamine concentration above the limit of detection, up to 200 mg/kg. Of the total samples, 22.8% originated from EU countries (Romania, Spain and other unspecified MSs), 19.2% from non-EU countries and for 58.0% of samples, origin information was not provided. In terms of sample collection locations, 30.4%, 19.2%, 12.8% and 6.0% of samples were taken from retail, border control posts, wholesale and cold storage, respectively. For 31.6% of samples, no specific collection information was available.

At the manufacturing level, all 18 samples tested negative and origin details were unavailable.

Fish sauce produced by fermentation of fishery products (food category 1.27a)

For food category 1.27a at the distribution level, 44 official control samples were reported. Of these, 11.4% had a histamine content between the limit of detection and 400 mg/kg, while 2.3% exceeded 400 mg/kg. Regarding the origin of the samples, 84.1% originated from EU countries (Poland, Italy and Spain) and 9.1% were from non-EU countries (Thailand), with no origin information provided for the remaining 6.8%.

D1.2 | Other surveillance, monitoring or outbreak investigation data for histamine

MSs also collected and analysed fishery products for surveillance, monitoring or outbreak investigation purposes, outside the scope of Commission Regulation (EC) 2073/2005 on microbiological criteria for foodstuffs.

Surveillance

A total of 2604 single sampling units and 90 batches were collected as part of surveillance activities, reported by 10 MSs. This included 1329 single sampling units and 90 batches at the distribution level, and 1275 sampling units at the manufacturing level.

At the distribution level, 91.2%, 8.5% and 0.30% of the 1329 sampling units were categorised as 1.26, 1.27 and 1.27a, respectively.

In category 1.26, 5.4% of the sampling units had a histamine content between the limit of detection and 100 mg/kg, 1.4% had histamine levels between 100 and 200 mg/kg and 0.66% had histamine levels exceeding 200 mg/kg, while 0.88% of category 1.27 sampling units contained histamine levels over 400 mg/kg.

In total, 63.8%, 14.2%, 13.5% and 5.0% of sampling units were taken from retail, wholesale, border control posts and a 'restaurant or cafe or pub or bar or hotel or catering service', respectively, while for 3.5% no specific information was reported.

Regarding origin, 77.3% were from EU countries (Italy and Spain), 13.8% from non-EU countries (Ecuador, Ghana, Indonesia, Philippines, Thailand, Türkiye and Morocco), while 8.9% had no origin information available.

All the batches ($N = 90$) taken at border control posts were categorised as 1.26 and all batches were negative. Origin details were not available for all batches.

At the manufacturing level, 1275 samples were taken at processing plants or farms. Of these, 87.9% were categorised as category 1.26, 11.8% as category 1.27 and 0.30% as category 1.27a. Only 7.8% of category 1.26 samples had a histamine content between the limit of detection and 100 mg/kg, and all sampling units in categories 1.27 and 1.27a were negative.

In terms of origin, 69.6% were from EU countries (Estonia, Greece, Italy and Romania) and 6.4% from non-EU countries (Norway and others), with the origin of 24.0% unreported.

Monitoring

A total of 60 single sampling units were collected as part of monitoring activities, reported by Bulgaria. These included 40 single sampling units at the distribution level and 20 sampling units at the manufacturing level. Regarding origin, all sampling units were from Bulgaria.

At the distribution level, 95.0% and 5.0% of the 40 sampling units were categorised as 1.26 and 1.27, respectively. All sampling units were negative.

In total, 65.0%, 30.0% and 5.0% of sampling units were taken from retail, wholesale and border control posts, respectively.

At manufacturing level, 65.0% and 5.0% of the 20 sampling units were categorised as 1.26 and 1.27, respectively. All sampling units were negative.

Outbreak investigation

Three single samples were collected as part of outbreak investigations, reported by Italy: two from retail and one from a household. All were categorised in 1.26 and two samples had a histamine content between the limit of detection and 100 mg/kg. All sampling units were from Italy.

D2 | STAPHYLOCOCCAL ENTEROTOXINS

D2.1 | Staphylococcal enterotoxin data in the context of Commission Regulation (EC) No 2073/2005

Seven MSs (Bulgaria, Greece, Italy, Romania, Slovenia, Slovakia and Spain) reported data on staphylococcal enterotoxins. Overall, 2544 official control samples were tested at the distribution level, resulting in one positive (0.04%) finding by Spain on 'cheeses made from sheep milk – hard' collected at the wholesale and retail levels. At the manufacturing level, 900 samples were tested, with Romania detecting one positive (0.11%) sample in 'cheeses made from cows' milk – soft and semisoft' collected at the processing plant.

D2.2 | Other surveillance data for staphylococcal enterotoxins

Twelve MSs reported data on staphylococcal enterotoxins detected in contexts outside those specified by Commission Regulation (EC) No 2073/2005. Out of 5784 samples tested, 22 (0.38%) were positive. The positive samples came from various food categories, including 'other processed food products and prepared dishes', 'cheeses made from unspecified milk or other animal milk', 'meat from bovine animals – meat products – cooked, ready-to-eat', 'cheeses made from sheep milk – hard – made from raw or low heat-treated milk', 'cheeses made from cows' milk – soft and semi-soft – made from pasteurised milk' and 'cheeses made from sheep milk – unspecified'.

