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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 2023–2024

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Abstract

This report presents the main findings of the 2023–2024 harmonised antimicrobial resistance (AMR) monitoring in *Salmonella* spp., *Campylobacter jejuni* and *Campylobacter coli* from humans, food-producing animals (broilers, laying hens, fattening turkeys, fattening pigs and bovines under 1 year of age), and derived meat. For animals and meat, AMR was also assessed for indicator commensal *Escherichia coli*, presumptive extended-spectrum beta-lactamase (ESBL)-/AmpC beta-lactamase (AmpC)–/carbapenemase (CP)-producing *E. coli, Enterococcus faecalis*, *Enterococcus faecium* and the occurrence of methicillin-resistant *Staphylococcus aureus* (MRSA). A high proportion of *Salmonella* and *Campylobacter* isolates from humans and animals were resistant to commonly used antimicrobials (ampicillin, tetracycline and sulfonamides), although *Salmonella* isolates from laying hens exhibited lower resistance. Increasing trends in ciprofloxacin resistance, a critically important antimicrobial (CIA) for human medicine, were detected in *Salmonella* from laying hens in certain Member States (MSs), and in human infections for a poultry-associated *Salmonella* serovar and for *C. jejuni* in more than half of the reporting countries. Combined resistance to CIA remained uncommon, but higher levels were observed for certain *Salmonella* serovars and *C. coli* from humans and animals in some countries. Resistance differed greatly between countries. In imported fresh meat of broilers and turkeys, very high and moderate levels of resistance to third-generation cephalosporins were observed in *Salmonella* and indicator *E. coli*, respectively. Although CP-producing *Salmonella* were not detected in animals, six human cases were reported in 2023 and five in 2024, predominantly carrying $bla_{\text{OXA-48}}$, but also $bla_{\text{OXA-181}}$, $bla_{\text{NDM-1}}$ and $bla_{\text{IMP-1}}$. CP-producing *E. coli* isolates harbouring diverse carbapenemase genes, were detected in broilers, turkeys, pigs, calves and pig meat in eight MSs, warranting a thorough follow-up. Trend analyses of Key Outcome Indicators (complete susceptibility (KOI_{CS}) and prevalence of ESBL-/AmpC- producing *E. coli*) indicate encouraging progress in reducing AMR in food-producing animals in several MSs over the past decade. At the EU level and in certain MSs, some previously declining resistance or increasing susceptibility trends in indicator *E. coli* from broilers and turkeys, and KOI_{CS}, have stabilised and plateaued, highlighting the need for sustained and strengthened AMR control efforts.

KEYWORDS

antimicrobial resistance, *Campylobacter*, indicator bacteria, MRSA, *Salmonella*, zoonotic bacteria

CONTENTS

SUMMARY

In 2023–2024, data on antimicrobial resistance (AMR) 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, targeted food-producing animals (fattening pigs, bovines under 1 year of age, broilers and fattening turkeys, and for *Salmonella* also laying hens) 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*, and methicillin-resistant *Staphylococcus aureus* (MRSA) from animals and derived meat were addressed as well as *Enterococci* from animals.[1] In 2024, it was mandatory to report AMR data from poultry and meat from poultry, while in 2023, it was mandatory to report AMR data from pigs and calves at slaughter and meat derived from these animals. 'Microbiological resistance' in the isolate populations was assessed using epidemiological cut-off (ECOFF) values. For 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 2024, resistance to ampicillin, sulfonamides and tetracyclines was observed in a high proportion of isolates, while resistance to third-generation cephalosporins was noted in overall low proportions of isolates (1.8% and 1.5% for cefotaxime and ceftazidime, respectively). A statistically significant decline in resistance to ampicillin and tetracycline in isolates from humans was observed in 19 and 14 countries, respectively, over the period 2014–2024. This was particularly evident in *S.* Typhimurium, and for tetracycline, also in monophasic *S.* Typhimurium. A high occurrence of resistance to ciprofloxacin (21.4%) was observed in isolates from human cases from 2024, with an extremely high proportion of resistant isolates noted in *S.* Kentucky (79.1%). Increasing trends in ciprofloxacin resistance were observed for *S.* Enteritidis in 15 countries over the period 2014–2024, with this serovar predominantly being associated with poultry.

In *Salmonella* spp. isolates from food-producing animals in 2023–2024, 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 calves and broilers, and at very low levels in laying hen and turkey flocks and fattening pigs. These findings mirror those observed in *Salmonella* isolates from human cases. 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*.

Between 2014 and 2024, a statistically significant decreasing trend in tetracycline resistance at the MS-group level was registered in isolates from broilers, while in turkeys, statistically significant decreasing trends were observed for both ampicillin and tetracycline resistance. Over the same period, a statistically significant increasing trend in ciprofloxacin resistance at the MS-group level was identified in laying hen flocks, while a decreasing trend was observed in turkeys.

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 calves, very low in broilers and laying hens and not detected in turkeys. While resistance to tigecycline was reported at low levels in pigs, calves, laying hens and turkeys, moderate levels in broilers were reported. Resistance to azithromycin and tigecycline in indicator *E. coli* was low to very low in all four animal populations monitored. Resistance to amikacin ranged from very low to low among *Salmonella* spp. isolates from the animal populations monitored, and it was not detected in calves. Resistance to colistin was very low in pigs, low in all the poultry populations but moderate in calves. 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 very low in *Salmonella* isolates in almost all animal populations, except for calves, where low levels were observed. Certain *Salmonella* serovars from poultry sources, such as *S.* Newport, *S.* Infantis and *S.* Kentucky from broilers and *S.* Infantis from turkeys, however, exhibited higher levels of combined resistance to ciprofloxacin and cefotaxime compared to other serovars. The same was observed in these serovars isolated from humans.

Overall, the data obtained in 2023–2024 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 2024 were also very high. Resistance to erythromycin was detected at rare to 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 (rare to moderate) and animals (low to high). The whole genome sequencing (WGS) results reported for erythromycin-resistant *C. jejuni* and *C. coli* isolates from food-producing animals in 2023–2024, mostly those highly resistant (MIC ≥ 512 mg/L), showed a predominant detection of the

[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).

mutation A2075G in the 23S rRNA gene in most isolates. One *C. coli* isolate from calves in 2023 and two *C. coli* isolates from fattening turkeys in 2024 were reported positive to the presence of *erm*(B). Among the three countries reporting WGS data for *Campylobacter* isolates from humans, no erythromycin resistance mechanisms were detected.

Over the period 2014–2024, ciprofloxacin resistance in *C. jejuni* from humans increased significantly in 12 countries, while erythromycin resistance decreased in 10 countries. Similar trends were observed in *C. jejuni* from broilers over the same period, where an increase in ciprofloxacin resistance and a decrease in erythromycin resistance were observed in seven countries each. Over the same period, in *C. coli* from humans, an increase in ciprofloxacin resistance was observed in four countries, while a decrease in resistance to erythromycin was observed in eight countries. Among *C. coli* isolates from animals, resistance to ciprofloxacin increased in two countries for broilers and fattening pigs, while erythromycin resistance decreased in fattening pigs in four countries. Decreasing trends in ciprofloxacin resistance among *C. jejuni* isolates were observed in five countries for humans, and in three and two countries for broilers and fattening turkeys, respectively. In contrast, a significant decreasing trend in ciprofloxacin resistance among *C. coli* isolates was observed only in one country for humans and in two countries for fattening pigs in 2023. Notably, resistance to erythromycin increased in *C. jejuni* from humans in two countries, and in *C. jejuni* and *C. coli* from broilers in one country each. The occurrence of combined resistance to ciprofloxacin and erythromycin in *Campylobacter* spp. is considered of high public health relevance as these antimicrobials are first-line treatment of *Campylobacter* infections in humans. 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 low in the considered animal species. Compared to *C. jejuni*, MDR was markedly higher in *C. coli* isolates from humans and all monitored animal populations, varying from very low to moderate in humans and from moderate to high in animals. 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 broilers and fattening turkeys in 2024 has been estimated at the 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 absent to high or very 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 in the prevalence of resistance was found for erythromycin resistance and gentamicin resistance, which varied from absent to low in *C. jejuni* and from absent to moderate in *C. coli*.

For indicator commensal *E. coli* isolates recovered from targeted food-producing animals in 2023–2024, EU MSs median levels of resistance to ampicillin, sulfamethoxazole, trimethoprim and tetracycline ranged from high to very high. Median levels of resistance to third-generation cephalosporins (cefotaxime and ceftazidime) were very low in all targeted animal populations. Resistance to (fluoro)quinolones (ciprofloxacin and nalidixic acid) was registered at high median levels among all targeted animal populations. Resistance to carbapenems (meropenem) was not detected in any isolates of indicator commensal *E. coli*.

At the EU MSs level, statistically significant decreasing trends in resistance for indicator *E. coli* were observed for ciprofloxacin and tetracycline in broilers and turkeys, and colistin and tetracycline in pigs and calves. No statistically significant increasing trends were detected. However, in certain MSs, changes in trend slopes were identified for specific resistance combinations, and CS in indicator *E. coli* from broilers and turkeys. Some previously declining resistance trends, or increasing complete susceptibility (CS) trends, have stabilised and recently plateaued.

The number of indicator commensal *E. coli* isolates recovered from imported meat sampled at border control posts in 2023–2024 was rather low. Overall, resistance was more common among isolates from imported poultry meat than in isolates from imported pig or cattle meat.

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

Within routine and specific monitoring (non-selective and selective media, respectively), the prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* varied between countries. At the EU level from specific monitoring, significant decreasing trends were observed for ESBL-producing *E. coli* in broilers, fattening turkeys, cattle under 1 year, broiler meat, pig meat and bovine meat. In 2023–2024, ESBL-producers predominated over AmpC-producers by phenotypic and genotypic results. WGS data confirmed that 3179 isolates carried ESBL genes, 295 plasmid-mediated AmpC genes and 385 an AmpC promoter mutation.

WGS results showed 70 isolates carrying CP-genes in *E. coli* in 2023–2024. No CP-encoding gene were detected in the routine monitoring in 2023. In the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*, one broiler isolate with $bla_{\text{VIM-1}}$ was detected in 2024. In 2023, two CP-producers were reported from cattle under 1 year ($bla_{\text{VIM-1}}$ or $bla_{\text{NDM-5}}$) and four isolates from fattening pigs (three with $bla_{\text{OXA-181}}$, one co-harbouring $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$).

In the specific monitoring of CP-producing *E. coli*, a single isolate from a broiler carrying the $bla_{\text{OXA-244}}$ gene was reported in 2024 and one presumptive CP-producing isolate was also detected in broilers, showing resistance to meropenem and ertapenem, for which no CP-encoding gene could be identified with the databases for resistance gene detection used. Additional findings in 2023 included 61 CP-producing isolates from fattening pigs (24 with $bla_{\text{OXA-181}}$, 21 with $bla_{\text{OXA-48}}$, 5 with $bla_{\text{NDM-5}}$, 4 with both $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$ simultaneously, and 1 with $bla_{\text{OXA-244}}$); five isolates from calves (four with

bla$_{OXA-181}$, one with *bla*$_{OXA-48}$) and one isolate carrying *bla*$_{NDM-5}$ was reported from pig meat. CP-producing *Salmonella* isolates were not detected in animals in 2023–2024, but in humans, six cases with CP-producing *Salmonella* were reported in 2023 and five in 2024 (six with *bla*$_{OXA-48/OXA-48-like}$, two with *bla*$_{OXA-181}$ and one each with *bla*$_{NDM-1}$ and *bla*$_{IMP-1}$). For one isolate, information on the gene was not available).

The voluntary monitoring of MRSA from food and healthy animals in 2023–2024 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 2023 and 2024, livestock-associated (LA) clonal complex (CC) 398 was by far the most reported CC, both in isolates from animals and food. An important observation from the 2023 to 2024 monitoring includes the detection of resistance to the critically important antimicrobials (CIAs) linezolid (1 isolate from meat from turkey), rifampicin (1 isolate from meat from turkey) and mupirocin (1 isolate from meat from broilers). Resistance to vancomycin was not detected in any of the reported MRSA isolates subjected to antimicrobial susceptibility testing.

In 2023–2024, the voluntary monitoring of *E. faecalis* and *E. faecium* was conducted in a limited number of countries, ranging from three to nine countries depending on the animal populations. Occurrence of resistance varied remarkably among *Enterococcus* species, animal populations and countries. Considering the results from all reporting MSs and animal populations, the highest levels of occurrence of resistance were observed for erythromycin and tetracycline in both *Enterococcus* spp. and, limited to *E. faecium*, for quinupristin-dalfopristin. Vancomycin resistance was exclusive to *E. faecium*, in cattle under 1 year (1.5%) and pigs (0.2%) and not detected in poultry populations. Linezolid resistance was detected at low levels in *E. faecalis* (the highest resistance found in isolates from cattle under 1 year of age, 6.6%) and very low levels in *E. faecium* (the highest resistance detected in fattening pigs, 0.6%), with no resistance detected in *E. faecium* from turkeys.

