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SCIENTIFIC REPORT

The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2022–2023

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The declarations of interest of all scientific experts active in EFSA's work are available at https://open.efsa.europa.eu/experts

Abstract

This report presents the main findings of the 2022–2023 harmonised antimicrobial resistance (AMR) monitoring in *Salmonella* spp., *Campylobacter jejuni* and *Campylobacter coli* from humans and food-producing animals (broilers, laying hens and fattening turkeys, fattening pigs and cattle under 1 year of age) and derived meat. For animals and meat, AMR data on indicator commensal *Escherichia coli*, presumptive extended-spectrum beta-lactamase (ESBL)-/AmpC beta-lactamase (AmpC)–/carbapenemase (CP)-producing *E. coli* and the occurrence of methicillin-resistant *Staphylococcus aureus* (MRSA) are also analysed. Generally, resistance differed greatly between reporting countries and antimicrobials. A high proportion of *Salmonella* spp. and *Campylobacter* isolates from humans and animals were resistant to commonly used antimicrobials (ampicillin, tetracycline and sulfonamides) in human and veterinary medicine, although *Salmonella* isolates from laying hens exhibited lower resistance. In humans, increasing trends in resistance to ciprofloxacin, one of two critically important antimicrobials (CIA) for human treatment, were observed in poultry-associated *Salmonella* serovars and in *Campylobacter*, in several reporting countries. Combined resistance to CIA was however observed in a low proportion of isolates except for some *Salmonella* serovars and *C. coli* from humans and animals in some countries. In imported fresh meat of broilers and turkeys sampled at border control posts, resistance to third-generation cephalosporins was observed respectively at very high and moderate levels in *Salmonella* and indicator *E. coli*. While CP-producing *Salmonella* isolates were not detected in animals in 2022–2023, five human cases of CP-producing *Salmonella* were reported in 2022 and six cases in 2023 (the majority harbouring $bla_{\text{OXA-48}}$ or $bla_{\text{OXA-48}}$-like genes). Detection of CP-producing *E. coli* isolates (carrying $bla_{\text{OXA-48}}$, $bla_{\text{OXA-181}}$, $bla_{\text{OXA-244}}$, $bla_{\text{NDM-5}}$ and $bla_{\text{VIM-1}}$ genes) in broilers, fattening turkeys, fattening pigs, cattle under 1 year of age and meat from pigs by seven member states (MSs) in 2022 and 2023, requires a thorough follow-up. The temporal trend analyses in key outcome indicators (complete susceptibility and prevalence of ESBL-/AmpC- producing *E. coli*) showed an encouraging progress in reducing AMR in food-producing animals in several EU MSs over the last 10 years.

KEYWORDS

antimicrobial resistance, ESBL, indicator bacteria, MRSA, zoonotic bacteria

CONTENTS

SUMMARY

In 2022–2023, data on antimicrobial resistance in zoonotic and indicator bacteria submitted by 27 EU Member States (MSs), the United Kingdom (Northern Ireland) and five non-MSs, were jointly analysed by the European Food Safety Authority (EFSA), the European Centre for Disease prevention and Control (ECDC) and EFSA's contractor. Resistance in zoonotic *Salmonella* and *Campylobacter* from humans, food-producing animals (fattening pigs, cattle under 1 year of age, broilers and fattening turkeys, and also laying hens for *Salmonella*) and meat derived from these animals, as well as resistance in indicator commensal *Escherichia coli*, presumptive extended-spectrum beta-lactamase (ESBL)-/AmpC beta-lactamase (AmpC)–/carbapenemase (CP)-producing *E. coli*, methicillin-resistant *Staphylococcus aureus* (MRSA) and *Enterococci* from animals and derived meat were addressed.[1] In 2022, it was mandatory to report AMR data from poultry and meat from poultry, while in 2023, it was mandatory to report AMR data from fattening pigs and cattle under 1 year of age at slaughter and meat derived from these animals. 'Microbiological resistance' in the isolate populations was assessed using epidemiological cut-off (ECOFF) values. For the countries reporting qualitative data on human isolates, the categories of 'clinically resistant' (R) and susceptible with increased exposure (I) were combined, thereby achieving close correspondence with the proportion of isolates with the ECOFF-defined microbiological resistance. See Appendix A – Materials and methods for further information.

In *Salmonella* spp. from human cases in 2023, resistance to ampicillin, sulfonamides and tetracyclines was observed in a high proportion of isolates, while resistance to third-generation cephalosporins was noted in overall very low to low proportions of isolates (1.6% and 1.3% for cefotaxime and ceftazidime, respectively). A statistically significant decline in resistance to ampicillin and tetracycline in isolates from humans was observed in 14 and 12 countries, respectively, over the period 2014–2023. This was particularly evident in *S*. Typhimurium. For cefotaxime, seven MSs reported significant declining trends while four MSs reported increasing trends. A high occurrence of resistance to ciprofloxacin (21.8%) was observed in isolates from human cases from 2023; with an extremely high proportion of resistant isolates noted in *S*. Kentucky (80.5%) and increasing trends in ciprofloxacin resistance observed for *S*. Enteritidis in 13 countries over the period 2014–2023, with this serovar predominantly being associated with poultry.

For *Salmonella* spp. and indicator commensal *E. coli* isolates recovered from food-producing animals in 2022–2023, resistance to ampicillin, tetracyclines and sulfonamides ranged from moderate to very high in most EU MSs. Resistance to third-generation cephalosporins (cefotaxime and ceftazidime) was reported at low levels in *Salmonella* spp. isolates from cattle under 1 year of age, broilers and turkey flocks, and at very low levels in laying hen flocks and fattening pigs. These findings mirror those observed in *Salmonella* isolates reported from human cases. Over the period 2014–2023, a statistically increasing trend in ampicillin resistance at the MS level was observed in *Salmonella* isolates from broilers, while a declining trend in tetracycline resistance was noted in turkey isolates. In imported fresh meat of broilers and turkeys sampled at border control posts, very high levels of resistance to third-generation cephalosporins were observed for *Salmonella*. Similarly, in indicator *E. coli*, resistance to third-generation cephalosporins was reported at very low or low levels in all animal populations and imported fresh meat of pigs and cattle, whereas, in imported fresh meat of broilers and turkeys, moderate levels of resistance were registered. Resistance to (fluoro)quinolones (ciprofloxacin and nalidixic acid) was registered at high to very high levels among *Salmonella* spp. and indicator commensal *E. coli* isolates recovered from broilers, fattening turkeys and imported poultry meat in 2022, and at low or moderate levels in isolates from pigs and cattle under 1 year of age in 2023. For *Salmonella* isolates, statistically significant increasing trends in ciprofloxacin resistance at the MS level were identified in broiler and laying hen flocks over the period 2014–2023.

The proportion of isolates resistant to the last-line antimicrobials azithromycin and tigecycline was overall low in *Salmonella* isolates from humans. In *salmonella* isolates from food-producing animals, resistance to azithromycin was overall low in pigs and cattle under 1 year of age, very low in broilers and turkeys and not detected in laying hens. While resistance to tigecycline was reported at low levels in pigs, cattle under 1 year of age, and laying hens but at moderate levels in turkeys and high levels in broilers. Resistance to azithromycin and tigecycline in indicator *E. coli* was low to very low in all four animal populations monitored. Resistance to amikacin was rare or very low among *Salmonella* spp. and *E. coli* isolates from the animal populations monitored. Resistance to colistin was uncommon among *Salmonella* spp. and *E. coli* isolates recovered from food-producing animals and poultry carcases. Moderate to very high resistance levels were observed in certain *Salmonella* serovars (*S*. Enteritidis) and in *Salmonella* isolates from cattle under 1 year of age (*S*. Dublin). Although not investigated this is probably not due to acquired resistance as these serovars belong to group D (serogroup O9) and are expected to show decreased susceptibility to colistin. The combined resistance to ciprofloxacin and cefotaxime, categorised as highest priority critically important antimicrobials (hpCIA) by WHO, was low in *Salmonella* isolates from humans and rare or very low in *Salmonella* isolates in almost all animal populations, with the exception of broilers, turkeys and cattle under 1 year of age, where low levels were observed. Certain *Salmonella* serovars from poultry sources, such as *S*. Kentucky from broilers and *S*. Infantis from turkeys, however, exhibited elevated levels of combined resistance to ciprofloxacin and cefotaxime compared to other serovars. The same was observed in these serovars isolated from humans. For *E. coli*, very low or low levels were registered in all animal populations, as well as in meat of pigs and cattle, whereas in poultry meat, the combined resistance was low to moderate.

[1]The monitoring is also described in EFSA interactive story maps, tailored to the public, and the results are presented in interactive dashboards. All available online (here).

The number of indicator commensal *E. coli* isolates recovered from imported meat sampled at border control posts was rather low even if the number of isolates recovered from meat of cattle and pigs increased between 2021 and 2023. Overall, resistance was more common among isolates from imported poultry meat than that of pigs or cattle.

Overall, the data obtained in 2022–2023 from *C. jejuni* and *C. coli* from human and animal origins showed high to extremely high levels of resistance to fluoroquinolones (ciprofloxacin). Due to these levels of resistance, fluoroquinolones can no longer be recommended for the treatment of *Campylobacter* infections in humans. Overall, the levels of resistance to ciprofloxacin in isolates obtained from food-producing animals were higher for *C. coli* than for *C. jejuni*, although the levels of resistance to ciprofloxacin obtained from *C. jejuni* isolates from poultry in 2022 were also very high. The lowest levels of resistance to ciprofloxacin in both *C. jejuni* and *C. coli* were observed in isolates from fattening pigs in 2023. Resistance to erythromycin (representing the macrolide class, a critically important antimicrobial (CIA) for the treatment of *Campylobacter* infections in humans) was detected at very low levels in *C. jejuni* from humans and at low levels in *C. jejuni* from animals. However, higher levels of resistance were observed in *C. coli* isolates from humans and animals. The whole genome sequencing (WGS) results reported for erythromycin-resistant *C. jejuni* and *C. coli* isolates from food-producing animals in 2022–2023, mostly those highly resistant (MIC ≥ 512 mg/L), showed detection of the mutation A2075G in the 23S rRNA gene and no detection of the transferable *erm*(B) gene in most isolates. A single isolate of *C. coli* from cattle under 1 year of age was reported positive to the presence of *erm*(B), and two isolates presented a mutated *rplV* gene (one *C. coli* from fattening pigs and one *C. jejuni* from cattle under 1 year of age). Among the three countries reporting WGS data for *Campylobacter* isolates from humans, no erythromycin resistance mechanisms were detected.

Over the period 2014–2023, ciprofloxacin resistance in *C. jejuni* from humans increased in 11 countries, while erythromycin resistance decreased in 10 countries. Similar trends were observed in *C. jejuni* from broilers over 2014–2023 for six countries where resistance to ciprofloxacin increased, and six countries where it decreased. Over the same period, resistance to ciprofloxacin in *C. jejuni* from turkeys increased in one country, while it decreased in two countries. Over 2014–2023, a decrease in resistance to erythromycin was observed in *C. coli* from humans in nine countries, and in *C. coli* from fattening pigs in four countries.

The occurrence of combined resistance to ciprofloxacin and erythromycin in *Campylobacter* spp. is considered of high public health relevance. Overall combined resistance to these antimicrobials was lower in *C. jejuni* isolates than in *C. coli* isolates from humans and food-producing animals. Multidrug resistance (MDR) levels were generally very low for *C. jejuni* isolated from humans and ranged from very low to moderate in the animal species considered. Compared to *C. jejuni*, MDR was markedly higher in *C. coli*, in humans and all monitored animal populations. These results agree with the higher levels of resistance to selected antimicrobials seen in *C. coli* isolates.

The prevalence of resistance to selected antimicrobials in *C. jejuni* and *C. coli* from fattening pigs and cattle under 1 year of age in 2023 has been estimated at country level as the product of the proportion of isolates showing microbiological resistance to each antimicrobial and the percentage of all caecal samples cultured for *C. jejuni or C. coli*. Between-country variability, from rare, low or moderate to extremely high levels, was observed in the prevalence of ciprofloxacin-resistant and tetracycline-resistant *C. jejuni* and *C. coli* isolates. Notably, a more limited between-country variability and lower levels of prevalence of resistance were found for erythromycin-resistant *Campylobacter*.

The monitoring also included assessment of the levels of presumptive extended-spectrum beta-lactamases (ESBL)-/AmpC beta-lactamases (AmpC)–/ carbapenemase (CP)-producers among *Salmonella* spp. from human cases, food-producing animals and imported fresh meat; as well as among indicator commensal *E. coli* isolates from food-producing animals and meat derived thereof. At the reporting MS group level, the proportion of presumptive ESBL- and/or AmpC-producers ranged from very low to low among *Salmonella* spp. isolates recovered from animals/carcases (broilers, laying hens, fattening turkeys, fattening pigs) and very low in isolates from human cases, although higher in some *Salmonella* serovars.

Within both the routine and specific monitoring (non-selective and selective media, respectively), varying occurrence/prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* were observed in different reporting countries. Statistically significant decreasing trends were evident in the prevalence of ESBL-producing *E. coli* in broilers, fattening turkeys, meat from broilers, meat from pigs, cattle under 1 year and meat from bovines at the EU level. A larger proportion of isolates were identified as presumptive ESBL-producers compared with AmpC-producers based on phenotypic methods in 2022 and 2023. This was also the case for countries reporting WGS data, where 2764 *E. coli* isolates carried ESBL genes, 284 isolates carried plasmid-mediated AmpC genes and 316 isolates had a point mutation in the AmpC promotor.

WGS results also revealed one CP-producing *E. coli* from a fattening turkey and carrying the $bla_{\text{OXA-181}}$ gene in the routine monitoring for indicator *E. coli* in 2022. No CP-producing *E. coli* were detected in the routine monitoring in 2023. Additionally, three CP-producing *E. coli* isolates from broilers carrying the $bla_{\text{VIM-1}}$ gene were reported in the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* in 2022. In 2023, two CP-producing *E. coli* from cattle under 1 year (each carrying either $bla_{\text{VIM-1}}$ or $bla_{\text{NDM-5}}$), and four isolates from fattening pigs (three carrying $bla_{\text{OXA-181}}$ and one co-harbouring $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$) were reported. In in the specific monitoring of CP-producing *E. coli*, a single CP-producing *E. coli* isolate from a fattening turkey, carrying the $bla_{\text{OXA-181}}$ gene, was reported in 2022. In 2023, CP-producers were reported in 55 isolates from fattening pigs (24 carrying $bla_{\text{OXA-181}}$, 21 with $bla_{\text{OXA-48}}$, 5 with $bla_{\text{NDM-5}}$, 4 with both $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$, and 1 with $bla_{\text{OXA-244}}$). Additionally, five isolates from cattle under 1 year (four with $bla_{\text{OXA-181}}$ and one with $bla_{\text{OXA-48}}$) were also reported. Further, one CP-producing isolate was detected in meat from pigs, carrying $bla_{\text{NDM-5}}$. CP-producing *Salmonella* isolates were not detected in animals in 2022–2023, but in humans five cases of CP-producing *Salmonella* were reported in

2022 and six in 2023, eight of these were carrying $bla_{\text{OXA-48/OXA-48-like}}$, one carried $bla_{\text{NDM-1}}$ and for two isolates, information on the gene was not available.

The voluntary monitoring of MRSA from food and healthy animals in 2022–2023 was performed in a limited number of countries and was not harmonised. Still, it provided useful information regarding the occurrence of MRSA in food-producing animals and food. Among MRSA isolates subjected to molecular typing in 2022 and 2023, livestock-associated (LA) clonal complex (CC) 398 was by far the most commonly reported CC, both in isolates from animals and food. The occasional detection of lineages of CA- and/or HA-MRSA primarily associated with humans is not surprising, since the sporadic interchange of strains between humans and animals may be expected. An important observation from the 2022 to 2023 monitoring includes the detection of resistance to the critically important antimicrobial rifampicin in isolates from breeding pigs, meat from pigs and meat from poultry. Resistance to linezolid and vancomycin, both considered critically important for treatment of human infections, were not detected in any of the reported MRSA isolates subjected to antimicrobial susceptibility testing.

In 2022–2023, the voluntary monitoring of *E. faecalis* and *E. faecium* was conducted in a limited number of countries, ranging from three to six RCs for *E. faecalis*, and from three to five for *E. faecium* over both years and showing notable differences in resistance patterns among isolates from food-producing animals. Overall, *E. faecium* exhibited higher resistance than *E. faecalis*. Vancomycin resistance was exclusive to *E. faecium*, ranging from very low to low with the highest resistance level detected in cattle under 1 year (1.5%). Linezolid resistance was either not detected or low in *E. faecalis* (the highest resistance found in cattle under 1 year of age, 6.6%) and very low in *E. faecium* (the highest resistance detected in fattening pigs, 0.6%), with minimal resistance detected in broilers and none in turkeys for either species.

The **key outcome indicators** for AMR in food-producing animals – complete susceptibility to the harmonised panel of antimicrobials in *E. coli* (KOI_{CS}) and the prevalence of ESBL-/AmpC-producing *E. coli* (KOI_{ESC}) – have also been analysed over the period 2014–2023. There are marked variations in both KOI among reporting countries. Statistically significant decreasing trends in KOI_{ESC} were observed in 19 MSs and two non-MS. A statistically significant increasing trend was identified in three MS and one non-MS. Statistically significant increasing trends in KOI_{CS} were registered in 12 MSs and decreasing trends in 1 MS. The increasing trends in CS and KOI_{CS} in indicator commensal *E. coli* isolates and decreasing trends in KOI_{ESC} reveal progress towards lower levels of resistance in some countries and in the MS-group. Both key outcome indicators show that encouraging progress has been registered in reducing AMR in food-producing animals in several EU MSs over the last years.

1 | INTRODUCTION

Terms of Reference

The European Union system for the monitoring and collection of information on zoonoses is based on **Directive 2003/99/EC**, which obliges the Member States (MSs) of the European Union (EU) to collect data on the occurrence of zoonoses, zoonotic agents, antimicrobial resistance (AMR), animal populations and food-borne outbreaks. The structure of the monitoring of AMR is further elaborated in Commission Implementing Decision 2020/1729 (EU).

- In accordance with Article 9 of Directive 2003/99/EC, the EU MSs are required to assess trends and sources of zoonoses, zoonotic agents and AMR, as well as food-borne outbreaks in their territory, submitting an annual report each year by the end of May to the European Commission (EC) covering the data collected.
- According to the same article, the EFSA shall examine the submitted national reports of the MSs and publish a summary report on the trends and sources of zoonoses, zoonotic agents and AMR in the EU.

EFSA is assigned the tasks of examining the data reported and publishing annual European Union Summary Reports (EUSR) in cooperation with the European Centre for Disease Prevention and Control (ECDC). ECDC provides and analyses the data on zoonotic infections in humans. Since 2007, data on human cases have been reported through The European Surveillance System (TESSy), maintained by the ECDC.

The annual EUSR regarding zoonotic agents and AMR in zoonotic and indicator bacteria from humans, animals and food, as well as illustrating dashboards and story maps assess the evolving situation regarding these matters in the EU.

The antimicrobial agents used in food-producing animal and human medicine in Europe are frequently the same or belong to the same classes. The route of administration and the administered quantities of antimicrobials differ between humans and food-producing animals. Comparable wide variations also occur between and within food-producing animal populations and countries. Nevertheless, frequently exposing the bacterial biota in both humans and animals to antimicrobial agents might result in the development of AMR by favouring the selection of resistant bacterial clones, regardless of whether these are pathogenic, commensal or environmental bacteria. This could, over time, change the population structure of microbial communities with serious consequences for human and animal health.

Antimicrobial-resistant bacteria derived from food-producing animals can spread to humans by ingestion of, or from handling, food contaminated with zoonotic bacteria such as *Campylobacter*, *Salmonella* or *Escherichia coli* (*E. coli*), from direct contact with animals, or sometimes, by environmental contamination. Infections with resistant bacteria may result in treatment failures or the need for second-line antimicrobials for therapy. The commensal bacterial flora can also form a reservoir of resistance genes, which may be transferred between bacterial species, including organisms capable of causing disease in humans and animals (EFSA, 2008).

The European Commission (EC) adopted an Action Plan to tackle AMR on 29 June 2017.[2] The Action Plan is underpinned by a One Health approach that addresses resistance in bacteria from both humans and animals. EU actions have focused on the areas with the highest added value for MSs, such as promoting the prudent use of antimicrobials via antimicrobial stewardship (AMS), enhancing cross-sectorial work, improving infection prevention and control (IPC) and consolidating surveillance of AMR and antimicrobial consumption (AMC). AMR monitoring in zoonotic and commensal bacteria in food-producing animals and foodstuffs entails specific and continuous data collection, analysis and reporting. It enables the understanding of the development and diffusion of resistance, the following of temporal trends in the occurrence and distribution of AMR, the identification of emerging or specific resistance patterns, it provides relevant risk assessment data and helps to evaluate targeted interventions.

Antimicrobial resistance

In this report, AMR is defined as the inability or reduced ability of an antimicrobial agent to inhibit the growth of a bacterium, which, in the case of a pathogenic organism, can lead to therapy failure. A bacterial strain can acquire resistance by mutation, by the uptake of exogenous genes by horizontal transfer from other bacterial strains or by the activation/triggering of a genetic cascade, thereby inducing the expression of resistance mechanisms (EMA and EFSA, 2017). AMR is also an acronym for the health problems arising, in humans and animals, when antimicrobial-resistant microorganisms spread within a population or society. The development and spread of resistance can be triggered by different factors such as use of antimicrobials in human and veterinary medicine, poor hygiene conditions and practices in healthcare settings or the food chain that facilitate the transmission of resistant microorganisms. Over time, this makes antimicrobials less effective.

[2]A European One Health Action Plan against Antimicrobial Resistance (AMR), https://health.ec.europa.eu/system/files/2020-01/amr_2017_action-plan_0.pdf.

1.1 | Monitoring and reporting of antimicrobial resistance in the EU

1.1.1 | Humans: Monitoring of antimicrobial resistance

The EU protocol for harmonised monitoring of AMR in human *Salmonella* and *Campylobacter* isolates was developed by ECDC in collaboration with its Food- and Waterborne Diseases and Zoonoses (FWD) network (ECDC, 2016). The document is targeted to the National Public Health Reference Laboratories (NPHRL) to guide the susceptibility testing required for EU surveillance and reporting to ECDC and to facilitate comparison of data across countries and with the food- and animal AMR monitoring. Based on the defined EU level surveillance objectives, the protocol describes the panel of antimicrobials to be tested, the methods to use (dilution or disc diffusion according to EUCAST recommended methods), how to perform screening and confirmation of ESBL, AmpC and carbapenemase-producing *Salmonella*, the interpretive criteria that should be applied and the reporting format when submitting data to ECDC. It has been agreed that for the joint report with EFSA, human data should be interpreted with EUCAST epidemiological cut-off values (ECOFFs). Countries are therefore since 2014 (2013 data collection) requested to report quantitative antimicrobial susceptibility test results per isolate. After Decision 2018/945/EU came into force in July 2018, EU Member States are legally required to report their AMR test results to ECDC following the methods and criteria specified in the EU protocol. The countries that do not perform AST at the NPHRL, however, continue to report data collected from clinical laboratories, interpreted with clinical breakpoints.

As WGS has started to replace phenotypical typing methods in the NPHRLs, ECDC has enabled the reporting of resistance predicted from WGS since 2020 and from 2023 ECDC is encouraging countries to report the raw sequences to ECDC to allow a harmonised AST interpretation.

ECDC is providing external quality assessment (EQA) schemes via a contracting laboratory to support laboratories in implementing the recommended test methods and antimicrobials and obtaining high-quality AST results. Further capacity building activities, including training, EQA schemes on WGS and networking activities are provided via the HaDEA funded FWD AMR RefLabCap project in 2021–2024.[3] ECDC has also in 2023 funded the sequencing of 100 *Salmonella* isolates and 50 *Campylobacter* isolates for countries that have not yet, or just started, implementing WGS for these pathogens.

1.1.2 | Animals and food: Monitoring of antimicrobial resistance

According to Commission Implementing Decision (EU) 2020/1729, which applies from 1 January 2021 to December 2027, monitoring of AMR is mandatory in *Salmonella* spp., *Campylobacter coli* (*C. coli*), *Campylobacter jejuni* (*C. jejuni*) and indicator commensal *E. coli*, in the major domestically produced food-producing animal populations and their derived meat. Further characterisation is required for *E. coli* and *Salmonella* isolates showing resistance to extended-spectrum cephalosporins and carbapenems. Moreover, specific monitoring of extended-spectrum beta-lactamases (ESBL)-, AmpC beta-lactamases (AmpC)- and carbapenemase (CP)-producing *E. coli* is also required. Monitoring is performed on a rotating basis, targeting fattening pigs and cattle under 1 year of age and meat derived thereof in odd-numbered years and poultry populations (broilers, laying hens, fattening turkeys) and meat derived thereof in even-numbered years, as specified by the legislation.

From 2021, monitoring of imported fresh meat at border control posts (BCPs) shall also be undertaken to complement AMR monitoring in food-producing animals domestically produced. MSs may also voluntarily perform complementary monitoring for MRSA. Representative random sampling of food-producing animals and derived meat is based on a generic proportionate stratified sampling and performed in accordance with the legislation and the technical specifications issued by EFSA.

Microdilution methods for testing should be used and results interpreted using EUCAST ECOFFs to understand microbiological resistance. The harmonised panels of antimicrobials used for *Salmonella*, *Campylobacter* and indicator commensal *E. coli* include substances important for human health, such as critically important antimicrobials (CIAs), and can provide clearer insight into the resistance mechanisms involved. The concentration ranges to be used encompass both the ECOFF and the clinical breakpoints (CBPs), as defined by EUCAST, allowing for comparison with data coming from humans. For *Salmonella* and *E. coli*, a supplementary panel of antimicrobial substances for testing isolates showing resistance to third-generation cephalosporins or carbapenems in the first panel is also used. From 2021, whole genome sequencing (WGS) is authorised as an alternate method to conventional phenotypic testing for isolates obtained for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* and for indicator commensal *E. coli* or *Salmonella* spp. isolates showing resistance to extended-spectrum cephalosporins and carbapenems from routine monitoring. WGS is also recommended for *Campylobacter* isolates expressing high levels of phenotypic resistance to erythromycin. WGS is authorised on a voluntary basis only; however, technical conditions on the WGS technique have been imposed to ensure data comparability (EFSA, 2020).

External quality assurance is provided by the EURL-AR, which distributes panels of well-characterised organisms to all MSs for susceptibility testing, arranges proficiency tests (PTs) trials for the National Reference Laboratories for Antimicrobial Resistance (NRLs-AR) of the MSs every year and together with EFSA and the MSs, performs a reference testing exercise that includes re-testing the antimicrobial susceptibility and WGS analysis of selected isolates (Appendix A – Materials and methods). The EURL-AR also provides a source of reference for MSs regarding the susceptibility test methodologies.

[3] https://www.fwdamr-reflabcap.eu/about-fwd-amr-reflabcap.

Data reporting is performed at the isolate level to enable analyses on the occurrence of resistance and patterns of multidrug resistance (MDR). The reporting of isolate-based data also allows in-depth phenotypic characterisation of certain resistance mechanisms, e.g. third-generation cephalosporin and carbapenem resistance. The voluntary reporting of WGS data from 2021 onwards on ESBL-/AmpC-/CP-producing *E. coli* and *Salmonella* isolates will facilitate an understanding of the potential contribution of food-producing animals and derived food to the burden of AMR in humans (EFSA, 2019).

1.2 | The 2022–2023 EU summary report on AMR

This EUSR presents data on AMR in zoonotic and indicator bacteria from humans, animals and food collected in 2022 and 2023, jointly analysed by EFSA and ECDC, with the assistance of EFSA's contractors. For data on food-producing animals and derived meat in 2022 and 2023, MSs and other reporting countries reported primarily data collected in accordance with Commission Implementing Decision (EU) 2020/1729. Quantitative antimicrobial susceptibility data for *Campylobacter*, *Salmonella* and indicator commensal *E. coli* isolates from animals and food were interpreted using ECOFFs. The occurrence of resistance, complete susceptibility (CS) and MDR were reported at both country and EU levels, along with the results from the phenotypic monitoring of resistance to third-generation cephalosporins and/or carbapenems caused by presumptive ESBL-/AmpC-/CP-producing *Salmonella* and *E. coli*. Data deriving from the voluntary monitoring of MRSA in food and animals were also addressed. The data analysed in this report and presented in the related communication tools were extracted from the EFSA AMR database on 3 December 2024.

For human data in 2023, MSs and non-MSs reported results from antimicrobial susceptibility testing of *Salmonella* spp. and *Campylobacter* spp. isolates from clinical cases of salmonellosis and campylobacteriosis. Phenotypic test results were reported by MSs to TESSy either as quantitative or categorical/qualitative data at the isolate level according to the EU protocol for harmonised monitoring of AMR in human *Salmonella* and *Campylobacter* (ECDC, 2016). Quantitative phenotypic data were interpreted using EUCAST ECOFFs, where available, to understand microbiological resistance. Qualitative phenotypic data were reported in the categories susceptible, susceptible with increased exposure or resistant, as interpreted with clinical breakpoints (CBPs). CBPs enable clinicians to choose the appropriate treatment based on information relevant to the individual patient while ECOFFs help epidemiologists identify small changes in bacterial susceptibility, which may indicate emerging resistance and allow for appropriate control measures to be considered. The breakpoints for clinical resistance are often less sensitive than the ECOFF for a specific bacterium–drug combination resulting in higher levels of microbiological resistance than clinical resistance. By combining the categories of clinically resistant (R) and 'susceptible with increased exposure' (I) into one category, however, close correspondence with the ECOFF can be achieved. A few countries reported genotypic data, either as resistance predicted from WGS or as sequences which were analysed at ECDC with ResFinder and PointFinder to identify resistance markers. Such genetic results are considered to correspond to the ECOFF with a separation between wild-type and non-wild-type isolates. For assessing MDR in *Salmonella* and *Campylobacter*, ECDC and EFSA have agreed on a harmonised panel of nine and four antimicrobial classes, respectively, for better comparison between the two sectors. Additional information on the human data reported in 2022 can also be found in the European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2021–2022 (EFSA and ECDC, 2024).

Since 2021, the only United Kingdom data reported to EFSA were 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) and data transmitted by the United Kingdom (Northern Ireland) have been assigned to the MSs group. In relation to AMR data from humans, no data for 2020–2023 were reported to ECDC by the United Kingdom due to their withdrawal from the EU on 31 January 2020.

This report includes an introduction section, followed by five main chapters on AMR in *Salmonella*, *Campylobacter*, indicator commensal *E. coli*, ESBL-/AmpC-/CP-producing *Salmonella* and *E. coli*, and MRSA, with sections detailing resistance in isolates from humans, food-producing animals and derived meat. A section on key findings is included at the beginning of each chapter. Appendices containing complementary information are located at the end of the report. Detailed information on the materials and methods used in this EUSR on AMR can be found in **Appendix A – Materials and methods**. Annexes to this report are listed in **Appendix B – Additional information and supporting data**, and available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.14645440.

Accompanying this report, EFSA has also published communication tools on the EFSA website: four Story Maps on the monitoring of AMR in *Salmonella, Campylobacter* and *E. coli* as well as the monitoring of MRSA, and two Dashboards on indicators of AMR, and AMR in *Salmonella*, *Campylobacter* and indicator commensal *E. coli* and the occurrence of MRSA. Data on AMR in *Salmonella* and *Campylobacter* from humans are available in the ECDC Surveillance Atlas of Infectious diseases on the ECDC website. The EU MSs, and other reporting countries, the EC and the EURL-AR were consulted while preparing the report. The efforts made by the EU MSs and other reporting countries are gratefully acknowledged.

The data on AMR collected by the EU MSs and compiled in the EUSR on AMR are also used to perform integrated analysis of the consumption of antimicrobials and AMR in animals, food and humans, under a One Health approach on a regular basis (ECDC, EFSA and EMA, 2024). The JIACRA IV report provides evidence-based analysis of the possible association between AMC and AMR in humans and food-producing animals by focusing on combinations of antimicrobials and bacterial species considered important for public health. The comparison of AMC in human and animal sectors, expressed in mg/kg of estimated biomass, at European level showed that between 2014 and 2021, total AMC in food-producing animals decreased by 44%, while in humans, it remained relatively stable. Positive associations between consumption of certain antimicrobials and resistance to those substances in bacteria from both humans and food-producing animals were observed. For certain combinations of bacteria and antimicrobials, AMR in bacteria from humans was associated with AMR in bacteria from food-producing animals which, in turn, was related to AMC in animals. The relative strength of these associations differed markedly between antimicrobial class, microorganism and sector. For certain antimicrobials, statistically significant decreasing trends in AMC and AMR were concomitant for food-producing animals (third-generation cephalosporins, aminopenicillins, tetracyclines and polymixins) and humans (quinolones and aminopenicillins) in several countries over 2014–2021. Similarly, a proportion of countries that significantly reduced total AMC also registered increasing susceptibility to antimicrobials in indicator *E. coli* from food-producing animals and *E. coli* originating from human invasive infections (i.e. exhibited 'complete susceptibility' or 'zero resistance' to a harmonised set of antimicrobials). Overall, the findings suggest that measures implemented to reduce AMC in food-producing animals and in humans have been effective in many countries. Nevertheless, these measures need to be reinforced so that reductions in AMC are retained and further continued, where necessary. This also highlights the importance of measures that promote human and animal health, such as vaccination and better hygiene, thereby reducing the need for the use of antimicrobials.

2 | ANTIMICROBIAL RESISTANCE IN *SALMONELLA* SPP.

2.1 | Key findings

- The number of reported ***Salmonella* spp.** isolates from human cases varied considerably among the 29 reporting countries, often reflecting differences in population size. Similarly, the number of *Salmonella* isolates reported from food-producing animals also varied considerably among reporting countries. In 2023, 25 MSs, the United Kingdom (Northern Ireland) and 1 non-MS reported *Salmonella* spp. from pigs, while 11 MSs reported data from cattle under 1 year of age. In 2022, AMR data on *Salmonella* was reported in poultry populations, namely broilers (24 MSs, the United Kingdom (Northern Ireland) and 2 non-MSs), laying hens (23 MSs, the United Kingdom (Northern Ireland) and 1 non-MS) and fattening turkeys (19 MSs).
- Overall resistance to **ampicillin, sulfonamides and tetracyclines** was observed at high levels in *Salmonella* spp. isolates from humans in 2023 and ranged from moderate to very high in isolates from food-producing animals and imported poultry meat, except in laying hens where low levels of resistance were reported.
- Over the period 2014–2023, statistically significant declining **trends** in resistance to ampicillin and tetracyclines in isolates from humans were observed in 14 and 12 countries, respectively, primarily driven by declining resistance in *S.* Typhimurium, a serovar commonly associated with pigs and cattle under 1 year of age. In poultry populations, an increasing trend in ampicillin resistance at MS level was registered in isolates from broilers, while a declining trend in tetracycline resistance was seen in turkey isolates.
- Overall resistance to **fluoroquinolones (ciprofloxacin)** was observed at moderate levels in *Salmonella* isolates from fattening pigs (14.9%) and cattle under 1 year of age (16.2%) from data reported in 2023, and at high to very high levels among isolates from laying hens (24.7%), broilers (55.5%) and fattening turkeys (57.9%) in 2022. In *Salmonella* isolates from humans reported in 2023, the overall resistance to ciprofloxacin was 21.8%, with the lowest levels observed in *S.* Derby (5.2%) and monophasic *S.* Typhimurium (10.1%) and high to extremely high levels in *S.* Infantis (42.4%) and *S.* Kentucky (80.5%). In *S.* Enteritidis, the most common *Salmonella* serovar detected in humans, resistance to ciprofloxacin was 30.1%. Resistance trends calculated for 2014 to 2023 for human data showed statistically significant increasing trends in resistance to ciprofloxacin in nine countries and decreasing trends in three, with the most noticeable increase in *S.* Enteritidis (13 countries with increasing trends) but also in *S.* Typhimurium and its monophasic variant and *S.* Infantis. Statistically significant increasing trends in ciprofloxacin resistance at MS level were also registered in *Salmonella* isolates from broiler and laying hen flocks.
- **Extremely high resistance to ciprofloxacin** was mostly reported in *S.* Kentucky isolates from humans and food-producing animals. In 2023, 2.3% of *Salmonella* from humans expressed high-level resistance to ciprofloxacin, of which 82.1% were *S.* Kentucky. Eight S. Kentucky were sequenced and six belonged to ST198 and displayed two mutations each in *par*C and *gyr*A, and one also to *parE*. Among the *Salmonella* isolates from pigs displaying ciprofloxacin resistance, 1.4% (three *S.* Kentucky) exhibited MICs of ≥ 4 mg/L. In 2022, 4.2% of the isolates from broilers (15 *S.* Kentucky, 14 *S.* Newport

and 12 *S*. Infantis), 3.3% from turkeys, (13 S. Kentucky) and 2.2% from laying hens (three *S*. Infantis, and one each *S*. Kentucky and *S*. Newport) exhibited high-level ciprofloxacin resistance.

- Overall resistance to **third-generation cephalosporins** was noted at low levels in isolates from humans in 2023 (1.6% resistance to ceftazidime and 1.3% to cefotaxime on average), at very low levels in laying hens (0.2% resistance to cefotaxime and ceftazidime) and pigs (0.8% resistance to cefotaxime and ceftazidime) and at low levels in cattle under 1 year of age (1.2% resistance to cefotaxime and ceftazidime), broiler flocks (1.4% resistance to cefotaxime and 1.3% to ceftazidime) and turkey flocks (2.2% resistance to cefotaxime and ceftazidime). Consequently, the overall proportion of presumptive **ESBL-/AmpC-producing** *Salmonella* spp. at MS level was generally very low/low in 2022 and 2023 among all food-producing animal populations and very low in isolates from human cases, although higher resistance was observed in specific *Salmonella* serovars.
- In 2022 and 2023, no *Salmonella* spp. isolates recovered from animals or meat were microbiologically resistant to meropenem. However, like in 2022, meropenem resistance in human isolates was reported (< 0.1%), with six countries reporting one resistant isolate each in 2023.
- Overall, **combined resistance to fluoroquinolones and cephalosporins** was low in isolates from humans and very low in food-producing animals. However, it was higher in certain *Salmonella* serovars, reaching high levels in *S*. Kentucky isolates from broilers (21.1%) and moderate levels in *S*. Infantis isolates from turkeys (16.9%).
- **Multidrug resistance (MDR)** was overall moderate (19.1%) among *Salmonella* spp. reported in human cases in the EU, ranging from low levels in *S*. Enteritidis (3.1%) to very high in monophasic *S*. Typhimurium 1,4,[5],12:i:- (65.9%) and extremely high in *S*. Kentucky (73.0%). Similarly, MDR was observed at high levels in *Salmonella* spp. recovered from pigs (43.3%) and cattle under 1 year of age (25.0%) in 2023, and broilers and turkeys in 2022 (43.0% and 38.9%, respectively). *Salmonella* spp. isolates from laying hens showed a markedly lower MDR level (7.5%). At the serovar level, the occurrence of MDR was similar across human and animal populations, except for *S*. Kentucky, which on average exhibited higher MDR levels in humans and turkeys than when recovered from other animals.
- Overall, in 2023, **complete susceptibility (CS)** in *Salmonella* spp. isolates from humans was observed in 58.0% of the tested isolates. In isolates from animals, CS was high in pigs (36.8%) and very high in cattle under 1 year of age (56.3%). For 2022 data, CS was high for broilers (35.4%) and turkeys (29.4%) and very high in laying hens (69.1%).

2.2 | Data on AMR in *Salmonella* spp. addressed

Monitoring of non-typhoidal Salmonellas

This section focuses on **non-typhoidal Salmonellas (NTS)** and summarises the occurrence and AMR patterns of isolates recovered from several food-producing animal populations and fresh meat of broilers and turkeys taken at the border control posts (BCPs). Typhoidal salmonellas are human host-adapted organisms causing typhoid and paratyphoid fever. Non-typhoidal strains can either infect or colonise a multitude of animal hosts or be host-specific for particular animal species (Crump et al., 2015). Typhoidal salmonellas belong to *Salmonella enterica* subsp. *enterica* serovars Typhi, Paratyphi A, Paratyphi B (d-tartrate negative) and Paratyphi C, while NTS include all other serovars within the subspecies *enterica* (including the d-tartrate positive Paratyphi B variant Java).

According to the World Health Organisation (WHO), the transmission of disease-causing bacterial infections from non-human sources to humans is more common in specific bacteria such as non-typhoidal *Salmonella*, *Campylobacter* spp. and *E. coli* (WHO, 2019). Thus, the WHO urges for the recognition of this transmission potential. In 2023, salmonellosis was the second most commonly reported food-borne zoonosis in the European Union, with 77,486 confirmed human cases and the most frequent causative agent in food-borne outbreaks accounting for 19.6% of all food-borne outbreaks reported in 2023 (EFSA and ECDC, 2024).

Commission Implementing Decision (EU) 2020/1729 lays down detailed protocols and rules for harmonising AMR monitoring and reporting in zoonotic and commensal bacteria. In 2023, the AMR monitoring in *Salmonella* isolates recovered from caecal contents of fattening pigs and bovine animals under 1 year of age, taken at slaughter, was mandatory. While for 2022, it was mandatory to monitor AMR in *Salmonella* isolates recovered from faecal samples and/or environmental samples (boot swabs or dust) of broiler, laying hen and fattening turkey flocks collected as part of National Control Programmes (NCPs) for *Salmonella* in poultry, and to monitor AMR in *Salmonella* isolates recovered from fresh meat from broilers and turkeys sampled at the border control posts (BCPs).

This chapter describes 2023 AMR data on *Salmonella* isolates from bovine animals under 1 year of age at slaughter (referred to as 'cattle under 1 year of age') and fattening pigs (referred to as 'pigs') and 2022 AMR data from faecal samples and/or environmental samples (boot swabs or dust) collected from flocks of broilers, laying hens and fattening turkeys. Data for *Salmonella* spp. isolated from human cases are reported for both 2022 and 2023. However, Section 2.3 presents data only for 2023, since 2022 data from humans were published in the EU Summary report for 2021/2022 (EFSA and ECDC, 2024).

Antimicrobial susceptibility testing (AST) results in *Salmonella* isolates from human cases include all tested serovars and are also presented separately for the most prevalent serovars in food-producing animals.

Results from data on *Salmonella* spp. isolates include all serovars reported from the different animal origins. According to Commission Implementing Decision (EU) 2020/1729, only one isolate per *Salmonella* serovar from the same epidemiological unit is tested for AMR each year. Since AMR can vary markedly among serovars, the relative contribution of different serovars can influence the overall resistance levels reported for *Salmonella* spp. in the different animal/meat origins. Therefore, results are also presented for selected serovars if they exhibit a high prevalence (i.e. a high recovery rate from samples) or if they are deemed relevant to public health.

In cases where fewer than 10 isolates were retrieved from a particular animal origin in a given country, their resistance profiles were also considered in the analysis. This approach ensures that serovars with low prevalence are not excluded, that emerging serovars are accounted for, and that all relevant data is included in the analysis. Note that some figures in this chapter only display individual MS data where 10 or more *Salmonella* spp. isolates were reported, although the occurrence of resistance at the MS-group level includes all reported isolates.

Variations in *Salmonella* prevalence from food-producing animals and their derived carcases

In 2022 and 2023, countries reported data on *Salmonella* spp. from different origins according to their national situation. Some MSs did not obtain any *Salmonella* isolates from animal or meat origins, therefore data are not presented for those countries. In 2023, the number of MSs reporting data from pigs was considerably higher than MSs reporting data from cattle under 1 year of age. Similarly, in 2022, the number of countries reporting results for broilers and laying hens was considerably higher than for fattening turkeys. This difference can be attributed to the small size of the cattle under 1 year of age and turkey sectors in certain MSs, with production levels falling below the threshold at which the monitoring is mandatory. Additionally, the number of isolates reported by countries varied due to different *Salmonella* prevalence. These factors may be a source of variation in the results when considering all reporting countries.

In 2025, EFSA has for the first time published (together with the present report) a story map on AMR in *Salmonella*, where further information on the topic can be found.

EFSA story map on monitoring AMR in *Salmonella*

The EFSA story map on antimicrobial resistance in *Salmonella* is a new interactive communication tool published by EFSA in 2025, tailored to the general public and available online here. This story map provides general information on the pathogen, explains the importance of monitoring resistance in *Salmonella*, and illustrates the main resistance mechanisms and modes of resistance spread. In addition, this story map describes the activities implemented in the EU for the monitoring of antimicrobial resistance in *Salmonella* from humans and animals and EFSA's role in these activities. Furthermore, the story map shows the key findings of the 2022–2023 EU monitoring of the occurrence of antimicrobial resistance in *Salmonella* and informs on how to prevent antimicrobial resistance. Users can easily display and explore the content of the different sections in the story map, browsing the dynamic infographics, text and plots.

Additionally, EFSA has for the first time published a dedicated dashboard on AMR in *Salmonella*. The dashboard is an online data visualisation tool where the user can interactively see all the information on the occurrence of resistance in *Salmonella* spp. and some selected serovars from animals. Similarly, data on AMR in *Salmonella* spp. from humans can be visualised and downloaded from the ECDC Surveillance Atlas of Infectious Diseases, available here.

EFSA dashboard on monitoring AMR in *Salmonella*

The EFSA dashboard on antimicrobial resistance in *Salmonella* (available online here) is a graphical user interface for searching and querying the data on AMR monitoring in *Salmonella* from animals reported to EFSA by EU MSs and other reporting countries, according to Commission Implementing Decision (EU) 2020/1729. In the dashboard, monitoring data and related statistics on the occurrence of resistance in *Salmonella* isolates from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age can be visualised interactively through maps and graphs. Temporal trends for the period 2014–2023 and the distribution of *Salmonella* serovars in different animal populations are also shown using dynamic graphs. The dashboard allows the user to select the reporting year, reporting country, animal population and antimicrobial substance. In this tool, the main statistics can also be viewed and downloaded in tabular format. Detailed information on the use and features of the antimicrobial resistance dashboard can be found in the user guide (a video embedded in the dashboard).

2.3 | Humans: Occurrence of antimicrobial resistance in *Salmonella*

2.3.1 | Data reported

For 2023, 27 MSs and 2 non-MSs reported data on AMR in *Salmonella* isolates from human cases of non-typhoidal salmonellosis. Twenty-one countries provided data as measured values (quantitative data), four as data interpreted with clinical breakpoints and four reported whole genome sequences that were analysed by ECDC and interpreted as predicted wild type or predicted non-wild type. Not all countries reported results for all antimicrobials in the harmonised panel (ECDC, 2016, 2021). The reported data represent 27.4% of the confirmed human cases with non-typhoidal *Salmonella* reported in the EU/EEA in 2023.

2.3.2 | Occurrence of resistance to commonly used antimicrobials in human and/or veterinary medicine

In **2023**, high proportions of human *Salmonella* isolates were resistant to **ampicillin** (21.3%), **sulfonamides** (20.8%) and **tetracyclines** (21.8%) (Figure 1; Table 1; Annex A.1, table 1). By serovar, resistance to these compounds ranged from 2.5% to 5.6% in *S*. Enteritidis to extremely high in monophasic *S*. Typhimurium 1,4,[5],12:i:- (76.1%–86.0%). The variation in the proportion of resistance was large. Overall, for all *Salmonella* spp., outliers in terms of high proportion of resistance were observed for ampicillin (41.1%) and tetracycline (39.2%) in Italy (Annex A.1, table 1). For *S*. Enteritidis, outliers with a higher proportion of resistance to ampicillin were observed in Belgium (18.2%), and for tetracycline in Bulgaria and Italy (6.7% in both countries) (Annex A.1, table 2). For *S*. Typhimurium, outliers with a higher proportion of resistance were observed in Estonia for ampicillin, sulfonamides and tetracycline (78.9% resistance to all three substances), in Iceland for ampicillin (91.7%, though the number of isolates was low, $N = 12$) and Belgium for tetracycline (60.9%) (Annex A.1, table 3). For *S*. Infantis, Slovakia and Slovenia reported a higher proportion of resistance to ampicillin (82.6% and 54.5%) (Annex A.1, table 5). For *S*. Derby, France was an outlier in reporting higher levels of resistance to sulfonamides (57.1%) (Annex A.1, table 7).

Overall, resistance to **gentamicin** was low (2.2%) across all reported serovars (Annex A.1, tables 1–7) except in *S*. Kentucky where gentamicin resistance was high (33.7%) at the EU level (Annex A.1, table 6). Similarly, levels of **trimethoprim** resistance were overall low among *Salmonella* spp. (5.6%) (Annex A.1, table 1), but moderate in *S*. Infantis (15.7%) and high in *S*. Kentucky (24.2%) (Annex A.1, tables 5 and 6).

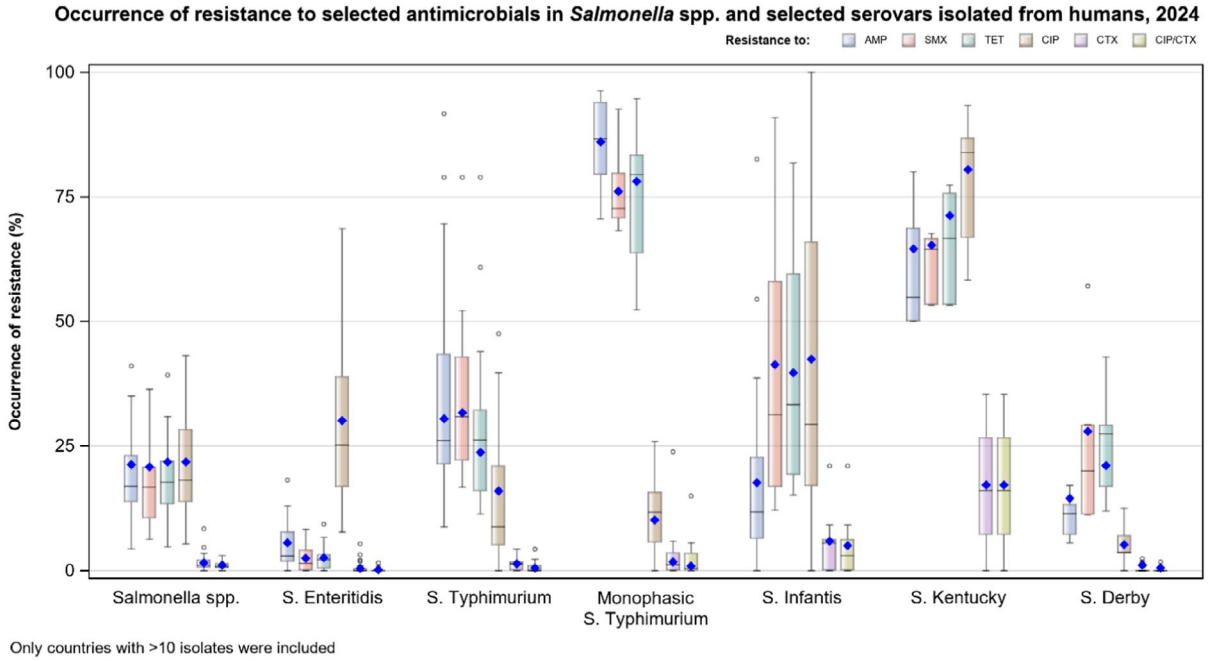


FIGURE 1 Occurrence of resistance to selected and critically important antimicrobials in *Salmonella* spp. and selected serovars isolated from humans, 2023.

AMP, ampicillin; CIP/CTX, combined microbiological resistance to ciprofloxacin and cefotaxime; CIP, ciprofloxacin; CTX, cefotaxime; SMX, sulfamethoxazole; TET, tetracycline; Horizontal lines represent median; Lower and upper box boundaries, 25th and 75th percentiles, respectively; Blue diamond: resistance at the reporting MS group level.

Only MSs reporting data for 10 or more isolates are shown in the graph; however, all isolates are included in the calculation of resistance at the reporting-MS group level.

TABLE 1 Occurrence of resistance to selected and critically important antimicrobials in *Salmonella* spp. and selected serovars from humans, 2023.

	AMP		SMX		TET		CIP		CTX		Combined CIP/CTX	
EU total	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**
Salmonella spp. (27 MSs)	19,593	21.3	10,428	20.8	16,391	21.8	18,477	21.8	17,356	1.6	17,297	1.1
S. Enteritidis (27 MSs)	7315	5.6	3811	2.5	5211	2.6	6354	30.1	5850	0.5	5816	0.2
S. Typhimurium (27 MSs)	1789	30.5	829	31.7	1482	23.7	1773	16	1588	1.4	1583	0.6
Monophasic *S.* Typhimurium (19 MSs)	2400	86	1497	76.1	2403	78.1	2404	10.1	2407	1.7	2404	0.9
S. Infantis (25 MSs)	772	17.6	368	41.3	723	39.7	767	42.4	759	5.9	756	5.0
S. Kentucky (18 MSs)	263	64.6	190	65.3	251	71.3	262	80.5	261	17.2	261	17.2
S. Derby (20 MSs)	359	14.5	183	27.9	350	21.1	364	5.2	355	1.1	355	0.6

Abbreviations: % Res, proportion of resistant isolates; AMP, ampicillin; CIP, ciprofloxacin/pefloxacin; CTX, cefotaxime; N, number of tested isolates; SMX, sulfamethoxazole; TET, tetracycline.

2.3.3 | Occurrence of resistance to highest priority 'critically important antimicrobials' (CIAs) and last resort antimicrobials

The proportion of *Salmonella* isolates resistant to the highest priority critically important antimicrobial (hpCIA) **ciprofloxacin** was overall 21.8% (Figure 1; Table 1). A high proportion of resistance to ciprofloxacin was observed in isolates of *S.* Enteritidis (30.1%, which was a marked increase compared to 2022 when it was 22.8%) and *S.* Infantis (42.4%), while an extremely high proportion was observed in *S.* Kentucky isolates (80.5%) (Figure 1, Annex A.1, tables 2, 5 and 6). At country-level, the highest level of ciprofloxacin resistance in *Salmonella* spp. in 2023 was observed in Poland and Greece (43.2% and 38.2%, respectively) and the lowest in Latvia and Iceland (9.5% and 5.4%, respectively). Cyprus and Greece reported the highest resistance in *S.* Enteritidis (62.2% and 68.6%, respectively) (Figure 2, Annex A.1, table 2). Croatia and Slovenia reported the highest resistance rates in *S.* Typhimurium (39.7% and 47.5%, respectively) and for *S.* Infantis, much higher rates than the EU average were reported in Austria, Ireland, Italy, Slovakia and Slovenia (66.1%–100%) (Annex A.1, tables 2 and 5). Caution should be taken when interpreting results for some countries as they report data on a small number of isolates.

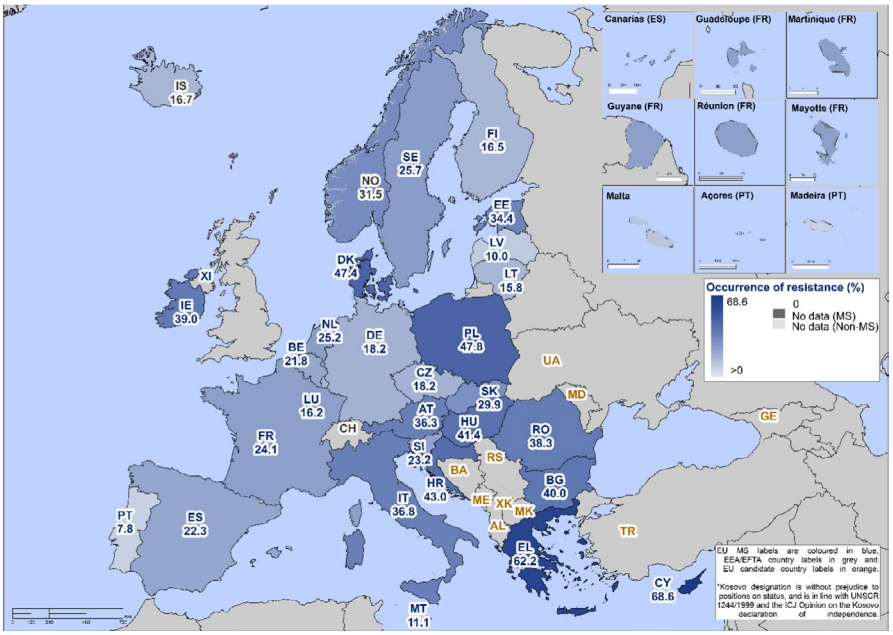


FIGURE 2 Spatial distribution of ciprofloxacin resistance among *S.* Enteritidis isolated from human cases, 2023. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

For **cefotaxime** and **ceftazidime**, representing third-generation cephalosporins, another class of hpCIAs for *Salmonella*, resistance levels were generally low among *Salmonella* spp. (1.6% and 1.3%, respectively) (Annex A.1, table 1), with low levels of resistance ranging from 0.4% to 17.2% across the serovars of interest (Annex A.1, tables 2–7). Resistance was more pronounced in *S.* Infantis and *S.* Kentucky isolates (5.9% and 17.2%) (Table 1; Annex A.1, tables 5 and 6). Outliers in terms of high resistance to third-generation cephalosporins were observed in Luxembourg and Belgium for *Salmonella* spp. (8.4% and 4.7%, respectively), in Luxembourg, Croatia and Belgium for *S.* Enteritidis (5.4%, 2.1% and 1.8%, respectively), in Slovenia for

monophasic *S*. Typhimurium (23.8%), in Italy for *S*. Infantis (21.0%), and in Italy and Germany for *S*. Derby (2.4% and 1.7%, respectively) (Annex A.1, tables 1, 2, 4, 5, and 7).

Sixteen and fourteen countries tested resistance to last-line antimicrobials **azithromycin** and **tigecycline**. Resistance was overall low among *Salmonella* spp. (0.9% and 3.0%, respectively), although Belgium observed a high resistance to tigecycline (21.1%; Annex A.1, table 1). Among the individual serovars, the highest level of resistance to azithromycin was observed in *S*. Kentucky (3.0%). The highest proportion of isolates resistant to tigecycline was observed in *S*. Infantis and *S*. Kentucky (16.8% and 13.9%, respectively; Annex A.1, tables 5 and 6). Resistance to **colistin** was detected in 9.5% of *Salmonella* isolates, with resistance being most pronounced in *S*. Enteritidis (29.7%) and *S*. Dublin (58.1%) isolates, both serovars belonging to group D *Salmonella* which tend to show a higher natural tolerance to colistin (Agersø et al., 2012; Ricci et al., 2020). Resistance mechanisms conferring resistance to polymyxins/colistin was only detected in 1 of 835 isolates (0.1%, a mutation in the PmrAB system) among the four countries reporting sequences for AMR.

Combined resistance to both ciprofloxacin and cefotaxime was overall low in *Salmonella* spp. in human cases (1.1%) (Figure 3A; Annex A.1, table 1) and very low overall in the serovar *S*. Enteritidis, *S*. Typhimurium, monophasic *S*. Typhimurium and *S*. Derby (0.2%, 0.6%, 0.9% and 0.6%, respectively, Annex A.1, tables 2–4 and 7). An exception was a moderate combined resistance in Slovenia for monophasic S. Typhimurium (15.0%) (Annex A.1, table 3). Overall higher levels of combined resistance were observed in *S*. Infantis (5.0%) and *S*. Kentucky (17.2%; Figure 3B,C, and Annex A.1, tables 5 and 6) where Italy reported the highest proportion of combined resistance in *S*. Infantis (21.0%), and for *S*. Kentucky, Austria, Germany, the Netherlands and Spain reported high levels of combined resistance (26.7%–35.4%).

(A)

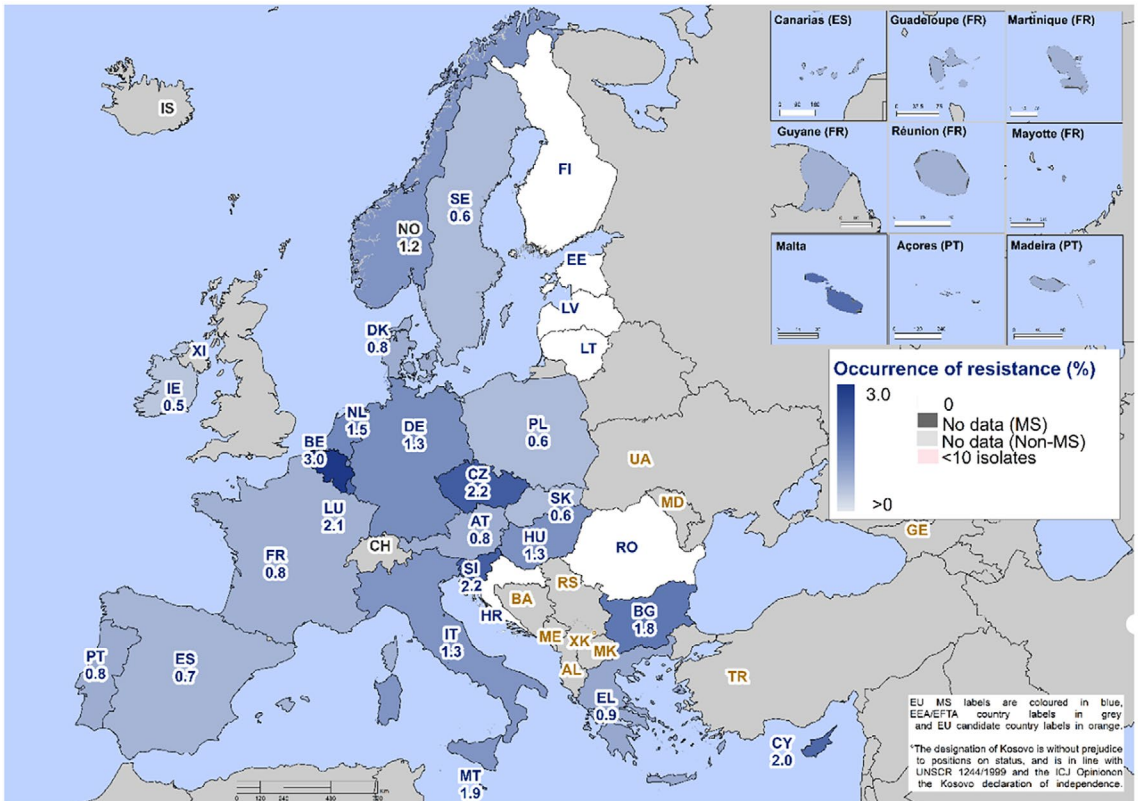


FIGURE 3 (Continued)

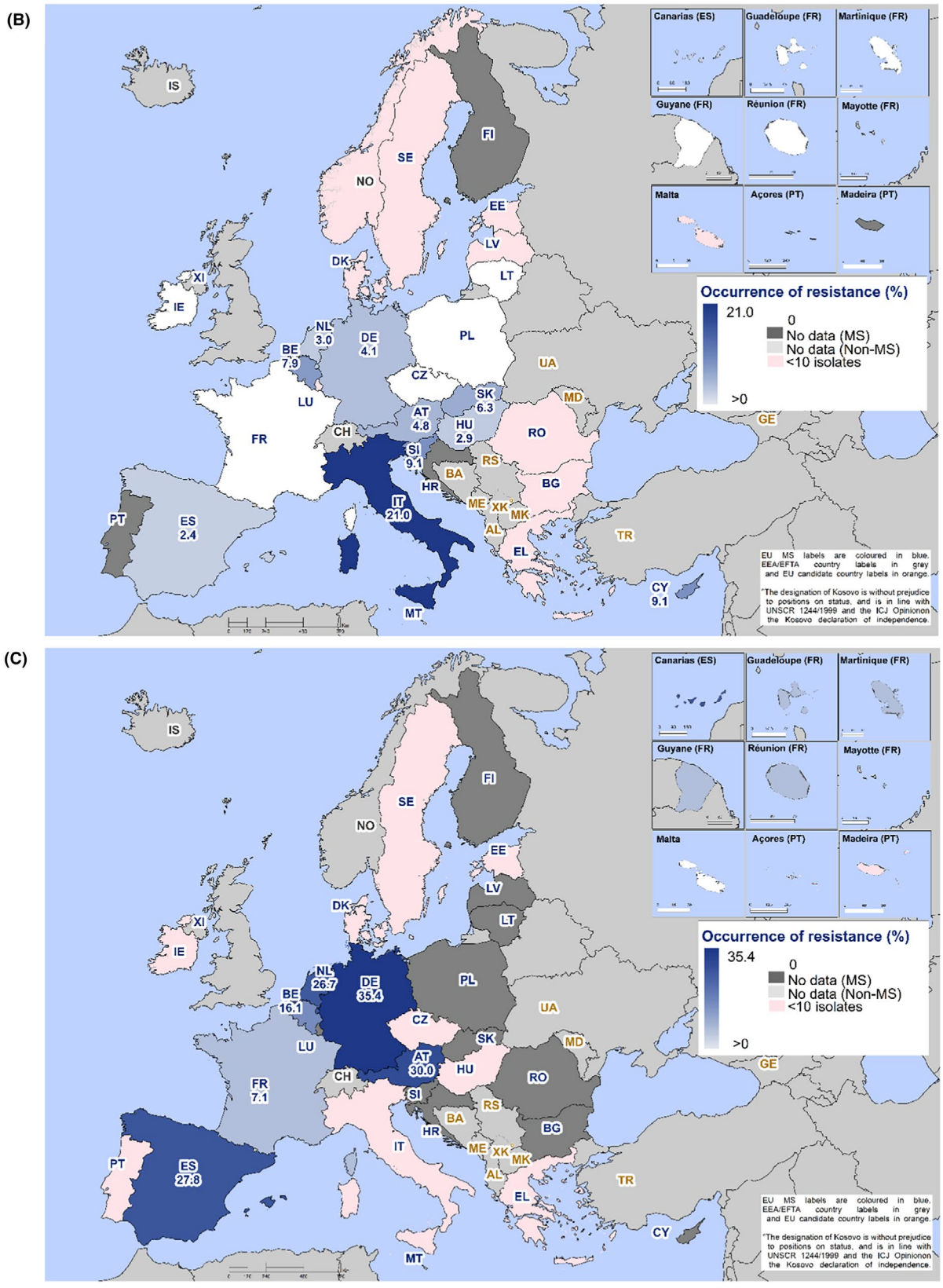


FIGURE 3 Spatial distribution of combined microbiological resistance to ciprofloxacin and cefotaxime among (A) *Salmonella* spp., (B) *S*. Infantis and (C) *S*. Kentucky isolated from human cases, 2023 (pink indicates fewer than 10 isolates tested). The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

2.3.4 | ESBL-, AmpC- and carbapenemase-producing *Salmonella*

Among the 27 MSs and 2 non-MS reporting data on **third-generation cephalosporins** in 2023, resistance was either not detected (4 MSs and Iceland) or found at very low/low levels. Resistant isolates were further tested for ESBL and/or AmpC (Table 2; Annex A.1, table 8). Seven countries (Belgium, Croatia, France, Germany, Hungary, Italy and Slovakia) had not confirmed all presumptive ESBL/AmpC isolates, possibly due to clinical breakpoints being used in routine AST and not ECOFFs. In the case of Italy, only two isolates were not further tested as the cases were epidemiologically linked to other cases confirmed with WGS in an outbreak (pers. comm. L. Villa, Istituto Superiore di Sanità, Italy, 9 September 2024). In the case of Belgium, since 2023, Belgium has entered a transitionary phase in which WGS analysis of invasive *Salmonella* isolates and 50% of *S*. Typhimurium and *S*. Enteritidis strains is performed. Therefore, only a fraction of the presumptive ESBL/AmpC positive isolates were confirmed (genotypically) (pers. comm. P-J Ceyssens, Sciensano, Belgium, 30 October 2024).

ESBL-producing *Salmonella* were identified in 0.8% of the tested isolates, ranging by country from 0% in Finland, Latvia, Lithuania, Romania and Iceland to 3.5% in Bulgaria (in the case of Bulgaria, whole genome sequencing was used as the test method and the sample size was fairly small, *N* = 57) (Annex A.1, table 8). AmpC was less frequent, identified in 0.1% of tested isolates, with the highest occurrence in Italy and Czechia (0.7% and 0.6%, respectively). No isolates were reported to be both AmpC- and ESBL-producing. Six isolates (0.03%) from six different countries carried a carbapenemase (Annex A.1, table 8). ESBL-producing isolates were reported in 28 serovars, with the highest proportions observed in isolates of *S*. Schwarzengrund (13.6%), *S*. Anatum (9.8%), *S*. Kentucky (8.4%), *S*. Heidelberg (7.1%), *S*. Muenster (4.0%) and *S*. Infantis (3.5%), among the isolates where at least 10 isolates had been tested (Table 2). AmpC-type beta-lactamases were overall reported in nine serovars, with the highest proportion observed in *S*. Goldcoast (9.7%), *S*. Uganda (7.1%) and *S*. Schwarzengrund (4.5%). Of the six meropenem resistant isolates, two were monophasic *S*. Typhimurium and one each was *S*. Agona, *S*. Give, *S*. Kentucky and monophasic *S*. *enterica* subspecies II (*salamae*). Four of the isolates carried $bla_{\text{OXA-48}}$, (Table 2; Annex A.1, table 8), one carried $bla_{\text{NDM-1}}$ and one had not been genotyped. It should be noted that in six of 27 reporting MSs, meropenem results were interpreted using the EUCAST clinical breakpoint (CBP), where the MIC is substantially higher (+4 dilutions) than the ECOFF.

TABLE 2 ESBL, AmpC and carbapenemase phenotypes and genotypes in *Salmonella* spp. isolates from humans by serovar in reporting EU/EEA countries, 2023.

			Resistance phenotype										
	Tested for CTX and/or CAZ	Res to CTX and/or CAZ	ESBL		AmpC		AmpC + ESBL		Carba-penemase		Negative for ESBL, AmpC, CP		
Serovar	*N*	*N*	*N*	%	*N*	%	*N*	%	*N*	%	*N*	%	Genotype
Agbeni	9	3	3	NA									CTX-M-15 (3)
Agona	216	4	2	0.9					1	0.5	1	0.5	CTX-M-1 (1), CTX-M-14 (1), CTX-M-55 (1)
Anatum	61	7	6	9.8									SHV-12 (6)
Apeyeme	8	1	1	NA									CTX-M-55 (1)
Bovismobificans	151	2	1	0.7							1	0.7	CTX-M-65 (1)
Braenderup	86	2	1	1.2									CTX-M-15 (1)
Cannstatt	1	1	1	NA									CTX-M-15 (1)
Carno	2	1	1	NA									CTX-M-15 (1)
Chester	383	4	4	1.0									CTX-M-1 (1), CTX-M-55 (1), CTX-M-65 (2)
Coeln	215	3	3	1.4									CTX-M-1 (1), CTX-M-3 (1), CTX-M-55 (1)
Derby	367	4	2	0.5									CTX-M-8 (1), CTX-M-55 (1)
Dublin	69	4	1	1.4									CTX-M-32 (1)
Enteritidis	6371	15	4	0.1	2	0.0					3	0.0	CTX-M (1), CTX-M-8 (1), CTX-M-15 (1), TEM-52b (1), DHA-1 (1), DHA-12 (1)
Give	48	2	1	2.1					1	2.1			CTX-M-55 (1)
Goldcoast	72	10	1	1.4	7	9.7							CMY-2 (7)
Heidelberg	28	2	2	7.1									CTX-M-15 (1), CTX-M-55 (1)
Infantis	774	46	27	3.5							2	0.3	CTX-M-1 (17), CTX-M-65 (6), CTX-M-3 (1)

TABLE 2 (Continued)

Serovar	Tested for CTX and/or CAZ	Res to CTX and/or CAZ	Resistance phenotype										Genotype
			ESBL		AmpC		AmpC + ESBL		Carba-penemase		Negative for ESBL, AmpC, CP		
	N	*N*	*N*	%	*N*	%	*N*	%	*N*	%	*N*	%	
Kentucky	262	49	22	8.4					1	0.4	3	1.1	CTX-M-14/14b (10), CTX-M-15 (1), CTX-M-27 (1), CTX-M-55 (2), CTX-M-like (7)
London	86	1	1	1.2									CTX-M-1 (1)
Mbandaka	111	3	3	2.7									CTX-M-1 (1), CTX-M-like (1)
Minnesota	5	1			1	NA							
Monophasic Typhimurium 1,4,[5],12:i:-	2425	46	32	1.3	3	0.1			2	0.1	4	0.2	CTX-M-1 (16), CTX-M-3 (1), CTX-M-9 (2), CTX-M-14 (4), CTX-M-15 (2), CTX-M-55 (2), CTX-M-65 (2), CTX-M-69 (1), SHV-12 (1), CMY-2 (2), CMY-167 (1), OXA-48 (2)
Muenchen	97	2	1	1.0									
Muenster	50	3	2	4.0									CTX-M-55 (1)
Newport	248	2	1	1.0									CTX-M-15 (1)
Saintpaul	137	5	2	1.5							2	1.5	CTX-M-15 (1)
Schwartzengrund	22	4	3	13.6	1	4.5							CTX-M-55 (3)
Stanley	254	3			1	0.4							DHA-1 and OXA-1 (1)
Subspecies II (4:b:-)	37	1							1	2.7			
Thompson	70	3	1	1.4	2	2.9							
Typhimurium	1878	24	15	0.8	4	0.2					2	0.1	CTX-M-1 (5), CTX-M-9 (1), CTX-M-15 (1), CTX-M-65 (1), CMY-2 (3)
Uganda	14	1			1	7.1							SHV-12 (6)

Note: Croatia did not perform confirmatory testing of resistant isolates and their results could therefore not be included in this table.

Abbreviations: %, percent of total tested within this serovar; CAZ, ceftazidime; CTX, cefotaxime; ESBL, extended-spectrum beta-lactamase; N, Number of isolates; NA, not applicable – if fewer than 10 isolates were tested, the percentage of resistance was not calculated.

2.3.5 | Complete susceptibility (CS) and multidrug resistance (MDR)

In this report, complete susceptibility (**CS**) is defined as susceptibility to each of the nine antimicrobial classes tested in the harmonised panel described by the ECDC (ECDC, 2016, 2021). **MDR** is defined as resistance to three or more antimicrobial classes among *Salmonella* isolates from human cases.

The level of CS in 2023 was 58.0% in *Salmonella* spp. from humans, with the highest proportion in *S.* Enteritidis (64.4%), *S.* Derby (62.3%), *S.* Typhimurium (54.8%) and *S.* Infantis (47.6%). The lowest levels of CS were observed in *S.* Kentucky (14.3%) and monophasic *S.* Typhimurium (6.8%) (Figure 4; Annex A.1, tables 9–14).

MDR was overall at 19.1% ($N = 10{,}394$) among *Salmonella* spp. (Figure 4; Annex A.1, table 9). Among the investigated serovars, MDR was most frequently reported among *S.* Kentucky (73.0%) and monophasic *S.* Typhimurium 1,4,[5],12:i:- (65.9%), followed by *S.* Infantis (42.4%), *S.* Typhimurium (25.4%), *S.* Derby (13.1%) and lastly *S.* Enteritidis (3.1%) (Figure 4; Annex A.1, tables 10–15). Thirteen isolates (five *S.* Infantis, four monophasic *S.* Typhimurium and one each of *S.* Carno, *S.* Give, *S.* Kentucky and *S.* Newport) were resistant to eight of the nine tested substances, eleven of which were only susceptible to meropenem while two were resistant to meropenem and only susceptible to either trimethoprim or sulfonamides (the two monophasic *S.* Typhimurium).

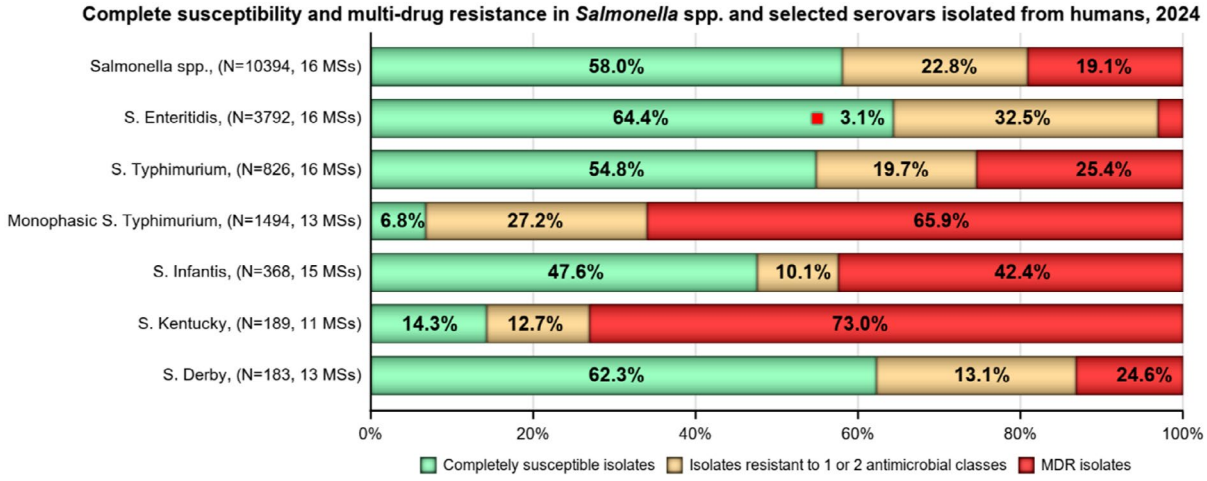


FIGURE 4 Proportion of *Salmonella* isolates from humans being completely susceptible, resistant to one and/or two antimicrobial classes or multidrug resistant (MDR) in 2023.

2.3.6 | Temporal trends

Trends in resistance over the 10-year period 2014–2023 were assessed with logistic regression. Trends varied by country for the different serovars and antimicrobials (Table 3; Figure 5; Annex A.1, figures 1–6). For *Salmonella* spp. overall, 14 and 12 countries out of 26 observed a statistically significant decrease in resistance to ampicillin and tetracycline respectively, whereas two and three countries reported an increase. Also for cefotaxime, more countries observed a statistically significant decrease (seven) than an increase (four), while for ciprofloxacin, a statistically significant increase in resistance was observed in nine countries, while three reported a decrease.

By serovar, statistically significant increasing trends in resistance to ciprofloxacin/quinolones were more commonly observed than decreasing trends in all investigated serovars except for *S*. Kentucky, and with the most notable increase observed in *S*. Enteritidis (13 countries). Respectively, 16 and 15 countries reported decreasing trends in resistance to ampicillin and tetracycline in *S*. Typhimurium, while resistance to ampicillin was increasing in *S*. Infantis and monophasic *S*. Typhimurium in 7 and 6 countries, respectively.

TABLE 3 Number of countries with statistically significant ($p < 0.05$) increasing or decreasing trends in resistance to selected antimicrobials for *Salmonella* spp. and selected serovars in humans in 2014–2023.

	Ampicillin		Cefotaxime		Ciprofloxacin/quinolones		Tetracycline	
Serovar	**Incr.**	**Decr.**	**Incr.**	**Decr.**	**Incr.**	**Decr.**	**Incr.**	**Decr.**
Salmonella spp. (24 MSs + 2 non-MS)	2 (FI, SI)	14 (CY, DE, DK, EL, ES, FR, IE, IT, LT, LU, NO, PT, RO, SE)	4 (HU, IT, SE, SI)	7 (BE, EE, ES, FR, MT, PL, SK)	9 (AT, DE, HU, LT, NL, NO, PL, RO, SK)	3 (ES, FR, MT)	3 (EE, SI, SK)	12 (DK, EL, ES, FR, HU, IE, IT, LU, NL, NO, PT, SE)
S. Enteritidis (23 MSs + 1 non-MS)	4 (AT, BE, NL, SK)	6 (DE, ES, LT, MT, PL, RO)	–	1 (PL)	13 (AT, BE, DE, EE, HU, LT, LU, NL, NO, PL, RO, SI, SK)	5 (ES, FR, MT, PT, SE)	7 (AT, BE, DE, IT, NL, SI, SK)	5 (ES, FR, LT, PL, RO)
S. Typhimurium (24 MSs + 2 non-MS)	–	16 (AT, CY, DE, DK, EE, ES, FI, FR, HU, IE, IS, LU, NO, PT, RO, SI)	2 (DE, HU)	1 (IE)	6 (DE, HU, LT, NO, SI, SK)	–	–	15 (AT, DE, EE, EL, ES, FI, FR, HU, IE, LU, NL, NO, PT, SE, SI)
Monophasic *S*. Typhimurium (15 MSs + 1 non-MSs)	6 (EE, HU, IT, LU, MT, NL)	2 (AT, ES)	2 (IT, SI)	2 (BE, ES)	5 (AT, HU, NL, PT, SI)	1 (NO)	2 (DK, SE)	7 (AT, ES, FR, HU, IE, PT, SI)
S. Infantis (12 MSs)	7 (AT, BE, FR, HU, LT, NL, SK)	2 (DE, ES)	1 (NL)	–	5 (BE, DE, ES, NL, SK)	2 (HU, MT)	3 (BE, ES, NL)	1 (DE)
S. Kentucky (7MSs)	–	1 (BE)	1 (BE)	1 (MT)	–	2 (ES, FR)	–	2 (AT, BE)

TABLE 3 (Continued)

Serovar	Ampicillin		Cefotaxime		Ciprofloxacin/quinolones		Tetracycline	
	Incr.	Decr.	Incr.	Decr.	Incr.	Decr.	Incr.	Decr.
S. Derby (7 MSs)	1 (LT)	1 (DE)	–	–	1 (DE)	–	1 (LT)	1 (FR)

Abbreviations: AT, Austria; BE, Belgium; BG, Bulgaria; CY, Cyprus; DE, Germany; DK, Denmark; EE, Estonia; EL, Greece; ES, Spain; FI, Finland; FR, France; HU, Hungary; IS, Iceland; IT, Italy; LT, Lithuania; LU, Luxembourg; LV, Latvia; MT, Malta; NL, Netherlands; NO, Norway; PL, Poland; PT, Portugal; RO, Romania; SE, Sweden; SI, Slovenia; SK, Slovakia.

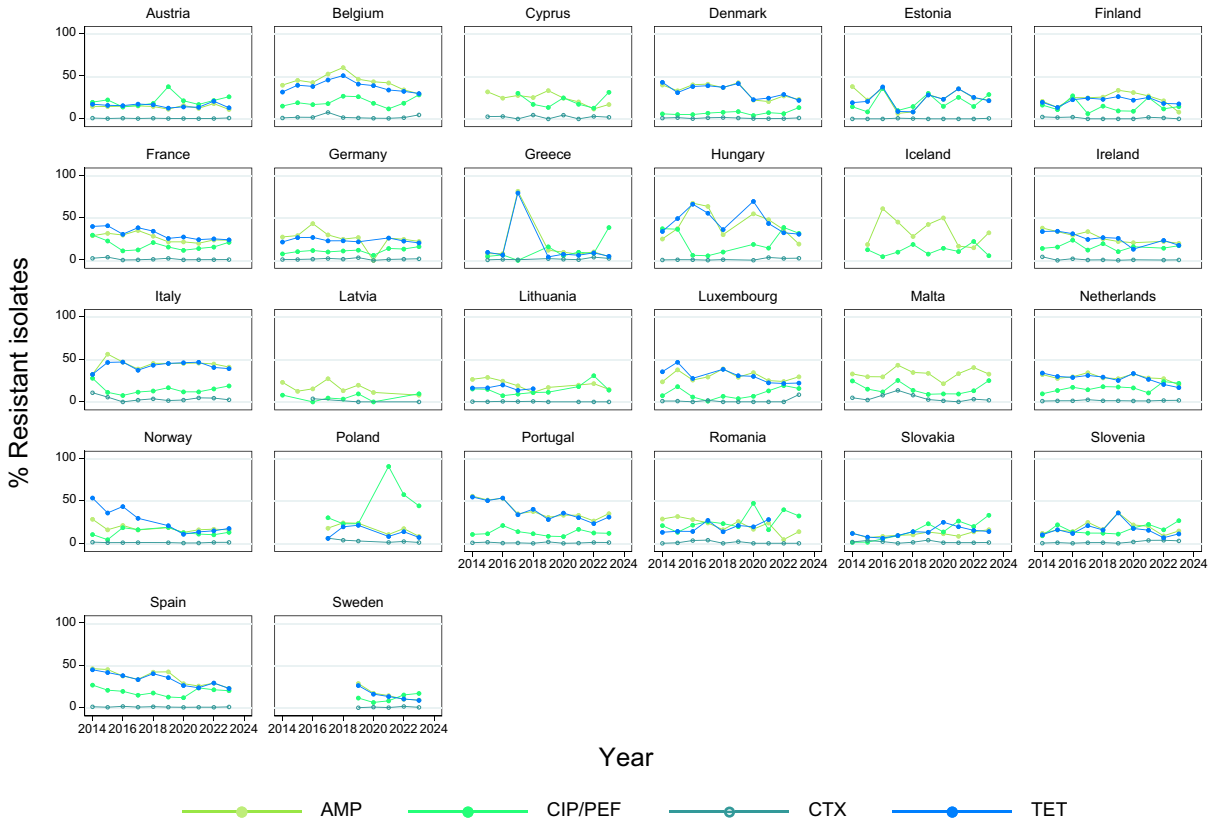


FIGURE 5 Trends in resistance to ampicillin, ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime and tetracycline in *Salmonella* spp. from humans in 26 reporting countries, 2014–2023.

2.3.7 | High-level ciprofloxacin resistance

In 2023, 2.3% ($N = 9095$) of *Salmonella* spp. from humans expressed high-level resistance to ciprofloxacin (MIC ≥ 4 mg/L, Table 4). Such isolates were reported from 9 of the 12 countries reporting MIC values for ciprofloxacin. Among the 15 serovars reported with MICs of ≥ 4 mg/L, high-level ciprofloxacin resistance was most frequently observed in *S.* Kentucky (in 83.7% of tested *S.* Kentucky) and this serovar accounted for 174 out of 212 isolates (82.1%) reported with high-level MIC. Eight *S.* Kentucky sequences were available within the 2023 official *Salmonella* AMR data submitted to ECDC. Six of these were of ST198 and they all displayed two mutations each in *parC* and *gyrA*, and one also to *parE*, which explains the high-level resistance to ciprofloxacin in ST198. The other two isolates, one ST314 and one ST152, only had the *parC* T57S mutation which on its own normally does not result in phenotypic resistance to fluoroquinolones (Chang et al., 2021).

TABLE 4 Occurrence of high-level resistance to ciprofloxacin (MIC ≥ 4mg/L) in *Salmonella* serovars from human cases in 2023.

Serovar	*N*	High-level resistance to ciprofloxacin (MIC ≥ 4 mg/L)	
		n	%
S. Agona	130	4	3.1
S. Corvallis	44	1	2.3
S. Enteritidis	2415	8	0.3

(Continues)

TABLE 4 (Continued)

Serovar	*N*	High-level resistance to ciprofloxacin (MIC ≥ 4 mg/L)	
		n	%
S. Hadar	40	1	2.5
S. Infantis	430	2	0.5
S. Isangi	19	1	5.3
S. Kentucky	208	174	83.7
S. Mbandaka	56	1	1.8
Monophasic *S.* Typhimurium	1346	5	0.4
S. Napoli	107	3	2.8
S. Paratyphi B var. Java	32	1	3.1
S. Saintpaul	90	2	2.2
S. Stanley	186	1	0.5
S. Thompson	34	1	2.9
S. Typhimurium	883	5	0.6
Unspecified serotype	206	2	1.0
Other	2869	–	0.0
Total (12 MSs)	**9095**	**212**	**2.3**

Abbreviations: %, percentage of isolates with MIC ≥ 4 mg/L; *n*, number of isolates with MIC ≥ 4 mg/L; *N*, number of tested isolates.

2.4 | Food-producing animals and meat thereof: Occurrence of antimicrobial resistance in *Salmonella*

2.4.1 | Data reported

In **2023**, 25 MSs, the United Kingdom (Northern Ireland) and 2 non-MSs reported AMR data on *Salmonella* isolates recovered from the caecal contents of pigs at slaughter, and 11 MSs reported AMR data on *Salmonella* isolates recovered from the caecal contents of cattle under 1 year of age at slaughter.

In **2022**, 24 MSs, the United Kingdom (Northern Ireland) and 2 non-MSs reported AMR data on *Salmonella* isolates recovered from broiler flocks, while 23 MSs, the United Kingdom (Northern Ireland) and 1 non-MS reported AMR data on *Salmonella* isolates recovered from laying hen flocks, and 19 MSs reported AMR data on *Salmonella* isolates recovered from fattening turkey flocks. Five and one MSs, respectively, reported data on *Salmonella* isolates recovered from fresh meat of broilers and turkeys sampled at the border control posts.

The relative contribution of the most frequently reported serovars recovered from each food-producing animal population at country level is illustrated in Figure 6. In **pigs**, four serovars (monophasic Typhimurium, Derby, Typhimurium and Rissen) accounted for 76.6% of *Salmonella* spp., while in **cattle under 1 year of age**, serovars Dublin, Typhimurium, Anatum and monophasic Typhimurium accounted for 55.0% of the total *Salmonella* spp. recovered from this origin. In **broilers**, two serovars (Infantis and Enteritidis) represented 51.4% of *Salmonella* isolates, while in **laying hens**, four serovars (Enteritidis, Kentucky, Infantis and Typhimurium) accounted for 53.8% and in **turkeys**, serovars Agona, Infantis, Derby and Bredeney represented 52.6% of *Salmonella* isolates.

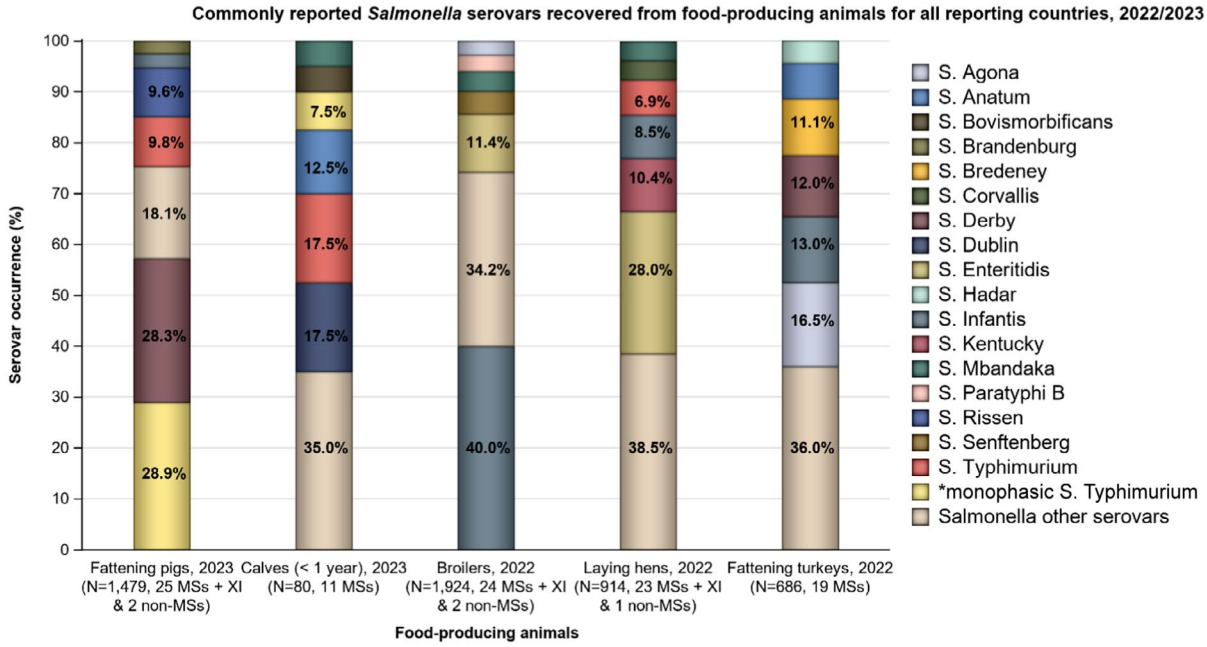


FIGURE 6 Commonly reported *Salmonella* serovars recovered from fattening pigs and cattle under 1 year of age (calves) in 2023, and broilers, laying hens and fattening turkeys in 2022, for all reporting countries.
*monophasic *S*. Typimurium includes all antigenic formulas; serovars in the legend are listed by alphabetical order.
MSs, Member States; *N*, total number of *Salmonella* spp. isolates reported by reporting countries; XI, United Kingdom (Northern Ireland).

The occurrence of AMR (%), CS, MDR and combined resistance to ciprofloxacin and cefotaxime in *Salmonella* spp. and selected serovars from pigs and cattle under 1 year of age (corresponding to 2023 data), and from broilers, laying hens and turkeys (corresponding to 2022 data) at both the MS and MS-group level are presented in Annex A.2 (Annex A.2 is available on the EFSA knowledge junction community on Zenodo at: https://doi.org/10.5281/zenodo.14645440).

Reporting isolate-based data allows for the analysis of MDR patterns, the detection of high-level ciprofloxacin resistance and combined resistance to ciprofloxacin and cefotaxime, which are first-line agents critically important for treating human salmonellosis. In accordance with Commission Implementing Decision (EU) 2020/1729, MSs also included information on serovars and production type. This enabled a detailed analysis of the occurrence of resistance and MDR by serovar for the different animal/meat origins (also shown in Annex A.3).

2.4.2 | Occurrence of resistance to commonly used antimicrobials in veterinary medicine

Since 2014, the antimicrobial substances included in the harmonised panel designed for monitoring and reporting AMR in *Salmonella* from food-producing animals and derived meat have ensured the continuity of monitoring data and epidemiological tracing of isolates (particularly serovars) exhibiting resistance patterns of interest to public health. The selection of these antimicrobial substances was done based on either their public health importance or their common use in veterinary medicine.

Antimicrobial substances such as ampicillin, sulfamethoxazole and tetracycline are widely used in veterinary medicine to treat infections in production animals. The WHO categorises ampicillin, sulfamethoxazole and tetracycline as 'highly important antimicrobials' (HIA) in human medicine (WHO, 2024).

Food-producing animals

In 2023, *Salmonella* spp. recovered from pigs and cattle under 1 year of age showed on average high resistance to **tetracycline** (48.4%; median = 47.3% in pigs, and 30.0%; median = 25.0% in cattle under 1 year of age) and **sulfonamides** (49.5%; median = 44.5% in pigs, and 30.0%; median = 25.0% in cattle under 1 year of age; Figure 7; Annex A.2, tables 1 and 6). **Ampicillin** resistance was also high in pigs (47.0%; median = 39.4%) and slightly lower in cattle under 1 year of age (22.5%; median = 23.1%) when compared to tetracycline and sulfamethoxazole. Resistance levels to **trimethoprim** were high in both, pigs (21.6%, median = 21.8%) and cattle under 1 year of age (20.0%, median = 16.7%), and ranged from moderate to high for **chloramphenicol** (17.0%, median = 16.4%; 20.0%, median = 12.5%, respectively). In contrast, resistance levels for **gentamicin** were low in isolates from both food-producing animals (5.2%, median = 1.2%; 2.5%, median = 0.0%, in pigs and cattle under 1 year of age, respectively).

In 2022, *Salmonella* spp. isolated from broiler flocks exhibited on average high resistance levels for **tetracycline** (40.2%; median = 24.4%) and **sulfonamides** (42.5%; median = 33.3%). Similarly, isolates from turkey flocks showed a high level of resistance to tetracycline (41.4%; median = 25.0%) and sulfonamides (26.7%; median = 16.7%), while, laying hen flocks

exhibited low resistance levels to both, tetracycline (9.1%; median = 3.9%) and sulfonamides (7.9%; median = 2.7%) (Figure 7; Annex A.2, tables 10, 14 and 18). The average resistance levels to **ampicillin** in broiler and laying hen flocks were generally lower than those for other antimicrobials commonly used in veterinary medicine, with low resistance in laying hens (5.4%; median = 0%) and moderate in broilers (19.1%, median = 12.2%). However, isolates from turkey flocks showed on average a very high resistance level to ampicillin (50.1%; median = 0%) (Figure 7; Annex A.2, table 18). Resistance levels in *Salmonella* isolates from poultry species varied from rare to very high for other commonly used antimicrobials in veterinary medicine (Annex A.2, tables 10, 14 and 18).