D3 | *CRONOBACTER SAKAZAKII*

D3.1 | *Cronobacter sakazakii* data in the context of Commission Regulation (EC) No 2073/2005

Regarding *Cronobacter sakazakii* in 'infant formulae' and 'foodstuffs intended for special nutritional uses' collected at distribution by eight MSs (Croatia, Cyprus, the Czech Republic, Hungary, Italy, Slovenia, Slovakia and Spain), none of the 1086 samples tested positive. Only a single sample was reported by Italy from the manufacturing level, which tested negative.

D3.2 | Other surveillance data for *Cronobacter sakazakii*

Eleven MSs provided data on *Cronobacter* spp. from sources outside the scope of Commission Regulation (EC) No 2073/2005. Samples of 'infant formulae', 'foodstuffs for special nutritional uses' and 'dairy products excluding cheeses' were gathered at retail, processing and wholesale levels, or in hospitals and medical facilities for surveillance or monitoring. In total, 1739 individual samples and 328 batches were analysed, with no positive detections.

KEY DEFINITIONS

The following definitions adopted by ECDC are used to describe the surveillance systems:

Legal character of surveillance

- ‘Compulsory’ (Co): the surveillance system has a legal basis (at the national administrative level or other) under which reporting of cases of the disease(s) under surveillance is compulsory.
- ‘Voluntary’ (V): the surveillance system is based on a voluntary agreement (at the national level or other) by which reporting of cases of the disease(s) under surveillance is voluntary.
- ‘Other’ (O): any system that does not fall under one of the above descriptions.
- ‘Unknown’: not specified/unknown.

Comprehensiveness of surveillance.

- ‘Comprehensive’ (Cp): Reporting is based on cases occurring within the whole population of the geographical area where the surveillance system is set up (national, regional, etc.).
- ‘Sentinel’ (Se): Reporting is based on a selected group of physicians/hospitals/laboratories or other institutions' notifications, and/or cases occurring within a selected population defined by age group, gender, exposure or other selection criteria.
- ‘Other’ (O): Reporting is based on a part of the population or group of physicians (or other institutions) which is not specified, for example reporting from laboratories with no selection criteria.
- ‘Unknown’: not specified/unknown.

National coverage.

- Defined as covering the entire population of the country or a part of it. May be unknown when not specified.

Origin of human cases.

- Domestic/locally acquired cases are defined as cases declared in the data set as ‘not imported’.
- Travel-related cases (or imported cases) are defined as cases declared in the data set as ‘imported’.
- Place of infection is defined in the data set as the probable country of infection.
- Cases of infection acquired in the EU (domestic cases + travel in EU).

Active/Passive (human surveillance).

- ‘Active’ (A): The surveillance system is based on the public health officials' initiative to contact the physicians, laboratory or hospital staff or other relevant sources to report data.
- ‘Passive’ (P): The surveillance system relies on the physicians, laboratory or hospital staff or other relevant sources to take the initiative to report data to the health department.
- ‘Unknown’: Not specified/unknown.

The following definitions are used to describe data provided to EFSA in the EUOHZ 2024:

- **Surveillance**: This programme type term infers to a careful observation of one or more food or feed businesses, food or feed business operators or their activities (in the context of the food and feed control Regulation (EC) No 882/2004). In general, it means a close and continuous observation for the purpose of control. As opposed to monitoring, active control measures are frequently taken when positive cases are detected. This type of programme does not necessarily have a defined target for reducing the occurrence of diseases/contamination.
- **Surveillance, based on Regulation 2073**: This programme type term is used to report the samples collected and analysed according to the Regulation 2073/2005 on microbiological criteria. These samples can be taken either to check the compliance with Process hygiene criteria (*Salmonella* in carcases (2.1.3, 2.1.4, 2.1.5)) or with Food Safety criteria (*Salmonella* in meat and meat products (1.4–1.20, 1.22; 1.23; 1.28), *Listeria monocytogenes* (1.1, 1.2, 1.3), *Staphylococcus* enterotoxins (1.21), *Cronobacter* (1.24), Histamine (1.26; 1.27; 1.27a), Shiga toxin-producing *Escherichia coli* (1.29)).
- **Active rabies surveillance**: This specific rabies programme type term is used for reporting of data on active testing in the context of the monitoring of the efficacy of oral rabies vaccination (ORV) campaigns in wildlife (i.e. in foxes, raccoon dog and/or jackals).

- **Monitoring**: This programme type term infers to a system of collecting, analysing and disseminating data on the occurrence of zoonoses, zoonotic agents and antimicrobial resistance related thereto. As opposed to surveillance, no active control measures are taken when positive cases are detected (Directive 2003/99/EC).
- **Objective sampling**: Objective sampling—planned strategy based on the selection of a random sample, which is statistically representative of the population to be analysed. Each unit, within the framework population, has a specified probability of being selected. This strategy provides data from which statistical inference can be implemented. That means that the results inferred are comparable. Objective sampling is often the case in monitoring and surveillance schemes as well as in surveys.