The key outcome indicators for AMR in food-producing animals – CS 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 2014–2024. There are marked variations in both KOI among reporting countries. Statistically significant increasing trends in KOI$_{CS}$ were registered at the MS-group level as well as in 11 individual MSs whereas a decreasing trend was not observed in any MS. Statistically significant decreasing trends in KOI$_{ESC}$ were observed in eight MSs and one non-MS. A statistically significant increasing trend was identified in only one MS.

The increasing trends in 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 within the MS-group. Both KOI show that encouraging progress has been registered in reducing AMR in food-producing animals in several EU MSs over the last 10 years. Still, at the EU level and in certain MSs, trend slope changes have been observed for specific resistance combinations, CS in indicator *E. coli* from broilers and turkeys, and KOI$_{CS}$, with some previously declining resistance trends or increasing susceptibility trends stabilising and plateauing. Although these changes are based on recent data points and require further investigation to determine whether the plateaus represent short-term fluctuations or a sustained shift, they highlight the continuing need for reinforced efforts to combat AMR.

1 | INTRODUCTION

Terms of Reference

The European Union's monitoring system for zoonoses is established under **Directive 2003/99/EC**, which mandates the Member States (MSs) to collect data on zoonoses, zoonotic agents, antimicrobial resistance (AMR), animal populations and food-borne outbreaks. The framework of AMR monitoring is further detailed in Commission Implementing Decision 2020/1729 (EU).

In accordance with Article 9 of Directive 2003/99/EC, MSs must annually assess trends and sources of zoonoses, zoonotic agents, AMR, and food-borne outbreaks within their territory, submitting report to the European Commission (EC) by the end of May each year. EFSA is tasked with reviewing and analysing these national data and publishing a European Union Summary Report (EUSR) on the trends and sources of zoonoses, zoonotic agents and AMR in the EU.

EFSA collaborates with the European Centre for Disease Prevention and Control (ECDC), which collects, provides and analyses data on zoonotic infections, including AMR, in humans, reported to ECDC from the MSs.

The annual EUSR on zoonotic agents and AMR integrates data from humans, animals and food. It is supplemented by interactive dashboards and story maps, to evaluate the evolving epidemiological situation within the EU.

Antimicrobial resistance (AMR) arises when bacteria lose or reduce susceptibility to antimicrobial agents, potentially causing treatment failure in pathogenic infections. Resistance can develop through genetic mutations, horizontal gene transfer or activation of intrinsic resistance mechanisms and represents a major public health challenge due to the spread of resistant microorganisms among humans and animals. The widespread use of similar antimicrobials in both human and veterinary medicine, coupled with varying dosages and administration routes across populations and countries, accelerates the selection of resistant strains and can alter microbial communities. Resistant bacteria from food-producing animals may reach humans through contaminated food, direct contact or environmental pathways, with commensal flora acting as reservoirs for resistance genes transferable to pathogenic species. Factors such as antimicrobial use, poor hygiene and inadequate food-chain practices facilitate this process, ultimately reducing antimicrobial efficacy. In response, the European Commission's 2017 Action Plan adopts a One Health approach, promoting prudent antimicrobial use, cross-sector collaboration, enhanced infection control and systematic surveillance of AMR and antimicrobial consumption, thereby supporting the identification of emerging resistance patterns, the detection of temporal trends in the occurrence and distribution of AMR and informing risk assessments and targeted interventions.

1.1 | Monitoring and reporting of antimicrobial resistance in the EU

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). It provides guidance to the National Public Health Reference Laboratories (NPHRL) on susceptibility testing for EU surveillance and reporting to ECDC, facilitating cross-country comparison and integration with food- and animal-based AMR data. Based on the defined EU level surveillance objectives, the protocol describes the panel of antimicrobials to be tested, recommended methods (dilution or disc diffusion according to EUCAST), procedures for screening and confirming of ESBL-, AmpC- and carbapenemase-producing *Salmonella*, interpretive criteria and the reporting format to ECDC. For the joint reports with EFSA, human data are interpreted using EUCAST epidemiological cut-off values (ECOFFs), with countries required since 2014 (2013 data collection) to report quantitative susceptibility results per isolate. Following Decision 2018/945/EU which came into force in July 2018, EU Member States are legally required to report AMR test results according to the EU protocol. However, countries that do not perform antimicrobial susceptibility testing (AST) at NPHRLs continue to submit data from clinical laboratories, interpreted using clinical breakpoints. As WGS has started to replace phenotypic typing in the NPHRLs, ECDC has enabled the reporting of WGS-predicted resistance since 2020 and, from 2023, is encouraging countries to submit raw sequence data to enable harmonised AST interpretation.

ECDC provides external quality assessment (EQA) schemes through a contracting laboratory to support laboratories in implementing the recommended test methods and antimicrobials and ensuring high-quality AST results. Further capacity building activities, including training, EQA schemes on WGS and networking, was provided via the HaDEA-funded FWD AMR RefLabCap project (2021–2024).[2] In 2023 and 2024, ECDC has also funded the sequencing of 100 *Salmonella* isolates and 50–70 *Campylobacter* isolates for countries that have not yet, or have only recently started, implementing WGS for these pathogens.

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

Animals and food: Monitoring of antimicrobial resistance

Under Commission Implementing Decision (EU) 2020/1729, in effect 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 major domestically produced food-producing animal populations and their derived meat. Further characterisation is required for *E. coli* and *Salmonella* isolates resistant 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: fattening pigs and cattle under 1 year of age and their derived meat are targeted in odd-numbered years, while poultry populations (broilers, laying hens and fattening turkeys) and their meat are monitored in even-numbered years, as specified by the legislation.

Monitoring imported fresh meat at border control posts (BCPs) has also been undertaken to complement AMR monitoring in domestically produced food-producing animals. MSs may also voluntarily perform complementary monitoring for MRSA and *Enterococcus* spp. Representative random sampling of animals and derived meat is carried out using proportionate stratified sampling, in accordance with legislation and EFSA's technical specifications.

Microdilution methods are recommended for susceptibility testing, with results interpreted using EUCAST ECOFFs to assess microbiological resistance. Harmonised antimicrobial panels for *Salmonella*, *Campylobacter* and indicator commensal *E. coli* include substances important for human health, such as critically important antimicrobials (CIAs), providing insights into the resistance mechanisms involved. Concentration ranges encompass both ECOFFs and the clinical breakpoints (CBPs), as defined by EUCAST, facilitating comparison with human data. For *Salmonella* and *E. coli*, a supplementary antimicrobial panel is applied to isolates resistant to third-generation cephalosporins or carbapenems. Since 2021, WGS has been authorised as an alternative to phenotypic testing for isolates monitored for ESBL-/AmpC-/CP-producing *E. coli*, as well as 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 exhibiting high levels of phenotypic resistance to erythromycin. Although WGS use remains voluntary, technical standards have been established to ensure data comparability (EFSA, 2020).

External quality assurance is coordinated by the EURL-AR, which annually distributes panels of well-characterised organisms to all MSs for susceptibility testing and organises proficiency testing (PT) trials for the National Reference Laboratories for Antimicrobial Resistance (NRLs-AR). In collaboration with EFSA and the MSs, the EURL-AR performs reference testing exercises, including re-testing antimicrobial susceptibility and performing WGS on selected isolates (Appendix A – Materials and methods). Additionally, the EURL-AR also serves as a reference resource for MSs on susceptibility testing methodologies.

Data reporting is performed at the isolate level to facilitate analysis of the occurrence of resistance and multidrug resistance (MDR) patterns. This approach enables in-depth phenotypic characterisation of specific resistance mechanisms, such as third-generation cephalosporin and carbapenem resistance. Since 2021, voluntary reporting of WGS data on ESBL-/AmpC-/CP-producing *E. coli* and *Salmonella* isolates has enhanced understanding of the role of food-producing animals and derived food in the human AMR burden (EFSA, 2019). Further information on monitoring AMR in animals and food is available in the online story map on antimicrobial resistance monitoring (available here).

1.2 | The 2023–2024 EU summary report on AMR

This EUSR presents data on AMR in zoonotic and indicator bacteria from humans, animals and food collected in 2023 and 2024, jointly analysed by EFSA and ECDC with support from EFSA's contractors.

Human AMR data reporting and interpretation in 2024

For 2024 human data, EU MSs and non-MSs reported AST results for *Salmonella* spp. and *Campylobacter* spp. isolates from clinical cases of salmonellosis and campylobacteriosis. Phenotypic test results were submitted to EpiPulse Cases (the new surveillance system that has replaced the European Surveillance System, TESSy, in 2025) at the isolate level, either as quantitative or categorical/qualitative data, following 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 detect microbiological resistance, while qualitative phenotypic data were reported as susceptible, susceptible with increased exposure, or resistant, based on CBPs. CBPs enable clinicians to choose the appropriate treatment based on information relevant to the individual patient, whereas ECOFFs help epidemiologists identify small changes in bacterial susceptibility, which may indicate emerging resistance and allow for appropriate control measures to be considered. Because CBPs are often less sensitive than ECOFFs, combining the clinically resistant (R) and 'susceptible with increased exposure' (I) categories closely aligns with the ECOFF-based interpretation.

A few countries also reported genotypic data, either as WGS-predicted resistance or raw sequences analysed at ECDC with ResFinder and PointFinder, corresponding to the ECOFF-based classification. For assessing MDR, ECDC and EFSA have agreed on a harmonised panel of nine antimicrobial classes for *Salmonella* and four for *Campylobacter*, enabling cross-sector comparison.

Additional information on the human data reported in 2023 can also be found in the 2022–2023 EU Summary Report on AMR in zoonotic and indicator bacteria (EFSA and ECDC, 2025b). No human AMR data from the United Kingdom were submitted to ECDC for 2020–2024 following its withdrawal from the EU on 31 January 2020.

Animal and food AMR data reporting in 2024

Data on food-producing animals and derived meat primarily for 2024 originated from MSs and other reporting countries following 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, CS and MDR were reported at country levels, alongside phenotypic monitoring results for resistance to third-generation cephalosporins and/or carbapenems due to presumptive ESBL-/AmpC-/CP-producing *Salmonella* and *E. coli*. Data from voluntary monitoring of MRSA and *Enterococcus* spp. in food and animals are also included. Since 2021, the only data reported to EFSA from the United Kingdom have originated from Northern Ireland. In accordance with the Withdrawal Agreement between the United Kingdom and the European Union, specifically Article 5(4) of the Windsor Framework (Joint Declaration No 1/2023, OJ L 102, 17.4.2023, p. 87) and section 24 of Annex 2 to the Framework, references to MSs under this regulation include the United Kingdom with respect to Northern Ireland. Consequently, EU data sampling requirements apply to Northern Ireland (XI), and data submitted by the United Kingdom (Northern Ireland) have been included within the MSs' dataset. The data analysed were extracted from the EFSA AMR database on 19 September 2025.

Classification of antimicrobials according to WHO and AMEG

Various organisations classify antimicrobials according to their significance in human and/or animal health. In this report, antimicrobials are categorised based on the World Health Organisation's *List of Medically Important Antimicrobials* (WHO, 2024) and the European Medicines Agency's Antimicrobial Advice Ad Hoc Expert Group (AMEG) classification of antibiotics by their relevance to human and animal health (EMA, 2019).

WHO categorisation considers both the significance for human medicine and the AMR risks and potential human health implications associated with of the use in non-human sectors. Based on this categorisation, antimicrobials fall in the following categories: **authorised for use in humans only**, **highest priority critically important** (HPCIA), **critically important** (CIA), **highly important** (HIA), **important to human medicine** and **authorised for use in animals only**.

AMEG categorisation classifies the antimicrobial substances based on their recommended use in veterinary medicine. **Group D** (**Prudence**) includes first-line treatment options; **Group C** (**Caution**) comprises antimicrobials which should be used only when Group D options are ineffective; **Group B** (**Restrict**) includes antimicrobials that require susceptibility testing prior to use and that should be reserved for cases where no Group C or D alternatives are effective; **Group A** (**Avoid**) covers antimicrobials that are not authorised for veterinary use in the EU and must not be administered to food-producing animals.

Further information on antimicrobial categorisations can be found in the EFSA's story map on monitoring antimicrobial resistance (available online here).