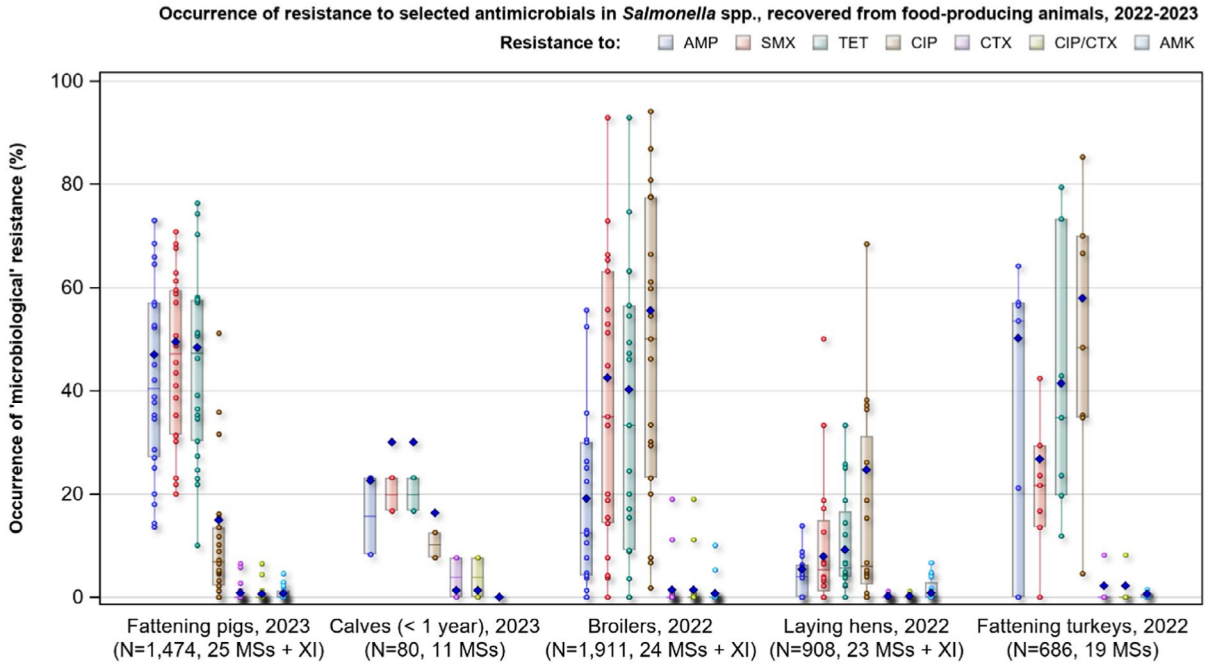


FIGURE 7 Occurrence of resistance to selected and critical important antimicrobials in *Salmonella* spp. recovered from fattening pigs and cattle under 1 year of age (calves) in 2023, and broilers, laying hens and fattening turkeys in 2022, in EU MSs and United Kingdom (Northern Ireland).
AMK, amikacin; AMP, ampicillin; CIP/CTX, combined microbiological resistance to ciprofloxacin and cefotaxime; CIP, ciprofloxacin; CTX, cefotaxime; MSs, Member State; *N*, total number of *Salmonella* spp. isolates reported by MSs; SMX, sulfamethoxazole; TET, tetracycline; XI, United Kingdom (Northern Ireland). Blue diamond shows resistance at the reporting-MS group level. Dots represent resistance in the different countries. Horizontal lines represent median; Lower and upper box boundaries, 25th and 75th percentiles, respectively.
Only MSs reporting data for 10 or more isolates are shown in the graph; however, all isolates are included in the calculation of resistance at the reporting-MS group level.

2.4.3 | Occurrence of resistance to highest priority critically important antimicrobials (hpCIAs) and last resort antimicrobials

Food-producing animals

In **2023**, overall resistance to **ciprofloxacin** was reported at a moderate level for both pigs (14.9%; median = 6.8%) and cattle under 1 year of age (16.3%; median = 0%). Resistance to **nalidixic acid** was also reported at moderate levels in pigs (13.2%, median = 4.7%) and cattle under 1 year of age (10.0%, median = 0%) (Figure 7; Annex A.2, tables 1 and 6).

Of the *Salmonella* isolates from pigs **resistant to ciprofloxacin** and **susceptible to nalidixic acid** ($n = 27$), seven were *S*. Derby (three from the United Kingdom (Northern Ireland) and one each from Estonia, Italy, Romania and Spain), six were monophasic *S*. Typhimurium (Spain, $n = 3$; Germany, $n = 1$; Ireland, $n = 1$; and United Kingdom (Northern Ireland), $n = 1$), four were *S*. Uganda (Spain), two each were *S*. Bredeney (Romania) and *S*. Livingstone (Germany), and one each was *Salmonella* unspecified (Germany), *S*. 4,12:-:- (Spain), *S*. Brandenburg (Italy), *S*. Kapemba (Spain), *S*. Ohio (Spain) and *S*. Typhimurium (Netherlands). Most isolates (40.7%) were reported by Spain. From cattle under 1 year of age, there were only six isolates, three *S*. Bovismorbificans (Italy, $n = 2$; Romania, $n = 1$), two *S*. Typhimurium (Italy) and one *S*. Dublin (Portugal).

In **2022**, overall resistance to **ciprofloxacin** was reported at a very high level for broilers (55.5%, median = 46.2%) and fattening turkeys (57.9%, median = 35.3%) and at a high level for laying hens (24.7%, median = 4.2%). Resistance to **nalidixic acid** was reported at similar levels, with 55.3%, 49.1% and 23.7% for broilers, turkeys and laying hens, respectively (Figure 7; Annex A.2, tables 10, 14 and 18).

Of the *Salmonella* isolates from broilers **resistant to ciprofloxacin and susceptible to nalidixic acid** ($n = 13$), three were *S*. Paratyphi B (Belgium), two each were *S*. Anatum (Portugal), *S*. Virchow (Belgium) and *S*. *enterica* subsp. *enterica* (Czechia), and one each were *S*. Derby (Belgium), *S*. Bovismorbificans (Spain), *S*. Enteritidis (Czechia) and *S*. Kedougou (Spain). From laying hens there were 10 isolates, two each were *S*. Infantis (Belgium and Romania) and *S*. Kentucky (Italy), and one each

were *S.* Bovismorbificans (Spain), *S.* Braenderup (Hungary), *S.* Enteritidis (Spain), *S.* Meleagridis (Spain), *S.* Molade (France) and *S.* Uganda (Spain). A high number ($n = 63$) of isolates from turkeys were resistant to ciprofloxacin and susceptible to nalidixic acid, of which 74.6% were *S.* Anatum (Hungary ($n = 2$), Italy ($n = 37$), Portugal ($n = 4$) and Slovenia ($n = 4$)).

In **2023**, most countries did not detect resistance to **third-generation cephalosporins** (i.e. cefotaxime and ceftazidime) in *Salmonella* isolates from pigs and cattle under 1 year of age (Annex A.2, tables 1 and 6). The few countries reporting resistance to both antimicrobials, **cefotaxime** and **ceftazidime**, in pigs, were Germany (6.5%, $N = 31$), Romania (5.8%, $N = 137$), Croatia (2.7%, $N = 37$) and Malta (1.3%, $N = 77$) (Annex A.2, table 1). Overall resistance to **cefotaxime** and **ceftazidime** was very low (0.8%; median = 0%, for each antimicrobial) in cattle under 1 year of age, Portugal ($N = 13$) was the only country reporting a single *S.* Dublin isolate resistant to both substances (Annex A.2, table 6).

Similarly, in **2022**, most countries did not report resistance to **third-generation cephalosporins** in *Salmonella* isolates from broilers, laying hens and fattening turkeys (Annex A.2, tables 10, 14 and 18). In broilers, only Italy (cefotaxime = 11.1% and ceftazidime = 9.5%, $N = 190$) and Malta (19.0% for both antimicrobials, $N = 21$) reported moderate resistance levels. While in laying hens and turkeys, only Italy reported 2 isolates (*S.* Infantis; $N = 174$) and 15 isolates (*S.* Infantis; $N = 184$), respectively, resistant to both substances (Annex A.2, tables 14 and 18).

In **2023**, overall **combined resistance to ciprofloxacin** and **cefotaxime** in *Salmonella* isolates from pigs and cattle under 1 year of age was reported only by four countries (pigs = 0.6%, median = 0%, cattle under 1 year of age = 1.2%, median = 0%). Specifically, in pigs, Romania reported six isolates (4.4%, $N = 137$), Germany two isolates (6.5%, $N = 31$) and Malta one isolate (1.3%, $N = 77$) (Figure 8; Annex A.2, table 1). For cattle under 1 year of age, a single isolate from Portugal ($N = 13$) was detected with combined resistance to both substances (Figure 8; Annex A.2, table 6).

In **2022**, overall **combined resistance to ciprofloxacin and cefotaxime** was also reported by a very few countries in broilers (1.4%, median = 0%), laying hens (0.2%, median = 0%) and turkey flocks (2.2%, median = 0%). In broiler flocks, only Italy (11.1%, $N = 190$) and Malta (19.1%, $N = 21$) reported moderate resistance levels (Figure 8; Annex A.2, table 10). While for laying hens and fattening turkeys, Italy was the only MS reporting combined resistance (1.1%, $N = 174$, and 8.2%, $N = 184$, respectively) (Figure 8; Annex A.2, tables 21 and 22). As shown in the figure, combined resistance to ciprofloxacin and cefotaxime was most frequently observed in poultry populations, predominantly in *S.* Infantis isolates.

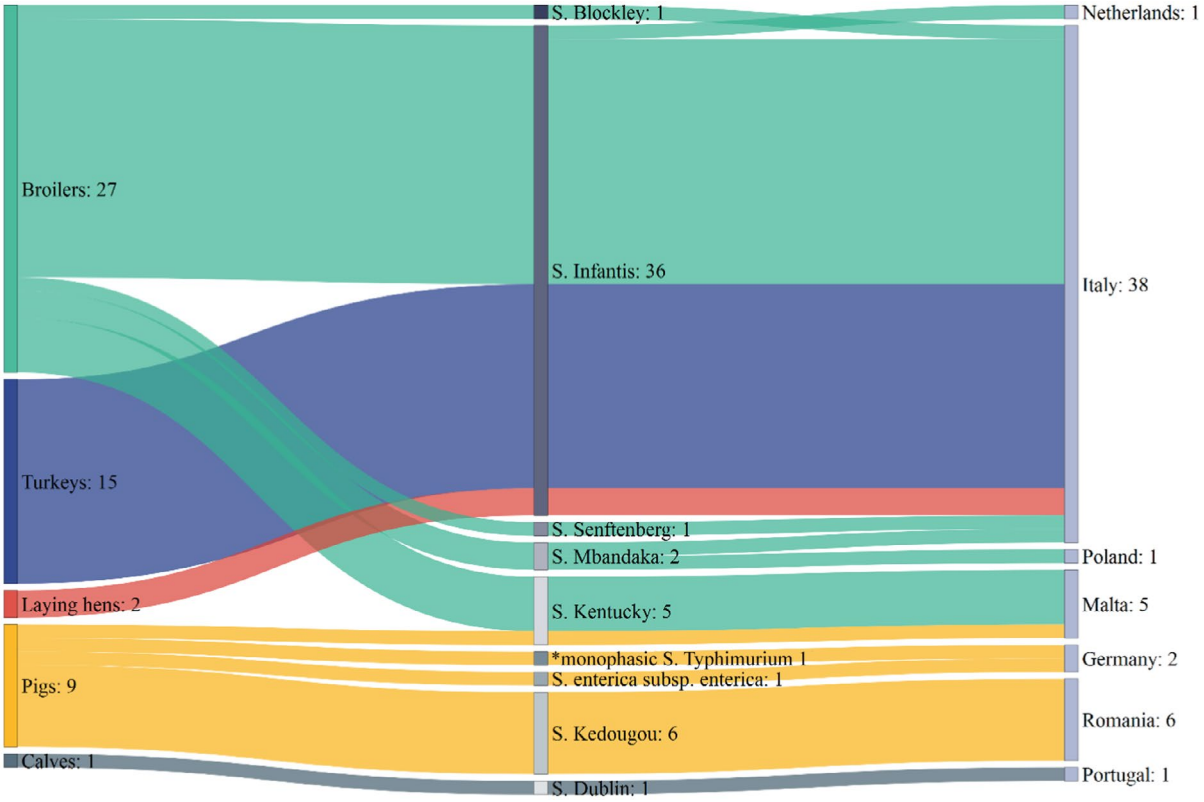


FIGURE 8 Sankey diagram showing the distribution of *Salmonella* isolates with combined resistance to ciprofloxacin and cefotaxime by serovar, food-producing animal and reporting MS, 2022–2023. *monophasic *S.* Typhimurium includes all antigenic formulas.

In **2023**, overall resistance to **azithromycin** in *Salmonella* isolates from pigs and cattle under 1 year of age was low (3.1%, median = 0%; 2.5%, median = 0%, respectively) (Annex A.2, tables 1 and 6). Among the few countries reporting azithromycin-resistant isolates, only Portugal (27.0%, $N = 74$) reported a high level of resistance in pigs, while in cattle under 1 year of age, two countries reported a single resistant isolate each: France ($N = 3$) and Portugal ($N = 13$). Similarly, in **2022**, very low levels of resistance were reported in broilers (0.5%, median = 0%) and turkeys (0.4%, median = 0%), and in laying hen flocks no resistance was detected (Annex A.2, tables 10, 14 and 18).

For **amikacin**, resistance was very low for all animal populations in both monitoring years, except for cattle under 1 year of age for which no resistance was reported in 2023 (Annex A.2, tables 1, 6, 10, 14 and 18). In pigs, very few countries reported resistant isolates (0.7%, median = 0%): three isolates from Romania (*N* = 137), two isolates from Bulgaria (*N* = 44), and one single isolate each from Latvia (*N* = 35), Belgium (*N* = 46), Portugal (*N* = 74), Malta (*N* = 77) and Poland (*N* = 78) (Annex A.2, table 1). In **2022**, low levels of resistance were reported in broilers (0.7%, median = 0%), by only four MSs, with Austria, Portugal, The Netherlands and Hungary reporting nine (*N* = 170), two (*N* = 20), one (*N* = 123) and one (*N* = 170) resistant isolates, respectively (Annex A.2, table 10). In laying hens, several MSs reported low levels of resistance to amikacin (Portugal, 6.7%, *N* = 15; Cyprus, 4.8%, *N* = 21; Austria, 4.4%, *N* = 45; Malta, 4.0%, *N* = 25; and Germany, 1.7%, *N* = 58). From turkeys (0.6%, median = 0%) four MSs, Austria (*N* = 4), France (*N* = 66), Hungary (*N* = 170) and Italy (*N* = 184), reported one resistant isolate each (Annex A.2, table 18).

Regarding **tigecycline**, the new ECOFF (MIC > 0.5 mg/L), laid down in the current legislation, was used to analyse the AMR data. Considering all MSs, overall resistance to tigecycline in **2023** was reported at a low level for pigs (7.3%, median = 3.9%) and cattle under 1 year of age (7.5%, median = 0%), which was similar to the levels reported in 2021 (7.0%, median = 4.4% for pigs and 10.1%, median = 0% for cattle under 1 year of age). In **2022**, resistance was reported at a high level in broilers (25.0%, median = 8.8%), at a moderate level in turkeys (18.4%, median = 0%) and at a low level in laying hens (2.9%, median = 0%). Lowering the tigecycline ECOFF from MIC > 1 mg/L to MIC > 0.5 mg/L may have contributed in part to a higher-than-expected level of resistance in *Salmonella* isolates from pigs, broilers and turkeys compared to previous years. Indeed, many of these isolates were reported with MICs within one dilution range of the new ECOFF. For instance, 6 out of 6 (100%), 88 out of 107 (82.2%), 409 out of 478 (85.6%), 84 out of 126 (66.7%) and 19 out of 26 (73.1%) tigecycline-resistant isolates from cattle under 1 year of age, pigs, broilers, turkeys and laying hens, respectively, had a MIC of 1 mg/L. If considering the previous legislation, these isolates would be categorised as susceptible to tigecycline. Furthermore, the instability of tigecycline in the Mueller-Hinton broth medium used in MIC-testing can lead to inconsistencies in MIC values (Bradford et al., 2005).

In **2023**, overall resistance to **colistin** in *Salmonella* isolates from pigs was very low (0.5%, median = 0%) but moderate for cattle under 1 year of age (13.8%, median = 12.5%) (Annex A.2, tables 1 and 6). While in **2022**, it was low in isolates from broilers (3.5%, median = 0%) and laying hens (5.4%, median = 0%), and very low in isolates from fattening turkeys (0.3%, median = 0%; Annex A.2, tables 10, 14 and 18). Attention should be given to the smaller overall sample size of *Salmonella* isolates from cattle under 1 year of age (*N* = 80) compared to the other animal groups (i.e. pigs, *N* = 1474; broilers, *N* = 1911; laying hens, *N* = 908; and turkeys, *N* = 686). This difference in sample sizes should be taken into consideration when interpreting these results. Across all animal populations, most individual countries reported no resistance or very low levels of resistance to colistin. However, some exceptions occurred where MSs reporting > 10 isolates, showed moderate to high levels of resistance to colistin. These countries included Portugal (23.1%, *N* = 13) for cattle under 1 year of age; Bulgaria (26.7%, *N* = 15) and Poland (19.2%, *N* = 167) for broiler flocks; and Cyprus (23.8%, *N* = 21), Czechia (16.7%, *N* = 12), the Netherlands (26.9%, *N* = 26) and Poland (17.3%, *N* = 81) for laying hen flocks (Annex A.2, tables 1, 10 and 14).

2.4.4 | Tigecycline and colistin resistance in *Salmonella* serovars

Tigecycline resistance in *Salmonella* spp.

Mechanisms of tigecycline resistance

Tigecycline is authorised for use in humans only and was previously categorised as a CIA by the WHO (WHO, 2024). It is considered a last-resort antimicrobial for the treatment of serious infections in adults caused by MDR bacteria. Tigecycline is structurally related to the tetracycline class of antibiotics and is active against Gram-positive and Gram-negative bacteria, as well as tetracycline-resistant bacteria and some anaerobes (Yaghoubi et al., 2022).

Resistance mechanisms to tigecycline include non-mobile *tet*(X) and mobile-plasmid-mediated transmissible *tet*(X), and resistance-nodulation-division (RND) efflux pump mediated by *tmexCD-toprJ* genes and *AcrB* (Anyanwu et al., 2022; Li et al., 2024). The spread of tigecycline resistance genes mediated by transferable plasmids, such as *tet*(X3) and *tet*(X4), is of the highest concern, as they confer high levels of resistance to all tetracyclines, including tigecycline (MICs of ≥ 32 mg/L). Two recent studies investigating the global distribution, evolution pattern and spread of *tet*(X) genes identified isolates carrying *tet*(X) genes from over 20 countries across five continents (Pan et al., 2020; Wang et al., 2021).

The first report of transferable high-level tigecycline (HLT) resistance by *tet*(X3) and *tet*(X4) genes in Enterobacteriaceae from food animals, meat and the environment came from China in 2019 (He et al., 2019). Another study from China in the same year identified *tet*(X4) MDR *E. coli* isolates from retail pork samples (Bai et al., 2019). The *tet*(X4) gene in these isolates was located on several conjugative plasmids of different replicon types, indicating that the gene may be captured by a range of mobile genetic elements circulating among bacterial strains. Since then, additional plasmid-mediated *tet*(X) genes, including *tet*(X5) and *tet*(X6), have been identified in over 10 different Gram-negative species, although rarely in *Salmonella* spp. (Wang et al., 2021). Recently, *tet*(X4) has been identified for the first time in *S.* Rissen (ST469) from pork in China (Zhang et al., 2024). The authors

found that the *tet*(X4) was located in the IncFIA(HI1)-IncHI1A-IncHI1B(R27) hybrid plasmid, suggesting an increasing transmission risk of the mobile tigecycline resistance gene *tet*(X4) beyond *E. coli* (Zhang et al., 2024).

While tigecycline is not used in food-producing animals, it is postulated that the excessive use of tetracyclines in these animals may contribute to the emergence of plasmid-mediated *tet*(X) genes, with the potential to spread to human bacterial species (Anyanwu et al., 2022; Pan et al., 2020). The potential for other bacteria within the Enterobacteriaceae family (such as *Salmonella*) to acquire such transferable tigecycline resistance genes is highlighted, and the importance of monitoring tigecycline resistance through the determination of MICs or by molecular investigation such as WGS is further underlined.

The number and percentage of tigecycline-resistant *Salmonella* isolates detected by MSs from pigs, cattle under 1 year of age and poultry flocks, and the predominant serovars accounting for this resistance are shown in Figure 9. Particular serovars displayed microbiological resistance to tigecycline, suggesting a clonal expansion of microbiologically-resistant strains of these serovars.

In **2023**, ***S.* Rissen** (39.3%, *n* = 42), **monophasic *S.* Typhimurium** (18.7%, *n* = 20), ***S.* Derby** (15.0%, *n* = 16) and ***S.* Typhimurium** (13.1%, *n* = 14) accounted for most of the tigecycline resistant isolates recovered from pigs (*n* = 107; Figure 9). For cattle under 1 year of age, of the six isolates resistant to tigecycline, four were ***S.* Typhimurium** and the remaining were ***S.* Rissen** and ***S.* Worthington**, one each (Figure 9).

In **2022**, serovar **Infantis** accounted for most of the tigecycline-resistant isolates recovered from broilers (82.2%, *n* = 393), laying hens (57.7%, *n* = 15) and turkeys (48.4%, *n* = 61). The second most predominant serovar among the tigecycline-resistant isolates in broilers, was **S. Newport**, 4.6% (*n* = 22), followed by ***S.* Paratyphi B** (2.5%, *n* = 12) and ***S.* Enteritidis** (1.7%, *n* = 8) In laying hens, ***S.* Enteritidis** and ***S.* Kentucky**, each 11.5% (*n* = 3), and in turkeys ***S.* Bredeney** and ***S.* Agona**, 31.7% (*n* = 40) and 7.9% (*n* = 10), respectively, accounted for the most tigecycline-resistant isolates recovered (Figure 9).

Considering individual countries, the highest levels of tigecycline resistance in pigs (*n* = 107) were reported by Portugal (29.7%, *n* = 22), Estonia (28.6%, *n* = 4) and Romania (19.7%, *n* = 27; Annex A.2, table 1). In cattle under 1 year of age, Italy reported three of the six tigecycline-resistant isolates (Annex A.2, table 6). Most of the tigecycline-resistant isolates in broilers were reported by Hungary (54.1%, *n* = 92), Slovenia (50.0%, *n* = 44), Poland (46.7%, *n* = 78) and Romania (40.6%, *n* = 69), while the highest levels of tigecycline in turkeys were reported by Hungary (42.9%, *n* = 73) and Italy (21.2%, *n* = 39; Annex A.2, tables 10 and 18).

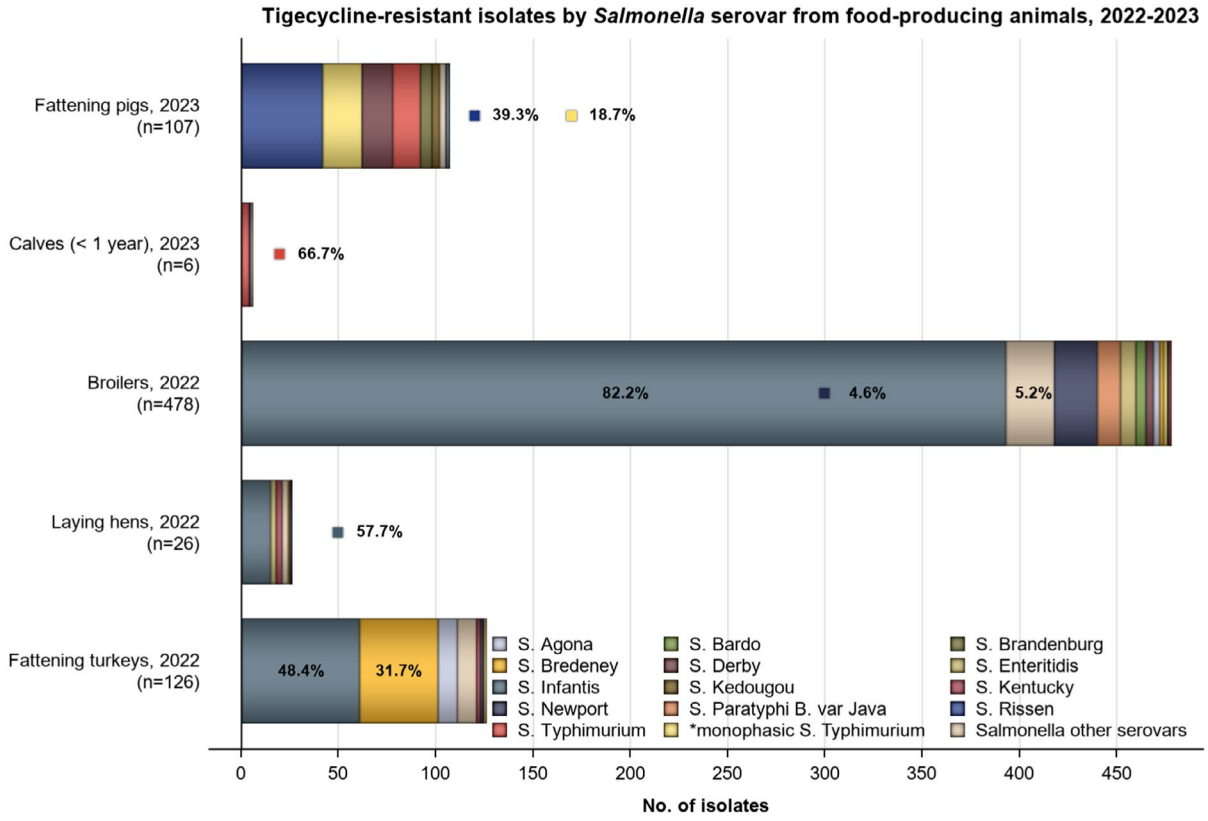


FIGURE 9 Breakdown of the number of tigecycline-resistant *Salmonella* isolates by serovar from fattening pigs and cattle under 1 year of age (calves < 1 year) in 2023 and broilers, laying hens and fattening turkeys in 2022, using harmonised ECOFFs.

n, total number of tigecycline-resistant isolates reported by MSs; predominant serovars are also expressed as a percentage.

*Monophasic *S.* Typhimurium includes all antigenic formulas; *Salmonella* serovars in the legend are listed by alphabetical order. The ECOFF used to determine tigecycline resistance was MIC > 0.5 mg/L.

Where **tigecycline** resistance was reported among certain serovars within the different food-producing animal populations, **MDR** was often a feature. For instance, in pigs, 75.7% of all tigecycline-resistant *Salmonella* spp. isolates were multidrug-resistant ($n = 81$). Of all tigecycline-resistant isolates from pigs that were MDR, 84.0% exhibited resistance to at least ampicillin, sulfamethoxazole and tetracycline (AMP-SUL-TET). ***S.* Rissen** ($n = 25$), **monophasic *S.* Typhimurium** ($n = 17$) and ***S.* Typhimurium** ($n = 11$) were the most common serovars with the above-mentioned characteristics. For cattle under 1 year of age, among the tigecycline-resistant isolates, three ***S.* Typhimurium** isolates and one ***S.* Rissen** were also MDR, showing resistance to four to six antimicrobial classes.

In **2022**, among broilers, of all tigecycline-resistant ***S.* Infantis** isolates, 97.2% were multidrug-resistant, with a consistent presence of resistance to ciprofloxacin, nalidixic acid, sulfamethoxazole and tetracycline (CIP-NAL-SUL-TGC-TET) across all these isolates, either alone or alongside additional resistances. This is a resistance pattern typical of some MDR broiler clones of ***S.* Infantis** (Alba et al., 2020; Alvarez et al., 2023; Nógrády et al., 2012). For laying hens, 20 tigecycline-resistant isolates (76.9%, $n = 26$) were MDR, with a similar resistance pattern to that described above for broilers. Among turkeys, of all tigecycline-resistant isolates, 98.4% (124 out of 126) were multidrug-resistant, with ampicillin, nalidixic acid, ciprofloxacin and tetracycline resistance being a feature.

Colistin resistance in *Salmonella* spp.

Mechanisms of colistin resistance

Colistin belongs to the polymyxin antimicrobial class and is considered a highest priority CIA (hpCIA) and a last resort antimicrobial for treating serious human infections caused by several Gram-negative bacteria (WHO, 2024). Although not frequently used in human medicine due to its nephrotoxic effects, colistin has been widely used in veterinary medicine for prophylactic/metaphylactic treatment (Kieffer et al., 2017). Several mechanisms of polymyxin resistance in Gram-negative bacteria have been described (lipopolysaccharide modifications, efflux pumps, capsule formation and overexpression of membrane protein, Hamel et al., 2021). Furthermore, transferable mobile colistin resistance (mcr) genes have also been detected in *Salmonella* isolates (Portes et al., 2022).

Among *Salmonella* isolates recovered in **2023** from pigs with resistance to **colistin** ($n = 8$), 37.5% were ***S.* Enteritidis** ($n = 3$), two isolates were **monophasic *S.* Typhimurium** (25.0%) and one isolate each was ***S.* London**, ***S.* Poona** and ***S.* Typhimurium** (Figure 10). While, of the 11 colistin-resistant isolates from cattle under 1 year of age, 9 were ***S.* Dublin** and 1 each was ***S.* Anatum** and ***S.* Enteritidis** (Figure 10).

In **2022**, resistance to colistin was generally observed in ***S.* Enteritidis** isolates (Figure 10). This serovar accounted for 86.6% and 87.8% of the colistin-resistant isolates recovered from broilers and laying hens, respectively. Only two colistin-resistant isolates were reported from turkeys, one of them being ***S.* Napoli**.

Figure 10 presents the number and percentage of colistin-resistant isolates detected from the different food-producing animal species reported by MSs and the predominant serovars accounting for this resistance. Notably, ***S.* Enteritidis**, ***S.* Dublin** and ***S.* Napoli** are **group D salmonellas** (serogroup O9). *Salmonella* belonging to group D tend to show a decreased susceptibility to colistin without having any known acquired or mutational colistin resistance mechanisms (Agersø et al., 2012; Ricci et al., 2020). This is exemplified by the proportion of colistin-resistant isolates belonging to ***S.* Enteritidis** (in poultry) and ***S.* Dublin** (in cattle under 1 year of age) in both reporting years. The remaining serovars listed do not belong to group D (serogroup O9).

One ***S.* Enteritidis** isolate from laying hens in 2022 showed markedly elevated colistin MICs (i.e. MIC ≥ 16 mg/L). In 2023, there were no isolates from pigs or cattle under 1 year of age showing markedly elevated colistin MICs.

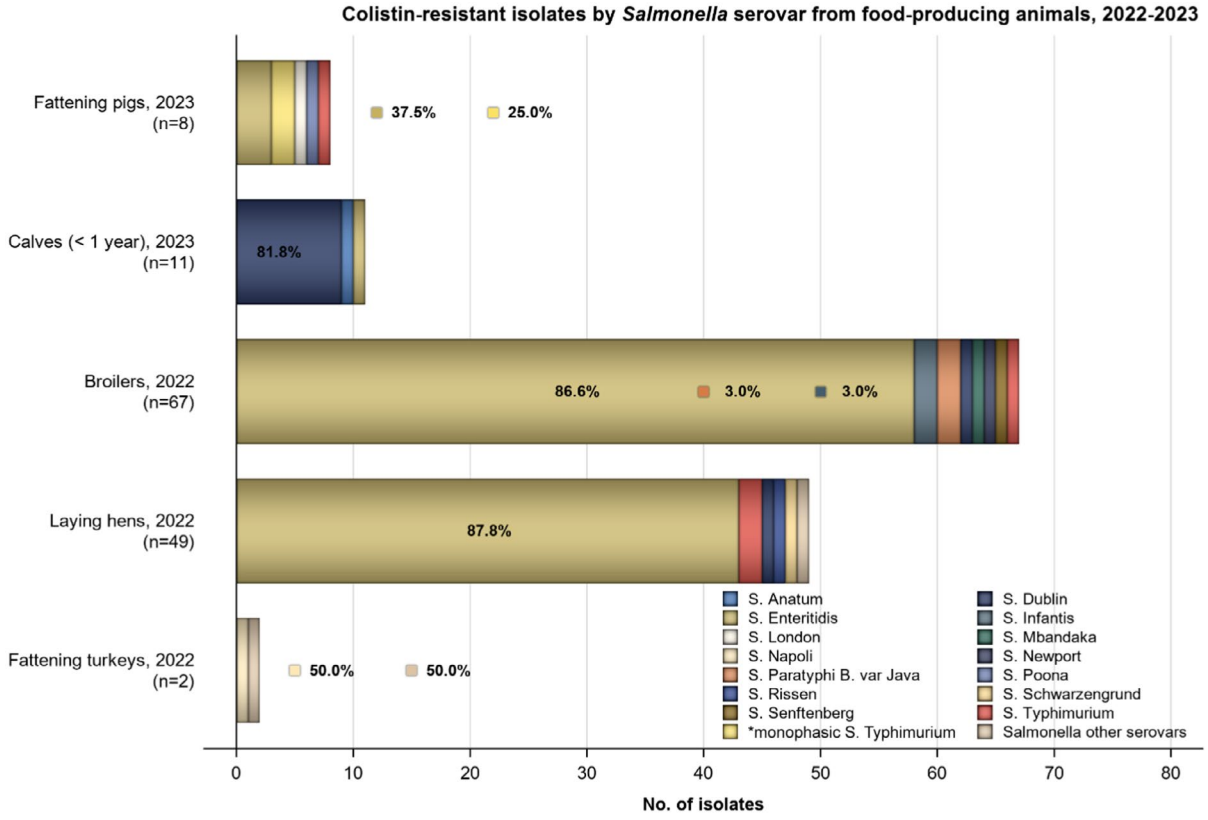


FIGURE 10 Breakdown of the number of colistin-resistant *Salmonella* isolates by serovar from fattening pigs and cattle under 1 year of age (calves < 1 year) in 2023 and broilers, laying hens and fattening turkeys in 2022.
n, total number of colistin-resistant isolates reported by the MSs; predominant serovars are expressed as a percentage.
*Monophasic *S.* Typhimurium includes all antigenic formulas; *Salmonella* serovars in the legend are listed by alphabetical order.

2.4.5 | Complete susceptibility (CS) and multidrug resistance (MDR)

The assessment of CS and MDR in *Salmonella* spp. isolates included the following list of antimicrobials: amikacin/gentamicin (aminoglycosides), ampicillin, cefotaxime/ceftazidime (third-generation cephalosporins), chloramphenicol, ciprofloxacin/nalidixic acid ((fluoro)quinolones), meropenem, sulfamethoxazole, tetracycline/tigecycline (glycylcyclines) and trimethoprim (also detailed in Appendix B – Additional information and supporting data). **CS** is defined as complete susceptibility to the selected antimicrobial substances listed above. **MDR** is defined as resistance to three or more antimicrobial classes listed above. Data from countries submitting less than 10 *Salmonella* isolates from the different animal origins are excluded from some of the analyses described in this section. The **levels of CS** and **MDR** among *Salmonella* isolates recovered from food-producing animals are shown in Figure 15. Only MSs reporting 10 or more isolates are included in the analysis. Annex A.2 includes tables with overall and individual country MDR and CS.

MDR at MS level was observed at high levels in isolates from pigs (43.3%, median = 38.8%), broilers (43.0%, median = 33.3%), turkeys (38.9%, median = 21.2) and cattle under 1 year of age (25.0%, median = 23.1%). Few countries reported zero MDR in any of these food-producing animal populations. Conversely, MDR was reported at a low level in isolates from laying hens (7.5%, median = 2.7%).

Across all MSs submitting data in **2023**, **MDR** in **pigs** was reported at extremely high levels by the United Kingdom (Northern Ireland) (70.8%, *N* = 89) and very high levels by seven MSs, namely: Croatia (64.9%, *N* = 37), Spain (63.5%, *N* = 170), Germany (61.3%, *N* = 31), Portugal (59.5%, *N* = 74), Estonia (57.1%, *N* = 14), Ireland (52.9%, *N* = 170) and Romania (51.1%, *N* = 137; Annex A.2, table 1). For **cattle under 1 year of age**, Spain and Portugal reported moderate and high MDR levels, respectively (12.5%, *N* = 24 and 23.1%, *N* = 13, respectively; Annex A.2, table 6). In **2022**, extremely high levels of **MDR in broilers** were reported by Cyprus (92.9%, *N* = 14) and Austria (72.9%, *N* = 170). In turkeys MDR was reported at very high levels by Hungary (69.4%, *N* = 170). In contrast, when considering laying hens, up to 12 countries reported zero MDR isolates (Annex A.2, tables 10, 14, and 18).

Conversely, in 2022 and 2023, overall **CS** at the MS level was observed at very high levels for laying hens (69.1%, median = 82.6%) and cattle under 1 year of age (56.3%, median = 50.0%), and high levels for pigs (36.9%, median = 41.0%), broilers (35.4%, median = 47.6%) and turkeys (29.4%. median = 41.2%; Annex A.2, tables 1, 6, 10, 14 and 18). However, the levels of CS varied widely among reporting countries, particularly in pig, broiler and turkey populations.

The **spatial distribution of CS** across all reporting countries can be seen in Figure 11. In **2023**, for pigs across all countries reporting data for > 10 isolates, Slovenia (80%, *N* = 10), Hungary (63.9%, *N* = 61) and Luxembourg (62.5%, *N* = 32) reported the highest CS levels, while Portugal (17.6%, *N* = 74) and the United Kingdom (Northern Ireland) (18.0%, *N* = 89), reported the lowest CS levels. Generally, Central and Northern Europe shows higher CS rates compared to parts of Southern and Eastern

Europe, where rates tend to be lower. For cattle under 1 year of age, only two countries, Portugal (76.9%, *N* = 13) and Spain (62.7%, *N* = 24), submitted AMR data on more than 10 isolates.

For **2022** broilers' data across all MSs reporting 10 or more isolates, France reported the highest level of CS (93.5%, *N* = 168; Annex A.2, table 10). For turkeys, France also reported an extremely high level of CS (77.3%, *N* = 66), followed by Portugal (43.5%, *N* = 23), Ireland (41.2% *N* = 17), Italy (30.4% *N* = 184), Croatia (26.7, *N* = 15) and Spain (22.9%, *N* = 170). For laying hens, the median CS was extremely high at 82.6%, with almost every country reporting CS above 60% except for Italy (28.7%, *N* = 174), Belgium (37.5%, *N* = 16), Luxembourg (50%, *N* = 2) and Poland (56.8%, *N* = 81).

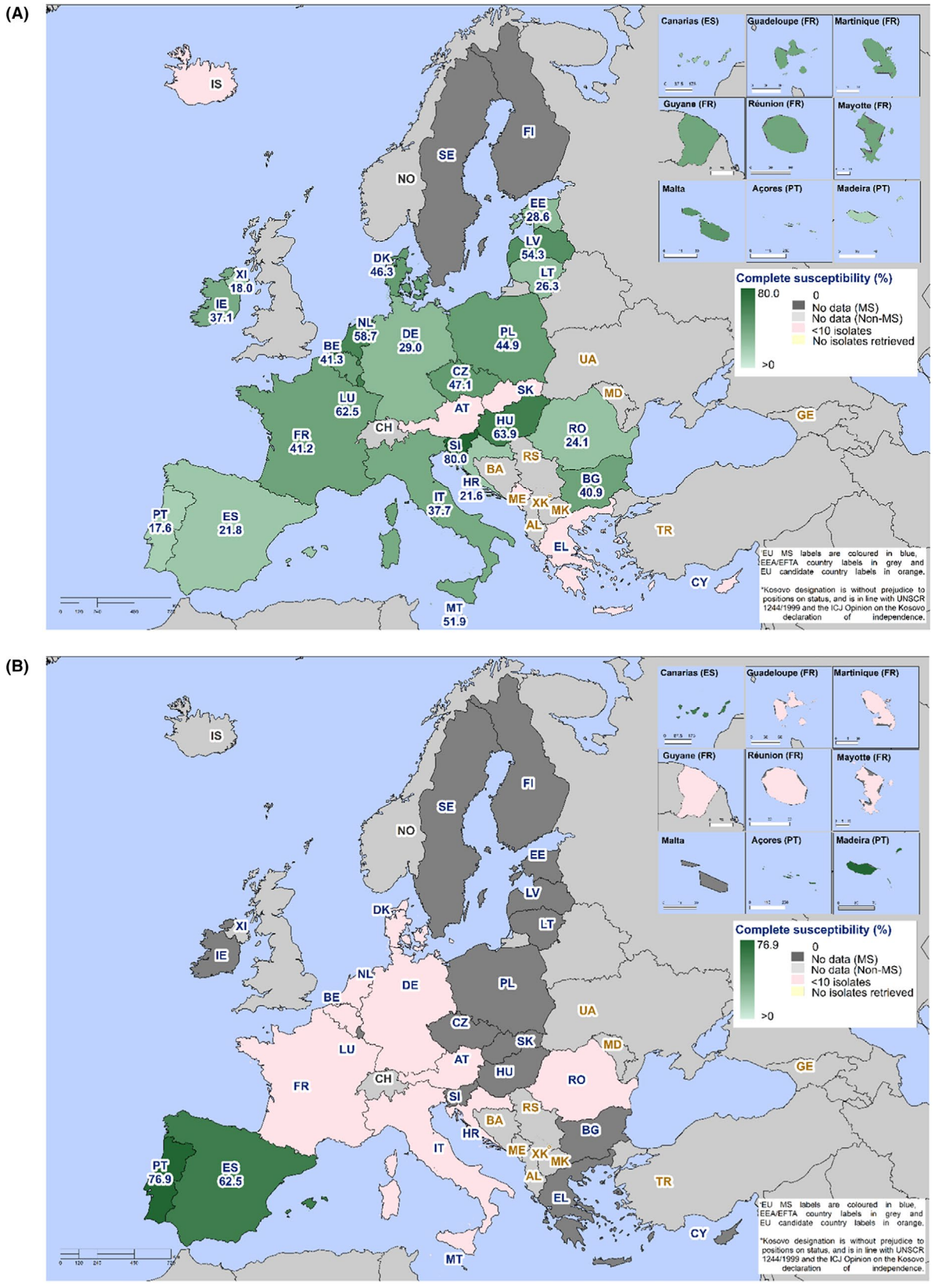
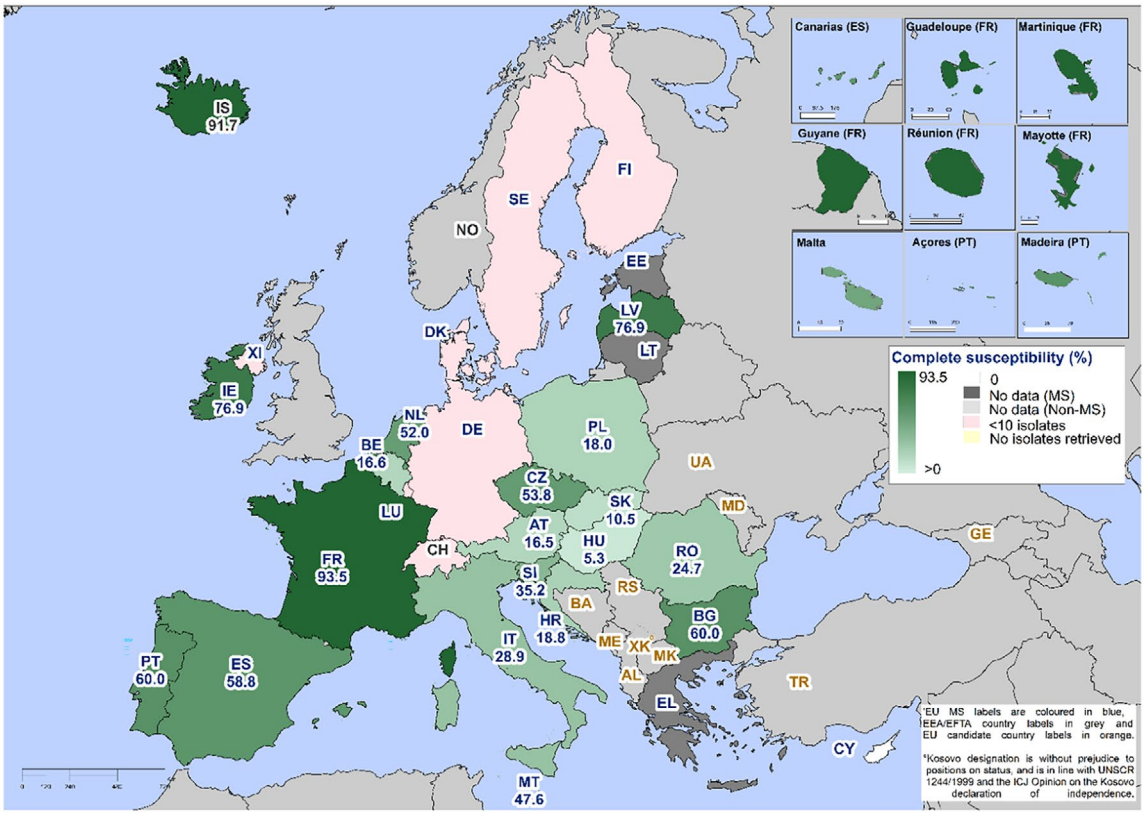


FIGURE 11 (Continued)

(C)



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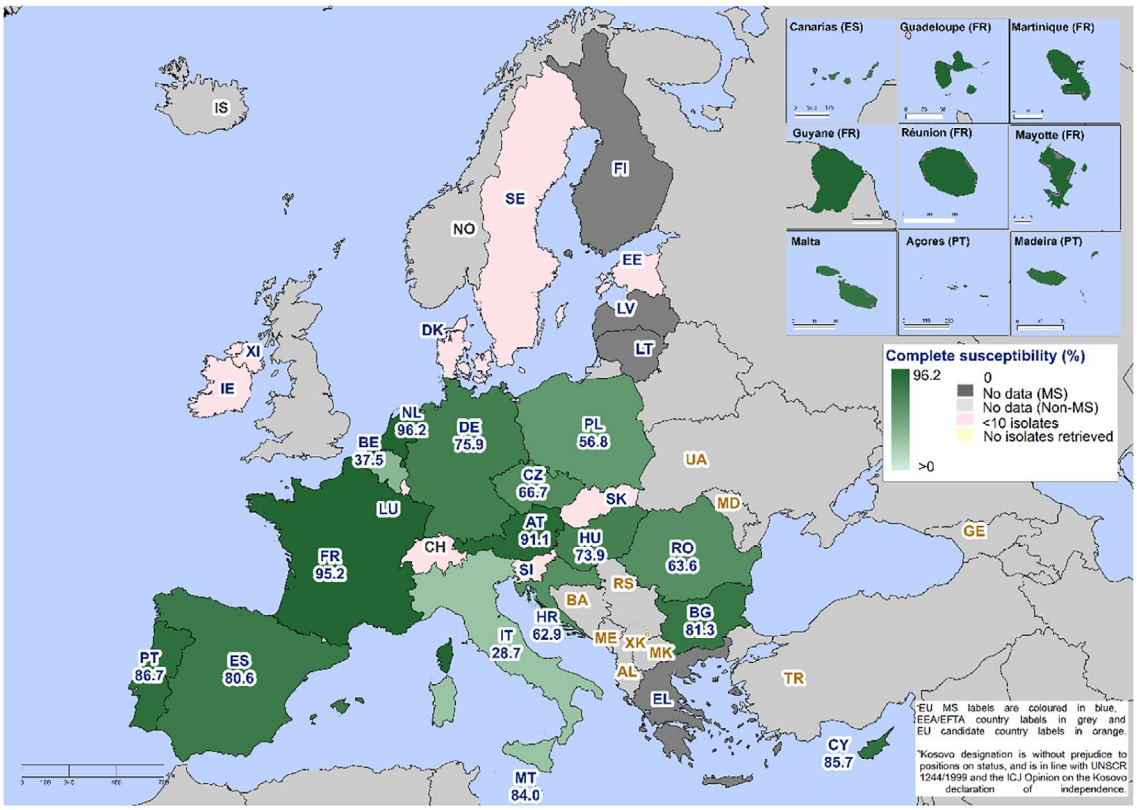


FIGURE 11 (Continued)

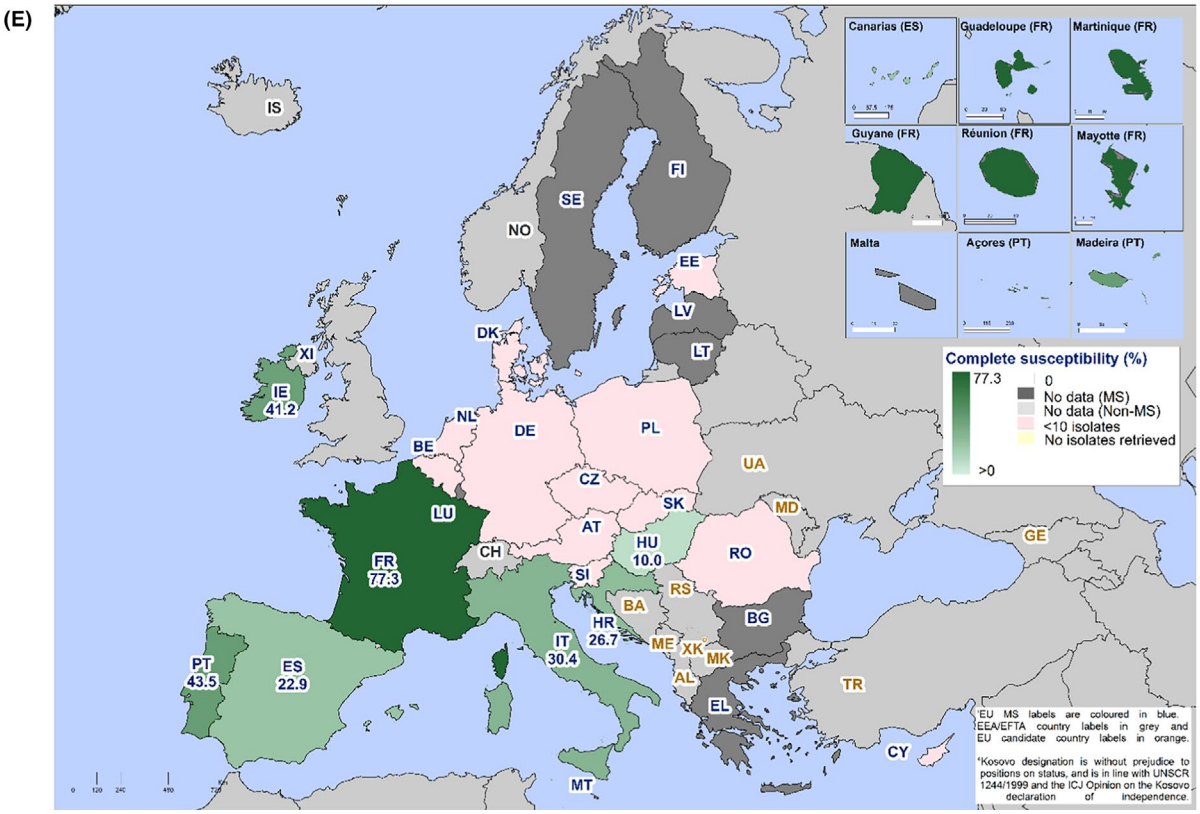


FIGURE 11 Spatial distribution of complete susceptibility to the selected antimicrobials tested among *Salmonella* spp. from (A) fattening pigs, (B) cattle under 1 year of age, (C) broilers, (D) laying hens and (E) fattening turkeys using harmonised ECOFFs. Maps are presented only when at least four Member States reported data. 'No data' refers to the absence of reported data by a MS or non-MS for a given matrix in a given reporting year; 'No isolates retrieved' refers to the MSs or non-MSs that tested for the presence of *Salmonella* spp. but retrieved no isolates in a given matrix in a given year. *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.*

Multidrug resistant serovars

The proportions of isolates that were **completely susceptible** and **multidrug-resistant** among particular *Salmonella* serovars within the different food-producing animal species are presented in Figure 12. In **2023**, the serovars that contributed most to multidrug resistance in *Salmonella* isolates from pigs were **monophasic *S.* Typhimurium** (54.4%), ***S.* Typhimurium** (12.9%) and ***S.* Derby** (10.5%). Similarly, *S.* Typhimurium and its monophasic variants (25.0% each) contributed most to MDR in *Salmonella* isolates from cattle under 1 year of age. In **2022**, ***S.* Infantis** contributed most to MDR in all poultry populations (74.4% for broilers, 32.4% for laying hens and 31.5% for turkeys), with monophasic *S.* Typhimurium (22.1%) and ***S.* Bredeney** (25.1%) the second biggest contributors to MDR in laying hens and turkeys, respectively.

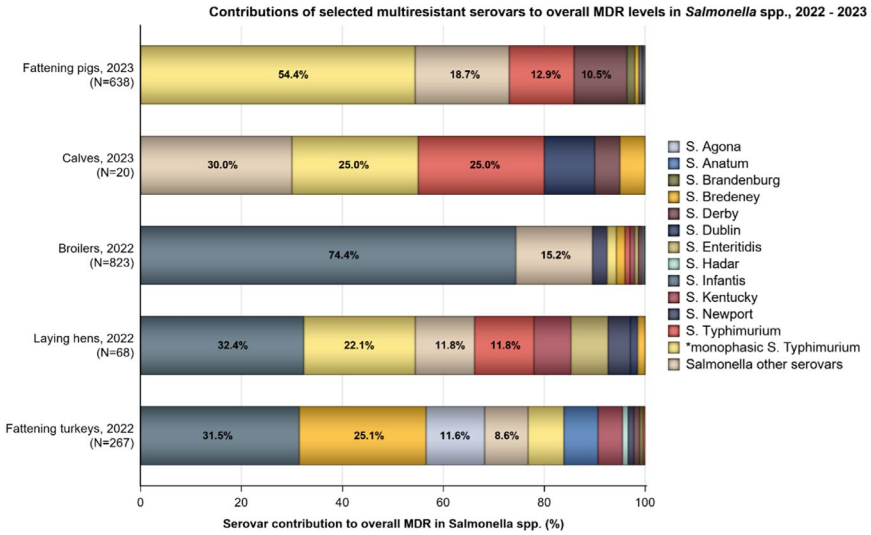


FIGURE 12 Proportions of certain serovars exhibiting multidrug resistance to overall MDR levels in *Salmonella* spp. recovered from each food-producing animal population, for all reporting countries in 2022–2023.
N, total number of multidrug-resistant isolates reported by the MSs; predominant serovars are expressed as a percentage.
*Monophasic *S.* Typhimurium includes all antigenic formulas; *Salmonella* serovars in the legend are listed by alphabetical order.

2.4.6 | Temporal trends

Temporal trends in resistance for countries reporting data for poultry population for at least 3 years over the period 2014–2022 were assessed with logistic regression (Appendix A – Materials and methods). Resistance trends for each selected antimicrobial varied by country and among different serovars (Figure 13; Annex A.3). For *Salmonella* spp. isolates from broilers, among the 18 MSs reporting data for at least 3 years from 2014 to 2022, statistically significant **decreasing trends** in the levels of **ampicillin** and **cefotaxime** resistance were observed in only three MSs, while increasing trends were reported in four and one country, respectively. Decreasing trends in ciprofloxacin and tetracycline resistance occurred in five MSs each, with increasing trends being reported in six and four MSs, respectively. Overall, at the **reporting country group level**, an **increasing trend** in resistance to **ampicillin** and **ciprofloxacin** in broilers can be observed. Similarly, an overall **increasing trend** in resistance to **ciprofloxacin** among *Salmonella* spp. isolates from **laying hens** was registered. Even though resistance levels to **cefotaxime** in turkeys remain low (2.2%), an **increasing trend** can be observed. Additionally, a concomitant **decreasing** trend in resistance to **ciprofloxacin** and **tetracycline** was also registered.

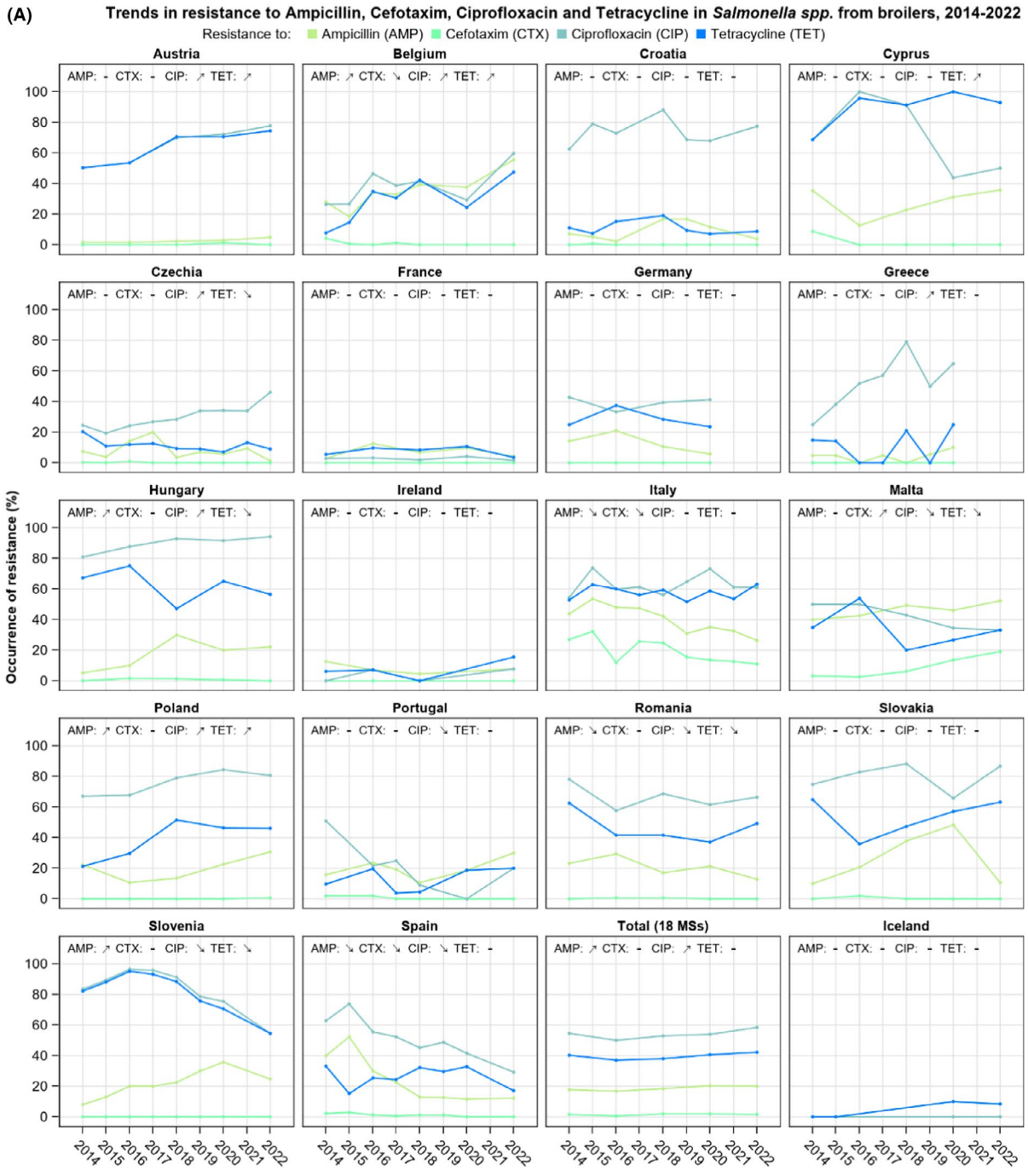


FIGURE 13 (Continued)

FIGURE 13 (Continued)

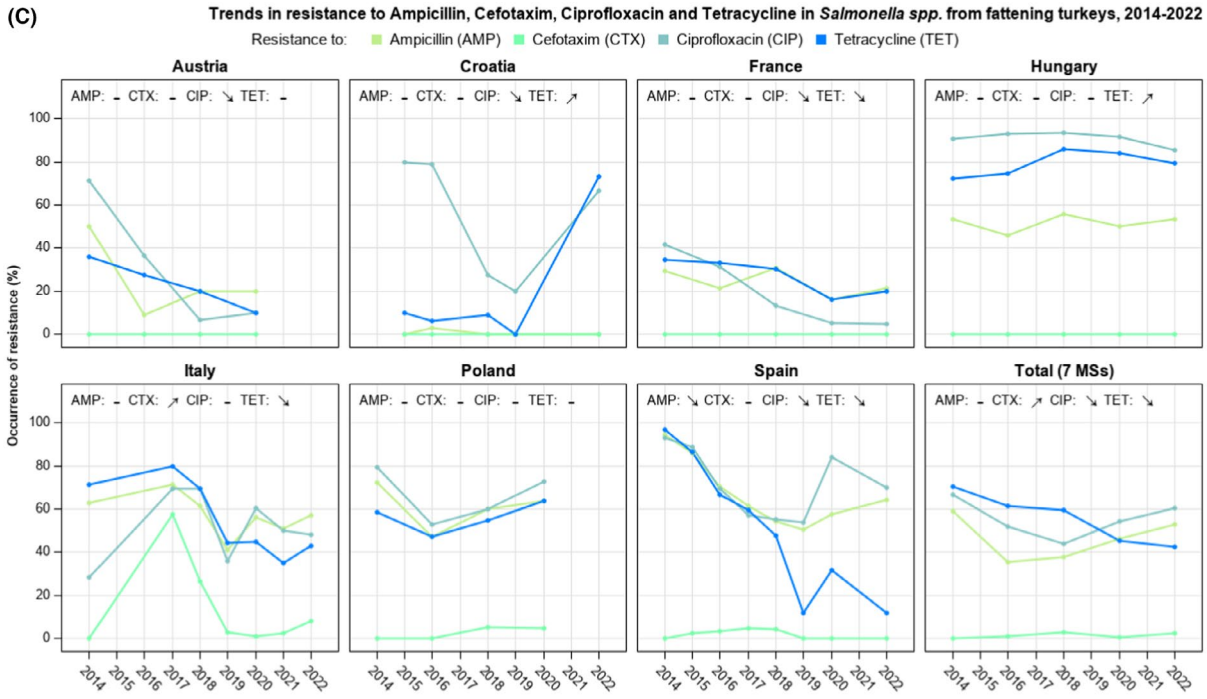


FIGURE 13 Trends in resistance to ampicillin, ciprofloxacin, cefotaxime and tetracycline in *Salmonella* spp. from broilers (A), laying hens (B) and turkeys (C) for all reporting countries, 2014–2022.
Only countries reporting > 10 isolates in a given year and reporting data for at least 3 years over the period 2014–2022 separated by not more than a 1 year gap between them, were included in the analysis. Overall temporal trend (shown in boxes 'Total (X MSs)') is presented only for Member States and for even years when the monitoring of AMR in poultry populations is mandatory in the EU, in accordance with Decision (EU) 2020/1729.

2.4.7 | High-level resistance to ciprofloxacin (CIP) in *Salmonella* spp.

The distribution of ciprofloxacin-resistant isolates displaying levels of microbiological resistance or high-level resistance (isolates with a MIC ≥ 4 mg/L) within each of the food-producing animal species is illustrated in Figure 14.

In **2023**, among the *Salmonella* isolates from **pigs** displaying ciprofloxacin resistance, only 1.4% ($n = 3$, all *S.* Kentucky) exhibited MICs of ≥ 4 mg/L. For **cattle under 1 year of age**, 13 isolates (16.3%; $N = 80$) were resistant to ciprofloxacin, but none exhibited high-level resistance. In **2022**, 4.2% of the isolates from **broilers** ($n = 44$, of which 15 *S.* Kentucky, 14 *S.* Newport and 12 *S.* Infantis), 3.3% from **turkeys**, ($n = 13$, all *S.* Kentucky) and 2.2% from **laying hens** ($n = 5$, of which 3 *S.* Infantis, and 1 each *S.* Kentucky and *S.* Newport) exhibited high-level ciprofloxacin resistance (Figure 14).

The serovars displaying **high-level resistance** to fluoroquinolones are of interest from both the epidemiological and the public/animal health perspectives. ***S.* Kentucky** was the most reported serovar exhibiting high-level ciprofloxacin resistance in pigs, broilers and turkeys. A detailed analysis of the high-level resistance to ciprofloxacin in *S.* Kentucky and other *Salmonella* serovars is presented in Annex A.3.

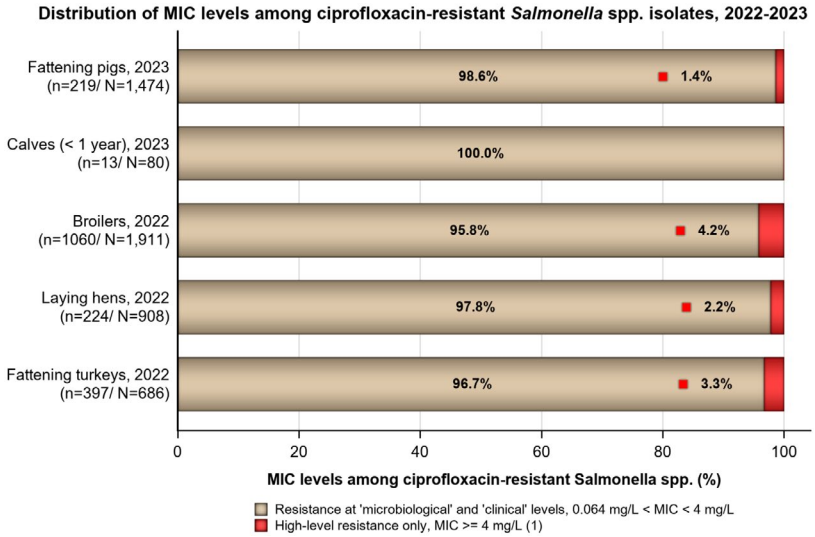


FIGURE 14 Distribution of MIC levels among ciprofloxacin-resistant *Salmonella* spp. isolates from fattening pigs, cattle under 1 year of age (calves), broilers, laying hens and fattening turkeys, for all reporting EU MSs, 2022–2023.
n, number of ciprofloxacin-resistant *Salmonella* isolates; *N*, total number of *Salmonella* spp. isolates reported by MSs.

2.4.8 | Phenotypic characterisation of third-generation cephalosporin and carbapenem resistance in *Salmonella* spp.

According to Decision 2020/1729/EU, any *Salmonella* isolate from food-producing animals or imported broiler and turkey fresh meat showing resistance to cefotaxime or ceftazidime or meropenem (i.e. presumptive ESBL-/AmpC-/CP-producing *Salmonella* isolates) should be further tested with a second panel of harmonised antimicrobial substances to confirm the phenotypic resistance to third-generation cephalosporins or carbapenems.

The proportion of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. at the MS level was generally very low or low in 2022 and 2023 (ranging between 0 and 2.2%, Annex A.2, tables 1, 6, 10, 14, and 18). The occurrence of ESBL-/AmpC-/CP-producing *Salmonella* in a specific animal population may be greatly influenced by the prevalence of different *Salmonella* serovars in each reporting country.

At the reporting MS-group level, the occurrence of presumptive ESBL-/AmpC-producing *Salmonella* in **2023** was 0.8% in pigs and 1.2% in cattle under 1 year of age, and in **2022** it was 2.2% in fattening turkeys, 1.4% in broilers and 0.2% in laying hens. Detailed data per country and matrix are presented in Annex D.2 and D.3. An overview of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. reported in 2022 and 2023 is given in Tables 5 and 6.

In **2023**, WGS data for *Salmonella* spp. was reported by one MS. Germany reported $\boldsymbol{bla_{CTX\text{-}M\text{-}1}}$ from a single monophasic *S.* Typhimurium isolate and $\boldsymbol{bla_{CTX\text{-}M\text{-}1}}$ from a single *S. enterica* subs. *enterica* from pigs. In **2022**, WGS data for *Salmonella* spp. was reported by three MSs (Germany, Italy and the Netherlands). Italy reported $\boldsymbol{bla_{CTX\text{-}M\text{-}1}}$ in 18 *S.* Infantis, one *S.* Blockley, one *S.* Mbandaka and one *S.* Senftenberg isolated from broiler flocks, 15 *S.* Infantis isolates from fattening turkeys and two *S.* Infantis from laying hens. Germany and the Netherlands also reported WGS data for imported meat sampled at BCPs (see specific textbox in the end of Chapter 4).

TABLE 5 Summary of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. from food-producing animals collected within the routine monitoring by serovar, all reporting MSs, 2022–2023.

Year	Matrix	Serovar	*n*	ESBL[a]	AmpC[b]	ESBL + AmpC[c]	Genotype (n_g)
2023	Cattle under 1 year of age (*n* = 1)	*S.* Dublin	1	1	–	–	–
	Fattening pigs (*n* = 12)	*S.* Bredeney	1	1	–		–
		S. Kedougou	7	6	–	1	–
		S. Kentucky	1	1	–	–	–
		S. Typhimurium, monophasic	2	2	–	–	$bla_{CTX\text{-}M\text{-}1}$ (1)
		S. enterica subs. *Enterica**	1	1			$bla_{CTX\text{-}M\text{-}1}$ (1)
2022	Broilers (*n* = 26)	*S.* Infantis	18	18	–	–	$bla_{CTX\text{-}M\text{-}1}$ (18)
		S. Mbandaka	2	2	–	–	$bla_{CTX\text{-}M\text{-}1}$ (1)
		S. Kentucky	4	4	–	–	
		S. Blockley	1	1	–	–	$bla_{CTX\text{-}M\text{-}1}$ (1)
		S. Senftenberg	1	1	–	–	$bla_{CTX\text{-}M\text{-}1}$ (1)
	Fattening turkeys (*n* = 15)	*S.* Infantis	15	15	–	–	$bla_{CTX\text{-}M\text{-}1}$ (15)
	Laying hens (*n* = 2)	*S.* Infantis	2	2	–	–	$bla_{CTX\text{-}M\text{-}1}$ (2)

Abbreviations: AmpC, AmpC beta-lactamase; CP, carbapenemase; ESBL, extended-spectrum betalactamase; *n*, number of presumptive ESBL-/AmpC-/CP-producing isolates; n_g, number of isolates harbouring a specific gene.

[a]All isolates showing clavulanate synergy with CTX or CAZ or both, suggesting ESBL phenotype, or reported presence of ESBL-encoding gene.

[b]Isolates with cefoxitin resistance, suggesting AmpC phenotype, or reported presence of AmpC-encoding gene.

[c]Isolates showing synergy with CTX or CAZ and cefoxitin resistance, suggesting ESBL- and AmpC-enzymes in the same isolates, or both ESBL- and AmpC-encoding genes reported.

**S. enterica* subs. *enterica* rough. Rough strains of *S. enterica* subspecies *enterica* lack the complete O-antigen structure, making them untypable by standard serotyping methods.

2.4.9 | Carbapenem resistance in *Salmonella* spp. from food-producing animals

Carbapenems are authorised for use in humans only and were previously categorised as hpCIAs (WHO, 2024). This antimicrobial class includes meropenem, an antimicrobial agent specified in the antimicrobial panel for monitoring and reporting AMR in *Salmonella* spp. as stipulated in the Commission Implementing Decision (EU) 2020/1729. The use of these antimicrobials in animals has been prohibited since 2022 in accordance with Commission Implementing Regulation (EU) 2022/1255 (Official Journal of the European Union, 2022).

In 2022 and 2023, none of the *Salmonella* isolates recovered from any of the animal populations exhibited microbiological resistance to **meropenem**. This is consistent with data from animal origins in 2021 and 2020.

2.4.10 | Resistance exhibited by dominant *Salmonella* serovars

The detailed reporting of results at the serovar level highlights the contribution of a few serovars to the overall occurrence of resistance when considering aggregated data for *Salmonella* spp. The resistance patterns associated with these different serovars have a marked influence on the overall resistance levels in *Salmonella* spp., as the proportion of completely susceptible and MDR isolates may vary significantly among serovars recovered from each of the studied food-producing animal populations and meat derived thereof. The analysis of AMR at the serovar level is presented in the section below (Comparison of resistance data in *Salmonella* from human and food-producing animals) and Annex A.3.

2.5 | Comparison of resistance data in *Salmonella* from human and food-producing animals

It is of note that the countries reporting data on particular *Salmonella* serovars from human cases are not always the same as those reporting corresponding serovar data within the animal categories. Additionally, the number of isolates reported from human cases and from animal origins varied, both at the MS and MS-group level. Further, *Salmonella* isolates have been derived from different scenarios; human data is from clinical cases while animal data comes from healthy animals. All of these factors may introduce a source of variation in results when comparing overall percentage of resistance to particular antimicrobials and MDR levels among human and animal isolates.

Moreover, the prevalence of particular *Salmonella* serovars within countries and animal populations, and their associated patterns of resistance, may explain some of the observed differences in the occurrence of AMR and MDR. Indeed, the spread of resistant clones and the presence of resistance genes within these clones can be exacerbated by selective pressure from using antimicrobials in human and animal populations.

The panel of nine antimicrobial classes comprising the MDR analysis of human isolates includes ampicillin, cefotaxime/ceftazidime, chloramphenicol, ciprofloxacin/pefloxacin/nalidixic acid, gentamicin, meropenem, sulfonamides/sulfamethoxazole, tetracyclines and trimethoprim/trimethoprim-sulfamethoxazole (co-trimoxazole) and does not include azithromycin and tigecycline. Not all MSs test clinical *Salmonella* isolates for the full panel, particularly when resistance testing is done in clinical laboratories where the antimicrobials tested reflect local or national prescribing habits and or treatment guidelines. For that reason, a smaller dataset is available for the MDR analysis for humans than compared to the full dataset. For animal isolates, the MDR analysis included the same nine antimicrobial classes, as well as tigecycline (glycylcycline class). Tigecycline was addressed together with tetracycline from the MDR analysis of animal isolates to align with the panel analysed from humans. As tigecycline resistance is less common than tetracycline resistance, this procedure has a very limited effect on the MDR outputs and negligible effect on human and animal comparisons.

Levels of CS and MDR

The occurrence of MDR, CS and resistance to one or two antimicrobial classes across humans in 2023 and food-producing animals for 2022–2023 in *Salmonella* spp. isolates and the serovars *S*. Typhimurium and its monophasic variant, *S*. Derby, *S*. Infantis, *S*. Enteritidis and *S*. Kentucky is summarised in Figure 15.

In **2023**, **MDR** was overall moderate (19.1%, *N* = 10,394) among ***Salmonella* spp**. reported in **human cases** in the EU, ranging from low levels among *S*. Enteritidis (3.1%, *N* = 3792) to extremely high among *S*. Kentucky (73.0%, *N* = 189). Monophasic *S*. Typhimurium exhibited very high MDR levels (65.9%, *N* = 1494), while MDR in *S*. Typhimurium and *S*. Infantis was reported at high levels (25.4%, *N* = 826 and 42.4%, *N* = 368, respectively).

MDR was observed at high levels in *Salmonella* spp. recovered from **pigs** (43.3%), **broilers** (43.0%), **turkeys** (38.9%) and **cattle under 1 year of age** (25.0%), while in **laying hens** a markedly lower MDR level (7.5%) was observed.

The highest levels of MDR among all animal populations were observed in monophasic *S*. Typhimurium isolates, followed by *S*. Infantis and *S*. Kentucky. MDR in **monophasic *S*. Typhimurium** and ***S*. Infantis** isolates from **broilers** (58.3%, *N* = 24 and 79.7%, *N* = 768, respectively) and **turkeys** (76.0%, *N* = 25 and 94.4%, *N* = 89, respectively) was reported at very high to extremely high levels, showing generally higher MDR values than those serovars recovered from humans. Similarly, monophasic *S*. Typhimurium isolates recovered from **pigs** (81.1%, *N* = 428) and **cattle under 1 year of age** (83.3%, *N* = 6) exhibited extremely high MDR levels. In contrast, MDR levels in *S*. Infantis from **laying hens** (28.2%, *N* = 78) and pigs (9.8%, *N* = 41) were lower than those in humans.

MDR levels in ***S*. Typhimurium** in humans were lower than in pigs (56.9%, *N* = 144) and cattle under 1 year of age (35.7%, *N* = 14). However, in poultry populations lower MDR levels were reported (ranging from 7.1% in turkeys to 15.7% in broilers).

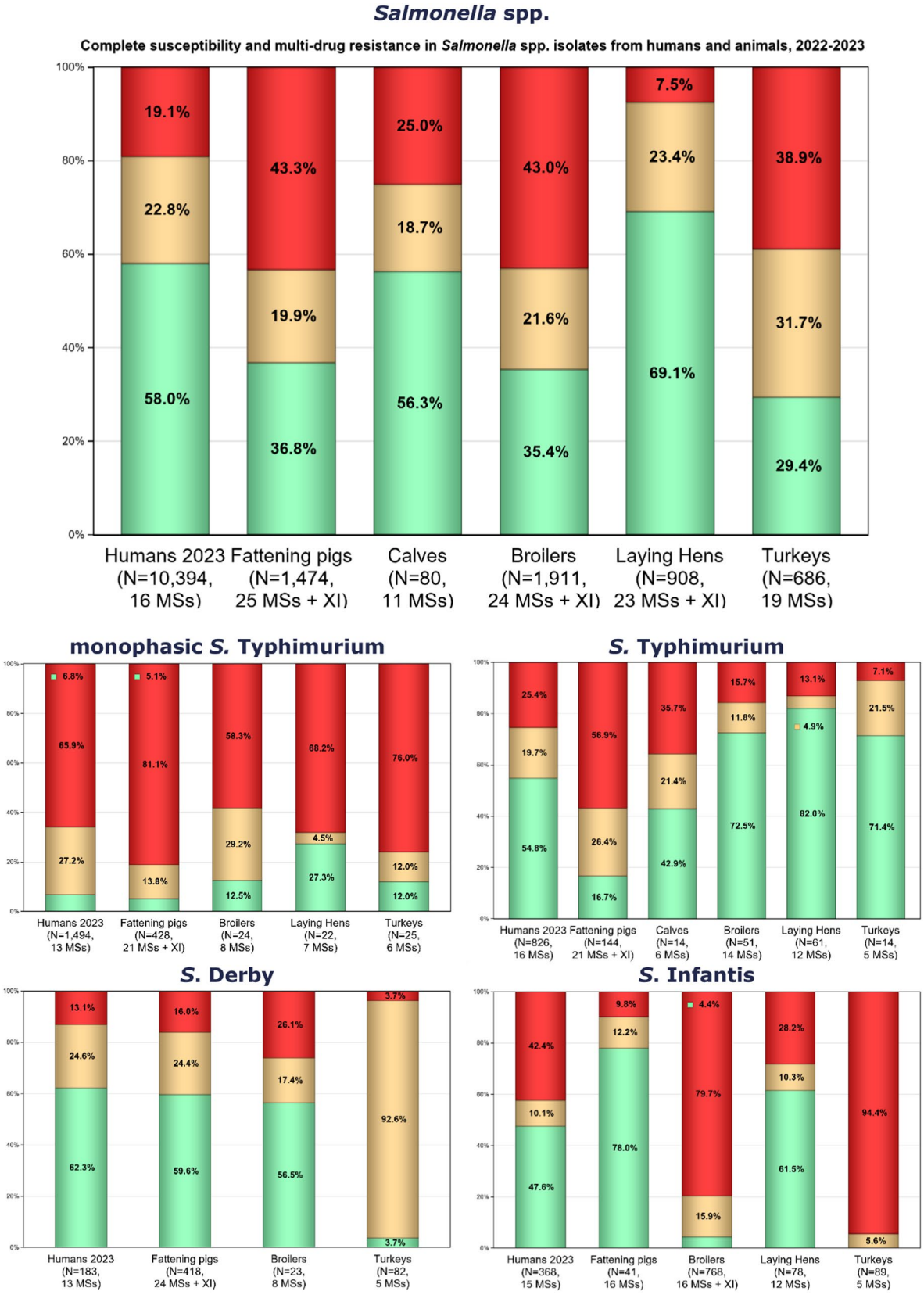
In ***S*. Derby** from humans, lower MDR levels were reported (13.1%, *N* = 183), with similar figures reported in pigs (16.0%, *N* = 418).

In general, ***S*. Enteritidis** from pigs and poultry populations showed a similar occurrence of MDR as in *S*. Enteritidis from humans. Namely, isolates from pigs (4.5%, *N* = 22), broilers (2.7%, *N* = 219) and laying hens (2.0%, *N* = 254) exhibited low MDR levels, while in turkeys (*N* = 11), as well as in cattle under 1 year of age (*N* = 2), no MDR was reported.

Differences in the occurrence of MDR levels in ***S*. Kentucky** from humans and turkeys are evident when compared to the other animal origins. All *S*. Kentucky isolates from turkeys (*N* = 13) were MDR followed by extremely high levels in humans

(73.0%, *N* = 189), while broilers (42.1%, *N* = 19) exhibited high MDR levels, and laying hens, where *S*. Kentucky was most commonly reported (5.3%, *N* = 95) showed markedly lower MDR levels. Two out of the seven *S*. Kentucky isolates from pigs were MDR, while no *S*. Kentucky isolates were found in cattle under 1 year of age.

Overall, in 2023, **CS** in ***Salmonella* spp.** isolates from humans was 58.0%. For animals CS was high for turkeys (29.5%), broilers (35.4%) and pigs (36.8%), and very high in cattle under 1 year of age (56.3%) and in laying hens (69.1%). The highest levels of CS were observed in *S*. Enteritidis isolates from humans and all animal populations, ranging from very high levels observed in broilers (56.6%, *N* = 219), humans (64.4%), laying hens (76.4%, *N* = 254) and pigs (72.7%, *N* = 22) to extremely high levels in turkeys (100% *N* = 11).



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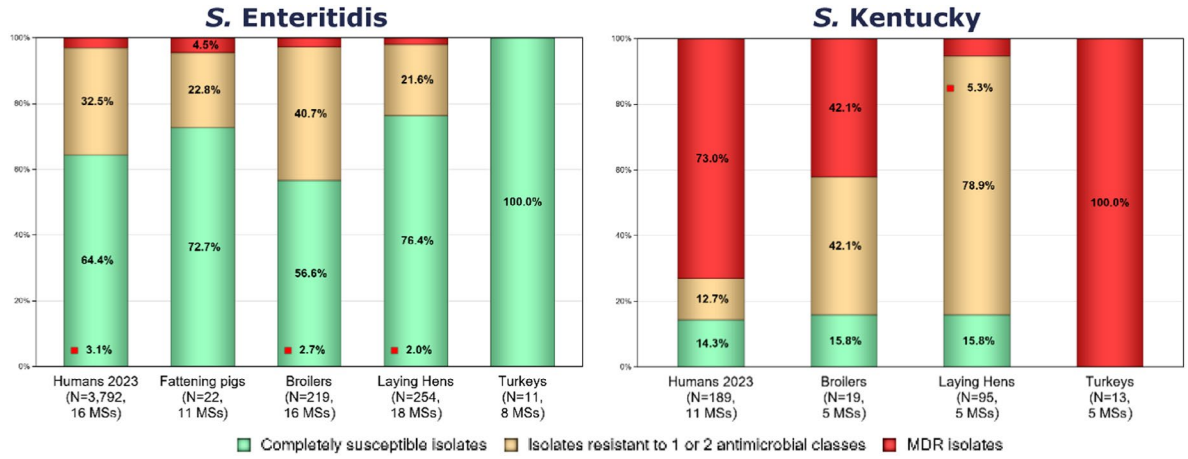


FIGURE 15 Multidrug resistance (MDR) and complete susceptibility (CS) in *Salmonella* spp. and selected serovars recovered from humans in 2023, fattening pigs and cattle under 1 year of age (calves) in 2023, and broiler, turkey and laying hen flocks in 2022, all reporting MSs.
MSs, EU Member States; *N*, total number of isolates belonging to a specific serovar reported by the MSs; XI, United Kingdom (Northern Ireland). The MDR analysis of animal isolates included the following antimicrobials: Amikacin/gentamicin, ampicillin, azithromycin, cefotaxime/ceftazidime, chloramphenicol, ciprofloxacin/nalidixic acid, meropenem, sulfamethoxazole, tetracycline/tigecycline and trimethoprim. MDR and complete susceptibility are expressed as percentages. Only animal populations with > 10 isolates reported for each specific serovar were included in the graph.

Resistance to selected antimicrobials

Overall resistance to **ampicillin**, **sulfonamides** and **tetracyclines** was observed at high levels in ***Salmonella* spp.** isolates from humans in 2023 and ranged from moderate to very high in isolates from food-producing animals, except in laying hens where low levels of resistance were reported (Figure 16). **Ciprofloxacin** resistance was observed at moderate levels in pigs (14.9%) and cattle under 1 year of age (16.3%) in 2023, with high levels reported in humans (21.8%) and laying hens (24.7%) and very high levels in broiler (55.5%) and fattening turkey flocks (57.9%; Figure 16). Overall **cefotaxime** resistance was noted at very low levels in human isolates in 2023 (1.6%) and was seldomly detected in food-producing animals in 2022–2023, except in cattle under 1 year of age (1.2%), and broiler and turkey flocks (1.4% and 2.2%, respectively; Figure 16).

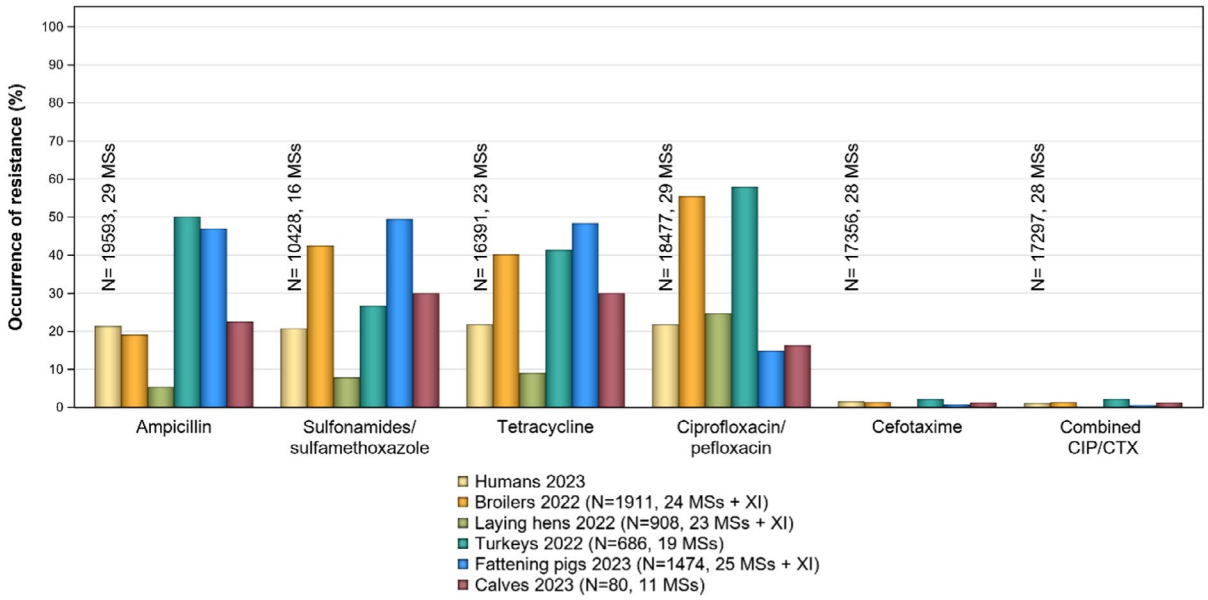


FIGURE 16 Occurrence of resistance to selected antimicrobials in *Salmonella* spp. from humans (2023) and animal populations (2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of *Salmonella* spp. isolates tested; XI, United Kingdom (Northern Ireland).

Resistance to selected antimicrobials by serovar

***S.* Typhimurium** was the second most common *Salmonella* serovar identified in human cases in 2023, with 5946 cases reported in the EU/EEA and the second and third most common serovar identified in cattle under 1 year of age and pigs, respectively. Considering all reporting MSs, the highest levels of resistance in *S.* Typhimurium from humans were observed for ampicillin (30.5%), sulfonamides (31.7%) and tetracycline (23.7%). In pigs ($N = 144$) and cattle under 1 year of age ($N = 14$)

considerably higher resistance levels to ampicillin (70.8% and 35.7%), sulfonamides (68.1% and 57.1%) and tetracycline (55.6% and 57.1%) were observed. On the other hand, isolates from laying hens ($N = 61$) and broilers ($N = 51$) exhibited lower resistance levels to these antimicrobials (Figure 17). Resistance levels to ciprofloxacin were moderate in humans (16.0%), pigs (17.4%), cattle under 1 year of age (14.3%) and broilers (11.8%), and lower in laying hens (3.3%) and turkey isolates (0%). Resistance to cefotaxime was only reported in human isolates (1.4%).

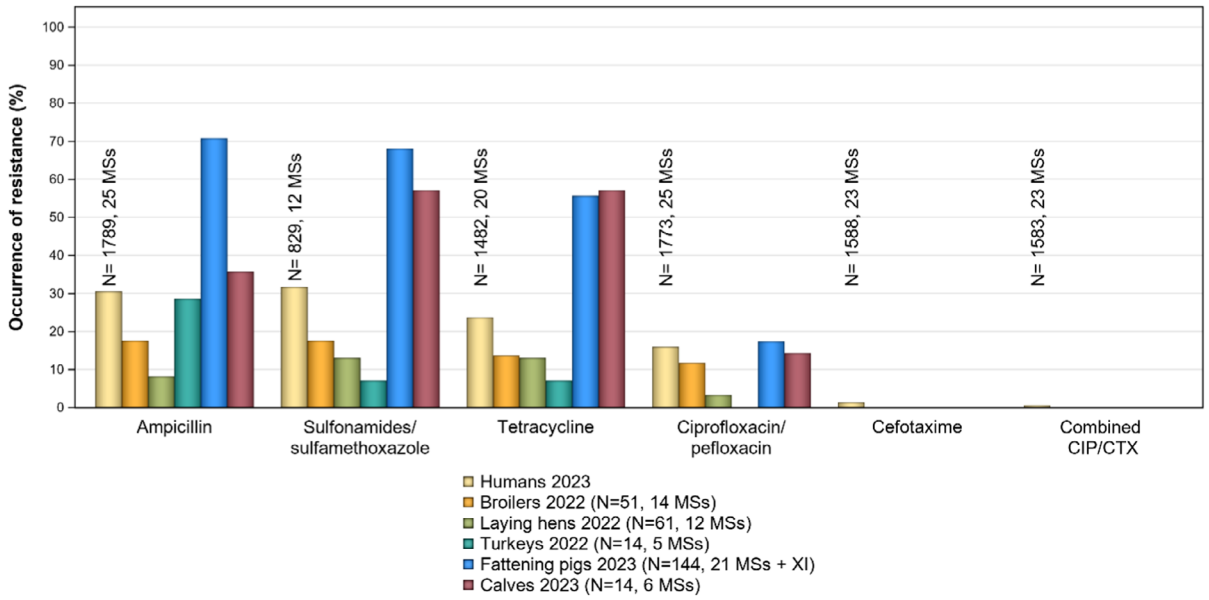


FIGURE 17 Occurrence of resistance to selected antimicrobials in *S.* Typhimurium from humans (2023) and animal populations (≥ 10 isolates in 2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of *S.* Typhimurium isolates tested; XI, United Kingdom (Northern Ireland).

Monophasic *S.* Typhimurium was the third most common serovar reported from human cases in 2023, with 5136 registered cases in the EU/EEA, the most common serovar reported in pigs and the fourth in cattle under 1 year of age and laying hens. Considering all reporting MSs, the highest levels of resistance in monophasic *S.* Typhimurium from humans were observed for ampicillin (86.0%), sulfonamides (92.6%) and tetracycline (78.1%), as were also for isolates from pigs and poultry populations (Figure 18). It is of note, that this serovar shows the highest levels of resistance to antimicrobials commonly used in veterinary medicine compared to the other serovars included in the analysis, ranging from very high (in laying hens) to extremely high levels of resistance (in humans, broilers, turkeys and pigs). Notably, this resistance pattern (together with resistance to streptomycin) is typical of monophasic *S.* Typhimurium (Hopkins et al., 2010).

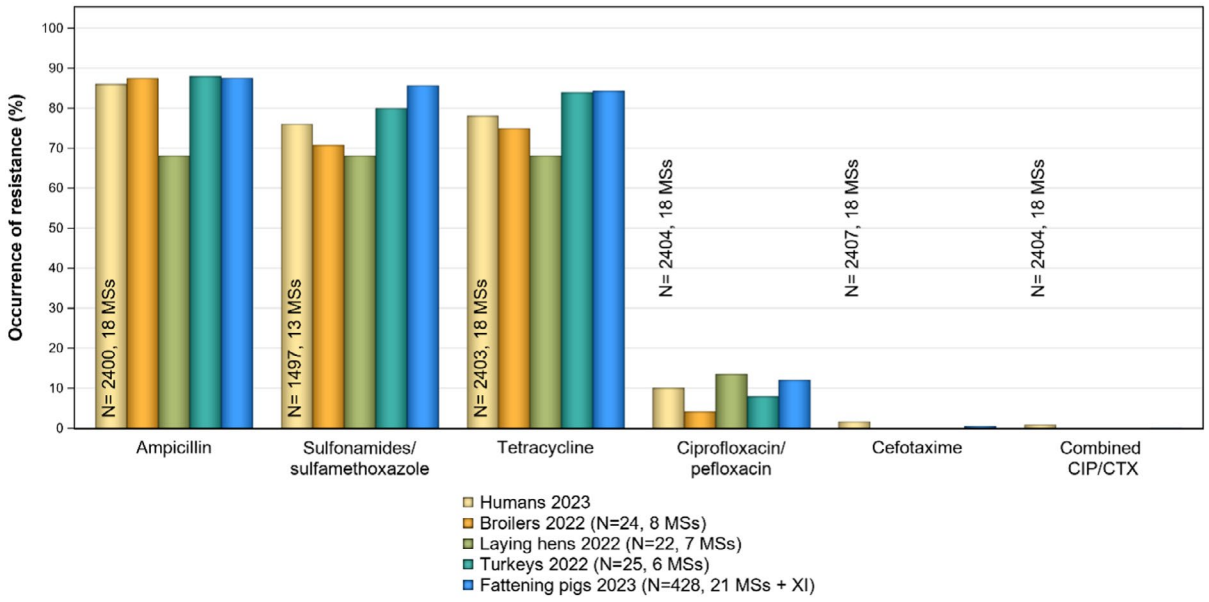


FIGURE 18 Occurrence of resistance to selected antimicrobials in monophasic *S.* Typhimurium from humans (2023) and animal populations (≥ 10 isolates in 2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of monophasic *S.* Typhimurium isolates tested; XI, United Kingdom (Northern Ireland).

***S.* Derby** was the sixth most common serovar reported from human cases in 2023, with 655 cases registered by EU/EEA countries, the second and the third most common serovar reported in pigs and turkeys, respectively. While MDR was not as frequently observed among human/animal *S.* Derby isolates in comparison to *S.* Typhimurium and its monophasic variant (Figure 15), resistance to sulfonamides and tetracycline was relatively common in *S.* Derby isolates from human cases (27.9% and 21.1%, respectively). This was also observed among *S.* Derby isolates from the animal origins (Figure 19). Notably, *S.* Derby from turkeys (*N* = 82) showed extremely high levels of resistance to ampicillin and ciprofloxacin (91.5% each). Most of these isolates (*N* = 75) were reported by a single country (Spain).

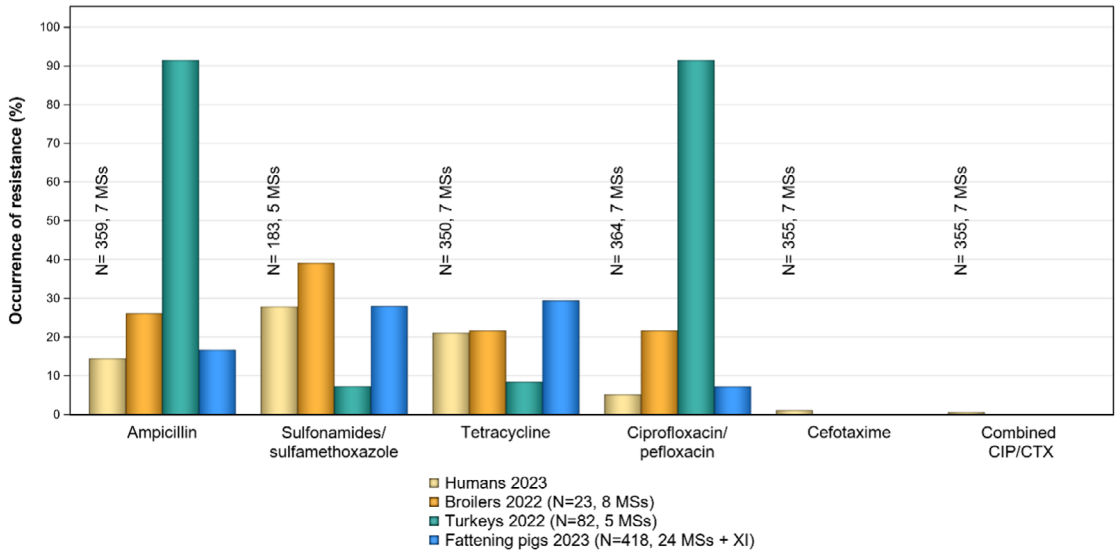


FIGURE 19 Occurrence of resistance to selected antimicrobials in *S.* Derby from humans (2023) and animal populations (≥ 10 isolates in 2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of *S.* Derby isolates tested; XI, United Kingdom (Northern Ireland).