Terms used to describe prevalence or proportion-positive values for EFSA data

In the EUOHZ report a set of standardised terms are used to characterise the proportion of positive sample units or the prevalence of zoonotic agents in animals and foodstuffs:

• Rare:	< 0.1%
• Very low:	0.1% to 1%
• Low:	> 1% to 10%
• Moderate:	> 10% to 20%
• High:	> 20% to 50%
• Very high:	> 50% to 70%
• Extremely high:	> 70%
• Majority of MSs:	60% (in 2024 this was 17 MSs)
• Most MSs:	75% (in 2024 this was 21 MSs)

ABBREVIATIONS

A	Aggregated data
ADIS	Animal Disease Information System
AE	Alveolar echinococcosis
AHL	Animal Health Law
AMR	Antimicrobial resistance
ANSES	French Agency for Food, Environmental and Occupational Health and Safety
ATLAS	Surveillance Atlas of Infectious Diseases
BBLV	Bokeloh bat lyssavirus
BIOHAZ	EFSA Scientific Panel on Biological Hazards
C	Case-based data
CA	Competent authority
CE	Cystic echinococcosis
CEN	European Committee for Standardisation
CFU	Colony-forming units
CI	Confidence Interval
CIR	Commission Implementing Regulation
DCF	EFSA's Data Collection Framework
DFS	Disease-free status
EBLV	European bat lyssavirus
EC	European Commission
ECDC	European Centre for Disease Prevention and Control
EEA	European Economic Area
EFTA	European Free Trade Association
Eg	*Echinococcus granulosus*
Em	*Echinococcus multilocularis*
ELISA	Enzyme-linked immunosorbent assay
EpiPulse Cases	The European Surveillance System (formerly TESSy)
EU-FORS	European Union Foodborne Outbreak Reporting System
EUOHZ	European Union One Health Zoonoses Report
EURL	European Reference Laboratory
FAO	Food and Agricultural Organization
FBO	Foodborne outbreak
FBOp	Food business operator
FBOs	Foodborne outbreaks
FSC	Food Safety Criteria
FWD	Food and Waterborne Diseases and Zoonoses
GAP	Good Agricultural Practices

GF-TADs	The Global Framework for the Progressive Control of Transboundary Animal Diseases
GMP	Good Manufacturing Practices
HACCP	Hazard Analysis and Critical Control Point
HUS	Haemolytic-uraemic syndrome
IgG	Immunoglobulin G
IgM	Immunoglobulin M
ISO	International Organization for Standardisation
MS	Member State
MSM	Mechanically separated meat
MSs	Member States
MTBC	*Mycobacterium tuberculosis* complex
MVST	Monophasic variant *Salmonella* Typhimurium
N	Number
NCHC	Not controlled housing conditions
NCP	National control programme
non-RTE	Non-ready-to-eat
NS	Not significant
NUTS	Nomenclature of territorial units for statistics
OCR	Official Controls Regulation
ORV	Oral rabies vaccination
PCR	Polymerase Chain Reaction
PHC	Process hygiene criteria
RABV	Rabies virus
ROA	Rapid Outbreak Assessment
RTE	Ready-to-eat
RT-qPCR	Real time-reverse transcription PCR
Salm	*Salmonella*
SE	*Salmonella* Enteritidis
SGE RAB	Standing Group of Experts on Rabies
s.l.	sensu lato
ST	Sequence Types
STEC	Shiga toxin-producing *Escherichia coli*
TESSy	Former European Surveillance System (included in EpiPulse Case)
TB	Tuberculosis
UEP	Under eradication programme
UK	United Kingdom
US	United States
WGS	Whole Genome Sequencing
WHO	World Health Organization
WNV	West Nile Virus
WOAH	World Organisation for Animal Health
ZOE	Zoonoses under a One health perspective in the EU

COUNTRY CODES

EU Member States

AT	Austria
BE	Belgium
BG	Bulgaria
HR	Croatia
CY	Cyprus
CZ	Czechia
DK	Denmark
EE	Estonia
FI	Finland
FR	France
DE	Germany
GR	Greece
HU	Hungary
IE	Ireland
IT	Italy
LV	Latvia

LT	Lithuania
LU	Luxembourg
MT	Malta
NL	the Netherlands
PL	Poland
PT	Portuga
RO	Romania
SK	Slovakia
SI	Slovenia
ES	Spain
SE	Sweden
XI	United Kingdom (Northern Ireland)

EU non-MS counties

AL	Albania
BA	Bosnia and Herzegovina
IS	Iceland
XK	Kosovo
LI	Liechtenstein
ME	Montenegro
MK	Republic of North Macedonia
NO	Norway
RS	Serbia
CH	Switzerland
TK	Türkiye

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