1.2.1 | Structure, contents and supplementary materials of the report

This report comprises an introduction, followed by six main chapters addressing AMR in *Salmonella*, *Campylobacter*, indicator commensal *E. coli*, ESBL-/AmpC-/CP-producing *Salmonella* and *E. coli*, *Enterococci* and MRSA. Each chapter includes sections on resistance in isolates from humans, food-producing animals and where applicable, derived meat, with key findings highlighted at the beginning of each chapter. Appendices containing complementary information are provided at the end of the report. Detailed descriptions of the materials and methods used in this EUSR on AMR are available in **AppendixA – Materials and methods**. Annexes are listed in **AppendixB** – **Additional information and supporting data** and can be accessed via the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17950222

EFSA communication tools on antimicrobial resistance

Accompanying this report, EFSA has published communication tools on the EFSA website, including four Story Maps covering AMR monitoring in *Salmonella, Campylobacter, E. coli* and MRSA, as well as two Dashboards presenting Key Indicators of AMR and data on AMR in *Salmonella*, *Campylobacter*, indicator commensal *E. coli* and the occurrence of MRSA.

The EFSA dashboard on AMR (available online here) is an online graphical user interface that enables interactive querying and visualisation of the large amount of AMR data collected each year by EFSA from the EU MSs and other reporting countries under the EU legislation. It displays yearly data and temporal trends in resistance to selected antimicrobials in the bacterial species investigated from broilers, fattening turkeys, fattening pigs and cattle under 1 year of age through charts, graphs and maps. The user can filter results by reporting year, country, animal population and antimicrobial substance. Key statistics are also available in downloadable tabular format.

Human AMR data for *Salmonella* and *Campylobacter* are accessible via the ECDC Surveillance Atlas of Infectious Diseases (on the ECDC website).

The EU MSs, other reporting countries, the EC and the EURL-AR were consulted during the report's preparation.

Ten years of harmonised monitoring in food-producing animals and meat

This year marks the 10th anniversary of the harmonised AMR monitoring programme targeting the most important food-producing animal populations domestically produced across Europe. It marks a decade of sustained commitment to combatting AMR across Europe. Over the past decade, this programme has ensured essential surveillance of key zoonotic (*Salmonella, Campylobacter*) and indicator bacteria (*E. coli*), offering critical insights into the occurrence and trends of AMR within these sectors. EU legislation – specifically Commission Implementing Decisions (EU) 2020/1729 and 2013/652/EU, Directive 2003/99/EC – has established monitoring priorities based on public health considerations, setting out the minimum mandatory requirements from 2014 onwards.

A major achievement of the programme has been the establishment of standardised methodologies of representative sampling designs and laboratory protocols, ensuring consistency in data collection and analysis across the EU Member States and participating countries, as well as over time. Antimicrobials have been selected based on their relevance to human therapy – especially highest priority critically important antimicrobials (CIAs) – and/or epidemiological significance. For example, colistin, tigecycline and carbapenems have been included for public health purposes in *E. coli* and *Salmonella*. Microbiological resistance is assessed using EUCAST ECOFFs to detect emerging resistance from an epidemiological perspective.

Selective monitoring of ESBL-, AmpC- and carbapenemase-producing *E. coli* has also been implemented. In addition, countries may voluntarily monitor MRSA, *Enterococcus faecium* and *Enterococcus faecalis*. The scope of harmonised AMR monitoring was expanded to include imported fresh meat at border control posts. Surveillance of ESBL-, AmpC- and CP-producing *E. coli* was also extended to specifically target CP-producing strains. Whole genome sequencing (WGS) has been introduced to complement phenotypic testing, particularly for isolates resistant to extended-spectrum cephalosporins and/or carbapenems. WGS is also recommended for *Campylobacter* isolates showing high-level phenotypic resistance to erythromycin.

The external quality assurance of the monitoring programme, provided through annual proficiency and reference testing, the standardised data collection, reporting and analysis framework put in place by EFSA, as well as the harmonised sampling designs and statistical appraisal of outputs has ensured robustness. The EFSA Network on the monitoring of AMR, which includes experts from MSs and reporting countries, have met regularly to review findings, discuss new developments and address harmonisation and emerging issues. This harmonisation has enhanced the quality, representativeness, reliability and comparability of AMR data, facilitating cross-country and longitudinal comparisons, creating a robust evidence base to support effective monitoring and intervention strategies at both national and EU levels.

Key outcome indicators (KOIs) have been established to track resistance trends to support the EU MSs in monitoring their progress in reducing AMR in food-producing animals. The KOIs aim to provide harmonised, quantitative measures that allow for the evaluation of long-term trends and the assessment of the effectiveness of national and EU-wide AMR reduction strategies. Two KOIs are currently defined as the proportion of indicator *E. coli* susceptible to all tested antimicrobials (KOI_{CS}), and the occurrence of ESBL-/AmpC-producing *E. coli* in samples from healthy animals and meat (KOI_{ESC}).

Over the past decade, the programme has played a pivotal role in identifying emerging resistance threats and tracking resistance trends, thereby informing risk assessments and contributing significantly to the protection of both animal and human health. Harmonised monitoring has notably facilitated the detection of specific multidrug-resistant *Salmonella* serovars (e.g. Infantis, Kentucky), the identification of high-level fluoroquinolone resistance in *S*. Kentucky and the screening for carbapenemase producers.

Among the programme's notable achievements are documented reductions in resistance levels in specific bacteria and animal populations, reflecting the positive impact of coordinated monitoring and intervention efforts of the MSs. Statistically significant decreases in resistance to certain antimicrobials, along with increasing trends in CS and KOI_{CS} values, demonstrate measurable progress in reducing AMR across several countries – particularly in broilers and turkeys. Over the past decade, the KOI_{CS} increased significantly with a rate of change of 47%.

Complementing routine AMR monitoring with targeted risk assessment, the ongoing 2025 EU-wide baseline survey (BLS) aims to determine the prevalence, genetic diversity and virulence traits of MRSA in fattening pigs. Although MRSA surveillance has been fragmented, national efforts continue to inform trends in genotype and resistance. The 2025 BLS will produce harmonised data, enabling comparison with the 2008 BLS in breeding pigs – conducted in 17 of 24 MSs and identifying ST398 as the dominant type – and provide a clearer view of temporal developments.

Following a One Health approach, representative and harmonised AMR data reported by the EU MSs and compiled in the EUSR on AMR have enabled integrated analyses of antimicrobial consumption (AMC) and AMR across animals, food and humans. These analyses are regularly published in the Joint Interagency Antimicrobial Consumption and Resistance Analysis (JIACRA) reports (ECDC, EFSA and EMA, 2024) and to date, four reports have been published, with the fifth expected in 2026. JIACRA analysis notably showed that countries reducing total AMC often reported increased susceptibility – manifested as 'CS' or 'zero resistance' – in indicator *E. coli* from animals and *E. coli* from human invasive infections. These findings indicate that implemented measures to reduce AMC have been effective in many countries.

The success of the harmonised monitoring of AMR in animals is the result of strong collaboration between EU institutions, MSs, national reference laboratories, who have worked together to enhance AMR surveillance. Still, at the EU level and in certain MSs, trend slope changes were identified for certain resistance combinations and CS in indicator *E. coli* from broilers and turkeys, as well as the KOI_{CS}: some previously declining resistance trends or increasing CS trends have stabilised and recently plateaued. Although these trend changes are based solely on recent data points and request further investigation to determine whether the plateaus reflect a short-term fluctuation or a sustained interruption of previous trends, they also underscore the need for reinforced efforts to combat AMR.

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 targeted food-producing animals also varied considerably among reporting countries. In 2024, AMR data on *Salmonella* spp. were reported in broilers (26 MSs, the United Kingdom (Northern Ireland) and 3 non-MSs), laying hens (26 MSs, the United Kingdom (Northern Ireland) and 1 non-MS) and fattening turkeys (20 MSs, the United Kingdom (Northern Ireland) and 1 non-MS). In 2023, 25 MSs, the United Kingdom (Northern Ireland) and 2 non-MSs reported *Salmonella* from pigs, while 11 MSs reported data from calves.
- Overall resistance to **ampicillin, sulfonamides** and **tetracyclines** was observed at high levels in *Salmonella* spp. isolates from humans in 2024 and ranged from moderate to very high in isolates from targeted food-producing animals, except in laying hens, where low levels of resistance were reported.
- Over the period 2014–2024, statistically significant declining **trends** in resistance to ampicillin and tetracyclines were observed in isolates from humans in 19 and 14 countries, respectively. This decline was primarily driven by a reduction in resistance in *S*. Typhimurium and for tetracycline, also in monophasic *S*. Typhimurium, both serovars commonly associated with pigs and calves. In poultry populations, a decreasing trend in tetracycline resistance at the MS-group level was registered in isolates from broilers, while in turkey isolates, decreasing trends were observed in both ampicillin and tetracycline resistance. No trend analyses were performed for pigs or calves due to an insufficient number of data points.
- Overall resistance to **fluoroquinolones (ciprofloxacin)** was observed at high to very high levels in *Salmonella* isolates from humans (21.2%), laying hens (22.0%), broilers (49.7%) and fattening turkeys (32.7%) in 2024 and at moderate levels in fattening pigs (14.9%) and calves (16.3%) in 2023. A statistically significant increasing trend in ciprofloxacin resistance was observed in 15 of 27 MSs in *Salmonella* spp. from humans in the period 2014–2024. A statistically significant increasing trend in ciprofloxacin resistance at the MS level was also registered in *Salmonella* isolates from laying hen flocks. Conversely, a decreasing trend was observed in fattening turkeys.
- **Extremely high resistance to ciprofloxacin** was mostly reported in *S*. Kentucky isolates from humans. In 2024, 2.5% of *Salmonella* from humans expressed high-level resistance to ciprofloxacin, of which 78.9% were *S*. Kentucky. Of the 10 ciprofloxacin-resistant *S*. Kentucky with sequences available, all belonged to ST198. Nine displayed two mutations each in *parC* and *gyrA*, and the tenth carried a *qnr*-gene. Among the *Salmonella* isolates from broilers displaying ciprofloxacin resistance, 5.4% (20 *S*. Newport, 17 *S*. Infantis, 14 *S*. Kentucky) exhibited MICs of ≥ 4 mg/L. While from turkeys and laying hens, 6.5% (12 *S*. Kentucky and 1 *S*. Newport) and 1.3% (2 *S*. Kentucky and 1 *S*. Enteritidis), respectively, also exhibited high-level ciprofloxacin resistance. This represents an increase in the proportion of isolates from broilers and turkeys exhibiting high-level resistance compared with 2022 data (4.2% and 3.3%, respectively). Compared to 2022, in 2024, serovars other than *S*. Kentucky were more commonly associated with high-level ciprofloxacin resistance in broilers, whereas in turkeys and laying hens, the predominance of this serovar was consistent across both years.
- Overall resistance to **third-generation cephalosporins** was noted at low levels in isolates from humans in 2024 (1.8%), at very low levels in turkeys (0.2%), laying hens (0.3%) and pigs (0.8%) and at low levels in broilers (1.0%) and calves (1.3%). Consequently, the overall proportion of presumptive ESBL-/AmpC-producing *Salmonella* spp. at the MS level was generally very low/low in 2023 and 2024 among all targeted food-producing animal populations and very low in isolates from human cases, although higher resistance was observed in specific *Salmonella* serovars.

- In 2023 and 2024, no *Salmonella* spp. isolates recovered from animals or meat were microbiologically **resistant to meropenem**. However, five isolates (< 0.1%) from humans were meropenem resistant in 2024, with one country reporting three patients with such isolates and another two countries one case each.
- Overall, **combined resistance to fluoroquinolones and cephalosporins** was low in isolates from humans and very low in food-producing animals. A clear decrease in combined resistance in the serovar Kentucky was observed in isolates from broilers when compared to 2022.
- **Multidrug resistance** (MDR) was overall moderate (18.7%) among *Salmonella* spp. reported in human cases in the EU, but varied by serovar from low in *S*. Enteritidis (3.2%) and *S*. Derby (5.2%) to very high in monophasic *S*. Typhimurium (64.6%) and *S*. Kentucky (67.8%). MDR was observed at high levels in *Salmonella* recovered from pigs (43.3%), broilers (35.1%), turkeys (22.9%) and calves (25.0%), while in laying hens, a markedly lower MDR level (6.0%) was observed. MDR in *S*. Infantis isolates from broilers (82.2%) and turkeys (80.0%) showed considerably higher MDR values than in laying hens (28.8%) and in humans (47.3%). *S*. Kentucky isolates exhibited higher MDR levels in humans and turkeys than when recovered from other animals.
- Overall, in 2024, **complete susceptibility** (CS) in *Salmonella* spp. isolates from humans was observed in 57.9% of the tested isolates. In isolates from animals, CS was high in broilers (38.1%) and pigs (36.8%), very high in turkeys (56.7%) and calves (56.3%), and extremely high in laying hens (72.4%).

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

This section focuses on **Non-Typhoidal Salmonellas (NTS)** and summarises the occurrence and AMR patterns of isolates recovered from the food-producing animal populations specified in the Commission Implementing Decision (EU) 2020/1729 and fresh meat from broilers and turkeys taken at the border control posts (BCPs). Typhoidal salmonellas are human host-adapted organisms causing typhoid and paratyphoid fever, while NTS 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 NTS, *Campylobacter* spp. and *E. coli* (WHO, 2019). Thus, the WHO urges the recognition of this transmission potential. In 2024, salmonellosis was the second most reported food-borne zoonosis in the European Union, with 79,703 confirmed human cases. It was the most frequent causative agent in food-borne outbreaks, accounting for 18.9% of all food-borne outbreaks reported in 2024 (EFSA and ECDC, 2025a).