***S.* Infantis** was the fourth most common serovar identified in human cases in 2023, with 1324 cases reported in the EU/EEA, the most common serovar reported in broilers and the second and third in turkeys and laying hens, respectively. Resistance to ciprofloxacin in humans was high (42.4%) with laying hens and pigs exhibiting similar and lower resistance levels (33.3% and 7.3%, respectively). Conversely, extremely high levels were reported in isolates from both broiler (94%) and turkey flocks (100%; Figure 20). Generally, resistance levels to sulfonamides and tetracycline were lowest in pigs and laying hens, reaching high levels in humans (41.3% and 39.7%, respectively), and extremely high levels in broilers (78.8% and 79.2%, respectively) and turkeys (94.4% each; Figure 20). These high resistance levels to fluoroquinolones, sulfonamides and tetracycline in broilers and turkeys align with the circulation of an *S.* Infantis clone harbouring a (pESI)-like megaplasmid, which is prevalent in Europe (Alba et al., 2020).

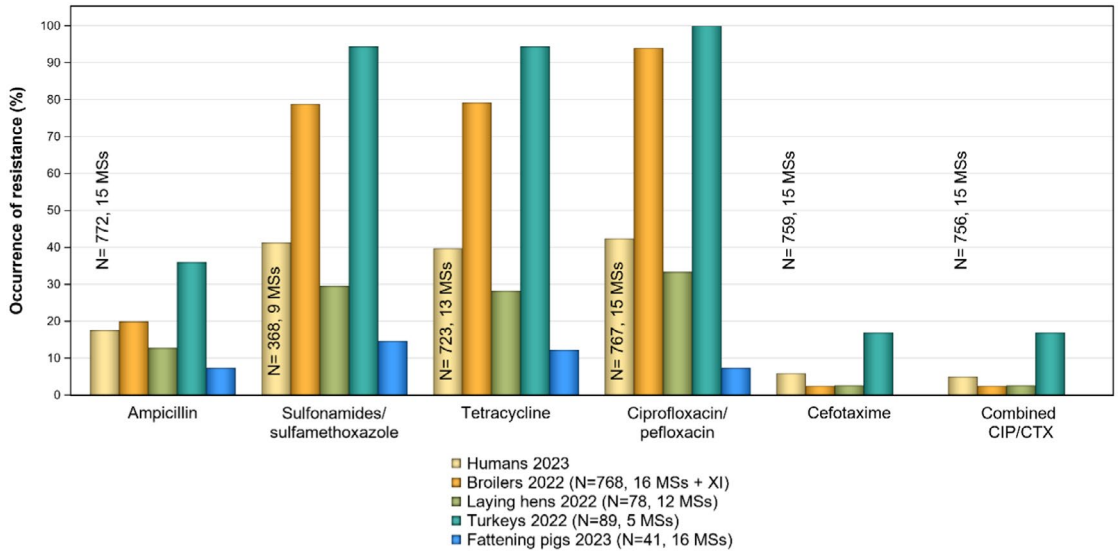


FIGURE 20 Occurrence of resistance to selected antimicrobials in *S.* Infantis from humans (2023) and animal populations (≥ 10 isolates in 2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of *S.* Infantis isolates tested; XI, United Kingdom (Northern Ireland).

***S.* Enteritidis** was the most common *Salmonella* serovar identified in human cases in 2023, with 32,805 cases reported in the EU/EEA. It was also the most common serovar reported in laying hens in 2022. While MDR was uncommon among *S.* Enteritidis isolates from both humans and poultry populations (Figure 15), resistance levels in *S.* Enteritidis from humans were high for ciprofloxacin (30.1%) and colistin (25.7%). Similar resistance levels to these AMs were reported in *S.* Enteritidis isolated from pigs (27.3% and 13.6%, respectively) and laying hens (20.9% and 16.9%, respectively), while in broilers ciprofloxacin resistance was reported at a higher level (Figure 21). Colistin resistance among *S.* Enteritidis is not uncommon, since this serovar belongs to group D salmonellas (serogroup O9) which tends to show decreased intrinsic susceptibility to colistin (Ricci et al., 2020).

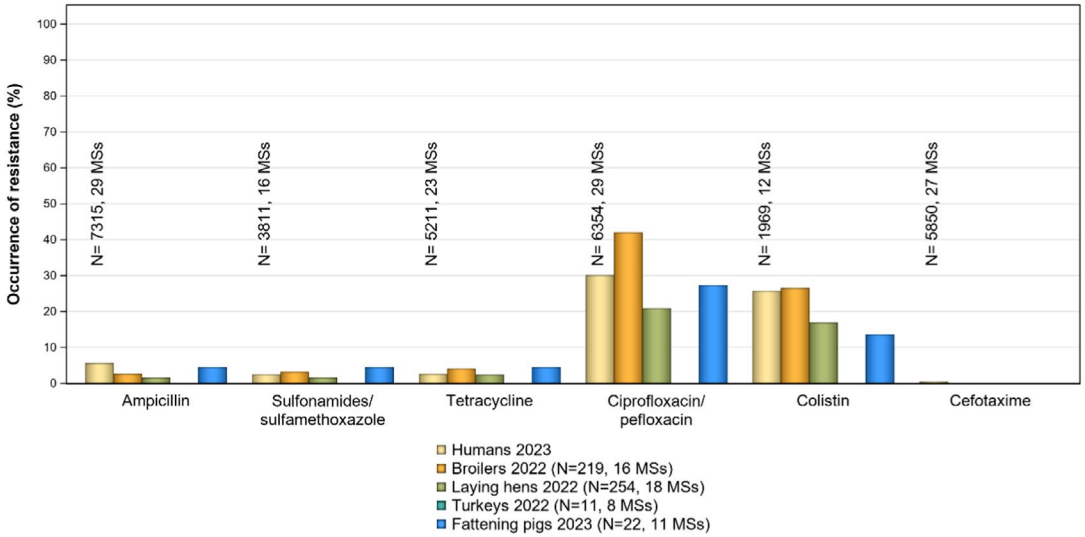


FIGURE 21 Occurrence of resistance to selected antimicrobials in *S.* Enteritidis from humans (2023) and animal populations (≥ 10 isolates in 2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of *S.* Enteritidis isolates tested; XI, United Kingdom (Northern Ireland).

Considering ***S.* Kentucky**, the 11th most reported serovar from human cases in 2023 with 413 cases reported in the EU/EEA, extremely high levels of resistance were noted to ciprofloxacin (80.5%). Resistance levels in poultry populations reached even higher resistance levels to ciprofloxacin (Figure 22). Additionally, *S.* Kentucky accounted for most of the *Salmonella* isolates recovered from poultry exhibiting high-level resistance to ciprofloxacin (Annex A.3). Similarly, *S.* Kentucky isolated from humans in 2023 accounted for 82.1% of the *Salmonella* isolates exhibiting high ciprofloxacin resistance. *S.* Kentucky isolates exhibiting high-level ciprofloxacin resistance are likely to belong to the ST198 clone, which has shown epidemic spread globally (Hawkey et al., 2019; Le Hello et al., 2011, 2013). All the *S.* Kentucky isolates exhibiting high-level ciprofloxacin resistance from poultry in 2022 displayed MICs of ≥ 8 mg/L.

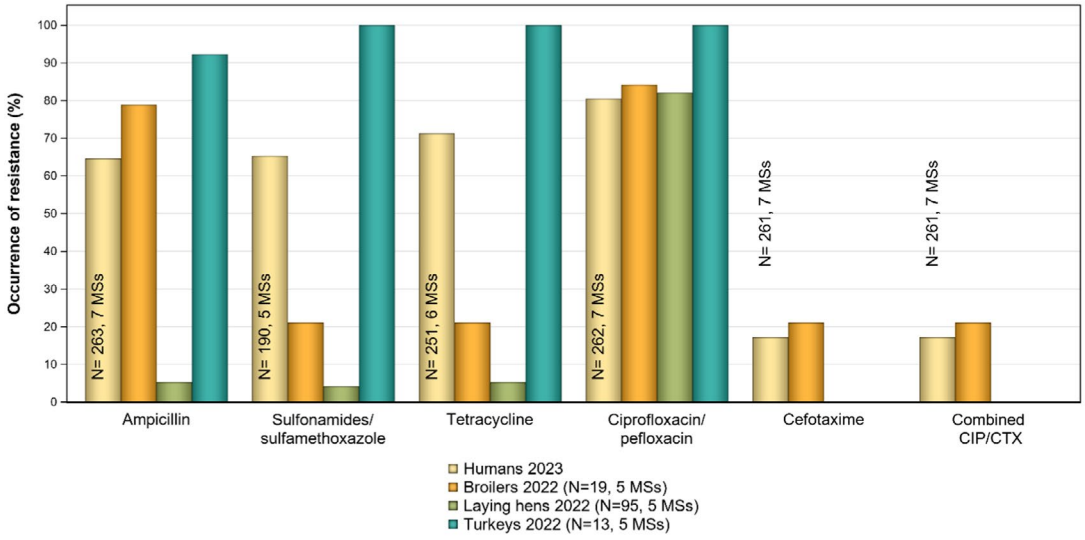


FIGURE 22 Occurrence of resistance to selected antimicrobials in *S.* Kentucky from humans (2023) and animal populations reporting ≥ 10 isolates (2022–2023), all reporting MSs. CIP/CTX, combined resistance to ciprofloxacin and cefotaxime; MSs, EU Member States; *N*, total number of *S.* Kentucky isolates tested; XI, United Kingdom (Northern Ireland).

Presumptive ESBL-/AmpC-CP-producing* Salmonella *spp.

The overall proportion of presumptive ESBL-/AmpC-producing *Salmonella* spp. at MS level was generally very low or low in 2022 and 2023 among all food-producing animal populations and very low in isolates from human cases (Table 6). In 2022 and 2023, no *Salmonella* spp. isolates recovered from animal origins were microbiologically resistant to meropenem. Similarly to 2022, meropenem resistance was in 2023 reported in *Salmonella* spp. isolates from humans (< 0.1%, Table 6), with six countries reporting one resistant isolate each.

TABLE 6 Summary of the presumptive ESBL-, AmpC- or CP-producing *Salmonella* spp. from humans and food-producing animals, subjected to supplementary testing (panel 2) or whole genome sequencing, EU MSs, 2022–2023.

Matrix	ESBL and/or AmpC[a] *n* (% *R*)	ESBL[b] *n* (% *R*)	AmpC[c] *n* (% *R*)	ESBL + AmpC[d] *n* (% *R*)	CP[e] *n* (% *R*)
Humans 2023 (*N* = 18,459, 27 MSs)	162 (0.9)	141 (0.8)	21 (0.1)	0 (0)	6 (< 0.1)
Humans 2022 (*N* = 14,058, 26 MSs)	150 (1.1)	122 (0.9)	24 (0.2)	4 (< 0.1)	4 (< 0.1)
Fattening pigs, 2023 (*N* = 1474, 25 MSs + XI)	12 (0.8)	11 (0.7)	0 (0)	1 (0.1)	0 (0)
Calves, 2023 (*N* = 80, 11 MSs)	1 (1.3)	1 (1.3)	0 (0)	0 (0)	0 (0)
Broilers, 2022 (*N* = 1911, 24 MSs + XI)	26 (1.4)	26 (1.4)	0 (0)	0 (0)	0 (0)
Fattening turkeys, 2022 (*N* = 686, 19 MSs)	15 (2.2)	15 (2.2)	0 (0)	0 (0)	0 (0)
Laying hens, 2022 (*N* = 908, 23 MSs + XI)	2 (0.2)	2 (0.2)	0 (0)	0 (0)	0 (0)

Abbreviations: % *R*, percentage of cephalosporin-resistant isolates presenting a presumptive phenotype; AmpC, AmpC beta lactamase; CP, carbapenemase; ESBL, extended-spectrum beta- lactamase; MSs, EU Member States; *n*, number of presumptive ESBL- and/or AmpC–/ CP-producing isolates; *N*, total number of isolates tested; XI, United Kingdom (Northern Ireland).

[a]According to EUCAST guidelines (EUCAST, 2017), only isolates showing MIC > 1 mg/L for CTX and/or CAZ or reported presence of ESBL-/AmpC-encoding gene were considered (see Appendix A – Materials and methods).

[b]All isolates showing clavulanate synergy with CTX or CAZ or both, suggesting ESBL phenotype or reported presence of ESBL-encoding gene.

[c]Isolates with cefoxitin resistance, suggesting AmpC phenotype, or reported presence of AmpC-encoding gene.

[d]Isolates showing synergy with CTX or CAZ and cefoxitin resistance, suggesting ESBL- and AmpC- enzymes in the same isolates, or both ESBL- and AmpC-encoding genes reported.

[e]Isolates with meropenem resistance or CP-encoding gene reported.

2.6 | Discussion

The continuous monitoring of AMR in *Salmonella* is essential to identify new and emerging resistance mechanisms in both human and animal populations. The harmonised monitoring of *Salmonella* from food-producing animals and imported fresh meat using phenotypic antimicrobial susceptibility testing aims to identify emerging risks. For instance, this monitoring helped identify MDR *S.* Kentucky with high resistance to fluoroquinolones and *S.* Infantis isolates exhibiting combined resistance to extended-spectrum cephalosporins, fluoroquinolones and colistin (EFSA, 2019).

In 2022 and 2023, the detection of resistant *Salmonella* isolates varied markedly based on their animal origins, serovars and reporting countries. These factors may introduce a source of variability in the results when considering data from all reporting countries. Thus, results should be interpreted cautiously.

Regarding data from humans, resistance predicted from WGS has been an accepted test method since 2019 and for 2023, four MSs used whole genome sequences as their official *Salmonella* AMR data submission. For two of them, this was facilitated through the ECDC sequencing support project of *Salmonella* and *Campylobacter* AMR in 2023–2024. WGS is increasingly recognised as a powerful tool for epidemiological surveillance of AMR in the 'One Health' context (WHO, 2020). It complements phenotypic methods by providing information on molecular determinants and mechanisms, genetic factors that facilitate transmission and geographical distributions of resistance genes. Several studies have reported a high concordance rate between WGS data and phenotypic data for *Salmonella* (Hendriksen et al., 2019; McDermott et al., 2016).

Occurrence of resistance to commonly used antimicrobials in veterinary medicine

In 2023, *Salmonella* isolates recovered from pigs and cattle under 1 year of age exhibited high resistance to **tetracyclines**, **sulfonamides** and **ampicillin**. **Monophasic *S.* Typhimurium** continues to be the leading serovar registering the highest resistance levels to these antimicrobials, a characteristic of the most frequent clone (ST34) circulating within the EU (Sun et al., 2020). In 2022, high levels of resistance to tetracycline and sulfonamides were also reported in broiler and turkey flocks, with laying hen flocks displaying comparatively lower resistance levels to both antimicrobials. Resistance to ampicillin was reported at lower levels in broiler and laying hen flocks. In contrast, turkey flocks showed very high resistance to ampicillin. For the first time, the presence of **temporal trends** at the RC level in *Salmonella* spp. and selected serovars from poultry populations were analysed. A statistically significant **increasing** trend in **ampicillin** resistance was observed in *Salmonella* spp. from broilers, while a **decreasing** trend in **tetracycline** resistance was seen in turkey flocks. Interestingly, declining trends in tetracycline resistance in isolates from humans were also registered. However, these were mostly led by declining resistance levels in *S.* Typhimurium, which is most prevalent in pigs and cattle under 1 year of age. Due to the

recent implementation of Commission Implementing Decision 2020/1729, limited number of data points from pigs and cattle under 1 year of age does not enable to assess the statistical significance of temporal trends, thus impeding a direct comparison. Similarly, decreasing trends in ampicillin resistance were also registered in *Salmonella* from humans led by a reduction in resistance levels in *S*. Typhimurium.

Occurrence of resistance to third-generation cephalosporins and fluoroquinolones

Third-generation cephalosporins and fluoroquinolones are categorised as hpCIAs because they are commonly used to treat gastrointestinal infections, including *Salmonella* infections, in humans (WHO, 2024). This sets the rationale for monitoring combined resistance to these antimicrobial classes within food-producing animals.

Resistance to **third-generation cephalosporins, cefotaxime and ceftazidime** in *Salmonella* isolates recovered from food-producing animals was either rare or detected at very low/low levels in most of the reporting MSs in 2022 and 2023. In *Salmonella* spp. isolated from human cases in 2023, resistance levels to cefotaxime and ceftazidime were also low. Temporal trends for **cefotaxime resistance** in turkey flocks showed a statistically significant **increase**, mostly due to cefotaxime-resistant *S*. Infantis from Italy. While in human *Salmonella* isolates, seven and four countries registered significantly decreasing and increasing trends, respectively, attributed across several serovars.

A very small number of isolates from food-producing animals were determined to be **presumptive ESBL-, AmpC- or ESBL + AmpC-producers**. The highest occurrence was observed in turkey flocks (2.2%), followed by broilers (1.4%), cattle under 1 year of age (1.3%), pigs (0.8%) and laying hen flocks (0.2%). Germany was the only MS submitting WGS data in 2023, while three MSs (Germany, Italy and the Netherlands) submitted it in 2022.

Among 2023 data, eleven ESBL phenotypes from pigs (six *S*. Kedougou), one from cattle under 1 year of age (*S*. Dublin) and one ESBL+AmpC phenotype from pigs (*S*. Kedougou) were reported; among poultry populations in **2022**, only ESBL phenotypes were reported. Germany reported a monophasic *S*. Typhimurium and a *S. enterica* subsp. *enterica* isolates, each harbouring $\boldsymbol{bla_{\text{CTX-M-1}}}$. Germany also reported six ESBL-producing monophasic *S*. Typhimurium isolates from humans of which five harboured $bla_{\text{CTX-M-1}}$ and one $bla_{\text{CTX-M-55}}$. ESBL-producing monophasic *S*. Typhimurium with ST34 has been reported previously in Germany, where this clone acquired different IncI1 plasmids harbouring $bla_{\text{CTX-M-1}}$ gene within different food-producing animals (mainly swine, but also cattle and sheep) (Rodríguez et al., 2012; Sun et al., 2020). Several other countries reported ESBL phenotypes in monophasic *S*. Typhimurium from humans where $bla_{\text{CTX-M-1}}$ was the most frequently identified ESBL gene. $bla_{\text{CTX-M-1}}$ was overall the most common ESBL gene found in *Salmonella* from humans in 2023, with 46 positive isolates in total – 17 in monophasic *S*. Typhimurium, 17 in *S*. Infantis and the remaining 12 in 9 different serovars. However, of the 28 *Salmonella* serovars exhibiting ESBL phenotypes, the highest proportions were observed in isolates of *S*. Schwarzengrund (13.6%), *S*. Anatum (9.8%), *S*. Kentucky (8.4%), *S*. Heidelberg (7.1%), *S*. Muenster (4.0%) and *S*. Infantis (3.5%).

In 2022, most ESBL phenotypes were associated with *S*. Infantis, suggesting the possible clonal expansion of this serovar, with all isolates harbouring $\boldsymbol{bla_{\text{CTX-M-1}}}$. In a recent Italian study, *S*. Infantis strains harbouring pESI-like plasmids, carrying $bla_{\text{CTX-M-1}}$ genes were reported, and core genome multilocus sequence typing (cgMLST) and single-nucleotide polymorphisms (SNP)-based analysis revealed the presence of one main cluster composed of strains isolated from the environment, animals, food and humans (Russo et al., 2024), suggesting clonal spread among animal populations and humans.

Moreover, both in 2022 and 2023, no *Salmonella* spp. isolates recovered from animal/meat origins were microbiologically resistant to **meropenem**. Similarly to 2022, six *Salmonella* spp. isolates from humans resistant to meropenem were recovered in several countries in 2023 however, at MS level the occurrence of meropenem resistance was < 0.1%. Four of the six meropenem-resistant isolates carried $bla_{\text{OXA-48}}$, one carried $bla_{\text{NDM-1}}$ and one had not been genotyped.

Ciprofloxacin/nalidixic acid resistance was reported at moderate levels in pigs, with *S*. Rissen, *S*. Typhimurium and monophasic *S*. Typhimurium showing the highest resistance levels. Fluoroquinolone resistance in cattle under 1 year of age was also found at moderate levels. Among *Salmonella* isolates recovered from broiler, *S*. Infantis exhibited the highest levels of resistance to ciprofloxacin and nalidixic acid whereas, in isolates from laying hens, this was seen in *S*. Kentucky. In the case of turkeys, both serovars presented the highest levels of resistance to these antimicrobials. This likely reflects the spread of resistant clones belonging to these serovars. From human data reported in 2023, *S*. Infantis and *S*. Kentucky also showed the highest resistance to these substances. Resistance to ciprofloxacin/nalidixic acid, sulfamethoxazole and tetracycline are typical of a clone of *S*. Infantis prevalent in Europe in broilers (Alba et al., 2020). Ciprofloxacin resistance was observed at very similar levels to nalidixic acid resistance in food-producing animals. However, *Salmonella* isolates exhibiting ciprofloxacin resistance and nalidixic acid susceptibility were most frequently found in turkeys, indicating the occurrence of plasmid-mediated quinolone resistance (PMQR) mechanisms. Several isolates from pigs were also reported, with most originating from Spain.

In both reporting years, the overall **combined resistance to ciprofloxacin and cefotaxime** in *Salmonella* isolates from human cases (1.1%) and food-producing animals ranged from very low to low, with most countries reporting no resistant isolates. However, higher combined resistance was reported in *S*. Infantis (5.0%) and *S*. Kentucky (17.2%) isolated from human cases in 2023, with several countries reporting moderate to high levels of combined resistance in *S*. Kentucky isolates. ESBL was reported in 8.4% of *S*. Kentucky from humans in 2023 however, an additional 23 isolates were resistant to cefotaxime and/or ceftazidime but not further tested. From food-producing animals, moderate and high levels of combined resistance were found in pigs (14.3%, $N = 7$) and broiler flocks (21.1%, $N = 19$) however, this was not seen in laying hens or turkey flocks with both poultry populations not reporting any combined resistance in *S*. Kentucky isolates. *S*. Kentucky

multilocus sequence type (ST) 198 is a globally disseminated clone, capable of rapid spread and accumulation of resistance determinants to last-line antimicrobials. Acquisition of *Salmonella* genomic island 1 (SGI1) and plasmids, as well as mutations in the Quinolone Resistance-determining regions (QRDR), were the only genetic features found to explain the global epidemiological success of the MDR *S*. Kentucky ST198 lineage which is highly resistant to ciprofloxacin (Coipan et al., 2020). In the WGS data submitted to ECDC from human isolates for 2023, no less than four mutations in the QRDR were identified in all *S*. Kentucky ST198 and one isolate had even five mutations.

Regarding *S*. Infantis isolates from humans, particularly high proportions of combined resistance were observed among *S*. Infantis isolates from Italy (a comparable observation for Italy was made in 2020–2022). This is due to a high carriage of ESBL in *S*. Infantis in Italy, where $bla_{\text{CTX-M-1}}$ was identified in all 13 isolates with an ESBL-phenotype in 2023. Similarly, Italy reported a moderate level of combined microbiological resistance to ciprofloxacin and cefotaxime (17.5%) in broiler flocks and it was the only MS reporting a high level of combined resistance (34.9%) in fattening turkeys for *S*. Infantis, where an increasing trend was observed. Several scientific publications in Europe highlight the involvement of plasmids, which appear to be responsible for resistance in many European MDR *S*. Infantis isolates (Alba et al., 2020; Alvarez et al., 2023; Franco et al., 2015; Nógrády et al., 2012).

High-level resistance to ciprofloxacin

In **2023**, high-level resistance to ciprofloxacin (MIC ≥ 4 mg/L) was detected in three *S*. Kentucky isolates from pig samples from Malta, and not detected in cattle under 1 year of age. In **2022**, high-level resistance to ciprofloxacin was observed in several isolates from poultry. While many serovars (including Newport and Infantis) exhibited high-level resistance among poultry, *S*. Kentucky was the most frequently reported. The same finding was also noted among isolates from human cases in 2023, where high-level ciprofloxacin resistance was most commonly found in *S*. Kentucky (in 83.7% of *S*. Kentucky isolates) among the 12 countries reporting MIC data. *S*. Kentucky isolates exhibiting high-level ciprofloxacin resistance are likely to belong to the above-mentioned ST198 clone, as discussed above. Sequence typing is not performed on isolates from food-producing animals, and further studies are needed to conclude on the presence of the ST198 clone. Two of the three *S*. Kentucky isolates showing MICs of ciprofloxacin ≥ 4 mg/L were MDR, with AMR profiles AMP-CTX-CAZ-CIP-NAL and CIP-NAL-SUL-TET. MDR was also common in poultry isolates, primarily showing resistance to ampicillin, gentamicin, nalidixic acid, sulfamethoxazole and tetracycline.

Occurrence of resistance to other highest priority critically important antimicrobials (hpCIAs) and last resort antimicrobials

Tigecycline resistance in pigs was mostly found in *S*. Rissen and monophasic *S*. Typhimurium, while in poultry populations in *S*. Infantis. In 2023, *S*. Infantis and *S*. Kentucky were the serovars exhibiting the highest tigecycline resistance in humans. Multidrug resistance was a common feature among tigecycline-resistant *Salmonella* serovars from animal populations. Determining the susceptibility to tigecycline is not straightforward as this compound can be inactivated by oxidation and exposure to light, which may lead to falsely elevated MIC values. In addition, upregulation of normal cell pathways or processes may also contribute to elevated tigecycline MIC values at levels above the ECOFF in Enterobacteriaceae (He et al., 2016). Two transferable plasmid-mediated tigecycline resistance genes, *tet(X3)* and *tet(X4)*, conferring higher levels of tigecycline resistance (MICs of ≥ 16 mg/L), have been reported in Enterobacteriaceae from animals and meat (chicken and pork) in China (Bai et al., 2019; He et al., 2019). Of note, *tet*(X4) has been identified for the first time in *S*. Rissen (ST469) from pork in China (Zhang et al., 2024). The authors found that the *tet*(X4) was located in the IncFIA(HI1)-IncHI1A-IncHI1B(R27) hybrid plasmid with structure *abh-tet*(X4)-ISCR2, suggesting an increasing transmission risk of the mobile tigecycline resistance gene *tet*(X4) beyond *E. coli* (Zhang et al., 2024). So far, neither *tet*(X3) nor *tet*(X4) have been reported in *Salmonella* spp. from humans in the European AMR monitoring.

As in previous years, resistance to **colistin** (MIC > 2 mg/L) was predominantly observed in *S*. Enteritidis and other group D salmonellas (serogroup O:9) from humans and food-producing animals. Group D salmonellas tend to exhibit intrinsic decreased susceptibility to colistin without having known acquired or mutational colistin resistance mechanisms. Phenotypical testing for colistin is complicated and EUCAST recommends performing testing using microbroth dilution or specific PCR. For that reason, colistin results from humans are only available from 12 of the 27 reporting MSs. EUCAST has temporarily removed the *Salmonella*-specific ECOFF until more comprehensive data is available, and a tentative ECOFF has been suggested for *S*. Dublin where a MIC of ≤ 16 mg/L would be considered wild type (EUCAST, 2023). The tentative ECOFF would facilitate the identification of isolates with acquired resistance, while further molecular characterisation of colistin-resistant isolates obtained from the EU AMR monitoring to determine the underlying genetic mechanisms would assist in identifying the emergence and dissemination of colistin-resistant *Salmonella* clones in human and animal populations. Among the four countries reporting sequences for AMR in humans in 2023, only 1 of 835 isolates (0.1%) carried resistance mechanisms to colistin –a mutation in the PmrAB system.

Amikacin and gentamicin are aminoglycosides and considered CIAs for human medicine. In both monitoring years, resistance to amikacin was very low for all animal populations, except for cattle under 1 year of age for which no resistance was reported in 2022. Resistance to gentamicin was mostly found at very low to low levels.

From the monitoring of food-producing animals in 2023 and 2022, the overall resistance levels to **azithromycin** ranged from zero, with no resistance observed in *Salmonella* isolates from laying hen flocks, very low levels in turkeys (0.4%) and

broilers (0.5%), and low levels in cattle under 1 year of age (2.5%) and pigs (3.1%). A small increase in azithromycin resistance was observed in isolates from pigs (1.9% in 2021).

Multidrug resistance (MDR)

In 2022 and 2023, MDR was found at high levels among *Salmonella* spp. from food-producing animals, except in laying hens (7.5%). MDR levels varied among serovars which may exhibit particular MDR patterns, so the relative contribution of individual serovars within the different animal populations and between countries should be considered when comparisons are made. For example, the overall lower level of MDR among isolates from laying hens most likely reflects the predominance of *S*. Enteritidis, which accounted for 28.0% of *Salmonella* isolates from laying hens reported by MSs, and where 76.4% of *S*. Enteritidis isolates exhibited complete susceptibility. In contrast, the high MDR levels observed in pigs reflect the high occurrence of monophasic *S*. Typhimurium (29.0%) and their extremely high MDR level (79.7%).

In *Salmonella* spp. strains from human cases, MDR was detected in 19.1% of the isolates. Generally, MDR levels showed good concordance in the different serovars isolated from humans and food-producing animals. Apparent differences in MDR levels in *S*. Kentucky between human and animal populations were observed. *S*. Kentucky isolates were most prevalent in laying hens, compared to other animal populations, where MDR was reported at low levels; however, all *S*. Kentucky isolates from turkeys ($N = 13$) were MDR, which suggests a higher risk can be attributed to this source. Although European studies where genotypic AMR among human and animal populations are lacking, a recent US study concluded that MDR and fluoroquinolone-resistant ST198 infections in humans may be linked to the consumption of food products that are imported or consumed while travelling (Tate et al., 2022). Similar studies at the EU level are needed to elucidate these differences.

Zoonotic *Salmonella* infections in humans tend to be self-limiting rarely leading to clinical conditions where patients should receive antibiotic treatment. In 2023, 8% of the *Salmonella* isolates tested for AMR were from either blood, urine, pus or spinal fluid, indicating that the patients had infections that needed antibiotic treatment. While this is likely a somewhat higher proportion than among all salmonellosis cases (bias introduced in the referral of isolates from primary laboratories to the Public Health National Reference Laboratories), it would still amount to several thousands of patients in the EU/EEA annually. Continuous monitoring of antibiotic resistance, particularly to antimicrobials used for critically ill patients such as the (hp)CIAs, is therefore pivotal. Additionally, monitoring resistance levels in *Salmonella* from food-producing animals and derived meat allows the assessment and evaluation of the progress in the efforts to tackle AMR within the EU.

3 | ANTIMICROBIAL RESISTANCE IN *CAMPYLOBACTER* SPP.

3.1 | Key findings

- For 2023, 24 MSs and 2 non-MS (Iceland and Norway) reported data on AMR in ***C. jejuni*** and ***C. coli*** from humans. In the same year, data on AMR in *C. jejuni* and *C. coli* from cattle under 1 year of age were reported by 11 MSs and 1 non-MS, whereas data on AMR in *C. coli* from fattening pigs were reported by 27 MSs and three non-MSs. In 2022, data on AMR in *C. jejuni* from broilers and from fattening turkeys were reported by 26 MSs, the United Kingdom (Northern Ireland) and 3 non-MSs, and by 10 MSs, respectively, whereas data on AMR in *C. coli* from broilers and from fattening turkeys were reported by 24 MSs, the United Kingdom (Northern Ireland) and 3 non-MSs, and by 11 MSs, respectively.
- Resistance rates differed greatly between reporting countries, between antimicrobials and between the two *Campylobacter* species, with overall higher values in *C. coli* than in *C. jejuni*.
- Levels of resistance to **ciprofloxacin** ranged from high and very high to extremely high, respectively, in *C. jejuni* and *C. coli* isolates, recovered from humans and food-producing animals in the EU. In 2023, levels of resistance to ciprofloxacin in human *C. jejuni* isolates ranged from 27.6% to 97.5% among the MSs while for *C. coli* isolates, 16 out of 18 countries reporting at least 10 *C. coli* isolates found levels of ciprofloxacin resistance higher than 70%. In food-producing animals, the highest levels of resistance to ciprofloxacin were observed in *C. coli* isolates, ranging from 54.3% in fattening pigs to 84.1% in fattening turkeys. An extremely high level of resistance to ciprofloxacin was also observed in *C. coli* isolates from cattle under 1 year of age (80.4%) in 2023, as well as in *C. jejuni* isolates from poultry (78.1% in fattening turkeys and 70.9% in broilers) in 2022.
- Resistance to **erythromycin** was very low to low in *C. jejuni* from humans and food-producing animals but was higher in *C. coli*, ranging from overall 6.7% in humans to 31.6% in cattle under 1 year of age.
- The whole genome sequencing results reported for erythromycin-resistant *C. jejuni* and *C. coli* isolates from food-producing animals in 2022–2023, mostly those highly resistant (MIC ≥ 512 mg/L), showed detection of the mutation A2075G in the 23S rRNA gene and no detection of the transferable *erm(B)* gene in most isolates. A single isolate of *C. coli* from cattle under 1 year of age was reported positive to the presence of *erm(B)*, and two isolates presented a mutated *rplV* gene (one *C. coli* isolate each from fattening pigs and from cattle under 1 year of age). Among the three countries reporting WGS data for *Campylobacter* isolates from humans, no erythromycin resistance mechanisms were detected.
- The **combined resistance to both ciprofloxacin and erythromycin**, two critically important antimicrobials for treating campylobacteriosis, was generally rare to low in *C. jejuni* from humans and food-producing animals. The combined resistance was higher in *C. coli* isolates, with low levels observed in humans (6.8%) and broilers (8.2%), moderate levels

in fattening pigs (10.6%) and fattening turkeys (17.4%), and high levels in cattle under 1 year of age (30.3%). This finding may be a cause for public health concern.

- The moderate and high observed levels of resistance to **gentamicin** and **ertapenem** in *C. coli* isolated from cattle under 1 year of age in 2023 (10.5% and 35.5%, respectively), and the moderate to very high levels of resistance to ertapenem in *C. jejuni* and *C. coli* isolated from poultry in 2022 might be a cause for public health concern as those are recommended antimicrobials for treatment in severe invasive *Campylobacter* infections in humans. Gentamicin resistance in *C. coli* from humans was observed at low levels except in one MS, while ertapenem is not yet included in the priority panel for *Campylobacter* monitoring of human isolates at EU level.
- Although findings on ertapenem resistance should be interpreted with caution due to the lack of a validated EUCAST epidemiological cut-off for ertapenem, the results show a shift towards higher MIC values for *Campylobacter* isolates from cattle under 1 year of age and from fattening pigs between 2021 and 2023.
- The **prevalence of resistance** to selected antimicrobials in *C. jejuni* and *C. coli* from cattle under 1 year of age and fattening pigs in 2023 has been estimated at country-level. Between-country variability, from rare, low or moderate to extremely high levels, was observed in the prevalence of ciprofloxacin-resistant and tetracycline-resistant *C. jejuni* and *C. coli* isolates. Notably, a more limited between-country variability and lower levels of prevalence of resistance were found for erythromycin-resistant *Campylobacter*.
- Overall, **complete susceptibility** (CS), defined in this report as susceptibility to ciprofloxacin, erythromycin, tetracycline and gentamicin, was higher in *C. jejuni* than in *C. coli* isolates. The overall CS observed in *C. jejuni* isolates was 25.5% in humans in 2023, and among *C. jejuni* from food-producing animals, it was lowest in fattening turkeys (16.5%) and highest in fattening pigs (51.1%). Regarding overall CS among *C. coli* isolates, it was moderate in humans (11.0%), broilers (13.1%) and fattening pigs (19.7%), and low in fattening turkeys (4.4%) and cattle under 1 year of age (4.5%).
- **Multidrug resistance** (MDR), defined in this report as resistance to at least three antimicrobials among ciprofloxacin, erythromycin, tetracycline and gentamicin, was generally very low for *C. jejuni* isolated from humans (0.6%) and ranged from very low to low (1.0% to 4.3%) in the animal species considered. Compared to *C. jejuni*, MDR was markedly higher in *C. coli*, specifically occurring in 8.6% of the isolates from humans, 34.8% of isolates from cattle under 1 year of age, 16.9% of isolates from fattening turkeys, 10.7% of isolates from fattening pigs and 8.3% of isolates from broilers. These results agree with the higher levels of resistance to selected antimicrobials seen in *C. coli* isolates.
- **Over the period 2014–2023**, **resistance to ciprofloxacin** in *C. jejuni* from humans increased in 11 MSs and decreased in three reporting countries (two MSs and one non-MS). In the same period, resistance to ciprofloxacin in *C. jejuni* increased in six MSs and in one MS from broilers and fattening turkeys, respectively, while it decreased in three MSs and in one MS from the same animal populations. Resistance to ciprofloxacin in *C. coli* from humans increased in two MSs and decreased in two MSs in the period 2014–2023. Similarly, in the same period, resistance to ciprofloxacin in *C. coli* from fattening pigs increased in two MSs and decreased in two non-MSs, while it increased in one MS in *C. coli* from broilers.
- In the same period, **erythromycin resistance** decreased in *C. jejuni* from humans in 10 countries (nine MSs and one non-MSs), from broilers in six MSs and from fattening turkeys in two MSs. Erythromycin resistance also decreased in *C. coli* from humans in nine MSs, and from fattening pigs in four MSs. An increasing trend in erythromycin resistance was observed in *C. jejuni* from humans in two MSs and from broilers in one MS, and in one MS in *C. coli* from humans.

3.2 | Data on antimicrobial resistance in *Campylobacter* spp. addressed

The two main *Campylobacter* species responsible for human infections are *C. jejuni*, which is a predominant species in poultry, followed by *C. coli* (Jehanne et al., 2020), frequently found in pigs and in poultry, sometimes at higher rates than *C. jejuni* (Pergola et al., 2017). *C. coli* is often more resistant than *C. jejuni* to several important antimicrobials and may contain and transfer resistance genes to *C. jejuni*.

Further information on AMR in *Campylobacter* can be found in a dedicated EFSA story map, an interactive online communication tool that is updated and published every year together with the current report (available online here).

Campylobacter AMR data from human infections either derive from monitoring programmes set up by national public health reference laboratories/services or are collected from primary or regional laboratories and integrated with the case information in the national surveillance of human *Campylobacter* infections. This report covers AMR data for *C. jejuni* and *C. coli* from human cases from 2023. Data from 2022 are presented in the 2021–2022 report (EFSA and ECDC, 2024).

In the framework of the Commission Implementing Decision (EU) 2020/1729, the monitoring of AMR in *Campylobacter* spp. from food-producing animals is focused on the species *C. jejuni* and *C. coli*. Since 2021, the AMR monitoring has been mandatory, every year for alternating animal populations, with broilers and fattening turkeys being monitored in even years and fattening pigs and cattle under 1 year of age in odd years. Both *Campylobacter* species are monitored in caecal samples from broilers and fattening pigs, and in countries where the national production of bovine meat or turkey meat is more than 10,000 tonnes per year, in caecal samples from cattle under 1 year of age and fattening turkeys, respectively.

This chapter includes data on *C. jejuni* and *C. coli* in cattle under 1 year of age and fattening pigs in 2023, and in broilers and fattening turkeys in 2022 resulting from mandatory monitoring. In addition, an overview of the voluntary monitoring of AMR in *Campylobacter* isolates recovered from meat samples at retail (of broilers, fattening turkeys, cattle under 1 year of age, fattening pigs and other animal species) performed in 2022 and 2023 is available as supporting documentation on the EFSA Knowledge Junction community on Zenodo at https://doi.org/10.5281/zenodo.14645440.

Data can be further visualised interactively using the EFSA dashboard on AMR in *Campylobacter*, available online here, and in the ECDC Surveillance Atlas of Infectious Diseases, available online here.

Detailed information on AMR data reporting including requirements, sample descriptions and codes for mandatory and voluntary reporting are presented in EFSA's manual for reporting AMR data within the framework of Directive 2003/99/EC and Commission Implementing Decision (EU) 2020/1729 (EFSA, 2024). Further consideration on the data used and the methodology applied in the analysis can be found in Appendix A – Materials and methods.

3.3 | Humans: Occurrence of antimicrobial resistance in *Campylobacter*

3.3.1 | Data reported

For 2023, 24 MSs and 2 non-MS (Iceland and Norway) reported data on AMR from *C. jejuni* and *C. coli* isolated from human cases of campylobacteriosis. Croatia and Latvia reported *Campylobacter* AMR data for the first time for 2023, facilitated by the ECDC sequencing support project for *Salmonella* and *Campylobacter* AMR. The three MS that did not report have no surveillance system in place for *Campylobacter* AMR, i.e. they do not collect AMR data from clinical laboratories or routinely perform *Campylobacter* AST at the national public health reference laboratory.

Seventeen countries reported measured values, four reported results interpreted as susceptible standard dosing regimen, susceptible increased exposure or resistant (SIR) according to the clinical breakpoints (CBPs) applied, and five countries reported results that were categorised as predicted wild type or predicted non-wild type based on analysis of bacterial genomes (Bulgaria, Croatia and Latvia providing sequences that were interpreted by ECDC and Ireland and the Netherlands providing already interpreted data) (Annex B.1, tables 1 and 2). Not all countries reported results for all antimicrobials in the harmonised panel (ECDC, 2016).

The reported data represented 22.1% and 25.5% of the confirmed human cases with *C. jejuni* and *C. coli*, respectively, reported in the EU/EEA in 2023.

3.3.2 | Occurrence of resistance

In 2023, high to extremely high levels of resistance to **ciprofloxacin** were reported in *C. jejuni* isolated from humans, ranging from around 28% in Ireland, Iceland and Norway (27.6%, 28.1% and 28.4%, respectively) to levels approaching nearly 100% in Poland, Portugal, Cyprus and Lithuania (range 93.8%–97.5%) (Annex B.1, table 1). The overall resistance level of ciprofloxacin in the EU was 71.9% (Figure 23; Table 7). The overall ciprofloxacin resistance level in *C. coli* in the EU was at a similar level (75.0%) however, the median level in *C. coli* was higher due to all countries – except for two – reporting very high to extremely high ciprofloxacin resistance levels (Figure 23; Table 7; Annex B.1, table 2).

The highest ciprofloxacin resistance levels in *C. coli* isolates were reported by Lithuania and Portugal (100% and 97.4%, respectively). The lowest resistance levels in *C. coli* were reported by Ireland (16.7%) and the Netherlands (0.0%). In the case of the Netherlands, the absence of ciprofloxacin resistance in *C. coli* appears to be due to a methodological problem after shifting from phenotypic susceptibility testing (with 71.7% resistance reported in 2021) to genotypic (no resistant isolated detected in 2022 or 2023) and will be further investigated.

The level of resistance to **erythromycin** in human *C. jejuni* isolates in the EU ranged from rare to low, with an overall level of erythromycin resistance of 0.8% (Table 7). The highest levels were reported by Ireland, Italy, Spain and Cyprus (4.2%, 4.0%, 3.0% and 2.6%, respectively). Erythromycin resistance was generally higher in *C. coli* compared to *C. jejuni*, with an overall EU resistance in *C. coli* of 6.7%, and ranging from rare to moderate by country. The highest erythromycin resistance was reported in Portugal, Cyprus, Italy and Denmark (22.1%, 18.2%, 15.4% and 15.0%, respectively) (Figure 23; Annex B.1, table 2).

In 2023, overall, MSs reported high **tetracycline** resistance in human *C. jejuni* (47.9%, Table 7) with levels ranging from moderate (14.4%, Norway) to extremely high (75.0%–76.9% in Cyprus, Lithuania, Poland and Portugal) (Annex B.1, table 1). The overall level of tetracycline resistance in human *C. coli* in the EU was very high (68.2%) with resistance levels varying from high (32.1%, Slovenia) to extremely high (88.3%, Portugal). Eight out of seventeen countries reporting at least 10 isolates obtained extremely high tetracycline resistance levels (Annex B.1, table 2).

Fifteen and eleven MSs reported data on **gentamicin** resistance from more than 10 isolates in respectively *C. jejuni* and *C. coli* (Annex B.1, tables 1 and 2). For *C. jejuni*, resistance levels in the EU were very low in general (0.5%, Table 7) with seven countries reporting 0.0% resistance and only two countries reporting low levels of resistance (Spain and Poland). Overall gentamicin resistance levels in *C. coli* were somewhat higher in the EU, but still considered low (2.5%, Table 7). All countries reporting resistance in *C. coli* in at least 10 isolates reported rare to low levels of resistance, except for one country (Italy, 15.4%, $N = 26$, data to be interpreted with caution due to low number of isolates tested).

Only a few countries reported at least 10 isolates tested in relation to **co-amoxiclav** resistance (five for *C. jejuni* and two for *C. coli*). For *C. jejuni* and *C. coli*, the overall EU resistance level was very low and low (0.6% and 1.2%, respectively) (Annex B.1, tables 1 and 2), though two countries reported moderate and high levels, respectively, of resistance to co-amoxiclav in *C. jejuni* and one country reported high levels in *C. coli* (Annex B.1, tables 1 and 2).

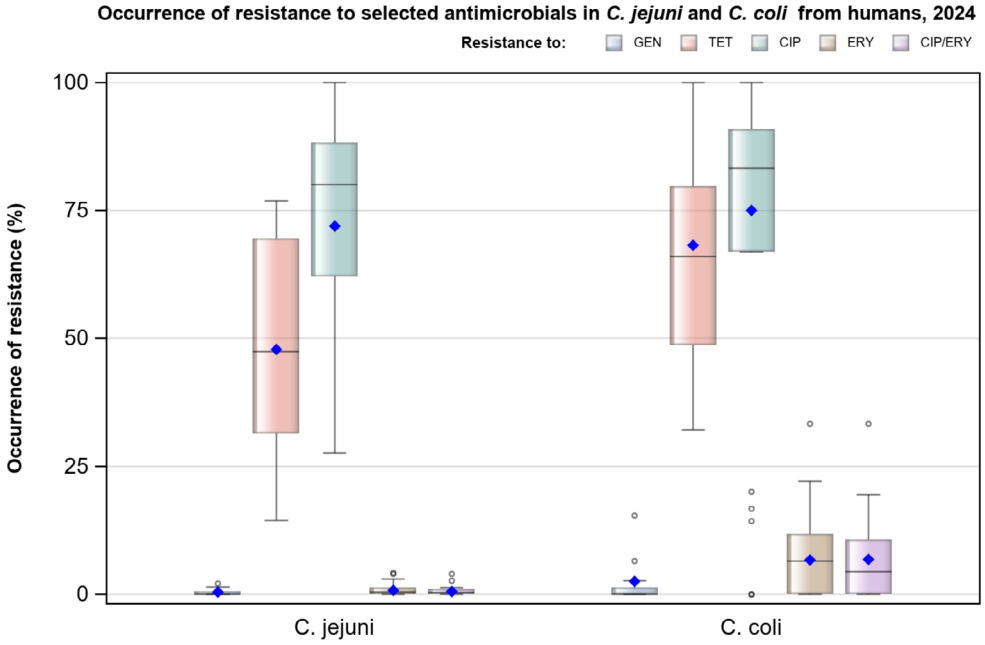


FIGURE 23 Boxplot of the occurrence of resistance to a selection of antimicrobials in *Campylobacter jejuni* and *C. coli* isolated from humans, 2023.
Horizontal line represents the median; blue diamond: overall resistance in the EU. Only countries reporting ≥ 10 isolates per species are included in the graph. CIP, ciprofloxacin; CIP/ERY, combined resistance to ciprofloxacin and erythromycin; ERY, erythromycin; GEN, gentamicin; TET, tetracycline.

TABLE 7 Overall resistance levels in the European Union in *Campylobacter jejuni* and *C. coli* isolated from humans, 2023.

	Ciprofloxacin		Erythromycin		Tetracycline		Gentamicin		Combined CIP/ERY	
***Campylobacter* species**	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**	***N***	**% Res**
C. jejuni (24 MSs)	16,033	71.9	16,805	0.8	14,682	47.9	9789	0.5	15,975	0.6
C. coli (24 MSs)	2296	75.0	2475	6.7	2148	68.2	1509	2.5	2290	6.8

Abbeviation: CIP/ERY, combined resistance to ciprofloxacin and erythromycin.

3.3.3 | Combined resistance to ciprofloxacin and erythromycin

Combined resistance to both ciprofloxacin and erythromycin, which are considered critically important antimicrobials for the treatment of campylobacteriosis, was overall very low at the EU level in *C. jejuni* (0.6%) and low (6.8%) in *C. coli* (Table 7; Annex B.1, tables 1 and 2). These percentages were very similar to the numbers reported in 2022. The levels of combined resistance to both ciprofloxacin and erythromycin in human *C. jejuni* isolates ranged from 0.0% to 4.0%, with the highest levels reported by Cyprus and Italy. The levels of combined resistance to both ciprofloxacin and erythromycin in human *C. coli* isolates ranged from 0.0% to 19.5%, with the highest levels reported by Cyprus and Portugal (Figure 24; Annex B.1, tables 1 and 2).

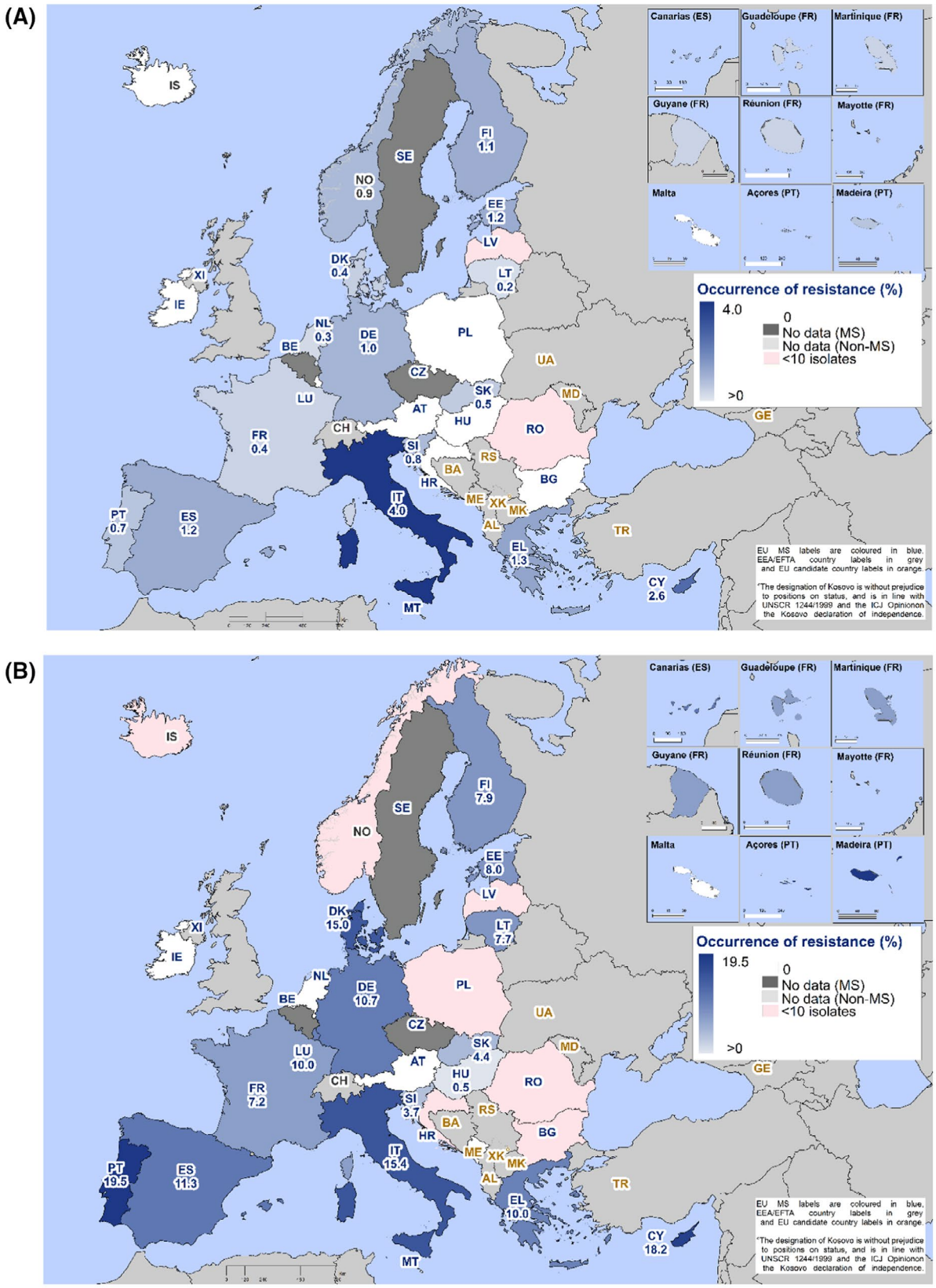


FIGURE 24 Spatial distribution of combined resistance to ciprofloxacin and erythromycin in (A) *Campylobacter jejuni* and (B) *C. coli* isolates from humans, 2023. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

3.3.4 | Complete susceptibility and multidrug resistance

Analyses of complete susceptibility (CS) and multidrug resistance (MDR) focus on critically important antimicrobials in humans, and the target substances were agreed by EFSA and ECDC to include ciprofloxacin (class: fluoroquinolones), erythromycin (class: macrolides), gentamicin (class: aminoglycosides) and tetracycline. It must be noted that the MDR analysis is based on data from fewer reporting countries as not all countries test gentamicin susceptibility. As the aim of such analyses

is to compare CS and MDR in animals and humans, the related findings are only presented in Section 3.5 on the comparison of human and animal data.

Detailed results at country level on the occurrence of MDR and CS in *C. jejuni* and *C. coli* isolates from humans are presented in Annex B.1, tables 3 and 4.

3.3.5 | Temporal trends

Temporal trends were analysed for countries reporting data for at least 3 years over the period 2014–2023 using logistic regression (Appendix A – Materials and methods). Trends in AMR to *C. jejuni* and *C. coli* varied by country depending on the respective antimicrobial (Table 8; Figures 25 and 26). Statistically significant ($p < 0.05$) increasing trends of **ciprofloxacin** resistance were observed in *C. jejuni* isolates from 11 EU MSs and in *C. coli* isolates from Slovenia and Slovakia. Statistically significant decreasing trends in *C. jejuni* were found for Spain, Finland and Norway, while for Spain and the Netherlands, decreasing trends were found in *C. coli*. Only two countries (Estonia and Spain) showed a significant increase in **erythromycin** resistance in *C. jejuni* isolates and one (Germany) in *C. coli*. Statistically significant decreases in *C. jejuni* and *C. coli* were respectively noted in 10 (including non-MS Norway) and 9 countries. Finally, **tetracycline** resistance in *C. jejuni* significantly increased for five MSs and decreased for five countries (including non-MS Norway). For *C. coli*, statistically increasing trends in time were seen for two countries (France and Slovakia) and decreasing trends in three countries (Austria, Slovenia and Spain).

TABLE 8 Number of countries with significantly* increasing or decreasing trends in resistance to selected antimicrobials for *Campylobacter jejuni* and *C. coli* in humans, 2014–2023.

	Ciprofloxacin		Erythromycin		Tetracycline	
***Campylobacter* species**	**Incr.**	**Decr.**	**Incr.**	**Decr.**	**Incr.**	**Decr.**
C. jejuni (21 MS + 2 non-MS)	11 (AT, BG, CY, DE, DK, FR, LT, MT, PL, SI, SK)	3 (ES, FI, NO)	2 (EE, ES)	10 (DE, DK, FI, IT, LT, MT, NL, NO, PT, SK)	5 (AT, LT, NL,PL, SK)	5 (ES, FI, FR, NO, PT)
C. coli (17 MSs)	2 (SI, SK)	2 (ES, NL)	1 (DE)	9 (AT, EE, ES, FI, FR, IT, MT, PT, SK)	2 (FR, SK)	3 (AT, ES, SI)

*$p < 0.05$, logistic regression.

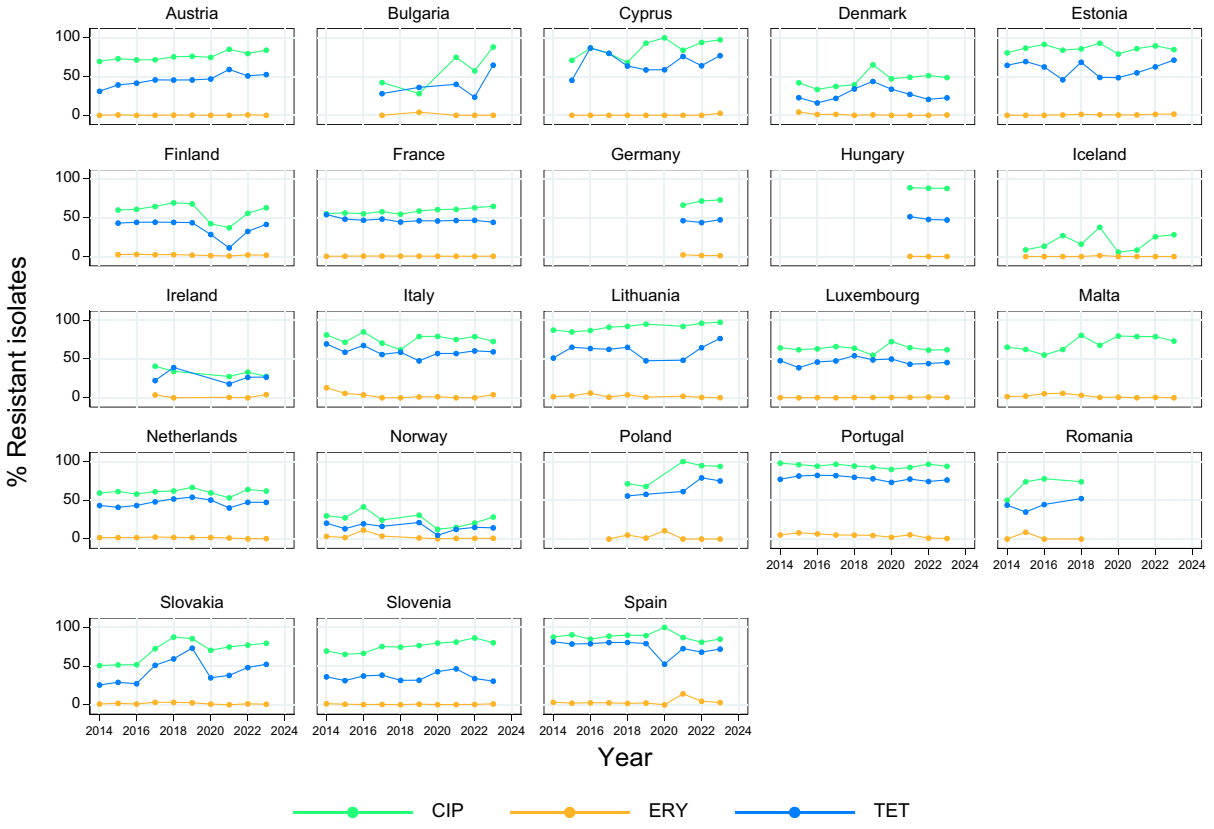


FIGURE 25 Trends in ciprofloxacin, erythromycin and tetracycline resistance in *Campylobacter jejuni* from humans in 23 reporting countries, 2014–2023.

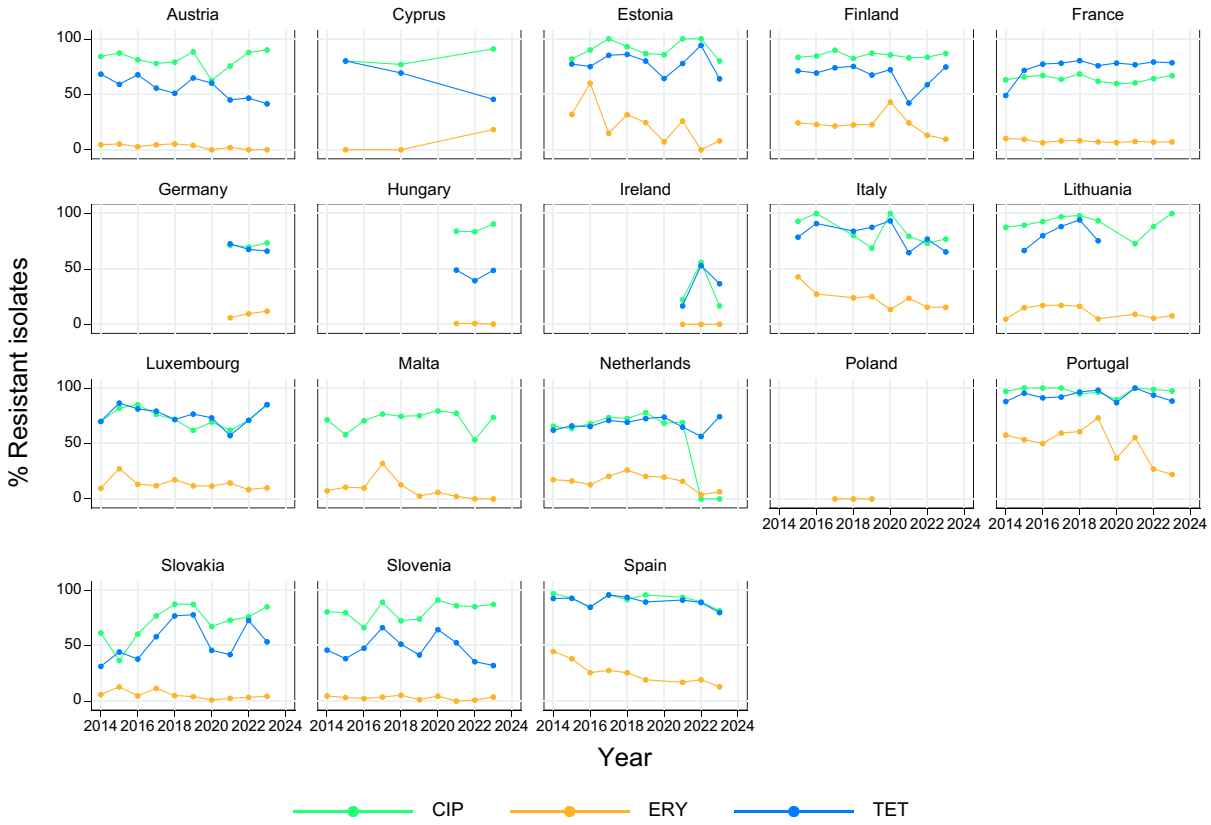


FIGURE 26 Trends in ciprofloxacin, erythromycin and tetracycline resistance in *Campylobacter coli* from humans in 18 reporting countries, 2014–2023.

3.3.6 | High-level resistance to erythromycin

High-level resistance to erythromycin (MIC > 128 mg/L) was assessed as a potential indication for transferrable erythromycin resistance due to the potential presence of the *erm(B)* gene (Qin et al., 2014). Of all *C. jejuni* isolates tested with MIC ($N = 2953$, eight MSs and one non-MS) 0.2% showed MIC values > 128 mg/L while for *C. coli* the percentage was higher, 3.9% ($N = 482$, eight MSs and one non-MS). No *erm(B)* genes were detected among the 74 *Campylobacter* sequences reported by three countries as their AMR data for 2023.

3.4 | Food-producing animals: Occurrence and prevalence of antimicrobial resistance in *Campylobacter*

3.4.1 | Data reported

In the present report, the 2022 AMR data on *Campylobacter* isolates from broilers and fattening turkeys are considered for comparison with 2023 resistance data on *Campylobacter* from fattening pigs and cattle under 1 year of age. In 2022, mandatory data on *Campylobacter jejuni* isolates recovered from caecal samples from broilers were reported by 26 MSs (all MSs, except Greece) and the United Kingdom (Northern Ireland), as well as by three non-MSs (Iceland, Norway and Switzerland) ($N = 2927$ and $N = 325$, respectively). Data on *C. jejuni* isolates recovered from caecal samples from fattening turkeys were reported by 10 MSs (Austria, Croatia, France, Germany, Ireland, Italy, Poland, Portugal, Romania and Spain) in 2022 ($N = 929$). Twenty-four MSs (all MSs, except Finland, Greece and Lithuania) and the United Kingdom (Northern Ireland), as well as three non-MS (Norway, Republic of North Macedonia and Switzerland) reported mandatory data on *Campylobacter coli* isolates recovered from caecal samples of broilers ($N = 1565$ and $N = 64$, respectively). Furthermore, 11 MSs (Austria, Croatia, France, Germany, Hungary, Ireland, Italy, Poland, Portugal, Romania and Spain) reported data on *C. coli* isolates recovered from caecal samples of fattening turkeys ($N = 1381$).

In 2023, 11 MSs (Austria, Belgium, Croatia, Denmark, France, Germany, Italy, the Netherlands, Portugal, Romania and Spain) and one non-MSs (Switzerland) reported mandatory data on *C. jejuni* isolates recovered from cattle under 1 year of age ($N = 1470$ and $N = 154$, respectively). Furthermore, 13 MSs (Austria, Bulgaria, Cyprus, Czechia, Estonia, Finland, Germany, Hungary, Ireland, Italy, Latvia, Luxemburg and the Netherlands) reported data on *C. jejuni* isolates recovered from fattening pigs ($N = 47$). Twenty-seven MSs, as well as three non-MSs (Iceland, Norway and Switzerland) reported mandatory data on *C. coli* isolates recovered from fattening pigs ($N = 4050$ and $N = 621$, respectively). Eleven MSs (Austria, Belgium, Croatia, Denmark, France, Germany, Italy, the Netherlands, Portugal, Romania and Spain) and one non-MS (Switzerland) reported mandatory data on *C. coli* isolates recovered from cattle under 1 year of age ($N = 465$ and $N = 8$, respectively).

Resistance data concerning food-producing animals, reported in 2022 and 2023, are presented in the following sections. Only AMR data collected in accordance with the legislative requirements laid down in Commission Implementing Decision (EU) 2020/1729 are presented in this report. The complete overview of all reported data (mandatory and voluntary) from food-producing animals and meat derived thereof, reported in 2022 and 2023, is available as supporting documentation on the EFSA Knowledge Junction community on Zenodo (https://doi.org/10.5281/zenodo.14645440).

According to the EU rules for the AMR monitoring in *Campylobacter* in place since 2021 (Commission Implementing Decision (EU) 2020/1729), the mandatory antimicrobials to be reported for *C. jejuni* and *C. coli* are: chloramphenicol, ciprofloxacin, ertapenem, erythromycin, gentamicin and tetracycline.

3.4.2 | Occurrence of antimicrobial resistance

In this report, data on the occurrence of resistance in *C. jejuni* and *C. coli* in caecal samples from broilers (2022), fattening turkeys (2022), fattening pigs (2023) and cattle under 1 year of age (2023) are presented in Table 9 and Figure 27. The detailed country-level information on the occurrence of resistance is presented in Annex B.2 (tables 1–6, 10, and 11).

Based on the animal data reported in the EU, the average level of resistance to **tetracycline** ranged from high to very high (from 38.3% in fattening pigs to 65.6% in cattle under 1 year of age) in *C. jejuni*, and from very high to extremely high (from 67.5% in broilers to 88.6% in cattle under 1 year of age) in *C. coli* isolates from all the animal populations. The highest levels of resistance to tetracycline were observed in *C. coli* isolated from cattle under 1 year of age in 2023 (88.6%; data from 11 MSs) and from fattening turkeys in 2022 (79.8%; data from 11 MSs). Overall, among the observed levels of resistance to all selected antimicrobials, the levels of resistance to tetracycline were the highest in *C. coli* and *C. jejuni* isolates from cattle under 1 year of age in 2023, and the second highest in *Campylobacter* isolates from fattening turkeys in 2022. Furthermore, the levels of resistance to tetracycline were higher for *C. coli* than for *C. jejuni* within each animal species.

High to extremely high average levels of resistance to **ciprofloxacin** were also observed in both *C. jejuni* (range from 34.0% in fattening pigs to 78.1% in fattening turkeys) and *C. coli* (range from 54.3% in fattening pigs to 84.1% in fattening turkeys) isolates from all the animal populations reported in EU MSs. The highest average level of resistance to ciprofloxacin was observed in *C. coli* isolated from fattening turkeys in 2022 (84.1%; data from 11 MSs). Likewise, an extremely high level of resistance to ciprofloxacin (80.4%) was obtained from *C. coli* isolated from cattle under 1 year of age in 2023 (data from 11 MSs). Overall, the levels of resistance to ciprofloxacin were higher for *C. coli* than for *C. jejuni* within an animal species, although the average level of resistance to ciprofloxacin obtained from *C. jejuni* isolates from broilers (70.9%) and fattening turkeys (78.1%) in 2022 were also extremely high (data from 26 MSs and the United Kingdom (Northern Ireland), and from 10 MSs, respectively). For both *C. jejuni* and *C. coli*, the lowest levels of resistance to ciprofloxacin were obtained from fattening pigs in 2023 (34.0% in *C. jejuni* and 54.3% in *C. coli*; data from 13 MSs and from 27 MSs, respectively).

Resistance to **gentamicin** ranged from absent to moderate among *C. jejuni* isolates from all the animal populations reported in the EU. The highest average level of resistance to gentamicin was observed in *C. coli* from cattle under 1 year of age (10.5%; data from 11 MSs), and the second highest in *C. jejuni* from fattening pigs (4.3%; data from 13 MSs), both in 2023. In 2022, resistance to this antimicrobial was absent for *C. jejuni* from turkeys (data from 10 MSs), and it varied between 0.1% for *C. jejuni* from broilers (data from 26 MSs and the United Kingdom (Northern Ireland)), 2.0% for *C. coli* from broilers (data from 24 MSs and the United Kingdom (Northern Ireland)) and 0.6% for *C. coli* from fattening turkeys (data from 11 MSs). Gentamicin resistance occurrence was also low in *C. jejuni* from cattle under 1 year of age (1.1%; data from 11 MSs) and in *C. coli* from fattening pigs (2.3%; data from 27 MSs) in 2023.

Average resistance to **erythromycin** among reporting EU MSs was detected at low levels in *C. jejuni* isolates for the different animal populations (range from 1.5% in broilers to 2.1% in fattening pigs). Notably higher average levels of resistance were reported in *C. coli* isolates (range from 8.8% to 31.6%). The highest average level of resistance to erythromycin was observed in *C. coli* isolates recovered from cattle under 1 year of age (31.6%; data from 11 MSs) in 2023, followed by fattening turkeys (18.0%; data from 11 MSs) in 2022, fattening pigs (13.0%; data from 27 MSs) in 2023 and broilers (8.8%; data from 24 MSs and the United Kingdom (Northern Ireland)) in 2022. High variability in erythromycin resistance was observed between countries in food-producing animals. Notably, in 2023, Portugal (52.7%) and Cyprus (62.8%) reported the highest occurrences of erythromycin resistance in *C. coli* from fattening pigs, while Belgium reported an extremely high occurrence of erythromycin resistance in *C. coli* from cattle under 1 year of age (75.9%).

Average resistance to **chloramphenicol** among reporting EU MSs in *Campylobacter* isolates from all animal populations considered in 2022 and 2023 varied from absent to very low (range from 0.0% to 0.7%), except for low average resistance in *C. coli* isolates from cattle under 1 year of age in 2023 (1.7%; data from 11 MSs).

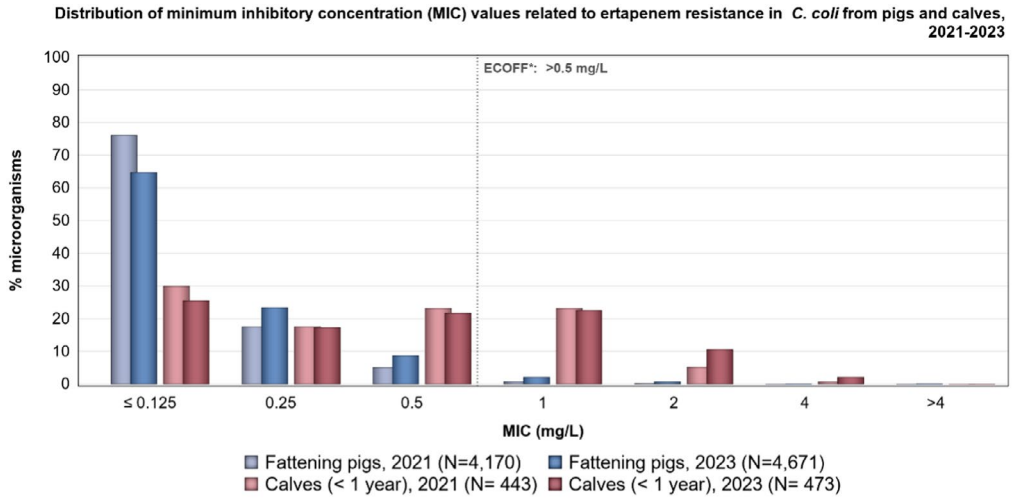
Resistance to **ertapenem** in *C. jejuni* isolates varied from absent to moderate on average among all reporting MSs (range from 0.0% in fattening pigs to 15.1% in fattening turkeys). Notably, *C. jejuni* isolated from fattening turkeys (15.1%; data from 10 MSs) and from broilers (10.2%; data from 26 MSs and the United Kingdom (Northern Ireland)) in 2022 presented higher levels of resistance compared to *C. jejuni* isolated from cattle under 1 year of age (2.4%; data from 11 MSs) and from fattening pigs (0.0%; data from 13 MSs) in 2023. It is noteworthy that a higher level of average resistance to ertapenem was reported in *C. coli*, varying from low to very high (range 3.4% in fattening pigs to 58.1% in fattening turkeys). Average ertapenem resistance in *C. coli* was highest in fattening turkeys (58.1%; data from 11 MSs), followed by broilers (43.1%; data from 24 MSs and the United Kingdom (Northern Ireland)), both in 2022, and then by cattle under 1 year of age (35.5%; data from 11 MSs) and fattening pigs (3.4%; data from 27 MSs) in 2023.

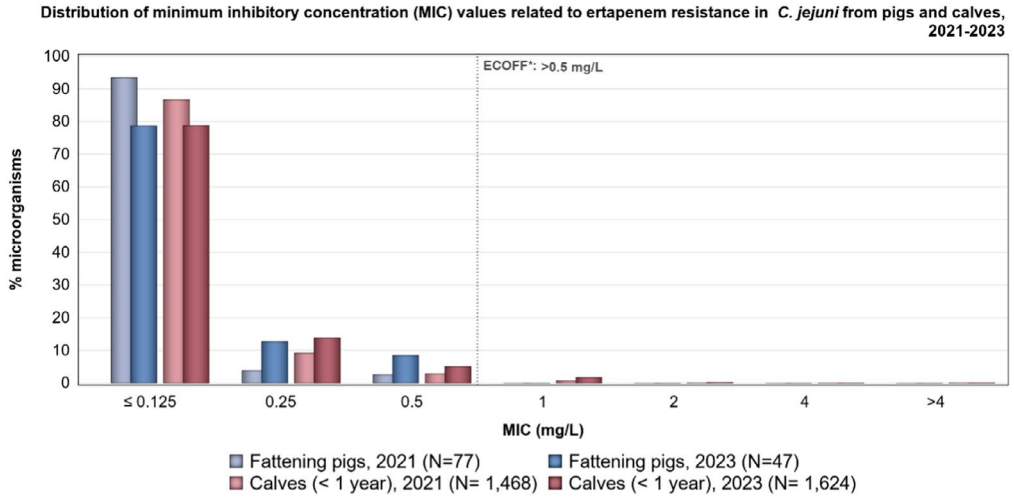
Further considerations on the levels of ertapenem resistance in *Campylobacter jejuni* and *C. coli* from fattening pigs and cattle under 1 year of age

Due to the absence of a validated threshold for resistance to ertapenem in *C. jejuni* and *C. coli* recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST), an epidemiological cut-off (ECOFF) of 0.5 mg/L has been used by EFSA since 2021 in agreement with the European Reference Laboratory for Antimicrobial Resistance (EURL-AR) (EFSA, 2024). This ECOFF is currently under further investigation in the project CarbaCamp, a collaboration between EFSA, ECDC, EUCAST and EURL-AR (EFSA and ECDC, 2024).

In 2023, minimum inhibitory concentration (MIC) values were reported for the second mandatory year for *C. jejuni* and *C. coli* from fattening pigs and cattle under 1 year of age, following the requirements of Commission Implementing Decision (EU) 2020/1729. Considering the data reported by all reporting countries, the occurrence of ertapenem resistance increased from 2021 to 2023 among *C. jejuni* from cattle under 1 year of age (from 1.2% to 2.2%), in *C. coli* from fattening pigs (from 1.1% to 3.0%) and in *C. coli* from cattle under 1 year of age (from 29.1% to 35.3%), while it remained absent in *C. jejuni* from fattening pigs.

MIC distribution (%) in ertapenem-resistant and susceptible *C. coli* and *C. jejuni* isolates from fattening pigs and cattle under 1 year of age in 2021 and 2023, reported by MSs and non-MSs, are presented below.





*Epidemiological cut-off.

The observed increases in occurrence of ertapenem resistance are a result of shifts in the ertapenem MIC distributions towards higher values in 2023, as shown in the figure above. Both *C. jejuni* and *C. coli* isolates, from fattening pigs and cattle under 1 year of age, presented an increased occurrence of higher MIC values in 2023 compared to 2021. In 2023, *C. coli* from cattle under 1 year of age presented higher occurrence of MIC values of 2 and 4 mg/L compared to 2021. In 2023, *C. coli* from fattening pigs presented 0.7%, 0.1% and 0.1% occurrence of MIC values 2 , 4 and >4 mg/L, respectively, while these values were not observed in 2021. Those three MIC values were also observed only in 2023 among *C. jejuni* isolates from cattle under 1 year of age (0.2%, 0.1% and 0.1%, respectively). Finally, although there were no ertapenem-resistant *C. jejuni* isolates from fattening pigs in both years, in 2023 there was a shift towards higher MIC values among those isolates also.

TABLE 9 Occurrence of resistance (%) to selected antimicrobials in *Campylobacter jejuni* and *C. coli* in caecal samples from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age using harmonised ECOFFs, 2022–2023, 27 MSs and United Kingdom (Northern Ireland).

Campylobacter species	Categories	Year	No. of isolates	Reporting countries (*N*)	GEN	CHL	ETP	CIP	ERY	TET	CIP/ERY
C. jejuni	Cattle under 1 year of age	2023	1470	AT, BE, DE, DK, ES, FR, HR, IT, NL, PT, RO (11)	1.1	0.0	2.4	57.6	1.1	65.6	0.8
	Fattening pigs	2023	47	AT, BG, CY, CZ, DE, EE, FI, HU, IE, IT, LV, LU, NL (13)	4.3	0.0	0.0	34.0	2.1	38.3	2.1
	Broilers	2022	2927	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, HR, HU, IE, IT, LT, LU, LV, MT, NL, PL, PT, RO, SE, SI, SK, XI (27)	0.1	0.0	10.2	70.9	1.5	50.7	1.1
	Fattening turkeys	2022	929	AT, DE, ES, FR, HR, IE, IT, PL, PT, RO (10)	0.0	0.1	15.1	78.1	1.7	59.0	1.6
C. coli	Cattle under 1 year of age	2023	465	AT, BE, DE, DK, ES, FR, HR, IT, NL, PT, RO (11)	10.5	1.7	35.5	80.4	31.6	88.6	30.3
	Fattening pigs	2023	4050	AT, BE, BG, CY, CZ, DE, DK, EE, EL, ES, FI, FR, HR, HU, IE, IT, LT, LU, LV, MT, NL, PL, PT, RO, SE, SI, SK (27)	2.3	0.4	3.4	54.3	13.0	68.4	10.6
	Broilers	2022	1565	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FR, HR, HU, IE, IT, LU, LV, MT, NL, PL, PT, RO, SE, SI, SK, XI (25)	2.0	0.7	43.1	73.0	8.8	67.5	8.2
	Fattening turkeys	2022	1381	AT, DE, ES, FR, HR, HU, IE, IT, PL, PT, RO (11)	0.6	0.0	58.1	84.1	18.0	79.8	17.4

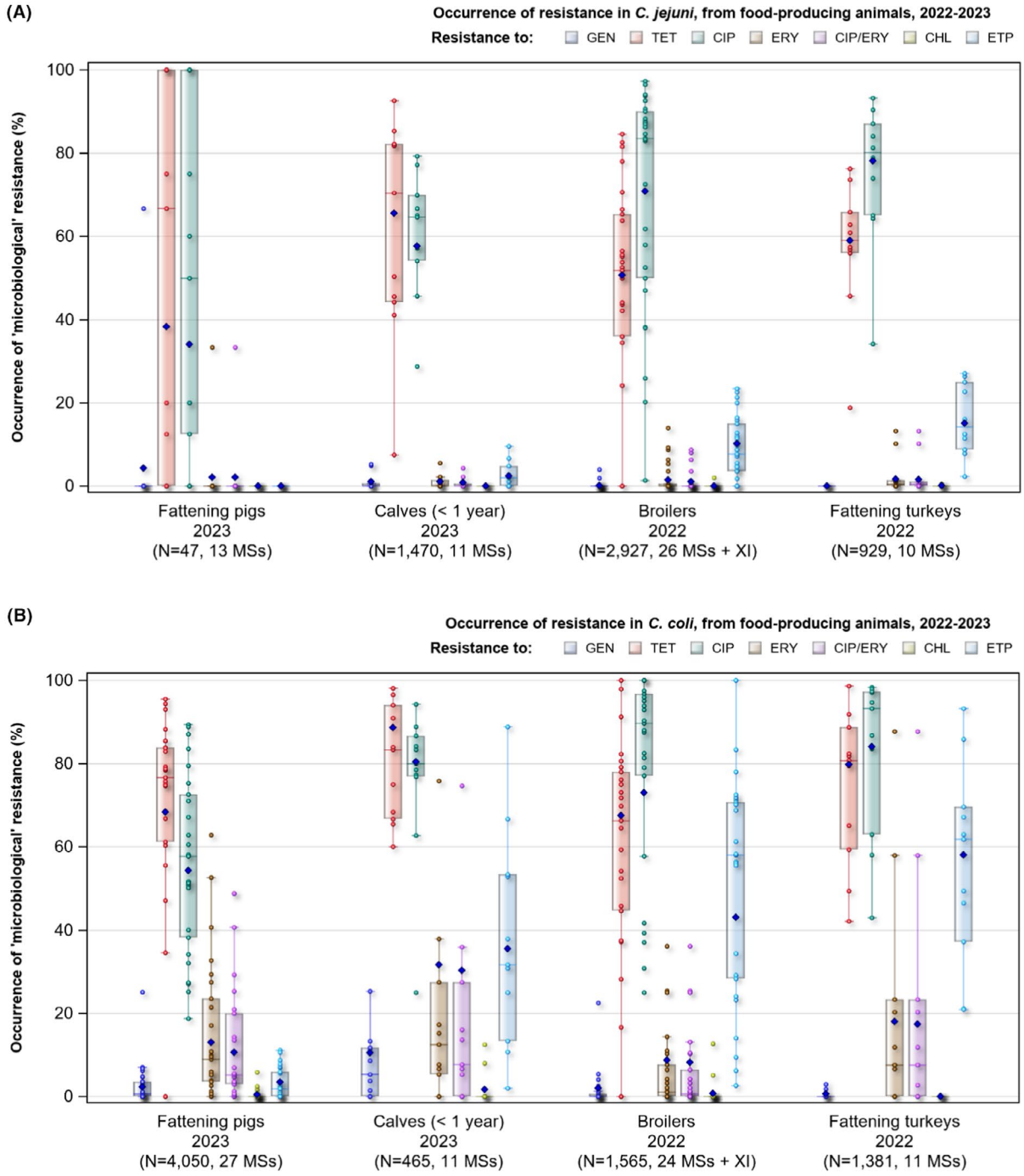


FIGURE 27 Occurrence of resistance to antimicrobials in (A) *Campylobacter jejuni* and (B) *C. coli* from food-producing animals, in EU MSs and United Kingdom (Northern Ireland), 2022–2023.
CHL, chloramphenicol; CIP, ciprofloxacin; CIP/ERY, combined resistance to ciprofloxacin and erythromycin; ERY, erythromycin; ETP, ertapenem; GEN, gentamicin; TET, tetracycline; XI, United Kingdom (Northern Ireland). Horizontal line represents the median; blue diamond: Overall resistance in the EU; dots represent resistance in the different countries.

3.4.3 | Combined resistance to ciprofloxacin and erythromycin

Since resistance to fluoroquinolones is common in *C. jejuni* and *C. coli*, macrolides are recognised as critically important antimicrobials (CIAs) for the treatment of *Campylobacter* infections in humans. According to the new WHO List of Medically Important Antimicrobials (WHO, 2024), macrolides are classified as CIA due to the limited therapy choices for *Campylobacter* infections, the fact that macrolide resistance may result from transmission from non-human sources, and because one or more macrolide substances are classified as Watch or Reserve in the WHO AWaRe list (WHO, 2021). Therefore, the occurrence of combined resistance to ciprofloxacin and erythromycin in *Campylobacter* spp. from food-producing animals is of great importance to public health, since it might hamper the treatment of human campylobacteriosis (Friedrich, 2019).

Overall average **combined resistance** to these antimicrobials among reporting EU MSs was higher in *C. coli* isolates than in *C. jejuni* isolates for all animal species tested (Table 9; Figure 27; see also detailed country-level information in Tables 1–6, 10, and 11). Low average levels of combined resistance to ciprofloxacin and erythromycin were reported in

C. jejuni isolates from broilers (1.1%; data from 26 MSs and the United Kingdom (Northern Ireland)) and fattening turkeys (1.6%; data from 10 MSs) in 2022 (Annex B.2, tables 2 and 4), and from cattle under 1 year of age (0.8%; data from 11 MSs) and fattening pigs (2.1%; data from 13 MSs) in 2023 (Annex B.2, tables 6 and 11). The highest average levels of combined resistance were reported in *C. coli* isolates from cattle under 1 year of age (30.3%; data from 11 MSs) in 2023 and from fattening turkeys (17.4%; data from 11 MSs) in 2022, followed by fattening pigs (10.6%; data from 27 MSs) in 2023 and broilers (8.2%; data from 24 MSs and the United Kingdom (Northern Ireland)) in 2022 (Annex B.2, tables 1, 3, 5, and 10).

Combined resistance to ciprofloxacin and erythromycin in *C. jejuni* from fattening pigs was detected in a single isolate from 1 MS (Italy), out of 47 isolates reported by 13 MSs in 2023 (Annex B.2, table 6). As all the 13 reporting MSs provided fewer than 10 isolates each, no map showing the spatial distribution of co-resistance in *C. jejuni* isolates from fattening pigs was presented. Combined resistance to ciprofloxacin and erythromycin in *C. coli* isolates from fattening pigs in 2023 was detected by 24 MSs (all except for Czechia, Estonia and Finland) and two non-MSs (Norway and Switzerland) out of 30 reporting countries, with levels of co-resistance ranging from 0.4% in Norway and the Netherlands, up to 48.8% in Cyprus and Portugal (Figure 29A; Annex B.2, table 5).

Combined resistance to ciprofloxacin and erythromycin in *C. jejuni* isolated from cattle under 1 year of age was detected in four MSs (Belgium, Germany, Italy and the Netherlands) out of 12 reporting countries in 2023, ranging from 0.5% to 4.3%, with the highest level of combined resistance reported by Belgium (Figure 28A; Annex B.2, table 11). Co-resistance to ciprofloxacin and erythromycin detected in *C. coli* isolates from cattle under 1 year of age was reported from eight MSs (Belgium, Croatia, France, Germany, Italy, the Netherlands, Portugal and Spain) out of 12 countries reporting data in 2023. The levels of combined resistance ranged from 5.3% reported by Spain to 74.7% reported by Belgium (Figure 29B; Annex B.2, table 10).

Combined resistance to ciprofloxacin and erythromycin in *C. jejuni* isolated from broilers was detected in five MSs (Belgium, Bulgaria, Czechia, Portugal and Romania) out of 26 MSs, the United Kingdom (Northern Ireland) and three non-MSs reporting data in 2022, ranging from 0.5% in Czechia to 8.8% in Romania (Figure 28B; Annex B.2, table 2). Co-resistance to ciprofloxacin and erythromycin detected in *C. coli* isolates from broilers was reported from 12 MSs (Belgium, Bulgaria, Cyprus, France, Germany, Ireland, Italy, Malta, the Netherlands, Portugal, Romania and Spain), United Kingdom (Northern Ireland) and one non-MS (Switzerland) out of 28 countries reporting data in 2022. In EU, the levels of combined resistance ranged from 0.6% reported by France to 36.1% reported by Portugal (Figure 29C; Annex B.2, table 1).

Combined resistance to ciprofloxacin and erythromycin in *C. jejuni* from fattening turkeys was detected in five MSs (France, Italy, Poland, Portugal and Romania), out of 10 reporting MSs in 2022 (Figure 28C; Annex B.2, table 4), ranging from 0.9% in France to 13.2% in Portugal. Combined resistance to ciprofloxacin and erythromycin in *C. coli* isolates from fattening turkeys in 2022 was detected by eight MSs (France, Germany, Ireland, Italy, Poland, Portugal, Romania and Spain) out of 11 MSs reporting 2022 data, with levels of co-resistance ranging from 2.7% in France, up to 58.0% and 87.7% in Portugal and Romania, respectively (Figure 29D; Annex B.2, table 3).

The combined resistance to ciprofloxacin and erythromycin in *C. jejuni* obtained from cattle under 1 year of age tested in 2023 remained similar to the average level reported in 2021 (0.8%) (data from 10 MSs in both years). The combined resistance to ciprofloxacin and erythromycin in *C. jejuni* obtained from fattening pigs reported in EU remained at a low level but increased from 1.0% in 2021 to 2.1% in 2023 (data from 12 and 13 MSs in 2021 and 2023, respectively).

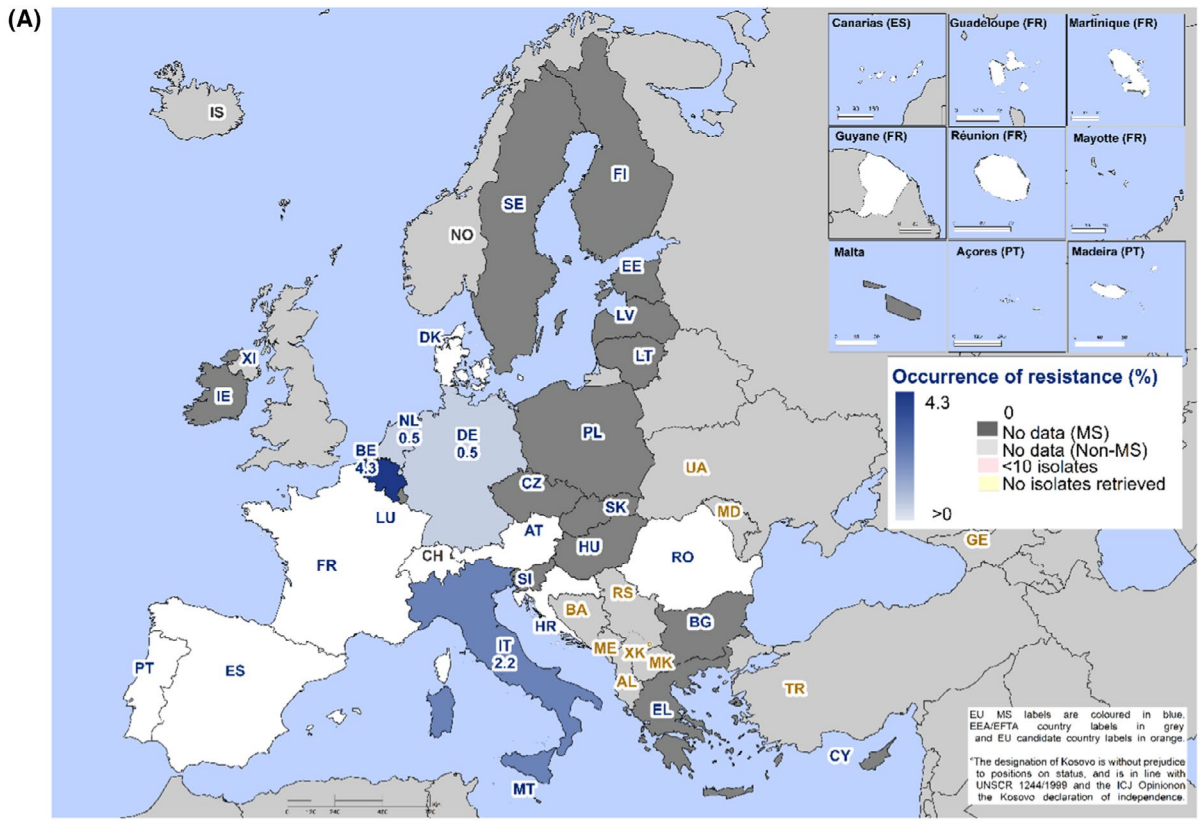


FIGURE 28 (Continued)

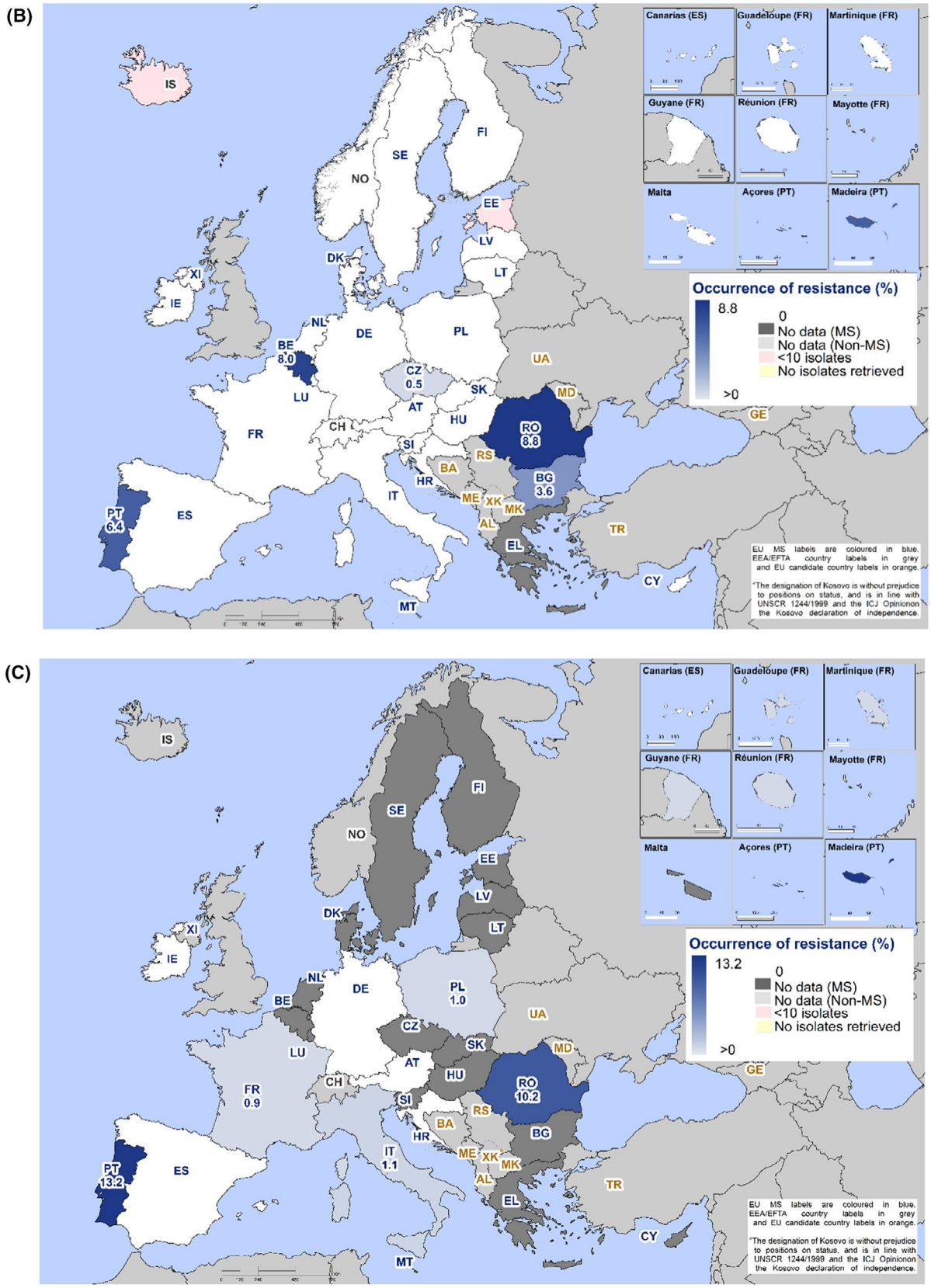


FIGURE 28 Spatial distribution of combined resistance to ciprofloxacin and erythromycin in *Campylobacter jejuni* isolates from (A) cattle under 1 year of age (11 MSs and one non-MS, 2023), (B) broilers (26 MSs, the United Kingdom (Northern Ireland) and three non-MSs, 2022), (C) fattening turkeys (10 MSs, 2022).