Further information on AMR in *Salmonella* 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).

Under Commission Implementing Decision (EU) 2020/1729, the harmonised AMR monitoring in *Salmonella* is conducted in food-producing animals on a biennial basis following a rotating scheme. Accordingly, this chapter describes 2024 AMR data on *Salmonella* isolates from faecal samples and/or environmental samples (boot swabs or dust) collected from broilers, laying hens and fattening turkeys under the National Control Programmes (NCPs), as well as fresh meat from broilers and turkey at border control posts (BCPs) (see textbox '**Monitoring AMR in imported fresh meat at BCP**'), and 2023 AMR data from bovine animals under 1 year of age at slaughter (referred to as 'calves') and fattening pigs. Results on *Salmonella* spp. isolates include all serovars reported from the different animal origins. 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.

Salmonella 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 *Salmonella* infections. This report covers AMR data for *Salmonella* spp. from human cases in 2024. Data from 2023 are presented in the 2022–2023 report (EFSA and ECDC, 2025b). Antimicrobial susceptibility testing (AST) results from *Salmonella* isolates from human cases include all tested serovars and are also presented separately for the most prevalent serovars in food-producing animals.

Data on AMR in *Salmonella* spp. from food-producing animals can be further visualised interactively using the EFSA dashboard on AMR in *Salmonella*, available online here and AMR data from human isolates 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 reporting, is 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, 2025). Further consideration on the data used and the methodology applied in the analysis can be found in Appendix A – Materials and methods.

Variations in *Salmonella* prevalence from targeted food-producing animals

In 2023 and 2024, countries reported data on *Salmonella* spp. from the different animal populations, depending on their national situation. Some MSs did not obtain any *Salmonella* isolates from animal or meat origins, and therefore, no data are presented for those countries.

In 2024, more MSs reported data from broilers and laying hens than from fattening turkeys. Similarly, in 2023, the number of countries reporting results for fattening pigs was higher than for calves. This difference can be attributed to the small size of the calves and fattening turkey sectors in certain MSs, where production levels fall below the threshold at which monitoring is mandatory. Additionally, the number of isolates reported varied across countries, reflecting different *Salmonella* prevalence. These factors may be a source of variation in the results when considering all reporting countries.

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

2.3.1 | Data reported

For 2024, 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), three as data interpreted with CBPs and five 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 26.8% 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 2024, high proportions of human *Salmonella* isolates were resistant to **ampicillin** (20.8%), **sulfonamides** (23.5%) and **tetracyclines** (21.8%) (Figure 1; Table 1; Annex A.1, table 1). By serovar, resistance to these compounds ranged from 3.1% to 5.6% in *S.* Enteritidis to extremely high in monophasic *S.* Typhimurium 1,4,[5],12:i:-(74.1%–82.9%). 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 in Italy (41.8%) and Portugal (45.1%), sulfonamides in Italy (44.8%) and tetracycline in Hungary (40.5%), Italy (46.2%) and Portugal (43.0%) (Annex A.1, table 1). In the case of Portugal, this was due to an increase in salmonellosis cases with *S.* Typhimurium and its monophasic variant. For *S.* Enteritidis, outliers with a higher proportion of resistance to sulfonamides were observed in Greece (35.5%) and Italy (10.1%) (Annex A.1, table 2). For monophasic *S.* Typhimurium, an outlier in terms of a lower proportion of resistance was observed in Denmark for ampicillin (39.1%) (Annex A.1, table 4). The low resistance in Denmark was due to a large outbreak with a fully susceptible strain of monophasic *S.* Typhimurium. For *S.* Infantis, Czechia, Slovakia and Slovenia reported much higher proportions of resistance to ampicillin (50.0%, 48.8% and 57.1%, respectively) compared to other countries (Annex A.1, table 5). For *S.* Kentucky, Sweden was an outlier in reporting much lower levels of resistance to ampicillin (26.7%) (Annex A.1, table 6).

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 (37.0%) at the EU level (Annex A.1, table 6). Similarly, levels of trimethoprim resistance were overall low among *Salmonella* spp. (5.9%) (Annex A.1, table 1), but moderate in monophasic *S.* Typhimurium (10.2%) and *S.* Infantis (13.0%) and high in *S.* Kentucky (25.6%) (Annex A.1, tables 4–6).

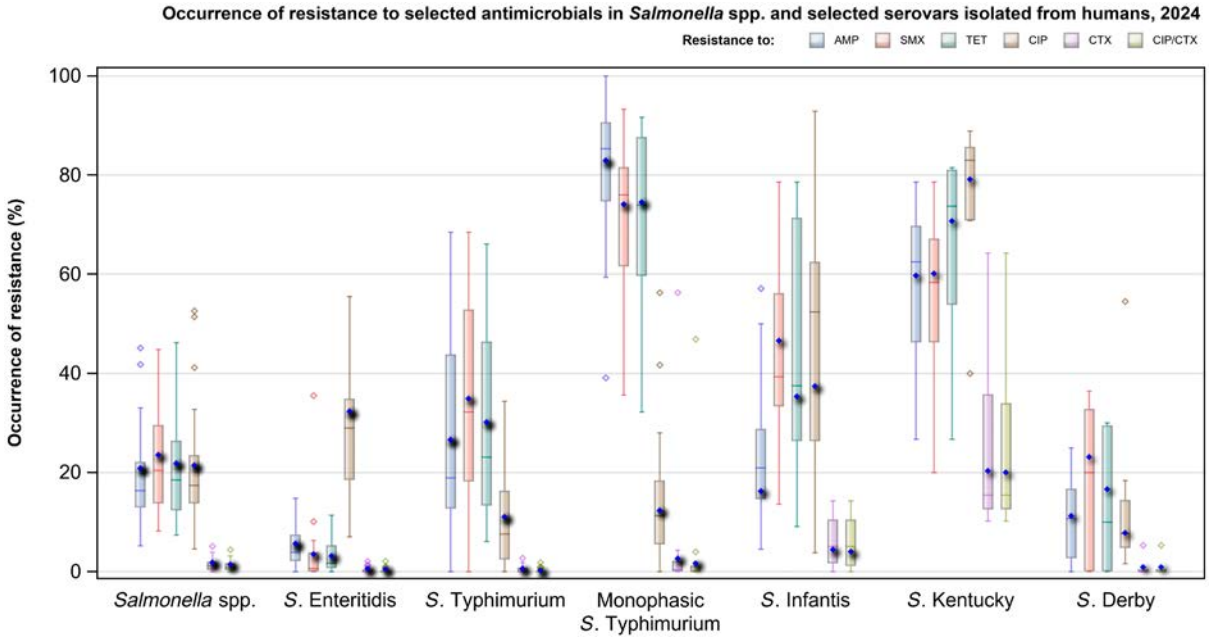


FIGURE 1 Occurrence of resistance to selected and critically important antimicrobials in *Salmonella* spp. and selected serovars isolated from humans, 2024.
Only MSs reporting data for 10 or more isolates are shown in the graph; however, all isolates are included in the calculation of resistance at the reporting MS-group level.
Abbreviations: AMP, ampicillin; Blue diamond, Resistance at the reporting MS-group level; CIP, ciprofloxacin; CIP/CTX, combined 'microbiological' resistance to ciprofloxacin and cefotaxime; Horizontal lines represent median; Lower and upper box boundaries, 25th and 75th percentiles, respectively; CTX, cefotaxime; SMX, sulfamethoxazole; TET, tetracycline.

TABLE 1 Occurrence of resistance to selected and critically important antimicrobials in *Salmonella* spp. and selected serovars from humans, 2024.

	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)	19,773	**20.8**	11,038	**23.5**	17,424	**21.8**	19,502	**21.4**	18,765	**1.8**	18,698	**1.4**
S. Enteritidis (27 MSs)	6360	**5.6**	3701	**3.5**	4854	**3.1**	6143	**32.3**	5794	**0.6**	5745	**0.5**
S. Typhimurium (27 MSs)	2078	**26.6**	1232	**34.9**	1862	**30.1**	2056	**11.0**	1959	**0.6**	1956	**0.2**
Monophasic *S.* Typhimurium (23MSs)	2499	**82.9**	1626	**74.1**	2416	**74.5**	2496	**12.3**	2499	**2.6**	2494	**1.6**
S. Infantis (26 MSs)	1198	**16.2**	401	**46.6**	1133	**35.3**	1194	**37.4**	1187	**4.4**	1186	**4.0**
S. Kentucky (20 MSs)	325	**59.7**	248	**60.1**	314	**70.7**	325	**79.1**	325	**20.3**	325	**20.0**
S. Derby (22 MSs)	322	**11.2**	143	**23.1**	301	**16.6**	319	**7.8**	316	**0.9**	316	**0.9**

Note: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. The correspondence between colour and resistance level categories can be found in the 'Definitions' section.

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' (HPCIAs) and last resort antimicrobials

The proportion of *Salmonella* isolates resistant to the HPCIA) **ciprofloxacin** was overall 21.4% (Figure 1; Table 1). A high proportion of resistance to ciprofloxacin was observed in isolates of *S.* Enteritidis (32.3%) and *S.* Infantis (37.4%), while an extremely high proportion was observed in *S.* Kentucky isolates (79.1%) (Figure 1, Annex A.1, tables 2, 5 and 6). At country-level, the highest level of ciprofloxacin resistance in *Salmonella* spp. in 2024 was observed in Poland, Romania and Slovakia (51.4%, 52.6% and 41.2%, respectively). Poland and Romania reported the highest resistance in *S.* Enteritidis (55.5% and 54.6%, respectively) (Figure 2A, Annex A.1, table 2) and Finland and Slovenia the highest resistance in monophasic *S.* Typhimurium (41.7% and 56.3%, respectively) (Annex A.1, table 4). Ciprofloxacin resistance varied greatly in *S.* Infantis from 3.8% in Lithuania to 92.9% in Slovenia (Figure 2B, Annex A.1, table 5). For *S.* Kentucky, Sweden reported much lower levels of ciprofloxacin (40.0%) while for *S.* Derby, Poland reported much higher levels (54.5%) (Annex A.1, tables 6, 7). Caution should be taken when interpreting results for some countries as they report data on a small number of isolates.

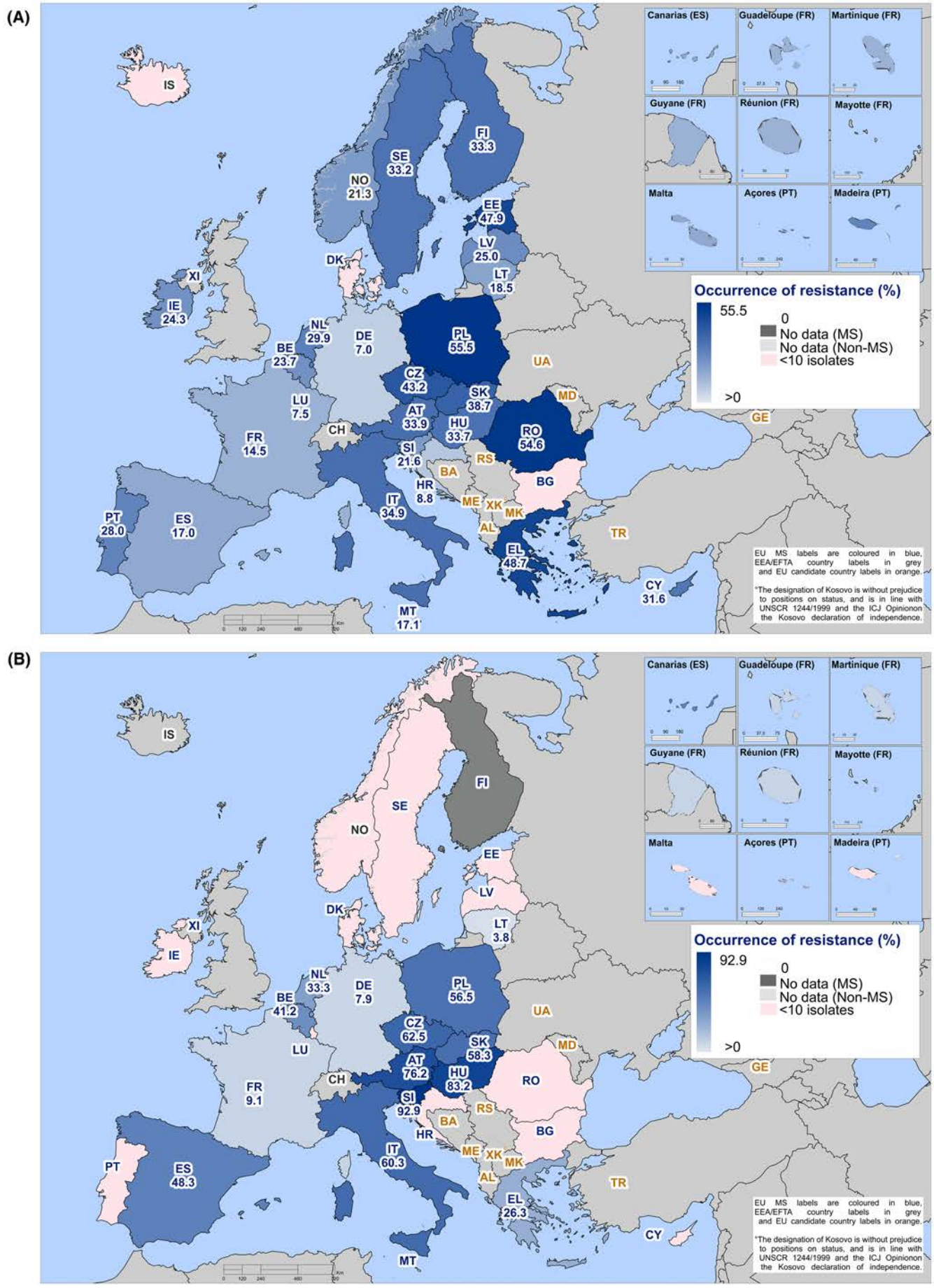


FIGURE 2 Spatial distribution of ciprofloxacin resistance among (A) *S*. Enteritidis; and (B) *S*. Infantis isolated from human cases, 2024. The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