Maps are presented only when at least four Member States reported data. The map showing the spatial distribution of co-resistance in *C. jejuni* isolates from fattening pigs was not included because all the reporting countries provided fewer than 10 isolates each. 'No data' refers to the absence of reported data by a MS or non-MS for a given matrix in a given reporting year; 'No isolates retrieved' refers to the RCs that tested for the presence of *C. jejuni* but retrieved no isolates in a given matrix in a given year. 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 average occurrence of combined resistance to ciprofloxacin and erythromycin observed in *C. coli* isolates from cattle under 1 year of age reported in EU remained high, with a slight decrease from 32.7% in 2021 to 30.3% in 2023, whereas it increased from low to moderate among *C. coli* isolates from fattening pigs, with 9.1% observed in 2021 and 10.6% in 2023. The number of reporting MSs and reported isolates did not differ considerably from 2021 to 2023 for these two animal species (data from 10 MSs in 2021 and from 11 MSs in 2023 for cattle under 1 year of age; data from 26 MSs and the United Kingdom (Northern Ireland) in 2021 and from 27 MSs in 2023 for fattening pigs).

The spatial distribution of combined resistance to both ciprofloxacin and erythromycin in *C. jejuni* and *C. coli* isolates from different animal populations is presented in Figures 28 and 29 when more than four countries have reported data.

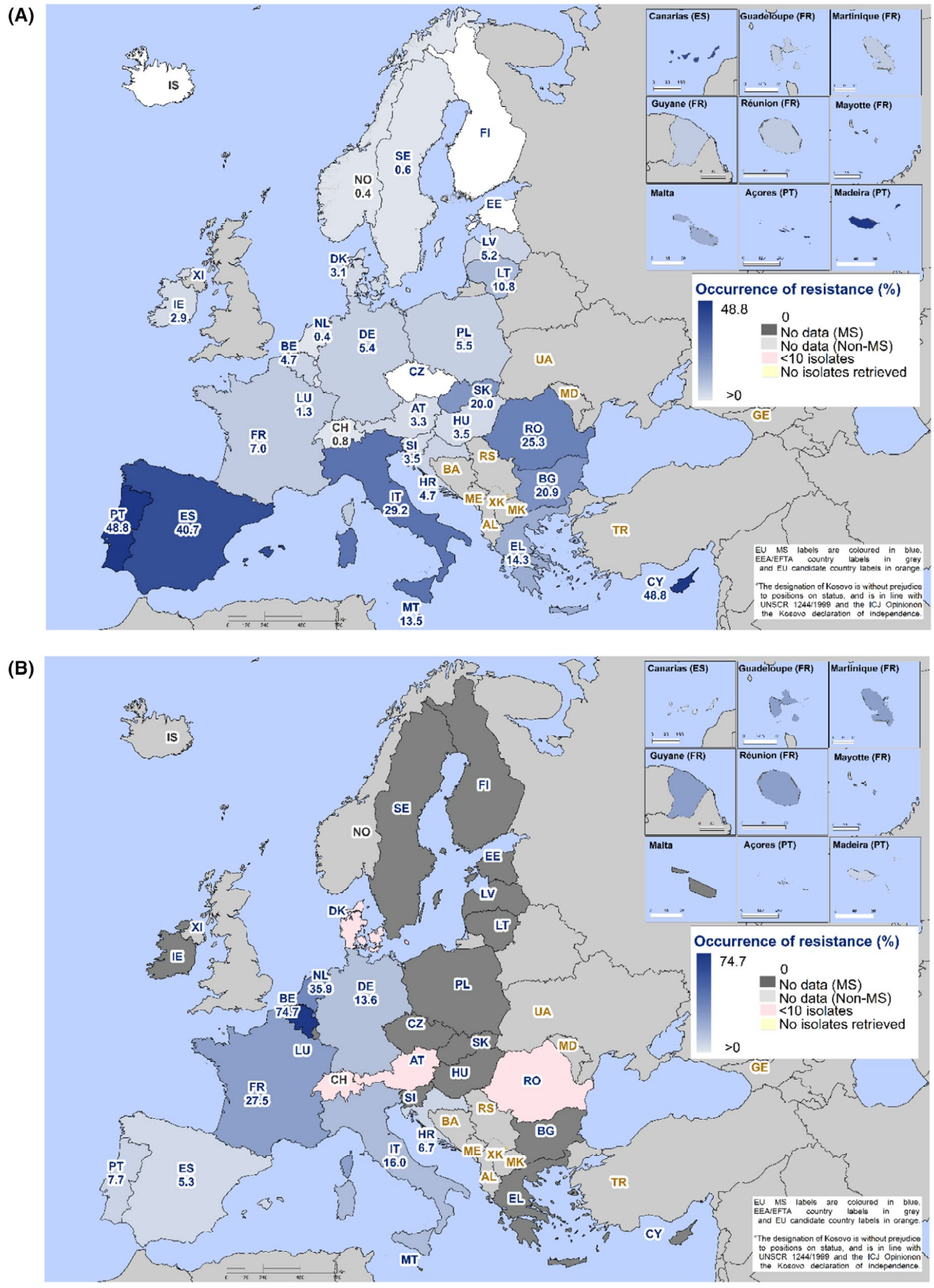


FIGURE 29 (Continued)

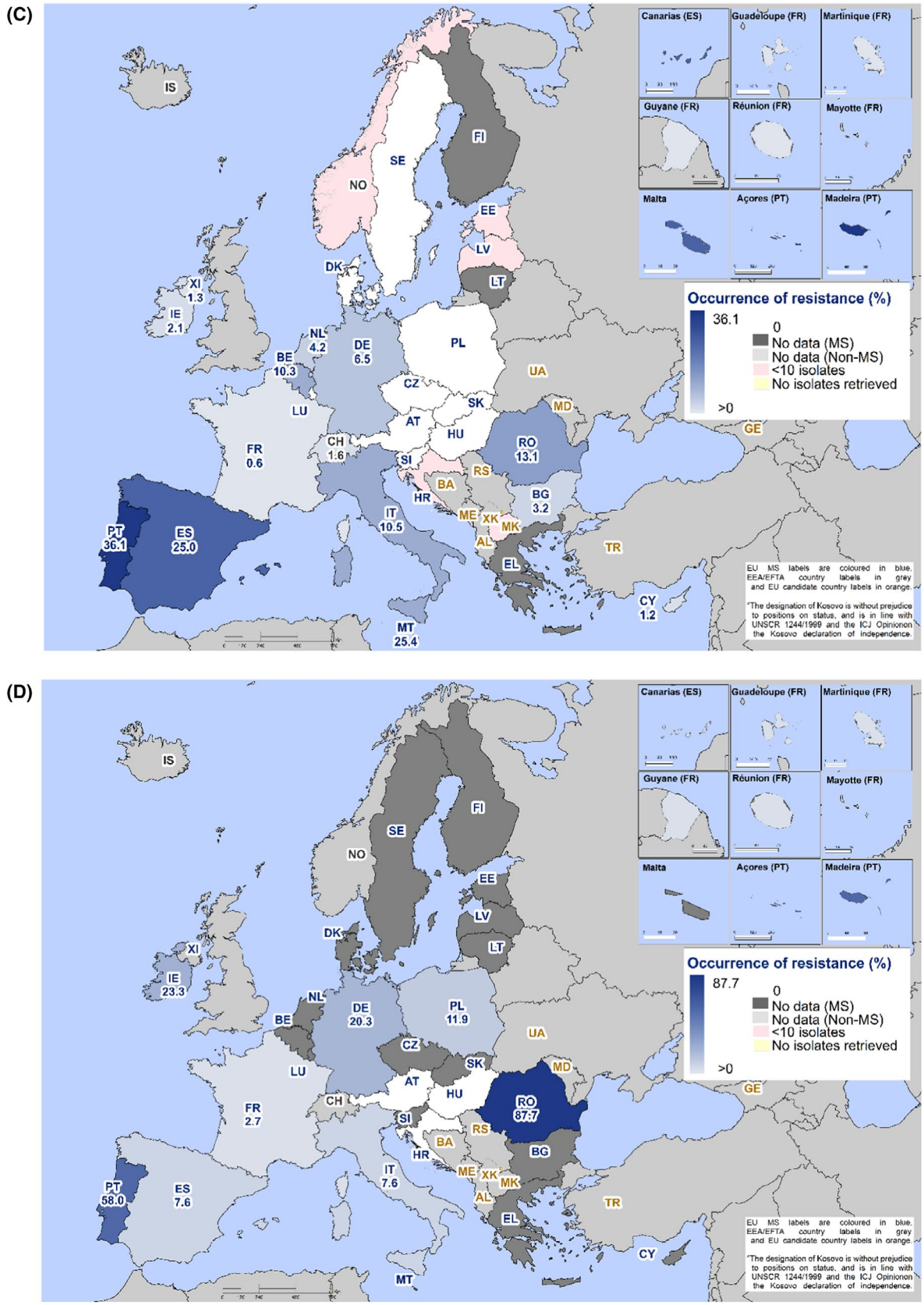


FIGURE 29 Spatial distribution of combined resistance to ciprofloxacin and erythromycin in *Campylobacter coli* isolates from (A) fattening pigs (27 MSs and three non-MSs, 2023), (B) cattle under 1 year of age (11 MSs and one non-MS, 2023), (C) broilers (24 MSs, the United Kingdom (Northern Ireland) and three non-MSs, 2022), (D) fattening turkeys (11 MSs, 2022).
Maps are presented only when at least four Member States reported data. 'No data' refers to the absence of reported data by a MS or non-MS for a given matrix in a given reporting year; 'No isolates retrieved' refers to the RCs that tested for the presence of *C. coli* but retrieved no isolates in a given matrix in a given year. 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.

3.4.4 | Prevalence of resistance to selected antimicrobials in *Campylobacter jejuni* and *C. coli*

The **prevalence of resistance** to selected antimicrobials in *C. jejuni* and *C. coli* from cattle under 1 year of age and fattening pigs has been estimated at country level as the product of the prevalence of *C. jejuni* or *C. coli* in caecal samples from the given animal species (Annex B.2, tables 7, 8, 12, and 13) and the percent occurrence of resistance in the corresponding isolates (Annex B.2, tables 5, 6, 10, and 11). Monitoring the prevalence of resistant *Campylobacter* enables to address together both evolving temporal trends in the prevalence of *C. jejuni* and *C. coli* and the occurrence of resistance in both species recovered from the different food-producing animals, through a unique indicator. This indicator is primarily intended to follow-up trends over time at the country level. The isolation method for *Campylobacter* has been harmonised across the EU in accordance with the protocol of the EURL for Campylobacter. Therefore, the prevalence of *C. coli* can be considered comparable between reporting countries. Similarly, the harmonised implementation of the antimicrobial susceptibility testing in *C. jejuni* and *C. coli* isolates allows comparability of the estimates of prevalence of resistance in isolates from all monitored food-producing animals across the EU. Although the sampling design for the monitoring of AMR in *C. jejuni* and *C. coli* from food-producing animals is harmonised according to the Commission Implementing Decision (EU) 2020/1729, still differences in the intensity of sampling effort exist across the EU MSs, as shown in the numbers of tested samples (tables 7, 8, 12, and 13 of Annex B.2). To account for these differences, 95% confidence intervals have been calculated together with the estimated prevalence of resistance, as presented in tables 9, 14, and 15 of Annex B.2, as well as in Figures 30–32.

The country-level estimates of the prevalence of resistance to selected antimicrobials in *C. jejuni* and *C. coli* from caecal samples of cattle under 1 year of age and fattening pigs are presented in Annex B.2 (tables 9, 14, and 15). In 2023, 13 MSs reported prevalence of *C. jejuni* in fattening pigs, all with values below 1%, with the number of isolates recovered from each MS ranging from one to eight. Due to the low number of isolates recovered at individual country level, prevalence of resistance was not estimated for *C. jejuni* from fattening pigs.

The country-level prevalence of resistance to ciprofloxacin, erythromycin and tetracycline in *C. jejuni* isolates from cattle under 1 year of age is presented in Figure 30, together with the 95% confidence intervals that provide an indication of the uncertainty around the point prevalence estimates. Between-country variability in the levels of prevalence of resistance in *C. jejuni* from cattle under 1 year of age was from moderate to high for ciprofloxacin resistance (ranging from 15.2% in Spain to 37.0% in Germany; Figure 30A) and from low to very high for tetracycline resistance (ranging from 5.8% in Denmark to 59.0% in Belgium; Figure 30C). Erythromycin-resistant *C. jejuni* from cattle under 1 year of age were detected in four out of 11 MSs (Belgium, Germany, Italy, the Netherlands) and in one non-MS (Switzerland), ranging from 0.3% to 3.5% (Figure 30B). Noteworthy, in three MSs (Belgium, France and Italy) *C. jejuni* from cattle under 1 year of age also presented positive prevalence of resistance to gentamicin (ranging from 0.2% to 3.1%) (Annex B.2, table 15). Belgium presented the highest prevalence of both erythromycin resistance and gentamicin resistance among *C. jejuni* from cattle under 1 year of age.

The country-level prevalence of resistance to ciprofloxacin, erythromycin and tetracycline in *C. coli* isolates is presented in Figure 31 for fattening pigs and Figure 32 for calves under 1 year of age, also including 95% confidence intervals. The prevalence of resistance in *C. coli* from fattening pigs showed high between-country variability among the 27 reporting MSs for ciprofloxacin resistance, tetracycline resistance and erythromycin resistance, ranging from absent or low to high or extremely high (from 8.7% in Bulgaria to 73.2% in Romania for ciprofloxacin; from 0.0% in Czechia to 33.3% in Cyprus for erythromycin; from 0% in Finland and Sweden to 82.1% in Austria for tetracycline) (Figure 31A–C; Annex B.2, table 9). Notably, one non-MS (Iceland) also presented extremely high prevalence of ciprofloxacin resistance (77.9%) in *C. coli* from fattening pigs. Lower between-country variability for prevalence of resistance in *C. coli* from fattening pigs was observed for gentamicin-, chloramphenicol- and ertapenem resistance. The country-level prevalence of resistance to gentamicin in *C. coli* from fattening pigs was higher than 0% in 17 of the 27 reporting MSs (varying between 0.2% prevalence from Bulgaria and 14.3% prevalence from Italy) and in two reporting non-MSs (0.3%). A similar level of between-country variability was observed for prevalence of ertapenem-resistant *C. coli* from fattening pigs, which was observed to be higher than 0% in 16 of the 27 reporting MSs (ranging from 0.3% prevalence from Bulgaria to 10.9% from Austria) and in one non-MS (Norway, 0.9%). The lowest between-country variability in prevalence of resistance in *C. coli* from fattening pigs was observed for prevalence of chloramphenicol resistance, with values above 0% observed in only four MSs, ranging between 0.5% from Malta and 3.3% from Italy (Annex B.2, table 9).

The prevalence of resistance to ciprofloxacin, erythromycin and tetracycline in *C. coli* from cattle under 1 year of age among the 11 reporting MSs and one non-MS varied from rare, very low or low to high levels, ranging from 0.9% in Croatia to 30.2% in Belgium for ciprofloxacin (Figure 32A), from 0.0% in Austria and Romania to 24.3% in Belgium for erythromycin (Figure 32B), and from 1.8% in Austria to 33.7% in the Netherlands for tetracycline (Figure 32C). A more limited between-country variability and notably lower levels of prevalence of resistance in *C. coli* from calves under 1 year of age were found for chloramphenicol and gentamicin, ranging from 0.0% in nine MSs and one non-MS to 2.6% in Belgium and from 0.0% in three MSs and one non-MS to 6.3% in Italy, respectively. Similarly, the prevalence of ertapenem-resistant *C. coli* from calves under 1 year of age was below 3% for eight MSs and one non-MS, while being estimated at 16.9% and 18.3% for two MSs (Belgium and the Netherlands, respectively) (Annex B.2, table 14). Overall, the prevalence of resistance in *Campylobacter* isolates from fattening pigs and cattle under 1 year of age in 2023 presented a high between-country variability for ciprofloxacin and tetracycline resistance, and a low to moderate between-country variability for resistance to erythromycin, gentamicin, chloramphenicol and ertapenem, with a few exceptions.

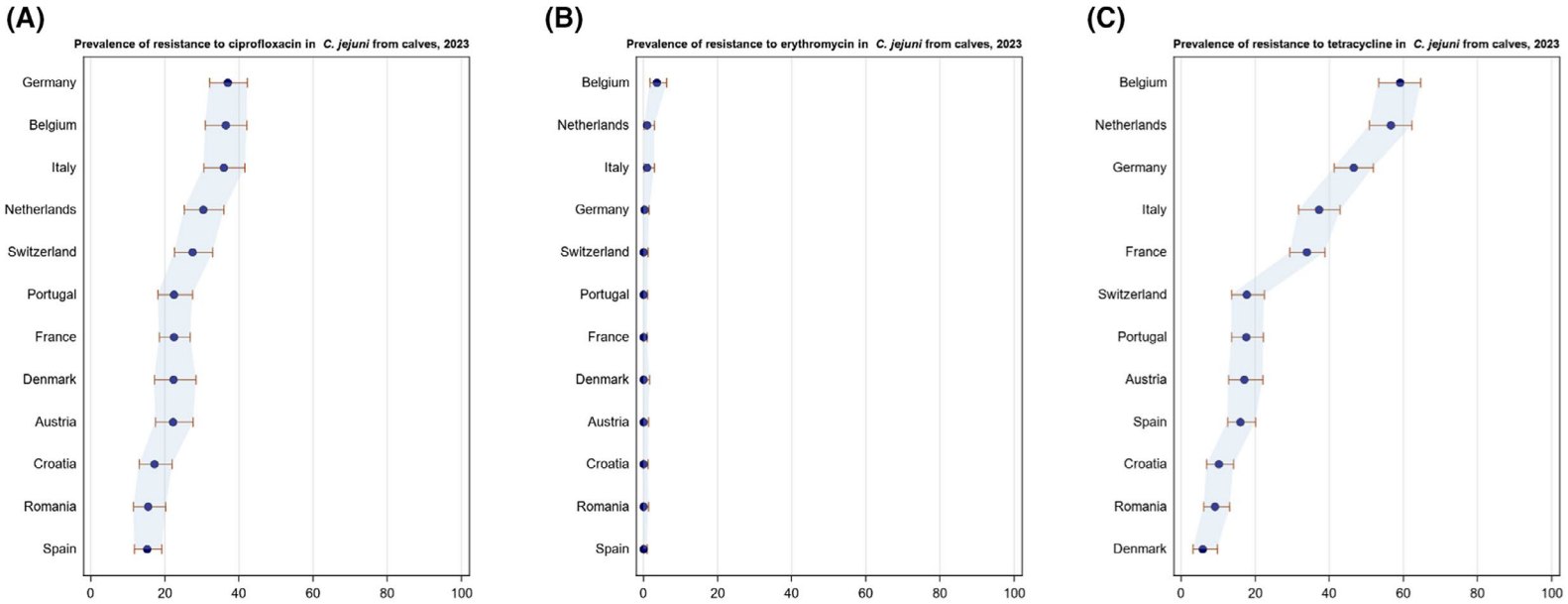


FIGURE 30 Prevalence of resistance to ciprofloxacin (A), erythromycin (B), tetracycline (C) and related 95% confidence intervals in *Campylobacter jejuni* from cattle under 1 year of age, per reporting country, 2023.

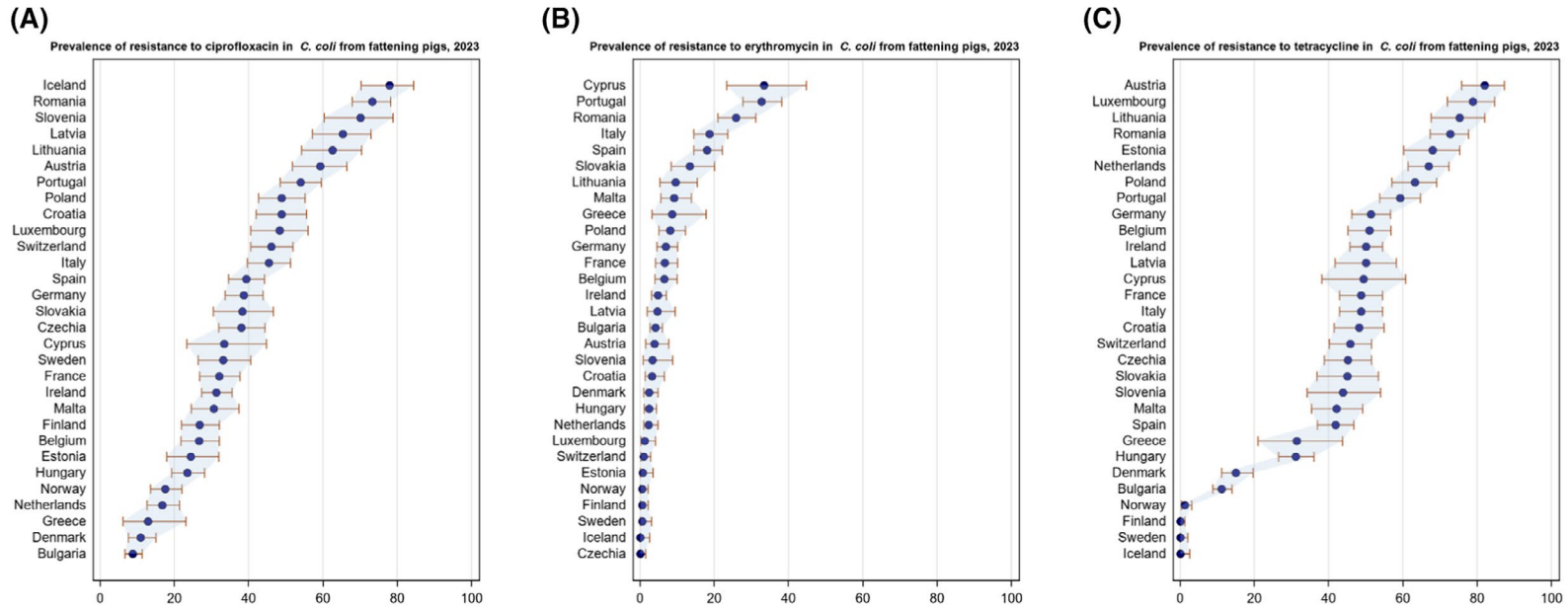


FIGURE 31 Prevalence of resistance to ciprofloxacin (A), erythromycin (B), tetracycline (C) and related 95% confidence intervals in *Campylobacter coli* from fattening pigs, per reporting country, 2023.

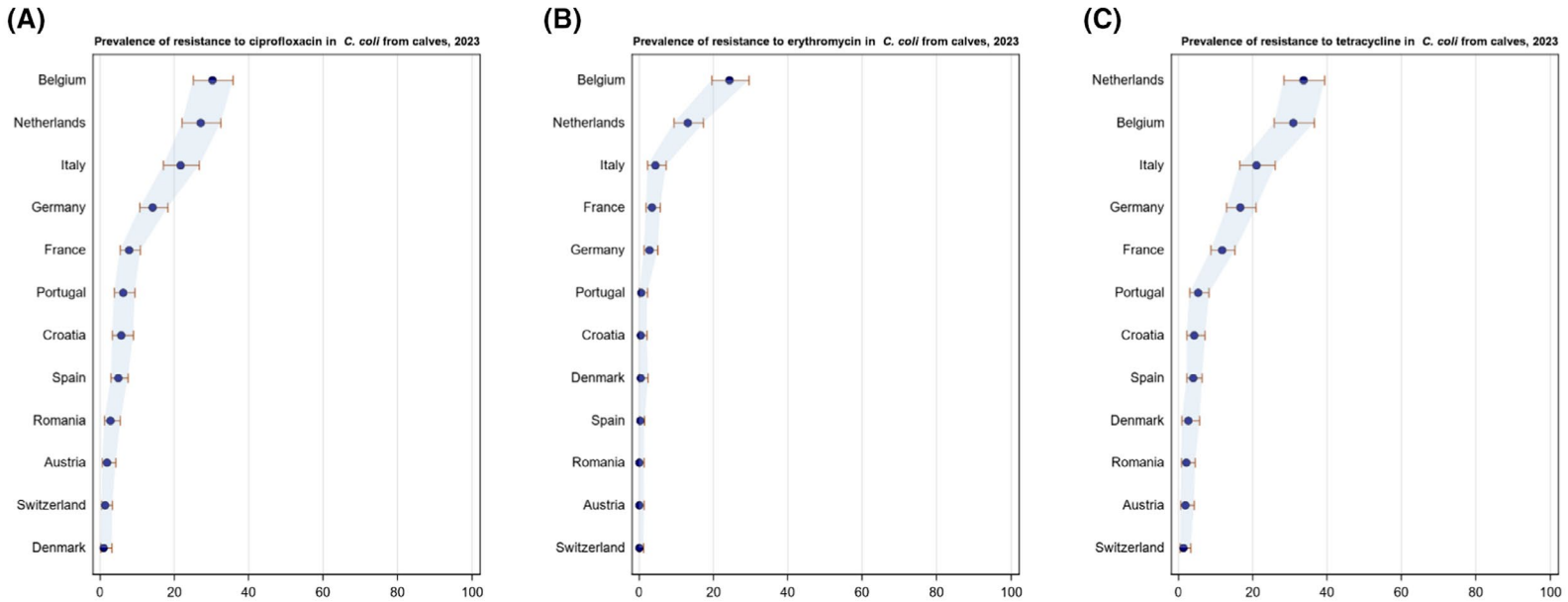


FIGURE 32 Prevalence of resistance to ciprofloxacin (A), erythromycin (B), tetracycline (C) and related 95% confidence intervals in *Campylobacter coli* from cattle under 1 year of age, per reporting country, 2023.

3.4.5 | Complete susceptibility and multidrug resistance

Analyses of complete susceptibility (CS) and multidrug resistance (MDR) focus on critically important antimicrobials for treatment of humans. The target substances that EFSA and ECDC agreed to include in the CS and MDR analyses are ciprofloxacin (class: fluoroquinolones), erythromycin (class: macrolides), gentamicin (class: aminoglycosides) and tetracycline. As the aim of such analyses is to compare CS and MDR in animals and humans, the related findings are only presented in Section 3.5 on the comparison of human and animal data.

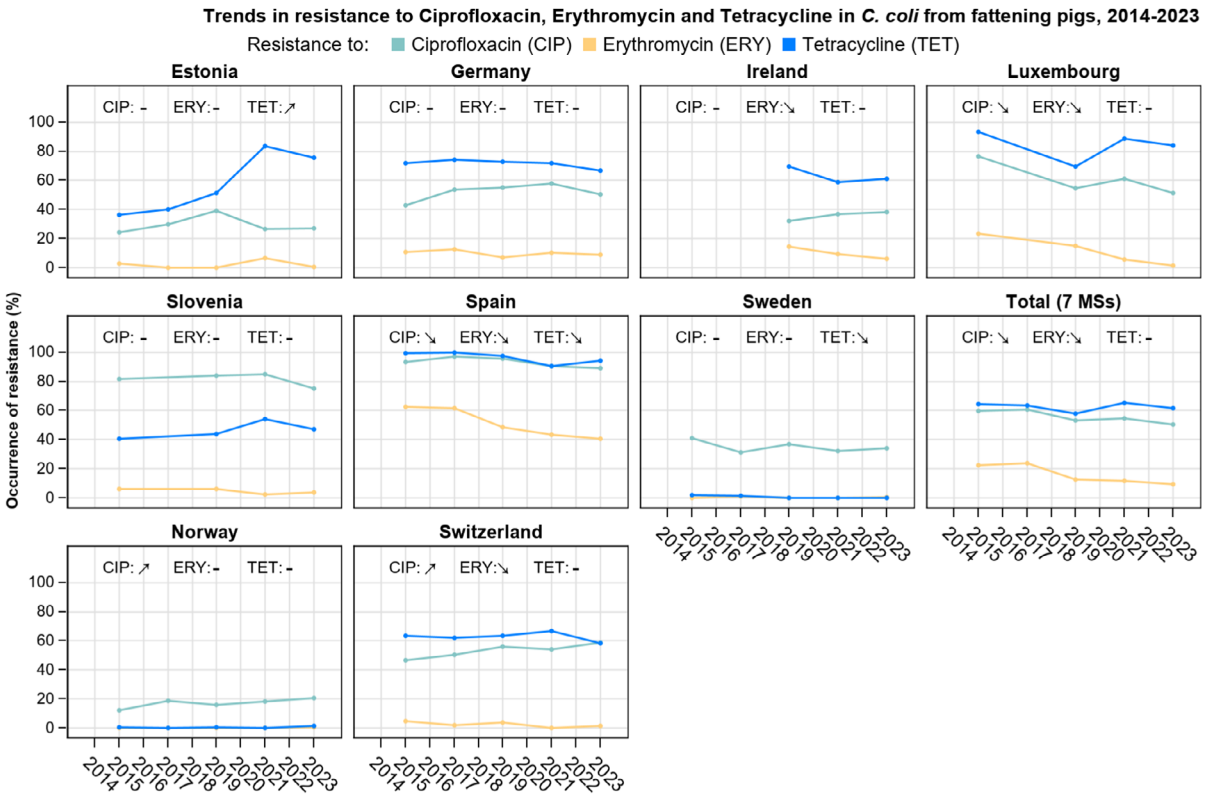
Detailed data on complete susceptibility and multidrug resistance in *C. jejuni* and *C. coli* isolates from different animal populations and in the different reporting countries are presented in Annex B.2 (tables 1–6, 10, and 11).

3.4.6 | Temporal trends

Evaluation of **temporal trends** in resistance to ciprofloxacin, erythromycin and tetracycline in *Campylobacter* isolates recovered from food-producing animals was performed for countries reporting data in the context of Commission Implementing Decision (EU) 2020/1729. The analysis included at least three years (three data points) within the period 2014–2023 separated by not more than a 1 year gap between them, with a minimum of 10 isolates per data point, and excluded RCs with more than one year gap during the last five-year period. When interpreting the results, it is important to note that trend analyses may be driven by particularly high or low levels of resistance reported in one or few data points leading to unexpected findings (e.g. detection of significant increasing or decreasing trends where the observed data do not seem to show any clear trend over the entire period). It is also relevant to note that between-year oscillations in the occurrence of resistance may not be captured in the evaluation of the trend for the entire period (2014–2023) and that very recent decreasing or increasing trends may therefore be masked by the overall trend. Moreover, trend results based on very few data points should be interpreted with caution, and more data and further analyses will be needed in the future for a more robust evaluation.

Temporal trends in resistance in* C. coli *from fattening pigs

Temporal trends showing resistance to selected antimicrobials in *C. coli* from fattening pigs, for the period 2014–2023, are shown in Figure 33 and Table 11 (see also Annex B.2, table 16). A significant increasing trend of resistance to ciprofloxacin was observed in two non-MSs (Norway and Switzerland), while a decreasing trend of resistance to ciprofloxacin was observed in two MSs (Luxembourg and Spain). No significantly increasing trend of resistance to erythromycin was observed among the reporting countries, while a significantly decreasing trend of resistance to erythromycin was found in four RCs (Ireland, Luxembourg, Spain and Switzerland). A significantly increasing trend of resistance to tetracycline was observed in Estonia, while the results indicated significantly decreasing tetracycline resistance in Spain and Sweden.



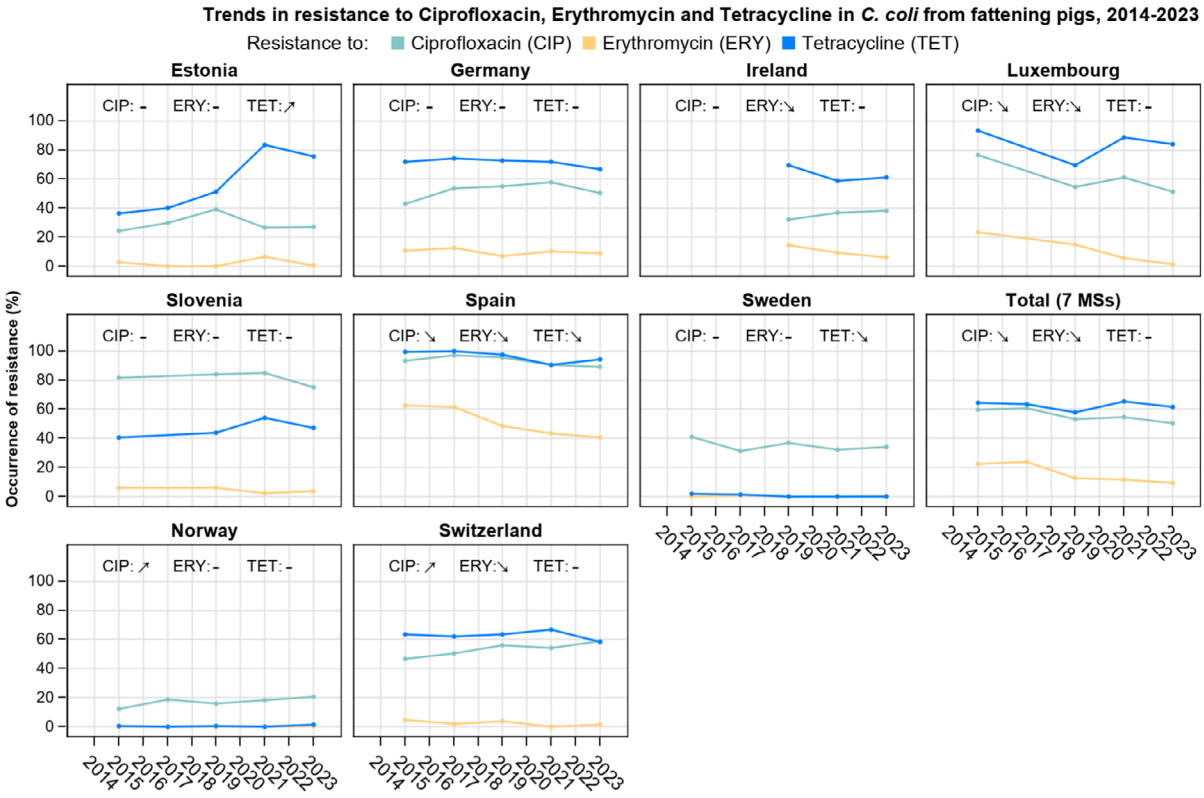


FIGURE 33 Trends in ciprofloxacin (CIP), erythromycin (ERY) and tetracycline (TET) resistance in *Campylobacter coli* from fattening pigs, 2014–2023. Only countries that reported data fulfilling all inclusion criteria explained in the text are shown. Overall temporal trend (shown in box 'Total (7 MSs)') is presented only for Member States and for odd years when the monitoring of AMR in EU in fattening pigs is mandatory according to Decision (EU) 2020/1729.

Temporal trends in resistance in Campylobacter isolates from cattle under 1 year of age

Due to the scarcity of comparable historical data on *C. jejuni* and *C. coli* from cattle under 1 year of age, the temporal trends in resistance to selected antimicrobials could not be analysed following the data inclusion criteria for this animal

population. Comparable data will be available in the coming years thanks to the implementation of the monitoring requirements laid down in Commission Implementing Decision (EU) 2020/1729.

Temporal trends in resistance in C. jejuni *and* C. coli *isolates from broilers*

The results from the analysis of temporal trends in resistance in *C. jejuni* isolated from broilers were obtained for the period 2014–2022 using data from 20 reporting MSs and 2 non-MSs (Table 11; see also Annex B.2, table 16; Annex B.3, figure 1A). For three MSs (Belgium, Finland and the Netherlands), data were available and considered for the period 2014–2023. The analysis of temporal trends in resistance to ciprofloxacin in *C. jejuni* from broilers indicated a significant increase in six MSs (Croatia, Denmark, Germany, Romania, Slovenia and Sweden). On the other hand, a significant decrease in resistance to ciprofloxacin in *C. jejuni* from broilers was detected in Finland, France and Latvia. A significant decrease in resistance to erythromycin was detected in six MSs (Bulgaria, Cyprus, Germany, Italy, Romania and Slovakia), while a significant decrease in resistance to tetracycline was seen in six MSs (Bulgaria, Finland, France, Italy, Spain and Sweden). A significant increase in resistance was detected for tetracycline in five MSs (Austria, Croatia, Denmark, Germany and Ireland), and for erythromycin in a single MS (Belgium).

The results from the analysis of temporal trends in resistance in *C. coli* from broilers were obtained using data from two MSs (Czechia and Slovenia) over the period 2014–2022, and from one MS (the Netherlands) over the period 2014–2023 (Table 11; see also Annex B.2, table 16; Annex B.3, figure 2). Three significant temporal trends were identified in *C. coli* isolated from broilers, including a decrease in tetracycline resistance in the Netherlands and in Slovenia, an increase in tetracycline resistance in Czechia and an increase in ciprofloxacin resistance in the Netherlands.

Temporal trends in resistance in C. jejuni *isolates from fattening turkeys*

Temporal trends in resistance to selected antimicrobials in *C. jejuni* isolates from fattening turkeys during the period 2014–2022 are displayed in Table 11 (see also Annex B.2, table 16; Annex B.3, figure 1B). The results from the analysis of temporal trends in resistance of *C. jejuni* isolated from fattening turkeys were obtained using data from seven reporting MSs (Austria, France, Germany, Italy, Poland, Portugal and Spain). Significant temporal trends in resistance in *C. jejuni* isolated from fattening turkeys were detected for ciprofloxacin in two MSs (an increasing trend in Poland and a decreasing trend in Portugal), as well as for tetracycline in three MSs (decreasing trend in France, Germany and Spain), and for erythromycin in two MSs (decreasing trends in Italy and Spain). No significant increase of resistance to tetracycline or erythromycin was detected.

Due to the scarcity of historical data on *C. coli* from fattening turkeys, the temporal trends of resistance to selected antimicrobials were not analysed for *C. coli* in this animal population. Comparable data will be available in the coming years thanks to the implementation of the monitoring requirements laid down in Commission Implementing Decision (EU) 2020/1729.

3.4.7 | High-level resistance to erythromycin

The distribution of MIC values related to **erythromycin resistance** in *Campylobacter* recovered from caecal samples of food-producing animals following legislative requirements in 2022 and 2023 are shown in Annex B.3 (Figure 3). It is interesting to note that even though MIC values were reported at low and moderate levels (ECOFF < MIC ≤ 128 mg/L), several isolates, especially *C. coli*, displayed high MIC (> 128 mg/L).

Figure 34 (see also Annex B.2, table 17) shows the number and proportion of erythromycin-resistant isolates (based on ECOFF values for *C. jejuni*: MIC > 4 mg/L and for *C. coli*: MIC > 8 mg/L) reported by MSs and non-MSs displaying resistance below or equal to 128 mg/L in comparison to those displaying high-level erythromycin resistance (128 mg/L < MIC ≤ 512 mg/L) and the highest level of erythromycin resistance (MIC > 512 mg/L) within each of the animal populations. A notable proportion of erythromycin-resistant isolates in both *Campylobacter* species displayed high MIC values, in particular *C. coli* isolates from cattle under 1 year of age (16.3% of isolates with MIC between 128 and 512 mg/L; 76.2% of isolates with MIC > 512 mg/L), from fattening pigs (47.2% of isolates with MIC between 128 and 512 mg/L; 39.1% of isolates with MIC > 512 mg/L), and from fattening turkeys (33.7% of isolates with MIC between 128 and 512 mg/L; 47.0% of isolates with MIC > 512 mg/L). Notably, a very high level of erythromycin resistance was also observed in erythromycin-resistant *C. jejuni* isolates from cattle under 1 year of age, although notably only a few *C. jejuni* isolates ($n = 24$) from cattle under 1 year of age were resistant to erythromycin.

Country-level findings on high-level resistance to erythromycin in *C. jejuni and C. coli* isolates are summarised in a dedicated text box in Annex B.3.

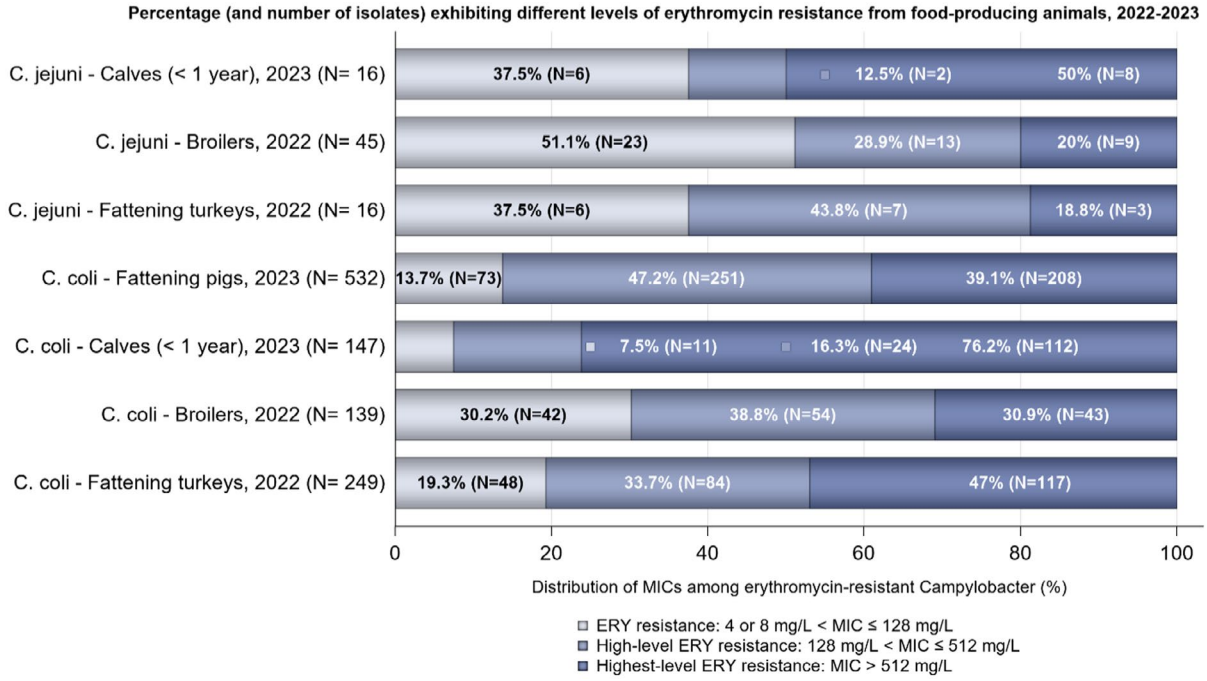


FIGURE 34 Percentage (and number) of *C. jejuni* and *C. coli* isolates exhibiting different levels of erythromycin resistance in fattening pigs, cattle under 1 year of age, broilers and fattening turkeys, in reporting MSs, United Kingdom (Northern Ireland) and non-MSs, 2023-2022.

3.4.8 | Summary of voluntary whole genome sequencing reporting

In 2022 and 2023, **whole genome sequencing** (WGS) information was reported on voluntary basis by some countries to further investigate the presence of genes (e.g. the *erm(B)* gene) or gene mutations (e.g. point mutations in the 23S rRNA ribosomal gene) that may confer high resistance against erythromycin. Additionally, three MSs also reported genes conferring resistance to gentamicin. The reported data is summarised in Table 10.

In 2022, WGS information on a total of 63 erythromycin-resistant isolates (1 *C. jejuni* from fattening turkeys, 27 *C. coli* from broilers and 35 *C. coli* from fattening turkeys from four MSs) were reported. The sequenced single *C. jejuni* isolate from fattening turkeys reported by Italy contained a 23S rRNA ribosomal gene A2075G mutation, even though it presented a MIC value of 64 mg/L. The A2075G mutation was equally detected in all 27 sequenced *C. coli* isolates from broilers, including three isolates with MIC 512 mg/L and eight isolates with MIC > 512 mg/L. Notably, most of the 17 *C. coli* isolates from broilers reported by Italy with the A2075G mutation presented MIC < 512 mg/L (13 isolates with MIC 128 mg/L, three isolates with MIC 64 mg/L and one isolate with MIC 512 mg/L). Among the 35 sequenced *C. coli* isolates from fattening turkeys, all but one presented the A2075G mutation, while a single isolate from Spain, with MIC > 512 mg/L presented the mutation A2074C in the same gene. Seventeen of the *C. coli* isolates from turkeys with the A2075G mutation presented MIC ≥ 512 mg/L (6 isolates with MIC 512 mg/L and 11 with MIC > 512 mg/L), while seventeen presented lower MIC values (12 isolates from Italy with MIC 128 mg/L, and 1 and 4 isolates, from Italy and Ireland, respectively, with MIC 256 mg/L).

In 2023, 30 isolates with the highest-level resistance to erythromycin (MIC > 512 mg/L) (2 *C. jejuni* and 4 *C. coli* from cattle under 1 year of age from 1 and 3 MSs, respectively, and 24 *C. coli* from fattening pigs from six MSs) were subjected to whole genome sequencing to determine their erythromycin resistance genotype. One *C. jejuni* isolate with MIC > 512 mg/L from cattle under 1 year of age from Italy presented the A2075G mutation in the 23S rRNA ribosomal gene. Among *C. coli* isolates from fattening pigs, of the 24 isolates with MIC > 512 mg/L, 11 presented a mutation in the 23S rRNA ribosomal gene (A2075G in all isolates except for one isolate from Portugal and one from Sweden). The *erm(B)* gene was not detected in *C. coli* isolates from fattening pigs with MIC > 512 mg/L. Also in 2023, among the four *C. coli* isolates from cattle under 1 year of age with the highest-level of erythromycin resistance, three isolates (two from Italy and one from Portugal) presented the A2075G mutation, while a single isolate from the Netherlands presented both the A2075G mutation and the *erm(B)* gene. The *erm(N)* gene was reported in one isolate from fattening pigs from Italy in 2023, although with a MIC value ≤ 512 mg/L.

In addition, three MSs (Italy, the Netherlands and Portugal) voluntarily reported WGS data for gentamicin resistance in *Campylobacter* isolates from food-producing animals. Gentamicin resistance genes were reported for seven and five *C. coli* isolates from broilers and fattening turkeys, respectively, from one MS in 2022 and in 2023 for 19 *C. coli* isolates from cattle under 1 year of age from the three MSs, for 48 *C. coli* isolates from fattening pigs from two MSs, for seven *C. jejuni* isolates from cattle under 1 year of age from one MS, and from two *C. jejuni* isolates from fattening pigs from one MS. Among all the isolates with reported gentamicin resistance genes, the most commonly detected genes were *aph(2″)-If and aph(2″)-Ii*, reported in 37 and 30 isolates, respectively. The gene *aph(2')-Ic* was detected in 17 isolates, and was the most common in *C. coli* from poultry (broilers and fattening turkeys). While *aph(3')-III* was only detected among poultry *C. coli* isolates, *aph(2')-Ic* was also found in *C. coli* from cattle under 1 year of age and fattening pigs. The gene *apmA*, a gene that confers broad-spectrum resistance to aminoglycosides, including gentamicin, was reported in a single *C. coli* isolate from cattle

under 1 year of age from Italy in 2023. Finally, the streptomycin resistance gene *aad9* was detected in a single *C. coli* isolate from pigs, and in two *C. coli* isolates from cattle under 1 year of age in Italy in 2023.

TABLE 10 Antimicrobial resistance genes and mutations conferring resistance to erythromycin and gentamicin reported for *Campylobacter jejuni* and *C. coli* from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age, 2022–2023.

Species	Animal population, year	ERY-resistant isolates	GEN-resistant isolates
C. coli	Cattle under 1 year of age, 2023	23S mutation 2075A>G (**IT(5), NL (1), PT(1)**)	*aph(2″)-If* (**IT (7)**)
		rplV mutation 103A>V (**IT(1)**)	*aph(2″)-Ii* (**IT (8)**)
		erm(B) (**NL(1)**)*	*aph(2″)-Ic* (**IT(1), NL(1), PT(1)**)
		–	*apmA* (**IT(1)**)
	Fattening pigs, 2023	23S mutation 2075A>G (**CY(3), IE(9), IT(30), PT(2)**)	*aph(2″)-Ic* (**IT(4), PT(3)**)
		23S mutation 2059A>G (**SE(1)**)	*aph(2″)-If* (**IT(22)**)
		erm(N) (**IT(1)**)	*aph(2″)-Ii* (**IT(17)**)
		rplV mutation 103A>V (**IT(1)**)	–
	Broilers, 2022	23S mutation 2075A>G (**IT (17), IE(2), ES(7), DE(1)**)	*aph(2′)-Ic* (**IT(4)**)
		–	*aph(3′)-If*; (**IT(2)**)
		–	*aph(3′)-III*; (**IT(1)**)
	Fattening turkeys, 2022	23S 2075A>G mutation (**DE(9), ES(2), IE(10), IT(13)**)	*aph(2′)-Ic* (**IT(3)**)
		23S 2074A>C mutation (**ES(1)**)	*aph(3′)-III* (**IT(2)**)
C. jejuni	Cattle under 1 year of age, 2023	23S 2075A>G mutation (**IT(2)**)	*aph(2′)-Ii* (**IT(5)**);
		–	*aph(2′)-If* (**IT(2)**)
	Fattening pigs, 2023	–	*aph(2′)-If* (**IT(2)**)
	Fattening turkeys, 2022	23S 2075A>G mutation (**IT(1)**)	–

Note: This table shows the number of individual isolates for which each AMR gene and mutation has been reported. Some of the reported isolates may harbour a combination of the indicated genes and mutations. Some of the reported isolates may have combined resistance to gentamicin and erythromycin.

*The *erm(B)* gene was reported in a *C. coli* isolate from cattle under 1 year of age where presence of the 23S 2075A>G mutation and the gentamicin resistance gene *aph(2′)-Ic* were also reported.

3.5 | Comparison of resistance data in *Campylobacter* spp. from humans and food-producing animals

The comparison of **occurrence of resistance** to selected antimicrobials and combined resistance to erythromycin and ciprofloxacin in *C. jejuni* and *C. coli* isolates between humans (2023) and food-producing animals (2022 and 2023) is presented in Figures 35 and 36, respectively.

Extremely high levels of resistance to **ciprofloxacin** were observed in isolates from humans (71.9% in *C. jejuni* by 24 MSs; 75.0% in *C. coli* by 24 MS) and from high to extremely high in food-producing animals (ranging from 34.0% in *C. jejuni* from fattening pigs to 84.1% in *C. coli* from fattening turkeys). In both humans and animals, the levels of resistance were higher for *C. coli* than for *C. jejuni*. The highest levels of resistance to ciprofloxacin among *Campylobacter* from food-producing animals were observed in *C. coli* from fattening turkeys in 2022 (84.1%), followed by *C. coli* from cattle under 1 year of age in 2023 (80.4%). However, isolates of *C. jejuni* from broilers (70.9%) and fattening turkeys (78.1%) presented very high occurrence as well. The lowest levels of resistance to ciprofloxacin were reported in both *C. jejuni* and *C. coli* from fattening pigs in 2023 (34.0% and 54.3%, respectively).

Overall resistance to **erythromycin** was reported at low levels for *C. jejuni* from both humans (0.8%) and food-producing animals (ranging from 1.5% in broilers to 2.1% in fattening pigs). Higher levels of resistance were observed in *C. coli* isolates from both humans (6.7%) and food-producing animals (ranging from 8.8% in broilers to 31.6% in cattle under 1 year of age). Overall, erythromycin resistance among animals was observed at the highest levels in *C. coli* isolates recovered from cattle under 1 year of age (31.6%) in 2023, followed by fattening turkeys (18.0%) in 2022, fattening pigs (13.0%) in 2023 and broilers (8.8%) in 2022.

Overall resistance to **gentamicin** was either absent or detected at low levels among *Campylobacter* isolated from food-producing animals (range from 0.0% in *C. jejuni* from fattening turkeys to 4.3% in *C. jejuni* from fattening pigs), except for moderate occurrence in *C. coli* from cattle under 1 year of age in 2023 (10.5%). Similarly, overall resistance to gentamicin was very low in human *C. jejuni* isolates (0.5%) and low in *C. coli* isolates from humans (2.5%).

The overall levels of resistance to **tetracycline** were high to very high in *C. jejuni* isolates from both humans (47.9%) and food-producing animals (ranging from 38.3% in fattening pigs to 65.6% in cattle under 1 year of age). Very high to extremely high levels of resistance to tetracycline were detected in *C. coli* isolates from humans (68.2%) and food-producing animals (ranging from 68.4% in fattening pigs to 88.6% in cattle under 1 year of age in 2023).

Overall levels of **combined resistance** to ciprofloxacin and erythromycin in *C. jejuni* were very low to low in both humans (0.6%) and food-producing animals (ranging from 1.1% in broilers to 2.1% in fattening pigs). Conversely, notable higher levels of co-resistance were observed in *C. coli* from both humans (6.8%) and animals, with the highest levels

reported in isolates from cattle under 1 year of age (30.3%) in 2023, followed by fattening turkeys (17.4%) in 2022, fattening pigs (10.6%) in 2023 and broilers (8.2%) in 2022.

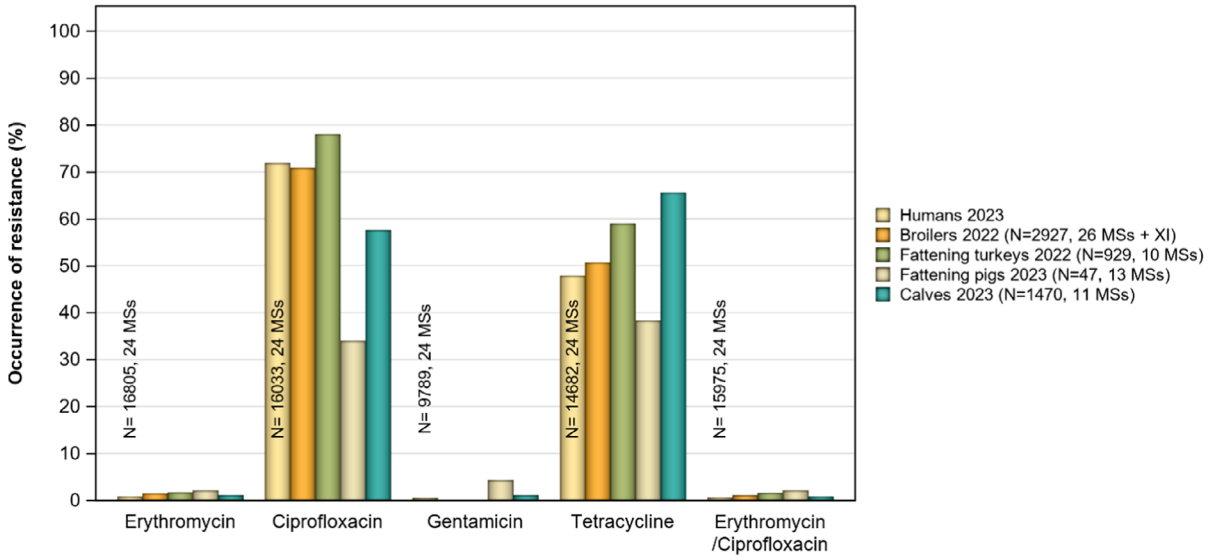


FIGURE 35 Comparison of *Campylobacter jejuni* occurrence of resistance between humans and food-producing animals, EU MSs, 2022–2023.

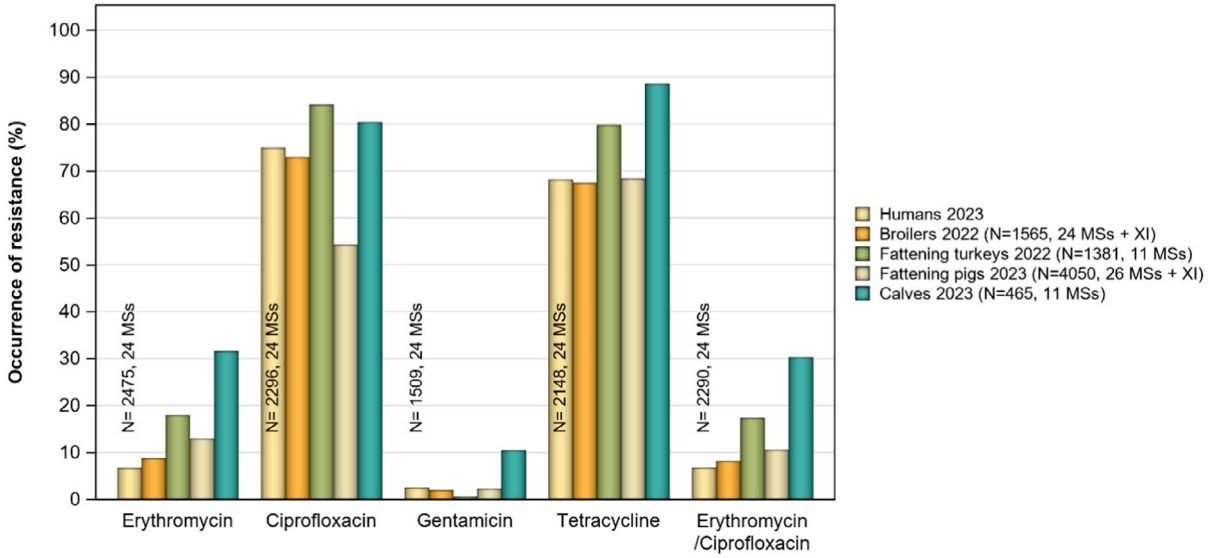


FIGURE 36 Comparison of *Campylobacter coli* occurrence of resistance between humans and food-producing animals, EU MSs, 2022–2023.

The analyses of CS and MDR in both humans and food-producing animals focus mainly on critically important antimicrobials for human treatment. For this reason, the target substances were agreed by EFSA and ECDC and include ciprofloxacin (class: fluoroquinolones), erythromycin (class: macrolides), gentamicin (class: aminoglycosides) and tetracycline. Levels of CS and MDR in *Campylobacter* isolates recovered from humans in 2023 and from food-producing animals in 2022–2023 by EU MSs are displayed in Figure 37. Detailed results on occurrence of complete susceptibility and multidrug resistance in *C. jejuni* and *C. coli* isolates from different animal populations and from humans, in the different reporting countries, are presented in Annex B.1 (tables 1–6, 10, ad 11) and Annex B.2 (tables 1 and 2), respectively.

Complete susceptibility to the four target antimicrobials was reported at levels of 25.5% in *C. jejuni* isolates from humans and at 11.0% in *C. coli* isolates (Figure 37). Similarly, in food-producing animals, the observed overall CS was higher in *C. jejuni* than in *C. coli* isolates. In *C. jejuni* isolates, the highest levels of CS were observed in fattening pigs (51.1%) in 2023, followed by broilers (23.9%) in 2022, cattle under 1 year of age (21.2%) in 2023 and fattening turkeys (16.5%) in 2022. Regarding *C. coli*, the overall CS observed was low for isolates from fattening turkeys (4.4%) in 2022 and cattle under 1 year of age (4.5%) in 2023 while it was higher for broilers (13.1%) in 2022 and fattening pigs (19.7%) in 2023. The average CS observed in *C. jejuni* and *C. coli* from fattening pigs and cattle under 1 year of age were mostly at levels like those observed in 2021, although slightly increased in *C. jejuni* from pigs (from 48.3% to 51.1%) and slightly decreased in *C. coli* from cattle under 1 year of age (from 6.3% to 4.5%).

Multidrug resistance, defined as resistance to at least three antimicrobials among the four target substances, was reported at levels of 0.6% in *C. jejuni* isolates and 8.6% in *C. coli* isolates from humans in 2023. Similarly, in food-producing animals, the observed overall MDR was higher in *C. coli* than in *C. jejuni* isolates (Figure 37). MDR was observed at low levels in *C. jejuni* isolates from broilers (1.0%) and fattening turkeys (1.6%) in 2022, and from cattle under 1 year of age (1.6%) and fattening pigs (4.3%) in 2023. The highest levels of MDR were reported in *C. coli* isolates from cattle under 1 year of age (34.8%), followed by fattening turkeys (16.9%), fattening pigs (10.7%) and broilers (8.3%). The MDR levels observed in *C. jejuni* and *C. coli* from fattening pigs and cattle under 1 year of age in 2023 were at similar levels to those reported in 2021, with deviations of up to 1%, except for MDR in *C. coli* from cattle under 1 year of age, which decreased from 39.3% in 2021 to 34.8% in 2023.

Interestingly, the proportions of CS and MDR *C. jejuni* and *C. coli* isolates recovered from humans showed the most similar results to isolates from broilers for both *Campylobacter* species, followed by isolates from cattle under 1 year of age for *C. jejuni* and by isolates from fattening pigs for *C. coli*.

The most common resistance pattern among MDR isolates in *C. jejuni* and *C. coli* isolates from humans was resistance to ciprofloxacin, erythromycin and tetracycline (in 60.0% and 72.9%, respectively). The second most common pattern in both species was resistance to gentamicin, ciprofloxacin and tetracycline (26.7% in *C. jejuni* and 14.0% in *C. coli*). Resistance against all four classes was observed in 8.3% ($n = 5$) and 13.2% ($n = 17$) of the MDR isolates of *C. jejuni* and *C. coli*, respectively. Among isolates recovered from food-producing animals, the most common MDR pattern across both *Campylobacter* species and all but one monitored animal populations was resistance to ciprofloxacin, erythromycin and tetracycline (ranging between 48.4% in cattle under 1 year of age in 2023 and 100% in fattening turkeys in 2022 for *C. jejuni* and between 72.2% in cattle under 1 year of age in 2023 and 97.4% in fattening turkeys in 2022 for *C. coli*). The predominant second most common MDR pattern was resistance to gentamicin, ciprofloxacin, erythromycin and tetracycline, ranging from 7.1% in *C. jejuni* from broilers in 2022 to 13.0% in *C. coli* from cattle under 1 year of age in 2023. One of the two MDR isolates of *C. jejuni* from fattening pigs was resistant to gentamicin, ciprofloxacin and tetracycline and the other was additionally resistant to erythromycin. Notably, the second most common pattern in *C. jejuni* from cattle under 1 year of age (50.0%) and *C. coli* isolates from fattening turkeys (2.2%) was combined resistance to gentamicin, ciprofloxacin and tetracycline. The least frequent MDR patterns were combined resistance to gentamicin, erythromycin and tetracycline (1.5% in *C. coli* from broilers, 0.5% in *C. coli* from fattening pigs and 0.6% in *C. coli* from cattle under 1 year of age) and combined resistance to gentamicin, ciprofloxacin and erythromycin (0.6% in *C. coli* from cattle under 1 year of age). Overall, a higher variation in the spectra of MDR patterns was observed among *C. coli* than among *C. jejuni* recovered from food-producing animals. Detailed results on the MDR patterns reported by individual countries, by *Campylobacter* species and animal category can be found in dedicated tables available on Zenodo at https://doi.org/10.5281/zenodo.14645440.

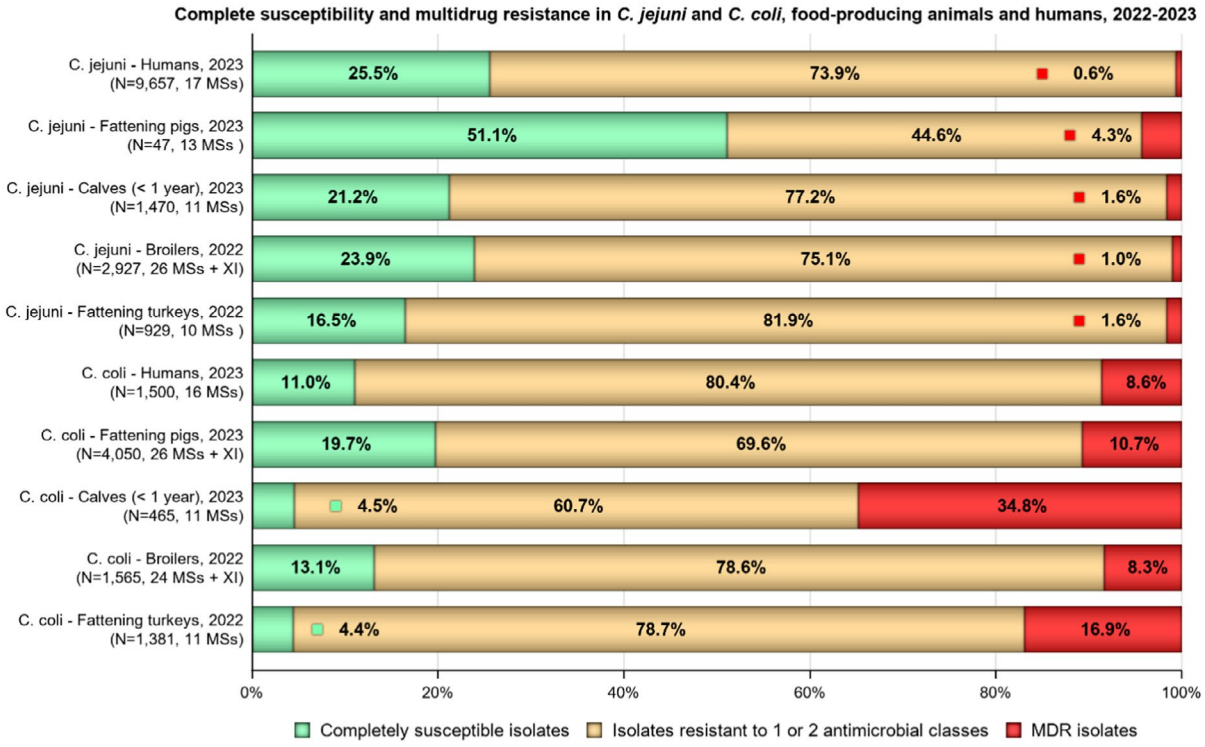


FIGURE 37 Proportion of isolates completely susceptible, resistant to one or two antimicrobial classes and multidrug resistant (MDR) among *Campylobacter jejuni* and *C. coli* from humans, broilers, fattening turkeys, fattening pigs and cattle under 1 year of age, in reporting EU MSs, 2022–2023.

Table 11 presents countries with significantly increasing or decreasing **trends in occurrence of resistance** to selected antimicrobials (ciprofloxacin, erythromycin and tetracycline) from human isolates and isolates from food-producing animals over the period 2014–2023. Factors such as the data collected and antibiotic usage may explain the variability observed between countries.

The most frequently detected country-level trends among *C. jejuni* isolates from both humans and food-producing animals were the increase in ciprofloxacin resistance (11 MSs for humans, 6 MSs for broilers and 1 MS for fattening turkeys) and the decrease in erythromycin resistance (10 MSs for humans, 6 MSs for broilers and 2 MSs for fattening turkeys). Significant decreases and increases in tetracycline resistance occurred in an approximately equal number of MSs for humans and broilers. A significant decrease in erythromycin resistance was also detected in *C. coli* from humans in nine MSs and from fattening pigs in four MSs. Significant decrease of ciprofloxacin resistance or increase of erythromycin resistance were rarely detected among the reporting countries included in the temporal trend analysis.

TABLE 11 Number of countries with significantly increasing or decreasing trends in resistance to selected antimicrobials for *Campylobacter jejuni* and *C. coli* from humans, broilers, fattening turkeys and fattening pigs, 2014–2023.

Campylobacter species	Origin	Ciprofloxacin		Erythromycin		Tetracycline	
		Increase	Decrease	Increase	Decrease	Increase	Decrease
C. jejuni	**Humans** (21 MSs + 2 non-MSs)	11 (AT, BG, CY, DE, DK, FR, LT, MT, PL, SI, SK)	3 (ES, FI, NO)	2 (EE, ES)	10 (DE, DK, FI, IT, LT, MT, NL, NO, PT, SK)	5 (AT, LT, NL, PL, SK)	5 (ES, FI, FR, NO, PT)
	Broilers (23 MSs + 2 non-MSs)	6 (DE, DK, HR, RO, SE, SI)	3 (FI, FR, LV)	1 (BE)	6 (BG, CY, DE, IT, RO, SK)	5 (AT, DE, DK, HR, IE)	6 (BG, ES, FI, FR, IT, SE)
	Fattening turkeys (7 MSs)	1 (PL)	1 (PT)	–	2 (ES, IT)	–	3 (DE, ES, FR)
C. coli	**Humans** (17 MSs)	2 (SI, SK)	2 (ES, NL)	1 (DE)	9 (AT, EE, ES, FI, FR, IT, MT, PT, SK)	2 (FR, SK)	3 (AT, ES, SI)
	Broilers (3 MSs)	1 (NL)	–	–	–	1 (CZ)	2 (NL, SI)
	Fattening pigs (7 MSs + 2 non-MSs)	2 (CH, NO)	2 (ES, LU)	–	4 (CH, ES, IE, LU)	1 (EE)	2 (ES, SE)

Abbreviations: AT, Austria; BG, Bulgaria; CH, Switzerland; CY, Cyprus; DE, Germany; DK, Denmark; EE, Estonia; EL, Greece; ES, Spain; FI, Finland; FR, France; HR, Croatia; IE, Ireland; IT, Italy; LT, Lithuania; LV, Latvia; MT, Malta; MSs, Member States; NL, Netherlands; NO, Norway; PL, Poland; PT, Portugal; RO, Romania; SE, Sweden; SI, Slovenia; SK, Slovakia.

3.6 | Discussion

Campylobacter is an important food-borne zoonotic agent and its occurrence in food-producing animals represents a risk for transmission to humans. Moreover, *Campylobacter* strains resistant to antibiotics may interfere with the treatment of human campylobacteriosis (Garcia & Heredia, 2013; Moore et al., 2006) and represent an important public health concern. The main species responsible for human infections is *C. jejuni*, which is usually predominant in poultry, followed by *C. coli* (Jehanne et al., 2020), more predominant in fattening pigs.

The implementation of harmonised EU monitoring of AMR in *C. jejuni* and *C. coli* from food-producing animals, according with Commission Implementing Decision (EU) 2020/1729, has improved integrated reporting and analysis of AMR in these species. This monitoring provides comparable data on the occurrence of AMR in the monitored animal populations, enabling trend assessments of AMR in animal production. However, it must be highlighted that the number of reporting countries and isolates may vary considerably, due to differences in national meat production.

Resistance in bacteria isolated from humans has been associated with resistance in bacteria from food-producing animals, and with antimicrobial consumption in both humans and animals. In the fourth joint inter-agency JIACRA report of the three EU agencies ECDC, EFSA and EMA, providing data from the respective networks on antimicrobial consumption and resistance in isolates from humans and animals, a statistically significant association was observed between resistance to fluoroquinolones, macrolides and tetracycline in *Campylobacter* spp. isolates from animals and isolates from humans in the EU (ECDC, EFSA and EMA, 2024).

Overall, the 2022–2023 AMR data from *C. jejuni* and *C. coli* isolates in humans and animal populations showed high to extremely high levels of resistance to fluoroquinolones (in this report represented by ciprofloxacin). Moreover, increasing trends of ciprofloxacin resistance were detected in *C. jejuni* from human isolates in 11 reporting countries (2014–2023) and from broilers in six countries, as well as from fattening turkeys in one MS. A similar trend was observed in *C. coli* from humans in nine countries, broilers in one country and fattening pigs in two non-Member States. These findings are consistent with the global increase in fluoroquinolone resistance in *Campylobacter* from human infections, with evidence of zoonotic transmission of resistant strains (Inglis et al., 2021; Ortega-Sanz et al., 2025; Yang et al., 2019). A recent genomic analysis

of *Campylobacter* isolates in Spain revealed a high occurrence of fluoroquinolone resistance, both in *C. jejuni* and *C. coli*, throughout the poultry supply chain and in clinical isolates from hospitalised humans (Ortega-Sanz et al., 2025). Notably, the analysis showed a higher diversity of resistance genetic determinants among isolates from hospitals and retail than those from the initial stages of the poultry supply chain, suggesting that resistance may not originate solely at the farm level. The high resistance levels observed in animal isolates at farm level suggest a continued high use of fluoroquinolones in food-producing animals, particularly in poultry production, where large numbers of animals may be affected by flock antimicrobial treatment.

The high level of ciprofloxacin resistance in *Campylobacter* is a concern, given that fluoroquinolones, like ciprofloxacin, are commonly used to treat diarrhoea in humans (Espinoza et al., 2020). Although antibiotic treatment for human campylobacteriosis is generally discouraged due to the self-limiting nature of the disease, it may be necessary for immunocompromised patients or those with co-morbidities (Yang et al., 2019). However, the high fluoroquinolone resistance in *Campylobacter* makes ciprofloxacin a less advisable treatment option, unless susceptibility testing confirms its effectiveness. Moreover, as ciprofloxacin is no longer recommended for treating human campylobacteriosis, even low levels of resistance to other critically important antimicrobials pose a public health concern.

The primary mechanism of resistance to quinolones and fluoroquinolones in *Campylobacter* involves the C257T mutation in the *gyrA* gene (Elhadidy et al., 2020; Espinoza et al., 2020; Garcia-Fernandez et al., 2024). Alterations in the expression of the CmeABC multidrug efflux pump in *Campylobacter* can lead to increased minimum inhibitory concentrations (MICs) of various antimicrobials, including fluoroquinolones, while also enhancing the bacterium's ability to survive in bile salts and colonise the host intestine (Lekshmi et al., 2023). Highly resistant *Campylobacter* isolates carrying a transferable 'super' efflux pump variant, RE-CmeABC, were first described in China (Yao et al., 2016). These isolates exhibited elevated MICs to ciprofloxacin, as well as florfenicol, chloramphenicol, erythromycin and tetracycline.

The RE-CmeABC efflux pump has been detected in recent studies of *Campylobacter* from poultry and humans with campylobacteriosis (Gao Fen et al., 2023; Gharbi et al., 2024; Ortega-Sanz et al., 2025). Furthermore, a recent investigation has identified plasmid-mediated quinolone resistance genes among *Campylobacter coli* isolates from poultry, including *qnrB*, *qnrS* and *qepA* (Gharbi et al., 2024). This finding raises concerns about the potential for horizontal transfer of quinolone resistance genes among *Campylobacter* populations, warranting further investigation.

Considering that fluoroquinolones are no longer a preferable option for the treatment of severe human campylobacteriosis in Europe, macrolides are now the main class of antibiotics used as first-line treatment of these infections. Therefore, monitoring resistance to macrolides in both humans and food-producing animals is of particular relevance for public health.

Resistance to erythromycin, belonging to macrolides, was either not detected or detected at very low levels in *C. jejuni* from humans, poultry and cattle under 1 year of age, but was higher in *C. coli* isolates from humans (overall, 6.7%), cattle under 1 year of age (overall, 31.6%), fattening turkeys (overall, 18.0%), fattening pigs (overall, 13.0%) and broilers (overall, 8.8%). High variability was observed between countries, with some countries reporting high levels of resistance to erythromycin in isolates from humans and food-producing animals. For example, in 2023, Portugal and Cyprus reported 22.1% and 18.2% erythromycin resistance, respectively, in *C. coli* isolates from humans, and reported the highest occurrences of erythromycin resistance in *C. coli* from fattening pigs (52.7% from Portugal and 62.8% from Cyprus). In 2023, Belgium also reported extremely high occurrence of erythromycin resistance in *C. coli* from cattle under 1 year of age (75.9%), but did not report data for *C. coli* in humans.

Interestingly, erythromycin resistance significantly decreased in *C. jejuni* from humans, broilers and fattening turkeys in 10, 6 and 2 reporting countries, respectively, over the period 2014–2023. In the same period, decreasing trends of resistance to erythromycin in *C. coli* were observed in nine and four reporting countries for humans and fattening pigs, respectively. Increasing trends of erythromycin resistance were rarely detected in the period under analysis. Notably, a high proportion of erythromycin-resistant isolates displayed very high MIC values (MIC > 512 mg/L), especially among isolates from cattle under 1 year of age. Three MSs (Belgium, France and the Netherlands) contributed the majority of *C. coli* isolates from cattle under 1 year of age with extremely high-level resistance to erythromycin (MIC > 512 mg/L). The underlying cause of these high erythromycin resistance levels is unclear, but it is possible that selection due to group treatments directly with macrolides, the second antimicrobial class used in Dutch veal farms (Mallioris et al., 2024), or cross-selection due to use of other antimicrobial classes contributes to this resistant pattern. For instance, the use of enrofloxacin has been shown to significantly alter the profiles of the calves' faecal microbiota and resistome, with high doses of enrofloxacin possibly inducing clonal expansion and transfer of AMR genes among gut microbial species (Beyi et al., 2021).

Macrolide resistance in *Campylobacter* is known to be mediated by mutations in the 23S rRNA gene (such as A2074G, A2074C and A2075G) (Garcia-Fernandez et al., 2024; Lekshmi et al., 2023; Luangtongkum et al., 2009), the presence of the transferable *erm(B)* gene and mutations in the *rplD* or *rplV* genes encoding 50S ribosomal proteins (Elhadidy et al., 2019, 2020). The *erm(B)* gene, often associated with multidrug resistance islands (MDRI) or plasmids in *Campylobacter*, may confer a high level of resistance to macrolides, lincosamides and/or streptogramin B antibiotics (Wang et al., 2014). An increase of the tested concentrations of erythromycin in susceptibility testing (up to 512 mg/L instead of 128 mg/L) has been implemented since 2021 according to Commission Implementing Decision (EU) 2020/1729. This change enables differentiation of isolates with low-level resistance (MIC < 128 mg/L), which are likely to be caused alone by polymorphisms of the L4 (*rplD* gene mutation) and L22 (*rplV* gene mutation) 50S ribosomal proteins, or the expression of the CmeABC efflux pump, from those with a high-level resistance (≥ 512 mg/L), which are more likely to carry the *erm(B)* gene, even though mutational resistance cannot be ruled out (Wang et al., 2014). Whole genome sequencing of *C. jejuni* and *C. coli* isolates from

food-producing animals in 2022–2023, revealed that most sequenced isolates harboured the A2075G mutation in the 23S rRNA gene. Notably, the *erm(B)* gene was found in a single *C. coli* isolate from fattening pigs reported by the Netherlands in 2023, which also harboured the A2075G mutation. Other relevant findings included a *C. coli* isolate from fattening turkeys reported by Spain in 2022 with an A2074C mutation, and a *C. coli* isolate from fattening pigs reported by Portugal in 2023 with multiple other mutations in the 23S rRNA gene. These findings support what is suggested by literature that point mutations in the 23S rRNA gene may confer levels of high resistance against erythromycin similar to those observed in *erm(B)*-mediated resistance in *Campylobacter*, especially in combination with the activity of the efflux pump CmeABC (Bejaoui et al., 2022; Wei & Kang, 2018).

Tetracycline resistance levels in humans and food-producing animals were moderate to extremely high in 2022 and 2023. High levels of resistance were reported in *C. jejuni* from cattle under 1 year of age in 2023 (65.6%) and for *C. coli* isolated from all food-producing animals (ranging between 67.5% in broilers in 2022 and 88.6% in cattle under 1 year of age in 2023). A decade-long review of AMR in *Campylobacter* isolates from animals and humans in Europe has revealed persistently high levels of tetracycline resistance (Barata et al., 2024). Notably, tetracyclines are the most used antimicrobial class in cattle production in some MSs (Mallioris et al., 2024), which may contribute to the high levels of occurrence observed in isolates from cattle under 1 year of age.

The prevalence of resistance to selected antimicrobials in *Campylobacter* isolates from food-producing animals in 2022 and 2023 was estimated at country level by combining the proportion of *C. jejuni* or *C. coli* isolates showing microbiological resistance with the percentage of all caecal samples positive for the corresponding *Campylobacter* species. This approach enables the monitoring of temporal trends in both the prevalence of *C. jejuni* and *C. coli* and the occurrence of resistance in each species, across different animal populations, through a single indicator at the country level. However, it is essential to consider that various factors, such as rearing conditions, feed, climate and others, may influence the true prevalence of resistance.

Between-country variability from low to high levels was observed in the prevalence of ciprofloxacin-resistant and tetracycline-resistant *C. jejuni* and *C. coli* in cattle under 1 year of age. This variability was even higher among *C. coli* isolates from fattening pigs, ranging from absent to extremely high between countries. Notably, the two MSs (Cyprus and Portugal) with the highest prevalence of erythromycin-resistant *C. coli* in fattening pigs in 2023 also reported moderate to high levels of erythromycin resistance in *C. coli* from humans, suggesting that fattening pigs could be a reservoir of erythromycin resistance for humans. Several studies have estimated that pig meat is a potential source of *C. coli* infections in humans (Hudson et al., 2021; Pascoe et al., 2024). This highlights the potential for zoonotic transmission of erythromycin-resistant *Campylobacter*, which is a significant public health concern given the increasing reliance on macrolides, such as erythromycin and azithromycin, as the first-line treatment of human campylobacteriosis.

MDR levels were generally lower in *C. jejuni* than in *C. coli* isolates from both humans and animals, ranging from very low in *C. jejuni* to low levels in *C. coli* from humans and broilers, moderate levels reported in *C. coli* from fattening turkeys and fattening pigs, and high levels in *C. coli* from cattle under 1 year of age. Notably, a comparison of CS and MDR *C. jejuni* and *C. coli* isolates from humans and animals showed similar results between humans and broilers for both *Campylobacter* species, suggesting that broilers may be also an important reservoir for the transmission of resistant *C. coli* to humans. This finding is consistent with recent studies that have identified chicken as the main or an important source of both *C. jejuni* and *C. coli* human campylobacteriosis in France (Jehanne et al., 2020), in the United Kingdom (FSA, 2021) and the United States (Hudson et al., 2021; Pascoe et al., 2024).

Chloramphenicol resistance varied between absent to very low among *Campylobacter* isolates from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age in 2022 and 2023, except for *C. coli* from cattle under 1 year of age, which showed a low occurrence of resistance to chloramphenicol (1.7%) in 2023.

Ertapenem resistance levels varied among *Campylobacter* isolates from different animal species. In 2022, moderate resistance was observed in *C. jejuni* from broilers and fattening turkeys, while high and very high resistance was seen in *C. coli* from broilers and fattening turkeys, respectively. In 2023, resistance levels ranged from absent to low in *C. jejuni*, and from high to low in *C. coli* from cattle under 1 year of age and fattening pigs, respectively. Despite the lack of a validated EUCAST epidemiological cut-off for ertapenem, the results presented in this report showed a shift towards higher MIC values among *Campylobacter* isolates from fattening pigs and cattle under 1 year of age between 2021 and 2023. This finding is of public health concern as carbapenems, including ertapenem, are recommended for treating invasive *Campylobacter* infections in humans (Dai et al., 2020; EFSA, 2019).

WGS of isolates, particularly those with multidrug resistance, high-level resistance to erythromycin or ciprofloxacin, or resistance to gentamicin or ertapenem is strongly encouraged to gain further insights into the AMR genes involved, their genetic origin and their potential of horizontal transmission. Moreover, WGS can contribute to the detection of prevalent resistant lineages or subtypes (Garcia-Fernandez et al., 2024; Mouftah et al., 2021; Webb et al., 2018) in different sources and enable comparison between animal and human isolates.

4 | ANTIMICROBIAL RESISTANCE IN INDICATOR *E. COLI*

4.1 | Key findings

- Resistance to **ampicillin, sulfamethoxazole, trimethoprim or tetracycline** was common and the median[4] levels of resistance to those substances were high or very high in all animal populations in 2022–2023. Resistance to quinolones was common in broilers and fattening turkeys for which median levels of resistance were very high and high, respectively. Resistance to other antimicrobials was less common.
- Resistance to **meropenem** was detected in one isolate from turkeys in 2022 but not in any isolates in 2023. The isolate was reported by Italy and was confirmed to carry the $bla_{\text{OXA-181}}$ gene.
- Large differences in the levels of AMR were recorded among countries. Lower levels were typically reported in Northern Europe.
- **Complete susceptibility (CS)** was more common in isolates from fattening pigs and cattle under 1 year of age than in those from broilers and fattening turkeys. Conversely, **Multidrug resistance (MDR)** was more frequent in isolates from broilers and turkeys than in those from pigs and cattle under 1 year of age. Marked differences in the levels of CS and MDR were observed among countries. The antimicrobials most often represented in the MDR patterns were tetracycline, ampicillin, sulfamethoxazole, trimethoprim and additionally, quinolones in broilers and turkeys.
- The **Key Outcome Indicator of complete susceptibility (KOI_{CS}),** accounting for the varying sizes of the different food-producing animal populations in a country, varied widely between countries, ranging from < 10% to > 80%. The highest KOI_{CS} were usually observed in Northern Europe.
- Resistance to highest priority Critically Important Antimicrobials (hpCIA) in human medicine was uncommon for **colistin, azithromycin and third-generation cephalosporins** (cefotaxime or ceftazidime), and median levels of resistance ranged between rare and low in all animal populations. Median levels of resistance to ciprofloxacin were low for pigs and cattle under 1 year of age but very high for broilers and high for fattening turkeys. Combined resistance to third-generation cephalosporins and fluoroquinolones was generally uncommon in all animal populations.
- Statistically significant decreasing **trends** in resistance to ampicillin, ciprofloxacin, cefotaxime, tetracycline and colistin, as well as increasing trends in CS and KOI_{CS} reveal progress towards lower levels of resistance in several reporting countries. Improvement in the situation has been most pronounced in broilers and fattening turkeys over the recent years.

4.2 | Monitoring resistance in indicator *E. coli*

The monitoring of AMR in indicator commensal *E. coli* collected from the intestinal flora of healthy food-producing animals and derived food provides insight into the potential reservoirs of resistant bacteria that could possibly be transferred between animal populations and humans. It also provides indirect information on the reservoirs of resistance determinants (genetic elements, such as genes and plasmids) that could be transferred to bacteria that are pathogenic to animals and/or humans. Such monitoring is therefore of great relevance for both public and animal health. The occurrence of AMR in indicator *E. coli* likely depends on several factors, including the selective pressure exerted by the use of antimicrobials in food-producing animals, clonal spread of resistant organisms, dissemination of resistance determinants and the effects of co-selection in bacteria exhibiting MDR. The monitoring concept is described in the EFSA interactive Story Map on AMR in indicator commensal *E. coli*, tailored to the general public and available online (here).

Since 2014, the EU legislation[5] has provided detailed requirements for the harmonised monitoring and reporting of AMR in zoonotic and commensal bacteria from food-producing animals. The monitoring of AMR in indicator *E. coli* isolates recovered from caecal contents of domestically produced fattening pigs and broilers is mandatory in odd- and even-numbered years, respectively. Furthermore, for the MSs with consistent production of cattle under 1 year of age and turkeys over a certain tonnage per annum, the monitoring of AMR in indicator *E. coli* is also mandatory. Since 1 January 2021, the scope of the monitoring has been enlarged to imported fresh meat from third countries. The antimicrobial substances included in the harmonised panel for the monitoring of AMR in *E. coli* have provided continuity of monitoring data and epidemiological tracing of isolates with resistance patterns of interest to public health. The substances of the panel have been selected either because of public health importance, epidemiological relevance, or common use in veterinary medicine. The AMR data are harmonised with respect to representative sampling design, laboratory methodologies, reporting and interpretation of resistance. Therefore, AMR data can be considered representative for the EU.

[4]The median level of AMR in indicator *E. coli* from a given animal population among the EU Member States is the value separating the higher half from the lower half of the occurrences of resistance registered in the EU Member States. It may be thought of as the middle value of the EU Member State data set.

[5]Commission implementing decision (EU) 2013/652 and the subsequent Commission implementing decision (EU) 2020/1729.

4.3 | Resistance in poultry, porcine and bovine populations

4.3.1 | The data reported

In 2023, 27 MSs, the United Kingdom (Northern Ireland) and 5 non-MSs[6] reported data on AMR in indicator *E. coli* from pigs, and 11 MSs and 2 non-MSs[7] submitted data on isolates from cattle under 1 year of age. In 2022, 27 MSs, the United Kingdom (Northern Ireland) and 4 non-MSs[8] reported data on isolates from broilers, and 13 MSs and 1 non-MSs[9] reported data on isolates from fattening turkeys.

Summary data on the occurrence of AMR to commonly used antimicrobials in veterinary medicine[10] and highest priority Critically Important Antimicrobials (hpCIAs)[11] as well as combined resistance to ciprofloxacin and cefotaxime are reported in this chapter. Additionally, results from the analysis of MDR patterns and complete susceptibility (CS) are also presented. Annex C presents detailed aggregated data on the occurrence of AMR, MDR, CS and combined resistance in *E. coli* from broilers and turkeys (2022), as well as pigs and cattle (2023), at both MS and MS-group levels. Resistance in indicator *E. coli* isolates recovered from imported fresh meat sampled at BCPs in 2022 and 2023 is also presented below in a dedicated Textbox.

Moreover, the findings of the specific monitoring of ESBL-, AmpC- or CP-producing *E. coli* using selective culturing methods, including the prevalence and occurrence of the presumptive ESBL-, AmpC- or CP-producing *E. coli* are presented in chapter 5.

EFSA dashboard on antimicrobial resistance in indicator commensal *E. coli*

The EFSA dashboard on AMR (available online here) is a graphical user interface for searching and querying the large amount of data collected each year by EFSA from the EU MSs and other reporting countries based on the EU legislation. Yearly data and temporal trends in occurrence of AMR to selected antimicrobials in indicator *E. coli* from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age can be displayed interactively using charts, graphs and maps. The user can select for reporting year, reporting country, animal population and antimicrobial substance. The main statistics can also be viewed and downloaded in tabular format. Detailed information on the use and features of the AMR dashboard can be found in the video user guide embedded in the dashboard.

4.3.2 | The occurrence of antimicrobial resistance

Resistance to antimicrobials commonly used

Resistance to **ampicillin**, **sulfamethoxazole**, **trimethoprim** and **tetracycline** was common among all four investigated animal populations, with high to very high median levels of resistance among the reporting EU MSs (Figure 1; Annex C). Large differences in resistance levels to ampicillin, sulfamethoxazole, trimethoprim and tetracycline between countries were, however, observed in all animal populations, ranging from 0.0% to 88.2%, 7.1% to 73.0%, 0.0% to 62.0% and 5.1% to 82.4%, respectively (Figure 1; Annex C, tables 1–4).

For **chloramphenicol**, the overall median resistance level for all reporting MSs was low to moderate for all animal populations (range 10.0%–13.8%). Some countries, however, reported high to very high resistance (Annex C, tables 1–4). The overall median level of resistance to **gentamicin** was very low or low in all four animal populations (range 1.4%–3.7%). Some countries reported, however, moderate levels of resistance and one country reported a high level of resistance among isolates from broilers (Annex C, tables 1–4).

Resistance to highest priority critically important antimicrobials

Among the antimicrobials tested in the mandatory monitoring of indicator *E. coli*, ciprofloxacin (fluoroquinolones), cefotaxime and ceftazidime (third-generation cephalosporins), colistin (polymyxins) and azithromycin (macrolides) have been categorised by WHO as highest priority Critically Important Antimicrobials (hpCIA) (WHO, 2019).

Resistance to **ciprofloxacin** and **nalidixic acid** was common in poultry, with very high median levels in broilers and high median levels in turkeys (Figure 1; Annex C, tables 1 and 2). For both ciprofloxacin and nalidixic acid resistance, large differences occurred between countries, ranging from 0.0% to 94.5% and 0.0% to 90.0%, respectively (Figure 1; Annex C).

[6]Iceland, Montenegro, Norway, Republic of North Macedonia and Switzerland.

[7]Republic of North Macedonia and Switzerland.

[8]Iceland, Norway, Republic of North Macedonia and Switzerland.

[9]Norway.

[10]Ampicillin, sulfamethoxazole and tetracyclines.

[11]Ciprofloxacin (fluoroquinolones), cefotaxime and ceftazidime (third-generation cephalosporins), colistin (polymyxins) and azithromycin (macrolides).

Very high levels of resistance to (fluoro)quinolones were recorded in isolates from broilers (median: **ciprofloxacin** 54.3%; **nalidixic acid** 50.3%), and high levels in isolates from turkeys (median: ciprofloxacin 32.6%; nalidixic acid 28.3%) (Figure 1; Annex C, tables 1 and 2). In contrast, the median levels of resistance to both these antimicrobials were low in pigs (median 8.1% and 4.9%, respectively) and cattle under 1 year of age (median 6.3% and 3.2%, respectively) (Figure 38; Annex C, tables 3 and 4). Furthermore, most countries reported nalidixic acid resistance at lower levels than ciprofloxacin resistance. This was most notable for pigs and cattle under 1 year of age, and at the MS-group level, nalidixic acid resistance was approximately half that for ciprofloxacin for both these animal populations. The largest differential was seen among isolates from turkeys with 4.3 percentage points difference.

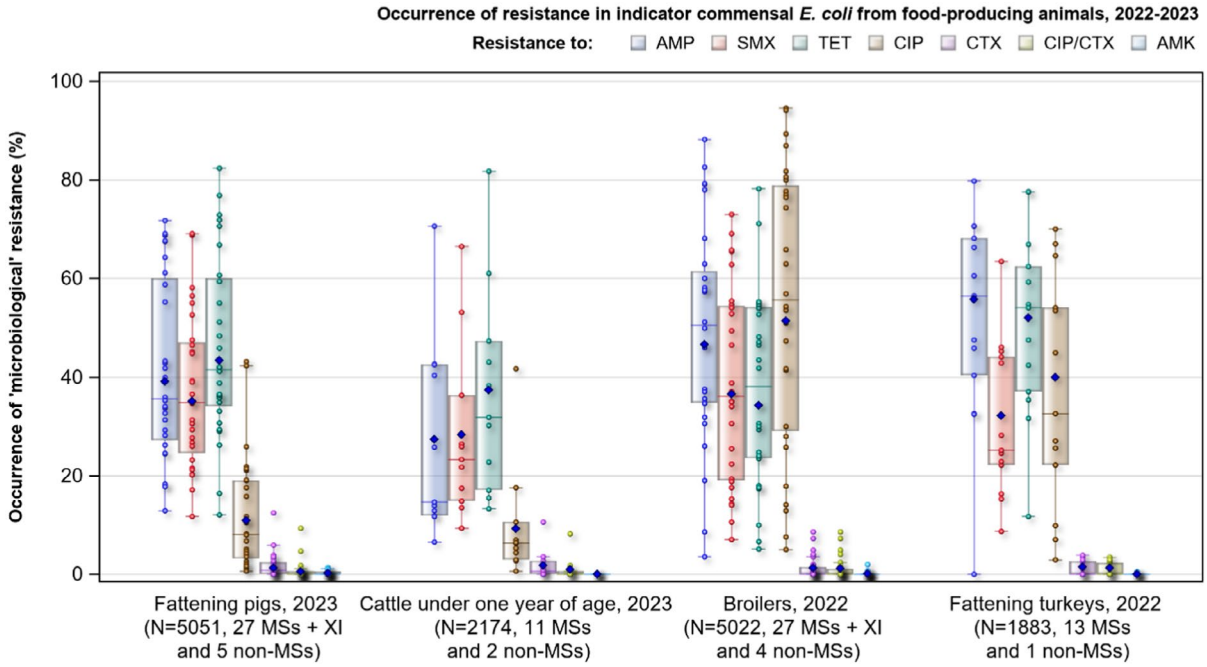


FIGURE 38 Distribution of the occurrence of resistance to selected antimicrobials in indicator commensal *E. coli* isolates recovered from fattening pigs and cattle under 1 year of age in 2023, and from broilers and fattening turkeys in 2022, EU MSs, XI and non-MSs.
AMK, amikacin; AMP, ampicillin; CIP/CTX, combined microbiological resistance to ciprofloxacin and cefotaxime; CIP, ciprofloxacin; CTX, cefotaxime; *N*, total number of indicator commensal *E. coli* isolates reported by MSs; SMX, sulfamethoxazol; TET, tetracycline; XI, United Kingdom (Northern Ireland). Blue diamond shows resistance at the reporting-MS group level. Horizontal lines in boxes represent median; Lower and upper box boundaries, 25th and 75th percentiles, respectively.

Resistance to **amikacin**, **azithromycin, cefotaxime**, **ceftazidime** and **colistin** was rare, very low or low in all four animal populations (Annex C, tables 1–4). Considering all reporting MSs, overall median **colistin** resistance was rare in all four animal populations (Annex C, tables 1–4). Resistance to **azithromycin** was generally uncommon with overall low median levels of resistance in pigs (1.5%), very low level in broilers (0.7%) and rare in turkeys (0.0%) and cattle under 1 year of age (0.0%). Resistance to both colistin and azithromycin was not observed in most countries (Annex C, tables 1–4). For both substances, moderate levels of resistance in broilers and turkeys were, however, registered. Levels of resistance to **tigecycline** were very low or low in all four animal populations (Annex C, tables 1–4). One country, however, reported a moderate level of resistance among isolates from pigs.