For **cefotaxime** and **ceftazidime**, representing third-generation cephalosporins, another class of HPCIAs for *Salmonella*, resistance levels were generally low among *Salmonella* spp. (1.8% and 1.5%, respectively) (Annex A.1, table 1), with very low to moderate levels of resistance ranging from 0.3% to 20.4% across the serovars of interest (Annex A.1, tables 2–7). Resistance was more pronounced in *S.* Infantis and *S.* Kentucky isolates (4.4% and 20.4% resistance to cefotaxime) (Table 1; Annex A.1, tables 5 and 6). Outliers in terms of high resistance to third-generation cephalosporins were observed in Slovenia for *Salmonella* spp. (5.1%), in Belgium and Hungary for *S.* Enteritidis (2.1% and 1.4%, respectively), in Hungary for *S.* Typhimurium (2.7%), in Slovenia for monophasic *S.* Typhimurium (56.3%), in Austria for *S.* Kentucky (64.3%) and in Hungary for *S.* Derby (5.3%) (Annex A.1, tables 1–4, 6, 7). Seventeen and fourteen countries tested resistance to last-line antimicrobials **azithromycin** and **tigecycline**. Resistance was overall low among *Salmonella* spp. (1.0% and 3.2%, respectively) (Annex A.1, table 1). Among the individual serovars, the highest level of resistance to azithromycin was observed in *S.* Kentucky (14.8%) and the highest level of resistance to tigecycline in *S.* Infantis (17.7%; Annex A.1, tables 6 and 5). Two isolates of *S.* Kentucky, in two different countries, were found to carry the transferrable plasmid-mediated tigecycline resistance gene *tet*(X4). Resistance to **colistin** was detected in 7.4% of *Salmonella* isolates, with resistance being most pronounced in *S.* Enteritidis (18.4%) and *S.* Dublin (68.2%) 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., 2020a, 2020b). Resistance mechanisms conferring resistance to polymyxins/colistin was not detected in any of 1590 isolates from the five countries reporting sequences for AMR. Only one isolate carried an mcr-9 gene, which however does not give phenotypic resistance to colistin (Tyson et al. 2020).

Combined resistance to both ciprofloxacin and cefotaxime was overall low in *Salmonella* spp. in human cases (1.4%) (Figure 3A; Annex A.1, table 1) and very low overall in the serovar *S.* Enteritidis, *S.* Typhimurium, monophasic *S.* Typhimurium and *S.* Derby (0.5%, 0.2%, 1.6% and 0.9%, respectively, Annex A.1, tables 2–4 and 7). An exception was a high combined resistance in Slovenia for monophasic *S.* Typhimurium (46.9%) (Annex A.1, table 3). Overall higher levels of combined resistance were observed in *S.* Infantis (4.0%) and *S.* Kentucky (20.0%; Figure 3B,C and Annex A.1, tables 5–6) where Austria reported the highest proportion of combined resistance in *S.* Kentucky (64.3%).

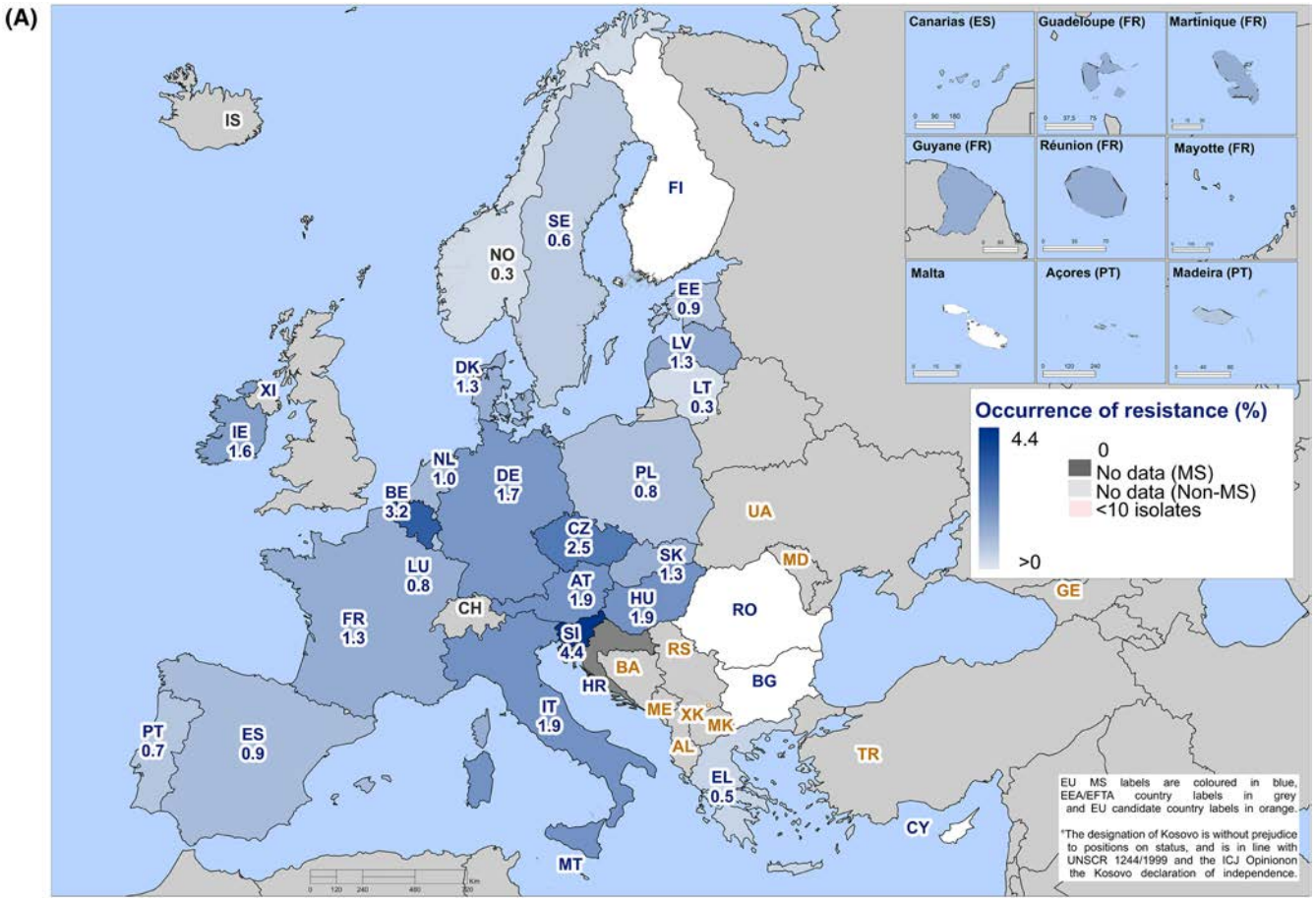


FIGURE 3 (Continued)

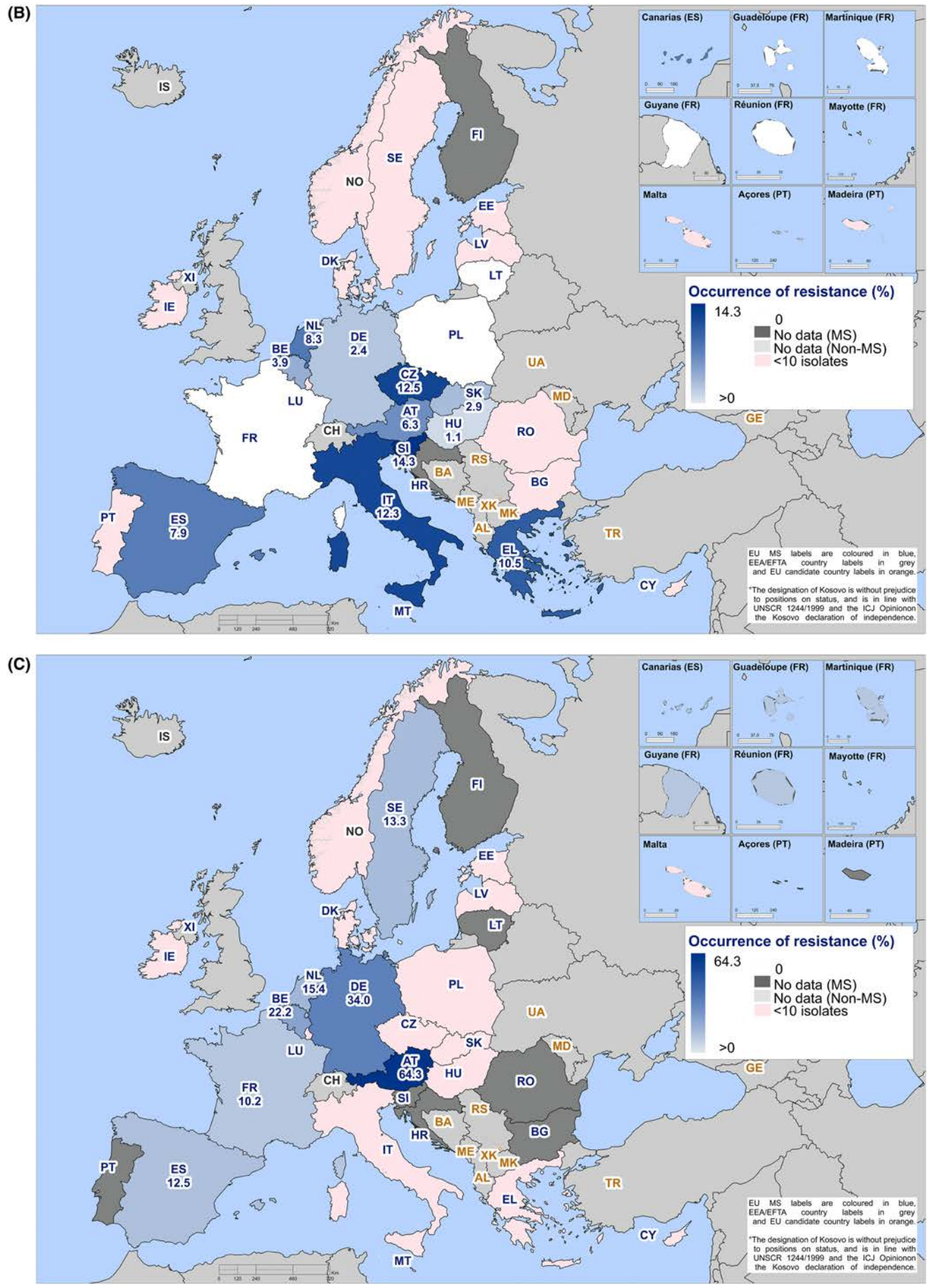


FIGURE 3 Spatial distribution of combined microbiological resistance to ciprofloxacin and cefotaxime among (A) *Salmonella* spp., (B) *S*. Infantis and (C) *S*. Kentucky isolated from human cases, 2024.
The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 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-MSs reporting data on **third-generation cephalosporins** in 2024, resistance was either not detected (5 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). Five countries (France, Germany, Italy, Slovakia and Spain) had not confirmed all presumptive ESBL/AmpC isolates, possibly due to CBPs being used in routine AST and not ECOFFs.

ESBL-producing *Salmonella* were identified in 0.9% of the tested isolates, ranging by country from 0% in Bulgaria, Cyprus, Finland, Malta, Romania and Iceland to 2.8% in Belgium (Annex A.1, table 8). AmpC was less frequent, identified in 0.1% of tested isolates, with the highest occurrence in Italy and Slovakia (both with 0.8%). Five isolates (0.03%) were reported to be both AmpC-and ESBL-producing. Five isolates (0.03%) from three different countries carried a carbapenemase (Annex A.1, table 8). ESBL-producing isolates were reported in 24 serovars, with the highest proportions observed in isolates of *S*. Kentucky (13.3%), *S*. Anatum (10.7%), *S*. Heidelberg (5.8%), *S*. Indiana (5.3%), *S*. Ohio (4.3%), *S*. Saintpaul (4.2%) and *S*. Infantis (4.1%), among the isolates where at least 10 isolates had been tested (Table 2). AmpC-type beta-lactamases were overall reported in 10 serovars, with the highest proportion observed in *S*. Minnesota (27.3%), *S*. Goldcoast (3.8%), *S*. Give (2.6%) and *S*. Newport (2.5%). Of the five meropenem resistant isolates, three were monophasic *S*. Typhimurium and one each was *S*. Agona and *S*. Eppendorf. Two of the isolates carried $bla_{\text{OXA-181}}$, two carried $bla_{\text{OXA-48}}$ and one carried $bla_{\text{IMP-1}}$ (Table 2; Annex A.1, table 8). It should be noted that in five 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, 2024.

	Tested for CTX and/or CAZ	Res to CTX and/or CAZ	Resistance phenotype								Tested negative for ESBL. AmpC, CP		Genotype (bla genes) (N)
			ESBL		AmpC		AmpC + ESBL		Carbapenemase				
Serovar	***N***	***N***	***N***	**%**	***N***	**%**	***N***	**%**	***N***	**%**	***N***	**%**	
Agona	196	3	1	0.5					1	0.5	1	0.5	IMP-1 (1), OXA-1 (1)
Anatum	56	8	6	10.7									SHV-12 (5), TEM_ SHV (1)
Bredeney	50	4	1	2.0							2	4.0	CTX-M-55 (1)
Chester	287	2	1	0.3									CTX-M-65 (1)
Concord	8	1	1	NA									CTX-M-15 (1)
Corvallis	84	1	1	1.2									CTX-M-15 (1)
Enteritidis	5999	23	11	0.2	1	0.0	4	0.1					CTX-M-1 (1), CTX-M-55 (1), DHA (1), TEM-52 (5), TEM-52B (1)
Eppendorf	3	1							1	NA			OXA-48 (1)
Give	38	1			1	2.6							DHA-like (1)
Goldcoast	52	3	1	1.9	2	3.8							CMY-2 (2), CTX-M-3 (1)
Heidelberg	52	3	3	5.8									CTX-M-15 (1), CTX-M-65 (2)
Indiana	19	1	1	5.3									VEB-1 (1)
Infantis	1017	49	43	4.2	1	0.1					2	0.2	CMY-2 (1), CTX-M-1 (14), CTX-M-15 (1), CTX-M-3 (7), CTX-M-55 (1), CTX-M-65 (17)
Isangi	32	1	1	3.1									
Kapemba	53	1			1	1.9							CMY-2 (1)
Kentucky	323	64	42	13.0	1	0.3					1	0.3	CMY-2 (1), CTX-M-14 (18), CTX-M-14 & CTX-M-15 (2), CTX-M-14b (2), CTX-M-15 (1), CTX-M-55 (3), CTX-M-like (13)
London	71	1	1	1.4									CTX-M-15 (1)
Mikawasima	195	1	1	0.5									CTX-M-32 (1)
Minnesota	11	4			3	27.3							CMY-2 (3)

(Continues)

TABLE 2 (Continued)

Serovar	Tested for CTX and/or CAZ	Res to CTX and/or CAZ	Resistance phenotype								Tested negative for ESBL. AmpC, CP		Genotype (bla genes) (N)
			ESBL		AmpC		AmpC + ESBL		Carbapenemase				
	N	*N*	*N*	%	*N*	%	*N*	%	*N*	%	*N*	%	
Monophasic typhimurium 1.4.[5].12:i:-	2091	46	33	1.5	5	0.2			3	0.1	2	0.1	CMY-2 (4), CMY-3 (1), CTX-M-1 (18), CTX-M-14 (2), CTX-M-15 (1), CTX-M-55 (1), CTX-M-65 (6), CTX-M-65, OXA-10 (1), CTX-M-9 (1), OXA-181 (2), OXA-48 (1), SHV-12 (2)
Muenster	99	1	1	1.0									CTX-M-55 (1)
Newport	353	21	3	0.8	9	2.5					2	0.6	CTX-M-1 (1), CTX-M-15 (1), DHA-1 (7)
Ohio	23	1	1	4.3									CTX-M-32 (1)
Saintpaul	119	6	5	4.2							1	0.8	CTX-M-55 (5)
Schwarzengrund	16	3	1	1.0									CTX-M-55 (1)
Stanley	122	1	1	0.8									CTX-M-15 (1)
Typhimurium	1914	8	5	0.3	2	0.1	1	0.0			2	0.1	CMY-2 (1), CTX-M-1 (1), CTX-M-15 (2)
Virchow	137	1	1	0.7									SHV-12 (1)

Note: Hungary 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 2024 was 57.9% in *Salmonella* spp. from humans, with the highest proportion in *S*. Derby (66.1%), *S*. Enteritidis (63.0%), *S*. Typhimurium (56.6%) and *S*. Infantis (42.5%). The lowest levels of CS were observed in *S*. Kentucky (18.4%) and monophasic *S*. Typhimurium (12.2%) (Figure 4; Annex A.1, tables 9–14). MDR was overall at 18.7% (*N* = 10,511) among *Salmonella* spp. (Figure 4; Annex A.1, table 9). Among the investigated serovars, MDR was most frequently reported among *S*. Kentucky (67.8%) and monophasic *S*. Typhimurium 1,4,[5],12:i:-(64.6%), followed by *S*. Infantis (47.3%), *S*. Typhimurium (16.8%), *S*. Derby (5.1%) and lastly *S*. Enteritidis (3.2%) (Figure 4; Annex A.1, tables 10–15). Seventeen isolates (six monophasic *S*. Typhimurium, 4 *S*. Infantis, 4 *S*. Saintpaul and 1 each of *S*. Agona, *S*. Goldcoast and *S*. Kentucky) were resistant to eight of the 9 tested substances, 15 of which were only susceptible to meropenem while two were resistant also to meropenem but susceptible to either gentamicin (*S*. Agona) or ciprofloxacin (one of the monophasic *S*. Typhimurium).

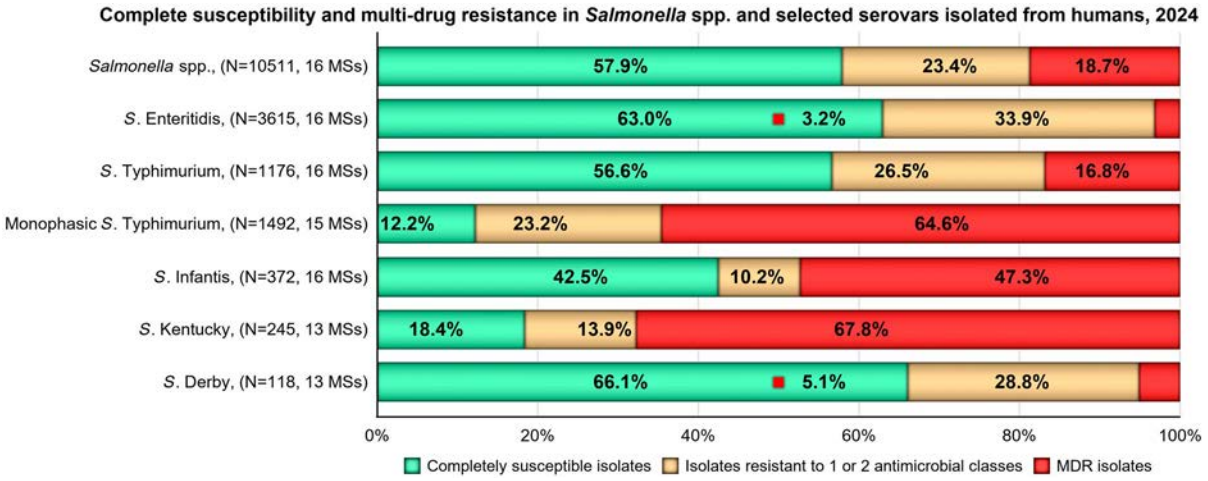


FIGURE 4 Proportion of *Salmonella* isolates from humans being completely susceptible, resistant to one and/or two antimicrobial classes or multidrug-resistant (MDR) in 2024.

2.3.6 | Temporal trends

Trends in resistance over the 11-year period 2014–2024 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, 19 and 14 countries out of 29 observed a statistically significant decrease in resistance to ampicillin and tetracycline respectively, whereas one country reported an increase in both. For ciprofloxacin, a statistically significant increase in resistance was observed in 15 countries, while 4 reported a decrease. For cefotaxime, five countries observed a statistically significant increase while four a decrease.

By serovar, statistically significant decreasing trends in resistance to ampicillin and tetracycline were observed in a large proportion of countries for *S*. Typhimurium (in about 60% and 40% of countries, respectively). Resistance to tetracycline decreased in monophasic *S*. Typhimurium in more than half of the countries reporting this serovar. Ciprofloxacin/quinolone resistance in *S*. Enteritidis, on the other hand, increased significantly in about 60% of countries and in about half of countries regarding monophasic *S*. Typhimurium and a quarter of countries regarding *S*. Typhimurium.

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 2014–2024.

	Ampicillin		Cefotaxime		Ciprofloxacin/Quinolones		Tetracycline	
Serovar	↑	↓	↑	↓	↑	↓	↑	↓
Salmonella spp. (27 MSs + 2 non-MSs)	1 (SK)	19 (BE, BG, CY, DE, DK, EL, ES, FR, HR, IE, IS, IT, LT, NL, NO, PL, PT, RO, SE)	5 (AT, DE, HU, LU, SI)	4 (FI, FR, MT, PL)	15 (AT, BE, DE, EL, HU, IT, LT, LU, LV, NL, PL, RO, SE, SI, SK)	4 (ES, FR, HR, MT)	1 (SK)	14 (BE, DE, DK, EL, ES, FR, HU, IE, LU, NL, NO, PL, PT, SE)
S. Enteritidis (25 MSs + 1 non-MS)	7 (AT, HU, IT, NL, NO, SI, SK)	8 (CY, DE, FI, FR, LT, PL, RO, SE)		1 (PL)	15 (AT, CY, DE, EE, EL, HU, IT, LT, LV, NL, NO, PL, RO, SI, SK)	1 (ES)	5 (AT, DE, IT, NO, SK)	6 (ES, FI, FR, LT, PL, RO)
S. Typhimurium (26 MSs + 2 non-MSs)	1 (HR)	17 (AT, BE, CY, DE, DK, ES, FI, FR, HU, IE, IT, LT, NL, NO, RO, SE, SI)	2 (DE, HU)	1 (IE)	7 (DE, EL, ES, HU, LT, SI, SK)	3 (EE, FR, HR)	2 (DK, RO)	11 (AT, BE, DE, ES, FR, HU, IE, LU, NL, NO, SI)
Monophasic *S*. Typhimurium (18 MSs + 1 non-MS)	4 (IT, MT, NO, PT)	6 (AT, BE, DK, ES, HU, SI)	3 (HU, IT, SI)	1 (BE)	9 (DK, ES, FR, HU, LU, NL, PT, SE, SI)	1 (NO)		10 (AT, DE, DK, ES, FR, HU, IE, NL, PT, SI)
S. Infantis (14 MSs)	3 (HU, SI, SK)	2 (DE, IT)		1 (IT)	3 (BE, ES, SK)	4 (DE, HU, LT, MT)	2 (ES, SK)	2 (DE, PL)
S. Kentucky (7MSs)		3 (BE, FR, MT)	4 (AT, BE, DE, FR)	1 (MT)		1 (MT)	1 (ES)	
S. Derby (7 MSs)	1 (LT)				1 (FR)		1 (LT)	1 (FR)

Note: ↓, statistically significant decreasing trends; ↑, statistically significant increasing trends.
Abbreviations for reporting countries can be found here.