In all monitored animal populations, overall median resistance to third-generation cephalosporins (**cefotaxime** and/or **ceftazidime**) was rare or very low (range 0.0%–0.8%) (Figure 38; Annex C, tables 1–4). A low number of indicator *E. coli* isolates from caecal samples from broilers and turkeys in 2022 and from pigs and cattle under 1 year of age in 2023 were detected as phenotypically resistant to third-generation cephalosporins (**cefotaxime** and/or **ceftazidime**) (Table 12). In the countries reporting resistant isolates, the levels of resistance were either very low or low apart from the moderate resistance observed in pigs in Cyprus and in cattle under 1 year of age in Italy. All isolates exhibiting resistance to third-generation cephalosporins (and/or carbapenems) were phenotypically characterised further for identification of presumptive production of ESBL-, AmpC- and/or CP-enzymes (on a second panel). The results of these investigations are reported in chapter 5 of this report.

TABLE 12 Occurrence of resistance to third-generation cephalosporins in indicator *E. coli* from pigs, cattle under 1 year of age, broilers and turkeys, EU MSs and non-MSs, 2022–2023.

Animal category	No. of MSs/no. of non-MSs	*N*	Cefotaxime		Ceftazidime	
			n	% *R*	*n*	% *R*
Fattening Pigs, 2023	27 + XI/5	5051	60	1.2	56	1.1
Cattle < 1 year of age, 2023	11/2	2174	41	1.9	37	1.7
Broilers, 2022	27 + XI/4	5022	57	1.1	56	1.1
Fattening Turkeys, 2022	13/1	1883	27	1.4	20	1.1

Abbreviations: % *R*, percentage of resistance; *n*, total number of resistant isolates; *N*, total number of reported; XI, United Kingdom (Northern Ireland).

None of the indicator *E. coli* isolates from pigs, cattle under 1 year of age and broilers exhibited microbiological resistance to carbapenems (**meropenem**) in 2022–2023, except one isolate from turkeys reported phenotypically resistant to meropenem (Annex C, tables 1–4) and confirmed carrier of the $bla_{\text{OXA-181}}$ gene by Italy.

Combined resistance to fluoroquinolones and 3rd-generation cephalosporins.

In most reporting countries, microbiological[12] **combined resistance** to **ciprofloxacin** and **cefotaxime** was either not detected or detected at very low levels in all four animal populations monitored (Figure 39; Table 13; Annex C, tables 1–4). The overall median of combined resistance was rare in all four animal populations. Clinical[13] combined resistance was not detected in isolates from any of the four animal populations in most countries, and where it was, resistance was low to very low (Annex C, tables 1–4). Isolates exhibiting combined resistance were more common in broilers, turkeys and in cattle under 1 year of age than in pigs.

TABLE 13 Combined resistance to ciprofloxacin and cefotaxime in indicator commensal *E. coli* from broilers, turkeys, pigs and cattle under 1 year of age applying ECOFFs and clinical breakpoints, as issued by EUCAST, EU MSs and non-MSs, 2022–2023.

Food-producing animal population	Microbiological combined resistance to CIP & CTX using ECOFFs			Clinical combined resistance to CIP & CTX using clinical breakpoints		
	N	% *R*	95% CI	*N*	% *R*	95% CI
Fattening Pigs, 2023[a]	24	0.5	0.3, 0.7	5	0.1	0.0, 0.2
Cattle < 1 year, 2023[b]	25	1.1	0.8, 1.7	7	0.3	0.2, 0.7
Broilers, 2022[c]	52	1.0	0.8, 1.4	21	0.4	0.3, 0.6
Fattening Turkeys, 2022[d]	23	1.2	0.8, 1.8	9	0.5	0.3, 0.9

Abbreviations: % *R*, percentage of resistance; 95% CI, 95% confidence interval ;CIP, ciprofloxacin (fluoroquinolones); CTX, cefotaxime (third-generation cephalosporins); *N*, number of isolates.

[a]27 MSs, United Kingdom (Northern Ireland), 5 non-MSs; 5053 isolates investigated.

[b]11 MSs, 2 non-MSs; 2174 isolates investigated.

[c]28 MSs, 4 non-MSs; 5022 isolates investigated.

[d]13 MSs, 1 non-MSs; 1883 isolates investigated.

[12]i.e. defining resistance by epidemiological cut-off value (ECOFF). See Appendix A – Materials and methods for the definition.

[13]i.e. defining resistance by clinical breakpoint. See Appendix A – Materials and methods for the definition.

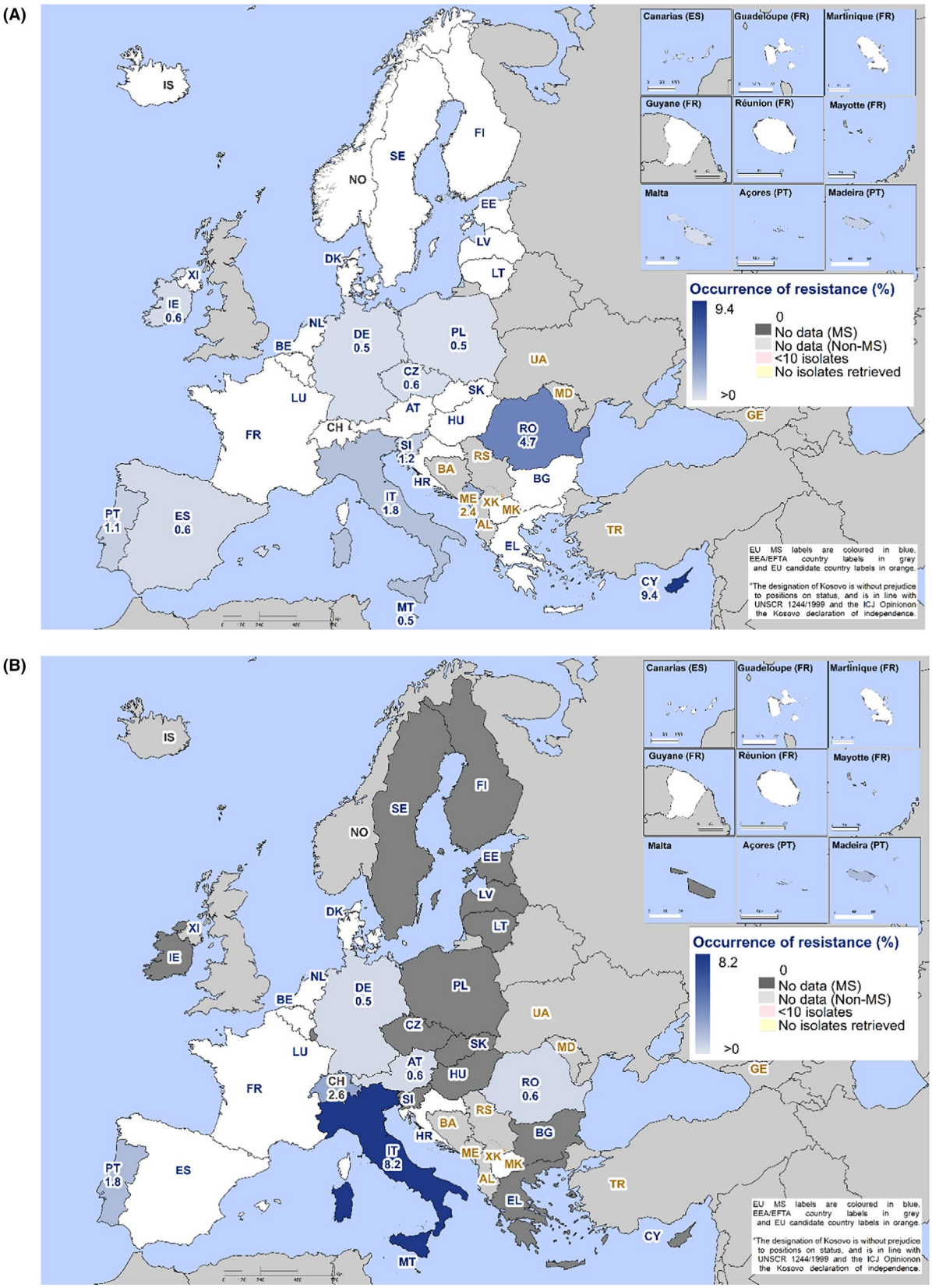


FIGURE 39 (Continued)

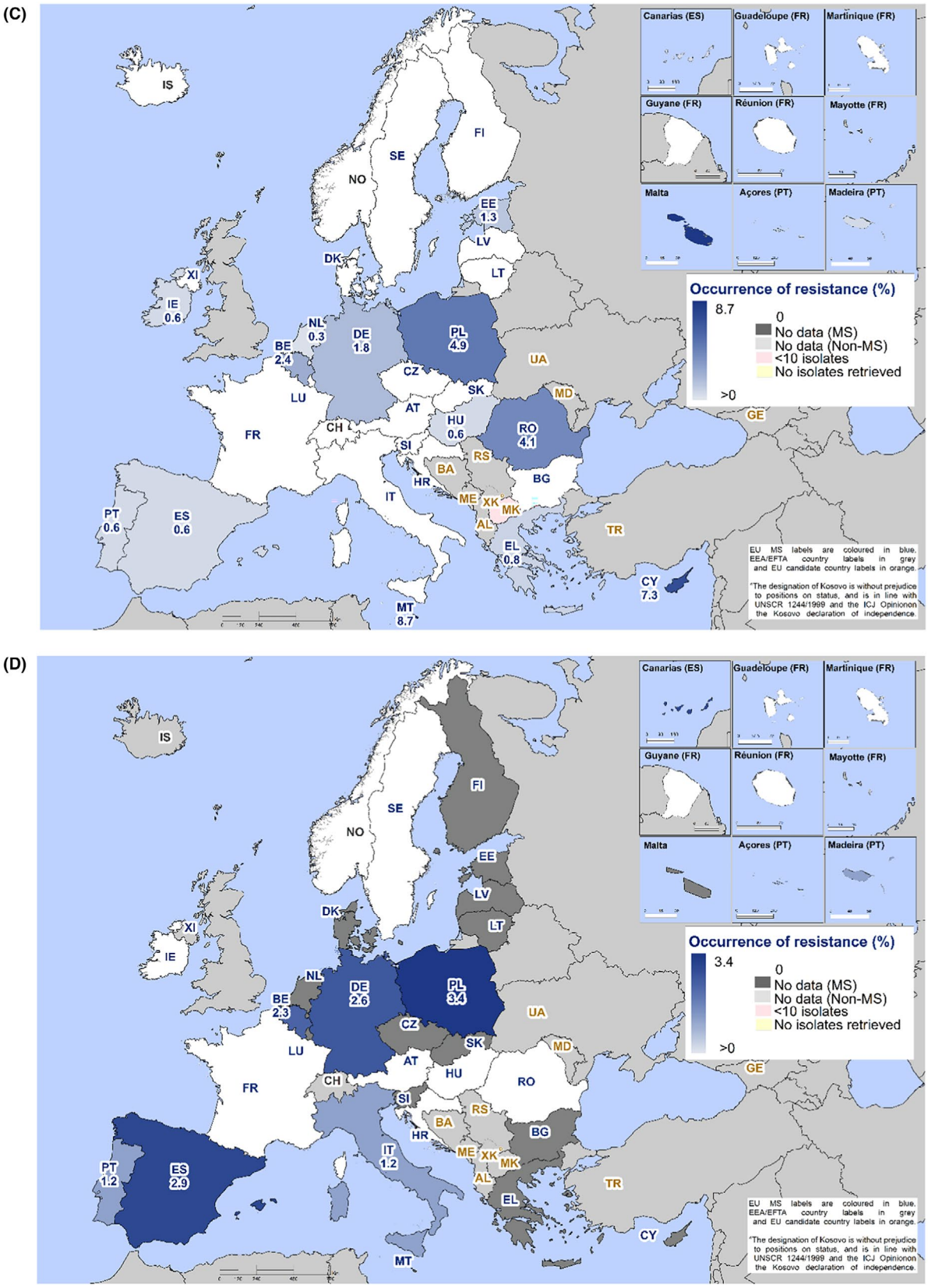


FIGURE 39 Spatial distribution of microbiological combined resistance to cefotaxime and ciprofloxacin in indicator commensal *E. coli* from (A) fattening pigs, 2023; (B) cattle under 1 year of age, 2023; (C) broilers, 2022; and (D) fattening turkeys, 2022, EU MSs and non-MSs. Note: The designation of 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.

4.3.3 | Multidrug resistance

Multidrug resistant isolates

Multidrug resistance (MDR) is defined as microbiological resistance to three or more antimicrobial classes of the harmonised panel of substances tested.

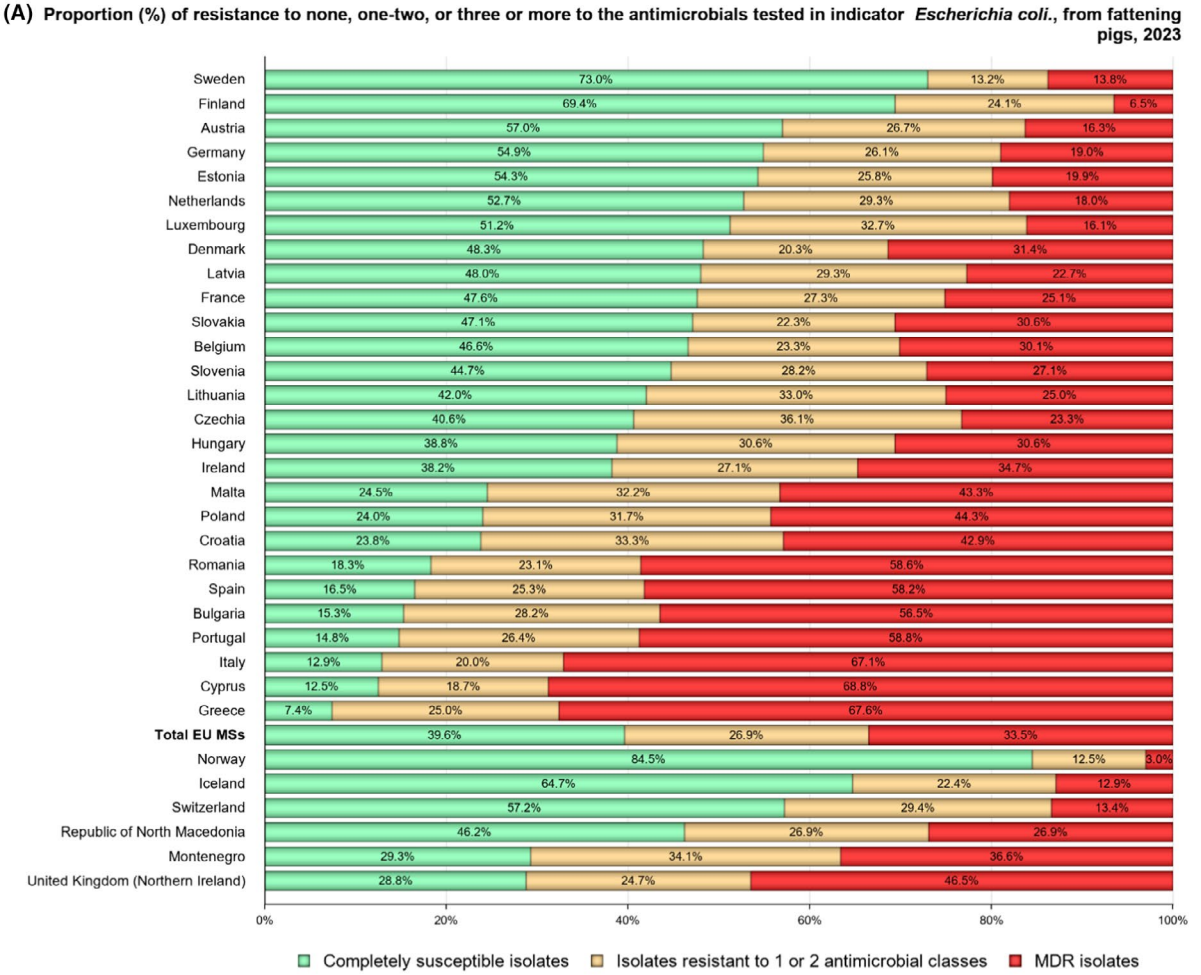
In 2022, the median MDR among MSs was 40.0% in indicator *E. coli* isolates from broilers and 43.4% in those from turkeys, while in 2023, the median MDR observed in *E. coli* isolates from pigs was 30.6%, and 22.9% in those isolated from cattle under 1 year of age. Large variations in MDR between reporting countries were observed, ranging from 3.5% to 85.5% in broilers, 0.0% to 75.3% in turkeys, 6.5% to 68.8% in pigs and 6.6% to 72.4% in cattle under 1 year of age (Figure 40, Annex C).

Multidrug resistance patterns

A wide variety of resistance patterns were observed in the MDR isolates recovered from all four animal populations. The antimicrobials most often represented in the MDR patterns of isolates from broilers were ampicillin, ciprofloxacin and nalidixic acid, often also in combination with tetracycline. In addition to this combination, many isolates were also resistant to sulfamethoxazole and trimethoprim. Resistance to chloramphenicol was also a common trait. Among isolates from turkeys, resistance to ampicillin, tetracyclines and ciprofloxacin, sometimes also combined with resistance to nalidixic acid, was the most common profile of MDR. In addition, many isolates were also resistant to sulfamethoxazole and trimethoprim.

Among isolates from pigs, the most common MDR pattern included resistance to ampicillin, sulfamethoxazole and trimethoprim. This pattern was in most cases also extended with resistance to tetracycline, and sometimes also with resistance against chloramphenicol. Among isolates from cattle under 1 year of age, the most common MDR pattern was resistance to ampicillin, sulfamethoxazole, trimethoprim and tetracyclines, sometimes also together with resistance to chloramphenicol. Resistance to ampicillin, sulfamethoxazole and tetracycline, either with or without resistance to chloramphenicol were also common MDR patterns.

None of the MDR-resistant patterns included resistance to azithromycin or tigecycline and in only nine isolates (eight from pigs, three from broilers and one from turkeys), the MDR pattern included resistance to amikacin. Resistance to colistin was a part of the MDR-resistant pattern in a few isolates from broilers ($n = 37$), pigs ($n = 3$) and cattle under 1 year of age ($n = 3$), but in a higher proportion (7.3%, $n = 56$) of MDR isolates from turkeys.



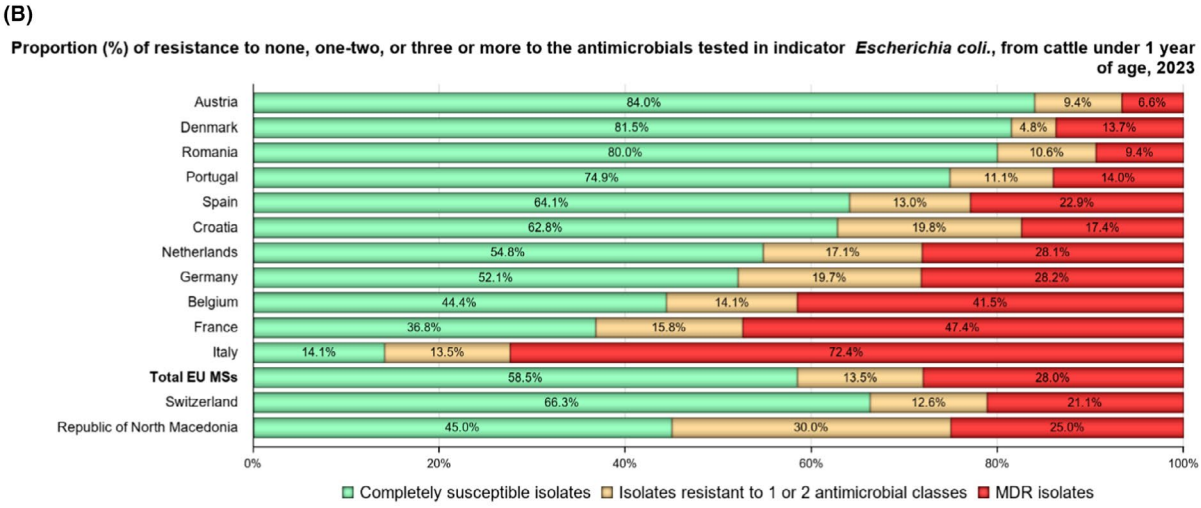
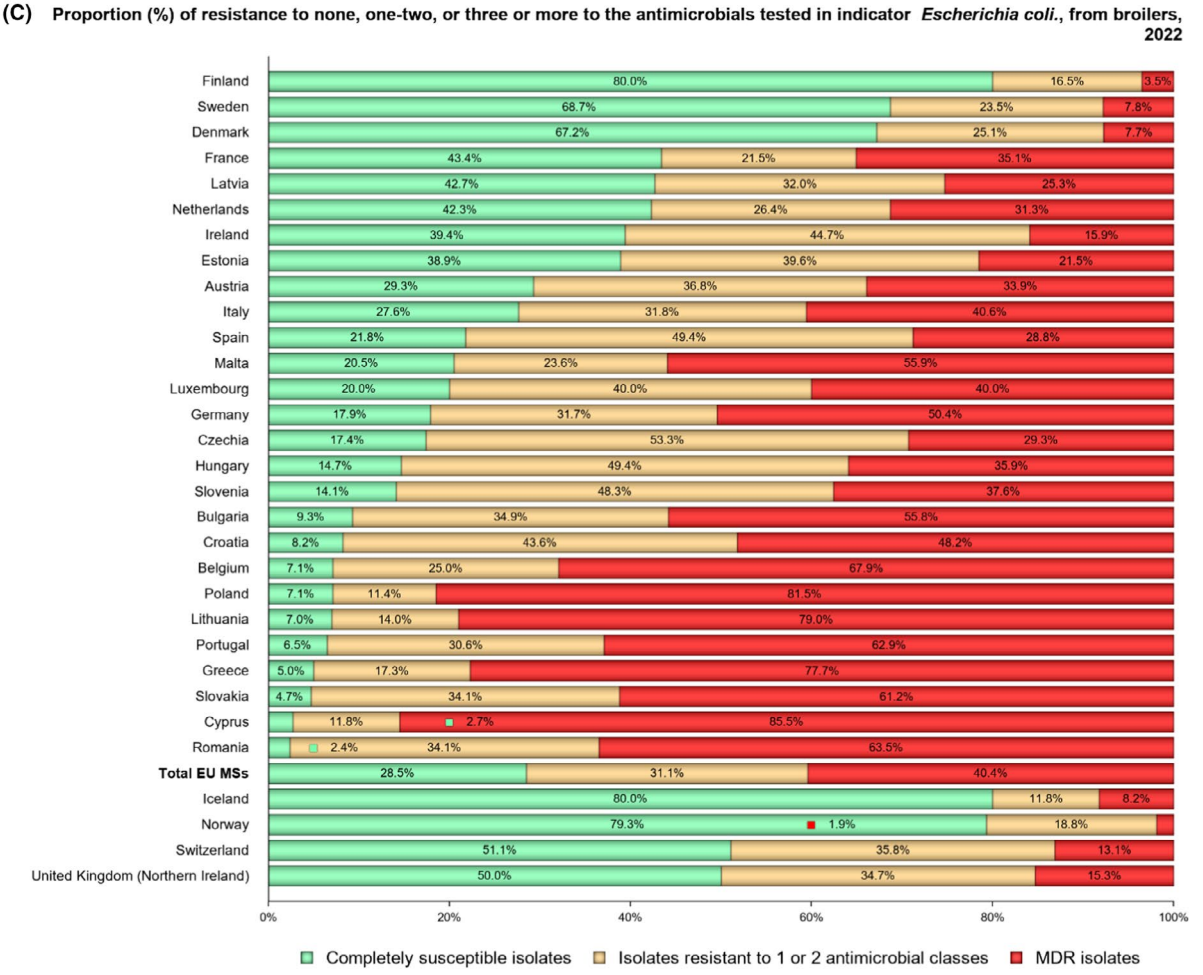


FIGURE 40 (Continued)



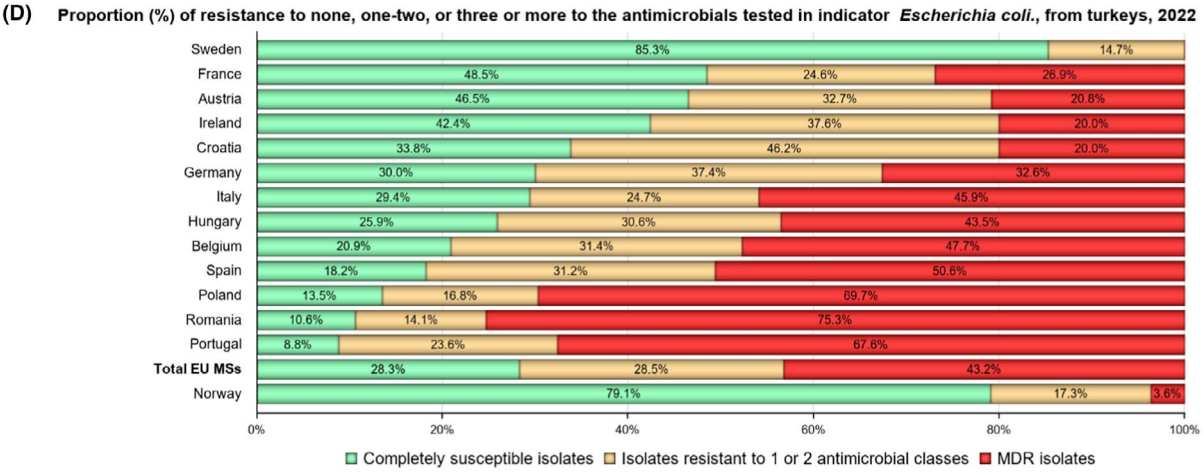


FIGURE 40 Occurrence of complete susceptibility to the antimicrobials tested, resistance to one or two substances or multidrug resistance in indicator commensal *E. coli*. (A) fattening pigs, 2023; (B) cattle under 1 year of age, 2023; (C) broilers, 2022; (D) fattening turkeys, 2022, EU MSs and non-EU MSs.

4.3.4 | Complete susceptibility

Completely susceptible isolates

The occurrence of resistance can be evaluated by considering the proportion of indicator *E. coli* isolates exhibiting susceptibility to all the 15 antimicrobials tested in the harmonised panel, using ECOFFs for interpretation. Such isolates are here called completely susceptible isolates (CS).

Considering all reporting MSs, the median CS among *E. coli* isolates was 20.0% in broilers, 28.9% in turkeys, 41.3% in pigs and 62.8% in cattle under 1 year of age (Annex C, tables 1–4). For all animal populations, CS varied widely between reporting countries and ranged from 2.4% to 80.0% in broilers, 8.8% to 85.3% in turkeys, 7.4% to 73.0% in pigs and 14.1% to 84.0%

in cattle under 1 year of age (Figure 41; Annex C, tables 1–4). Typically, the highest levels of CS in all four animal populations were observed in isolates from the Nordic countries, with levels generally decreasing in a north-to-south gradient and, to a lesser extent, in a west-to-east gradient.

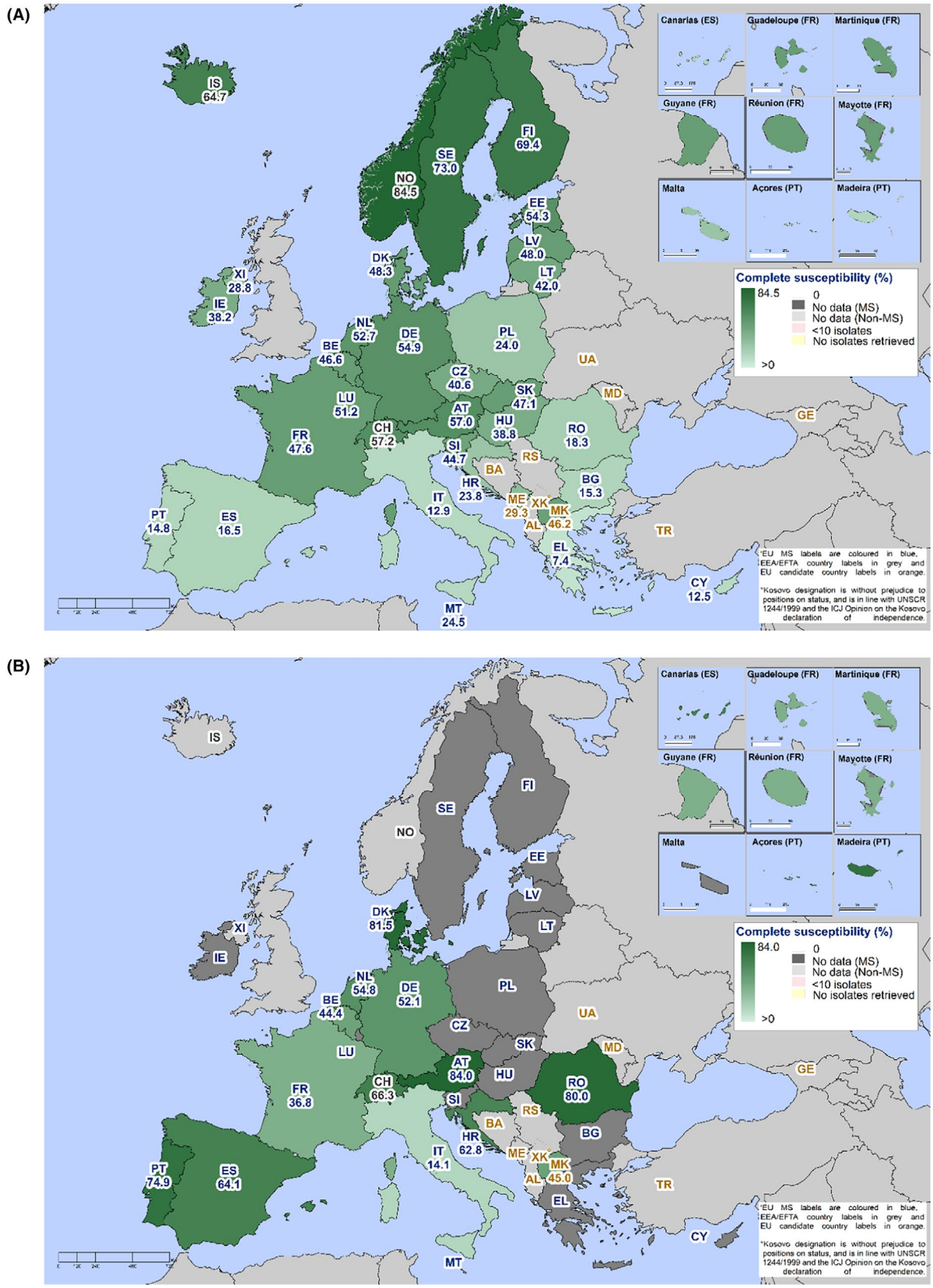


FIGURE 41 (Continued)

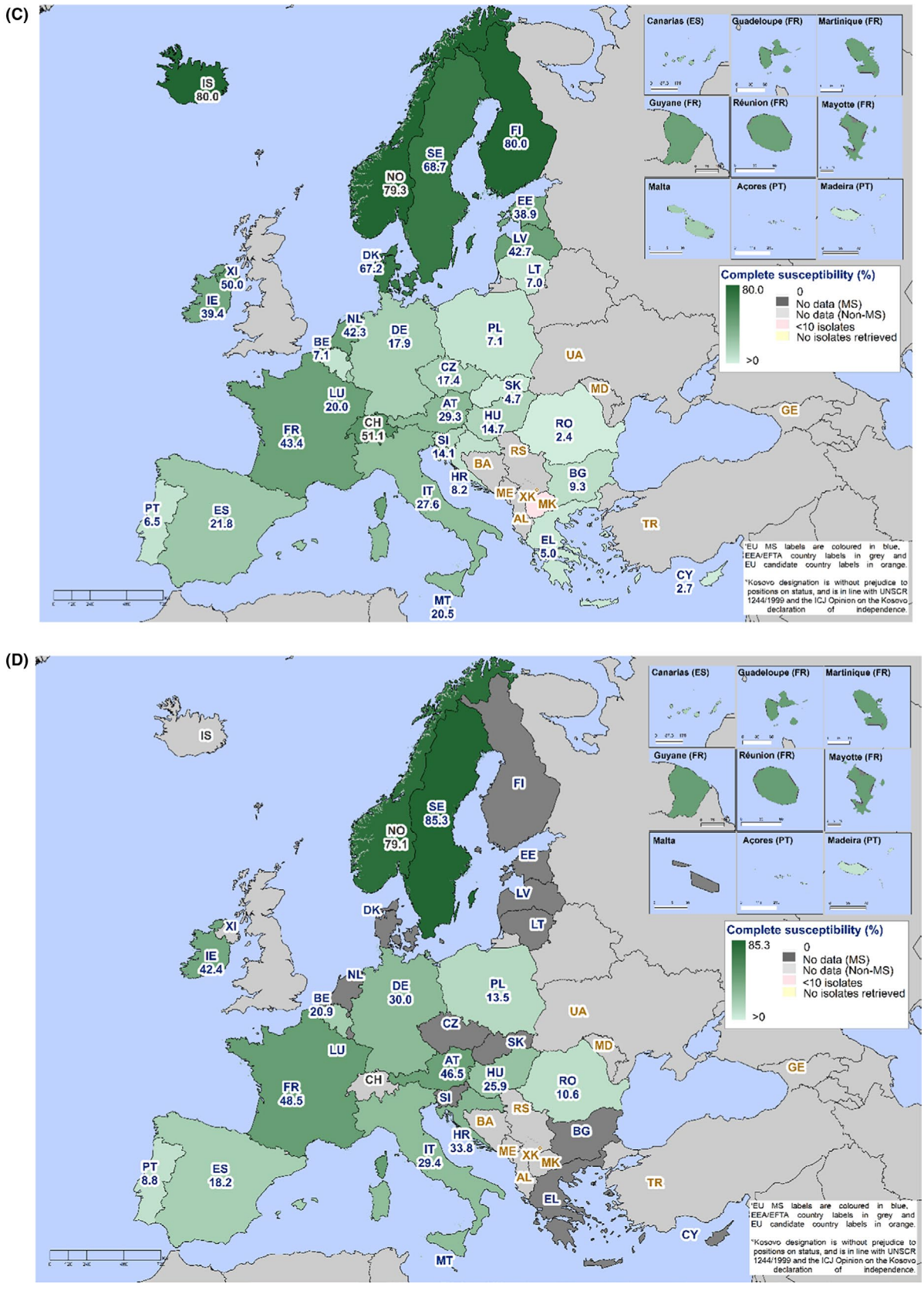


FIGURE 41 Spatial distribution of complete susceptibility to the antimicrobials tested in indicator commensal *E. coli*. (A) fattening pigs, 2023; (B) cattle under 1 year of age, 2023; (C) broilers, 2022; (D) fattening turkeys, 2022, EU MSs and non-EU MSs. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

Trends in complete susceptibility

Temporal trends in CS in indicator *E. coli* from broilers, turkeys, pigs and cattle under 1 year of age were assessed for countries that reported data for three or more years over the period 2014–2023.

For the four animal populations, a total of 33 statistically significant increasing and three decreasing trends were detected among all the reporting countries (Figure 42). France, Portugal and Spain reported increasing trends in all four monitored animal populations whereas Ireland reported increasing trends in all animal populations for which they reported data. Some countries have been reporting CS at high levels during years and in that case, increasing trends cannot be expected.

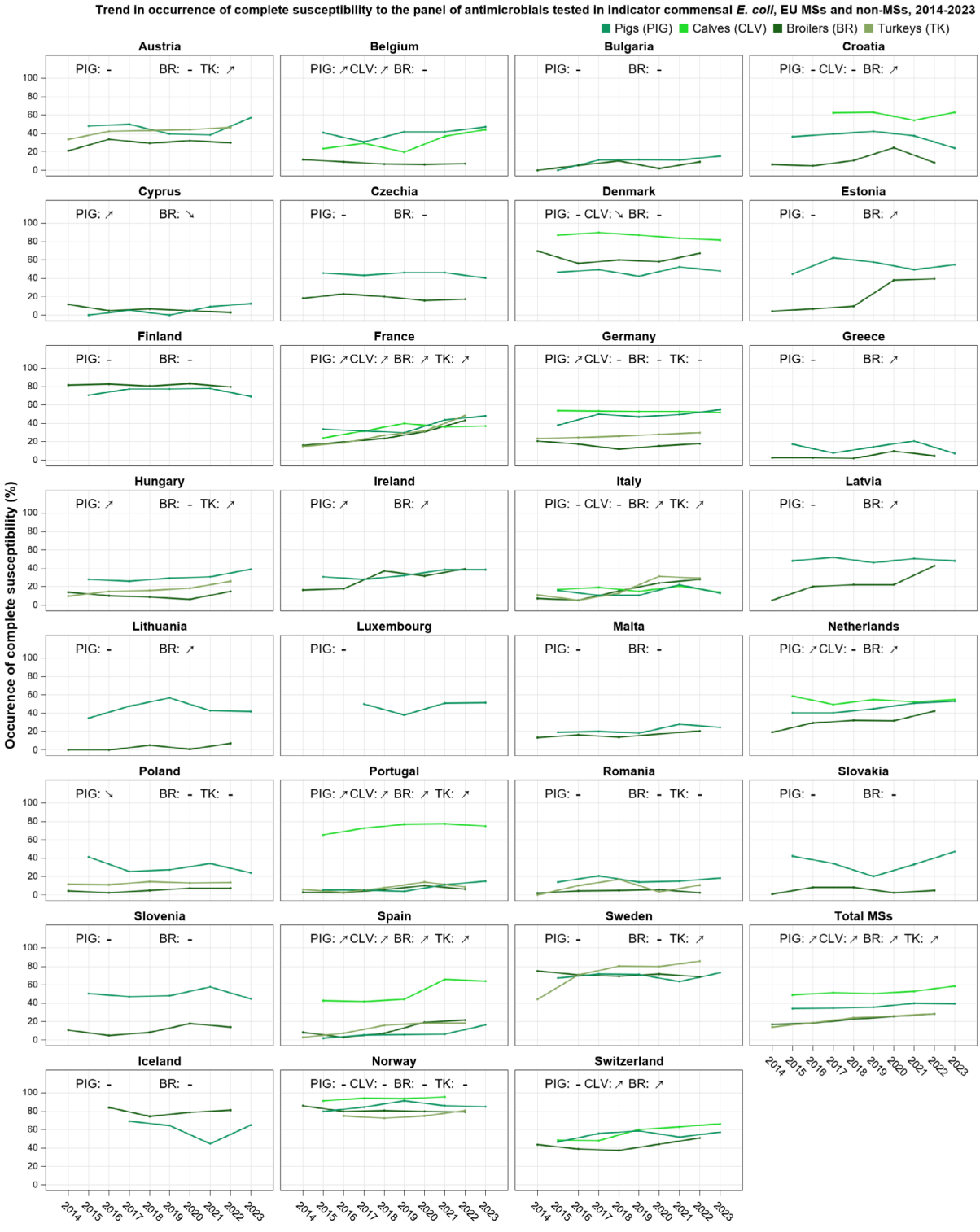


FIGURE 42 Trends in the occurrence of complete susceptibility to the panel of antimicrobials tested in indicator commensal *E. coli* from fattening pigs, cattle under 1 year of age, broilers and fattening turkeys, EU MSs and non-MSs, 2014–2023.

4.3.5 | Temporal trends in resistance

Temporal trends in resistance to ampicillin, ciprofloxacin, cefotaxime, tetracyclines and colistin in indicator *E. coli* from pigs, cattle under 1 year of age, broilers and turkeys were assessed for countries that provided data for three or more years over the period 2014–2023. Ampicillin and tetracycline have been the most used antimicrobials in food-producing animals in Europe (EMA, 2023). Monitoring temporal trends in resistance to those substances is therefore of great relevance, as decreasing trends in resistance are believed to primarily reflect changes in usage (ECDC, EFSA, EMA, 2024). Trends in resistance to the hpCIAs ciprofloxacin and cefotaxime were also addressed, as such resistance in *E. coli* from food-producing animals may impact human health. The statistical significance ($p < 0.05$) of trends was tested by logistic regression (see Appendix A – Materials and methods for details on the methodological approach).

Sufficient data for assessing the significance of temporal trends were available from 31 countries for pigs, 29 for broilers, 12 for cattle under 1 year of age and 11 for turkeys. Thus, 415 different animal/substance combinations were available and analysed for statistical significance of trends in resistance to **ampicillin**, **ciprofloxacin**, **cefotaxime**, **tetracyclines**, and **colistin**. For broiler and turkey data in 2022, 200 analyses were performed, and a total of 78 combinations had statistically significant ($p < 0.05$) decreasing trends, while 15 combinations had statistically significant increasing trends (Table 14). For pig and cattle data in 2023, 215 analyses were performed, and in a total of 31 combinations had statistically significant ($p < 0.05$) decreasing trends, while 10 combinations had statistically significant increasing trends (Table 14). In several countries, the levels of resistance were stable over time at low levels, and major changes cannot be expected.

TABLE 14 Summary of trends in resistance to ampicillin, cefotaxime, ciprofloxacin, tetracyclines and colistin in indicator commensal *E. coli* from fattening pigs and cattle under 1 year of age over 2014–2023, and broilers and fattening turkeys over 2014–2022, EU MSs and non-MSs.

Animal population	AMP			CTX			CIP			TET			COL			Total		
	↓	↑	↔	↓	↑	↔	↓	↑	↔	↓	↑	↔	↓	↑	↔	↓	↑	↔
Pigs, 2023 27 MSs, 4 non-MSs	4	2	25	1	2	28	2	4	25	14	0	17	1	0	30	22	8	125
Cattle < 1 year, 2023 9 MSs, 3 non-MSs	2	0	10	0	1	11	2	0	10	4	1	7	1	0	11	9	2	49
Total, 2023	6	2	35	1	3	39	4	4	35	18	1	24	2	0	41	31	10	174
Broilers, 2022 26 MSs, 3 non-MSs	13	3	12	13	1	16	13	5	11	12	2	15	3	3	23	54	14	77
Turkeys, 2022 10 MSs, 1 non-MSs	6	0	5	2	0	9	6	0	5	6	0	5	4	1	6	24	1	30
Total, 2022	19	4	17	14	1	25	19	5	16	18	2	20	7	4	29	78	15	107

Abbreviations: ↓, statistically significant decreasing trends; ↑, statistically significant increasing trends; ↔, statistically non-significant trends; AMP, ampicillin; CIP, ciprofloxacin; COL, colistin; CTX, cefotaxime; TET, tetracycline.

Fattening pigs

For the 31 countries reporting AMR data on indicator *E. coli* from pigs between 2014 and 2023, a total of 22 decreasing trends and eight increasing trends were statistically significant (Table 13; Figure 43). In Cyprus, Spain and the Republic of North Macedonia, statistically significant decreasing trends in three[14] of the five antimicrobials were observed. Only Romania registered statistically significant increasing trends in resistance to two substances. Notably, tetracycline resistance decreased in 14 countries and increased in none. In 13 countries, no statistically significant changes in trends were observed.

[14]Ampicillin, ciprofloxacin and tetracycline in Cyprus and the Republic of North Macedonia, ampicillin, colistin and tetracycline in Spain.

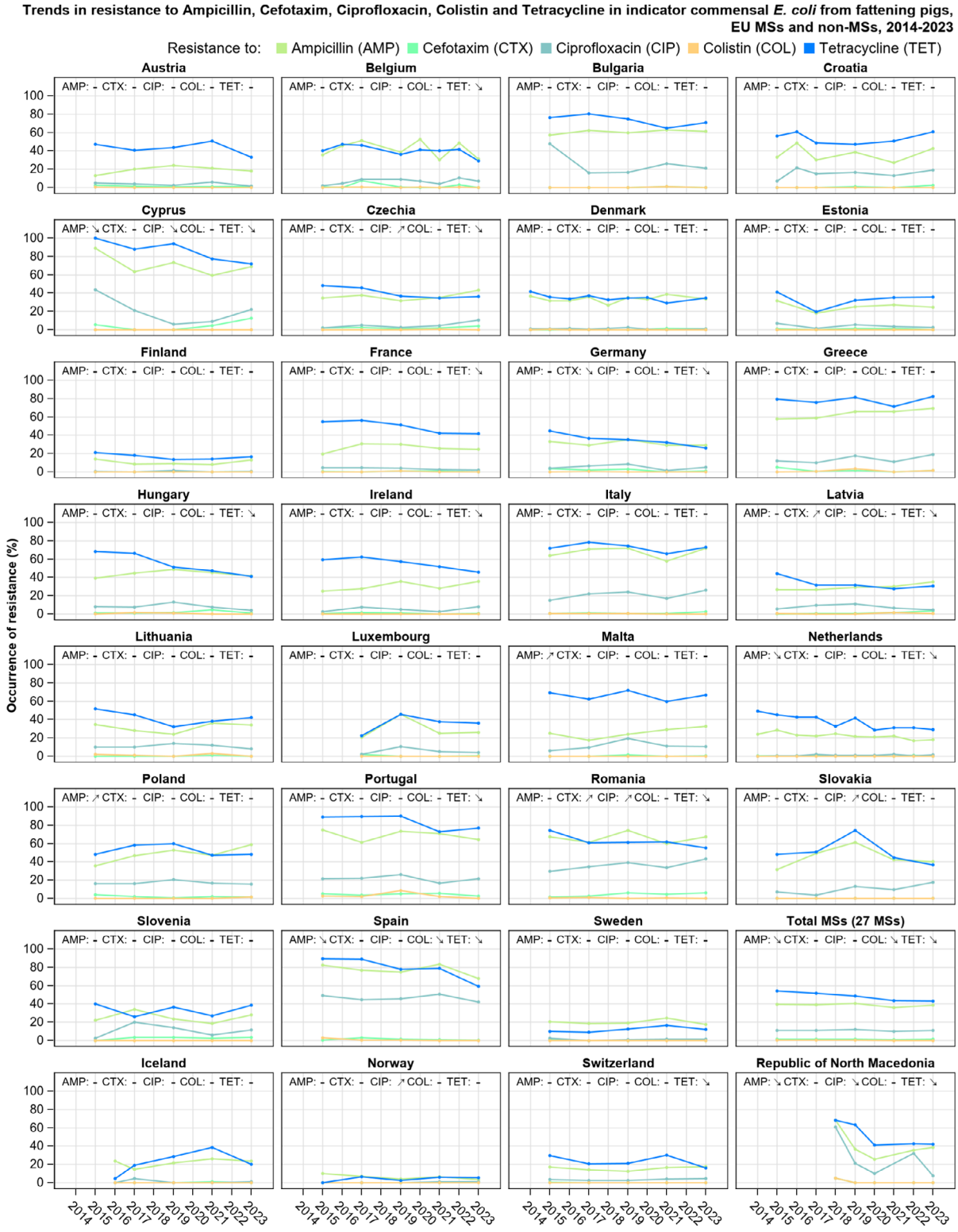


FIGURE 43 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, tetracyclines and colistin in indicator commensal *E. coli* from fattening pigs, EU MSs and non-MSs, 2014–2023.

Cattle under 1 year of age

In the 12 countries reporting data on indicator *E. coli* from cattle under 1 year of age between 2014 and 2023, nine decreasing trends and two increasing trends were observed (Table 13; Figure 44). In Switzerland, decreasing trends for three[15] of the five antimicrobials were registered. Furthermore, in France and Spain, decreasing trends for two[16] of the five antimicrobials were recorded. An increasing trend was detected in only two countries (tetracycline in Denmark and cefotaxime in Italy). In five countries, no statistically significant changes in trends were observed.

[15]Ampicillin, ciprofloxacin and tetracycline.

[16]Ciprofloxacin and tetracycline in France and ampicillin and tetracycline in Spain.

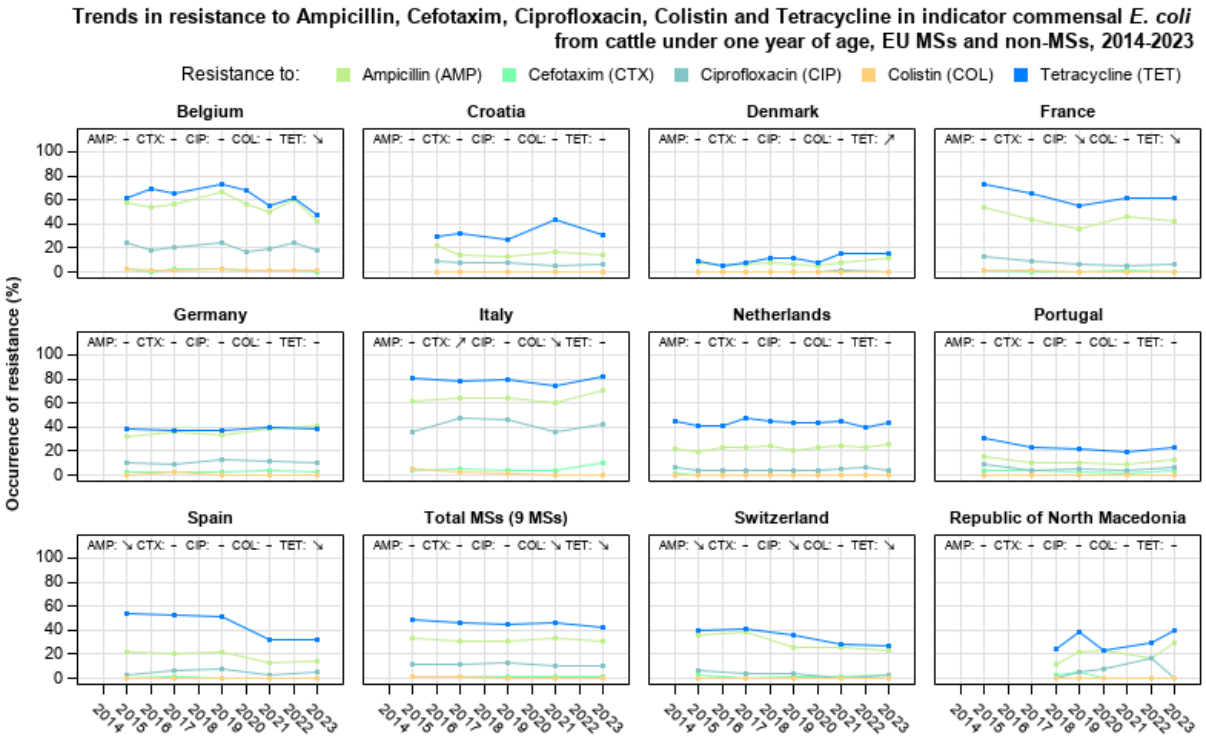


FIGURE 44 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, tetracyclines and colistin in indicator commensal *E. coli* from cattle under 1 year of age, EU MSs and non-MSs, 2014–2023.

Broilers

In the 29 countries reporting data on isolates from broilers, 54 decreasing and 14 increasing trends were registered (Table 14; Figure 45). In Italy and Portugal, decreasing trends for all five antimicrobials were detected. In five countries, decreasing trends for four[17] of the five antimicrobials were observed. In Cyprus and Norway, increasing trends for more than one substance were seen. In four countries, no statistically significant changes in trends were observed.

[17]Ampicillin, cefotaxime, ciprofloxacin and tetracycline in France, Ireland, Latvia, the Netherlands and Spain.

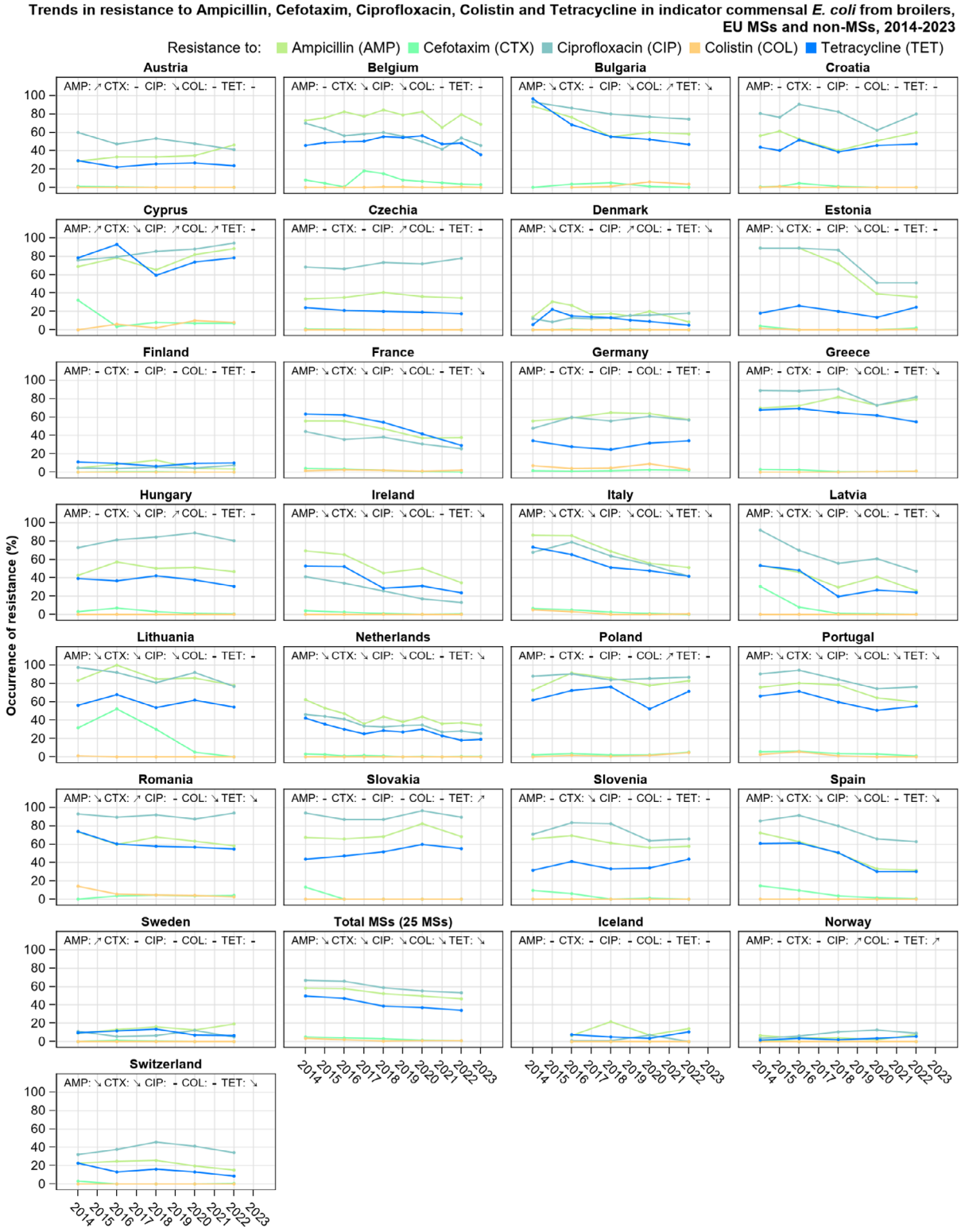


FIGURE 45 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, tetracyclines and colistin in indicator commensal *E. coli* from broilers, EU MSs and non-MSs, 2014–2022.

Fattening turkeys

In the 11 countries reporting data on isolates from fattening turkeys, there were 24 decreasing trends and only 1 increasing trend observed (Table 13; Figure 46). In Spain, decreasing trends for all five antimicrobials were reported. In France, Italy and Portugal, decreasing trends for four[18] of the five antimicrobials were registered. In Austria and Norway, no statistically significant changes in trends were observed.

[18]Ampicillin, ciprofloxacin, tetracycline and colistin.

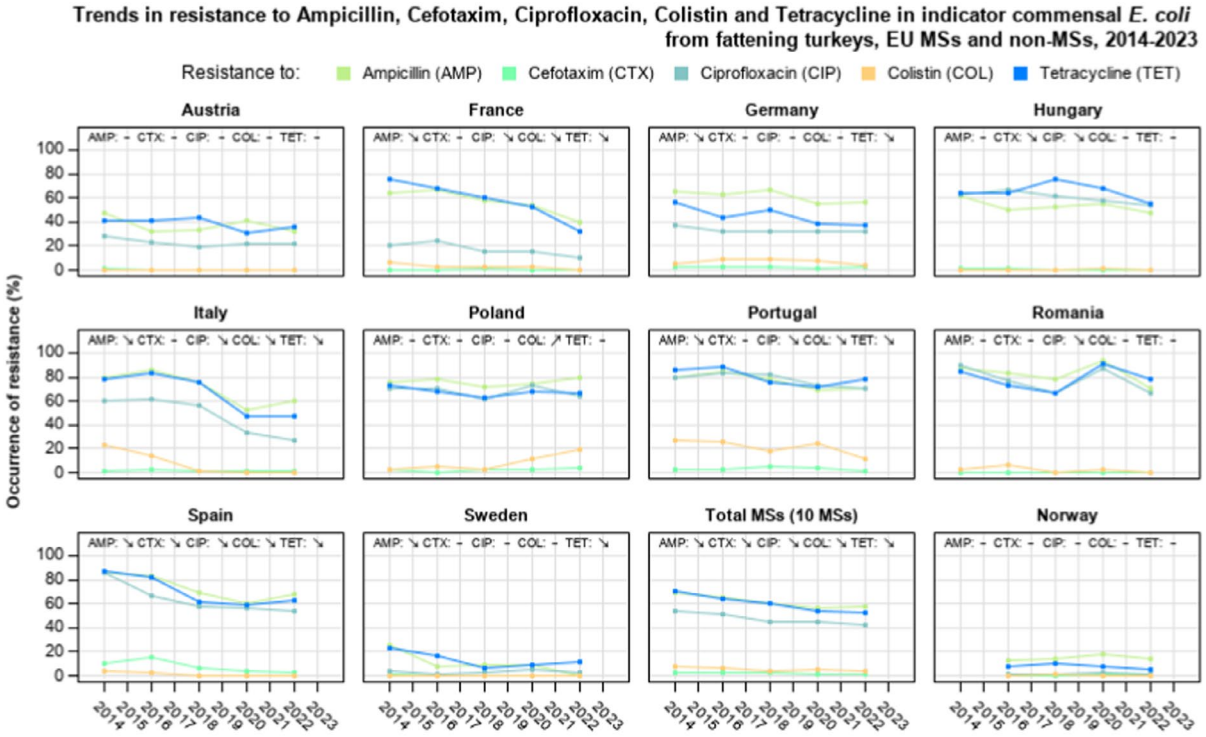


FIGURE 46 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, tetracycline and colistin in indicator commensal *E. coli* from fattening turkeys, EU MSs and non-MSs, 2014–2022.

4.3.6 | Key outcome indicator of complete susceptibility

The occurrence of CS indicator *E. coli* isolates from the most important food-producing animals (broilers, fattening turkeys, fattening pigs, cattle under 1 year of age) is used as a key outcome indicator (KOI_{CS}) or the overall AMR situation in food-producing animals in a country.

To account for differences in the relative size of food-producing animal populations in a country, the KOI_{CS} was calculated as the weighted mean of the proportions of completely susceptible indicator *E. coli* isolates in each of the four animal populations monitored. For the calculation of the KOI_{CS}, the occurrence of CS in each animal population was weighted in relation to the relative size of the populations within a country using the 'population correction unit' (PCU), as established by EMA (2011).

To calculate the KOI_{CS}, data reported in two consecutive years were used. The KOI_{CS} values were calculated from CS data on broilers and fattening turkeys reported in even-numbered years and data on fattening pigs and cattle under 1 year of age reported in the immediately preceding/following odd-numbered years. Data for broilers and pigs were included in the calculation for each country, whereas data for turkeys and cattle under 1 year of age were included in the calculation only in those countries reporting such data. See also, Appendix A – Materials and methods.

Marked variations in KOI_{CS} were observed among the 30 countries reporting consistently over the study period (Figure 47). In 2022–2023, levels of KOI_{CS} were < 10% in 2 countries, 10%–20% in 4 countries, 20%–40% in 11 countries, 40%–60% in 9 countries, 60%–80% in 3 countries (Finland, Iceland and Sweden) and > 80% in 1 country (Norway).

Furthermore, in 13 countries, a statistically significant increasing trend in the KOI_{CS} was observed and some of these showed a substantial improvement. Conversely, in one country a statistically significant decreasing trend in the KOI_{CS} was observed.

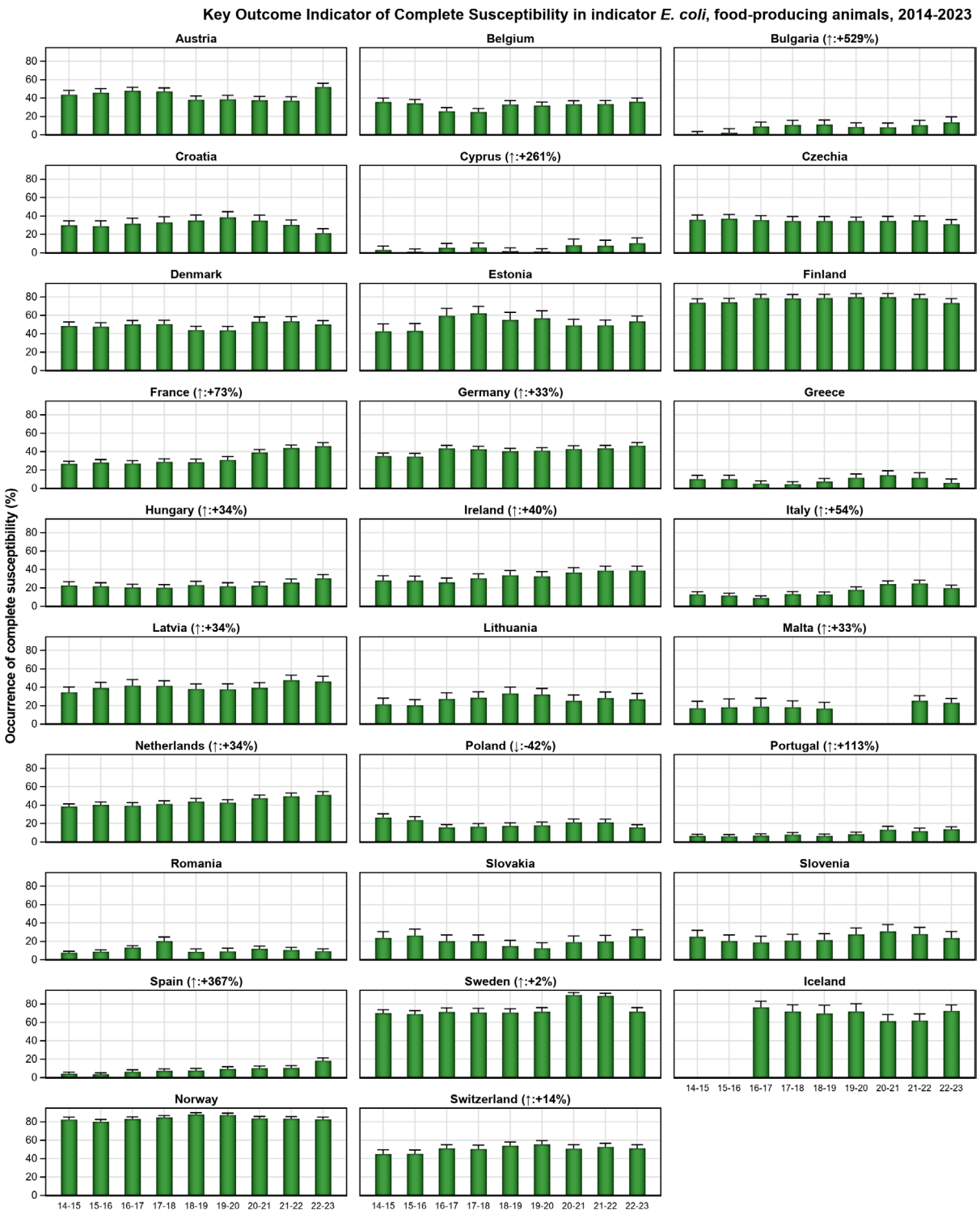


FIGURE 47 Trends in the key outcome indicator of complete susceptibility (KOI_{CS}) in indicator commensal *E. coli* from food-producing animals (broilers, fattening turkeys, fattening pigs and cattle under 1 year of age), 27 EU MSs and 3 non-MSs, 2014–2023.

4.4 | Discussion

An abundant and ubiquitous commensal bacterial species, *E. coli* has been selected as a reporting organism because it is considered more relevant in representing the overall resistance situation, including transmissible genes, in food-producing naimals than less abundant zoonotic bacterial species.

Resistance to hpCIAs[19] are of particular interest regarding the risk of possible spread to humans along the food chain. At the EU level, no significant differences in the low-level occurrence of resistance to cefotaxime, ceftazidime, azithromycin and colistin were observed between the four animal populations monitored. Meropenem resistance was reported in one

[19]Of the antimicrobials tested within the mandatory monitoring of indicator *E. coli*, ciprofloxacin (fluoroquinolones), cefotaxime and ceftazidime (third-generation cephalosporins), colistin (polymyxins) and azithromycin (macrolides) have been categorised by WHO as hpCIA (WHO, 2019).

isolate of indicator *E. coli* from turkeys in Italy in 2022. Resistance to carbapenem is still uncommon in commensal *E. coli* from food-producing animals in Europe. These findings regarding resistance to third-generation cephalosporins (cefotaxime and ceftazidime) and carbapenem relate to commensal *E. coli* isolates recovered using non-selective culture methods. Within the mandatory monitoring, samples of caecal contents are also cultured on selective media to specifically detect the presence of *E. coli* resistant to third-generation cephalosporins and carbapenems. In this latter part of the monitoring, *E. coli* exhibiting resistance to carbapenems are more easily detected, especially in samples from pigs. The results of these analyses are presented in more detail in chapter **Extended-spectrum β-lactamase (ESBL)-, AmpC- and /or carbapenemase (CP)- producing *Salmonella* and *E. coli***.

The median levels of resistance to **ciprofloxacin** and **nalidixic acid** among *E. coli* isolates from pigs and cattle under 1 year of age were low at the EU level. In contrast, the median levels of ciprofloxacin and nalidixic acid resistance were very high in broilers and high in turkeys. Notably, a substantial proportion of isolates from all animal populations exhibited resistance to ciprofloxacin but not to nalidixic acid; a resistance pattern which generally indicates the presence of transmissible genes mediating quinolone resistance (Jacoby et al., 2014).

Although the median levels of **azithromycin** resistance were rare, low or very low in all four animal populations, certain countries reported higher levels of resistance for some animal populations (broilers in Malta and Romania and turkeys in Romania). Azithromycin, which is an azalide, a subclass of macrolide antimicrobials, is not used in animals. The selective pressure exerted using other related macrolides in food-producing animals may have favoured the emergence of azithromycin resistance.

Considering all reporting MSs, the median level of resistance to **colistin** was rare in all four animal populations. Higher levels of resistance were, however, registered in broilers in Cyprus and turkeys in Poland and Portugal. Statistically significant decreasing trends in the levels of colistin resistance were reported among isolates from specific animal populations by some countries. This is in line with the fact that sales of polymyxins (e.g. colistin) for use in animals have decreased by over 40% in Europe between 2017 and 2022 (EMA, 2023).

At the MS-group level, resistance to **ampicillin**, **sulfamethoxazole**, **trimethoprim** as well as **tetracyclines** were generally common in indicator *E. coli* for all animal populations, apart from trimethoprim resistance in isolates from cattle under 1 year of age and turkeys. In poultry, resistance to ciprofloxacin and nalidixic acid was also common. The occurrence of resistance to most antimicrobials differed markedly between the reporting countries. Regarding pigs and broilers, the situation was generally more favourable in Northern Europe than in Southern and Eastern Europe. For turkeys, a similar pattern as that for pigs and broilers was discerned, albeit less marked.

The frequent occurrence of resistance to these substances in indicator *E. coli* likely reflects the widespread past and present use of these antimicrobials in food-producing animals in several MSs (ECDC, EFSA and EMA, 2024; Queenan et al., 2016). The disparities in the levels of consumption of antimicrobials among the animal populations, but also possibly the modes of administration, is likely mirrored in the differences in resistance observed between animal species. In poultry, flock treatment is almost exclusively practised, whereas pigs and cattle under 1 year of age are in some countries typically treated individually. Similarly, tetracycline, ampicillin, sulfamethoxazole and trimethoprim were often represented in the patterns of MDR isolates from all animal populations. Among isolates from broilers and turkeys, resistance to (fluoro)quinolones (ciprofloxacin/nalidixic acid) was also a common trait in the patterns of MDR.

Similarly, the frequent occurrence of tetracycline, ampicillin, sulfamethoxazole and trimethoprim, as core components of MDR patterns in *E. coli* from all animal populations, as well as that of (fluoro)quinolones (ciprofloxacin/nalidixic acid), as an additional common trait of MDR patterns in *E. coli* from broilers and turkeys, also likely reflect an extensive use in several countries over many years. The frequent links between the genes conferring resistance to these substances on mobile genetic elements also result in co-selection.

Overall, in several countries, statistically significant trends towards reduction of resistance in indicator *E. coli*, notably in broilers and turkeys, were revealed. For several antimicrobials and countries, statistically significant associations were demonstrated between both trends in use of antimicrobials in food-producing animals and in the occurrence of resistance in indicator *E. coli* from these animals (ECDC, EFSA and EMA, 2024). The decreasing trends in several countries are, therefore, believed to be due to the overall decline in sales of antimicrobials for use in animals since 2011, as documented in the ESVAC report (EMA, 2023).

To overcome the issue of co-selection and co-resistance when monitoring AMR and analysing the relationship between use of antimicrobials and AMR, CS has been consistently addressed by the harmonised monitoring of AMR in food-producing animals. The levels of CS vary markedly between countries in all four animal populations. Generally, completely susceptible isolates from pigs, broilers, and to some extent, turkeys were more common in Northern than in Southern and Eastern Europe. Considering all reporting countries, the median percentage of indicator *E. coli* isolates exhibiting CS to all antimicrobial classes tested was lower in broilers (21.1%) and turkeys (29.7%) than in pigs (44.7%) and cattle under 1 year of age (62.8%). Unsurprisingly, isolates exhibiting MDR were more common in broilers (median 35.5%) and turkeys (median 38.1%) than in pigs (median 30.1%), and cattle under 1 year of age (median 22.9%). Contrastingly, for cattle under 1 year of age, the picture was more complex, as in Austria, Denmark, Portugal and Romania, the occurrence of CS was >70%. This indicates that the situation in one animal production sector in a given country does not necessarily parallel the situation in other sectors in the same country.

As the association between overall use of antimicrobial and CS has been demonstrated (ECDC, EFSA and EMA, 2024), it also indicates that there are differences in consumption of antimicrobials not only among countries but also among different animal populations within a country. In the future, it will also be possible to compare levels of resistance in different animal populations in general and in specific countries with actual use data reported in accordance with Regulation (EU) 2019/6 on veterinary medicinal products. This could give further insight into differences seen within and among countries.

Trends in CS available at the level of each animal population monitored complement well that in KOI_{cs} so that any positive or negative trend occurring in one animal population of small relative size may not go unnoticed .

The KOI_{cs} has been retained as the primary indicator of AMR in food-producing animals, considered as a whole. It is relevant in the overall assessment of risks related to AMR in food-producing animals, as KOI_{cs} accounts for differences in the relative size of food animal populations in a country. Marked variations in KOI_{cs} were registered from < 10% in two MSs to > 80% in one country (Norway). The KOI_{cs} has been used to assess the development of AMR in relation to the total use of antimicrobials in food-producing animals (ECDC, EFSA and EMA, 2024; Queenan et al., 2016), and a statistically significant negative association has been demonstrated between KOI_{cs} and overall use. Therefore, it is to be expected that a reduction in the use of antimicrobials in food-producing animals would eventually result in an improvement of this indicator. Indeed, this is already the case in some countries, as concomittant improving trends regarding KOI_{cs} and overall use can be discerned in a number of countries (ECDC, EFSA and EMA, 2024).

The statistically significant decreasing trends in resistance to individual substances, which reveal progress towards reduced resistance in several countries, have been further highlighted by statistically significant trends towards higher levels of CS and KOI_{cs} in a number of countries. It should, however, be noted that, in some countries, the situation regarding AMR has already been favourable for a number of years and major changes, especially not improving trends, cannot be expected. Efforts to maintain, and even further improve the situation should however be made also in those countries.

Monitoring antimicrobial resistance in imported fresh meat sampled at border control posts

***Salmonella* spp.**

In 2022, *Salmonella* spp. isolates from imported fresh meat from broilers sampled at the BCPs were reported by five MSs: Germany (*N* = 5), Ireland (*N* = 8), the Netherlands (*N* = 32), Poland (*N* = 19) and Spain (*N* = 12). Overall, *Salmonella* isolates exhibited very high to extremely high levels of resistance to tetracycline (63.2%), sulfonamides (71.1%) and ampicillin (60.5%), while resistance to gentamicin (4.0%), chloramphenicol (5.3%) and trimethoprim (7.8%) was low. Resistance to ciprofloxacin and nalidixic acid was reported at an extremely high level (83%, *N* = 76, each antimicrobial). Furthermore, among the *Salmonella* isolates displaying ciprofloxacin resistance, one isolate (*S*. Heidelberg), exhibited high-level ciprofloxacin resistance (MIC ≥ 4 mg/L). Regarding resistance to third-generation cephalosporins, *Salmonella* isolates from imported broiler meat exhibited very high resistance (at 55.3% for each antimicrobial). Resistance to tigecycline in *Salmonella* isolates from imported fresh meat from broilers was reported at a high level (38.2%, *N* = 76). Low levels of colistin resistance were reported from broiler meat (4.0%).

Only the Netherlands reported data on fresh meat from turkeys sampled at BCPs (*N* = 3). All isolates were resistant to tetracycline, while two out of three isolates were resistant to sulfonamides and ampicillin, and only one to chloramphenicol. All three isolates were susceptible to gentamicin and trimethoprim. For fresh meat from turkeys, all isolates (*N* = 3) were resistant to both ciprofloxacin and nalidixic acid. Regarding resistance to third-generation cephalosporins, *Salmonella* isolates from turkey meat exhibited very high resistance (at 66.7% for each antimicrobial). No tigecycline-resistant nor colistin-resistant *Salmonella* isolates from fresh meat from turkeys were reported (*N* = 3).

Lastly, no resistance to azithromycin nor amikacin was reported in *Salmonella* isolates from meat sampled at BCPs.

Indicator commensal E. coli

Occurrence of resistance

For indicator commensal *E. coli* isolates recovered from fresh meat samples taken at BCPs, five MSs, United Kingdom (Northern Ireland), and one non-MS provided data from meat from pigs and seven MSs, United Kingdom (Northern Ireland), and two non-MSs provided data from meat from bovines in 2023. In 2022, eight MSs provided data from meat from broilers and three MSs provided data from meat from turkeys.

In total, 11 MSs reported data on 1100 indicator commensal *E. coli* isolates from imported fresh meat of the four kinds monitored, with the majority coming from meat from broilers (*N* = 399), meat from bovines (*N* = 349) and meat from pigs (*N* = 298) with fewer isolates (*N* = 54) from meat from turkeys (Table 15; Annex C, tables 5–8). Among isolates from imported fresh meat from broilers, resistance was high to very high for **ampicillin, ciprofloxacin** and **nalidixic acid, sulfamethoxazole, trimethoprim** and **tetracycline**. Furthermore, resistance to cefotaxime and ceftazidime was moderate. Somewhat similarly, among isolates from imported fresh meat from turkey, resistance to ampicillin, ciprofloxacin, nalidixic acid, sulfamethoxazole and tetracycline was high to very high. For cefotaxime and trimethoprim, resistance was moderate.

Among isolates from imported meat from bovines resistance was uncommon, with median levels of resistance being rare, very low or low. Among isolates from imported meat from pigs, the median level of resistance to tetracycline was high and median levels of resistance to ampicillin, sulfamethoxazole and trimethoprim was moderate.

Resistance to **meropenem** was not detected in any isolates from imported fresh meat. Resistance to **amikacin** was only detected in a few isolates from meat from pigs (0.7%) and meat from bovines (1.1%). Resistance to **colistin** was not detected in indicator *E. coli* isolates from imported meat from pigs or turkeys (Annex C, tables 5 and 8). In imported meat from bovines and broilers, very low to low levels of resistance were detected, 0.3% for meat from bovines and 2.5% for meat from broilers, respectively (Annex C, tables 6 and 7). Resistance to **azithromycin** was not detected in indicator *E. coli* isolates from imported meat from bovines or turkeys (Annex C, tables 6 and 8). In imported meat from pigs and broilers, very low to low levels of resistance were detected, 1.0% for meat from pigs and 1.3% for meat from broilers, respectively (Annex C, tables 5 and 7).

For **nalidixic acid** and **ciprofloxacin**, the overall level of resistance was very low and low in isolates from imported meat from bovines and low in imported meat from pigs (Annex C, tables 5 and 6). In contrast, the overall levels of resistance for both substances were very high among isolates from fresh meat from broilers and high among isolates from fresh meat from turkeys, 54.6% and 31.5% for nalidixic acid and 58.6% and 38.9% for ciprofloxacin, respectively (Annex C, tables 7 and 8). A similar situation was seen for **cefotaxime** and **ceftazidime** where the overall levels of resistance were very low in imported meat from bovines and low in meat from pigs (Table 16; Annex C, tables 5–8). Also among isolates from meat from turkeys, the levels of resistance were low, but at a higher level than for meat from pigs. Among isolates from meat from broilers, the levels of resistance were moderate (Table 15: Combined resistance to ciprofloxacin and cefotaxime in indicator *E. coli* from imported fresh meat from broilers, turkeys, pigs and bovines, applying ECOFFs and clinical breakpoints, as issued by EUCAST, EU MSs and United Kingdom (Northern Ireland), 2022–2023; Table 16; Annex C, tables 5–8).

Combined resistance to ciprofloxacin and cefotaxime

Microbiological combined resistance to ciprofloxacin and cefotaxime was moderate in fresh meat from broilers (11.8%) and low in fresh meat from turkeys (9.3%). Conversely, microbiological combined resistance was very low fresh meat from pigs and bovines (Table 15; Annex C, tables 5–8).

TABLE 15 Combined resistance to ciprofloxacin and cefotaxime in indicator *E. coli* from imported fresh meat from broilers, turkeys, pigs and bovines, applying ECOFFs and clinical breakpoints, as issued by EUCAST, EU MSs and United Kingdom (Northern Ireland), 2022–2023.

	Microbiological combined resistance to CIP & CTX (using ECOFFs)			Clinical combined resistance to CIP & CTX (using clinical breakpoints)		
Imported fresh meat	***N***	**% *R***	**95% CI**	***N***	**% *R***	**95% CI**
Meat from pigs,[a] 2023	2	0.7	0.2, 2.4	1	0.3	0.1, 1.9
Meat from bovines,[b] 2023	1	0.3	0.1, 1.6	0	0.0	0.0, 1.1
Meat from broilers,[c] 2022	47	11.8	9.0, 15.3	27	6.8	4.7, 9.7
Meat from turkeys,[d] 2022	5	9.3	4.0, 19.9	2	3.7	1.0, 12.5

Abbreviations: % *R*, percentage of resistance; 95% CI, 95% confidence interval; CIP, ciprofloxacin (fluoroquinolones); CTX, cefotaxime (third-generation cephalosporins); *N*, number of isolates.

[a]5 MSs, United Kingdom (Northern Ireland); 298 isolates investigated.

[b]7 MSs, United Kingdom (Northern Ireland); 349 isolates investigated.

[c]8 MSs; 399 isolates investigated.

[d]3 MSs; 54 isolates investigated.

TABLE 16 Occurrence of resistance to third-generation cephalosporins in indicator commensal *E. coli* isolates from imported fresh meat from broilers, turkeys, pigs and bovines, EU MSs and United Kingdom (Northern Ireland), 2022–2023.

			Cefotaxime		Ceftazidime	
Imported fresh meat	**No. of MSs**	***N***	***n***	**% *R***	***n***	**% *R***
Meat from pigs, 2023	5 + XI	298	4	1.3	4	1.3
Meat from bovines, 2023	7 + XI	349	1	0.3	3	0.9
Meat from broilers, 2022	8	399	60	15.0	60	15.0
Meat from turkeys, 2022	3	54	5	9.3	3	5.6

Abbreviations: % *R*, percentage of resistance; *n*, number of indicator *E. coli* resistant isolates; *N*, number of *E. coli* isolates tested; XI, United Kingdom (Northern Ireland).

Complete susceptibility and multidrug resistance

Considering all reporting MSs, the median CS among *E. coli* isolates from imported fresh meat was 14.7% from meat from broilers, 9.1% from meat from turkeys, 51.1% from meat from pigs and 88.2% from meat from bovines (Annex C, tables 5–8).

The level of MDR among indicator *E. coli* isolates from imported meat from broilers and turkeys was high; 48.4% and 48.1%, respectively. Contrastingly, the level of MDR among isolates from imported meat from bovines was rare (0.3%), while the level of MDR among isolates from fresh meat from pigs was moderate (11.9%), (Annex C, tables 5–8).

The antimicrobials most often represented in the MDR patterns of isolates from fresh meat from broilers were ampicillin, sulfamethoxazole and trimethoprim, often also in combination with tetracycline. Resistance to ciprofloxacin and nalidixic acid was also a common trait among MDR-resistant isolates, sometimes without the inclusion of sulfamethoxazole and trimethoprim. Among isolates from imported meat from turkeys, the most common MDR patterns were resistance to ampicillin and tetracycline in combination with sulfamethoxazole or ciprofloxacin and nalidixic acid.

Among isolates from meat from pigs, the antimicrobials most often represented in the MDR patterns were sulfamethoxazole, trimethoprim and tetracycline, often also in combination with ampicillin. Among isolates from meat from bovines, the antimicrobials most often represented in the MDR patterns were ampicillin, sulfamethoxazole, trimethoprim and tetracycline.

None of the MDR-resistant patterns included resistance to amikacin or azithromycin and only two isolates from meat from pigs included resistance or tigecycline. Resistance to colistin was a part of the MDR-resistant pattern in nine isolates from fresh meat from broilers and one isolate from meat from bovines but not in any isolates from fresh meat from pig or turkeys.

Routine monitoring: ESBL-/AmpC-/CP-producing Salmonella spp.

In 2022, ESBL-/AmpC-/CP-producing *Salmonella* spp. were detected in 42 samples from imported meat from broilers and two isolates from imported meat from turkeys collected at BCPs (Table 17, see also EFSA and ECDC, 2024). Germany detected the bla_{CMY-2} gene in one *S.* Heidelberg and one *S.* Minnesota isolate from imported meat from broilers. bla_{CMY-2} was also reported in 13 *S.* Minnesota and 12 *S.* Heidelberg from imported meat from broilers and two *S.* Heidelberg from imported meat from turkeys by the Netherlands. The Netherlands also reported $bla_{CTX-M-2}$ in two *S.* Minnesota isolates from imported meat from broilers.

Routine monitoring: ESBL-/AmpC-/CP-producing indicator *E. coli*

In 2022 and 2023, ESC-resistant *E. coli* were detected in imported meat from broilers, turkeys, pigs and bovines, sampled at BCPs (Table 17). As for meat sampled at retail, ESBL-/AmpC-/CP-producing *E. coli* was detected more frequently in imported meat from poultry compared to imported meat from pigs and bovines.

Germany, Ireland and the Netherlands reported WGS data for isolates recovered from imported meat form broilers in 2022. The most commonly reported ESBL-encoding gene was $bla_{CTX-M-55}$ ($n = 21$), followed by $bla_{CTX-M-2}$ ($n = 12$), $bla_{CTX-M-8}$ ($n = 5$), $bla_{CTX-M-14}$ ($n = 1$) and $bla_{CTX-M-65}$ ($n = 1$). One of the isolates reported by the Netherlands co-harboured $bla_{CTX-M-8}$ and $bla_{CTX-M-55}$. Further, the Netherlands reported WGS data for isolates from imported meat from turkeys, where $bla_{CTX-M-8}$, $bla_{CTX-M-15}$, bla_{SHV-12} and bla_{CMY-2} were reported in one isolate each.

In 2023, WGS data were reported by the Netherlands for isolates originating from imported meat from pigs. One isolate harboured $bla_{CTX-M-14}$ and one isolate harboured $bla_{CTX-M-15}$.

TABLE 17 Occurrence of presumptive ESBL-, AmpC- or CP-producing *Salmonella* spp. and indicator commensal *Escherichia coli* from imported fresh meat sampled at border control posts, routine monitoring, EU MSs, 2022–2023.

	ESBL and/or AmpC[a]	ESBL[b]	AmpC[c]	ESBL + AmpC[d]	CP[e]
Matrix	***n* (% *R*)**	***n* (% *R*)**	***n* (% *R*)**	***n* (% *R*)**	***n* (% *R*)**
***Salmonella* spp.**					
Imported meat from broilers at BCP, 2022 ($N = 42$, 4 MSs)	42 (100)	4 (9.5)	38 (90.5)	0 (0)	0 (0)
Imported meat from turkeys at BCP, 2022 ($N = 2$, 1 MS)	2 (100)	0 (0)	2 (100)	0 (0)	0 (0)

TABLE 17 (Continued)

Matrix	ESBL and/or AmpC[a] *n* (% *R*)	ESBL[b] *n* (% *R*)	AmpC[c] *n* (% *R*)	ESBL + AmpC[d] *n* (% *R*)	CP[e] *n* (% *R*)
Indicator *Escherichia coli*					
Imported meat from broilers at BCP, 2022 (*N* = 62, 6 MS)	60 (96.8)	49 (79.0)	7 (11.3)	4 (6.5)	0 (0)
Imported meat from turkeys at BCP, 2022 (*N* = 5, 1 MS)	5 (100)	3 (60.0)	1 (20.0)	1 (20.0)	0 (0)
Imported meat from pigs at BCP, 2023 (*N* = 4, 3 MSs)	4 (100)	3 (75.0)	1 (25.0)	0 (0)	0 (0)
Imported meat from bovines at BCP, 2023 (*N* = 2, 2 MSs)	1 (50.0)	1 (50.0)	0 (0)	0 (0)	0 (0)

Abbreviations: % *R*, percentage of isolates with the resistance phenotype; AmpC, AmpC beta-lactamase; CP, carbapenemase; ESBL, extended-spectrum beta-lactamase; *n*, number of isolates with the phenotype; *N*, number of isolates investigated with Panel 2.

[a]According to EUCAST guidelines (EUCAST, 2017), only isolates showing MIC > 1 mg/L for cefotaxime and/or ceftazidime or reported presence of ESBL- and/or AmpC-encoding gene were considered (see Appendix A – Materials and methods).

[b]Isolates showing clavulanate synergy with cefotaxime, ceftazidime or both, suggesting an ESBL phenotype, or reported presence of ESBL-encoding gene.

[c]Isolates with cefoxitin resistance, suggesting AmpC phenotype or reported presence of AmpC-encoding gene.

[d]Isolates showing synergy with cefotaxime, ceftazidime or both and cefoxitin resistance, suggesting ESBL- and AmpC enzymes in the same isolate, or reported presence of both ESBL- and AmpC-encoding genes.

[e]Isolates with meropenem resistance or reported presence of CP-encoding gene.

Specific monitoring of ESBL-/AmpC-/CP-producing E. coli

Nine countries (Estonia, France, Germany, Hungary, Ireland, the Netherlands, Portugal, Romania and Spain) collected samples of imported meat at BCPs in 2022, while 15 countries (Belgium, Denmark, Estonia, France, Germany, Ireland, Italy, Malta, the Netherlands, Portugal, Romania, Spain, Sweden, Switzerland and the United Kingdom – Northern Ireland) did so in 2023. Overall, 204 of 332 (61.4%) of isolates from imported meat from broilers and 32/45 (71.1%) of isolates from imported meat from turkeys sampled in 2022 were positive for presumptive ESBL-/AmpC-/CP-producing *E. coli*. In imported meat from pigs and bovines the occurrence was markedly lower, with 12/290 (4.1%) of isolates from meat from pigs and 3/742 (0.4%) from meat from bovines positive for presumptive ESBL-/AmpC-/CP-producing *E. coli*. Compared to meat sampled at retail, the prevalence of presumptive ESBL-/AmpC-/CP-producing *E. coli* was higher in imported meat from poultry, while it was lower in imported meat from pigs and bovines. However, the number of samples investigated at BCPs for each food category was much lower than the number of samples collected at retail. Detailed information is presented in Annex D1.

WGS data for isolates collected in the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* were reported by Germany and the Netherlands in 2022 and 2023. In imported meat from broilers, Germany reported $bla_{\text{CTX-M-55}}$ ($n = 20$), $bla_{\text{CTX-M-2}}$ ($n = 12$), $bla_{\text{CTX-M-8}}$ ($n = 8$), $bla_{\text{CMY-2}}$ ($n = 3$), $bla_{\text{CTX-M-15}}$ ($n = 1$), and co-carriage of $bla_{\text{CTX-M-55}}$ and $bla_{\text{CMY-2}}$ ($n = 1$). A similar pattern was seen in the Netherlands, who reported $bla_{\text{CTX-M-55}}$ ($n = 24$), $bla_{\text{CTX-M-8}}$ ($n = 16$), $bla_{\text{CTX-M-2}}$ ($n = 9$), $bla_{\text{CTX-M-15}}$ ($n = 4$), $bla_{\text{CMY-2}}$ ($n = 3$), $bla_{\text{CTX-M-1}}$ ($n = 2$), $bla_{\text{SHV-12}}$ ($n = 2$) and $bla_{\text{CTX-M-14}}$ ($n = 1$) in isolates from imported meat from broilers, and $bla_{\text{CTX-M-8}}$ ($n = 11$), $bla_{\text{CTX-M-55}}$ ($n = 9$), $bla_{\text{CTX-M-15}}$ ($n = 2$), and $bla_{\text{SHV-12}}$ ($n = 2$), $bla_{\text{CMY-2}}$ ($n = 2$) and $bla_{\text{CTX-M-2}}$ ($n = 1$) in isolates from imported meat from turkeys. In 2023, the Netherlands reported $bla_{\text{CTX-M-15}}$ ($n = 3$) and $bla_{\text{CTX-M-1}}$ ($n = 2$) in imported meat from pigs, while Germany reported $bla_{\text{CTX-M-55}}$ ($n = 1$) in imported meat from bovines.

The ESBL-encoding genes most frequently reported from isolates of imported meat from broilers and imported meat from turkeys sampled at BCP differed from those genes dominating in poultry meat sampled at retail. The ESBL-encoding genes $bla_{\text{CTX-M-55}}$ and $bla_{\text{CTX-M-8}}$ dominated among imported meat from broilers, while $bla_{\text{CTX-M-8}}$ was most common in imported meat from turkeys, followed by $bla_{\text{CTX-M-55}}$. These ESBL-encoding genes are commonly occurring in Brazil, which was the country of origin for the majority of imported meat samples from poultry (Adur et al., 2022; Casella et al., 2018; Egervärn et al., 2014; Soncini et al., 2022).

Specific monitoring of CP-producing E. coli

Within the specific monitoring of CP-producing *E. coli*, a total of 192 samples from imported meat from broilers and six samples from imported meat from turkeys were collected in 2022, and 199 samples from imported meat from pigs and 687 samples from imported meat from bovines were collected in 2023. No presumptive CP-producers were detected in any of the samples.

5 | EXTENDED-SPECTRUM β-LACTAMASE (ESBL)-, AMPC- AND/OR CARBAPENEMASE (CP)- PRODUCING *SALMONELLA* AND *E. COLI*

5.1 | Key findings

- In *Salmonella* spp. and indicator commensal *E. coli* collected in the routine monitoring, the **occurrence** of ESBL-/AmpC-/CP-producers was in general very low or low in 2022 and 2023.
- In 2022, **Whole Genome Sequencing (WGS)** data were reported by seven countries,[20] whereas 10 countries[21] reported WGS data in 2023.
- In both 2022 and 2023, a variety of ESBL- and AmpC-encoding genes were reported. Overall, the most reported ESBL-encoding genes in *E. coli* were ***bla*$_{\text{CTX-M-1}}$** followed by ***bla*$_{\text{CTX-M-15}}$**. In poultry and poultry meat, ***bla*$_{\text{SHV-12}}$** was also frequently reported. The ***bla*$_{\text{CMY-2}}$** gene was the most commonly reported plasmid-mediated AmpC-encoding gene in 2022 and 2023. Further, the **point mutation C-42T** in the chromosomal *ampC* gene causing an AmpC phenotype was frequently detected, especially in isolates from fattening turkeys, fattening pigs, cattle under 1 year of age and meat from these animal populations.
- In general, there was a high degree of **correspondence** between phenotype determined by MIC testing and phenotype predicted from genotype for isolates where both phenotypic and genotypic data were reported.
- Major differences were observed in the **spatial distribution** of the prevalence of ESBL-/AmpC-producing *E. coli*.
- The **prevalence** of ESBL-/AmpC-producing *E. coli* was still high in some countries, but statistically significant decreasing trends were observed in several countries for both animal populations and meat categories.
- Overall, the ESBL phenotype was more common than the AmpC phenotype in all animal populations and food categories tested.
- Statistically significant decreasing **trends** in the key outcome indicator of prevalence of ESBL- and/or AmpC-producing *E. coli* (KOI_{ESC}) were observed in 19 MSs and two non-MS, while a statistically significant increasing trend was observed in three MSs and one non-MS. In the remaining countries, no statistically significant trend was discerned.
- In 2022, one indicator commensal *E. coli* from fattening turkeys was reported to harbour the CP-encoding gene $bla_{\text{OXA-181}}$.
- In the **specific monitoring of ESBL-/AmpC-/CP-producing *E. coli***, three isolates from broilers were reported to harbour the $bla_{\text{VIM-1}}$ gene in 2022. In 2023, $bla_{\text{OXA-181}}$ was reported in three isolates from fattening pigs, $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$ in one isolate from fattening pigs, $bla_{\text{NDM-5}}$ in one isolate from cattle under 1 year of age and $bla_{\text{VIM-1}}$ in one isolate from cattle under 1 year of age.
- In the **specific monitoring of CP-producing *E. coli*** in 2022, one isolate from fattening turkeys was reported to carry the $bla_{\text{OXA-181}}$ gene. In 2023, $bla_{\text{OXA-181}}$ was found in 24 isolates from fattening pigs and four isolates from cattle under 1 year of age, $bla_{\text{OXA-48}}$ in 21 isolates from fattening pigs and 1 isolate from cattle under 1 year of age, $bla_{\text{NDM-5}}$ in 5 isolates from fattening pigs and $bla_{\text{OXA-244}}$ in 1 isolate from fattening pigs. Additionally, one isolate from pig meat was also reported, carrying the $bla_{\text{NDM-5}}$ gene.
- In 2023, five isolates from fattening pigs were reported to co-harbour two CP-encoding genes simultaneously: $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$. Four isolates were detected in the specific monitoring of CP-producers and one in the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*.

5.2 | Data on ESBL-, AmpC- and/or carbapenemase (CP)-producing *Salmonella* and *E. coli* addressed

It is mandatory to perform the routine monitoring of indicator *E. coli* and *Salmonella* spp. in caecal samples from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age. Further, it is mandatory to perform the specific monitoring of ESBL-, AmpC- and/or CP-producing *E. coli* in caecal samples and from retail meat, from the same animals. In 2023, gathering caecal samples from fattening pigs and cattle under 1 year of age, as well as meat from pigs and meat from bovines collected at retail was mandatory. Since 2021, it has also been mandatory to report AMR data from imported fresh meat from third countries sampled at border control posts (BCPs). Table 18 gives an overview of the number of MSs and non-MSs reporting data for the different animal populations and food categories (sampled at retail or BCPs) in 2022 and 2023.

[20]Czechia, Finland, Germany, Italy, the Netherlands, Norway and Sweden.

[21]Austria, Belgium, Czechia, Finland, Germany, Italy, the Netherlands, Norway, Sweden and the United Kingdom (Northern Ireland).

TABLE 18 Overview of countries performing the specific monitoring of ESBL-, AmpC- and/or CP-producing *Escherichia coli* in 2022 and 2023.

		Number of countries reporting data	
Year	**Matrix**	**MSs***	**Non-MSs**
2023	Fattening pigs	28	3
	Cattle under 1 year of age	12	1
	Meat from pigs (retail)	28	2
	Meat from bovines (retail)	28	2
	Meat from pigs (BCPs)	9	
	Meat from bovines (BCPs)	13	1
2022	Broilers	27	3
	Fattening turkeys	12	1
	Meat from broilers (retail)	26	2
	Meat from turkeys (retail)	22	2
	Meat from broilers (BCPs)	9	
	Meat from turkeys (BCPs)	3	

Abbreviations: BCPs, border control posts; MSs, EU Member States; non-MSs, non-EU Member States.
*Including United Kingdom (Northern Ireland).

All prevalence and occurrence tables on ESBL-, AmpC- and/or CP-producers from the 2022 and 2023 monitoring, as well as tables on resistance mentioned in this chapter can be found in Annex D1 and the *Salmonella* spp. documents available on Zenodo (https://doi.org/10.5281/zenodo.14645440). Materials and methods are presented in Appendix A – Materials and methods. Additionally, data can be further visualised interactively using the EFSA dashboard on Indicators of Antimicrobial Resistance available online (here). Results from imported meat sampled at BCPs are presented in the textbox 'Monitoring antimicrobial resistance in imported fresh meat sampled at Border Control Posts'.

Whole genome sequencing (WGS) was introduced as an alternative method to the phenotypic testing of indicator *E. coli* and *Salmonella* isolates displaying phenotypic resistance to extended-spectrum cephalosporins (ESC) and/or carbapenems in Panel 1, and for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* in 2021. The EURL-AR developed harmonised protocols to ensure data comparability between countries reporting WGS data. Reporting WGS data will facilitate and improve understanding of potential role and contribution of food-producing animals and food derived thereof to the human burden of AMR (EFSA, 2019). An overview of countries reporting WGS data for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* in 2022 and 2023 is shown in Table 19.

TABLE 19 Overview of countries reporting WGS data for the specific monitoring of ESBL-/AmpC-/CP-producing *Escherichia coli* in 2022 and 2023.

Year	Matrix	Number of countries	Countries reporting WGS results
2022	Broilers	7	CZ, DE, FI, IT, NL, SE, NO
	Fattening turkeys	3	DE, IT, NO
	Retail meat from broilers	6	CZ, DE, FI, IT, NL, SE
	Retail meat from turkeys	3	CZ, DE, IT
2023	Fattening pigs	9	AT, BE, CZ, DE, FI, IT, NL, SE, NO
	Cattle under 1 year of age	5	AT, BE, DE, IT, NL
	Retail meat from pigs	8	AT, BE, CZ, DE, IT, NL, XI, NO
	Retail meat from bovines	8	AT, BE, CZ, DE, FI, IT, NL, XI

Abbreviations: AT, Austria; BE, Belgium; CZ, Czechia; DE, Germany; FI, Finland; IT, Italy; NL, the Netherlands; NO, Norway; SE, Sweden; XI, United Kingdom (Northern Ireland); WGS, whole genome sequencing.

5.3 | Routine antimicrobial resistance monitoring: Presumptive ESBL-, AmpC- and/or CP-producers and related WGS data

Presumptive ESBL-, AmpC- and/or CP-producing *Salmonella* spp. and indicator *E. coli* collected within the framework of the routine monitoring were subjected to susceptibility testing using Panel 2 or WGS in accordance with the updated EU legislation.[22]

[22]All *Salmonella* and indicator *E. coli* isolates tested with the harmonised panel of antimicrobial substances (Panel 1) and exhibiting microbiological resistance to cefotaxime, ceftazidime or meropenem were subsequently subjected to further testing using a supplementary panel of substances (Panel 2) to obtain more detailed phenotypic characterisation (See Appendix A – Materials and methods).

ESBL/AmpC/CP phenotypes and genotypes in *Salmonella* spp.

In 2022 and 2023, the proportion of presumptive ESC-resistant *Salmonella* spp. collected within the routine monitoring based on phenotypic results was generally very low or low (ranging between 0.2% and 2.2%) at the MS level (Annex A2). The prevalence of different Salmonella serovars in some countries may greatly influence the occurrence of ESC-resistant *Salmonella* in a specific animal population. At the MS-group level, the occurrence of presumptive ESC-resistant *Salmonella* was 1.4% in broilers, 2.2% in fattening turkeys, 0.2% in laying hens, 0.8% in fattening pigs and 1.3% in cattle under 1 year of age. Detailed data per animal populations and food categories are presented in Annex D1. Table 3 gives an overview of the presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. isolates reported in 2022 and 2023. Additional information and WGS results for presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. from food-producing animals collected within the routine monitoring are presented in Chapter 2 **Antimicrobial resistance in Salmonella spp**.

ESBL/AmpC/CP phenotypes and genotypes in indicator commensal *E. coli*.

In 2022 and 2023, the proportion of ESC-resistant indicator commensal *E. coli* collected within the routine monitoring was generally low. The occurrence of ESC resistance ranged from 0% to 8.7% in broilers, 0% to 4.7% in fattening turkeys, 0% to 12.5% in fattening pigs and 0% to 10.6% in cattle under 1 year of age, among the reporting MSs. At the MS-group level, the occurrence of presumptive ESBL-/AmpC-/CP-producing indicator commensal *E. coli* was 1.3% in broilers, 1.5% in fattening turkeys, 1.3% in fattening pigs and 1.8% in cattle under 1 year of age. In all animal populations and food categories investigated, the ESBL phenotype was more common than the AmpC phenotype (Table 20).[23]

TABLE 20 Summary of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. and indicator commensal *Escherichia coli* subjected to supplementary testing (Panel 2) or whole genome sequencing, EU MSs, 2022–2023.

	ESBL and/or AmpC[a]	ESBL[b]	AmpC[c]	ESBL + AmpC[d]	CP[e]
Matrix	***n* (% *R*)**	***n* (% *R*)**	***n* (% *R*)**	***n* (% *R*)**	***n* (% *R*)**
***Salmonella* spp.**					
Broilers, 2022 (*N* = 1911, 24 MSs + XI)	26 (1.4)	26 (1.4)	0 (0)	0 (0)	0 (0)
Fattening turkeys, 2022 (*N* = 686, 19 MSs)	15 (2.2)	15 (2.2)	0 (0)	0 (0)	0 (0)
Laying hens, 2022 (*N* = 908, 23 MSs + XI)	2 (0.2)	2 (0.2)	0 (0)	0 (0)	0 (0)
Fattening pigs, 2023 (*N* = 1474, 25 MSs + XI)	12 (0.8)	11 (0.7)	0 (0)	1 (0.1)	0 (0)
Cattle under 1 year of age, 2023 (*N* = 80, 11 MSs)	1 (1.3)	1 (1.3)	0 (0)	0 (0)	0 (0)
Indicator commensal *E. coli*					
Broilers, 2022 (*N* = 4341, 27 MSs + XI)	48 (1.1)	39 (0.9)	6 (0.1)	3 (0.1)	0 (0)
Fattening turkeys, 2022 (*N* = 1773, 13 MSs)	18 (1.0)	17 (1.0)	1 (0.1)	0 (0)	1 (0.1)
Fattening pigs, 2023 (*N* = 4368, 27 MSs + XI)	50 (1.1)	38 (0.9)	12 (0.3)	0 (0)	0 (0)
Cattle under 1 year, 2023 (*N* = 1964, 11 MSs)	32 (1.6)	22 (1.1)	9 (0.5)	1 (0.1)	0 (0)

Abbreviations: % *R*, percentage of cephalosporin-resistant isolates presenting a presumptive phenotype; AmpC, AmpC beta lactamase; CP, carbapenemase; ESBL, extended-spectrum beta- lactamase; MSs, EU Member States; *n*, number of presumptive ESBL- and/or AmpC–/CP-producing isolates; *N*, total number of isolates tested; XI, United Kingdom (Northern Ireland).

[a]According to EUCAST guidelines (EUCAST, 2017), only isolates showing MIC > 1mg/L for cefotaxime and/or ceftazidime or with reported presence of ESBL-/AmpC-encoding gene were considered (see Appendix A).

[b]Isolates showing clavulanate synergy with cefotaxime or ceftazidime or both, suggesting an ESBL phenotype or reported presence of ESBL-encoding gene.

[c]Isolates with cefoxitin resistance, suggesting AmpC phenotype or reported presence of AmpC-encoding gene.

[d]Isolates showing synergy with cefotaxime and/or ceftazidime and cefoxitin resistance, suggesting ESBL- and AmpC-enzymes in the same isolate, or reported presence of both ESBL- and AmpC-encoding genes.

[e]Isolates with meropenem resistance or reported presence of CP-encoding gene.

In 2022, WGS data for ESC-resistant indicator commensal *E. coli* were reported by Germany, Italy and the Netherlands. **In 2023**, WGS data were reported by Norway in addition to the before mentioned countries. The genes reported are shown in Table 21.

[23]Detailed data per country are presented in Annex D1.

TABLE 21 ESBL-/AmpC-/CP-encoding genes reported in the routine monitoring of indicator commensal *Escherichia coli*, 2022–2023.

Year	Animal population	ESBL-encoding gene	AmpC-encoding gene	CP-encoding gene	Country (*n*)
2022	Broilers	bla_{SHV-12}			DE (3)
		$bla_{TEM-52B}$			NL (1)
	Fattening turkeys	$bla_{CTX-M-27}$			DE (1)
		bla_{SHV-12}			IT (1)
				$bla_{OXA-181}$	IT (1)
2023	Cattle (< 1 year)	$bla_{CTX-M-1}$			DE (2), IT (2)
		$bla_{CTX-M-15}$			IT (5)
		$bla_{CTX-M-32}$			NL (1)
		bla_{SHV-12}			DE (1), IT (4)
			bla_{CFE-1}		IT (6)
			bla_{CMY-1}		IT (1)
	Fattening pigs	$bla_{CTX-M-1}$			DE (1), IT (1)
		bla_{SHV-12}			IT (1)
			bla_{CFE-1}		IT (1)
			bla_{DHA-1}		IT (1)
			C-42T mutation		DE (1), NO (1)

Abbreviations: AmpC, AmpC beta lactamase; CP, carbapenemase; DE, Germany; ESBL, extended-spectrum beta- lactamase; IT, Italy; *n*, number of isolates harbouring the gene; NL, the Netherlands; NO, Norway.

5.4 | Specific monitoring of presumptive ESBL-, AmpC, and/or CP-producing *Escherichia coli* and related WGS data

5.4.1 | Prevalence and occurrence of presumptive ESBL-, AmpC- and/or CP-producing *E. coli*

The specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* includes selective culturing of samples on media containing 1 mg/L cefotaxime, as recommended by EUCAST, facilitating the detection of very low numbers of resistant isolates in a sample.[24] The prevalence of presumptive ESBL- or AmpC-producing *E. coli* in all animal populations and food categories tested in 2022 and 2023 is visualised in Figure 48. Detailed information regarding prevalence and occurrence per country and matrix is presented in tables available online at Zenodo (https://doi.org/10.5281/zenodo.14645440), while the overall prevalence at the MS level is presented in Table 22.

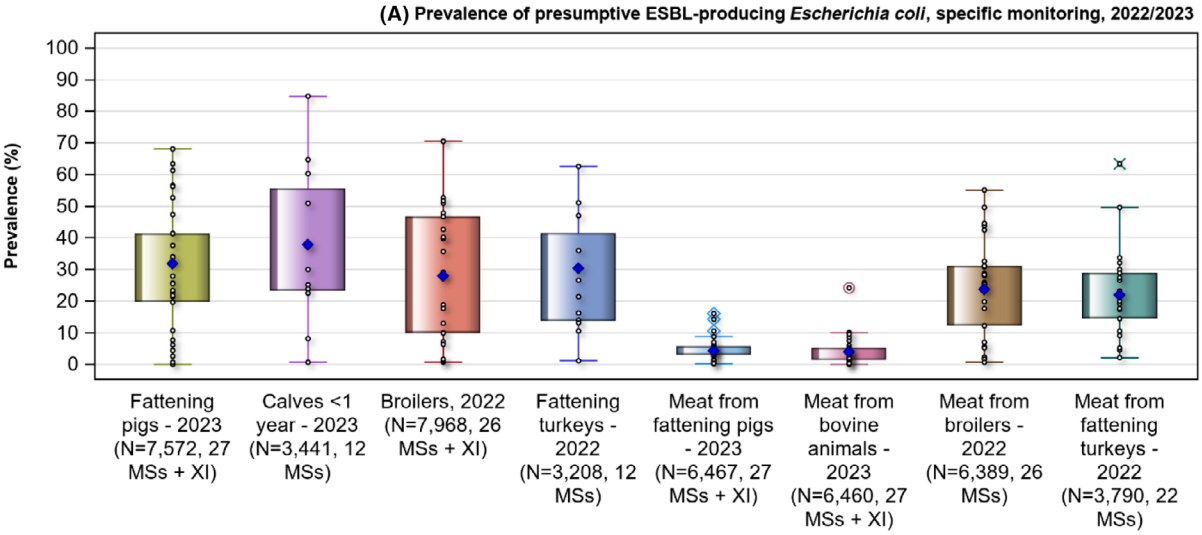
The **prevalence** of presumptive ESBL- and/or AmpC-producing[25] *E. coli* in **food-producing animals** varied markedly between the reporting countries in 2022–2023. When MIC data were considered, the prevalence ranged from 0% (Iceland) to 86.0% (Slovakia) in broilers, from 0% (Sweden) to 63.1% (Spain) in fattening turkeys, from 1.4% (Iceland) to 81.8% (Spain) in fattening pigs and from 0% (Sweden) to 54.1% (Portugal) in cattle under 1 year of age (see Annex D1 for detailed information). Further, the prevalence of ESBL- and/or AmpC-producing *E. coli* also varied between the MSs reporting WGS data. In 2022, the prevalence in broilers ranged from 0.6% (Norway) to 46.8% (Italy) in broilers and from 10.0% (Norway) to 39.0% (Germany) in fattening turkeys. In 2023, the prevalence ranged from 3.3% (Sweden) to 71.0% (Italy) in fattening pigs and from 27.9% (Austria) to 88.7% (Italy) in cattle under 1 year of age. When considering the prevalence of ESBL-producing *E. coli* and AmpC-producing *E. coli* separately, marked differences were also observed between the MSs (Annex D1).

In **meat sampled at retail**, the **prevalence** of presumptive ESBL- and/or AmpC-producing *E. coli* also varied considerably between the reporting countries. It ranged from 0% (Norway) to 61.3% (Hungary) in meat from broilers, from 0% (Finland and Norway) to 64.0% (Spain) in meat from turkeys, from 0% (Cyprus, Finland and Sweden) to 21.5% (Slovakia) in meat from pigs and from 0% (Cyprus, Sweden and Norway) to 24.9% (Hungary) in meat from bovines among countries reporting MIC data (Annex D1). Also, for meat, marked differences were observed between the MSs when the prevalence of ESBL- or AmpC-producing *E. coli* were assessed separately (Annex D1). Among MSs reporting WGS data, the prevalence of ESBL- and/or AmpC-producing *E. coli* ranged from 1.7% (Finland and Sweden) to 40.1% (Italy) in meat from broilers, from 17.1% (Czechia) to 35.1% (Germany) in meat from turkeys, from 0.3% (the Netherlands) to 8.8% (Czechia) in meat from pigs and from 0.3% (Finland) to 10.0% (Italy) in meat from bovines. The overall prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* at the MS-group level was low in retail meat from pigs (5.4%) and retail meat from bovines (4.4%), while it was high in retail meat from broilers (29.6%) and retail meat from turkeys (24.2%). A high overall prevalence at the MS-group level was observed for all animal populations investigated, with 35.0% in broilers, 32.1% in fattening turkeys, 40.9% in fattening pigs and 41.4% in cattle under 1 year of age (Annex D1).

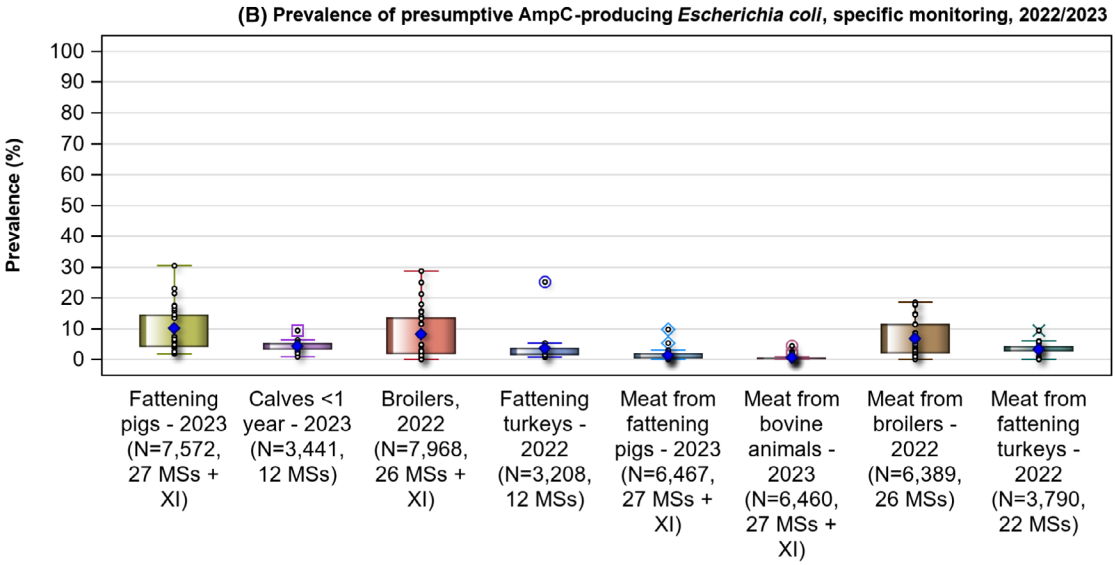
[24]The method is described in detail in Appendix A – Materials and methods and protocols are available at: https://www.eurl-ar.eu/protocols.aspx.

[25]*E. coli* exhibiting an ESBL-, AmpC- or ESBL+AmpC-producing phenotype.

The prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* in food-producing animals and meat derived thereof are visualised in Figures 50 and 51. An overview of meat samples collected at retail and BCPs is presented in Annex D1.



Genotypic data was added to phenotypic data for Germany and Italy (fattening pigs, calves (<1 year), fattening turkeys, broilers, meat from fattening turkeys, meat from broilers, meat from fattening pigs and meat from bovine animals), Belgium and Austria (fatttening pigs, calves (<1 year), meat from fattening pigs and meat from bovine animals), Czechia (fattening pigs, broilers, meat from fattening turkeys, meat from broilers, meat from fattening pigs and meat from bovine animals), Finland (fattening pigs, broilers, meat from bovine animals, meat from broilers), Netherlands (fatttening pigs, calves (<1 year), broilers, meat from fattening pigs, meat from bovine animals and meat from broilers) and Sweden (fattening pigs, broilers and meat from broilers)



Genotypic data was added to phenotypic data for Germany and Italy (fattening pigs, calves (<1 year), fattening turkeys, broilers, meat from fattening turkeys, meat from broilers, meat from fattening pigs and meat from bovine animals), Belgium and Austria (fatttening pigs, calves (<1 year), meat from fattening pigs and meat from bovine animals), Czechia (fattening pigs, broilers, meat from fattening turkeys, meat from broilers, meat from fattening pigs and meat from bovine animals), Finland (fattening pigs, broilers, meat from bovine animals, meat from broilers), Netherlands (fatttening pigs, calves (<1 year), broilers, meat from fattening pigs, meat from bovine animals and meat from broilers) and Sweden (fattening pigs, broilers and meat from broilers)

FIGURE 48 Prevalence of presumptive (A) ESBL-producing and (B) AmpC-producing *Escherichia coli* from the specific monitoring of ESBL-/AmpC-producing *Escherichia coli*, EU MSs and non-MSs, 2022–2023.

N, number of samples tested; diamonds with white outline are the data (one data point per country); blue diamond is Total EU. Outliers (> 1.5 IQR from 75 percentile) are visualised using a different symbol for each matrix (i.e. circle for fattening turkeys). MSs, EU Member States; XI, United Kingdom (Northern Ireland).

TABLE 22 Summary of the presumptive ESBL–/ and/or AmpC-producing isolates from food-producing animals and derived meat, specific monitoring of ESBL-/AmpC-/CP-producing *Escherichia coli* in 2022 and, EU MSs 2022–2023.

	ESBL- and/or AmpC-producers[a]			ESBL-producers[b]			AmpC-producers[c]			ESBL + AmpC-producers[d]		
Matrix	***n***	**Occ %**	**Prev%**	***n***	**Occ %**	**Prev%**	***n***	**Occ %**	**Prev%**	***n***	**Occ %**	**Prev%**
Meat from broilers at retail, 2022 (*Ns* = 6389; *N* = 1915; 26 MSs)	1882	98.3	29.6	1460	76.2	23.0	382	19.9	6.0	60	3.1	0.9
Meat from turkeys at retail, 2022 (*Ns* = 3790; *N* = 923; 22 MSs)	915	99.1	24.3	800	86.7	21.2	92	10.0	2.4	35	3.8	0.9
Meat from pigs at retail, 2023 (*Ns* = 6467; *N* = 351; 27 MSs + XI)	351	100	5.4	263	75.0	4.1	77	21.9	1.2	11	3.1	0.2
Meat from bovines at retail, 2023 (*Ns* = 6460; *N* = 271; 27 MSs + XI)	270	99.6	4.4	235	86.7	3.9	29	10.7	0.5	6	2.2	0.1
Broilers, 2022 (*Ns* = 7968; *N* = 2804; 26 MSs + XI)	2768	98.7	35.0	2123	75.7	26.8	556	19.8	7.0	95	3.4	1.2
Fattening turkeys, 2022 (*Ns* = 3208; *N* = 1028; 12 MSs)	1021	99.3	32.1	908	88.3	28.6	56	5.4	1.8	57	5.5	1.8
Fattening pigs, 2023 (*Ns* = 7572; *N* = 3120; 27 MSs + XI)	3081	98.8	40.9	2320	74.3	30.8	683	21.9	9.1	80	2.6	1.1
Cattle under 1 year of age, 2023 (*Ns* = 3441; *N* = 1427; 12 MSs)	1409	98.7	41.4	1260	88.3	37.0	124	8.7	3.6	25	1.8	0.7

Note: Prevalence was calculated using the formula presented in Appendix A – Materials and methods.

Abbreviations: AmpC, AmpC beta lactamase; CP, carbapenemase; genotypic data was added to phenotypic data for Austria, Belgium, Czechia, Germany, Finland, Italy, the Netherlands, Norway, Sweden and XI, United Kingdom (Northern Ireland) when reporting WGS results; ESBL, extended-spectrum beta lactamase; *N*, number of isolates tested; *n*, number of presumptive ESBL-/AmpC-/CP-producing isolates; *Ns*, total number of samples tested; Occ %, percentage of cephalosporin-resistant isolates presenting a presumptive phenotype; Prev %, percentage of samples harbouring a presumptive ESBL-/AmpC-producing *E. coli*.

[a]According to EUCAST guidelines (EUCAST, 2017), only isolates showing MIC > 1 mg/L for CTX and/or CAZ or reported presence of ESBL-/AmpC- encoding gene were considered (see Appendix A – Materials and methods).

[b]All isolates showing clavulanate synergy with CTX or CAZ or both, suggesting ESBL phenotype, or reported presence of ESBL- encoding gene.

[c]Isolates with cefoxitin resistance, suggesting AmpC phenotype, or reported presence of AmpC- encoding gene.

[d]Isolates showing synergy with CTX or CAZ and cefoxitin resistance, suggesting ESBL- and AmpC- enzymes in the same isolates, or both ESBL- and AmpC- encoding genes reported.

5.4.2 | ESBL-, AmpC- and/or CP-results based on WGS data

In 2022, seven countries (Czechia, Finland, Germany, Italy, the Netherlands, Norway and Sweden) reported WGS data for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*. In addition to the above countries, also Austria, Belgium and the United Kingdom (Northern Ireland) reported WGS data **in 2023**. WGS data were provided for isolates from broilers ($n = 528$), fattening turkeys ($n = 260$), meat from broilers ($n = 387$) and meat from turkeys ($n = 232$) in 2022, and for isolates from fattening pigs ($n = 916$), cattle under 1 year of age ($n = 860$), meat from pigs ($n = 86$) and meat from bovines ($n = 79$) in 2023. Detailed information regarding ESBL-, AmpC- and/or CP-encoding genes reported under WGS programme codes can be found in Annex D3 (https://doi.org/10.5281/zenodo.14645440).

ESBL-encoding genes were more frequently reported than AmpC-encoding genes. This is comparable to the phenotypic results, where ESBL phenotypes were found more frequently than AmpC phenotypes in all matrices tested. A summary of CP-producers identified in 2022 and 2023 can be found in **Section 5.5 Monitoring of carbapenemase-producing Escherichia coli**.

A variety of different **ESBL-encoding genes** were detected (Annex D3 and Figure 49A,B). In broilers, the most commonly reported ESBL-encoding genes were $bla_{\text{CTX-M-1}}$ ($n = 164$), followed by $bla_{\text{SHV-12}}$ ($n = 141$). While in meat from broilers, a reverse pattern was observed, with $bla_{\text{SHV-12}}$ ($n = 109$) being the most frequently reported gene, followed by $bla_{\text{CTX-M-1}}$ ($n = 106$). For fattening turkeys, and meat from turkeys, $bla_{\text{CTX-M-15}}$ ($n = 65$ and $n = 82$, respectively) was the most common gene, followed by $bla_{\text{SHV-12}}$ ($n = 63$) in fattening turkeys, and $bla_{\text{CTX-M-1}}$ ($n = 41$) in meat from turkeys. $bla_{\text{CTX-M-1}}$ followed by

bla$_{CTX-M-15}$ were also the most frequently reported genes in fattening pigs ($n = 424$ and $n = 66$, respectively), cattle under 1 year of age ($n = 301$ and $n = 277$, respectively), meat from pigs ($n = 42$ and $n = 6$, respectively) and meat from bovines ($n = 35$ and $n = 17$, respectively). Further, *bla*$_{SHV-12}$ was also reported in six isolates originating from meat from pigs.

The C-42T mutation was the most frequently reported **AmpC resistance mechanism** (Figure 49C,D) in fattening turkeys ($n = 20$), meat from turkeys ($n = 14$), fattening pigs ($n = 203$), meat from pigs ($n = 12$), cattle under 1 year of age ($n = 31$) and meat from bovines ($n = 6$). C-42T was also the second most common AmpC genotype reported in broilers ($n = 25$). However, in broilers and meat from broilers, *bla*$_{CMY-2}$ gene was the most commonly reported gene ($n = 94$ and $n = 64$, respectively). Further, *bla*$_{CMY-2}$ was the second most common gene reported in fattening turkeys ($n = 7$), fattening pigs ($n = 34$) and meat from pigs ($n = 6$). In meat from turkeys, the second most commonly reported gene was *bla*$_{CMY-101}$ ($n = 5$), while *bla*$_{CMY-2}$ and *bla*$_{CFE-1}$ were the second most commonly reported genes in cattle under 1 year of age ($n = 6$ of each) and meat from bovines ($n = 1$ of each).

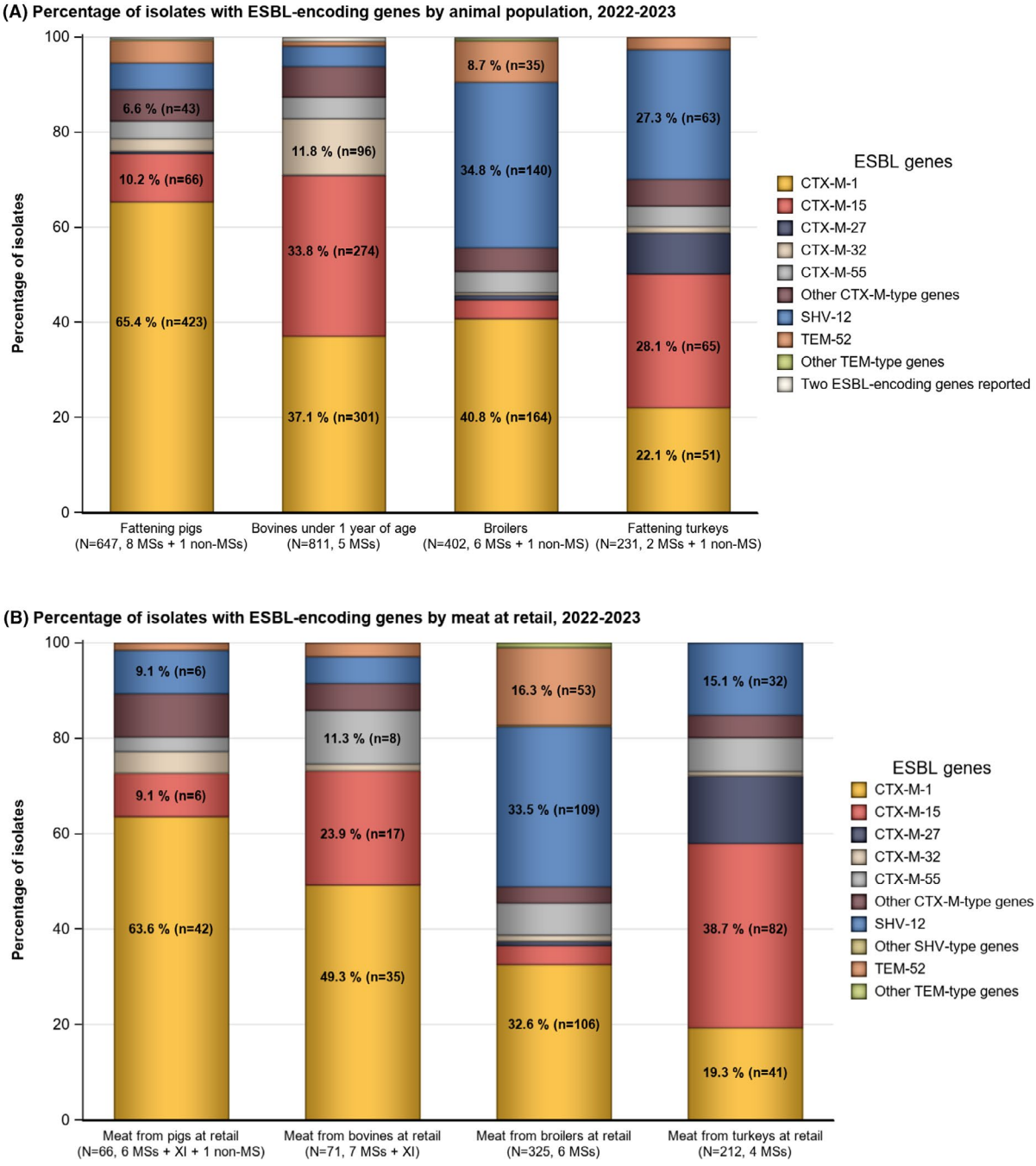


FIGURE 49 (Continued)

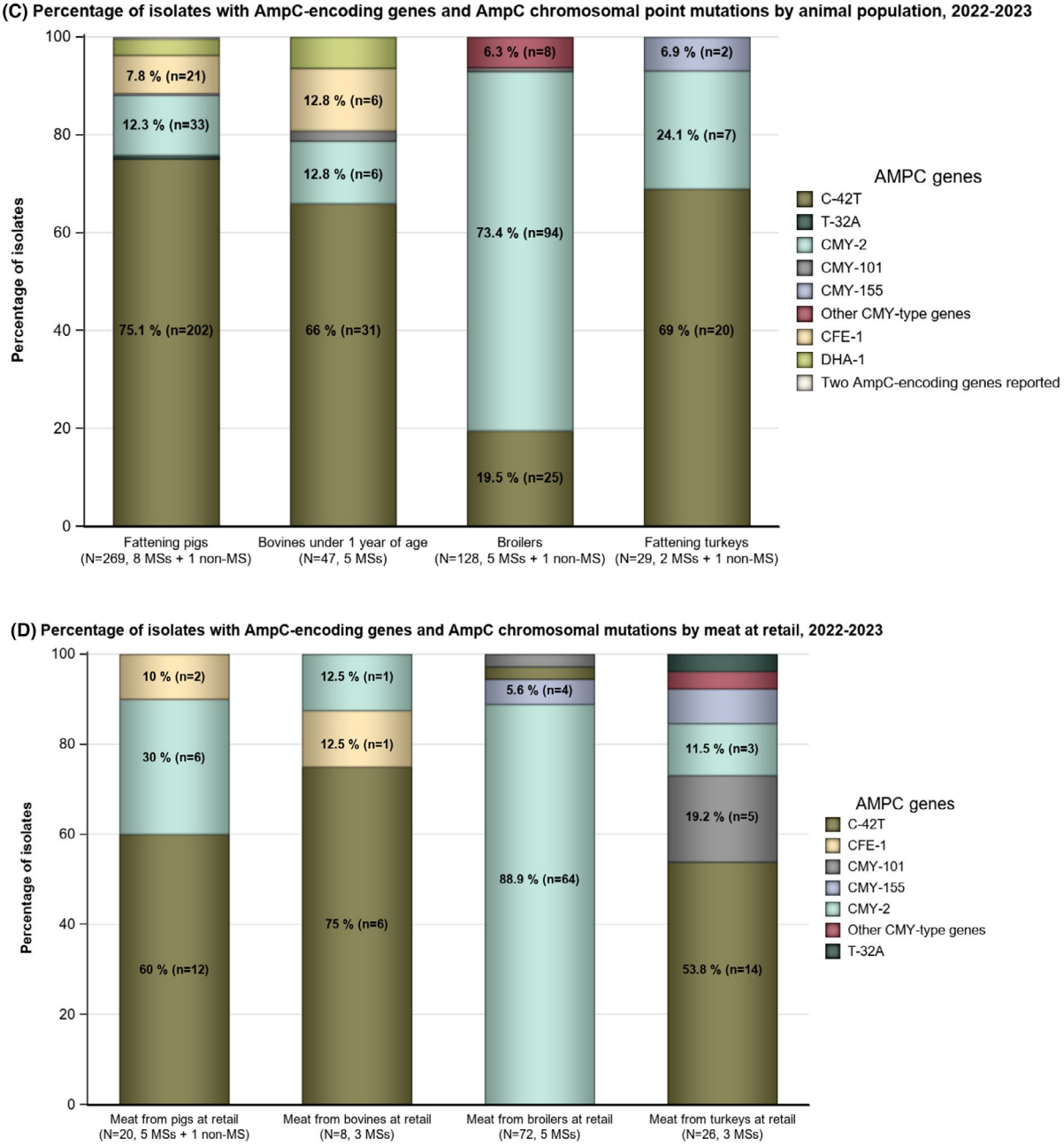


FIGURE 49 *Escherichia coli* isolates harbouring (A) ESBL-encoding genes in animals, (B) ESBL-encoding genes in retail meat, (C) AmpC-encoding genes and AmpC chromosomal point mutations in animals and (D) AmpC-encoding genes and AmpC chromosomal point mutations in retail meat, EU MSs and non-MSs, 2022/2023.

The figures include only data from countries reporting WGS results and indicating that these data should be used for analysis instead of MIC values. This excludes countries that provided both MIC results and WGS results voluntarily. The category TEM-52 also includes isolates with TEM-52B and TEM-52C. The category 'Two ESBL-genes reported' includes three isolates from fattening pigs, carrying CTX-M-1 + CTX-M-14 ($n = 1$), CTX-M-32 + SHV-12 ($n = 1$) or CTX-M-55 + CTX-M-65 ($n = 1$), seven isolates from cattle under 1 year of age carrying CTX-M-14 + CTX-M-55 ($n = 1$), CTX-M-15 + CTX-M-55 ($n = 1$), CTX-M-15 + SHV-12 ($n = 2$), CTX-M-189 + CTX-M-55 ($n = 2$) or CTX-M-32 + TEM-52 ($n = 1$), and two isolates from broilers carrying CTX-M-15 + TEM-207 ($n = 1$) or SHV-12 + TEM-106 ($n = 1$). The category 'Two AmpC-encoding genes reported' includes one isolate from fattening pigs, carrying CMY-2 + C-42T point mutation.

AmpC, AmpC beta-lactamase; ESBL, extended-spectrum beta-lactamase; MSs, EU Member States; *n*, number of isolates harbouring a specific gene or point mutation; *N*, number of isolates harbouring an ESBL- or AmpC-encoding gene; non-MS, Non-EU Member States; XI, United Kingdom (Northen Ireland).

Correspondence between MIC values and reported genes

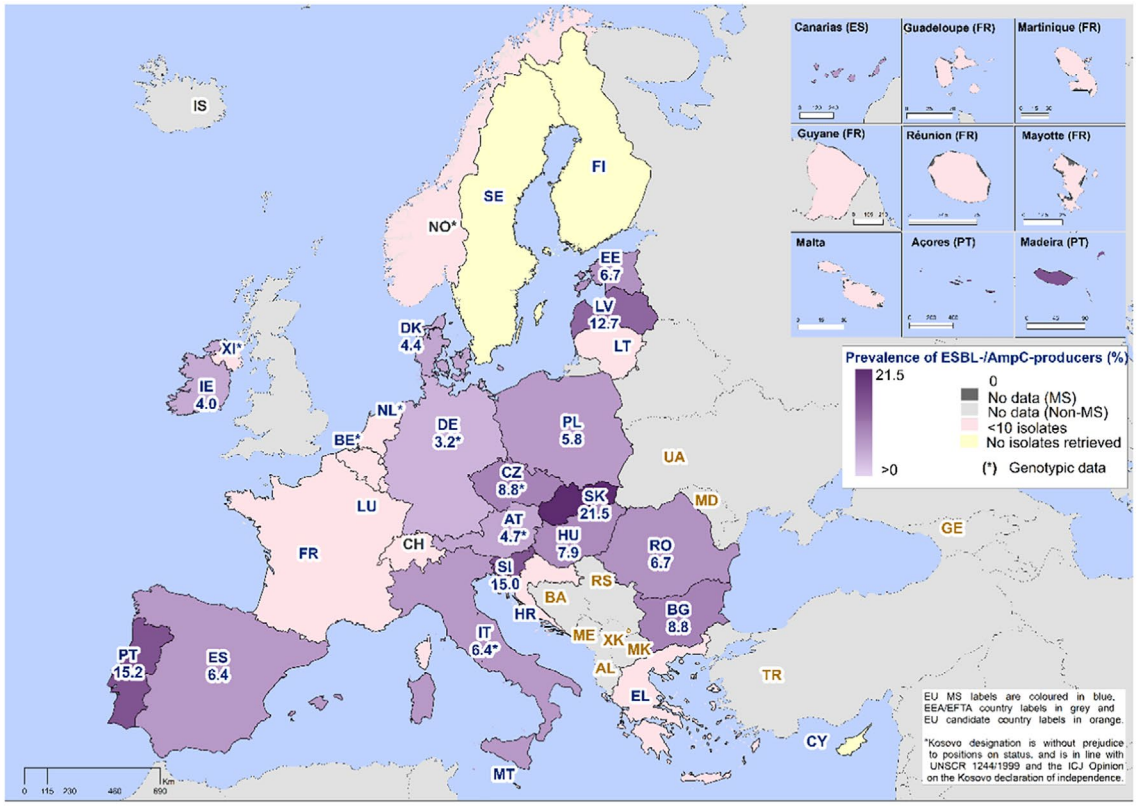
Both phenotypic and genotypic data for ESBL-/AmpC-/CP-producing *E. coli* were reported by six MSs (Austria, Finland, Ireland, Italy the Netherlands and Sweden) and Norway in 2022 and by five MSs (Finland, the Netherlands, Portugal Spain and Sweden), the United Kingdom (Northern Ireland) and Iceland in 2023. In general, there was high correspondence (i.e. ≥ 90% of the isolates carrying the gene also exhibited the expected phenotype) between the presence of an ESBL-/AmpC-/CP-encoding gene and the phenotype predicted based on the MIC data. However, for some genes, the overall correspondence was < 90%. A table showing reported genes and corresponding phenotype based on MIC data and a

summary table of correspondence between genotype and phenotype. In addition, concordance assessing the degree of agreement between phenotypic and genotypic results was measured using Cohen's kappa. Considering for example 2023 data, Cohen's kappa was assessed at 0.78 (95%IC: 0.73, 0.83), reflecting an agreement interpreted as good, between phenotypic and genotypic methods. Discrepancies may be partly explained by the fact that genes may be present and detected by WGS, but not expressed. The discrepant pairs would request detailed investigations for genes reported in ≥ 10 isolates is available in (Table 3 - Summary) on Zenodo: https://doi.org/10.5281/zenodo.14645440.

5.4.3 | Relative abundance (occurrence) of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. and indicator commensal *Escherichia coli* subjected

According to the monitoring protocols, only a single isolate from each positive sample is further investigated and characterised. Thus, if both ESBL- and AmpC-producing *E. coli* are present in a positive sample, the probability of detecting *E. coli* with either phenotype is influenced by the relative abundance of the phenotypes present in the sample. In the animal populations monitored, the occurrence of presumptive ESBL-producing *E. coli* isolates exceeds that of presumptive AmpC-producing isolates in most countries (Figure 52; Annex D1). Considerable variations in the occurrence of different phenotypes were observed for certain matrices between the reporting countries. When excluding countries testing less than 10 presumptive ESBL-/AmpC-producing isolates, the occurrence of isolates with an ESBL phenotype ranged from 24.6% (Latvia) to 97.7% (Germany) in broilers, from 18.2% (Norway) to 97.5% (Spain) in fattening turkeys, from 0% (Finland) to 93.8% (Austria) in fattening pigs, from 15.4% (Denmark) to 98.2% (Germany) in cattle under 1 year of age and from 25.0% (Ireland) to 93.3% (Austria) in retail meat from pigs (Annex D1). Less pronounced differences were observed for the remaining matrices, ranging from 50.8% (Latvia) to 96.2% (Luxembourg) in retail meat from broilers, from 62.5% (France) to 94.3% (Latvia) in retail meat from turkeys and from 46.2% (Slovenia) to 97.6% (Hungary) in retail meat from bovines (Annex D1). As it is not mandatory for countries with limited production of turkeys and cattle to investigate these matrices, only some countries report such data (Figure 53).

(A)



(B)

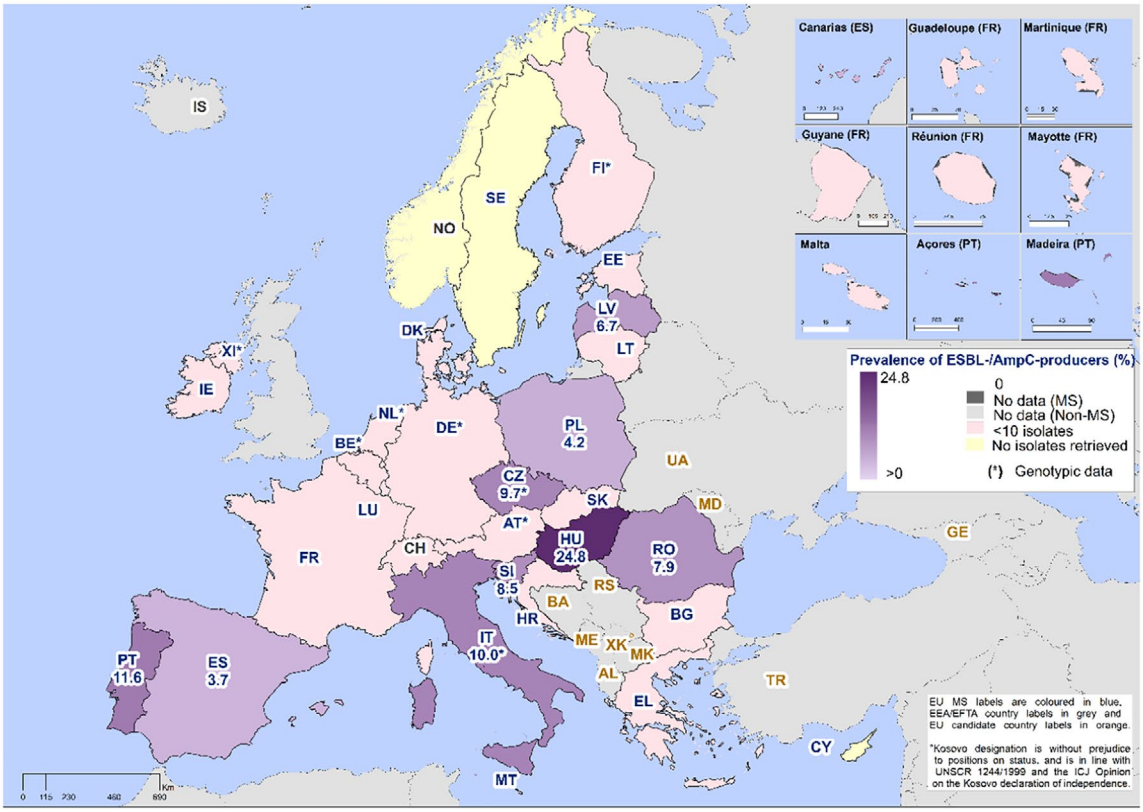


FIGURE 50 (Continued)

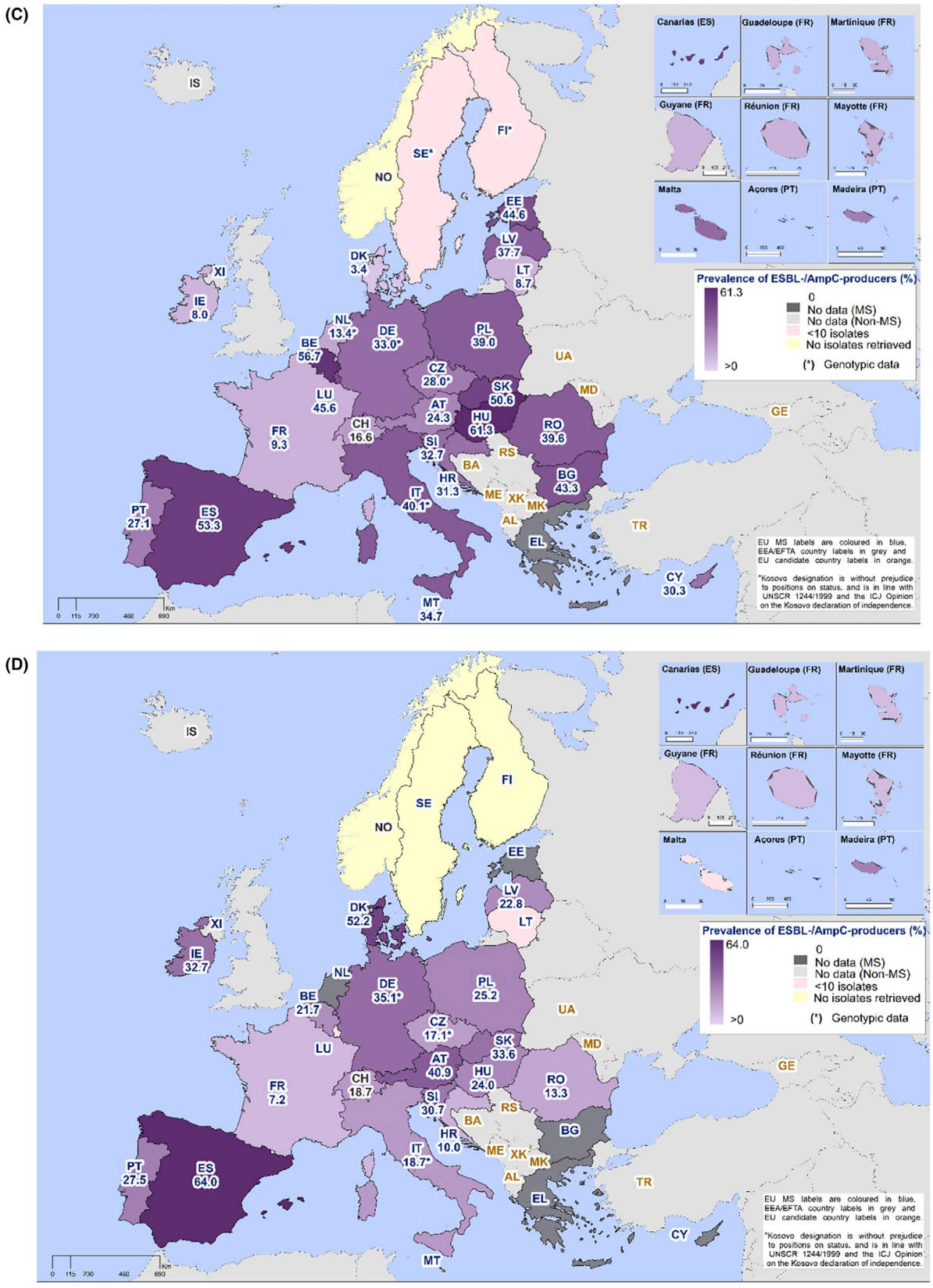


FIGURE 50 Spatial distribution of the prevalence of presumptive ESBL- and/or AmpC-producing *Escherichia coli* from (A) meat from pigs in 2023, (B) meat from bovines in 2023, (C) meat from broilers in 2022 and (D) meat from turkeys in 2022, EU MSs and non-MSs, 2022–2023. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

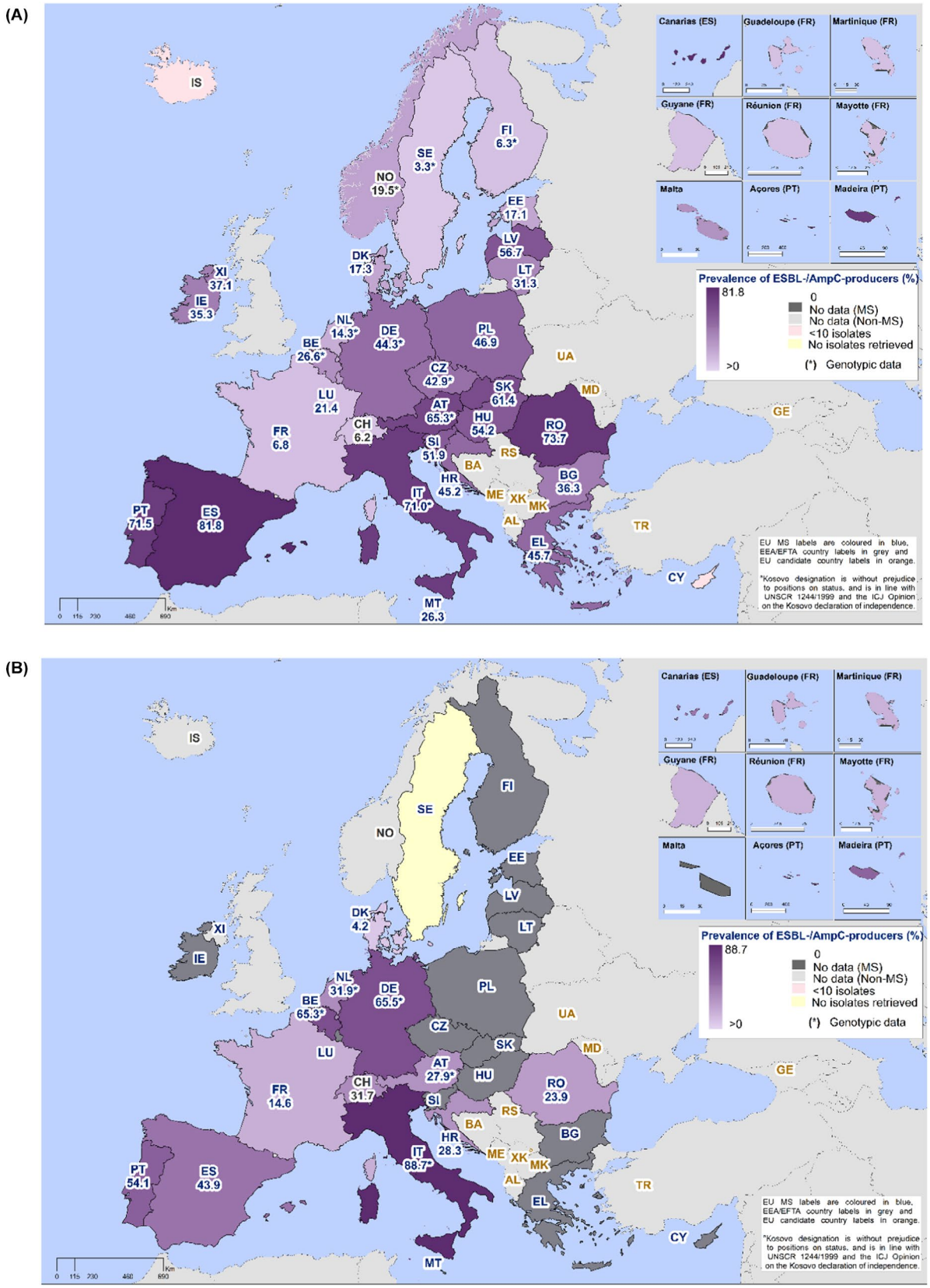


FIGURE 51 (Continued)

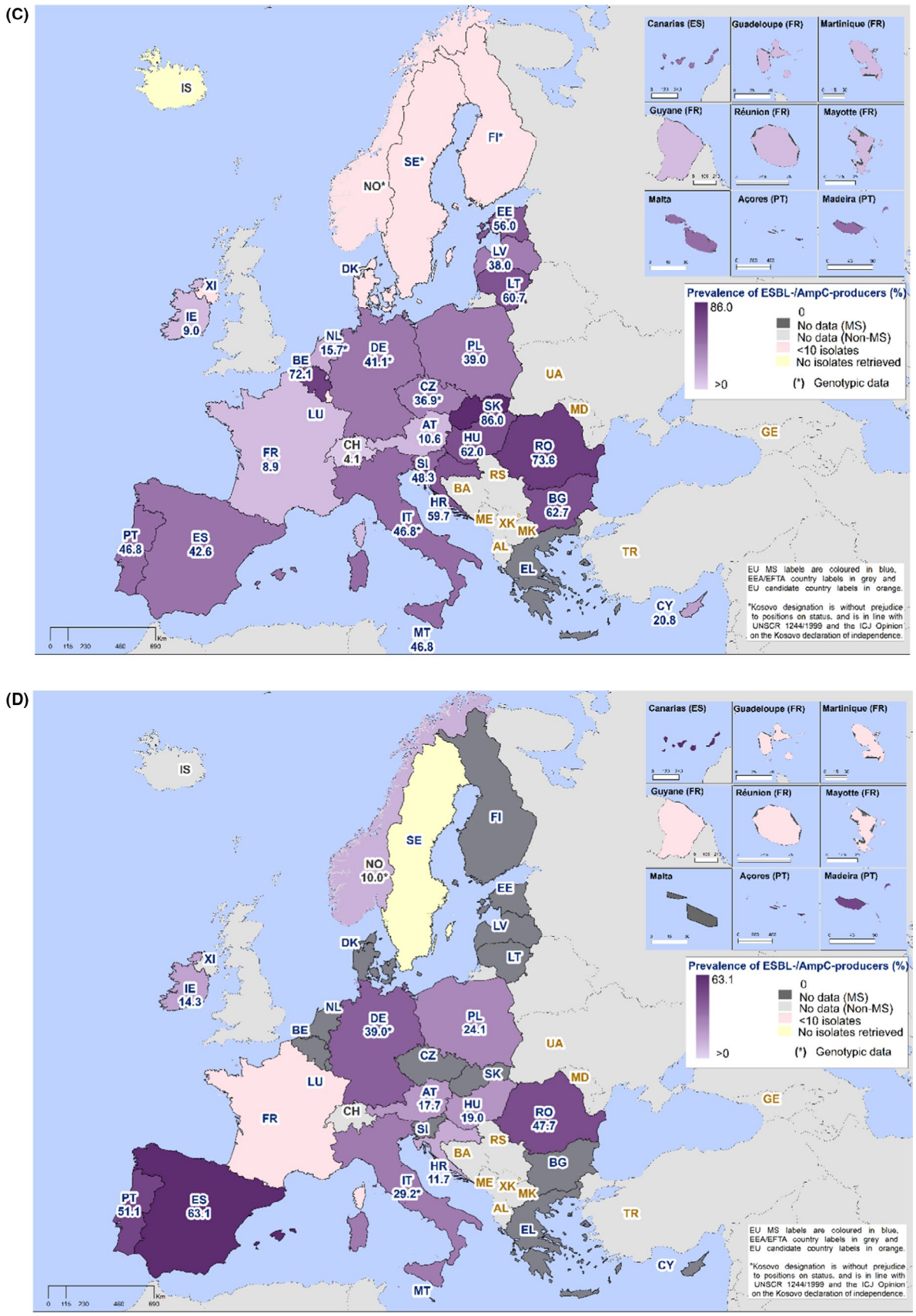
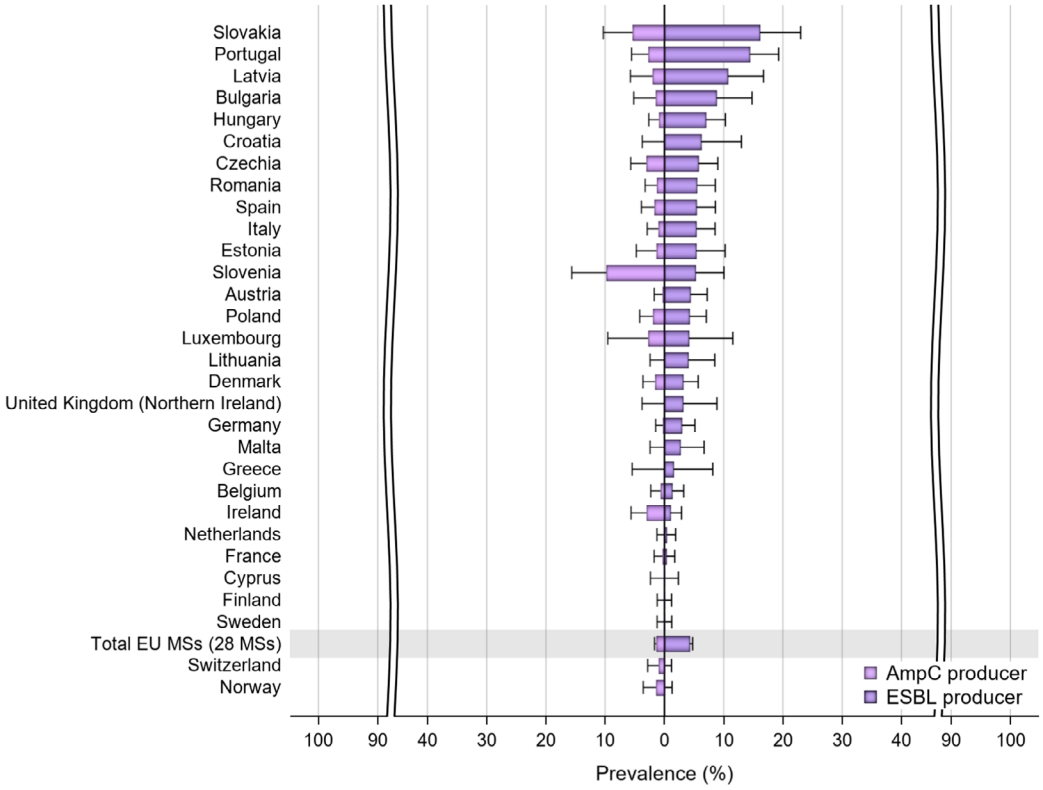


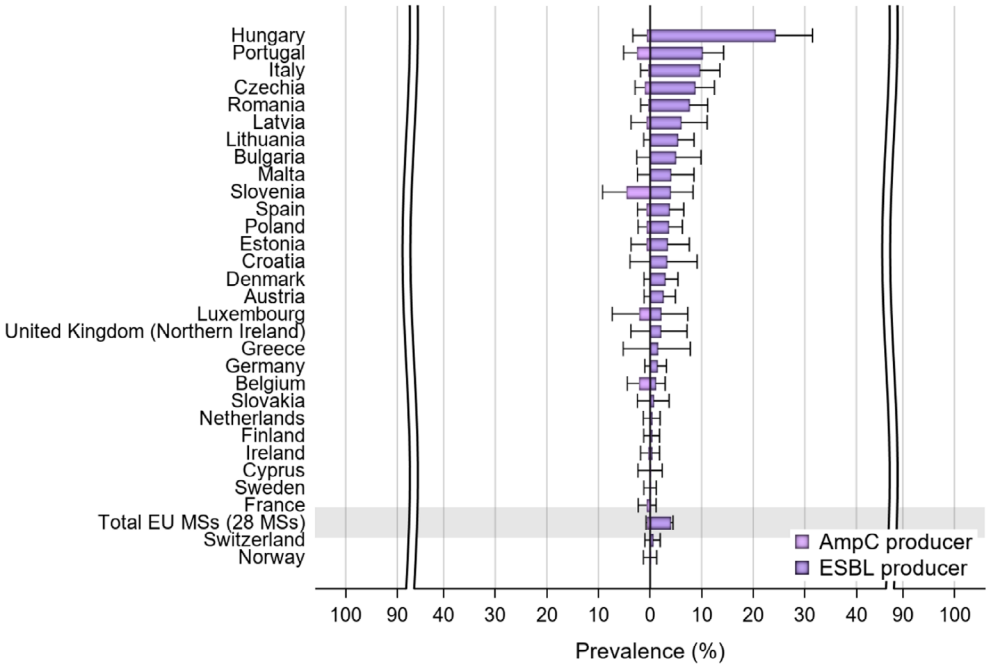
FIGURE 51 Spatial distribution of the prevalence of presumptive ESBL- and/or AmpC-producing *Escherichia coli* fromc (A) fattening pigs in 2023, (B) cattle under 1 year of age in 2023, (C) broilers in 2022 and (D) fattening turkeys in 2022, EU MSs and non-MSs, 2022/2023. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

(A) Prevalence of presumptive ESBL- and AmpC-producing *E. coli* in meat from pigs, specific monitoring, 2023



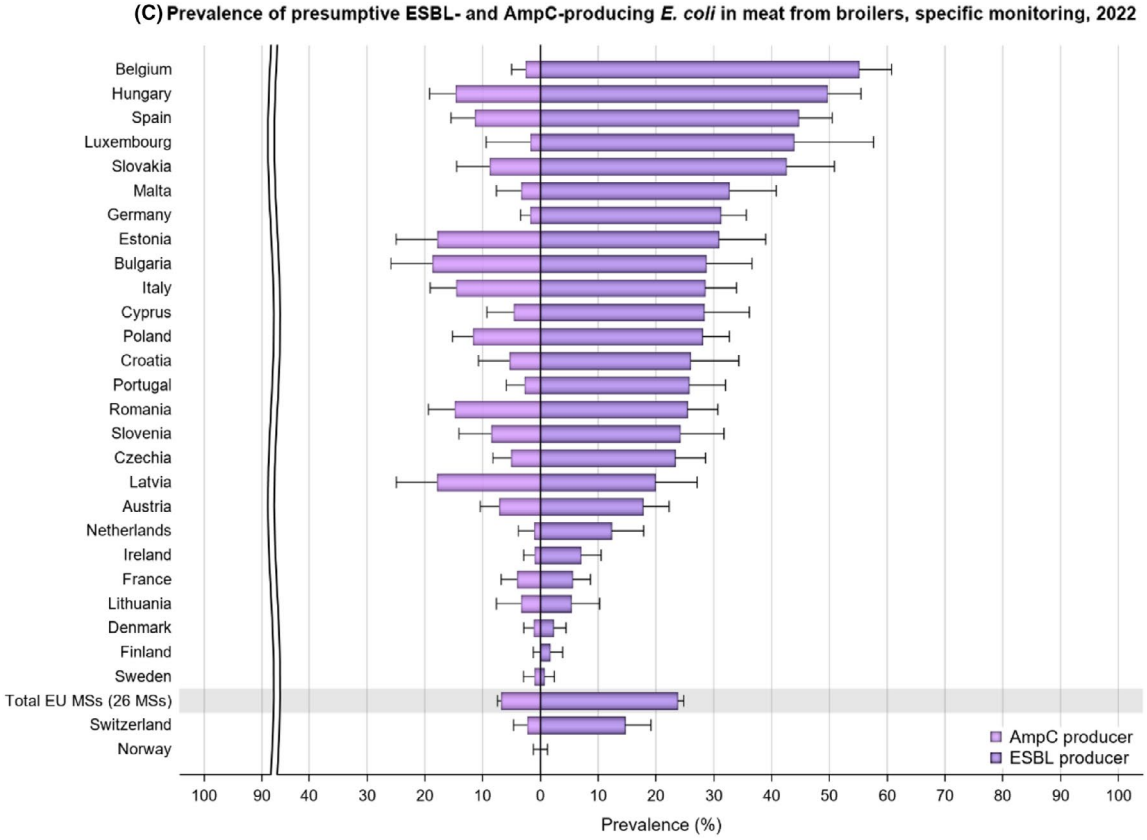
Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, IT and NL for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scalesused for the x-axis in the subfigures to improve the visibility of the variations among countries

(B) Prevalence of presumptive ESBL- and AmpC-producing *E. coli* in meat from bovines, specific monitoring, 2023



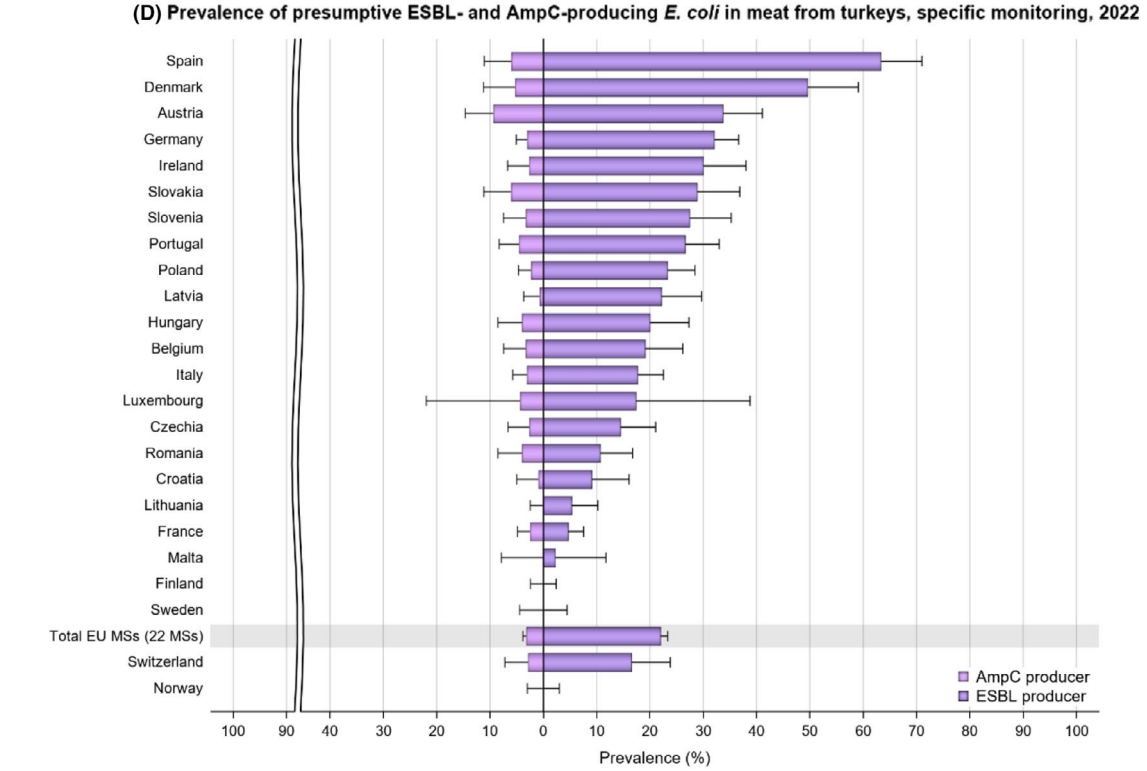
Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, FI and IT, for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

FIGURE 52 (Continued)



Prevalence estimates derive from phenotypic data, with the exception of CZ, DE, FI, IT, NL, and SE for which genotypic data have been used to assess prevalence

The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

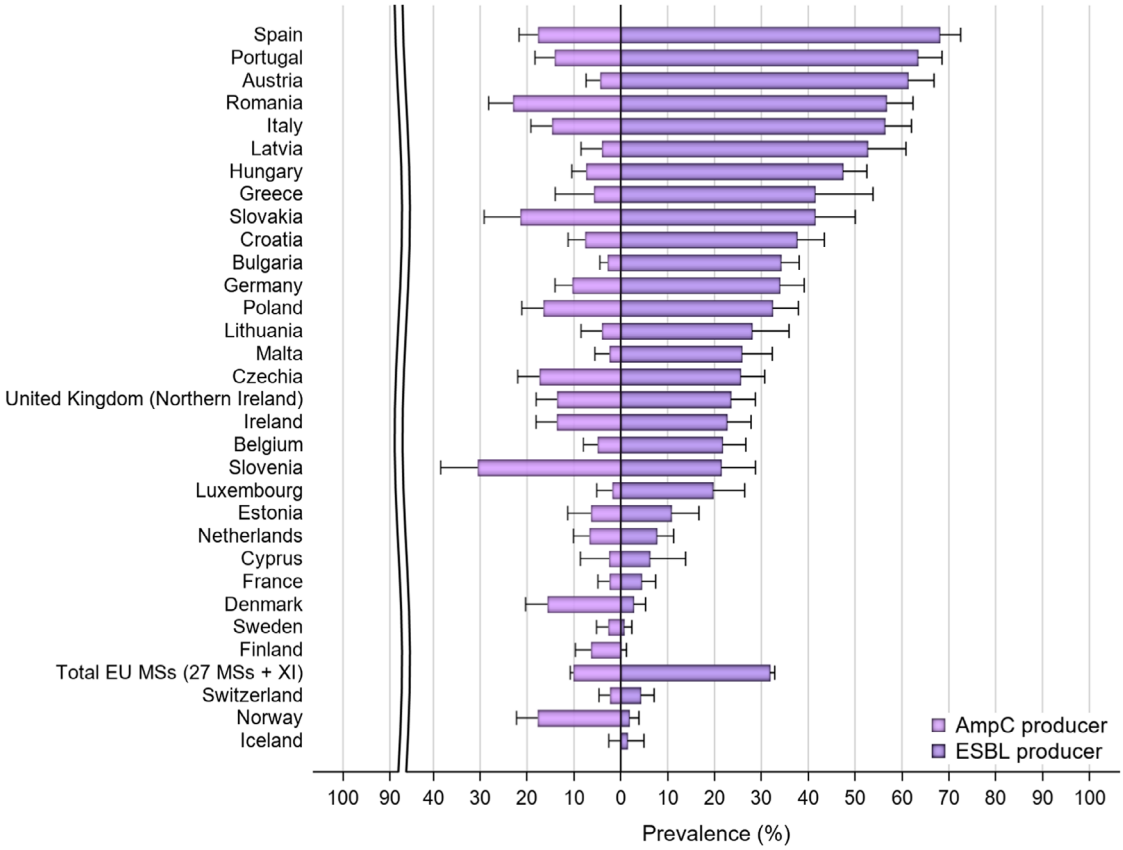


Prevalence estimates derive from phenotypic data, with the exception of CZ, DE and IT for which genotypic data have been used to assess prevalence

The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

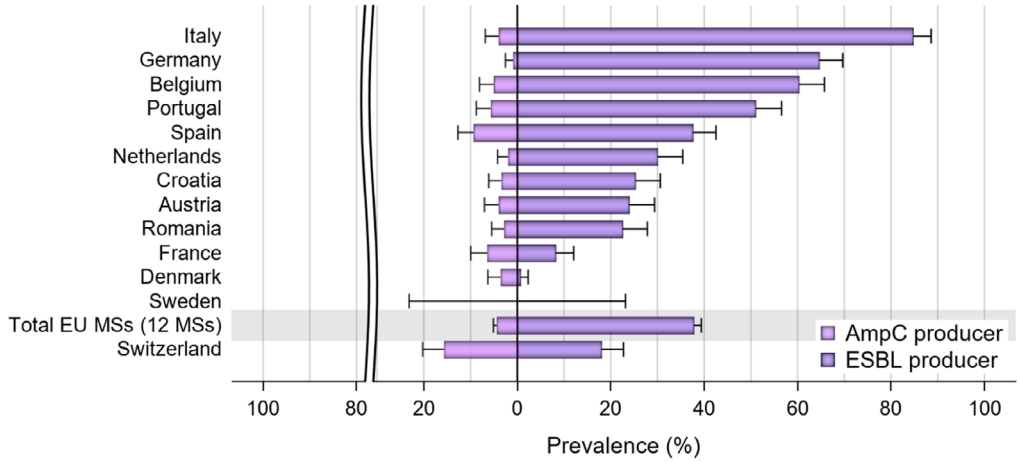
FIGURE 52 Prevalence of presumptive ESBL-producing versus AmpC-producing *Escherichia coli* from (A) meat from pigs 2023, (B) meat from bovines 2023, (C) meat from broilers 2022 and (D) meat from turkeys 2022, EU MSs and non-MSs.

(A) Prevalence of presumptive ESBL- and AmpC-producing *E. coli* in fattening pigs, specific monitoring, 2023



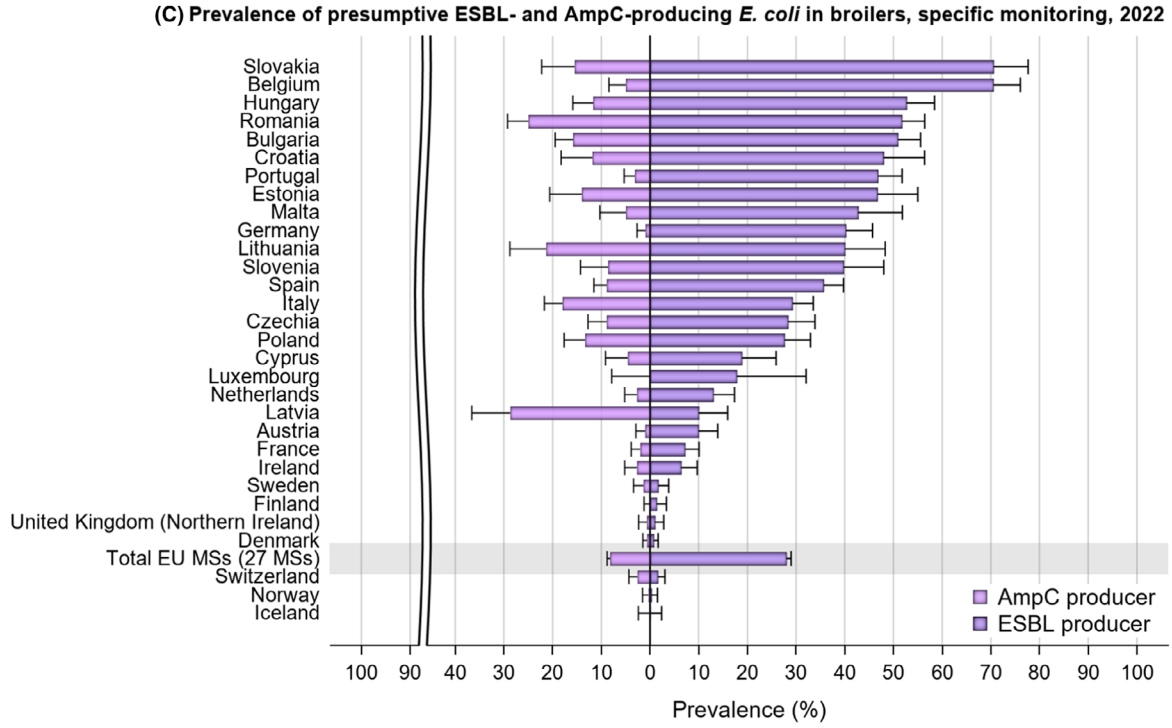
Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, FI, IT, NL and SE for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

(B) Prevalence of presumptive ESBL- and AmpC-producing *E. coli* in calves under 1 year of age, specific monitoring, 2023



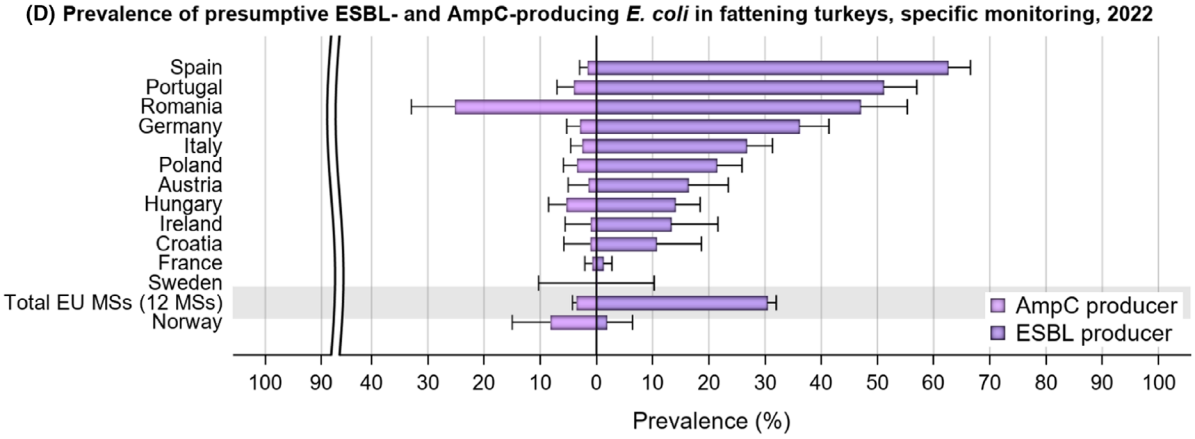
Prevalence estimates derive from phenotypic data, with the exception of AT, BE, DE, IT and NL, for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

FIGURE 53 (Continued)



Prevalence estimates derive from phenotypic data, with the exception of CZ, DE, FI, IT, NL, NO and SE for which genotypic data have been used to assess prevalence

The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries



Prevalence estimates derive from phenotypic data, with the exception of DE, IT, and NO, for which genotypic data have been used to assess prevalence

The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing E. coli are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

FIGURE 53 Prevalence of presumptive ESBL-producing versus AmpC-producing *Escherichia coli* from (A) fattening pigs 2023, (B) cattle under 1 year of age 2023, (C) broilers 2022 and (D) fattening turkeys 2022, EU MSs and non-MSs.

5.4.4 | Temporal trends

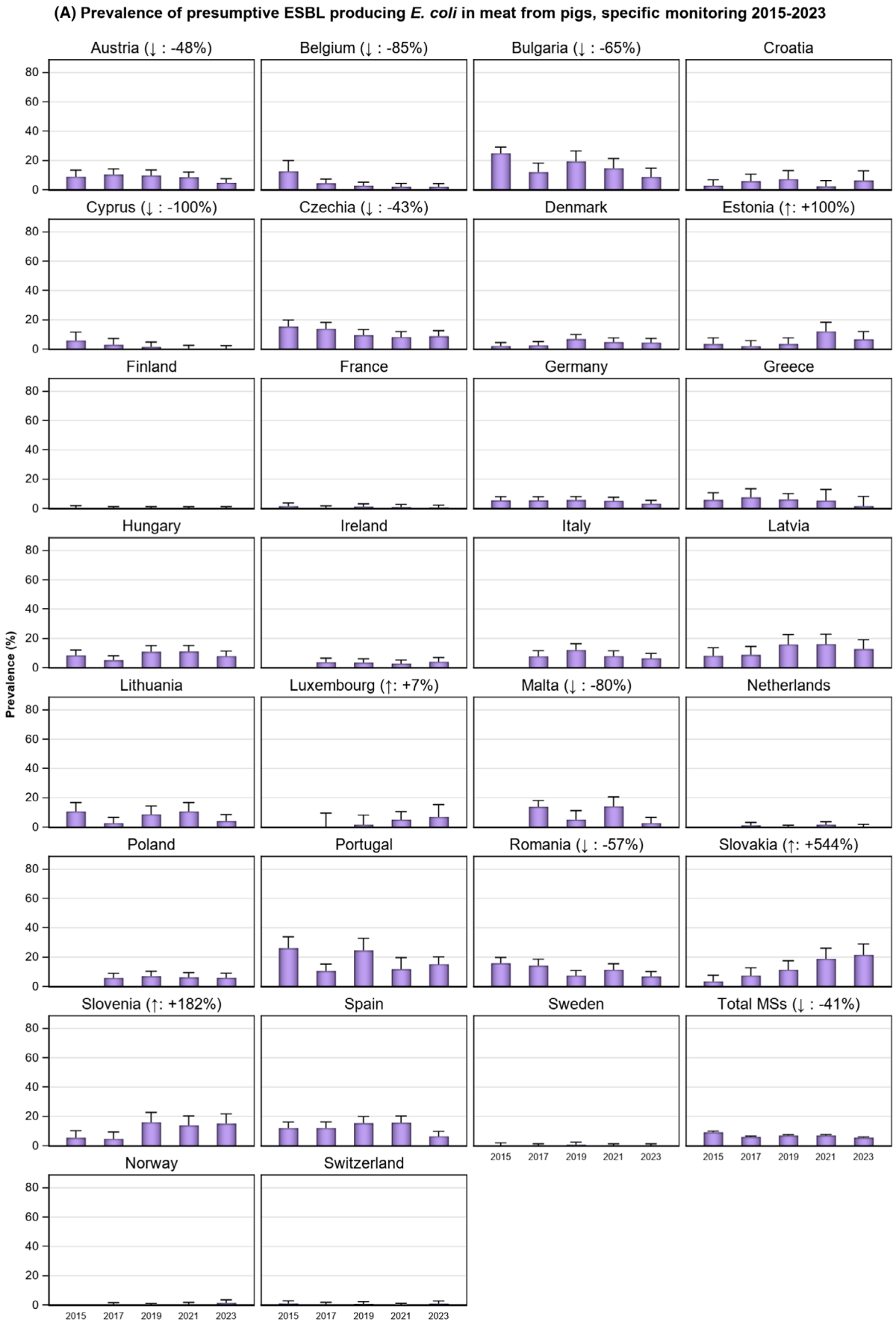


FIGURE 54 (Continued)

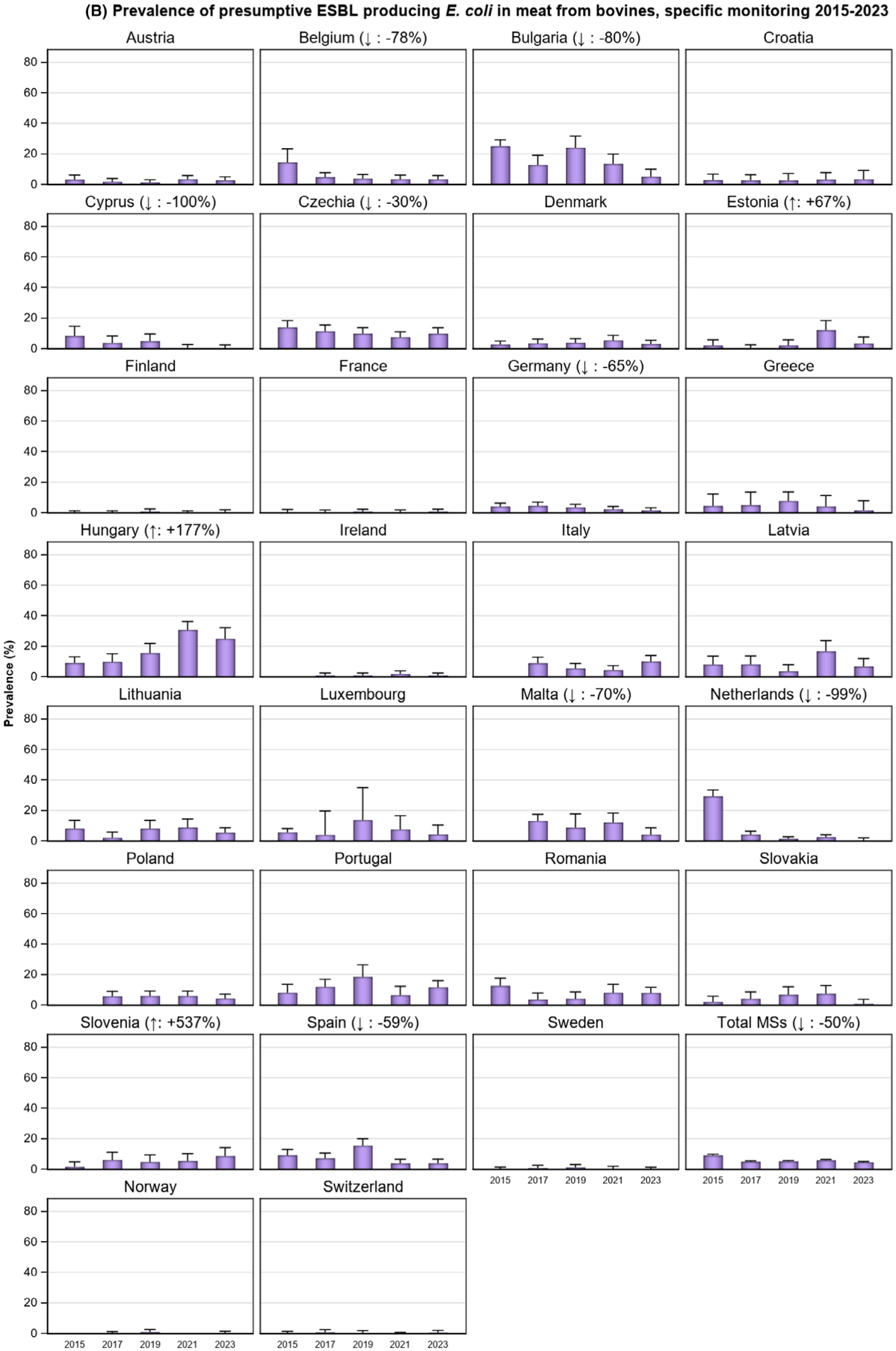


FIGURE 54 (Continued)

(C) Prevalence of presumptive ESBL-and/or AmpC-producing *E. coli* in meat from broilers, specific monitoring, 2014-2022

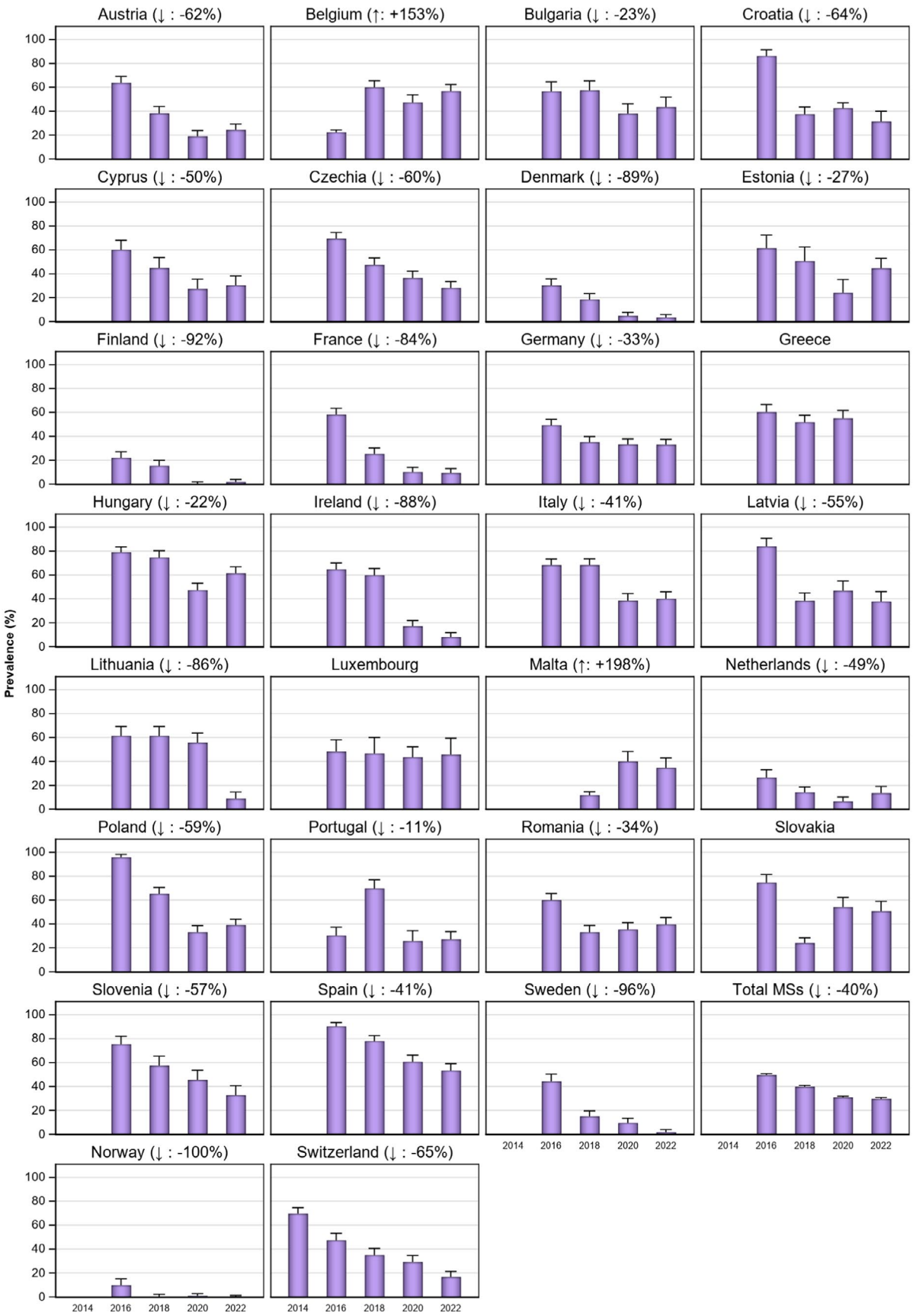


FIGURE 54 Trends on the prevalence of presumptive ESBL- and/or AmpC-producing *Escherichia coli* in (A) meat from pigs and (B) meat from bovines and (C) meat from broilers, EU MSs and non-MSs, 2016–2023.
Arrows indicate statistically significant decreasing/increasing trends over the period.

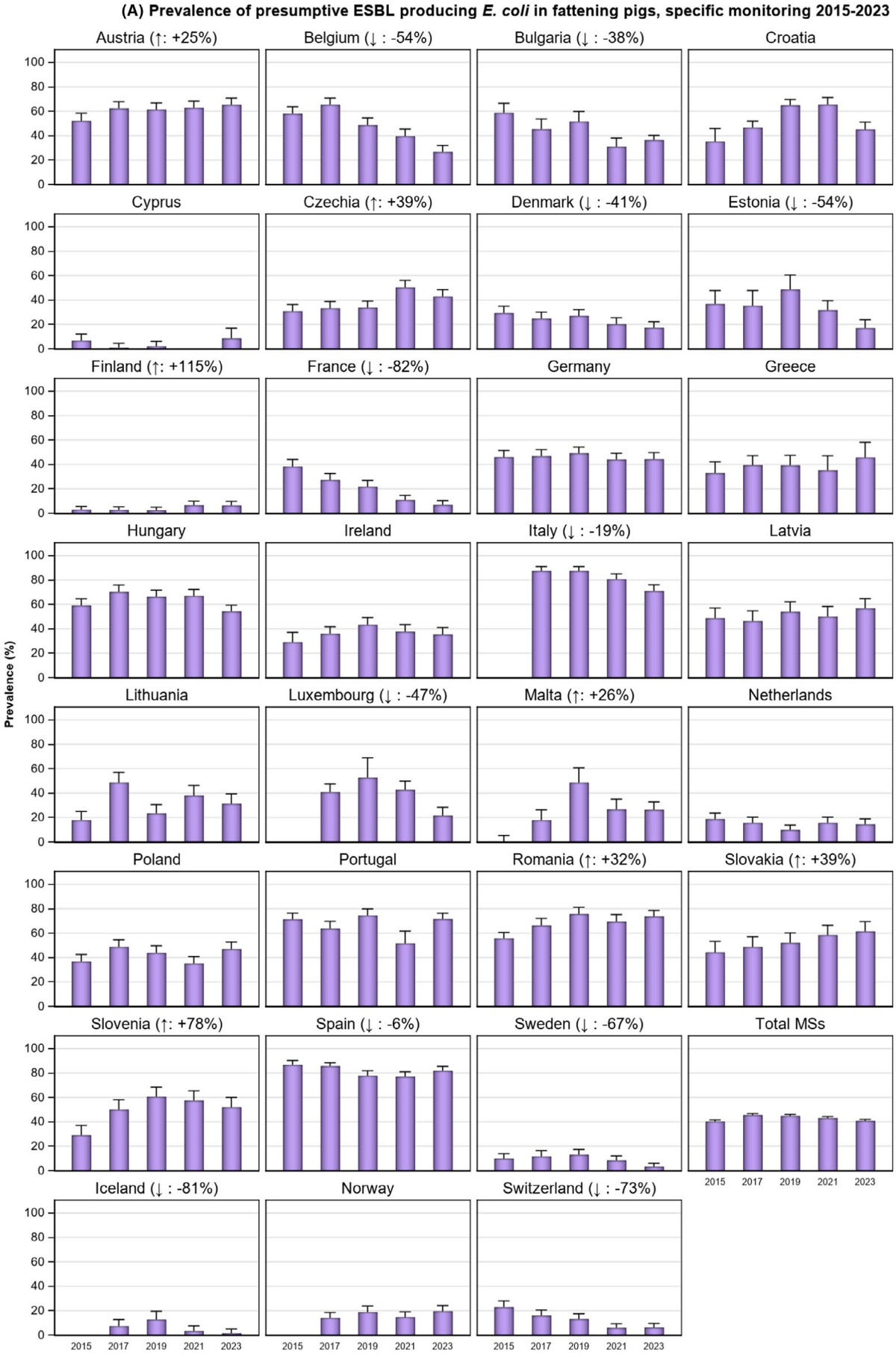


FIGURE 55 (Continued)

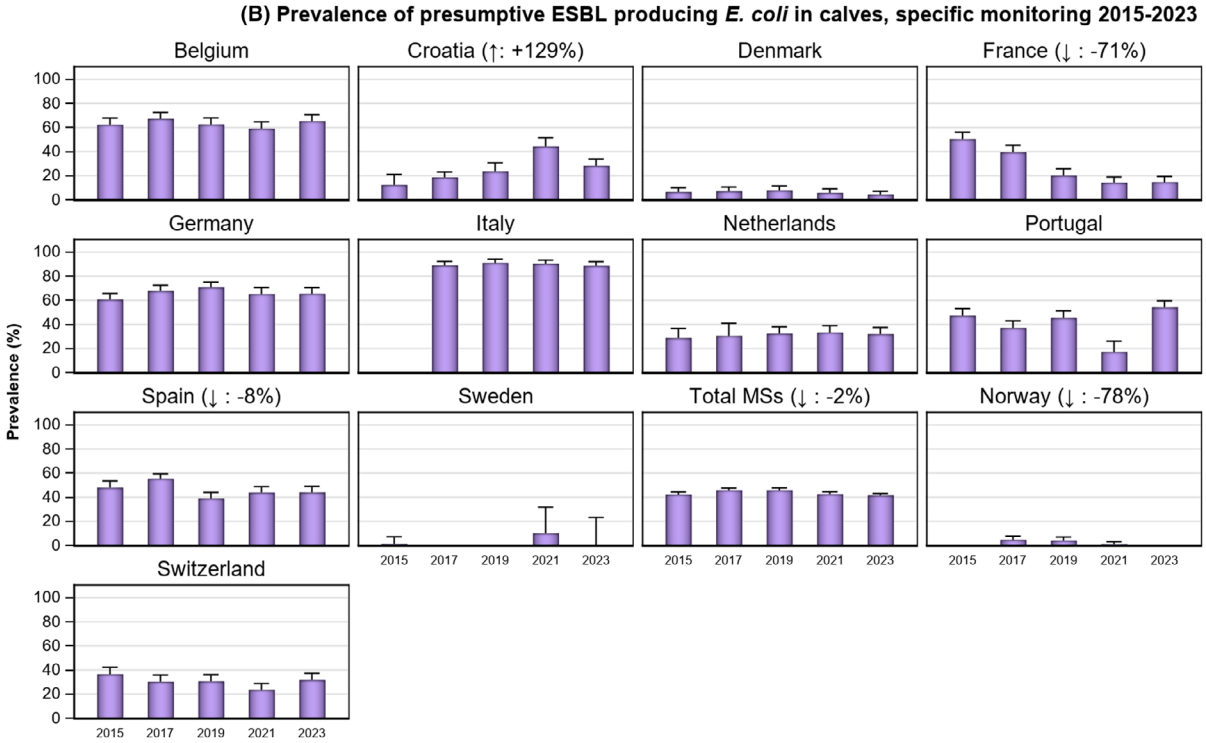


FIGURE 55 (Continued)

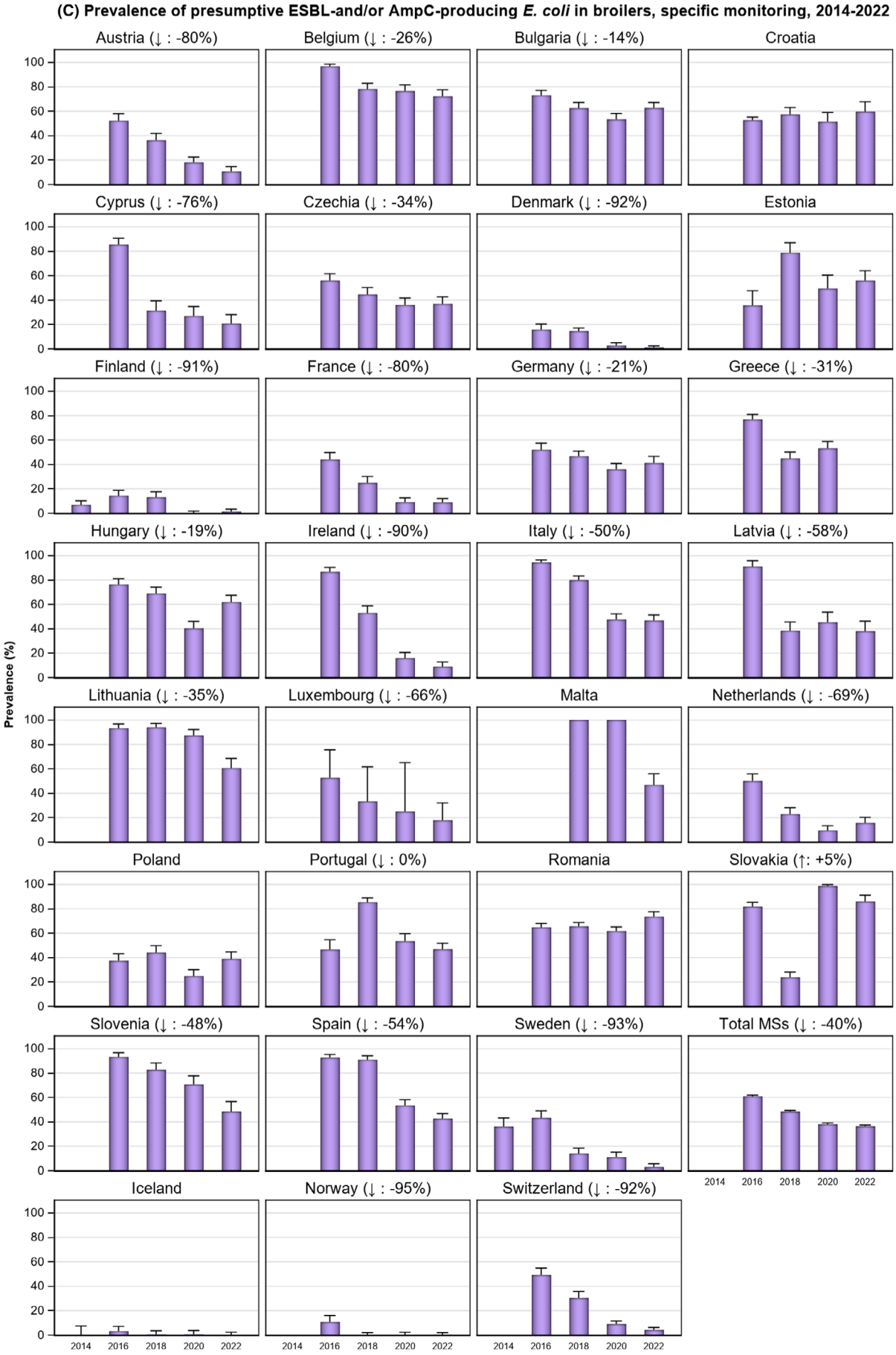


FIGURE 55 (Continued)

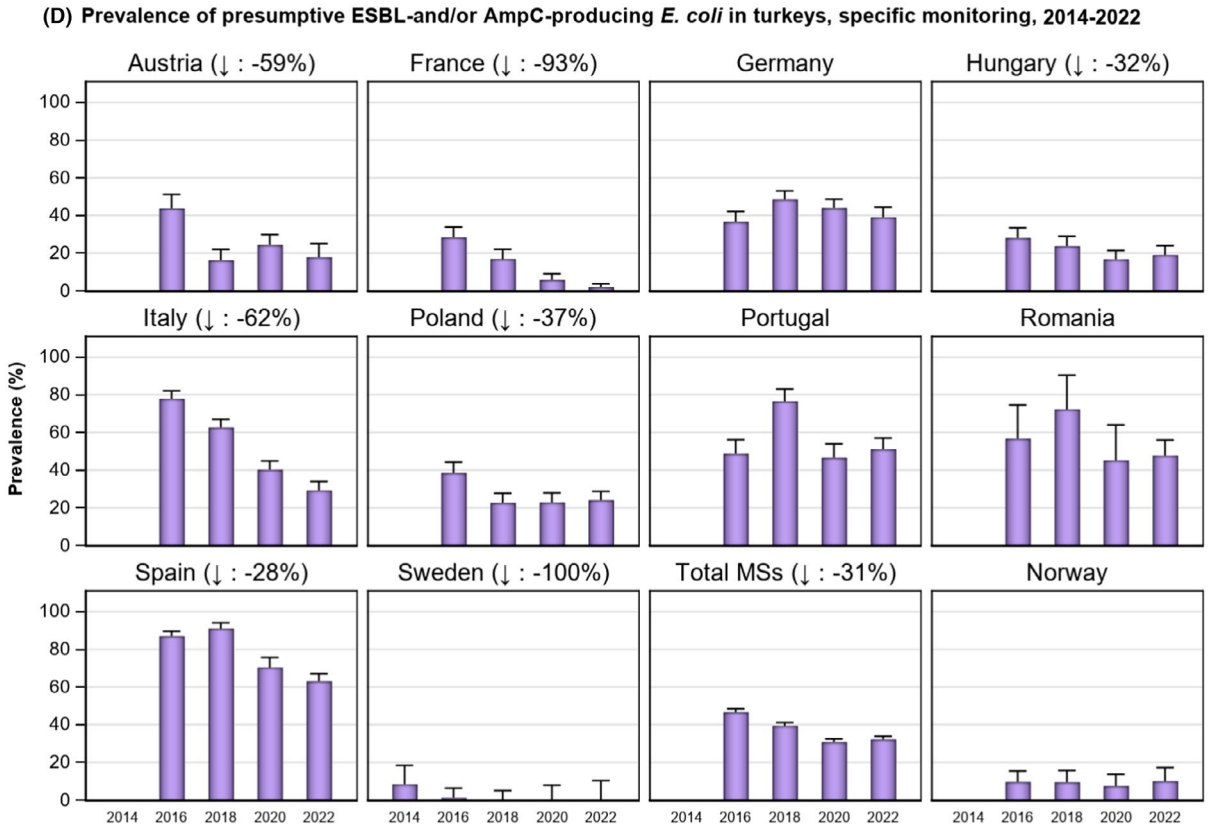


FIGURE 55 Trends on the prevalence of presumptive ESBL- and/or AmpC-producing *Escherichia coli* in (A) fattening pigs, (B) cattle under 1 year of age, (C) broilers and (D) fattening turkeys, EU MSs and non-MSs, 2016–2023.
Arrows indicate statistically significant decreasing/increasing trends over the period.