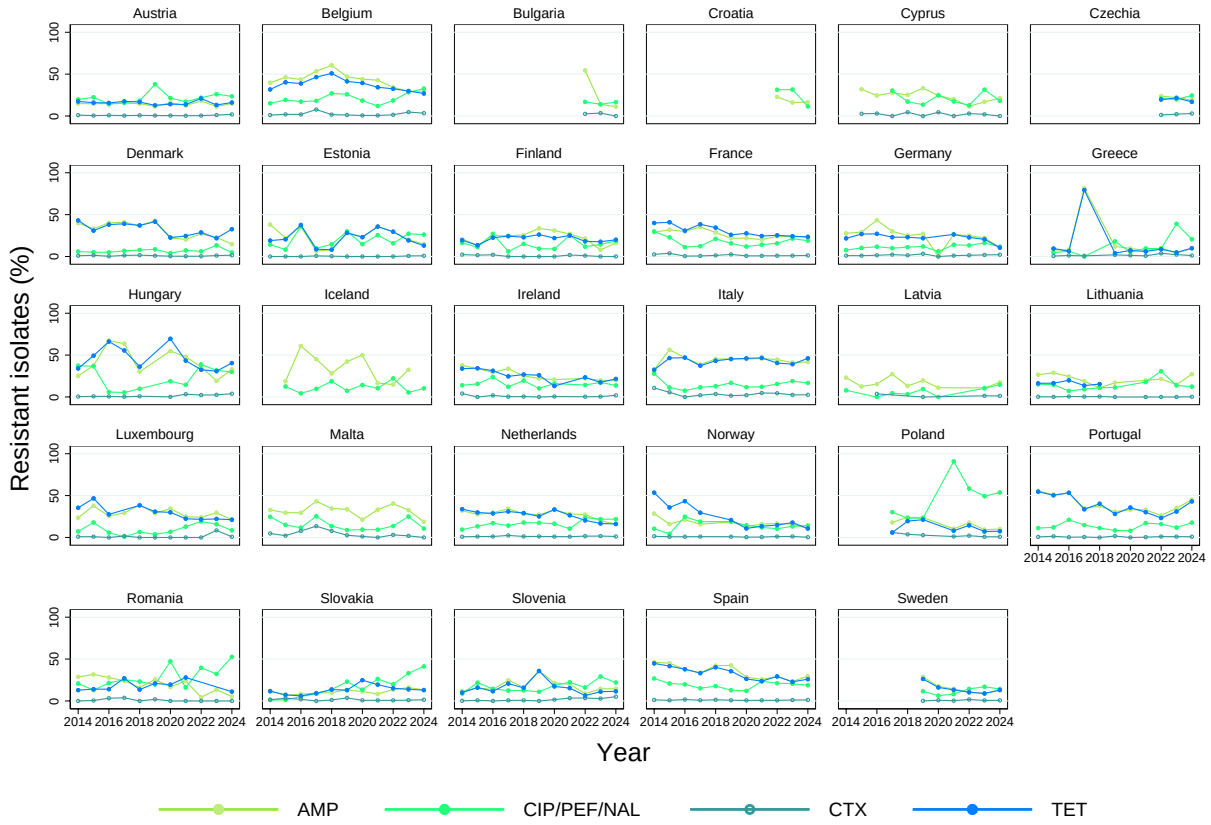


FIGURE 5 Trends in resistance to ampicillin, ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime and tetracycline in *Salmonella* spp. from humans in 29 reporting countries, 2014–2024.

2.3.7 | High-level ciprofloxacin resistance

In 2024, 2.6% ($N = 8666$) of *Salmonella* spp. from humans expressed high-level resistance to ciprofloxacin (MIC ≥ 4 mg/L, table 4). Such isolates were reported from 12 of the 13 countries reporting MIC values for ciprofloxacin. Among the 10 serovars reported with MICs of ≥ 4 mg/L, high-level ciprofloxacin resistance was most frequently observed in *S.* Kentucky (in 78.9% of tested *S.* Kentucky) and this serovar accounted for 198 out of 220 isolates (90.0%) reported with high-level MIC.

Of the 21 *S.* Kentucky sequences available within the *Salmonella* AMR data from humans in 2024, 10 carried resistance markers for ciprofloxacin. All 10 were ST198 and nine of these displayed two mutations each in *parC* and *gyrA* while the tenth carried a qnrB19-gene. The remaining *S.* Kentucky, eight ST198 and three ST314, 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 2024.

		High-level resistance to ciprofloxacin (MIC ≥4 mg/L)	
Serovar	***N***	***n***	**%**
S. Agona	128	3	2.3
S. Bareilly	41	1	2.4
S. Enteritidis	2128	2	0.1
S. Infantis	689	3	0.4
S. Kentucky	251	198	78.9
Monophasic *S.* Typhimurium	804	4	0.5
S. Newport	181	1	0.6
S. Saintpaul	82	6	7.3
S. Typhimurium	797	1	0.1
S. Wandsworth	5	1	20.0
Other	3560	–	0.0
Total (13 MSs)	**8666**	**220**	**2.5**

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

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

2.4.1 | Data reported

An overview of the number of MSs and non-MSs reporting data for targeted food-producing animals in 2023 and 2024 is presented in Table 5.

TABLE 5 Overview of countries reporting antimicrobial resistance data for *Salmonella* spp. from targeted food-producing animals, 2023–2024.

			Reporting countries (*N*)	
Year	**Animal population**	**No. of tested isolates**	**MS**	**Non-MS**
2024	Broilers	2068	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HR, HU, IE, IT, LT, LU, LV, MT, NL, PL, PT, RO, SI, SK, XI (27)	CH, IS, NO (3)
	Laying hens	1150	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HR, HU, IE, IT, LT, LU, MT, NL, PL, PT, RO, SE, SI, SK, XI (27)	CH (1)
	Fattening turkeys	573	AT, BE, CZ, DE, DK, EE, ES, FR, GR, HR, HU, IE, IT, NL, PL, PT, RO, SE, SI, SK, XI (21)	CH (1)
2023	Fattening pigs	1479	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FR, GR, HR, HU, IE, IT, LT, LU, LV, MT, NL, PL, PT, RO, SI, SK, XI (26)	IS, ME (2)
	Calves	80	AT, BE, DE, DK, ES, FR, HR, IT, NL, PT, RO (11)	

Abbreviations: *N*, number of countries reporting data; Abbreviations for reporting countries can be found here.

The relative contribution of the most frequently reported serovars recovered from each food-producing animal population is illustrated in Figure 6. Serovars Infantis, Enteritidis and Paratyphi B represented 53.7% of *Salmonella* spp. isolates from **broilers**, while in **laying hens**, Enteritidis, Infantis and Kentucky were the most reported (52.4%). In **fattening turkeys**, serovars Agona, Anatum, Infantis and Enteritidis were the most prevalent (47.1%). In **pigs**, four serovars (monophasic Typhimurium, Derby, Typhimurium and Rissen) accounted for 76.6% of *Salmonella*, while in **calves**, serovars Dublin, Typhimurium, Anatum and monophasic Typhimurium accounted for 55.0%.

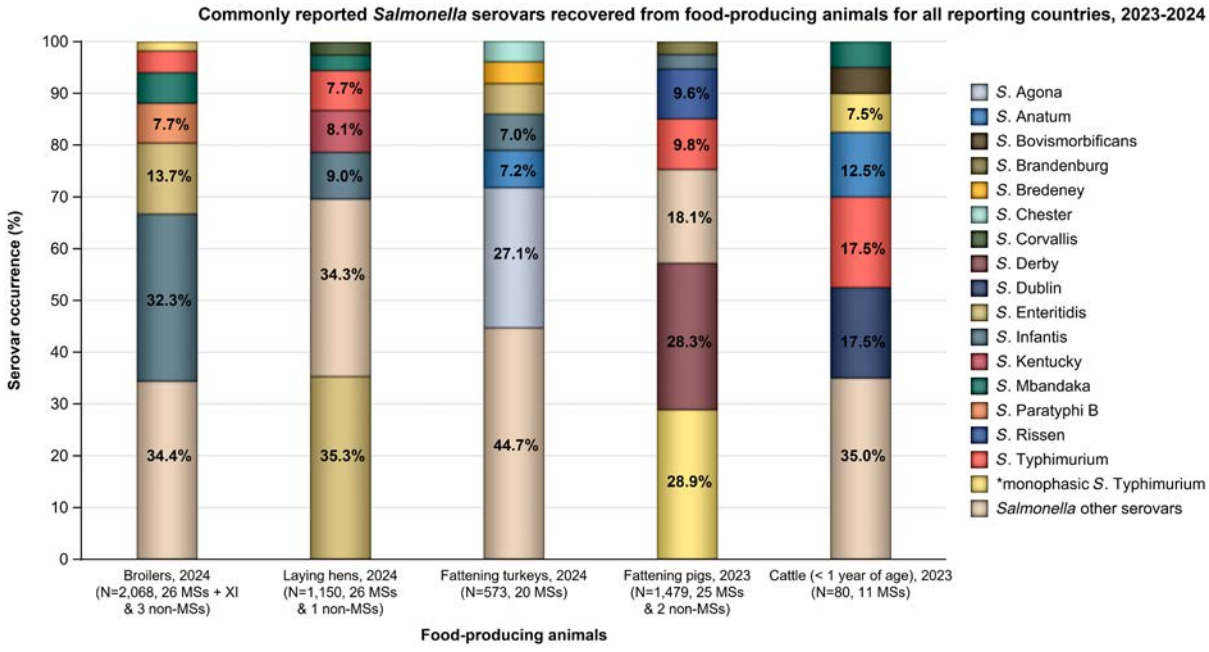


FIGURE 6 Commonly reported *Salmonella* serovars recovered from targeted food-producing animals, EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.
*Monophasic *S*. Typhimurium includes antigenic formulas; serovars in the legend are listed by alphabetical order.
Abbreviations: *N*, Total number of *Salmonella* spp. isolates reported by reporting countries; MSs, Member States; 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 food-producing animals (2023–2024) 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.17950222).

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 origins (also shown in Annex A.3).

2.4.2 | Occurrence of resistance

Since 2014, the antimicrobial substances included in the harmonised panel 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 public health interest. The selection of these antimicrobial substances was based on either their public health importance or their common use in veterinary medicine. Until 2023, antimicrobial substances in this report were categorised according to the WHO guidelines (WHO, 2024). From 2024 onwards, this report will also adopt the categorisation established by the Antimicrobial Advice Ad hoc Expert Group (AMEG) (EMA, 2019).

Under the AMEG framework, antimicrobial substances are categorised based on their recommended use in veterinary medicine. Group D (Prudence) includes first-line treatment options such as ampicillin, sulfamethoxazole, trimethoprim and tetracycline. Group C (Caution) comprises antimicrobials such as amikacin, gentamicin, chloramphenicol and azithromycin, which should be used only when Group D options are ineffective. Group B (Restrict) includes colistin, ciprofloxacin, nalidixic acid and third-generation cephalosporins (cefotaxime and ceftazidime), which require susceptibility testing and should be reserved for cases where no Group C or D alternatives are effective. Group A (Avoid) covers meropenem and tigecycline, which are not authorised for veterinary use in the EU and must not be administered to food-producing animals. Data on the occurrence of resistance in *Salmonella* isolates from fattening pigs and calves in 2023, and broilers, laying hens and fattening turkeys in 2024 are presented in Figure 7 and Tables 6, 7 and 8. The detailed country-level information on the occurrence of resistance is presented in Annex A.2 (Tables 1, 6, 10, 14, 18).

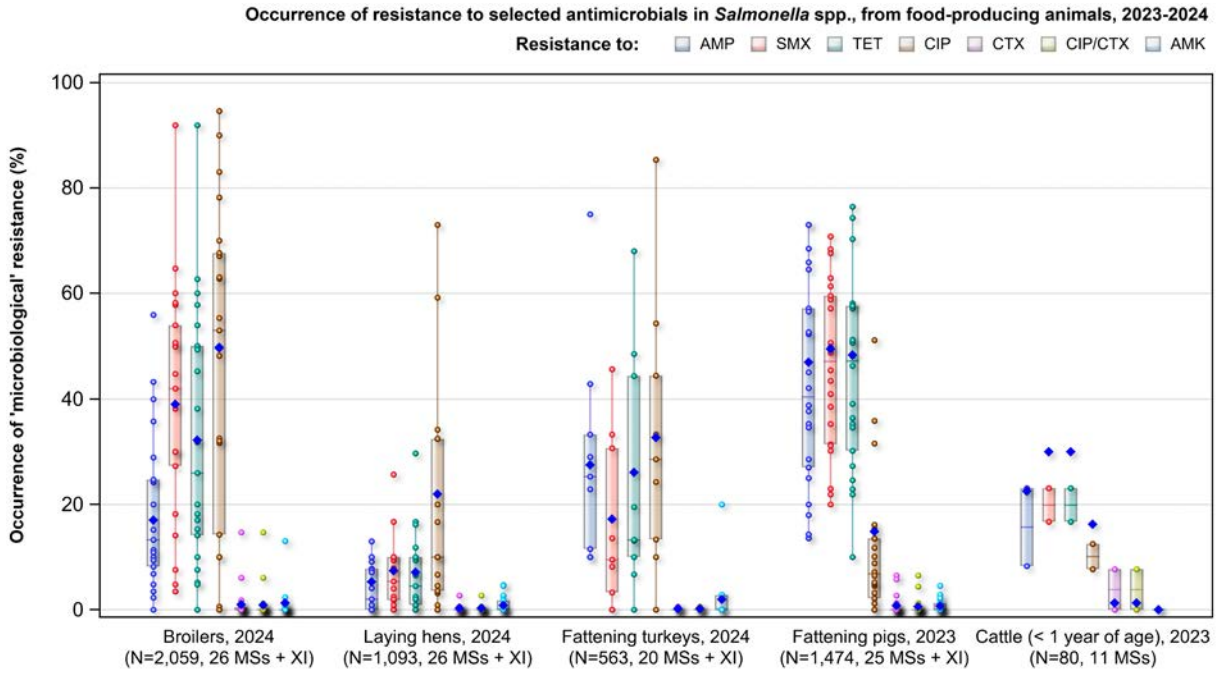


FIGURE 7 Occurrence of resistance to selected antimicrobials in *Salmonella* spp. recovered from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
Only MSs reporting data for 10 or more isolates are shown in the graph; however, all isolates are included in the calculation of resistance at the reporting MS-group level.
Abbreviations: AMK, amikacin; AMP, ampicillin; CIP/CTX, combined 'microbiological' resistance to ciprofloxacin and cefotaxime; CIP, ciprofloxacin; CTX, cefotaxime; MS, 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 the median; Lower and upper box boundaries, 25th and 75th percentiles, respectively.