Overall, at the MS-group level, the prevalence of presumptive ESBL-, AmpC- and/or CP-producing *E. coli* decreased significantly in broilers and in meat from broilers (40% decrease in both) between 2016 and 2022. Statistically significant decreasing trends in broilers were reported by 21 MSs[26] and 2 non-MSs.[27] Also, 22 MSs[28] and 2 non-MSs[29] recorded statistically significant decreasing trends in meat from broilers. In fattening turkeys, the prevalence at the MS-group level also decreased significantly (31% decrease) between 2016 and 2022, and seven MSs[30] registered statistically significant decreasing trends.

In fattening pigs, the prevalence of presumptive ESBL-/AmpC-/CP-producing *E. coli* at the MS-group level was comparable to previous years, while a significantly decreasing trend (2% decrease) was seen at the MS-group level for cattle under 1 year of age from 2015–2023. Eleven countries[31] reported statistically significant decreasing trends in fattening pigs, and three countries,[32] reported statistically decreasing trends in cattle under 1 year of age.

Statistically significant decreasing trends at the MS-group level was also seen in meat from pigs (41% decrease) and meat from cattle (50% decrease) from 2015 to 2023. However, a statistically significant increase was reported by four MSs[33] for meat from pigs and by three MSs[34] in meat from bovines from 2015 to 2023.

Several countries have decreasing trends in the prevalence of presumptive EBSL-/AmpC-producing *E. coli* for all animal populations and meat categories investigated. However, some MSs have an increasing or consistently high prevalence. Figures 54 and 55 and Annex D1 present detailed data on the prevalence per country, animal population and meat category for 2022 and 2023. Historical data can be found in previously published reports.

[26]Austria, Belgium, Bulgaria, Cyprus, Czechia, Denmark, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, the Netherlands, Portugal, Slovenia, Spain, Sweden.

[27]Norway and Switzerland.

[28]Austria, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Hungary, Ireland, Italy, Latvia, Lithuania, the Netherlands, Poland, Portugal, Romania, Slovenia, Spain, Sweden.

[29]Norway and Switzerland.

[30]Austria, France, Hungary, Italy, Poland, Spain and Sweden.

[31]Belgium, Bulgaria, Denmark, Estonia, France, Italy, Luxembourg, Spain, Sweden, Iceland and Switzerland.

[32]France, Spain and Norway.

[33]Estonia, Luxembourg, Slovakia and Slovenia.

[34]Estonia, Hungary and Slovenia.

5.4.5 | Key outcome indicator of prevalence of ESBL-/AmpC-producing *E. coli*

The proportion of samples from the different animal populations that are positive for presumptive ESBL- and/or AmpC-producing *E. coli* according to Commission Implementing Decision 2020/1729/EU, weighted by 'population correction unit' (PCU), has been retained as a summary indicator.

A weighted key outcome indicator of the prevalence of ESBL- and/or AmpC-producing *E. coli* (KOI_{ESC}) was calculated to account for differences in the relative size of animal populations in a country. The indicator is the weighted mean of the prevalence of ESBL- and/or AmpC-producing *E. coli* in each of the four monitored animal populations. The value for each population was weighted in relation to the relative size of the population within a country using the PCU for calculation of the mean. PCU is a technical unit of measurement used as an indicator of animal population size developed by the European Medicines Agency (EMA), primarily to estimate sales of antimicrobials corrected by the animal population in each country. The ESVAC report 'Sales of veterinary antimicrobial agents in 31 European countries in 2022' (EMA, 2023) includes a detailed description of data sources and methodology for calculation of PCU. KOI_{ESC} was calculated using data for two consecutive years for each country to account for all four animal populations. Thus, values for 2015–2016 included data from fattening pigs and cattle under 1 year of age for 2015 and data from broilers and fattening turkeys in 2016. Changes in KOI_{ESC} are presented in Figure 56.

A statistically significant decreasing trend in the KOI_{ESC} was seen in 19 MSs, although some of these countries started at very high or extremely high levels. Three MSs registered[35] a significantly increasing trend in KOI_{ESC}.

[35]Croatia, Romania and Slovakia.

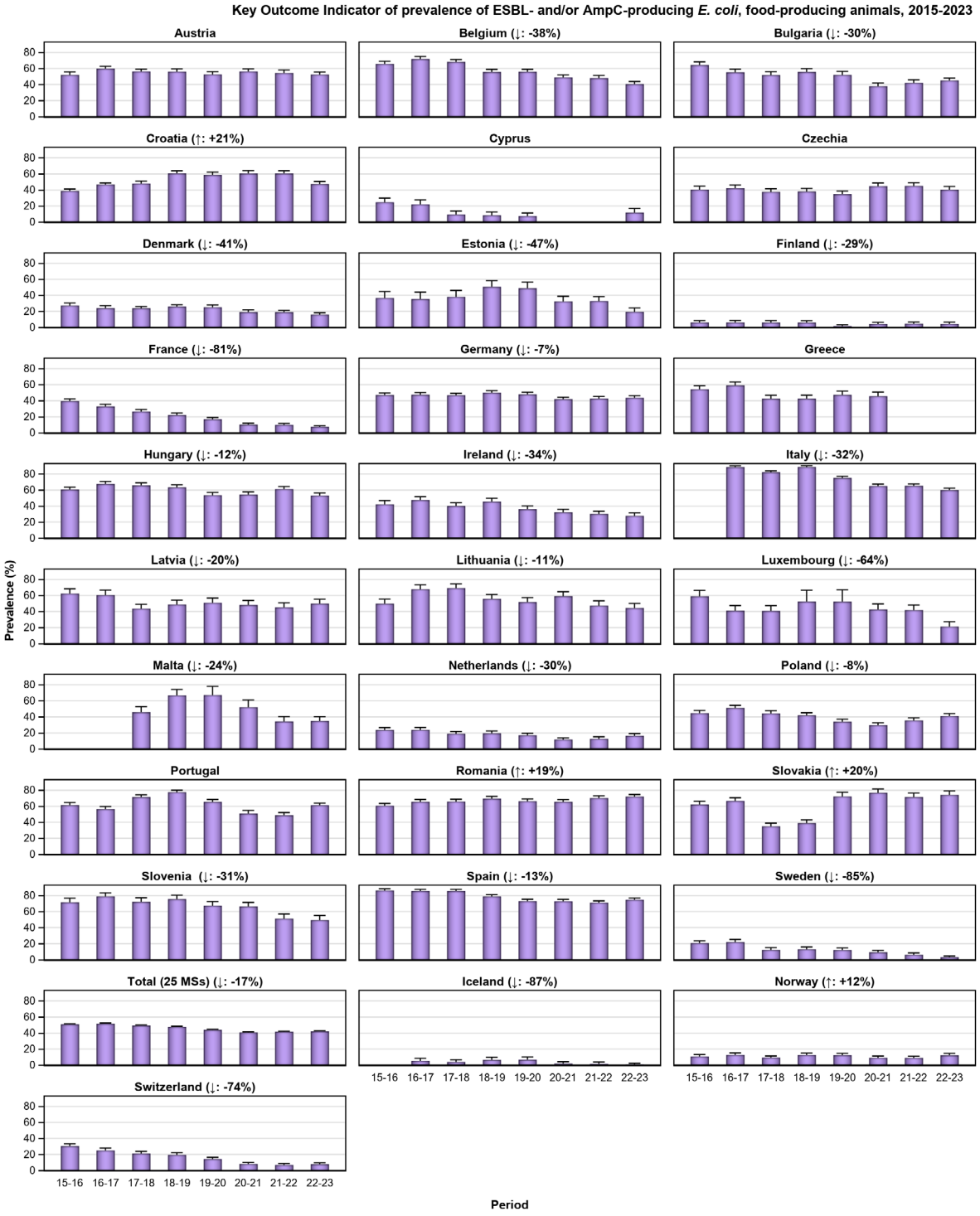


FIGURE 56 Changes in key outcome indicator of ESBL- and/or AmpC-producing *Escherichia coli* (KOI_{ESC}), 27 EU MSs and 3 non-MSs, 2015–2023. (↑/↓): indicates statistically significant decreasing/increasing trends over the 2015-2023 period. Rates of change are shown for the statistically significant decreasing/increasing trends observed.

5.4.6 | Discussion

The presence of ESBL-, AmpC- and/or CP-producing bacteria in animals is undesirable as they represent a potential risk for human acquisition via animals and their food products. Additionally, bacteria from animals carrying such resistance represent a reservoir of resistance genes that may transfer to other bacteria, including food-borne zoonotic bacteria such as *Salmonella* spp., further adding to the public health concern. Although the latest JIACRA report on antimicrobial consumption and resistance in bacteria from humans and food-producing animals did not detect a statistically significant association between resistance to ESCs in indicator *E. coli* from animals and invasive *E. coli* from humans (ECDC, EFSA and EMA, 2024), the complexity in the epidemiology of these bacteria cannot be underestimated.

The prevalence of ESBL-/AmpC-/CP-producing indicator commensal *E. coli* and *Salmonella* spp. collected in the **routine monitoring** was still low in 2022 and 2023.

In the **specific monitoring** of ESBL-/AmpC-/CP-producing *E. coli*, the ESBL phenotype was more commonly reported than the AmpC phenotype in all animal populations and meat categories monitored at the EU level. This was also observed in the majority of reporting countries. Similarly, when providing WGS results, the main proportion of reported genes were ESBL-encoding, followed by AmpC-encoding genes. The prevalence of ESBL- and AmpC phenotypes varied, however, considerably between countries. For example, in broilers in Latvia, fattening turkeys in Norway and fattening pigs in Denmark, Finland, Slovenia, Sweden and Norway, the AmpC phenotype dominated.

Interestingly, the prevalence of ESBL-/AmpC-/CP-producing *E. coli* was lower in meat from pigs and meat from bovines than in fattening pigs and cattle under 1 year of age. In poultry and meat from poultry, on the other hand, the prevalence of ESBL-/AmpC-/CP-producing *E. coli* was comparable. This may be related to the differences in slaughter processes for broilers and turkeys compared to those for pigs and cattle, resulting in less contamination of intestinal bacteria from pigs and cattle compared to poultry. This trend has also been observed in previous years (EFSA and ECDC, 2024).

In 2022 and 2023, $bla_{\text{CTX-M-1}}$ and $bla_{\text{CTX-M-15}}$ were the most commonly reported ESBL-encoding genes overall. These genes were the two most commonly detected in fattening pigs, cattle under 1 year of age and their derived meat. In broilers, $bla_{\text{CTX-M-1}}$ was also the most common, followed by $bla_{\text{SHV-12}}$; while in meat from broilers the pattern was reversed. In contrast, in fattening turkeys and derived meat, $bla_{\text{CTX-M-15}}$ was the predominant gene, followed by $bla_{\text{SHV-12}}$ and $bla_{\text{CTX-M-1}}$, respectively. The $bla_{\text{CTX-M-1}}$ and $bla_{\text{CTX-M-15}}$ genes are frequently reported in food-producing animals and their derived meat in Europe (Day et al., 2016; Ewers et al., 2012, 2021; Käsbohrer et al., 2019). Further, $bla_{\text{SHV-12}}$ is a well-known cause of ESC resistance in poultry (Ewers et al., 2012, 2021). The observed differences in ESBL-encoding genes reported by different countries indicate variations of genes present in animal populations in these countries. This may be linked to differences in animal husbandry, breeds, antimicrobial usage etc. between the countries.

The point mutation C-42T in the chromosomal *ampC* gene was the most common cause of an AmpC phenotype in isolates from all animal populations and meat categories except broilers and meat from broilers. $bla_{\text{CMY-2}}$ was the most commonly observed plasmid-mediated AmpC-encoding gene in broilers, meat from broilers, fattening turkeys, fattening pigs and meat from pigs, and the most common AmpC-encoding gene reported in broilers and derived meat. In 2023, the plasmid-mediated $bla_{\text{CFE-1}}$ gene was also reported as a cause of an AmpC phenotype in isolates from fattening pigs and cattle under 1 year of age and their derived meats. $bla_{\text{CFE-1}}$ has not been detected in the EU monitoring of AMR in previous years, but has been reported as a cause of ESC resistance in cheese and salami products in Italy (Crippa et al., 2024). Both $bla_{\text{CTX-M-1}}$ and $bla_{\text{CMY-2}}$ have persisted in European pig- and broiler production for several years, and their successful dissemination are suggested to be linked to epidemic plasmids circulating in the animal production chains (Bevan et al., 2017; Mo et al., 2016).

ESBL- and/or AmpC-producing *E. coli* were detected in caecal samples and meat from all monitored animal populations. However, at the MS-level the prevalence of ESBL-/AmpC-producing *E. coli* has decreased in both broilers and fattening turkeys since 2014, which is probably a result of the discontinuation of off-label use of extended-spectrum cephalosporins in poultry (EMA/CVMP, 2018).

5.5 | Monitoring of carbapenemase-producing *Escherichia coli*

5.5.1 | Routine monitoring of indicator *E. coli* and *Salmonella* spp.

In 2022, one indicator commensal *E. coli* from a fattening turkey was reported to harbour the CP-encoding gene $bla_{\text{OXA-181}}$. No CP-resistant indicator commensal *E. coli* or *Salmonella* spp. were reported in 2023.

5.5.2 | Specific monitoring of ESBL-, AmpC- and/or CP-producing *Escherichia coli*

The use of selective media (supplemented with 1 mg/L cefotaxime) in the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* also enables the detection of isolates with certain mechanisms for carbapenem resistance. In 2022, three CP-producing *E. coli* harbouring the $bla_{\text{VIM-1}}$ gene were reported. All three isolates originated from broilers and were reported by Austria ($n = 2$) and Italy ($n = 1$). In 2023, six CP-producing *E. coli* were reported. Two isolates were from cattle under 1 year of age, one reported by Germany harbouring the $bla_{\text{VIM-1}}$ gene and the other reported by Italy carrying the $bla_{\text{NDM-5}}$ gene. Further, four CP-producing isolates from fattening pigs were reported, three harbouring $bla_{\text{OXA-181}}$ (Italy, Portugal and Spain) and one harbouring $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$ (Portugal).

5.5.3 | Specific monitoring of carbapenemase-producing *Escherichia coli*

Specific monitoring of CP-producing bacteria using selective media for CP-producers in accordance with the protocol developed by EURL-AR[36,37] was made mandatory in 2021 (Appendix A – Materials and methods). In 2022 and 2023, 27 MSs, the

[36] https://www.eurl-ar.eu/CustomerData/Files/Folders/21-protocols/530_esbl-ampc-cpeprotocol-version-caecal-v7-09-12-19.pdf.
[37] https://www.eurl-ar.eu/CustomerData/Files/Folders/21-protocols/529_esbl-ampc-cpeprotocol-version-meat-v7-09-12-19.pdf.

United Kingdom (Northern Ireland) and 3 non-MSs investigated 8377 samples from broilers, 3031 samples from fattening turkeys, 7725 samples from fattening pigs, 3621 samples from cattle under 1 year of age, 6279 samples from meat from broilers at retail, 3567 samples from meat from turkeys, 6692 samples from retail meat from pigs and 6487 samples from retail meat from bovines (Annex D1).

In 2022, one isolate from fattening turkeys in Italy was reported in the specific monitoring of CP-producers. This isolate carried $bla_{\text{OXA-181}}$ (Annex D3).

In 2023, CP-producers were detected in fattening pigs from Czechia ($n = 5$), Italy ($n = 19$), Portugal ($n = 7$), Romania ($n = 1$) and Spain ($n = 23$), in cattle under 1 year of age in Italy ($n = 4$) and Spain ($n = 1$) and in meat from pigs from Spain ($n = 1$) (Annex D3). Genes encoding carbapenem resistance reported in 2022 and 2023 are summarised in Table 23.

TABLE 23 Summary table on carbapenemase-encoding genes reported in *Escherichia coli* sampled in the routine monitoring, the specific monitoring of ESBL-/AmpC-/CP-produ-cers and the specific monitoring of CP-producers in 2022–2023.

Year	Matrix	Gene	Number of isolates	Countries detecting the isolates (*n*)
Routine monitoring of indicator commensal *E. coli*				
2022	Fattening turkeys	$bla_{\text{OXA-181}}$	1	IT (1)
Specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*				
2022	Broilers	$bla_{\text{VIM-1}}$	3	AT (2), IT (1)
2023	Cattle under 1 year of age	$bla_{\text{VIM-1}}$	1	DE (1)
		$bla_{\text{NDM-5}}$	1	IT (1)
	Fattening pigs	$bla_{\text{OXA-181}}$	3	ES (1), IT (1), PT (1)
		$bla_{\text{OXA-181}} + bla_{\text{NDM-5}}$	1	PT (1)
Specific monitoring of CP-producing *E. coli*				
2022	Fattening turkeys	$bla_{\text{OXA-181}}$	1	IT (1)
2023	Fattening pigs	$bla_{\text{OXA-181}}$	24	ES (4), IT (19), PT (1)
		$bla_{\text{NDM-5}}$	5	CZ (5)
		$bla_{\text{OXA-48}}$	21	ES (19), PT (1), RO (1)
		$bla_{\text{OXA-181}} + bla_{\text{NDM-5}}$	4	PT (4)
		$bla_{\text{OXA-244}}$	1	PT (1)
	Cattle under 1 year of age	$bla_{\text{OXA-181}}$	4	IT (4)
		$bla_{\text{OXA-48}}$	1	ES (1)
	Meat from pigs	$bla_{\text{NDM-5}}$	1	ES (1)

Abbreviations: AT, Austria; CZ, Czechia; DE, Germany; IT, Italy; *n*, number of CP-producing isolates.

The relationship between the investigated animal populations, the CP-encoding genes and the countries where CP-producing isolates were detected, is illustrated in Figure 57. Notably, fattening pigs seem to be a significant source of isolates associated with carbapenem resistance, while a limited number of CP-producers are reported from cattle under 1 year of age and poultry. CP-producing *E. coli* from fattening pigs mainly carry $bla_{\text{OXA-181}}$, predominantly found in Italy, Spain and Portugal, followed by $bla_{\text{OXA-48}}$, mainly detected in Spain and Portugal and $bla_{\text{NMD-5}}$ detected in Czechia and Portugal. The $bla_{\text{OXA-181}}$ gene is also the most common CP-encoding gene in cattle under 1 year of age and fattening turkeys. In contrast, $bla_{\text{VIM-1}}$ is a gene that seems predominantly associated with broilers. Finally, the detection of five isolates from fattening pigs co-harbouring $bla_{\text{OXA-181}}$ and $bla_{\text{NMD-5}}$ is of specific concern.

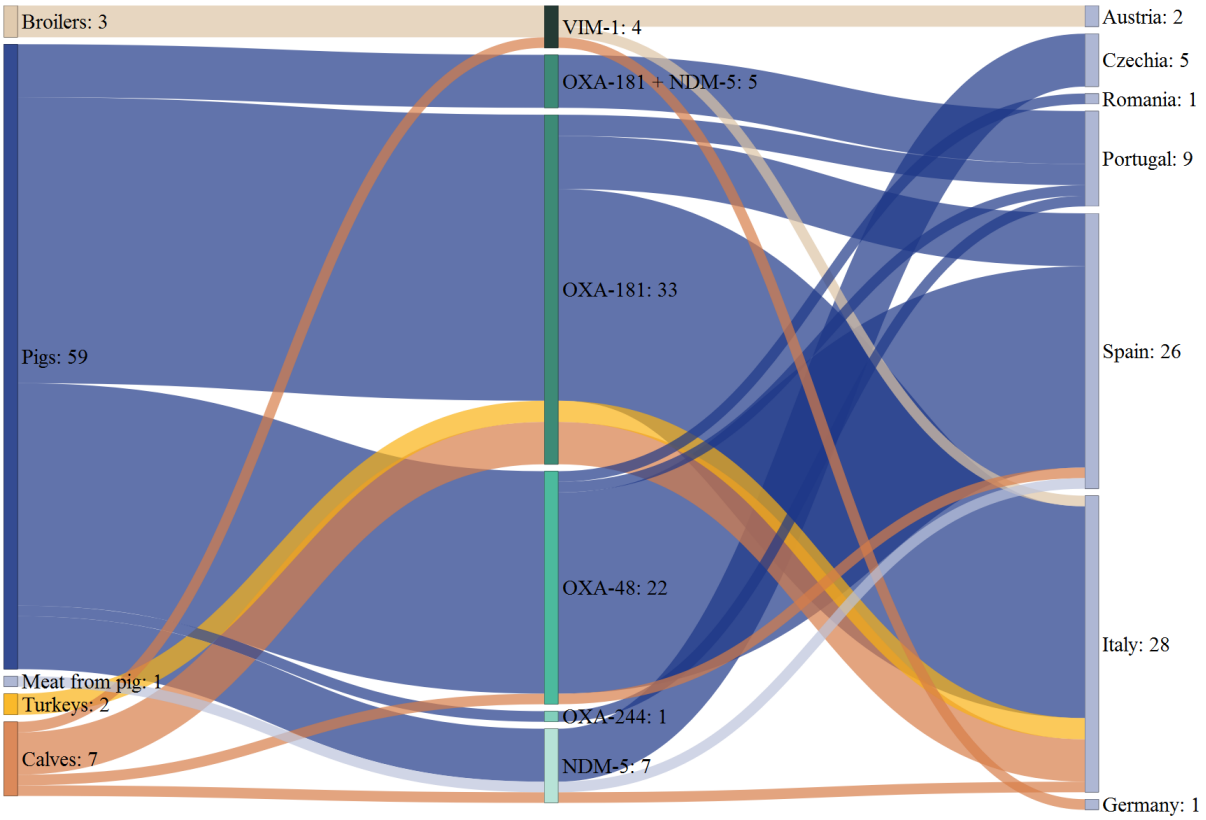


FIGURE 57 Distribution of carbapenemase-encoding genes detected in *Escherichia coli* isolated in the routine monitoring of indicator commensal *Escherichia coli*, specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* and specific monitoring of CP-producing *E. coli* in 2022–2023.
The figure only includes data from countries that have reported CP-producing isolates and for which the CP gene has been identified. This encompasses countries that submitted WGS and/or MIC results.

Additional information on CP-producing *E. coli* isolates detected in bovine animals other than those under one year of age and seafood

In 2023, carbapenem-resistant E.*coli* isolates were detected for the first time in food-producing animals in Norway. The caecal sample was taken from a healthy cow at slaughterhouse. Two *E.coli* isolates, both harbouring the bla_{NMD-5} gene, were reported. One isolate was identified following the protocol for the specific monitoring of ESBL-/AmpC- and/or CP- producing *E.coli*, while the other was found using the protocol of the specific monitoring of CP-producing *E.coli* isolates. The Norwegian Food Safety Authority initiated comprehensive follow-up sampling which was performed twice (October 2023 and January 2024) at the farm of origin, including both faecal and environmental samples. In the first follow-up sampling in October, CP-producing *E.coli* were detected in two of 30 samples analysed, while none of the samples collected and analysed in the second follow-up were positive for CP-producing *E.coli* (NORM/NORM-VET, 2023)

Additionally, the Netherlands sampled 62 batches of shrimps at BCP, in 2023, mainly originating from farms in Africa and Asia. For the first time, a CP-producing *E.coli* carrying the bla_{NMD-1} gene, was detected in a shrimp from India, through selective culturing (de Greeff et al., 2024).

5.5.4 | Discussion

In 2022 and 2023, a total of 49,634 samples were investigated in the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* and 44,779 samples in the specific monitoring of CP-producing *E. coli*. Of these, a total of 72 isolates were confirmed as CP-producers. Nine of these were identified in the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*, while 62 were reported in the specific monitoring of CP-producers. Of specific concern is also the detection of five isolates from fattening pigs co-harbouring two CP-encoding genes, namely $bla_{OXA-181}$ and bla_{NDM-5}. Further, a single CP-producing isolate was reported in the routine monitoring of commensal indicator *E. coli* in 2022. This isolate was from fattening turkeys and carried $bla_{OXA-181}$. Identification of a CP-producing isolate without the use of selective detection methods may indicate a high proportion of CP-producers in the sample. As carbapenems are last resort critically important antimicrobials reserved for treatment of severe human infections (WHO, 2024), these are both worrying findings. According to EMA's AMEG categorisation, carbapenems also belong to Category A with the indication 'Avoid' use in veterinary medicine in the EU (EMA, 2019). Substances in

this category are not authorised in veterinary medicine. Moreover, the use of carbapenems for food-producing animals is prohibited in Europe since 2022 as stated in the Commission Implementing Regulation (EU) 2022/1255.[38]

Although the number of CP-producing *E. coli* is still low, an increasing number of isolates is reported compared to previous years (EFSA and ECDC, 2022). From 2015 to 2017, a total of 48,184 isolates were investigated and only three CP-producing *E. coli* reported. In 2019, Germany reported three CP-producing *E. coli* from fattening pigs (bla_{GES-5} and bla_{OXA-48}) and meat from pigs (bla_{VIM-1}), while Austria reported one CP-producing *E. coli* from broilers (bla_{VIM-1}) in 2020 (EFSA and ECDC, 2022). The specific monitoring of CP-producers was made mandatory in 2021. When the harmonised monitoring will have been conducted for some years, it will be possible to evaluate trends. Currently, CP-producing *E. coli* are more frequently reported in fattening pigs and cattle under 1 year and derived meats compared to poultry and poultry meat. In 2022, no CP-producing *E. coli* were reported from poultry meat, while a single CP-producing isolate was reported from meat from pigs in 2023 harbouring the bla_{NDM-5} gene.

The $bla_{OXA-181}$ gene was the most commonly reported genetic determinant for carbapenem resistance overall in both the specific monitoring of ESBL-/AmpC-/CP-producers ($n = 4$) and in the specific monitoring of CP-producers ($n = 33$). It was also reported in a single isolate from fattening turkeys collected in the routine monitoring in 2022. In 2022, bla_{VIM-1} ($n = 3$) was the most commonly reported gene, followed by $bla_{OXA-181}$ ($n = 2$). The bla_{VIM-1} gene was reported in broilers from Austria, from which the same gene was also reported in 2020 (EFSA and ECDC, 2023). In 2023, bla_{OXA-48} ($n = 20$) was the second most reported gene, followed by bla_{NDM-5} ($n = 11$), $bla_{OXA-244}$ ($n = 1$) and bla_{VIM-1} ($n = 1$). The genes $bla_{OXA-181}$, bla_{OXA-48} and bla_{NDM-5} were also reported from fattening pigs and cattle under 1 year of age in 2021 (EFSA and ECDC, 2024). The $bla_{OXA-181}$ gene, belonging to class D carbapenemases, has mainly been associated with humans, the first report of its isolation from porcine *E. coli* was in Italy in 2016 (Pulss et al., 2017), and has since then been reported in swine, dairy cows, beef cattle, fattening turkeys and companion animals (Carfora et al., 2022; EFSA and ECDC, 2024; Ramírez-Castillo et al., 2023). The bla_{NDM-5} gene, which belongs to the New Delhi metallo-beta-lactamases (NDMs), has previously been reported from food-producing animals including dairy cows in Algeria, pigs and poultry in China, and cattle in India (Ramírez-Castillo et al., 2023). Further, the bla_{NDM-5} gene was shown to be the most frequently reported CP-encoding gene in *E. coli* from humans in Europe in a structured survey conducted in 36 European countries in 2019 (ECDC, 2018, 2023). The occurrence of *E. coli* with bla_{NDM-5} is increasing in Europe, and this has been linked to an ongoing global expansion of certain *E. coli* sequence types (STs) carrying this gene. Currently, this represents a significant concern in EU/EEA countries (ECDC, 2023). In 2023, $bla_{OXA-244}$ was reported for the first time in the AMR monitoring. Although detected in pig production and in dogs in Egypt (Khalifa et al., 2020; Sadek et al., 2022) this gene has not previously been reported in isolates from animals or food in Europe (ECDC, 2021). $bla_{OXA-244}$ is an increasing concern in human medicine, with several reported outbreaks in Europe in recent years (ECDC, 2020, 2021; Falgenhauer et al., 2020; Izdebski et al., 2024; Lindemann et al., 2023; Welker et al., 2020), and a considerable increase in detection of isolates carrying OXA-244 was reported between 2021 and 2023 in Europe (Kohlenberg et al., 2024). Isolates carrying the $bla_{OXA-244}$ gene can be difficult to detect in the laboratory (Hoyos-Mallecot et al., 2017), and there is a need to increase awareness and capacity for detecting this gene (ECDC, 2020). Thus, it is possible that the occurrence of *E. coli* with OXA-244 in animals and food is currently underestimated. Further studies including epidemiological and genetic analyses are needed to clarify the transmission dynamics of CP-producing *E. coli* among animals, food and humans.

In 2023, CP-producing *E. coli* co-harbouring $bla_{OXA-181}$ and bla_{NMD-5}, were reported for the first time in ceacal samples from pigs. Several recent publications have described the emergence of *E. coli* ST410 carrying both $bla_{OXA-181}$ and bla_{NDM-5} in human patients (Chudejova et al., 2021; Kim et al., 2021; Miller et al., 2017; Roer et al., 2018), and it is suggested to be a 'high-risk' clone (Roer et al., 2018). As information regarding STs is not provided by reporting countries, it is uncertain if the CP-producing isolates from fattening pigs belong to ST410. However, this finding underlines the importance of further studies taking genomic data into account in order to elucidate the epidemiology and possible transmission routes of these CP-producing isolates between food-producing animals and humans and vice versa. It has also been suggested that evolutionary- and clinical studies and surveillance is needed to contribute to knowledge needed for establishing prevention and management strategies in order to curb the dissemination of CP-resistant *E. coli*, which is of high importance for both human and veterinary medicine (Pitout et al., 2024).

In addition to CP-producing isolates collected in the harmonised EU monitoring (Bortolaia et al., 2021; Carfora et al., 2022; Diaconu et al., 2020; EFSA and ECDC, 2023, 2024; Garcia-Graells et al., 2020), CP-producing Enterobacterales have also been reported from companion animals (Ramírez-Castillo et al., 2023; Rincon-Real & Suárez-Alfonso, 2022), food-producing animals and meat derived thereof, seafood and vegetables (Brouwer et al., 2018; Irrgang et al., 2019, 2020; Köck et al., 2018; Liu et al., 2018; Ramírez-Castillo et al., 2023; Slettemeås et al., 2017; Touati et al., 2017; Zurfluh et al., 2015). Spill-over of CP-encoding genes and/or bacteria from humans has been suggested as a potential source of these bacteria in food production (Irrgang et al., 2020; Madec et al., 2017), as carbapenems are not authorised for veterinary use in the EU. Horizontal and/or vertical spread within the food chain has also been suggested after observing similar or closely related CP-encoding genes in isolates from different farms in certain regions (Carfora et al., 2022). Hopefully, actions to preserve the situation as it is will be effective, as CP-producing Enterobacterales still seem to be emerging in the animal populations and food categories investigated in the EU monitoring. This can prevent food-producing animals and food from becoming an important source for human acquisition of CP-producing bacteria.

[38] https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32022R1255.

There is a need to closely monitor and follow-up possible developments in the occurrence of CP-producing bacteria in food-producing animals and food, as CP-producing *E. coli* and *Salmonella* can be both pathogens and vectors for resistance mechanisms for public health. Also, the presence of CP-producers in food-producing animals highlights the critical importance of implementing specifically designed monitoring protocols for the early and sensitive detection of such isolates, even when present in low numbers. If CP-producers would be amplified in high-intensity animal production systems, food-producing animals may end up representing a significant source for exposure and acquisition of such bacteria in humans, which is an undesirable scenario (Carfora et al., 2022). Since the specific monitoring of CP-producing *E. coli* was made mandatory in 2021, more countries have reported the detection of CP-producing isolates. The introduction of WGS has also seemingly contributed to detection of more CP-producers compared to the use of phenotypic methods and will hopefully help facilitate the detection and characterisation of CP-producing isolates when present in investigated samples.

6 | ANTIMICROBIAL RESISTANCE IN METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA)

6.1 | Key findings

- The voluntary monitoring of MRSA in 2022 and 2023 was performed in a limited number of countries and was not harmonised. Still, it provided useful information regarding the occurrence of MRSA in food-producing animals and food. The results emphasise the need for continued monitoring and molecular characterisation of MRSA isolates in order to follow trends and evaluate potential effects on human health caused by the presence of MRSA in food-producing animals and food.
- Among MRSA isolates subjected to molecular typing in 2022 and 2023, livestock-associated (LA) clonal complex (CC) 398 was by far the most commonly reported CC, both in isolates from animals and food. Certain *spa*-types commonly associated with community-associated (CA)- and healthcare-associated (HA)- MRSA were also reported.
- MRSA assigned to CCs other than CC398 were more common in isolates of food origin than in isolates of animal origin.
- The clear majority of MRSA isolates subjected to antimicrobial susceptibility testing were MDR with extremely high levels of tetracycline resistance reported.
- Resistance to linezolid and vancomycin, both considered critically important for treatment of human infections, were not detected in any of the reported MRSA isolates subjected to antimicrobial susceptibility testing.
- In 2022 and 2023 resistance to the critically important antimicrobial rifampicin was detected in a limited number of isolates in meat from broiler, meat from turkey, meat from pig and breeding pigs.

6.2 | Data on MRSA addressed

Methicillin-resistant *S. aureus* (MRSA) can colonise the skin and mucosa of animals and humans and can cause severe infections. Three broad categories can be used to divide different MRSA: community-associated (CA)- MRSA, healthcare-associated (HA)- MRSA and livestock-associated (LA)- MRSA. The categories differ in means of epidemiology, resistance phenotype and molecular characterisation (i.e. SCC*mec* type), but there is no strict separation between them. The distinction between CA- and HA-MRSA is increasingly blurred (Hou et al., 2023). CA- and HA-MRSA predominantly include strains affecting humans, and are less frequently reported in food-producing animals. LA-MRSA have been detected in most food-producing animal populations, including those covered by the AMR monitoring according to Commission Implementing Decision 2020/1729/EU. Introduction of a fourth category, namely wildlife-associated (WA)- MRSA, has been discussed, due to the link of certain MRSA sequence types (STs) and clonal complexes (CCs) carrying the *mecC* gene to wild animals, especially European hedgehogs (Larsen et al., 2022). Further information on MRSA can be found in specific sections of the dedicated EFSA story map on MRSA, available online (here).

In 2025, a baseline study on the prevalence of MRSA in fattening pigs in EU will be performed (EFSA, 2022), as described in the Commission Implementing Decision (EU) 2023/1017. The aim is to estimate the prevalence of MRSA in the EU population of fattening pigs, using healthy fattening pigs at slaughter as the target population. Details on sampling design and testing requirements are presented in Decision (EU) 2023/1017 (online).

Findings on MRSA from humans are not specifically addressed in this chapter but are presented in the 'Antimicrobial resistance in the EU/EEA (EARS-Net) – Annual epidemiological report for 2023' published by ECDC (ECDC, 2024). Antimicrobial susceptibility in invasive *S. aureus* from humans is reported to TESSy by the European Antimicrobial Resistance Surveillance Network (EARS-Net) hosted by ECDC. In 2024, these data were reported by all EU Member States and EEA countries except France due to recent changes in the reporting from the French surveillance system. MRSA typing data are not reported, and possible links to the animal reservoir of LA-MRSA are therefore not easily detected at the European level. The estimated EU (excluding the UK and France) incidence of MRSA bloodstream infections decreased significantly from 5.63 per 100,000 population in 2019 to 4.64 per 100,000 population in 2023 (2023 EU/EEA country range: 0–15.5). The EU/EEA (excluding the UK and France) population-weighted mean percentage of MRSA among invasive *S. aureus* isolates reported to EARS-Net also decreased significantly from 18.2% in 2019 to 15.8% in 2023 (2023 EU/EEA country range: 1.5–51.1).

As of 2023, there are recommended EU targets on AMR (Council of the European Union, 2023). For MRSA, the target is to reduce the total EU incidence of MRSA bloodstream infections by 15% by 2030 against the baseline year 2019. In 2023, the

estimated total EU incidence of MRSA bloodstream infections was 17.6% lower than in 2019 (baseline year). As a result, the EU target for the incidence of MRSA bloodstream infections had already been reached by 2023. Still, combined resistance to another antimicrobial group was quite common, and MRSA percentages were high in several European countries. Thus, MRSA remains an important human pathogen in the EU/EEA (ECDC, 2024).

In EU, the monitoring of MRSA and related AMR in the veterinary sector is voluntary. As a result, only limited number of countries provided occurrence data for 2022 and 2023. Some countries also reported molecular data, including information on *spa*-types, sequence types and/or clonal complex, and data on antimicrobial susceptibility. This chapter summarises the MRSA data reported for food and animals in 2022 and 2023. Due to the voluntary and non-harmonised nature of monitoring, comparable data on MRSA over time are limited. Consequently, it is not possible to assess temporal trends in MRSA occurrence, and therefore this information is not presented in the current report.

Additional tables and graphs on MRSA in food and food-producing animals can be found in Annex E, available on Zenodo (https://doi.org/10.5281/zenodo.14645440). Occurrence data on MRSA in foods and animals can be visualised interactively using the EFSA dashboard on MRSA (here).

6.3 | Food and animals: MRSA

Six MSs (Belgium, Germany, Italy, the Netherlands, Slovakia and Spain) and one non-MS (Norway) reported data on the occurrence of MRSA in food and animals in 2022. In addition, isolate-based data on antimicrobial susceptibility was reported by Germany and Spain. In 2023, occurrence data on MRSA was reported by five MSs (Austria, Belgium, Germany, the Netherlands and Slovakia) and two non-MSs (Norway and Switzerland). Austria, Germany and Switzerland also reported isolate-based data on antimicrobial susceptibility. Although, the isolation method used for MRSA detection is not taken into account in the results presented in this chapter, this information is available as a filter for data visualisation in the MRSA dashboard (here). It is of note that the 1 step (S) isolation method, which is currently recommended by the EU Reference Laboratory for antimicrobial resistance (EURL-AR) (EURL-AR, 2023), may provide increased sensitivity compared to the 2-S isolation method (Larsen et al., 2017; Pauly et al., 2019). Comparison between countries should be done with caution as the monitoring of MRSA is not harmonised. Further, differences in the sensitivity of analytical methods used as well as sampling strategies, sample types collected and sampling stage may influence the MRSA prevalence. This should be considered when interpreting and comparing the results presented below.

6.3.1 | Food: Monitoring of MRSA

A limited number of countries reported data on MRSA in food in 2022 and 2023. In 2022, Germany, the Netherlands and Spain provided data on MRSA occurrence on meat from broilers (Germany, the Netherlands and Spain) and in meat from turkeys (Germany and the Netherlands). Further, Germany reported data on MRSA in meat from ducks, while the Netherlands also reported data on MRSA in meat from pigs, meat from cattle, meat from deer (venison), meat from farmed game (land mammals), meat from wild game (birds), meat from other animal species (not specified) and fruits (Annex E, table 1). In 2023, Austria, Germany, the Netherlands and Slovakia reported data. The occurrence of MRSA was investigated in meat from pigs (Austria, Germany, the Netherlands and Slovakia) and meat from cattle (Austria, Germany and the Netherlands). Germany also investigated the occurrence of MRSA in prawns from domestic aquaculture, while the Netherlands also reported data on MRSA occurrence in meat from broilers, meat from turkeys, meat from duck, meat from deer (venison), farmed game, wild game (birds) and meat from sheep (Annex E, table 2). Occurrence of MRSA in food reported from monitoring performed in 2022 and 2023 is presented in Figure 58. Please note that only food origins where positive isolates were obtained are included in this figure.

In both 2022 and 2023, MRSA was most frequently detected in meat from turkey with 53.7% of turkey carcases and 34.3% of retail meat from turkey reported positive by Germany in 2022, and 50.0% and 28.6% of retail meat from turkey reported positive by the Netherlands in 2022 and 2023, respectively (Annex E, table 1). It is of note that the Netherlands only provided data on a limited number of samples ($n = 8$ in 2022 and $n = 7$ in 2023). The MRSA occurrence in retail meat from broilers ranged from 1.1% in Spain (2022) to 9.7% in the Netherlands (2023). A slight increase from 7.5% in 2022 to 9.7% in 2023 was reported by the Netherlands. In 2022 Germany reported MRSA in 4.9% of samples from retail meat from broilers, while 16.7% of broiler carcases sampled at slaughterhouses were MRSA positive. In samples of retail meat from pigs, the Netherlands reported an MRSA occurrence of 6.9% in 2023 and 7.2% in 2022. Germany reported MRSA in 10.3% of retail meat from pigs, while the highest occurrences were reported by Austria (14.4%) and Slovakia (15.4%) in 2023. In meat from cattle, the Netherlands reported higher MRSA occurrence in samples collected at processing plants in 2022 and 2023 (9.1% and 13.6%, respectively), compared to retail meat from cattle (6.1% and 3.9%, respectively). Austria detected MRSA in 1.9% of retail meat from cattle samples, while Germany reported MRSA in 6.8% of samples from imported meat from cattle at border control posts. Germany also reported MRSA in retail meat from duck (1.9%) and duck carcases sampled at slaughterhouse (0.9%) in 2022, while the Netherlands reported MRSA in 4.6% of retail meat from sheep sampled in 2023. For detailed information regarding food samples investigated for MRSA in 2022 and 2023, please see and Annex E (tables 1 and 2).

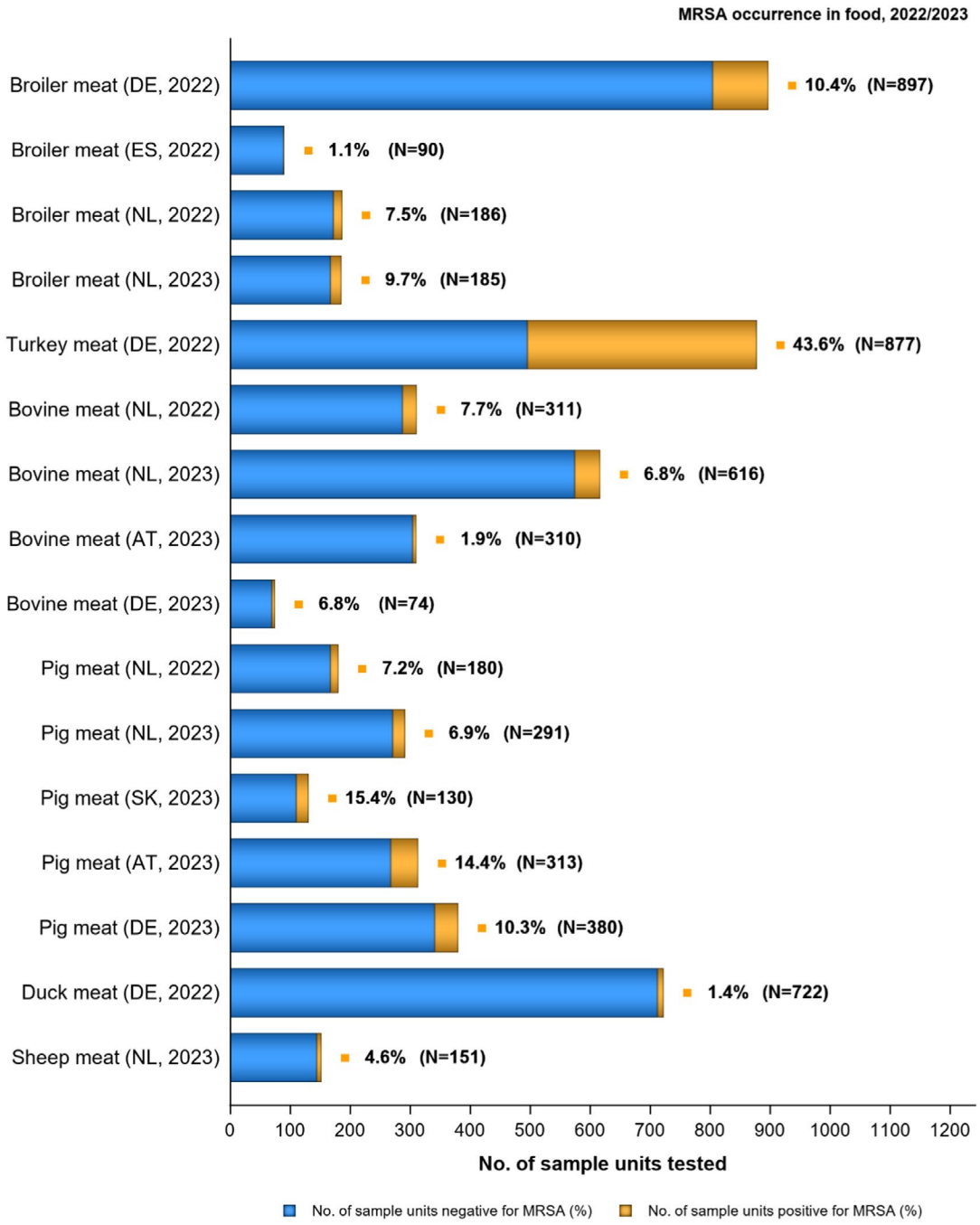


FIGURE 58 Methicillin-resistant *Staphylococcus aureus* in food, 2022/2023. Note: Only food categories where positive isolates were obtained and countries investigating > 10 samples are presented in this graph. The isolation method used for detection of MRSA is not considered in this analysis. AT, Austria; DE, Germany; ES, Spain; *N*, total number of sample units tested; NL, the Netherlands; SK, Slovakia. Blue: number of units negative for MRSA (%); Orange: number of units positive for MRSA (%).

Clonal complexes and *spa*-types (number of isolates):

Meat from broilers (DE, 2022): t1430 ST9 CC1 (1), CC398 spa-types: t011 (34), t034 (39), t571 (3), t899 (1), t1451 (1), t2011 (2), t2330 (1), t6575 (1), t10485 (1), molecular data not reported (9). Meat from broilers (ES, 2022): CC398 *spa*-type t6228 (1). Meat from turkeys (DE, 2022): CC1 *spa*-types: t127 (5), t235 (1), t1430 (6), t10204 (3), t242 CC5 (2), CC8 *spa*-types: t008 (1), t009 (1), CC398 *spa*-types: t011 (39), t034 (227), t538 (1), t588 (2), t899 (46), t1255 (4), t1451 (1), t1580 (1), t1793 (1), t2011 (7), t2346 (1), t2576 (1), t2922 (1), t5452 (2), t14089 (1), t21217 (1), CC398 *spa*-type not reported (2), t1422 CC692 (5), molecular data not reported (20). Meat from bovines, border control posts (DE, 2023): CC5 t002 (4), CC8 t008 (1). Meat from bovines (AT, 2023): t011 (3), t034 (3), all CC398. Meat from pigs (AT, 2023): CC1, ST9 *spa*-types: t899 (1), t1430 (3), CC398 *spa*-types: t011 (20), t034 (12), t1255 (1), t1451 (2), t2011 (4), t5524 (1), CC398 *spa*-type not provided (1). Meat from pigs (DE, 2023): CC1 *spa*-types: t127 (1), t693 (1), t899 (8), t1419 (1), t1430 (2), t3512 (1), t20072 ST22 CC22 (1), t008 CC8 (1), CC398 *spa*-types: t011 (10), t034 (7), t1451 (1), t1580 (1), t2011 (2), molecular data not reported (2).

Broiler meat reported by DE in 2022 were from carcases ($n = 412$) and fresh meat ($n = 485$). Broiler meat reported by ES in 2022 were from skinned meat ($n = 45$) and fresh meat with skin ($n = 45$). Bovine meat reported by NL in 2022 were from meat preparation ($n = 147$) and fresh meat ($n = 164$). Duck meat reported by DE in 2022 were from fresh meat ($n = 372$) and carcases ($n = 350$). Turkey meat reported by DE in 2022 were from fresh meat ($n = 460$) and carcases ($n = 417$). Bovine meat reported by NL in 2023 were from fresh meat ($n = 468$) and meat preparation ($n = 148$). Sheep meat reported by NL in 2023 were from fresh meat ($n = 134$) and meat preparation ($n = 17$).

6.3.2 | Animals: Monitoring of MRSA

6.3.2.1 | *Monitoring of MRSA in healthy animals*

In 2022, three MSs (Belgium, the Netherlands and Slovakia) and one non-MS (Norway) reported MRSA occurrence data from food-producing animals. In 2023, MRSA occurrence data in food-producing animals were reported by four MSs (Belgium, Germany, the Netherlands and Slovakia) and two non-MSs (Norway and Switzerland). MRSA data originated from monitoring, surveys and control and eradication programmes. In 2022/2023, monitoring of MRSA was performed on cattle under 1 year of age, dairy cows, broilers, laying hens, breeding pigs, fattening pigs and fattening turkeys.

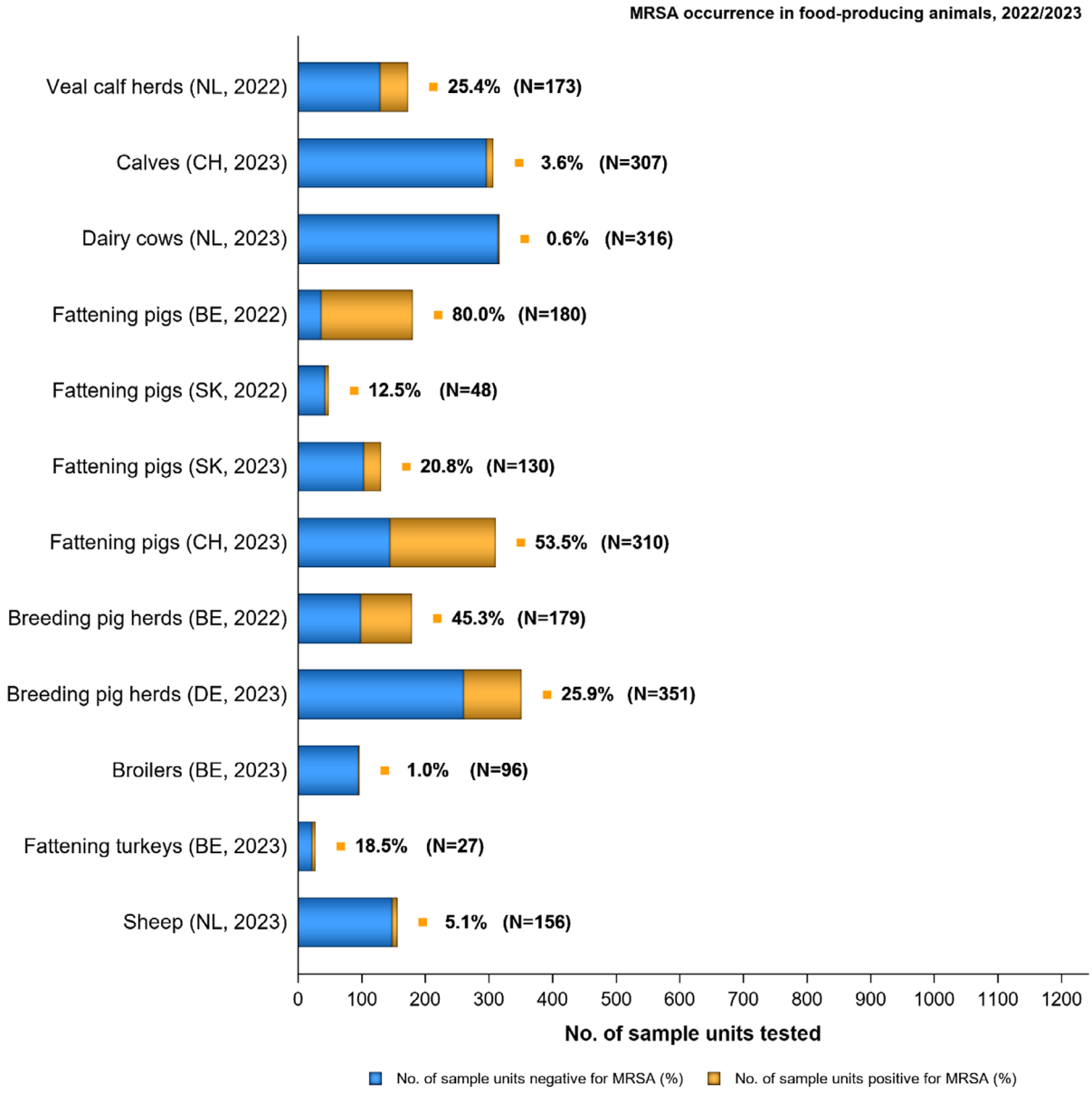


FIGURE 59 Methicillin-resistant *Staphylococcus aureus* in food-producing animals, 2022–2023. Note: Only food-producing animal populations where positive isolates were obtained and countries investigating > 10 samples are presented in this graph. The isolation method used for detection of MRSA is not considered in this analysis. BE, Belgium; CH, Switzerland; DE, Germany; *N*, total number of sample units tested; SK, Slovakia. Blue: number of units negative for MRSA (%); Orange: number of units positive for MRSA (%).
Clonal complexes and spa-types (number of isolates):
Fattening pigs (BE, 2022): CC398 *spa*-types t011 (63), t034 (26), t779 (1), t1255 (1), t1451 (1), t1580 (2), t2011 (2), t3423 (1), CC398 *spa*-type not reported (1), *spa*-type CC and/or ST not reported (46). Breeding pigs (BE, 2022): CC398 *spa*-types t011 (46), t034 (16), t588 (1), t1451 (1), t1457 (1), t2011 (3), t3423 (1), t5104 (1), t6575 (1), t15528 (1), *spa*-type not reported (9). Breeding pigs (DE, 2023): CC398 *spa*-types t011 (19), t034 (38), t108 (1), t1451 (2), t1456 (1), t2011 (6), t2922 (2), t3075 (1), t4652 (1), t6575 (3) t6608 (1), t16666 (1), t19248 (1), CC1 ST9 t899 (6), CC9 t10204 (1), *spa*-type not reported (7). Broilers (BE, 2023): CC398 t011 (1). Fattening turkeys (BE, 2023): CC398 t011 (5).
Norway tested a large number of pig herds in 2022 ($n = 591$) and 2023 ($n = 541$), but no MRSA were detected. Belgium tested laying hens ($n = 33$) in 2023, but no MRSA were detected.

MRSA was most frequently detected in pigs in both 2022 and 2023 (Figure 59). The occurrence in fattening pigs ranged from 12.5% in Slovakia (2022) to 53.5% in Switzerland (2023) and 80% in Belgium (2022). Further, MRSA was reported in

45.3% of breeding pig herds in Belgium (2022) and 25.9% of breeding pig herds in Germany (2023). In Norway, a large number of pig herds from different age groups were tested, but MRSA was not detected in 2022 and 2023 (Urdahl et al., 2023, 2024) (Annex E, tables 3 and 4). The results are similar to those observed in previous years.

Switzerland reported MRSA in 3.6% of cattle under 1 year of age in 2023, while the Netherlands reported MRSA in 25.4% of veal calf herds sampled in 2022 and 0.6% of dairy cows sampled in 2023. In 2023, Belgium reported MRSA in 18.5% of fattening turkeys and 1.0% of broilers. Further, the Netherlands reported MRSA in 5.1% of meat production sheep (2023).

6.3.2.2 | *Monitoring of MRSA in animals following clinical investigations*

Clinical investigations differ from monitoring studies as the sampling is usually biased, and selective culturing methods are normally not used. Although it is relevant to know the animal population affected and MRSA lineage in question, these data are not suited to infer occurrence data or to be extrapolated to the population level. In 2023, no countries reported data on monitoring of MRSA in animals following clinical investigations. Data from 2022 are included in Annex E (table 5).

6.3.3 | Food and animals: Results of molecular typing of isolates

In 2022, molecular typing data was reported for 447 (out of 544) isolates from food reported by Germany ($n = 446$) and Spain ($n = 1$), and for 170 (out of 275) isolates from food-producing animals from Belgium (Annex E, table 8).

In 2023, molecular typing data were reported for 93 (out of 205) isolates originating from food reported by Austria ($n = 51$) and Germany ($n = 42$) and 90 (out of 311) isolates from food-producing animals, originating from Belgium ($n = 6$) and Germany ($n = 84$) (Annex E, table 9). The *spa*-type results can be explored interactively in the MRSA dashboard (link). Molecular typing results are presented in Figure 60, Tables 24 and 25.

In both 2022 and 2023, the most frequently reported (confirmed and inferred) clonal complex (CC) in both food and food-producing animals was CC398. The CC was commonly associated with *spa*-types t011 and t034. In food, t011 or t034 were reported in 339 of 420 (80.7%) and 55 of 67 (82.1%) of CC398 isolates with *spa*-type information in 2022 and 2023, respectively. In food-producing animals, t011 or t034 were reported in 151 of 169 (89.3%) and 63 of 83 (75.9%) of CC398 isolates with *spa*-type information in 2022 and 2023, respectively. Similar results have been reported in previous years (EFSA and ECDC, 2022, 2023, 2024).

In addition to t011 and t034, 32 other *spa*-types were reported in CC398 isolates (Table 24). Of these, t899, 62 isolates, was the third most common *spa*-type following t011 and t034. This *spa*-type has been associated with both CC398 and CC1 (former CC9), with t899-CC398 being a mosaic strain primarily containing a CC398 chromosome but with a CC1 region containing the *spa*-gene (Larsen et al., 2016; Price et al., 2012). In 2022, ST and CC were not reported for isolates with *spa*-type t899, and they were therefore included in the CC398 group based on previous publications from MSs (Broens et al., 2011; Price et al., 2012; Simon et al., 2020). In 2023, t899 isolates were reported to belong to ST9/CC1, and were therefore included in the non-CC398 LA-MRSA group. Several *spa*-types associated with CC398 in 2022 and 2023 were also reported in the EU baseline study in breeding pigs performed in 2008 (EFSA, 2009a), indicating that the same strains may have persisted in the European pig production. Table 24 shows a complete overview of *spa*-types associated with MRSA CC398 in 2022 and 2023.

Non-CC398 isolates belonged to a range of different CCs and *spa*-types. A complete overview of *spa*-types found in non-CC398 isolates is shown in Table 25. The most frequently reported *spa*-type found in non-CC398 isolates was t899 (ST9, CC1) in 2023 and t1430 (ST9, CC1). Isolates with *spa*-type t899 were reported from breeding pigs and meat from pigs in 2023, while isolates with t1430 were reported in meat from broilers and meat from turkeys in 2022 and meat from pigs in 2023.

If only *spa*-type or ST was reported for an isolate, the CC was inferred based on reports in the literature. The following clarifications were made:

- *spa*-types t011, t034, t108, t571, t588, t1255, t1451, t1456, t1580, t1793, t2011, t2330, t2346, t2576, t2922, t5452, t6228, t6575, t10485, t19248 were classified as CC398 (Battisti et al., 2010; EFSA, 2009a; Kinross et al., 2017; Köck et al., 2013; Pauly et al., 2019; Tkadlec et al., 2023).
- If ST and/or CC was not specified, *spa*-type t899 was classified as CC1/CC398 (EFSA, 2009a; Guardabassi et al., 2009; Larsen et al., 2016).
- *spa*-type t127 was classified as CC1, LA-MRSA (EFSA, 2009a; Merialdi et al., 2019).
- *spa*-types t002 and t242 were classified as CC5 (Asanin et al., 2019; Köck et al., 2013).
- *spa*-types t008 and t009 were classified as CC8 (Boost et al., 2012; Cuny et al., 2016).
- *spa*-types t1419, t1430 and t10204 were associated to ST9 (EFSA, 2009a; Hasman et al., 2010; Köck et al., 2013), and classified as CC1 (PubMLST[39]).
- *spa*-type t1422 was classified as CC692 (Silva et al., 2020).
- *spa*-type t3512 was classified as ST2343 (Chen et al., 2018) and CC1 (PubMLST[1]).
- STs 9 and 8325 were classified as CC1 by PubMLST.[1]
- ST22 was classified as CC22 by PubMLST.[1]

[39] https://pubmlst.org/bigsdb?db=pubmlst_saureus_seqdef&page=query.

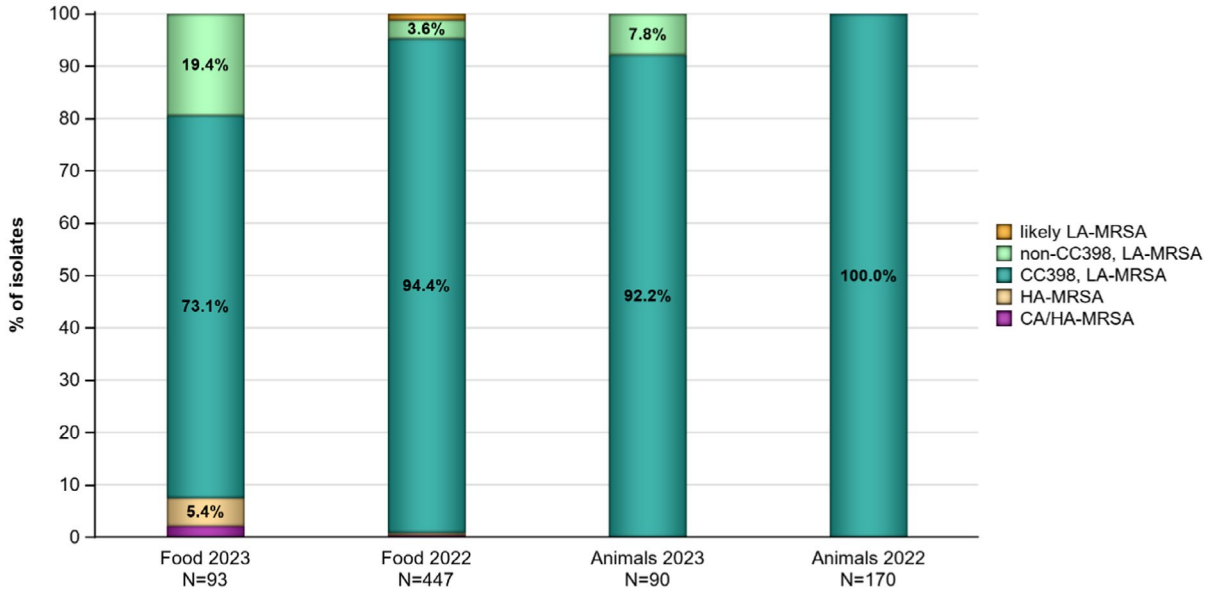


FIGURE 60 Methicillin-resistant *Staphylococcus aureus* types reported from food and animals in 2022 and 2023, inferred from molecular typing data.

CA-MRSA, community-associated MRSA; CC, clonal complex; HA-MRSA, hospital-associated MRSA; LA-MRSA, livestock-associated MRSA; *N*, number of isolates with typing data. The category 'likely LA-MRSA' includes CC692 associated with birds (Monecke et al., 2016). Molecular typing data included *spa*-type information, except for one isolate from pigs in Belgium, two isolates from meat from turkey in Germany and one isolate from meat from pigs in Austria where only information on CC and/or ST was provided. If data on CC was not provided, the CC was inferred based on findings in the literature. Detailed information on *mec*-genes, *spa*-types, STs and CCs reported and CCs inferred are shown in Annex E (tables 8 and 9).

TABLE 24 *spa*-types of methicillin-resistant *Staphylococcus aureus* CC398 and their detection in animals and food, 2022 and 2023.

spa-type	Year	Animals (number of isolates)	Tot	Food (number of isolates)	Tot
t034	2023	Breeding pigs (38)	38	Meat from cattle (3), Meat from pigs (19)	22
	2022	Breeding pigs (16), Fattening pigs (26)	42	Meat from broilers (39), Meat from turkeys (227)	266
t011	2023	Broilers (1), Breeding pigs (19), Fattening turkeys (5)	25	Meat from cattle (3), Meat from pigs (30)	33
	2022	Breeding pigs (46), Fattening pigs (63)	109	Meat from broilers (34), Meat from turkeys (39)	73
t899*	2022			Meat from broilers (1), Meat from turkeys (46)	47
t2011	2023	Breeding pigs (6)	6	Meat from pigs (6)	6
	2022	Breeding pigs (3), Fattening pigs (2)	5	Meat from broilers (2), Meat from turkeys (7)	9
t1451	2023	Breeding pigs (2)	2	Meat from pigs (3)	3
	2022	Breeding pigs (1), Fattening pigs (1)	2	Meat from broilers (1), Meat from turkeys (1)	2
t1255	2023			Meat from pigs (1)	1
	2022	Fattening pigs (1)	1	Meat from turkeys (4)	4
t6575	2023	Breeding pigs (3)	3		
	2022	Breeding pigs (1)	1	Meat from broilers (1)	1
t1580	2023			Meat from pigs (1)	1
	2022	Fattening pigs (2)	2	Meat from turkeys (1)	1
t571	2022			Meat from broilers (3)	3
t588	2022	Breeding pigs (1)	1	Meat from turkeys (2)	2
t2922	2023	Breeding pigs (2)	2		
	2022			Meat from turkeys (1)	1
t3423	2022	Breeding pigs (1), Fattening pigs (1)	2		
t5452	2022			Meat from turkeys (2)	2
t108	2023	Breeding pigs (1)	1		
t538	2022			Meat from turkeys (1)	1
t779	2022	Fattening pigs (1)	1		
t1456	2023	Breeding pigs (1)	1		

(Continues)

TABLE 24 (Continued)

spa-type	Year	Animals (number of isolates)	Tot	Food (number of isolates)	Tot
t1457	2022	Breeding pigs (1)	1		
t1793	2022			Meat from turkeys (1)	1
t2330	2022			Meat from broilers (1)	1
t2346	2022			Meat from turkeys (1)	1
t2576	2022			Meat from turkeys (1)	1
t3075	2023	Breeding pigs (1)	1		
t4652	2023	Breeding pigs (1)	1		
t5104	2022	Breeding pigs (1)	1		
t5524	2023			Meat from pigs (1)	1
t6228	2022			Meat from broilers (1)	1
t6608	2023	Breeding pigs (1)	1		
t10485	2022			Meat from broilers (1)	1
t14089	2022			Meat from turkeys (1)	1
t15528	2022	Breeding pigs (1)	1		
t16666	2023	Breeding pigs (1)	1		
t19248	2023	Breeding pigs (1)	1		
t21217	2022			Meat from turkeys (1)	1

Note: Molecular data were reported by Belgium (breeding pigs, *n* = 179; fattening pigs, *n* = 180), Germany (broiler carcases, *n* = 412; imported meat from broilers, *n* = 49; retail meat from broilers, *n* = 485; turkey carcases, *n* = 417; retail meat from turkey, *n* = 460) and Spain (meat from broilers, *n* = 90) in 2022. In 2023, molecular data were reported by Austria (retail meat from bovines, *n* = 310; retail meat from pigs, *n* = 313), Belgium (broilers, *n* = 96; fattening turkeys, *n* = 27) and Germany (breeding pigs, *n* = 351; imported meat from bovines, *n* = 74; retail meat from pigs, *n* = 380).

*t899 may also be attributed to CC1 (previously CC9). In 2022, ST and CC for t899 isolates were not reported, and they are therefore considered CC398.

TABLE 25 *spa*-types of other methicillin-resistant *Staphylococcus aureus* clonal complexes and their occurrence in animals and food, 2022 and 2023.

spa-type	Clonal complex (sequence type)	Year	Animals (number of isolates)	Tot	Food (number of isolates)	Tot
t899*	1 (9)	2023	Breeding pigs (6)	6	Meat from pigs (9)	9
t1430	1 (9)	2023			Meat from pigs (5)	5
		2022[a]			Meat from broilers (1), Meat from turkeys (6)	7
t127[a]	1	2023			Meat from pigs (1)	1
		2022			Meat from turkeys (5)	5
t1422[a]	692	2022			Meat from turkeys (5)	5
t002[a]	5	2023			Meat from cattle (4)	4
t10204[a]	1	2023	Breeding pigs (1)	1		
		2022			Meat from turkeys (3)	3
t008[a]	8	2023			Meat from cattle (1), Meat from pigs (1)	2
		2022			Meat from turkeys (1)	1
t242[a]	5	2022			Meat from turkeys (2)	2
t009[a]	8	2022			Meat from turkeys (1)	1
t235[a]	1 (8325)	2022			Meat from turkeys (1)	1
t693[a]	1 (9)	2023			Meat from pigs (1)	1
t1419[a]	1	2023			Meat from pigs (1)	1
t3512[a]	1	2023			Meat from pigs (1)	1
t20072[a]	22 (22)	2023			Meat from pigs (1)	1

[a]The CC associated with the *spa*-types (and, when reported, ST) is based on information from the literature, and not data reported from the countries.

*t899 may also be attributed to CC398. In 2023, t899 isolates were reported to belong to ST9, CC1, and are therefore reported under non-CC398 *spa*-types.

Note: Molecular data were reported by Belgium (breeding pigs, *n* = 179; fattening pigs, *n* = 180), Germany (broiler carcases, *n* = 412; imported meat from broilers, *n* = 49; retail meat from broilers, *n* = 485; turkey carcases, *n* = 417; retail meat from turkey, *n* = 460) and Spain (meat from broilers, *n* = 90) in 2022. In 2023, molecular data were reported by Austria (retail meat from bovines, *n* = 310; retail meat from pigs, *n* = 313), Belgium (broilers, *n* = 96; fattening turkeys, *n* = 27) and Germany (breeding pigs, *n* = 351; imported meat from bovines, *n* = 74; retail meat from pigs, *n* = 380).

6.4 | Summary data on the occurrence and susceptibility of MRSA

Antimicrobial susceptibility testing of MRSA provides valuable information regarding the situation in animals and food. This monitoring of AMR patterns in different MRSA lineages is important, as for example LA-MRSA CC398, which is considered to have a lower pathogenicity for humans, still can be a source of resistance genes with potential to disseminate to other more virulent *S. aureus* strains (Haaber et al., 2017; Sahibzada et al., 2017).

Antimicrobial susceptibility data were reported by Germany and Spain in 2022, and by Austria, Germany and Switzerland in 2023 (Annex E, tables 10 and 11). Broth microdilution and EUCAST epidemiological cut-offs (ECOFFs) were used to determine the antimicrobial susceptibility of the MRSA isolates.

Detailed data on occurrence of resistance to selected antimicrobials are presented in Annex E (figures 1 and 2, tables 10 and 11). None of the MRSA isolates subjected to susceptibility testing in 2022 and 2023 displayed resistance to the critically important antimicrobials linezolid or vancomycin, nor resistance to fusidic acid. However, resistance to rifampicin was reported in a limited number of isolates originating from pigs, meat from pigs, meat from broilers and meat from turkeys. Rifampicin is critically important for treatment of human infections, as it is a first-line antibiotic for treatment of tuberculosis, and can be used to improve treatment outcome of MRSA infections in combination with other antimicrobials (Nandhini et al., 2022; WHO, 2019). Resistance to mupirocin, an antimicrobial used for MRSA decolonisation (Deeny et al., 2015; Hetem & Bonten, 2013; Poovelikunnel et al., 2015), was also reported in one isolate from pigs. Tetracycline resistance was reported at extremely high levels in most animal populations and food categories tested. This was expected as most isolates were CC398, in which tetracycline resistance commonly occurrs (Price et al., 2012). High levels of tiamulin resistance were reported in all matrices investigated, most commonly in meat from broilers and meat from turkeys. Tiamulin, a pleuromutilin, is used almost exclusively in veterinary settings (EMA/CVMP, 2014). As expected, all tested isolates were also resistant to the beta-lactams, penicillin and cefoxitin. For the remaining antimicrobial substances, the levels of resistance varied markedly between the different animal populations and food categories tested (Annex E, tables 10 and 11).

The majority of isolates (99.8%) were considered MDR, (i.e. resistant to three or more antimicrobial classes). It is of note that penicillin and cephalosporins were considered as two separate antimicrobial classes in this analysis. However, even if penicillin and cefoxitin are considered as one class, the majority of isolates are still classified as MDR (93.1% and 90.7% in 2022 and 2023, respectively). The most commonly reported MDR pattern in both 2022 and 2023 was penicillin, cefoxitin, erythromycin, clindamycin, quinupristin/dalfopristin, tiamulin, trimethoprim and tetracycline. This MDR pattern was reported in 166/446 (37.2%) MDR isolates in 2022 and in 43/353 (12.2%) of MDR isolates in 2023.

6.5 | Discussion

The monitoring of MRSA in animals and food is performed on a voluntary basis, resulting in limited country participation in reporting occurrence and resistance data to EFSA.

Furthermore, the lack of harmonisation in monitoring protocols and varying methodologies between years hinders the comparability of data across and within countries. Additionally, MRSA prevalence may be affected by factors such as sampling strategies, sampling locations, analytical techniques, sample types and sample sizes. When evaluating results from different countries and across years, these limitations should be taken into consideration to ensure accurate interpretation of the data.

In 2022 and 2023, MRSA was detected in all animal populations investigated, including companion animals. However, the levels of MRSA varied markedly between animal populations and countries, with examples ranging from 0% of pigs in Norway to 80% of pigs in Belgium. Several different food matrices were also investigated in 2022 and 2023, and MRSA was detected in most of these at varying levels. Although food is not considered a primary source of human MRSA acquisition (Tang et al., 2017; Wendlandt et al., 2013), the presence of MRSA in food is a public health concern (Lozano et al., 2020). Notably, both Germany and Denmark have reported increasing levels of LA-MRSA strains colonising and infecting humans, with meat implicated as a potential source (Köck et al., 2013; Larsen et al., 2016).

Some countries reported molecular typing data on *spa*-types, STs and/or CCs. Consistent with previous years, CC398 was the most commonly reported or inferred CC overall (EFSA and ECDC, 2022, 2023, 2024). Among isolates with typing data from animals collected in 2022 and 2023, nearly all were CC398, with the exception of seven isolates LA-MRSA CC398 was first described in 2005 (Armand-Lefevre et al., 2005; Voss et al., 2005), and has since then persisted in the European pig production. This may partly be explained by a single-nucleotide polymorphism (SNP) in chromosome 12 of pigs, which is significantly associated with nasal carriage of MRSA (Skallerup et al., 2015). CC398 was also the most commonly reported CC in food categories. Interestingly, most non-CC398 *spa*-types reported where found in isolates from meat, indicating that the animal of origin is not the sole source of contamination. MRSA contamination might also occur during slaughter, meat processing and management of the meat at retail level (Jackson et al., 2013; Tang et al., 2017; van Loo et al., 2007). *spa*-type t899 is of particular interest, as it was the third most commonly reported *spa*-type in 2022 and 2023, following t034 and t011. Moreover, t899 has also been associated to both CC1 (previously CC9) and CC398, and MRSA t899 can be a mosaic strain with the CC398 chromosomal backbone and a smaller ST9 region carrying the *spa*-gene (Guardabassi et al., 2009; Larsen et al., 2016). The CC1/CC398 mosaic strain has been linked to poultry, with a subpopulation that appears to be better adapted to humans and poultry (Larsen et al., 2016; Tegegne et al., 2021).

All MRSA isolates for which molecular data were reported in 2022 and 2023 carried the *mecA* gene. The *mecC* gene has only been detected in a limited number of isolates in previous years (EFSA and ECDC, 2021, 2022, 2023, 2024). Although the primary host for *mecC* MRSA appears to be the European hedgehog (*Erinaceus europaeus*), it has also been described in food-producing animals, including dairy cows, goats, sheep and pigs in Europe (Angen et al., 2017; Bengtsson et al., 2017; Cui et al., 2021; Giacinti et al., 2017; Haenni et al., 2014; Schauer et al., 2018; Unnerstad et al., 2013). It has also been suggested that a subpopulation of *mec*C MRSA belonging to CC425 has adapted to ruminants (Larsen et al., 2022).

In 2022 and 2023, resistance to the critically important antimicrobials vancomycin and linezolid was not reported, nor was resistance to fusidic acid reported. Resistance to rifampicin and mupirocin resistance was however reported in a limited number of isolates. Resistance to linezolid has been attributed to the *cfr*-genes, conferring resistance tooxazolidinones, phenicols, streptogramin A, lincosamides and pleuromutilins (EMA/CVMP/AWP, 2014). In Europe, *cfr* has been described in isolates from or related to pigs, but the occurrences have generally been extremely low (Iurescia et al., 2023; Kehrenberg et al., 2009; Leão et al., 2022; Ruiz-Ripa et al., 2021; Schouls et al., 2022). The use of tiamulin in food-producing animals have given rise to concerns regarding proliferation of the *cfr* gene (EMA/CVMP/AWP, 2014). However, Belgium reported the presence of *cfr* in one isolate from sows and two isolates from fattening pigs in 2022, but antimicrobial susceptibility data were not available for these isolates, making it unclear whether they exhibited phenotypic linezolid resistance. It is important to consider that only a limited number of isolates undergo susceptibility testing, and therefore, the actual occurrence of resistance to critically important antimicrobials might be higher than reported.

MDR phenotypes were observed in most isolates subjected to susceptibility testing, with tetracycline resistance commonly reported in isolates from both animals and food. This is linked to the common association between CC398 and tetracycline resistance (Crombé et al., 2012). Notably, the occurrence of resistance to antimicrobials used to treat and control human MRSA infections was overall rare or very low.

A strong correlation exists between antimicrobial consumption and the emergence of resistant bacteria (Chantziaras et al., 2014) it would therefore be reasonable to believe that the occurrence of resistant bacteria, including MRSA, would also decrease. However, MRSA continues to be detected at very high or extremely high levels in some reporting countries, especially in pigs. Recent studies have reported extremely high levels of MRSA in pigs in Hungary (82.5%) and Portugal (98.8%) (Albert et al., 2023; Leão et al., 2022). It has been suggested that other MRSA reservoirs, for example colonised veterinarians or farm workers, could contribute to persistence of MRSA in the animal populations (Crespo-Piazuelo & Lawlor, 2021). Human-to-animal transmission has been identified as a source of MRSA introduction and outbreaks in Norwegian pig production (Elstrøm et al., 2019; Grøntvedt et al., 2016). Additionally, MRSA transmission between animals can occur during transportation and lairage (Bangerter et al., 2016; Grøntvedt et al., 2016). Dissemination through the production pyramid and introduction through imported breeding stock and semen has also been suggested as possible sources (Höjgård et al., 2015; Olsen et al., 2018). Thus, it is crucial to maintain high levels of biosecurity and hygiene standards at all levels of animal production to minimise the probability of MRSA introduction and/or transmission (Grøntvedt et al., 2016; Komodromos et al., 2022).

7 | ANTIMICROBIAL RESISTANCE IN *ENTEROCOCCUS* SPP.

7.1 | Key findings

- The voluntary monitoring of ***E. faecalis*** and ***E. faecium*** (Commission Implementing Decision (EU) 2020/1729) in 2022 and 2023 was performed in a limited number of countries, ranging from three to six reporting MSs for *E. faecalis* and from three to five for *E. faecium* over both years.
- Resistance rates differed greatly among *E. faecalis* and *E. faecium* isolates from different food-producing animals and antimicrobials tested, with overall higher resistance observed in *E. faecium* compared with *E. faecalis*.
- Resistance to **vancomycin** was only observed among *E. faecium* isolates, ranging from very low to low, with the highest level reported in cattle under 1 year of age (1.5%).
- Resistance to **linezolid** ranged from absent to low among *E. faecalis* (0.0%–6.6%), with the highest levels reported in cattle under 1 year of age (6.6%), followed by fattening pigs (2.0%). fattening turkeys in both enterococci species.

7.2 | Data on *Enterococcus* spp. addressed

In gram-positive bacteria, the *Enterococcus* species *E. faecalis* and *E. faecium* are suitable indicators of AMR, as both species are commonly found as commensals in the animal gastrointestinal tract and faeces (Nguyen et al., 2024). *E. faecium* and *E. faecalis* in the intestinal tract of animals or on food may constitute a reservoir of resistance genes which may be transferred either to pathogenic bacteria or to other commensal bacteria making them important opportunistic pathogens (Torres et al., 2018). The risk of clonal transmission and horizontal transference of mobile genetic elements is higher in *E. faecalis* than in *E. faecium*, which is most host-specific (Bortolaia & Guardabassi, 2023). The adaptability capacity and ability to acquire virulence and resistance genes make them adequate to assess the spread of AMR and pathogenic traits (Monteiro Marques et al., 2023).

In accordance with Commission Implementing Decision (EU) 2020/1729 (EC, 2020) and EFSA Technical specifications, the harmonised monitoring[41] and reporting of AMR in *Enterococcus* spp. from food-producing animals focuses on the species *E. faecalis* and *E. faecium* and is voluntary. Only a limited number of countries reported data on *E. faecalis* and *E. faecium* from cattle under 1 year of age and fattening pigs for 2023, and from broilers and fattening turkeys for 2022 due to the voluntary nature of the monitoring. The data reported (Annex F1, tables 1–4) are presented and considered for comparison in this chapter. The complete overview of all reported data from food-producing animals, reported in 2022 and 2023, is available as supporting documentation on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.14645440.

7.3 | Occurrence of antimicrobial resistance in *Enterococcus*

7.3.1 | Occurrence of antimicrobial resistance

Extremely high levels of resistance to **tetracyclines** (Table 1; Annex F1, tables 1–4) were observed among *E. faecalis* (70.4%–82.8%) and high to very high among *E. faecium* isolates (39.5%–60.6%) among all the animal populations monitored. The highest level of resistance to tetracyclines was observed in ***E. faecalis*** from cattle under 1 year of age (82.8%) followed by isolates from broilers (76.0%), fattening pigs (70.4%) and fattening turkeys (70.4%). Likewise, a very high level of resistance to tetracyclines was obtained from ***E. faecium*** isolated from fattening turkeys (60.6%), while lower levels of resistance were observed in the remaining animal populations monitored.

Resistance to **ampicillin** (Table 1; Annex F1, tables 1–4) varied unevenly among all MSs for *E. faecium* with ranges from low to moderate (5.7%–12.9%). The highest levels of resistance in *E. faecium* were reported in fattening turkeys (12.9%), followed by cattle under 1 year of age (9.8%). For *E. faecalis*, resistance to ampicillin was not detected in nearly all animal populations, except for broilers where a low level (1.0%) was observed (speciation of those *E. faecalis* isolates is ongoing).

Similarly, the observed **erythromycin** resistance (Table 1; Annex F1, tables 1–4) varied from very high to extremely high among *E. faecalis* (range from 50.5% to 73.4%) and high to very high in *E. faecium* (range from 23.9% to 51.5%) isolates from all the animal populations. Overall, erythromycin resistance was higher in *E. faecalis* than in *E. faecium*. The highest level of resistance was observed in *E. faecalis* from broilers in 2022 (73.4%). Likewise, a very high level of resistance to erythromycin (51.5%) was registered in *E. faecium* from fattening turkeys in 2022, whereas the lowest resistance was recorded in *E. faecium* from fattening pigs in 2023 (23.9%).

Resistance to **gentamicin** (Table 1; Annex F1, tables 1–4) ranged from very low to moderate among *E. faecalis* isolates (0.3%–13.6%) and very low to low among *E. faecium* isolates (0.4%–4.2%), across all animal populations and among all MSs. In both *E. faecalis* and *E. faecium*, the highest levels of resistance were observed in isolates from cattle under 1 year of age (13.6% and 4.2%, respectively) and fattening pigs (11.6% and 1.6%, respectively). In 2022, for both enterococci species, resistance to gentamicin was very low in fattening turkeys and broilers (0.3%–0.7%).

Resistance to **ciprofloxacin** (Table 1; Annex F1, tables 1–4) ranged from very low to low in *E. faecalis* (0.8%–5.2%) and remained low in *E. faecium* isolates (4.1%–9.5%) in all MSs. The highest levels of resistance were observed in fattening turkeys for both *E. faecium* (9.5%) and *E. faecalis* (5.2%), while rare resistance was reported for *E. faecalis* isolates from broilers (0.8%). In the remaining animal populations, low levels of resistance were reported in both *E. faecium* and *E. faecalis* isolates 4.7% and 3.0%, for cattle under 1 year of age, respectively, and 4.1% and 4.0%, for fattening pigs respectively), as well as for *E. faecium* from broilers (5.0%).

Resistance to **linezolid** (Table 1; Annex F1, tables 1–4) ranged from rare to low among *E. faecalis* (0.0%–6.6%) and remained rare among *E. faecium* (0.0%–0.6%). The highest levels of resistance were registered in *E. faecalis* from cattle under 1 year of age (6.6%) and in the second place for fattening pigs (2.0%). This pattern was reversed, among *E. faecium* isolates, where the highest levels were reported in fattening pigs (0.6%) followed by cattle under 1 year of age (0.3%). In broilers, *E. faecalis* and *E. faecium* exhibited very low levels of linezolid resistance (0.3% and 0.1%, respectively), whereas linezolid resistance was not detected in isolates from fattening turkeys in both enterococci species.

Resistance to **tigecycline** (Table 1; Annex F1, tables 1–4) ranged from rare to low in both *E. faecalis* (0.0%–1.8%) and *E. faecium* (0.0%–1.5%) isolates tested among all MSs. The highest levels of resistance in *E. faecalis* were registered for broilers (1.8%) and in *E. faecium* from cattle under 1 year of age (1.5%). In fattening pigs, *E. faecalis* and *E. faecium* exhibited low resistance to this antimicrobial (1.0%, both). No resistance to tigecycline was discerned in *E. faecalis* from cattle under 1 year of age and *E. faecium* from fattening turkeys.

Among all MSs, resistance to **vancomycin** (Table 1; Annex F1, tables 1–4) were only observed among *E. faecium* isolates, ranging from very low to low (0.1%–1.5%). The highest vancomycin resistance was registered for cattle under 1 year of age (1.5%) and fattening pigs (0.2%). Only *E. faecium* from broilers registered very low vancomycin resistance values (0.3%) and, no resistance was reported for fattening turkeys.

Resistance to **teicoplanin** (Table 1; Annex F1, tables 1–4) was only reported in *E. faecium* isolates at rare levels in broilers (0.1%) and no resistance was observed in the remaining animal populations.

Moreover, resistance to **daptomycin** (Table 1; Annex F1, tables 1–4) was only observed among *E. faecalis* isolates from broilers at very low levels (0.3%) and from fattening pigs at low levels (1.3%).

[41] In accordance with Commission Implementing Decision (EU) 2020/1729, the harmonised panel of antimicrobials for *E. faecalis* and *E. faecium* includes ampicillin, chloramphenicol, ciprofloxacin, daptomycin, erythromycin, gentamicin, linezolid, quinupristin/dalfopristin, teicoplanin, tetracycline, tigecycline and vancomycin.

Resistance to **quinupristin/dalfopristin** (Table 1; Annex F1, tables 1–4) ranged from very high to extremely high (64.5%–82.8%) in *E. faecium* isolates from all the animal populations monitored in all MSs. Overall, among the observed levels of resistance to all antimicrobials tested, the levels of resistance to quinupristin/dalfopristin were the highest in *E. faecium* isolates from all animal populations in 2022 and 2023. Furthermore, the levels of resistance to tetracyclines were higher for *E. faecalis* than for *E. faecium* within each animal species.

Resistance to **chloramphenicol** (Table 1; Annex F1, tables 1–4) ranged from very low to high among *E. faecalis* isolates (0.8%–37.4%) and very low to low among *E. faecium* (0.3%–2.2%) isolates from all the animal populations. The highest resistance levels were observed in *E. faecium* from cattle under 1 year of age (37.4%) and fattening pigs (22.9%), whereas in poultry, chloramphenicol resistance in both enterococci species varied from very low to low (0.3%–2.2%). Similarly to *E. faecalis*, the highest resistance in *E. faecium* was reported for cattle under 1 year of age (2.2%) and fattening pigs (2.0%) The lowest resistance in both *E. faecalis* and *E. faecium* was observed in broilers (0.8% and 0.3%, respectively; Table 26).

TABLE 26 Occurrence of resistance (%) to selected antimicrobials in *Enterococcus faecalis* and *Enterococcus faecium* in caecal samples from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age using harmonised ECOFFs, 2022–2023 and 6 MSs.

Enterococcus species	Categories	Year	No. of isolates	Reporting MSs (*N*)	AMP	CHL	CIP	DPT	ERY	GEN	LZD	Q/D*	TEC	TET	TGC	VAN
E. faecalis	Cattle under 1 year of age	2023	198	BE, DE, ES, IT (4)	0.0	37.4	3.0	0.0	60.1	13.6	6.6	94.6	0.0	82.8	0.0	0.0
	Fattening pigs	2023	301	BE, DE, DK, ES, IT, SI (6)	0.0	22.9	4.0	1.3	50.8	11.6	2.0	98.3	0.0	70.4	1.0	0.0
	Broilers	2022	387	BE, DE, DK, ES, SI (5)	1.0	0.8	0.8	0.3	73.4	0.3	0.3	99.7	0.0	76.0	1.8	0.0
	Fattening turkeys	2022	388	BE, DE, ES (3)	0.0	1.3	5.2	0.0	50.5	0.5	0.0	97.2	0.0	70.4	0.3	0.0
E. faecium	Cattle under 1 year of age	2023	408	BE, DE, ES, IT (4)	9.8	2.2	4.7	0.0	49.0	4.2	0.3	82.4	0.0	51.5	1.5	1.5
	Fattening pigs	2023	510	BE, DE, ES, IT, SI (5)	5.7	2.0	4.1	0.0	23.9	1.6	0.6	82.8	0.0	51.0	1.0	0.2
	Broilers	2022	747	BE, DE, DK, ES, SI (5)	6.3	0.3	5.0	0.0	38.7	0.7	0.1	64.5	0.1	39.5	0.3	0.3
	Fattening turkeys	2022	264	BE, DE, ES (3)	12.9	0.4	9.5	0.0	51.5	0.4	0.0	76.5	0.0	60.6	0.0	0.0

Abbreviations: AMP, ampicillin; BE, Belgium; CHL, chloramphenicol; CIP, ciprofloxacin; DE, Germany; DK, Denmark; DPT, daptomycin; ERY, erythromycin; ES, Spain; GEN, gentamicin; IT, Italy; LZD, linezolid; *N*, Total number of reporting Member States (MSs); Q/D, quinupristin/dalfopristin; SI, Slovenia; TEC, teicoplanin; TET, tetracycline; TGC, tigecycline; VAN, vancomycin.

**E. faecalis* is intrinsically resistant to Q/D.

Gray-shaded values indicate a high level of resistance to the antimicrobial, which is expected due to the intrinsic resistance of *E.faecalis* to this antimicrobial (quinupristin/dalfopristin).

ABBREVIATIONS

% f	percentage frequency of isolates tested
% Occ	percentage of cephalosporin-resistant isolates presenting a presumptive phenotype
% Prev	percentage of samples harbouring a presumptive ESBL/AmpC-producing *E. coli*
% Res	percentage of resistant isolates
AMC	antimicrobial consumption
AMR	antimicrobial resistance
AMS	antimicrobial stewardship
AST	antimicrobial susceptibility test
BCP	Border control posts
CA-MRSA	Community-associated MRSA
CASFM	Comité de l'Antibiogramme de la Société Française de Microbiologie
CBP	clinical breakpoints
CC	clonal complex
CI	confidence interval
CIA	critically important antimicrobial
CLSI	Clinical and Laboratory Standards Institute
CP	carbapenemase
CS	complete susceptibility
DD	disc diffusion method
DL	dilution/dilution method
DLG	dilution with gradient step
EARS-Net	European Antimicrobial Resistance Surveillance Network
ESBL	extended-spectrum β-lactamase
ECDC	European Centre for Disease Prevention and Control
ECOFF	Epidemiological cut-off value
EEA	European Economic Area
EFTA	European Free Trade Association
EMA	European Medicines Agency
ESBL	extended-spectrum beta-lactamase
ESC	extended spectrum
EUCAST	European Committee on Antimicrobial Susceptibility Testing
EURL-AR	EU Reference Laboratory for Antimicrobial Resistance
EUSR	European Union Summary Report
HaDEA	European Health and Digital Executive Agency
HA-MRSA	hospital-associated MRSA
hpCIA	highest priority critically important antimicrobials
I	susceptible with increased exposure
IEC	immune evasion cluster
IPC	Infection prevention and control
KOI_{CS}	key outcome indicator of completely susceptibility (susceptible to all tested substances) *E. coli*
KOI_{ESC}	Key outcome indicator of ESBL- and/or AmpC-producing *E. coli*
LA-MRSA	livestock-associated MRSA
MDR	multidrug resistant
MDRI	multidrug resistant islands
MIC	minimum inhibitory concentration
MLST	multi locus sequence typing
MRSA	methicillin-resistant *Staphylococcus aureus*
MS	Member State
NA	not applicable/not available
NCP	National Control Programme
NRL	National Reference Laboratory
NTS	non-typhoidal Salmonellas
OECD	Organisation for Economic Cooperation and Development
PCR	polymerase chain reaction
PCU	population correction unit
PMQR	plasmid-mediated quinolone resistance
PVL	Panton valentine leukocidin
Q	quantitative
QRDR	quinolone resistance-determining regions
R	resistant
RCs	Reporting countries

res1–res9	resistance to one antimicrobial substance/resistance to nine antimicrobial substances of the common set for *Salmonella*
S	susceptible
SIR	susceptible, intermediate, resistant
ST	sequence type
SYN	synergy
TESSy	The European Surveillance System
WGS	whole genome sequencing

ANTIMICROBIAL SUBSTANCES

AMC	Amoxicillin/clavulanate
AMK	Amikacin
AMP	Ampicillin
AZM	Azithromycin
CFT/FOX	Cefoxitin
CHL	Chloramphenicol
CIP	Ciprofloxacin
CLA	Clavulanate
CLI	Clindamycin
COL	Colistin
CTX	Cefotaxime
CTZ/CAZ	Ceftazidime
ERT/ETP	Ertapenem
ERY	Erythromycin
FEP	Cefepime
FUS	Fusidic acid
GEN	Gentamicin
IMI	Imipenem
KAN	Kanamycin
LZD	Linezolid
MEM	Meropenem
MUP	Mupirocin
NAL	Nalidixic acid
PEF	Pefloxacin
PEN/PNC	Penicillin
QD	Quinupristin/Dalfopristin
RIF	Rifampicin
SMX	Sulfonamides
STR	Streptomycin
SUL	Sulfonamides
SXT	Sulfamethoxazole
TEM	Temocillin
TET/TCY	Tetracycline
TGC	Tigecycline
TIA	Tiamulin
TMP	Trimethoprim

MSs OF THE EU AND OTHER REPORTING COUNTRIES

AT	Austria
BE	Belgium
BG	Bulgaria
CY	Cyprus
CZ	Czechia
DE	Germany
DK	Denmark
EE	Estonia
EL	Greece
ES	Spain
FI	Finland
FR	France
HR	Croatia
HU	Hungary

IE	Ireland
IT	Italy
LT	Lithuania
LU	Luxembourg
LV	Latvia
MT	Malta
NL	Netherlands
PL	Poland
PT	Portugal
RO	Romania
SE	Sweden
SI	Slovenia
SK	Slovakia
XI	United Kingdom (Northern Ireland)

NON-MSs REPORTING COUNTRIES

AL	Albania
CH	Switzerland
IS	Iceland
ME	Montenegro
MK	Republic of North Macedonia
NO	Norway
UK	United Kingdom

DEFINITIONS

'Antimicrobial-resistant isolate'	In the case of quantitative data, an isolate was defined as 'resistant' to a selected antimicrobial when its minimum inhibitory concentration (MIC) value (in mg/L) was above the cut-off value or the disc diffusion diameter (in mm) was below the cut-off value. The cut-off values, used to interpret MIC distributions (mg/L) for bacteria from animals and food, are shown in Appendix A – Materials and methods, tables F.5–F.7. In the case of qualitative data, an isolate was regarded as resistant when the country reported it as resistant using its own cut-off value or break point
'Level of antimicrobial resistance'	The percentage of resistant isolates among the tested isolates
'Reporting MS group'	Member States (MSs) that provided data and were included in the relevant table for antimicrobial resistance data for the bacteria–food/animal category–antimicrobial combination
Terms used to describe the levels of antimicrobial resistance	Rare: < 0.1% Very low: 0.1%–1.0% Low: > 1.0%–10.0% Moderate: > 10.0%–20.0% High: > 20.0%–50.0% Very high: > 50.0%–70.0% Extremely high: > 70.0%
Complete susceptibility	A completely susceptible isolate is defined as an isolate without resistance (MIC < ECOFF) to the tested antimicrobial substances
Multidrug resistant	A multidrug resistant isolate is defined as an isolate resistant to at least three of the tested antimicrobial substances

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APPENDIX A

Materials and methods

Antimicrobial susceptibility data from humans available in 2023

Data reported to The European Surveillance System (TESSy)

EU Member states (MSs) report results from antimicrobial susceptibility testing of *Salmonella* spp. and *Campylobacter* spp. isolated from clinical cases to European Centre for Disease Prevention and Control (ECDC) on an annual basis. Data can be submitted to the ECDC and The European Surveillance System (TESSy) in different formats. Phenotypic test results can be reported either as measured values (inhibition zone diameters or minimum inhibitory concentrations (MIC)) in the isolate-based reporting or as results interpreted with clinical breakpoints via the case-based reporting of *Salmonella* and *Campylobacter* infections. Genomic-based test results can be submitted either as the laboratory's prediction of the phenotype from sequencing of the bacterial genome, or from year 2023, submission of sequences directly to TESSy for analysis of resistance determinants and predicted phenotype in ECDC using ResFinder and PointFinder. The reporting of phenotypic quantitative data via the isolate-based reporting is so far the preferred format, as stipulated in the EU protocol for harmonised monitoring of antimicrobial resistance (AMR) in human *Salmonella* and *Campylobacter* isolates (ECDC, 2016).

Salmonella spp.: For 2023, 27 MSs, plus Iceland and Norway provided data on antimicrobial resistance (AMR) in human *Salmonella* isolates. Twenty-one countries reported measured values and four reported results interpreted as susceptible standard dosing regimen, susceptible increased exposure or resistant (SIR) according to the clinical breakpoints (CBPs) applied. Four countries reported whole genome sequences that were analysed by ECDC and interpreted as predicted wild type or predicted non-wild type (Table B.1)

Campylobacter spp.: For 2023, 24 MSs, plus Iceland and Norway provided AMR data from human isolates. Seventeen countries reported measured values, four reported results interpreted as susceptible standard dosing regimen, susceptible increased exposure or resistant (SIR) according to the CBPs applied and five countries reported results that were categorised as predicted wild type or predicted non-wild type based on analysis of bacterial genomes (two countries reporting interpreted data and three countries submitting whole genome sequences which were analysed at ECDC) (Table B.2)

Harmonised testing

Most laboratories follow the 'EU protocol for harmonised monitoring of antimicrobial resistance in human *Salmonella* and *Campylobacter* isolates' (ECDC, 2016) on the antimicrobial panel to be tested. The antimicrobials tested, the method used (dilution, disk diffusion, gradient strip, whole genome sequencing (WGS)), the type of data provided and the interpretive criteria applied are presented in Table A.1 for *Salmonella* and in Table A.2 for *Campylobacter*. For *Salmonella*, eight MSs, plus Iceland and Norway used only disk diffusion methods (DDs) for their antimicrobial susceptibility testing (AST), six MSs used dilution methods (DLs) and another nine MSs used various combinations of DD and DL or dilution with gradient strip (DLG) methods. Four countries used sequencing (Table A.1). For *Campylobacter*, eight MSs and Iceland used only DDs for their AST, five MSs used DL, Norway used DLG and three MS used a combination of DD and DLG or DL and DGL. Five countries used sequencing and bioinformatics tools were applied to predict phenotypic resistance from the genome. Two MSs did not provide the methodology (Table A.2). All data on measured MIC or zone mm values were results of AST performed at the national public health reference laboratories, with the exception of Italy for *Salmonella* where a few regional laboratories also contributed, and Finland for *Campylobacter* where the quantitative data had been collected from regional laboratories. Data interpreted with clinical breakpoints were normally from local or regional laboratories and reported together with the information on the clinical case. In these cases, AST had primarily been performed with the purpose of treatment of the case rather than AMR monitoring. For this reason, the number of tests per antimicrobial varied.

Salmonella test panel

The national public health laboratories within the Food- and Waterborne Diseases and Zoonoses (FWD) network has agreed on a panel of priority antimicrobials and optional antimicrobials to test for and report to ECDC (ECDC, 2016). Compared with earlier recommendations, a second beta-lactam (ceftazidime) and a carbapenem (meropenem) were added. For 2023, all MSs reported results on meropenem and all but one for ceftazidime. Three last-line antimicrobials – azithromycin, colistin and tigecycline – are also included in the priority list. For colistin, however, the methodology is complicated due to chemical properties of the substance and a joint European Committee on Antimicrobial Susceptibility Testing (EUCAST) and Clinical and Laboratory Standards Institute (CLSI) subcommittee confirmed that broth microdilution is so far the only valid method for colistin susceptibility testing (EUCAST, 2017). Disk diffusion does not work because of poor diffusion of the large colistin molecule into the agar, and tested gradient strips also underestimate colistin MIC values, again most likely due to poor diffusion into the agar (Matuschek et al., 2018). Therefore, only countries performing broth microdilution or

those predicting resistance from WGS should report on colistin resistance. Fourteen MSs reported AST results on colistin, fifteen and one non-MS on azithromycin and fourteen on tigecycline for 2023.

Due to the problems in detecting low-level fluoroquinolone resistance in *Salmonella* spp. using disk diffusion, nalidixic acid was, for a long time, used as a marker for fluoroquinolone resistance. After the discovery that plasmid-mediated fluoroquinolone resistance is often not detected using nalidixic acid, EUCAST studied alternative disks and concluded that pefloxacin was an excellent surrogate marker (except for isolates having the aac(6')-Ib-cr gene as the only resistance determinant) (Skov & Monnet, 2016). Since 2014, EUCAST has recommended this agent for screening of low-level fluoroquinolone resistance in *Salmonella* with disk diffusion (EUCAST, 2014) and, since June 2016, this is also reflected in the EU protocol. In 2023, all countries reporting measured values for disk diffusion tested with pefloxacin instead of ciprofloxacin. Eleven countries reported the combination drug co-trimoxazole (trimethoprim–sulfamethoxazole) in addition to, or instead of, testing the substances separately, partly because this combination is used for clinical treatment and partly because no EUCAST interpretive criterion exists for sulfamethoxazole for *Salmonella*.

Campylobacter **test panel**

The antimicrobials included in the 2023 report followed the panel of antimicrobials from the EU protocol for harmonised monitoring of AMR in human *Salmonella* and *Campylobacter* isolates (ECDC, 2016). The priority panel for *Campylobacter* includes ciprofloxacin, erythromycin, tetracyclines and gentamicin. Gentamicin was added in 2016 and is recommended for screening of invasive isolates. Co-amoxiclav (combination drug with amoxicillin and clavulanic acid) was included from the list of optional antimicrobials. In 2023, all reporting countries tested the isolates against the three main antimicrobials ciprofloxacin, erythromycin and tetracycline (although two countries tested less than 10 isolates). In relation to *Campylobacter jejuni* isolates, 18 reporting countries also tested for gentamicin and 7 tested for co-amoxiclav. With regards to *Campylobacter coli* isolates, 17 reporting countries also tested these isolates for gentamicin and 6 tested for co-amoxiclav (Annex B.1, tables 1 and 2).

Analyses of antimicrobial resistance testing

Harmonised interpretation of data with animal and food data

Data reported as measured values were interpreted by ECDC based on the EUCAST epidemiological cut-off (ECOFF) values, when available. For MIC data, the same criteria as used by EFSA were applied (Tables A.5 and A.6) except for when EUCAST had changed the ECOFF after the regulation for animal and food AMR monitoring had been implemented, e.g. as for ampicillin in 2021 for *Salmonella* enterica (MIC lowered by one dilution). Where EUCAST had removed the ECOFF (colistin, meropenem, tigecycline and trimethoprim-sulfamethoxazole for *Salmonella*), the same criteria were applied as recommended by EFSA (EFSA, 2024). For zone diameter data, corresponding EUCAST disk diffusion ECOFF values were applied with a few exceptions (Tables A.1 and A.2). Regarding data reported as SIR values, the categories of 'susceptible, increased exposure' (I) and 'clinically' resistant (R) were combined into one group. Alignment of the susceptible category with the 'wild type' category based on epidemiological cut-off values (ECOFFs) and of the I + R category with the ECOFF-based 'non-wild type' category provides better comparability and more straightforward interpretation of the data for most antimicrobial agents included (Figures A.1 and A.2). The exceptions are tetracycline for *Salmonella* and ciprofloxacin for *Campylobacter*, where only the R category was included. For *Salmonella*, this procedure results in good concordance (±1 dilution) across categories with the exception of meropenem where the MIC for non-susceptible category is substantially higher (+4 dilutions) than the ECOFF. For *Campylobacter*, there is full agreement across interpretive categories, with the exception of the EUCAST ECOFF for tetracycline in *C. jejuni* which is one dilution below the EUCAST CBP.

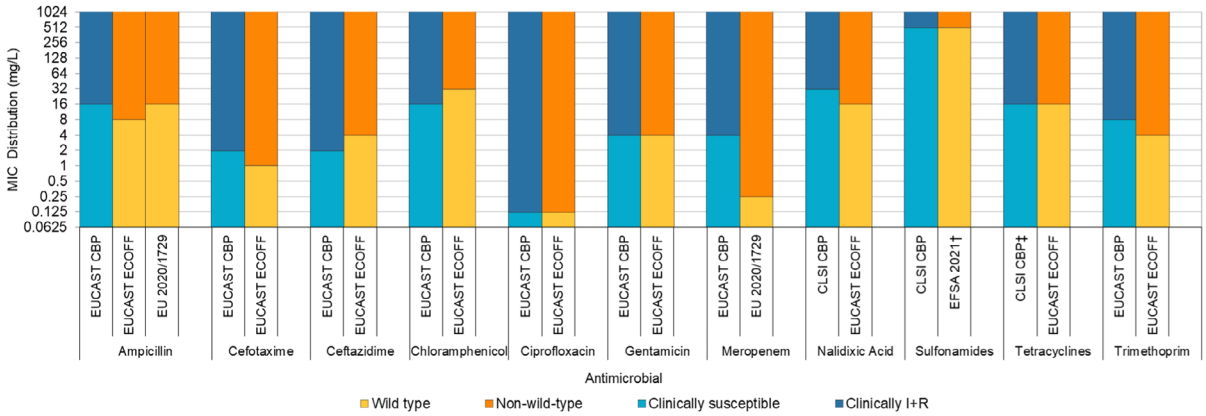

FIGURE A.1 Comparison of clinical breakpoints and epidemiological cut-off values used to interpret MIC data reported for *Salmonella* spp. from humans, animals or food.
†EFSA Manual for reporting 2023 antimicrobial resistance data within the framework of Directive 2003/99/EC and Decision 2020/1729/EU. ‡Only R category included.

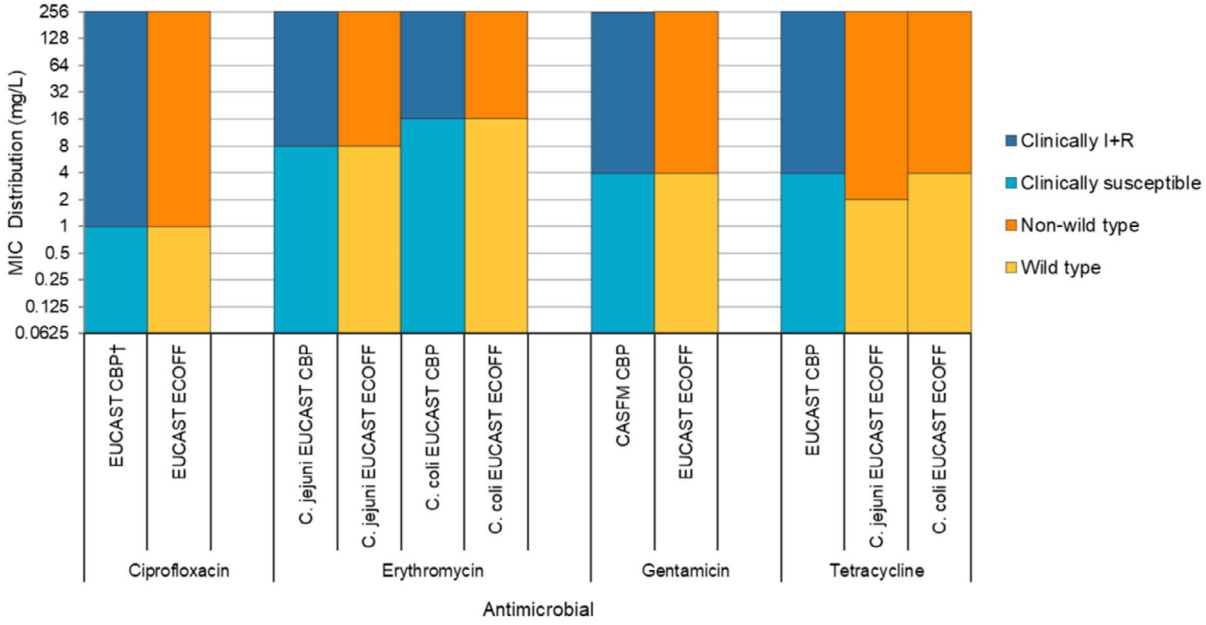

FIGURE A.2 Comparison of clinical breakpoints (CBPs) and epidemiological cut-off values (ECOFFs) used to interpret MIC data reported for *Campylobacter* spp. from humans and food-producing animals.
†Only R category included.

Separation by species or serovar

As resistance levels differ substantially between *Salmonella* serovars, results are presented separately for selected serovars of importance in humans. The serovars presented in the report are *S.* Enteritidis, *S.* Typhimurium, monophasic *S.* Typhimurium, *S.* Infantis, *S.* Kentucky and *S.* Derby. AMR data on the 10 most common serovars in human cases in the last years are also available in the ECDC Surveillance Atlas for Infectious Diseases (https://atlas.ecdc.europa.eu/public/index.aspx). For *Campylobacter*, resistance levels differ quite substantially between the two most important *Campylobacter* species, *C. jejuni* and *C. coli*, and data are therefore presented by species. The proportion of resistant isolates is only shown when at least 10 isolates were reported by a MS.

Exclusion of travel-associated cases

To better assess the impact of food consumed within each reporting country on the AMR levels found in human isolates, cases known to have travelled outside of the country during the incubation period were excluded from the analysis. However, as several countries had not provided any information on travel status of their cases, cases with unknown travel status were also included in addition to domestically-acquired cases. The exception to this is Denmark and Finland, where it has been agreed that cases of unknown travel status should be excluded from analyses for *Salmonella* spp. and for

Denmark also for *Campylobacter* spp. The proportions of travel-associated, domestic and cases with unknown travel status among the tested isolates are presented in Tables A.3 and A.4.

Temporal trends in resistance

Temporal trends in the proportion of resistant human isolates to selected antimicrobials over the period 2014–2023 were analysed by country. The statistical significance was assessed with logistic regression in Stata 17.0 and $p < 0.05$ was considered to be significant. Only countries testing at least 10 isolates per year and for at least 3 years in the 10-year period were included. For *Salmonella*, the antimicrobials analysed were ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime, ampicillin and tetracycline. For *Campylobacter*, the corresponding antimicrobials were ciprofloxacin, erythromycin and tetracycline.

Maps for critically important antimicrobial resistance

For *Salmonella*, the proportions of human isolates resistant to both of the critically important antimicrobials for treatment of severe *Salmonella* infections (WHO, 2024), fluoroquinolones (ciprofloxacin/pefloxacin) and third-generation cephalosporins (cefotaxime), were presented in maps to provide an overview of the geographical distribution of resistance in the EU/EEA. Combined 'microbiological resistance' was presented for *Salmonella* spp. and selected serovars (tables with combined resistance are also available in Annex A.1). In addition, the proportion of ciprofloxacin resistance in *S*. Enteritidis was also presented in a map. For *Campylobacter*, the proportions of human isolates resistant to both critically important antimicrobials for treatment of severe *Campylobacter* infections (WHO, 2024), fluoroquinolones (ciprofloxacin) and macrolides (erythromycin), were presented in maps to provide an overview of the geographical distribution of this combined resistance in the EU/EEA. Combined 'microbiological' resistance (using EUCAST ECOFFs and EUCAST CBPs) were presented for *C. jejuni* and *C. coli*.

Analysis of multidrug resistance

Multidrug resistance (MDR) of human *Salmonella* spp. to nine antimicrobial classes was analysed. Multidrug resistance of an isolate was defined as resistance to at least three different antimicrobial classes (Magiorakos et al., 2012). The antimicrobials included were ampicillin, cefotaxime/ceftazidime, chloramphenicol, ciprofloxacin/pefloxacin/nalidixic acid, gentamicin, meropenem, sulfonamides/sulfamethoxazole, tetracyclines and trimethoprim/trimethoprim-sulfamethoxazole (co-trimoxazole). Resistance to nalidixic acid, ciprofloxacin and pefloxacin were addressed together, as they belong to the same class of antimicrobials: quinolones. Isolates that were non-wild type or I + R to any of these antimicrobials were classified as microbiologically resistant to the class of quinolones. The same method was applied to the two third-generation cephalosporins cefotaxime and ceftazidime. Trimethoprim and co-trimoxazole were also addressed together, as a few countries had only tested for susceptibility to the combination. This approach was considered appropriate because among the countries that provided data on both trimethoprim alone and the combination co-trimoxazole, the proportion of resistant isolates corresponded closely between the two. Multidrug resistance of a *C. jejuni* or *C. coli* isolate was defined as resistance to at least three different antimicrobial classes (Magiorakos et al., 2012). The antimicrobials in the MDR analysis were harmonised between EFSA and ECDC and included ciprofloxacin, erythromycin, gentamicin and tetracycline.

Analysis of ESBL, AmpC and carbapenemase-production in *Salmonella*

All countries reported results from AST of third-generation cephalosporins in 2023. Those which reported findings of ESBL and/or AmpC or non-wild type results to third-generation cephalosporins and ampicillin, were contacted by mail to provide further details on phenotypic and/or genotypic results. Seven countries (Belgium, Croatia, France, Germany, Hungary, Italy and Slovakia) had not tested all presumptive ESBL/AmpC isolates, possibly due to clinical breakpoints being used in routine AST and not ECOFFs. In the case of Belgium, the reason was a shift in methodology in 2023, where phenotypic testing was gradually replaced by WGS.

TABLE A.1 Antimicrobials reported, method used, type of data reported and interpretive criteria applied by MSs for *Salmonella* isolates from humans in 2023.

Country	Gentamicin	Chloramphenicol	Ampicillin	Cefotaxime	Ceftazidime	Meropenem	Tigecycline	Nalidixic acid	Ciprofloxacin/pefloxacin	Azithromycin	Colistin	Sulfonamides	Trimethoprim	Trimethoprim-sulfamethoxazole	Tetracyclines	Method used	Quantitative (Q) or categorical (SIR or PWT/PNWT)	Interpretive criteria
Austria	•	•	•	•	•	•	•	•	•[a]	•		•	•		•	DD	Q	Interpreted by ECDC. EUCAST ECOFFs for all except CLSI CBP for SUL
Belgium	•	•	•	•	•	•	•		•	•		•	•		•	DL	Q	Interpreted by ECDC, as for Austria
Bulgaria	•	•	•	•	•	•	•	•	•	•	•	•	•		•	WGS	PWT/PNWT	Interpreted by ECDC using ResFinder and PointFinder
Croatia	•		•	•	•	•			•[a]					•		DD	Mix of Q & SIR	EUCAST CBP applied to all data
Cyprus	•		•	•	•	•			•		•			•		DL/DLG	Q	Interpreted by ECDC, as for Austria, except for CTX, MEM and SXT where EUCAST CBP were used
Czechia	•	•	•	•	•	•	•		•[a]	•	•		•	•	•	DL/DD	Q	Interpreted by ECDC, as for Austria except, for SXT where no MIC ECOFF available and CBP were used
Denmark	•	•	•	•	•	•	•	•	•	•	•	•	•		•	DL	Q	Interpreted by ECDC, as for Austria
Estonia	•	•	•	•	•	•	•	•	•	•	•	•	•		•	DL	Q	Interpreted by ECDC, as for Austria
Finland	•	•	•	•		•		•	•[a]				•		•	DD	Q	Interpreted by ECDC, as for Austria
France	•	•	•	•	•	•	•	•	•	•	•	•	•		•	DL	Q	Interpreted by ECDC, as for Austria
Germany	•	•	•	•	•	•		•	•				•	•	•	DL	Q	Interpreted by ECDC, as for Austria except, for SXT where no MIC ECOFF available and CBP were used
Greece	•	•	•	•	•	•		•	•[a]	•		•	•		•	DD	Q	Interpreted by ECDC, as for Austria
Hungary	•	•	•	•	•	•			•				•	•	•	DD	SIR	EUCAST CBP except CLSI CBP for TET
Iceland	•	•	•		•	•			•[a]	•			•	•		DD	Q	Interpreted by ECDC, as for Austria

(Continues)

TABLE A.1 (Continued)

Country	Gentamicin	Chloramphenicol	Ampicillin	Cefotaxime	Ceftazidime	Meropenem	Tigecycline	Nalidixic acid	Ciprofloxacin/pefloxacin	Azithromycin	Colistin	Sulfonamides	Trimethoprim	Trimethoprim-sulfamethoxazole	Tetracyclines	Method used	Quantitative (Q) or categorical (SIR or PWT/PNWT)	Interpretive criteria
Ireland	•	•	•	•	•	•	•	•	•	•	•	•	•		•	WGS	PWT/PNWT	Interpreted by ECDC using ResFinder and PointFinder
Italy	•	•	•	•	•	•	•	•	•[a]	•	•	•	•		•	DL/DD	Q	Interpreted by ECDC, as for Austria
Latvia	•	•	•	•	•	•	•	•	•	•	•	•	•		•	WGS	PWT/PNWT	Interpreted by ECDC using ResFinder and PointFinder
Lithuania	•	•	•	•	•	•			•				•	•		DL/DD	SIR	EUCAST CBP
Luxembourg	•	•	•	•	•	•			•[a]					•	•	DD/DLG	Q	Interpreted by ECDC, as for Austria
Malta	•		•	•	•	•			•[a]		•					DL/DD/DLG	Q	Interpreted by ECDC, as for Austria, except for CTX and MEM where EUCAST CBP were used
Netherlands	•	•	•	•	•	•	•	•	•	•	•	•	•		•	DL	Q	Interpreted by ECDC, as for Austria
Norway		•	•	•	•	•			•[a]						•	DD	Q	Interpreted by ECDC, as for Austria
Poland	•	•	•	•	•	•	•	•	•	•	•	•	•		•	DL/DD	Q	Interpreted by ECDC, as for Austria
Portugal	•	•	•	•	•	•	•	•	•[a]	•		•	•	•	•	DD	Q	Interpreted by ECDC, as for Austria
Romania	•	•	•	•	•	•		•	•[a]				•	•	•	DD	Q	Interpreted by ECDC, as for Austria.
Slovakia		•	•	•	•	•			•					•	•	DD/DL	SIR	EUCAST CBP except CLSI CBP for TET
Slovenia	•	•	•	•	•	•			•[a]			•	•	•	•	DD/DLG	Q	Interpreted by ECDC, as for Austria
Spain	•	•	•	•	•	•		•	•[a]			•	•		•	DD	Q	Interpreted by ECDC, as for Austria
Sweden	•	•	•	•	•	•	•	•	•	•	•	•	•		•	WGS	PWT/PNWT	Interpreted by ECDC using ResFinder and PointFinder

Abbreviations: AST, antimicrobial susceptibility testing; CBP, clinical breakpoint; CLSI, Clinical and Laboratory Standards Institute; CTX, cefotaxime; DD, disk diffusion; DL, dilution; DLG, dilution with gradient strip; ECDC, European Centre for Disease Prevention and Control; ECOFF, epidemiological cut-off; EUCAST, European Committee on Antimicrobial Susceptibility Testing; MEM, meropenem; NAL, nalidixic acid; PWT/PNWT, predicted wild type/predicted non-wild type (categorical); Q, quantitative data; SIR, susceptible standard dosing regimen, susceptible increased exposure, resistant (categorical data); SUL, sulfonamides; TET, tetracycline; WGS, whole genome sequencing.

[a]Pefloxacin used in disk diffusion.

TABLE A.2 Antimicrobials reported, method used, type of data reported and interpretive criteria applied by MSs for *Campylobacter* isolates from humans in 2023.

Country	Gentamicin	Co-amoxiclav	Ciprofloxacin	Erythromycin	Tetracyclines	Method used	Quantitative (Q) or categorical (SIR)	Interpretive criteria
Austria	•		•	•	•	DL	Q	Interpreted by ECDC. EUCAST ECOFF (CIP, ERY, GEN, TET)
Bulgaria	•	•	•	•	•	WGS	PWT/PNWT	Interpreted by ECDC using ResFinder and PointFinder
Croatia	•	•	•	•	•	WGS	PWT/PNWT	Interpreted by ECDC, as for Bulgaria
Cyprus			•	•	•	DD	Q	Interpreted by ECDC, as for Austria.
Denmark	•		•	•	•	DL	Q	Interpreted by ECDC, as for Austria.
Estonia	•		•	•	•	DL	Q	Interpreted by ECDC, as for Austria.
Finland			•	•	•	DD/DLG	Q	Interpreted by ECDC, as for Austria.
France	•	•	•	•	•	DD	SIR	EUCAST CBP (CIP, ERY, TET), CA-SFM CBP (AMC, GEN)
Germany	•		•	•	•	DL	Q	Interpreted by ECDC, as for Austria
Greece	•	•	•	•	•	DD	Q	Interpreted by ECDC, plus CA-SFM CBP 2023 (AMC)
Hungary			•	•	•	No information	SIR	No information available.
Iceland			•	•	•	DD	Q	Interpreted by ECDC, as for Austria.
Ireland			•	•	•	WGS	PWT/PNWT	Interpreted by IE using ResFinder and BioNumerics
Italy	•		•	•	•	DD	Q	Interpreted by ECDC, as for Austria.
Latvia	•	•	•	•	•	WGS	PWT/PNWT	Interpreted by ECDC, as for Bulgaria
Lithuania			•	•	•	DD	SIR	EUCAST CBP
Luxembourg	•		•	•	•	DD	Q	Interpreted by ECDC, as for Greece.
Malta	•	•	•	•	•	DLG/DL	Q	Interpreted by ECDC, as for Greece.
Netherlands	•		•	•	•	WGS	PWT/PNWT	Interpreted by NL using in-house pipeline based on PointFinder and Resfinder.

(Continues)

TABLE A.2 (Continued)

Country	Gentamicin	Co-amoxiclav	Ciprofloxacin	Erythromycin	Tetracyclines	Method used	Quantitative (Q) or categorical (SIR)	Interpretive criteria
Norway	•		•	•	•	DLG	Q	Interpreted by ECDC, as for Austria.
Poland	•		•	•	•	DL/DLG	Q	Interpreted by ECDC, as for Austria.
Portugal	•		•	•	•	DD	Q	Interpreted by ECDC, as for Austria.
Romania			•	•	•	DD	Q	Interpreted by ECDC, as for Austria.
Slovakia	•	•	•	•	•	No information	SIR	No information available.
Slovenia			•	•	•	DD/DL	Q	Interpreted by ECDC, as for Austria.
Spain	•		•	•	•	DL	Q	Interpreted by ECDC, as for Austria.

Abbreviatios: AMC, amoxicillin/clavulanate; AST, antimicrobial susceptibility testing; CA-SFM, French Society for Microbiology; CBP, clinical breakpoint; CIP, ciprofloxacin; DD, disk diffusion; DL, dilution; DLG, dilution with gradient strip; ECDC, European Centre for Disease Prevention and Control; ECOFF, epidemiological cut-off; ERY, erythromycin; EUCAST, European Committee on Antimicrobial Susceptibility Testing; GEN, gentamicin; MSs, Member States; PWT/PNWT, predicted wild type/predicted non-wild type (categorical); Q, quantitative data; SIR, susceptible standard dosing regimen/susceptible increased exposure/resistant (categorical data); TET, tetracycline; WGS, whole genome sequencing.

TABLE A.3 Proportion of tested *Salmonella* spp. isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country, 2023.

	Total *Salmonella* tested	Travel-associated	Domestic	Unknown
Country	***N***	**%**	**%**	**%**
Austria	1221	0.0	0.0	100.0
Belgium	449	10.5	16.5	73.1
Bulgaria	57	0.0	0.0	100.0
Croatia	1141	0.0	0.0	100.0
Cyprus	124	0.0	0.0	100.0
Czechia	205	11.7	83.9	4.4
Denmark	617	42.8	57.2	0.0
Estonia	182	9.9	68.1	22.0
Finland	135	7.4	92.6	0.0
France	1328	14.2	17.4	68.4
Germany	3651	2.4	97.6	0.0
Greece	434	0.0	0.0	100.0
Hungary	1970	0.5	99.5	0.0
Ireland	333	35.4	36.9	27.6
Italy	1694	1.0	3.9	95.1
Latvia	71	11.3	88.7	0.0
Lithuania	336	7.4	92.6	0.0
Luxembourg	157	39.5	34.4	26.1
Malta	52	0.0	0.0	100.0
Netherlands	1443	14.0	0.0	86.0
Poland	484	0.0	0.0	100.0
Portugal	611	0.0	5.7	94.3
Romania	126	0.0	0.0	100.0
Slovakia	1210	1.7	98.3	0.0
Slovenia	297	4.7	35.4	59.9
Spain	2072	0.1	74.7	25.1
Sweden	570	12.3	86.1	1.6
Total (27 MSs)	**20,970**	**5.7**	**50.5**	**43.8**
Iceland	55	32.7	30.9	36.4
Norway	398	38.4	47.0	14.6

Abbreviations: MSs, Member States; *N*, number of isolates tested.

TABLE A.4 Proportion of tested *Campylobacter jejuni* and *C. coli* isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country in 2023.

	Total *C. jejuni* & *C. coli* tested	Travel-associated	Domestic	Unknown
Country	**N**	**%**	**%**	**%**
Austria	499	3.6	89.6	6.8
Bulgaria	24	0.0	0.0	100.0
Croatia	40	0.0	0.0	100.0
Cyprus	50	0.0	0.0	100.0
Denmark	335	20.6	79.4	0.0
Estonia	290	2.8	50.7	46.6
Finland	1481	0.0	0.0	100.0
France	7506	0.0	0.0	100.0
Germany	1328	0.5	99.5	0.0
Greece	184	0.0	0.0	100.0
Hungary	1915	0.4	99.6	0.0
Ireland	257	0.8	3.5	95.7

(Continues)

TABLE A.4 (Continued)

	Total *C. jejuni* & *C. coli* tested	Travel-associated	Domestic	Unknown
Country	**N**	**%**	**%**	**%**
Italy	181	2.8	13.3	84.0
Latvia	4	0.0	0.0	100.0
Lithuania	546	0.9	99.1	0.0
Luxembourg	233	0.0	0.0	100.0
Malta	183	0.0	0.0	100.0
Netherlands	446	10.1	0.0	89.9
Poland	50	2.0	72.0	26.0
Portugal	648	0.0	100.0	0.0
Romania	10	0.0	100.0	0.0
Slovakia	1746	0.9	99.1	0.0
Slovenia	995	4.5	37.8	57.7
Spain	626	0.0	43.9	56.1
Total (24 MSs)	**19,577**	**1.2**	**39.5**	**59.3**
Iceland	127	47.2	28.3	24.4
Norway	363	37.7	46.8	15.4

Abbreviations: MSs, Member States; *N*, number of isolates tested.

Antimicrobial susceptibility data from animals and food in 2022–2023

Data reported under Directive 2003/99/EC, Commission Implementing Decision (EU) 2020/1729

EU MSs reported mandatory data collected following AMR monitoring programs during 2022 and 2023. 'Directive 2003/99/EC requires Member States to ensure that monitoring provides comparable data on the occurrence of antimicrobial resistance ('AMR') in zoonotic agents and, in so far as they present a threat to public health, other agents'. 'Directive 2003/99/EC also requires Member States to assess the trends and sources of AMR in their territory and to transmit a report every year covering data collected in accordance with that Directive to the Commission.' Furthermore, some non-MSs reported AMR data and some EU MSs and non-MSs also reported voluntary data from samples that were not included in the mandatory programmes per reporting year.

The Commission Implementing Decision (EU) 2020/1729 of 17 November 2020 lays down the rules for antimicrobial resistance monitoring performed from 2021 onwards. This Decision specifies harmonised rules for the period 2021–2027 for the monitoring and reporting of AMR to be carried out by MSs in accordance with EU Regulations. It also determines specific technical requirements for AMR testing and reporting in relation to sampling in food-producing animals and derived meat (at retail and at border control posts). The new legislation also authorises WGS as an alternative method to extended phenotypic testing of isolates with resistance to third-generation cephalosporins and/or carbapenems. The new rules apply until December 2027.

The Commission Implementing Decision (EU) 2020/1729 indicates that the monitoring and reporting of AMR shall cover the following bacteria: (a) *Salmonella* spp.; (b) *Campylobacter coli* (*C. coli*); (c) *Campylobacter jejuni* (*C. jejuni*); (d) Indicator commensal *Escherichia coli* (*E. coli*); (e) *Salmonella* spp. and *E. coli* producing the following enzymes: (i) Extended-spectrum beta-Lactamases (ESBL); (ii) AmpC beta-Lactamases (AmpC); (iii) Carbapenemases (CPs). Therefore, during 2022 and 2023, AMR data were collected from the bacteria listed above.

Countries may also report AMR data from other agents of public health importance such as methicillin-resistant *Staphylococcus aureus* (MRSA). According to Commission Implementing Decision (EU) 2020/1729 the monitoring and reporting of AMR may also cover indicator commensal *Enterococcus faecalis* (*E. faecalis*) and *Enterococcus faecium* (*E. faecium*).

A scientific report published by EFSA in 2019 included technical specifications on the harmonised monitoring and reporting of antimicrobial resistance in MRSA in food-producing animals and food (EFSA, 2019). Detailed rules were specified for harmonised monitoring and reporting on the prevalence of resistant microorganisms in food-producing animals and food, in particular as regards the microorganisms to be included, the origin of the isolates, the number of isolates to be tested, the antimicrobial susceptibility tests to be used, the specific monitoring of MRSA and ESBL-/AmpC-/CP-producing bacteria and the collection and reporting of the data. Comparison between human data and data from food-producing animals and the food sector was ensured by the involvement of ECDC.

The Commission Implementing Decision (EU) 2020/1729 specifies that the monitoring and reporting of AMR shall cover the following food-producing animal populations and food: (a) broilers; (b) laying hens; (c) fattening turkeys; (d) bovine animals under 1 year of age; (e) fattening pigs; (f) fresh meat from broilers; (g) fresh meat from turkeys; (h) fresh meat from pigs; (i) fresh meat from bovine animals. Fresh meat includes meat sampled at retail and imported meat from third countries sampled at border control posts (BCPs). This European Commission Decision indicates the sampling frequency for MSs to

carry out the AMR monitoring and reporting in accordance with the following rotational system: (a) In the years 2021, 2023, 2025 and 2027: in fattening pigs, bovine animals under 1 year of age, pig meat and bovine meat. (b) In the years 2022, 2024 and 2026: in laying hens, broilers, fattening turkeys and fresh meat derived from broilers and turkeys.

Therefore, following relevant EU legislation, AMR data presented in this Report were collected from poultry populations and derived meat thereof in 2022 and from pigs and cattle under 1 year of age in 2023.

The Commission Implementing Decision (EU) 2020/1729 lays down detailed rules for sampling design and sample size as well as for antimicrobial susceptibility testing for the different bacteria. This European Commission Decision indicates the analytical methods for detection and antimicrobial susceptibility testing that shall be performed by the laboratories referred to in Article 3(2). AMR testing shall be performed by using the broth microdilution method according to the reference method ISO 20776-1:2019.

For AMR testing, isolates were obtained through harmonised national programmes. The broth microdilution testing method was widely used for susceptibility testing following EU legislation.

The resulting quantitative isolate-based data were reported to EFSA and considered for this report. Resistance was interpreted using EUCAST ECOFF values (see text box below for further information). The antimicrobials incorporated in this report were selected based on their public health relevance and as representatives of different antimicrobial classes. Data on MRSA and other microorganisms apart from those required by legislation were reported on a voluntary basis.

Harmonised representative sampling and monitoring

Representative sampling and AMR monitoring should be performed following the current legislation and the technical specifications published by EFSA (EFSA, 2019). Regulation (EC) No 2073/200533 Article 4 indicates that: 'Food business operators shall perform testing as appropriate against the microbiological criteria set out in Annex I, when they are validating or verifying the correct functioning of their procedures based on HACCP principles and good hygiene practice.'

***Salmonella* spp.**

The Commission Implementing Decision (EU) 2020/1729 lays down rules for antimicrobial resistance monitoring performed from 2021 onwards. The Commission Implementing Decision (EU) 2020/ 1729 determines specific technical requirements for AMR testing and reporting in relation to sampling in food-producing animals and derived meat (at retail and at border control posts). In 2022, MSs collected representative *Salmonella* spp. isolates for AMR monitoring from the populations of broilers, laying hens and fattening turkeys sampled following the *Salmonella* National Control Programmes (NCPs) set up in accordance with Article 5(1) of the Regulation (EC) No. 2169/2003. For the purposes of sampling design and representativeness, no more than one isolate per *Salmonella* serovar from the same epidemiological unit (herd/holding/flock of birds) per year should be included in the AMR monitoring programme. Moreover, samples of imported fresh meat from broilers and fattening turkeys were collected at the border control posts. In most MSs, the isolates tested for AMR formed a representative subsample of the total *Salmonella* isolates available at the National Reference Laboratory (NRL) and/or other laboratories involved. The sampling was performed in such a way as to ensure geographical representativeness and even distribution throughout the year. However, when sampling from low prevalence areas, all the *Salmonella* isolates available should be tested for susceptibility.

In 2023, MSs collected representative *Salmonella* spp. isolates for AMR monitoring from samples of caecal content taken at slaughter from cattle under 1 year of age where the production of meat thereof was more than 10,000 tonnes per year sampled for testing and verification of compliance, in accordance with point 2.1.3 of chapter 2 of Annex I of Regulation (EC) No 2073/2005. Also in 2023, representative *Salmonella* isolates for AMR monitoring were obtained by MSs from samples of caecal content taken at slaughter from fattening pigs sampled for testing and verification of compliance, in accordance with point 2.1.4 of chapter 2 of Annex I of Regulation (EC) No 2073/2005. In compliance with EU legislation and EFSA guidelines, MSs sampled the caecal contents of fattening pigs and of cattle under 1 year of age at the slaughterhouse. MSs employed a two-stage stratified sampling design (with slaughterhouses as primary sampling units and carcases as secondary units) based on proportional allocation of the number of samples to the annual throughput of the slaughterhouse.

***Campylobacter* spp.**

The Commission Implementing Decision (EU) 2020/1729 lays down rules for antimicrobial resistance monitoring performed from 2021 onwards.

Regarding AMR testing of *C. coli* and *C. jejuni* isolated from different animal species (depending on the year), the Commission Implementing Decision (EU) 2020/1729 specifies where the isolates shall be obtained from (referred to in point 1(b)(i) to (iv)). MSs shall test at least 170 isolates of the nationally most prevalent species of *Campylobacter* (among *C. coli* and *C. jejuni*) obtained from samples referred to in point 1(b)(i) to (iii) or, for Member States making use of the derogation referred to in the second paragraph of point 3(1)(b), all isolates obtained from these samples. By way of derogation, where Member States have a national annual production of less than 100,000 tonnes of broiler meat, they may decide to test a minimum of 85 isolates instead of 170 isolates. MSs shall also test up to 170 isolates of the nationally less prevalent species of *Campylobacter* (among *C. coli* and *C. jejuni*) identified while recovering the isolates of the most prevalent *Campylobacter* species obtained from samples referred to in point 1(b)(i) to (iii). Moreover, MSs shall test at least 170 isolates of *C. coli*

obtained from samples referred to in point 1(b)(iv) or, for Member States making use of the derogation referred to in the second paragraph of point 3(1)(b), all isolates obtained from these samples. By way of derogation, where Member States have a national annual production of less than 100,000 tonnes of pig meat, they may decide to test a minimum of 85 isolates instead of 170 isolates.

In 2022, MSs collected at least 170 isolates of the nationally most prevalent species of *Campylobacter* (*C. coli* and *C. jejuni)* from samples obtained from broilers and fattening turkeys following regulations and technical requirements for AMR testing, and up to 170 isolates of the least prevalent *Campylobacter* species (among *C. coli* and *C. jejuni*). The sample collection was approximately evenly distributed over the year 2022. One representative caecal sample (pooled) per epidemiological unit (i.e. batch of birds sent to the slaughterhouse) was gathered to account for clustering. Isolates were recovered from caecal samples in accordance with EFSA's recommendations (EFSA, 2019, 2020).

In 2023, MSs collected at least 170 isolates of the nationally most prevalent species of *Campylobacter* (*C. coli* and *C. jejuni*) from samples obtained from cattle under 1 year of age and up to 170 isolates of the nationally least prevalent *Campylobacter* species following regulations and technical requirements for AMR testing. Moreover, MSs collected at least 170 isolates of *C. coli* from samples obtained from fattening pigs and voluntarily up to 170 isolates from *C. jejuni* following regulations and technical requirements for AMR testing. The sample collection was approximately evenly distributed over the year 2023. One representative caecal sample (single) per epidemiological unit (i.e. batch of animals sent to the slaughterhouse) was gathered to account for clustering. Isolates were recovered from caecal samples (single) in accordance with EFSA's recommendations (EFSA, 2019, 2021).

Indicator commensal *E. coli*

Routine monitoring of indicator commensal *E. coli*

Indicator commensal *E. coli* isolates were collected by MSs as part of their national AMR monitoring programme according to the provisions of the Commission Implementing Decision (EU) 2020/1729. In 2023, MSs collected indicator *E. coli* isolates based on random sampling of caecal samples gathered at slaughter from fattening pigs and cattle under 1 year of age where the production of cattle meat in the MSs is more than 10,000 tonnes slaughtered per year as specified in Annex Part A paragraph 1(c) (iv). In 2022, MSs collected indicator *E. coli* isolates based on random sampling of caecal samples gathered at slaughter from broilers and fattening turkeys where the production of turkey meat in the MSs is more than 10,000 tonnes slaughtered per year as specified in Annex Part A paragraph 1(c) (ii). One representative caecal sample (single or pooled) per epidemiological unit (herds), was gathered to account for clustering. Isolates were recovered from caecal samples (single or pooled), in accordance with regulations and EFSA's recommendations (EFSA, 2019, 2020).

As per Regulations, MSs shall test at least 170 isolates obtained from samples referred to in points 1(c)(i-iv). By way of derogation, where MSs have a national annual production of less than 100,000 tonnes of pig meat, less than 100,000 tonnes of broiler meat or less than 100,000 tonnes of turkey meat, they may test a minimum of 85 isolates instead of 170 isolates for each specific animal population (depending on the mandatory testing every year).

A two-stage stratified sampling design was applied in the reporting countries, with slaughterhouses as primary sampling units and carcases as secondary units, accounting for proportional allocation of the number of samples to the annual throughput of the slaughterhouse. Only one representative caecal sample (single or pooled) per epidemiological unit (batch of carcases deriving from the same flock), was gathered to account for clustering. Isolates were recovered from caecal contents samples (single or pooled), in accordance with EFSA's recommendations (EFSA, 2019). The sample collection was approximately evenly distributed over the respective years.

Specific monitoring of ESBL-, AmpC- and/or CP-producing *Escherichia coli*

In 2023, MSs obtained caecal samples from fattening pigs and cattle under 1 year of age at slaughter, in those MSs where the production of cattle meat was more than 10,000 tonnes slaughtered per year. Moreover, samples of fresh meat from pigs and bovines were collected at retail and at border control posts. In 2022, MSs collected caecal samples from broilers and fattening turkeys at slaughter, where the production of turkey meat was more than 10,000 tonnes slaughtered per year, and samples of fresh meat from broilers and turkeys gathered at retail and at border control posts. Only one representative caecal sample (single or pooled) per epidemiological unit (batch of carcases deriving from the same herd/flock), was collected to account for clustering. Isolates were recovered from caecal contents samples (single or pooled), in accordance with relevant Regulations and EFSA's recommendations (EFSA, 2014, 2019, 2020). The sample collection as described above was approximately evenly distributed over the years 2022 and 2023. The same sampling design was used to collect indicator *E. coli* isolates, whether dedicated to the routine monitoring of AMR or the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*.

Epidemiological cut-off values (ECOFFs) and clinical breakpoints (CBPs)

A microorganism is defined as 'clinically' resistant when the degree of resistance shown is associated with a high likelihood of therapeutic failure. The microorganism is categorised as resistant by applying the appropriate CBP in a defined phenotypic test system, and this breakpoint may alter with legitimate changes in circumstances (for example alterations in dosing regimen, drug formulation and/or patient factors). A microorganism is defined as wild type for a bacterial species when no acquired or mutational resistance mechanisms are present to the antimicrobial in question. A microorganism is categorised as wild type for a given bacterial species when presenting a lower MIC to the antimicrobial in question than the appropriate ECOFF in a defined phenotypic test system. This cut-off value will not be altered by changing circumstances (such as alterations in frequency of antimicrobial administration). Wild-type microorganisms may or may not respond clinically to antimicrobial treatment. A microorganism is defined as non-wild type for a given bacterial species by the presence of an acquired or mutational resistance mechanism to the antimicrobial in question. A microorganism is categorised as non-wild type for a given bacterial species by applying the appropriate ECOFF value in a defined phenotypic test system; non-wild type organisms are considered to show 'microbiological' resistance (as opposed to 'clinical' resistance). CBPs and ECOFFs may be the same, although it is often the case that the ECOFF is lower than the CBP. EUCAST has defined CBPs and ECOFFs.

Clinical breakpoints (clinical resistance)

The clinician, or veterinarian, choosing an antimicrobial agent to treat humans or animals for a bacterial infection requires information that the antimicrobial selected is effective against the bacterial pathogen. Such information will be used, together with clinical details such as the site of infection, ability of the antimicrobial to reach the site of infection, formulations available and dosage regimes, when determining an appropriate therapeutic course of action. In 2019, EUCAST updated their definitions of susceptibility testing categories susceptible (S), intermediate (I) and resistant (R) (EUCAST, 2019). The updated definitions are as follows;

S: Susceptible, standard dosage regimen: when there is a likelihood of therapeutic success using a standard dosing regimen of the agent.

I: Susceptible, increased exposure: when there is a high likelihood of therapeutic success because exposure to the agent is increased adjusting the dosing regimen or by its concentration at the site of infection.

R: Resistant: when there is a high likelihood of therapeutic failure even when there is increased exposure.

The in vitro susceptibility of the bacterial pathogen can be determined and CBPs used to ascertain whether the organism is likely to respond to treatment. CBPs will take into account the distribution of the drug in the tissues of the body following administration and assume that a clinical response will be obtained if the drug is given as recommended and there are no other adverse factors which affect the outcome. Different dosing regimens can lead to the development of different CBPs, as occurs in some countries for certain antimicrobials where different therapeutic regimes are in place. Although the rationale for the selection of different CBPs may be clear, their use makes the interpretation of results from different countries problematic, as the results are not directly comparable between those different countries.

Epidemiological cut-off values (microbiological resistance)

For a given bacterial species, the pattern of the MIC distribution (i.e. the frequency of occurrence of each given MIC plotted against the MIC value) can enable the separation of the wild type population of microorganisms from those populations that show a degree of acquired resistance. The wild type susceptible population is assumed to have no acquired or mutational resistance and commonly shows a normal distribution. When bacteria acquire resistance by a clearly defined and efficient mechanism, such as a plasmid bearing a gene which produces an enzyme destroying the antimicrobial, the MIC distribution commonly shows two major subpopulations. One is a fully susceptible normal distribution of isolates and the other a resistant population which has acquired the resistance mechanism. Resistance may be achieved by a series of small steps, such as changes in the permeability of the bacterial cell wall to the antimicrobial or other mechanisms which confer a degree of resistance. In this case, there may be populations of organisms which occur lying between the fully susceptible population and more resistant populations. The ECOFF value indicates the MIC or zone diameter above which the pathogen has some detectable reduction in susceptibility. ECOFFs are derived by testing an adequate number of isolates to ensure that the wild type population can be confidently identified for a given antimicrobial. The clinical breakpoint, which is set to determine the therapeutic effectiveness of the antimicrobial, may fail to detect emergent resistance. Conversely, the ECOFF detects any deviation in susceptibility from the wild-type population, although it may not be appropriate for determining the likelihood of success or failure for clinical treatment.

MRSA

MRSA isolates may have been collected by reporting countries using different monitoring approaches, either by active surveillance and monitoring of animals and foods or, in some cases, by passive monitoring (for example based on diagnostic submission of samples from clinical cases of disease in animals or from foods sampled as part of investigatory work). Furthermore, countries may apply different sampling strategies and collect different types of samples from different animal populations and food matrices. Isolation methods also differ between countries.

Harmonised antimicrobial susceptibility testing

Routine monitoring antimicrobial susceptibility

MSs followed Commission Implementing Decision (EU) 2020/1729 and recommendations from EFSA regarding the use of epidemiologic cut-off values for AMR monitoring. MSs tested antimicrobials and interpreted the results using the ECOFFs and concentration ranges shown in tables F.5 and F.6 to determine the susceptibility of the following microorganisms: *Salmonella* spp., *C. coli*, *C. jejuni* and indicator commensal *E. coli*. Under the new legislation (Commission Implementing (EU) 2020/1729), changes were made to the ECOFFs and clinical breakpoints for several antimicrobial substances included in the harmonised panel for testing of *Salmonella* spp. and *E. coli*. The substances with changes to ECOFFs and or clinical breakpoints included tigecycline, nalidixic acid and ciprofloxacin (table F.5). Since 2021, data from pigs, calves, poultry and meat from BCPs, the occurrence of resistance to tigecycline, nalidixic acid and ciprofloxacin is determined using the new ECOFFs and clinical breakpoints. Also, in 2021, a new substance, amikacin, was added to the harmonised panel for both *Salmonella* spp. and *E. coli*. For *Campylobacter* spp., no changes were made to ECOFFs and clinical breakpoints for the substances included in the harmonised panel. However, two new substances were added (chloramphenicol and ertapenem) and two substances were removed (nalidixic acid and streptomycin).

Presumptive ESBL-/AmpC-/CP-producing *E. coli* identified through the specific monitoring, as well as presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. and *E. coli* from the routine monitoring should be further tested with a second panel of antimicrobial substances (table F.**7**) or investigated using WGS. The second panel includes cefoxitin, cefepime and clavulanic acid in combination with cefotaxime and ceftazidime for the detection of presumptive ESBL- and AmpC-producing isolates. Moreover, the second panel contains imipenem, meropenem and ertapenem to phenotypically verify presumptive CP-producers.

Specific monitoring of ESBL-, AmpC- and/or CP-producing *E. coli*

To isolate presumptive ESBL-/AmpC-/CP-producing *E. coli* in the specific monitoring, samples were first subjected to a non-selective pre-enrichment step followed by inoculation on selective MacConkey agar. The selective agar contains 1 mg/L cefotaxime, in accordance with the detailed protocol for standardisation of the EU Reference Laboratory for Antimicrobial Resistance (EURL-AR).[42] Following this protocol, presumptive CP-producing isolates can also be recovered. If available, one presumptive ESBL-/AmpC-/CP-producing *E. coli* isolate obtained from each positive caecal sample and meat sample was tested for its antimicrobial susceptibility to the first panel of antimicrobials (Table A.5). This step was performed to confirm the microbiological resistance to cefotaxime (expected as the antimicrobial is present in the isolation medium at a concentration higher than the ECOFF), as well as to identify possible resistance to cefotaxime and/or ceftazidime and/or meropenem. In a second step, the isolate should be tested using the second panel of antimicrobials (Table A.6) to infer the presumptive ESBL-/AmpC-/CP-producing phenotypes according to the beta-lactams resistance phenotypes obtained (Figure A.3). WGS can be used as a replacement for the phenotypic testing of presumptive ESBL-/AmpC-/CP-producing *E. coli* from the specific monitoring.

Specific monitoring of CP-producing microorganisms

From 2021, the specific monitoring of CP-producing microorganisms is mandatory. For the specific monitoring of CP-producing microorganisms, isolation required the use of non-selective pre-enrichment and subsequent selective plating on carbapenem-containing media, in accordance with the most recent version of the detailed protocol of the EURL-AR. The microbial species was identified using appropriate methods. If available, one presumptive CP-producing isolate (primarily ***E. coli***, but also ***Salmonella***) obtained from each positive caecal sample and meat sample should be tested for its antimicrobial susceptibility to the first panel of antimicrobials (Table A.5) to confirm the microbiological resistance to meropenem and to identify possible resistance to other antimicrobials such as cefotaxime and/or ceftazidime. In a second step, the isolate should be tested against the second panel of antimicrobials (Table A.7) to infer the presumptive CP-producer phenotype according to the beta-lactam resistance phenotypes obtained (Figure A.3). The EUCAST epidemiological cut-off values applied for the antimicrobial susceptibility testing (Tables A.5–A.7) are based on Commission Implementing Decision (EU) 2020/1729.

[42]Available online:www.eurl-ar.eu.

TABLE A.5 Panel of antimicrobial substances included in AMR monitoring, thresholds for interpreting resistance and concentration ranges tested in *Salmonella* spp. and indicator commensal *E. coli* (first panel) based on Commission Implementing Decision (EU) 2020/1729 and EFSA Technical Report 2021.

Antimicrobial	*Salmonella* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	*E. coli* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	Concentration range, mg/L (no. of wells)
Amikacin	> 4[a]	> 8	4–128 (6)
Ampicillin	> 8	> 8	1–32 (6)
Azithromycin	NA[b]	NA[b]	2–64 (6)
Cefotaxime	> 0.5	> 0.25	0.25–4 (5)
Ceftazidime	> 2	> 0.5	0.25–8 (6)
Chloramphenicol	> 16	> 16	8–64 (4)
Ciprofloxacin	> 0.06	> 0.06	0.015–8 (10)
Colistin	NA[c]	> 2	1–16 (5)
Gentamicin	> 2	> 2	0.5–16 (6)
Meropenem	> 0.125	> 0.125	0.03–16 (10)
Nalidixic acid	> 8	> 8	4–64 (5)
Sulfamethozaxole	NA[d]	> 64	8–512 (7)
Tetracycline	> 8	> 8	2–32 (5)
Tigecycline	NA[e]	NA[e]	0.25–8 (6)
Trimethoprim	> 2	> 2	0.25–16 (7)

Abbreviations: AMR, antimicrobial resistance; ECOFFs, epidemiological cut-off values; EUCAST, European Committee on Antimicrobial Susceptibility Testing; NA, not available.

[a]EUCAST epidemiological cut-off (ECOFF) value for *Salmonella* is tentative.

[b]UCAST epidemiological cut-off (ECOFF) not available, > 16 mg/L was used.

[c]EUCAST epidemiological cut-off (ECOFF) value for *Salmonella* spp. not available, > 2 mg/L was used.

[d]EUCAST epidemiological cut-off (ECOFF) not available, > 256 mg/L was used.

[e]EUCAST epidemiological cut-off (ECOFF) not available, > 0.5 mg/L was used.

*EUCAST epidemiological cut-off values. '>' than the ECOFF, criteria used to determine microbiological resistance.

TABLE A.6 Panel of antimicrobial substances included in AMR monitoring, thresholds for interpreting resistance and concentration ranges tested in *C. jejuni* and *C. coli* based on Commission Implementing Decision (EU) 2020/1729 and EFSA Technical Report 2021.

Antimicrobial	*C. jejuni* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	*C. coli* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	Concentration range, mg/L (no. of wells)
Chloramphenicol	> 16	> 16	2–64 (6)
Ciprofloxacin	> 0.5	> 0.5	0.12–32 (9)
Ertapenem	> 0.5	> 0.5	0.125–4 (6)
Erythromycin	> 4	> 8	1–512 (10)
Gentamicin[a]	> 2	> 2	0.12–16 (7)
Tetracycline	> 1	> 2	0.5–64 (8)

Abbreviations: AMR, antimicrobial resistance; ECOFFs, epidemiological cut-off values; EUCAST, European Committee on Antimicrobial Susceptibility Testing.

[a]The updated EUCAST epidemiological cut-off (ECOFF) value for both species is at 1 mg/L.

*EUCAST epidemiological cut-off values. '>' than the ECOFF, criteria used to determine microbiological resistance.

TABLE A.7 Panel of antimicrobial substances, EUCAST ECOFFs and concentration ranges used for testing *Salmonella* spp. and indicator commensal *E. coli* isolates resistant to cefotaxime, ceftazidime or meropenem (second panel).

Antimicrobial	*Salmonella* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	*E. coli* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	Concentration range, mg/L (no. of wells)
Cefepime[a]	> 0.125	> 0.125	0.06–32 (10)
Cefotaxime	> 0.5	> 0.25	0.25–64 (9)
Cefotaxime + clavulanic acid	> 0.5	> 0.25	0.06–64 (11)
Cefoxitin	> 8	> 8	0.5–64 (8)
Ceftazidime	> 2	> 0.5	0.25–128 (9)
Ceftazidime + clavulanic acid	> 2	> 0.5	0.125–128 (11)

(Continues)

TABLE A.7 (Continued)

Antimicrobial	*Salmonella* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	*E. coli* EU surveillance 2022/2023 EUCAST ECOFF* (mg/L)	Concentration range, mg/L (no. of wells)
Ertapenem[b]	> 0.06	> 0.06	0.015–2 (8)
Imipenem	> 1	> 0.5	0.12–16 (8)
Meropenem	> 0.125	> 0.125	0.03–16 (10)
Temocillin	> 16	> 16	0.5–128 (9)

Abbreviations: AMR, antimicrobial resistance; ECOFFs, epidemiological cut-off values; EUCAST, European Committee on Antimicrobial Susceptibility Testing.

[a]EUCAST epidemiological cut-off (ECOFF) value for *E. coli* is 0.25 mg/L.

[b]EUCAST epidemiological cut-off (ECOFF) value for *E. coli* is tentative 0.03 mg/L.

*EUCAST epidemiological cut-off values. '>' than the ECOFF, criteria used to determine microbiological resistance.

Data validation

Validation against business rules

The reported data were first validated automatically by a series of 'business rules', applied in the EFSA data collection system. This process constitutes the first validation of incoming data. The positive result of the automatic validation process makes the data available for further steps of validation performed by EFSA.

Scientific data validation

The scientific validation of the data collected by the MSs and non-MSs and submitted to EFSA consisted of the data reviewing and making comparisons between data reported for the same antimicrobials when tested by different panels. Special attention was given to carbapenems, colistin, azithromycin and tigecycline and to possible discrepancies between results for antimicrobials present in both panels (i.e. cefotaxime, ceftazidime, meropenem). MSs were contacted by EFSA asking for clarifications. If necessary, MSs were asked to confirm the MIC results and the species identification of the reported isolates.

Reference testing

To ensure the quality of the data submitted, a reference testing exercise was run by the EURL-AR in close collaboration with the MSs. The exercise consisted in re-doing the AST of the isolates received using both Panel 1 and Panel 2 of antimicrobials, as well as WGS analyses of the isolates. Based on the data submitted to EFSA, a selection of 362 isolates was made in 2022 and 330 isolates in 2023. The selection of these isolates was based on different criteria:

- Isolates not showing resistance to any of the tested substances.
- *Escherichia coli* isolates showing resistance to colistin (MIC > 2 mg/L).
- *Salmonella* spp. and *E. coli* isolates showing high resistance to amikacin (MIC > 128 mg/L).
- *Salmonella* spp. and *E. coli* isolates showing resistance to both gentamicin (MIC > 16 mg/L) and amikacin (MIC > 128 mg/L).
- *Salmonella* spp. and *E. coli* isolates showing resistance to tigecycline (MIC > 0.5) but susceptibility to tetracycline (MIC< 8).
- *Campylobacter coli* and *C. jejuni* isolates showing the highest-level resistance to erythromycin (MIC > 512 mg/L).
- *Campylobacter coli* and *C. jejuni* isolates showing resistance to both gentamicin (MIC > 16 mg/L) and erythromycin (MIC > 512 mg/L).
- Isolates showing multidrug resistance to the highest number of substances (≥ 6 substances for *Salmonella* spp. and *E. coli*, ≥ 6 substances for *C. coli* and *C. jejuni*).
- Isolates representing the categorisations presumptive ESBL-, AmpC- and ESBL + AmpC- producers or with such genes reported.
- Isolates representing the category presumptive CP-producers or with such genes reported.
- Isolates where phenotypic and genotypic data were not in accordance with each other.
- MSs sent the selected isolates to the EURL-AR, where they were retested. EFSA, EURL-AR and MSs liaised together to address possible discrepancies found.

Analyses of antimicrobial resistance data

Data are reported in separate sections dedicated to each microorganism. Clinical investigation data were not accounted for in this report.

Overview tables of the resistance data reported

Data generated from the antimicrobial susceptibility testing and reported as quantitative at the isolate level by MSs have been described in the overview tables included in the Annexes A–E published on the EFSA Knowledge Junction community on Zenodo (https://doi.org/10.5281/zenodo.14645440). The tables also display complete susceptibility, multidrug resistance and co-resistance. These analyses are described in Section 2.4.

Epidemiological cut-off values and the occurrence of resistance

ECOFFs, as listed in Commission Implementing Decision (EU) 2020/1729, have been used in this report to interpret the isolate-based reported MIC data and determine non-wild type organisms also termed 'microbiologically' resistant organisms (i.e. displaying a decreased susceptibility), and to ensure that results from different MSs are comparable. In this report, 'microbiologically' resistant organisms are referred to as 'resistant' for brevity. This report also incorporates re-evaluation of the historical data accounting for the revised EU legislation, which included the revised ECOFFs. Under the new legislation, the ECOFF used to determine microbiological resistance of *Salmonella* isolates to tigecycline changed from > 1 to > 0.5 mg/L. To note for tigecycline testing is the instability of the substance in aged (> 12 h old) Mueller-Hinton broth medium used in MIC-testing, which may result in elevated MIC for some isolates (Bradford et al., 2005). The reported instability of tigecycline during testing, coupled with the lower ECOFF, may result in elevated reporting of resistance to tigecycline in *Salmonella* and *E. coli* isolates with MICs within one dilution range of the ECOFF.

Starting in 2021, new legislative requirements listed in Commission Implementing Decision (EU) 2020/1729, require MSs to test target bacterial isolates for new substances. For *Salmonella* spp., and *E. coli*, the new substance to be tested is amikacin. For *Campylobacter* spp., the new substances are chloramphenicol and ertapenem. Nalidixic acid and streptomycin were removed from the harmonised panel for *Campylobacter* spp.

The occurrence of resistance to a number of antimicrobials was determined for *Salmonella*, *Campylobacter*, and indicator commensal *E. coli* isolates and are tabulated at the production-type level in this report. The occurrence of resistance (i.e. resistance levels) in reporting MS groups was calculated as totals (the total number of resistant isolates out of the total number of tested isolates across reporting MSs), and, in the *E. coli* chapter, also as weighted means to account for the animal population sizes.

Data description

Throughout the report, level or occurrence of AMR means the percentage of resistant isolates as a proportion of the isolates tested of that microorganism. MSs reporting group means the MSs that provided data and were included in the relevant table of antimicrobial resistance for that bacterium–food or animal category–antimicrobial combination. Terms used to describe the levels or occurrence of antimicrobial resistance are 'rare': < 0.1%, 'very low': 0.1%–1.0%, 'low': > 1%–10.0%, 'moderate': > 10.0%–20.0%, 'high': > 20.0%–50.0%, 'very high': > 50.0%–70.0%, 'extremely high': > 70.0%. Although these terms are applied to all antimicrobials, the significance of a given level of resistance depends on the particular antimicrobial and its importance in human and veterinary medicine.

Temporal trends in resistance

Temporal trends show the resistance to different antimicrobials over time, by plotting the level of resistance for each year of sampling and for different species, such as humans and different food-producing animals. Trend graphs were generated for data meeting the minimum criteria for inclusion, e.g. 10 or more isolates reported and with three or more time points since 2014. Additional criteria, where applicable, are indicated in the specific chapters. To assess the statistical significance of temporal trends, the proportions of resistance were modelled using logistic regression. Logistic regression models used resistance as the outcome variable (with resistant (1)/non-resistant (0)) and year as a covariate. This analysis was carried out using the PROC LOGISTIC function of SAS 9.2. for each country reporting at least 10 total tested isolates, where there were 3 years or more of available data to use in the model. The PROC LOGISTIC function uses a logit transformation to model the proportions against year and provides estimates for both intercepts and slope. Models where the likelihood ratio test suggested it to be meaningful and resulting in a p-value associated with a slope of < 0.05 were significant (linear model fit). It is important to note that between-year fluctuations in the occurrence of resistance (%) may not be captured in the evaluation of the linear trend over the entire time period (2014–2023) and that very recent decreasing or increasing trends may therefore be masked by the overall trend. Also, when interpreting the results, it is important to note that trend analyses may be driven by particularly high or low levels of resistance reported in one or few data points leading to unexpected findings (e.g. detection of significant increasing or decreasing trends where the observed data do not show any clear trend over the entire period). The withdrawal of the UK from the EU had an impact on the AMR data reported at the EU level in 2020. In this report, data at the EU level are reported in accordance with the membership of the EU, whether before 2020 (EU including the UK) or after 2020 (EU without the UK). However, Northern Ireland is counted as an EU MS in this report. As monitoring of MRSA is not mandatory and harmonised, the availability of comparable data over time is limited. Thus, temporal trends were not assessed for MRSA.

Spatial analysis of resistance through maps

MS-specific AMR levels for selected bacterium–food category/animal population combinations were plotted in blue, purple or green shaded maps for 2022 and 2023, using ArcGIS 9.3. In the maps, resistance levels are presented with colours reflecting the continuous scale of resistance to the antimicrobial of interest among reporting MSs; so, there might be some apparent discrepancies between the colours and resistance levels between maps.

Resistance in *Salmonella* serovars of public health importance

In this report, AMR in tested *Salmonella* isolates were aggregated to give a value for *Salmonella* spp. for each country and animal/meat category. In addition, the most prevalent *Salmonella* serovars were also reported separately for each animal category. Additional tables were included in this report to describe the occurrence of AMR among selected *Salmonella* serovars of public health importance or with high prevalence in animals. To present a complete overview of the animal populations in which specific *Salmonella* serovars of public health importance have been recovered, all the data reported (even those derived from fewer than four reporting countries and less than 10 isolates tested) have been included.

Analysis of multidrug resistance, complete susceptibility and co-resistance data

The analysis of MDR and co-resistance data is important considering the emergence of multiresistant bacteria. The intention was to focus mainly on multi–/co-resistance patterns involving critically important antimicrobials (WHO, 2019), such as cephalosporins, fluoroquinolones and macrolides. The occurrence of isolates of certain serotypes/resistance patterns of interest was studied both at the MS level and at the EU level (by grouping data for all MSs and where also relevant for MSs and other reporting countries), as the overall picture for all MSs might show a more definite pattern of emergence and spread.

Analysis of multidrug resistance and complete susceptibility

For the analysis of MDR and complete susceptibility, a multidrug resistant isolate is defined as an isolate resistant to at least three of the tested antimicrobial substances. In contrast, a completely susceptible isolate is one defined as non-resistant (MIC < ECOFF) to these antimicrobial substances. For indicator commensal *E. coli* and *Salmonella* spp., the following substances from the harmonised test panel laid out in Commission Implementing Decision (EU) 2020/1729 were included in the assessment of MDR, as done in the previous EUSR on AMR including 2020–2021 data.

For *E. coli* the substances included were amikacin/gentamicin (assessed together as aminoglycoside antimicrobial class), ampicillin, cefotaxime/ceftazidime (assessed together as third-generation cephalosporin), chloramphenicol, ciprofloxacin/nalidixic acid (assessed together as quinolone antimicrobial class), colistin, meropenem, sulfamethoxazole, tetracycline/tigecycline (assessed together as glycylcycline antimicrobial class) and trimethoprim.

For *Salmonella* spp. the substances included were amikacin/gentamicin (assessed together as aminoglycoside antimicrobial class), ampicillin, cefotaxime/ceftazidime (assessed together as third-generation cephalosporin), chloramphenicol, ciprofloxacin/nalidixic acid (assessed together as quinolone antimicrobial class), meropenem, sulfamethoxazole, tetracycline/tigecycline (assessed together as glycylcycline antimicrobial class) and trimethoprim. For *C. coli* and *C. jejuni*, the substances included were ciprofloxacin, erythromycin, gentamicin and tetracycline.

Key outcome indicators

To support EU countries in their progress to reduce use of antimicrobials and AMR a list of key outcome indicators has been jointly published by ECDC, EFSA and EMA (ECDC, EFSA and EMA, 2017). Two of these key outcome indicators (KOI) are included in the report: (1) The key outcome indicator of complete susceptibility (KOI_{CS}) in indicator commensal *E. coli*; and (2) the key outcome indicator of the prevalence of ESBL- and/or AmpC-producing *E. coli* (KOI_{ESC}). KOI_{CS} is the proportion of fully susceptible indicator *E. coli* isolates, weighted by the size of the populations of the most important production animals (broilers, fattening turkeys, fattening pigs, cattle under 1 year of age) and is used as an indicator for the overall AMR situation in food-producing animals. KOI_{ESC} is the weighted mean of the prevalence of ESBL- and/or AmpC-producing *E. coli* in each of the four animal populations monitored. The KOI_{CS} and KOI_{ESC} account for differences in the relative size of food animal populations in a country and are therefore relevant in the evaluation of risks related to resistance in food-producing animals. These KOIs are displayed in bar charts showing changes in KOI over the years. The statistical significance of the trends was analysed using a simple linear regression over time. The F-test was used to assess the overall significance of the models (p-value < 0.05).

Combined resistance patterns of interest

The term combined resistance is used in this report to indicate phenotypic resistance to two or more different classes of antimicrobials, exhibited by the same bacterial isolate. In *Salmonella* and *E. coli* isolates, combined resistance to cefotaxime

(CTX) and ciprofloxacin (CIP) was estimated, as these two antimicrobials are of particular interest in human medicine. In 2023, co-resistance was addressed using both ECOFFs (CTX > 0.25 mg/L and CIP > 0.064 mg/L) and CBPs (CTX > 2 mg/L and CIP > 0.064 mg/L) for *E. coli*. In *C. jejuni* and *C. coli* isolates, co-resistance to ciprofloxacin and erythromycin (ERY) was estimated, as these two antimicrobials are of particular interest in human medicine in the treatment of severe campylobacteriosis. The interpretive ECOFFs used to address co-resistance to ciprofloxacin and erythromycin were, for *C. jejuni*, CIP > 0.5 mg/L and ERY > 4 mg/L and, for *C. coli*, CIP > 0.5 mg/L and ERY > 8 mg/L. These values may be considered very similar to CBPs.

Identification of presumptive ESBL-, AmpC- and/or CP-producers

Definition of ESBL-, AmpC-, ESBL + AmpC-, CP- phenotypes

The categorisation of isolates resistant to third-generation cephalosporins and/orcarbapenems in presumptive ESBL-, AmpC- or CP-producers was carried out based on the EUCAST guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance (EUCAST, 2017). In these expert guidelines and, based on other EUCAST and CLSI guidelines to detect ESBL/AmpC-producers, a screening breakpoint of > 1 mg/L is recommended for cefotaxime and ceftazidime (EUCAST, 2017). This screening breakpoint is higher than the ECOFFs applied for antimicrobial susceptibility of *E. coli* to both antimicrobials, and of *Salmonella* to cefotaxime. For this report, a first condition for classifying isolates as presumptive ESBL/AmpC-producers related to their MIC for either cefotaxime or ceftazidime, was to apply the screening breakpoint of MICs > 1 mg/L. Only isolates that presented MIC values complying with this requisite (as expected for most of the ESBL/AmpC-producers) were further considered. In total, for the third-generation cephalosporin- and/or carbapenem-resistant isolates, five main categorisations are made: (1) ESBL phenotype; (2) AmpC phenotype; (3) ESBL + AmpC phenotype; (4) CP-phenotype; and (5) Other phenotypes (Figure A.3).

1. To detect the production of ESBLs, a synergy test for cefotaxime and ceftazidime, in combination with clavulanic acid was performed. An eightfold reduction in the MIC for the cephalosporin combined with clavulanic acid compared with that obtained for the cephalosporin alone was interpreted as a positive synergy test. In all other cases, the synergy test was considered negative. For the present report, isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime and a synergy test positive for any of these antimicrobials, together with susceptibility to cefoxitin (≤ 8 mg/L) and meropenem (MEM ≤ 0.125 mg/L, see CP phenotype) were classified as **ESBL phenotype**.
2. For the AmpC phenotype, the combination MIC > 8 mg/L (ECOFF) for cefoxitin together with MICs > 1 mg/L for cefotaxime and/or ceftazidime was used as phenotypic criteria to investigate the presence of AmpC production in *E. coli*. It should be underline that some AmpC enzymes (i.e. ACC-1) do not confer resistance to cefoxitin, and there are some other mechanisms (porin loss, presence of carbapenemases, a few ESBL genes (i.e. CTX-M-5)) that may generate similar MIC values for the different antimicrobials (EFSA, 2012; EUCAST, 2017). Phenotypic AmpC confirmation tests (i.e. cloxacillin synergy) were not required for the present monitoring. For the present report, isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime and cefoxitin MIC > 8 mg/L together with negative synergy test for both cefotaxime and ceftazidime/clavulanic acid, together with susceptibility to meropenem (MEM ≤ 0.125 mg/L) were classified as **AmpC phenotype**. No distinction was made between acquired AmpC and chromosomal AmpC.
3. For the present report, isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime, positive synergy tests for any of these antimicrobials with clavulanic acid and cefoxitin MIC > 8 mg/L, together with susceptibility to meropenem (MEM ≤ 0.125 mg/L) were classified under the **ESBL + AmpC phenotype category**. In some isolates, several mechanisms can be present at the same time, making it very difficult to differentiate the phenotypes. Also, the high-level expression of AmpC beta-lactamases can mask the presence of ESBLs. AmpC can also be present in isolates with positive ESBL tests (clavulanic acid synergy). In this case, the cefepime/clavulanic acid synergy test should be used to overturn or confirm the presence of ESBLs in these isolates (EUCAST, 2017) but, unfortunately, the combination cefepime/clavulanic acid was not included among the substances tested for monitoring. The inclusion of resistance to cefepime with an MIC value ≥ 4 mg/L as an additional criterion proposed elsewhere (EFSA, 2012), could be useful to ascertain the presence of an ESBL-producer.
4. For the classification of isolates into the putative carbapenem producers (CPs), a meropenem screening cut-off of > 0.125 mg/L (which coincides with the harmonised ECOFF) was chosen. It is known that other mechanisms (i.e. hyperproduction or combination of ESBLs and/or AmpC and porin loss) can also affect to the MIC values generated for the different carbapenems, especially for ertapenem. The confirmation of the carbapenemase-production recommended by the EUCAST guidelines cannot be inferred from the carbapenem susceptibility testing data reported but needs further phenotypic or molecular testing. MSs that reported data suggesting the presence of putative CPs were recommended to validate the results by performing further confirmatory testing, and the EURL-AR offered to apply WGS of the isolates. For the present report, isolates with MIC > 0.125 mg/L for meropenem would be considered as presumptive CP-producers and were classified under the **CP phenotype**. The presence of other resistance mechanisms (ESBLs, AmpC, etc.) within the isolates placed in this group cannot be ruled out.
5. In this group, phenotypes not included in the categorisations defined above were included: isolates with an MIC > 0.125 for ertapenem and/or MIC > 1 mg/L for imipenem (EUCAST screening cut-offs, one dilution step higher than the currently defined ECOFFs) but no resistance to meropenem (MIC < 0.125 mg/L) were classified under the category 'other

phenotype'. Finally, isolates with MICs ≤ 1 mg/L for cefotaxime and ceftazidime would be considered as not ESBL and/or AmpC-producers. This implied that some isolates considered as microbiologically resistant (MICs over the ECOFFs) would not be further classified, as probably other mechanisms or technical issues in the MIC testing (i.e. MIC value close to the ECOFF) would be responsible for the MIC values obtained. For the present report, cefotaxime- and ceftazidime-resistant isolates with MICs ≤ 1 mg/L for both antimicrobials were considered as putative on-ESBL/AmpC-producers and were classified under the category **'other phenotype'**.

Without a further molecular characterisation of the isolates, it will not be possible to know exactly which resistance mechanisms are present. For epidemiological purposes and based on the EUCAST guidelines, the classification of 'presumptive' producers for the different mechanisms conferring resistance to third-generation cephalosporins and/or carbapenems was considered. Molecular characterisation of these mechanisms is recommended.

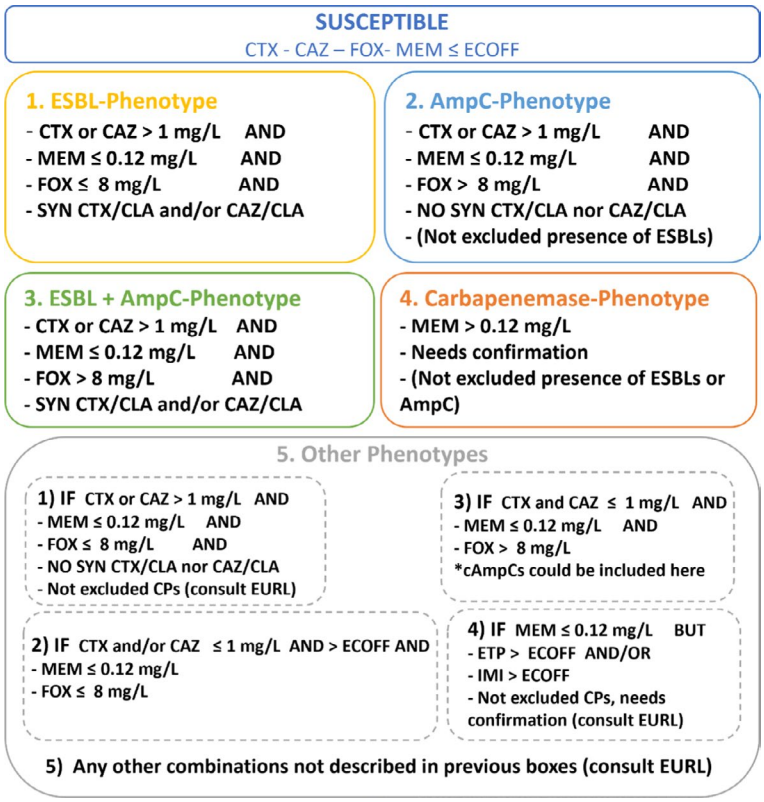

FIGURE A.3 Phenotypes inferred based on the resistance to the beta-lactams included in Panel 2.
Presumptive ESBL-producers include isolates exhibiting phenotype 1 or 3.
Presumptive AmpC-producers include isolates exhibiting phenotype 2 or 3.

For the occurrence and prevalence tables, as well as the violet shaded maps and graphics shown in Section 'Extended-spectrum beta-lactamase (ESBL)-, AmpC- and/or CP-producing *Salmonella* and *Escherichia coli*', presumptive ESBL-producers were considered as those exhibiting an ESBL and/or ESBL + AmpC phenotype and presumptive AmpC-producers, those with an AmpC and/or ESBL + AmpC phenotype (see below).

For the present report, the terms:

'**Presumptive ESBL-/AmpC-producers'** refers to those isolates who present an ESBL and/or and AmpC and/or an ESBL + AmpC phenotype (presumptive ESBL-producers and/or presumptive AmpC-producers).

'**Presumptive ESBL-producers'** refers to those isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime and a synergy test positive for any of these antimicrobials and susceptibility to meropenem (MEM ≤ 0.125 mg/L, see CP phenotype). These isolates may also harbour other resistance mechanisms (e.g. AmpC-encoding genes).

'**Presumptive ESBL-cefotaximase-producers'** refers to those presumptive ESBL-producers with MICs > 1 mg/L for cefotaxime and a synergy test positive for cefotaxime only. These isolates may also harbour other resistance mechanisms.

'**Presumptive ESBL-ceftazidimase-producers'** refers to those presumptive ESBL-producers with MICs > 1 mg/L for ceftazidime and synergy test positive for ceftazidime only. These isolates may also harbour other resistance mechanisms.

'**Presumptive AmpC-producers'** refers to isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime and cefoxitin MIC > 8 mg/L together with susceptibility to meropenem (MEM ≤ 0.125 mg/L, see CP phenotype). No distinction between

plasmid-mediated AmpC and chromosomal AmpC was made. These isolates may also harbour other resistance mechanisms (e.g. ESBL-encoding genes).

'**Presumptive ESBL + AmpC-producers'** refers to isolates with the ESBL + AmpC phenotype described above.

'**Presumptive CP-producers'** refers to those isolates with the CP phenotype described above.

Data on ESBL/AmpC/CP-genes

From 2021, MSs and non-MSs can choose to report WGS data for characterisation of presumptive ESBL-/AmpC-/CP-producing *E. coli* and *Salmonella* spp. isolates from the routine monitoring (if resistance to cefotaxime, ceftazidime and/or meropenem was detected in the first panel) or from the specific ESBL-/AmpC-/CP-producing *E. coli* monitoring. Definitions for genotypic interpretation of AMR data for 2022 and 2023 are listed below:

- Positive isolate is an isolate where at least one ESBL- or AmpC- or CP-gene was detected using WGS.
- Negative isolate is an isolate where no ESBL- or AmpC- or CP-genes are detected using WGS.

It is important to highlight that genotypic complete susceptibility is not the same as phenotypic complete susceptibility because not all genes that are detected are phenotypically expressed.

For the analysis with genotypic data the following definitions are applied:

- Genotypic prevalence will be defined using the following formula:

$$\text{Prevalence} = \frac{\text{Number of positive samples}}{\text{Number of samples tested}} \times \frac{\text{Number of positive isolates}}{\text{Number of isolates tested}} \times 100.$$

- Genotypic occurrence will be defined as the proportion (%) of ESBL-/AmpC-/CP-producing *E. coli* or *Salmonella* positive isolates (associated with at least one ESBL-/AmpC-/CP-gene) divided by the total number of ESBL- or AmpC- or CP- isolates tested.

Bar charts were also used to present the WGS data.

The list of ESBL-/AmpC-/CP-encoding genes used for the analysis of the ESBL-/AmpC-/CP-producing isolates can be consulted in the catalogue browser https://github.com/openefsa/catalogue-browser/wiki.

For countries reporting both genotypic and phenotypic data, the correspondence between phenotype predicted by genotype and phenotype predicted by MIC testing was calculated as follows:

$$\text{Correspondence} = \frac{\text{number of isolates with same phenotype predicted by both genotype and MIC}}{\text{Total number of isolates reported to harbour the specific gene}} \times 100.$$

Correspondence was considered to be high if ≥ 90% of the isolates carrying a gene also exhibited the expected phenotype encoded by the gene. Additionally, Cohen's kappa coefficient (κ) was used to assess the concordance between phenotypic and genotypic results, providing a measure of the agreement. This statistical analysis compares the categorical outcomes from both methods, considering the proportion of observed agreement and expected agreement by chance. Confidence intervals (95% CI) were also computed to assess the precision of the κ estimate. This analysis was conducted using SAS 9.2.

Data on methicillin-resistant *Staphylococcus aureus* (MRSA)

The occurrence of MRSA and its susceptibility to antimicrobials in various food categories (including meat samples from various species) and food-producing animals was reported by few MSs. MRSA occurrence data reported from clinical investigations of food-producing and/or companion animals in 2022–2023 were also reported. Details of the antimicrobials selected are provided in the section on MRSA. For further information on reported MIC distributions and the number of resistant isolates, refer to the submitted and validated MS data published on the EFSA website. The methods for collecting and testing samples for MRSA are not harmonised between MSs. The different methods employed for MRSA monitoring are explained in detail within the section on MRSA to enable readers to better follow the procedures carried out by individual countries.

APPENDIX B

Additional information and supporting data

List of Annexes

The annexes are available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.14645440.

The annexes contain the following information:

Annex A. Data reported on antimicrobial resistance in *Salmonella* spp.

The annex contains tables on antimicrobial resistance data:

- Antimicrobial resistance in *Salmonella* spp. from humans by country, including occurrence of ESBL, AmpC and carbapenemases,2023 and trend graphs for individual serotypes for 2014–2023 period – Annex A1;
- Occurrence of resistance to selected antimicrobials in *Salmonella* spp. from animals, 2022–2023 – Annex A2;
- Occurrence of resistance to selected antimicrobials in specific *Salmonella* serovars – Annex A3.

Annex B. Data reported on antimicrobial resistance in *Campylobacter* spp.

The annex contains tables and figures showing antimicrobial resistance data:

- Occurrence of resistance to selected antimicrobials in *C. jejuni* and *C. coli* from humans, by country, in 2023 – Annex B1;
- Occurrence and prevalence of resistance to selected antimicrobials in *C. jejuni* and *C. coli* from food-producing animals, for 2022/2023 – Annex B2;
- Trends of resistance in broilers and in fattening turkeys (2014–2023) – Annex B3.

Annex C. Data reported on antimicrobial resistance in indicator commensal *Escherichia coli* from food-producing animals and derived meat

- The annex contains tables in excel sheets on data reported on AMR in indicator commensal *Escherichia coli* from food-producing animals and derived meat (data from pigs and cattle under 1 year from 2023 and data from poultry from 2022).

Annex D. Data on presumptive ESBL-, AmpC- and/or carbapenemase-producing microorganisms (routine and specific monitoring)

The annex contains tables with the data reported on presumptive ESBL-, AmpC- and/or carbapenemase-producing microorganisms for poultry (2022), pigs and cattle (2023) and meat thereof, and their resistance occurrence (routine and specific monitoring programmes):

- ESBL-, AmpC-producers prevalence and occurrence tables – pigs and cattle and meat thereof, 2023 – in Annex D1
- ESBL-, AmpC-, carbapenemase-producers prevalence and occurrence tables – poultry 2022 – in Annex D1
- Specific carbapenemase-producing *E. coli* monitoring 2022–2023 – in Annex D1
- ESBL-, AmpC-producers prevalence maps – pigs and cattle and meat thereof, 2023 – Annex D2
- ESBL-, AmpC- producers prevalence maps – poultry and meat thereof 2022 – Annex D2

Further, the annex contains tables with WGS data reported under WGS programme codes in the specific monitoring of ESBL-, AmpC- and/or CP- producing *E. coli* and the specific monitoring of CP-producing *E. coli*, and complementary to MIC values for presumptive ESBL-/AmpC-/CP-producing *E. coli* collected in the routine monitoring (when isolates resistant to cefotaxime, ceftazidime and/or meropenem were detected in the first panel), as well as for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* and specific monitoring of CP-producers:

- ESBL- and AmpC-encoding genes reported in WGS ESBL MON, 2022 and 2023 – Annex D3;
- CP-encoding genes reported in WGS CARBA MON, 2022 and 2023 – Annex D3;
- ESBL-, AmpC- and/or CP-encoding genes reported in AMR MON pnl2, ESBL MON pnl2 or CARBA MON pnl2 in 2022 and 2023 – Annex D3.

Annex E. Data reported on antimicrobial resistance in MRSA from food-producing animals and derived meat

The annex contains tables and data reported on the prevalence, genetic diversity and antimicrobial resistance of MRSA from food-producing animals and derived meat collected in 2022 and 2023.

Annex F. Data reported on antimicrobial resistance in *Enterococci* from food-producing animals and derived meat

The annex contains tables in excel sheets on data reported on the occurrence of resistance to selected antimicrobials in *Enterococcus faecalis* and *E. faecium* from food-producing animals (data from pigs and cattle under 1 year from 2023 and data from poultry from 2022).

Supporting data

All tables produced for the European Union Summary Report on Antimicrobial Resistance in Zoonotic and Indicator Bacteria from Humans, Animals and Food in 2022–2023 are available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.14645440.

The aggregated dataset submitted on the negative results for extended-spectrum β-lactamases (ESBL) and carbapenemase-producers is also available on the Knowledge Juntion at: https://doi.org/10.5281/zenodo.14723959. The 2023 prevalence of MRSA aggregated dataset is also available on the Knowledge Junction at: https://doi.org/10.5281/zenodo.14723545.

A table showing ESBL-/AmpC-/CP-encoding genes and corresponding MIC data for cephalosporins and carbapenems reported in 2022 and 2023 is also available on the knowledge junction at: https://doi.org/10.5281/zenodo.14645440.

Country datasets

All country datasets containing the tables on the occurrence of antimicrobial resistance per each country are available on the EFSA Knowledge Junction community on Zenodo – please see below the list and corresponding link to the datasets.

The countries that submitted datasets on the 2022/2023 monitoring years are: the 27 EU Member States and United Kingdom (Northern Ireland), the 3 non-EU Member States, as well as Montenegro and Republic of North Macedonia as pre-accession countries.

Country	Link to the dataset
EU Member States	
Austria	https://doi.org/10.5281/zenodo.14713717
Belgium	https://doi.org/10.5281/zenodo.14720296
Bulgaria	https://doi.org/10.5281/zenodo.14718483
Croatia	https://doi.org/10.5281/zenodo.14720131
Cyprus	https://doi.org/10.5281/zenodo.14717630
Czechia	https://doi.org/10.5281/zenodo.14713481
Denmark	https://doi.org/10.5281/zenodo.14713093
Estonia	https://doi.org/10.5281/zenodo.14720337
Finland	https://doi.org/10.5281/zenodo.14713283
France	https://doi.org/10.5281/zenodo.14713657
Germany	https://doi.org/10.5281/zenodo.14713363
Greece	https://doi.org/10.5281/zenodo.14717885
Hungary	https://doi.org/10.5281/zenodo.14718525
Ireland	https://doi.org/10.5281/zenodo.14720203
Italy	https://doi.org/10.5281/zenodo.14712883
Latvia	https://doi.org/10.5281/zenodo.14713603
Lithuania	https://doi.org/10.5281/zenodo.14713540
Luxembourg	https://doi.org/10.5281/zenodo.14718438
Malta	https://doi.org/10.5281/zenodo.14720260
Netherlands	https://doi.org/10.5281/zenodo.14718767
Poland	https://doi.org/10.5281/zenodo.14720522

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Country	Link to the dataset
Portugal	https://doi.org/10.5281/zenodo.14718840
Romania	https://doi.org/10.5281/zenodo.14713134
Slovakia	https://doi.org/10.5281/zenodo.14718713
Slovenia	https://doi.org/10.5281/zenodo.14717812
Spain	https://doi.org/10.5281/zenodo.14713433
Sweden	https://doi.org/10.5281/zenodo.14724207
United Kingdom (Northern Ireland)	https://doi.org/10.5281/zenodo.14719738
Non-EU countries	
Iceland	https://doi.org/10.5281/zenodo.14718670
Montenegro	https://doi.org/10.5281/zenodo.14724278
Norway	https://doi.org/10.5281/zenodo.14720240
Republic of North Macedonia	https://doi.org/10.5281/zenodo.14720169
Switzerland	https://doi.org/10.5281/zenodo.14717953