Resistance to commonly used antimicrobials in human and/or veterinary medicine

Resistance to **ampicillin**, **sulfamethoxazole**, **trimethoprim** and **tetracycline** was common among food-producing animals, with moderate to high resistance levels reported among EU MSs (Table 6). The exception was seen in *Salmonella* spp. isolates from laying hens, which showed low resistance levels to these antimicrobials (Table 6). However, large differences in resistance levels to ampicillin, sulfamethoxazole, trimethoprim and tetracycline between countries were observed, with resistance levels varying most in *Salmonella* isolates from broilers (Figure 7; Annex A.2, tables 1, 6, 10, 14, 18).

TABLE 6 Occurrence of resistance to commonly used antimicrobials in human and/or veterinary medicine in *Salmonella* spp. isolates from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

Animal population	AMP %R	SMX %R	TET %R	TMP %R
Broilers, 2024 (*N* = 2059; 26 MSs + XI)	17.0	39.0	32.2	16.7
Fattening turkeys, 2024 (*N* = 563; 21 MSs)	27.5	17.2	26.1	6.2
Laying hens, 2024 (*N* = 1093; 26 MSs + XI)	5.3	7.4	7.1	1.9
Calves, 2023 (*N* = 80; 11 MSs)	22.5	30.0	30.0	20.0
Fattening pigs, 2023 (*N* = 1474; 25 MSs + XI)	47.0	49.5	48.4	21.6

Notes: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. A blank cell represents no resistance. The correspondence between colour and resistance level can be found in the 'Definitions' section.

Abbreviations: AMK, Amikacin; AMP, ampicillin; AZT, azithromycin; CHL, chloramphenicol; GEN, gentamicin; %R, percentage of resistant isolates; SMX, sulfamethoxazole; TET, tetracycline; TMP: trimethoprim.

Resistance to 'critically important antimicrobials' (CIAs) in human medicine and of cautious use in veterinary medicine

Resistance to **amikacin**, **gentamicin** and **azithromycin** was found at very low to low levels among food-producing animals from EU MSs (Table 7). **Chloramphenicol** resistance was found at low levels in poultry populations in 2024, while in 2023, moderate levels of chloramphenicol resistance were reported in isolates from pigs and calves (Table 7). In 2024, no resistance to azithromycin was found in *Salmonella* isolates from fattening turkeys, and in 2023, no amikacin resistance was detected in calves. Variations among MSs were small (Annex A.2, tables 1, 6, 10, 14, 18). Of note are the moderate amikacin resistance levels reported by Austria in *Salmonella* isolates from broilers (13.0%, *N* = 161) and fattening turkeys (20.0%, *N* = 30; Figure 7).

TABLE 7 Occurrence of resistance to 'critically important antimicrobials' in human medicine and of cautious use in veterinary medicine in *Salmonella* spp. isolates from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

Animal population	AMK %R	GEN %R	AZM %R	CHL* %R
Broilers, 2024 (*N* = 2059; 26 MSs + XI)	1.3	0.8	0.4	1.9
Fattening turkeys, 2024 (*N* = 563; 21 MSs)	2.0	1.2	0.0	4.8
Laying hens, 2024 (*N* = 1093; 26 MSs + XI)	0.8	0.5	0.2	1.4
Calves, 2023 (*N* = 80; 11 MSs)	0.0	2.5	2.5	20.0
Fattening pigs, 2023 (*N* = 1474; 25 MSs + XI)	0.7	5.2	3.1	17.0

Notes: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. A blank cell represents no resistance. The correspondence between colour and resistance levels can be found in the 'Definitions' section.

Abbreviations: AMK, amikacin; AZM, azithromycin; CHL, chloramphenicol; GEN, gentamicin; %R, percentage of resistant isolates.

*Chloramphenicol belongs to the 'highly important antimicrobials' (HIA) list on the WHO list.

*R*esistance to highest priority 'critically important antimicrobials' (CIAs) and last resort antimicrobials

Resistance to fluoroquinolones was common in poultry populations, with high resistance levels to **ciprofloxacin** and **nalidixic acid** reported in isolates from broilers, followed by fattening turkeys and then laying hens (Table 8; Annex A.2, tables 10, 14 and 18). Lower, yet still moderate, resistance levels were reported among isolates from pigs and calves (Table 8; Annex A.2, tables 1 and 6).

TABLE 8 Occurrence of resistance to 'highest priority critically important antimicrobials' (HPCIAs) and last resort antimicrobials in *Salmonella* spp. isolates from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland) 2023–2024.

Animal population	CIP %R	NAL %R	CTX %R	CAZ %R	Combined CIP/CTX %R	TGC %R	COL %R
Broilers, 2024 (*N* = 2059; 27 MSs)	49.7	48.9	1.0	0.7	0.9	16.2	4.4
Fattening turkeys, 2024 (*N* = 563; 21 MSs)	32.7	23.1	0.2	0.0	0.2	8.3	1.2
Laying hens, 2024 (*N* = 1093; 27 MSs)	22.0	21.4	0.3	0.3	0.3	2.7	6.7
Calves, 2023 (*N* = 80; 11 MSs)	16.3	10.0	1.3	1.3	1.3	7.5	13.8
Fattening pigs, 2023 (*N* = 1474; 26 MSs)	14.9	13.2	0.8	0.8	0.6	7.3	0.5

Notes: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. A blank cell represents no resistance. The correspondence between colour and resistance level can be found in the 'Definitions' section.

Abbreviations: CAZ, ceftazidime; CIP, ciprofloxacin; COL, colistin; CTX, cefotaxime; NAL, nalidixic acid; %R, percentage of resistant isolates; TGC, tigecycline.

Of the *Salmonella* isolates from broilers **resistant to ciprofloxacin and susceptible to nalidixic acid** (*n* = 24), nine isolates were ***S.* Mbandaka** (Spain). From laying hens, there were 10 isolates, of which three were ***S.* Braenderup** (Hungary). Noteworthy is the high number (*n* = 54) of isolates from turkeys resistant to ciprofloxacin and susceptible to nalidixic acid,

of which 28 were ***S.* Anatum** (Hungary, *n* = 1; Italy, *n* = 16; Portugal, *n* = 8; and Slovenia, *n* = 3) and 13 ***S.* Agona** (Croatia and Austria, *n* = 1 each; Italy, *n* = 11).

Of the *Salmonella* isolates from pigs **resistant to ciprofloxacin** and **susceptible to nalidixic acid** (*n* = 28), most were ***S.* Derby** (*n* = 7), followed by **monophasic *S.* Typhimurium** (*n* = 6). Spain reported the highest number of isolates belonging to different serovars (40.7%). Only six isolates from calves were reported (*S.* Bovismorbificans, *n* = 3; *S.* Typhimurium, *n* = 2; and *S.* Dublin, *n* = 1).

Most countries did not detect resistance to **third-generation cephalosporins** (i.e. cefotaxime and ceftazidime) in *Salmonella* isolates from targeted animal food-producing animals (Annex A.2, tables 1, 6, 10, 14 and 18). Overall resistance levels were very low in *Salmonella* isolates from laying hens, fattening turkeys and pigs, and low from broilers and calves (Table 8).

In **2024**, overall **combined resistance to ciprofloxacin and cefotaxime** was reported at very low levels in poultry (Table 8). In broiler flocks, Italy and Malta reported the highest resistance levels (Figure 8; Annex A.2, table 10). For laying hens and fattening turkeys, combined resistance was reported in very few isolates (Figure 8). In **2023**, combined resistance in *Salmonella* isolates from pigs was reported at very low levels (Table 8), with *S.* Kedougou the most reported serovar (Figure 8). Combined resistance to ciprofloxacin and cefotaxime was most frequently observed in broilers, predominantly in *S.* Infantis isolates (Figure 8).

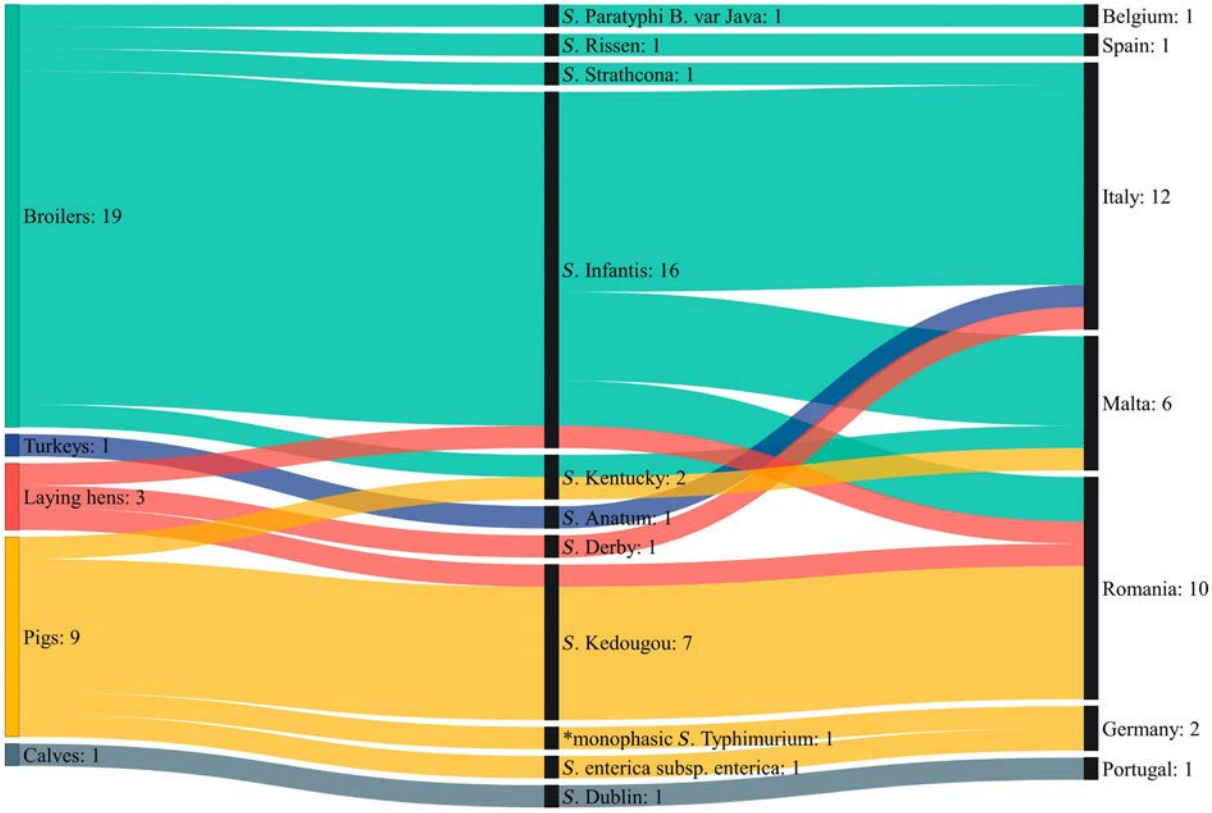


FIGURE 8 Sankey diagram showing the distribution of *Salmonella* isolates with combined resistance to ciprofloxacin and cefotaxime by serovar, food-producing animal and reporting MS, 2023–2024.

Resistance to **tigecycline** was reported at low levels in most targeted food-producing animals, except in broilers, where it was moderate (Table 8). However, 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 previous years, since the change of the ECOFF for tigecycline, resistance levels to tigecycline were higher than expected (EFSA, 2024, 2025), with most resistant isolates having a MIC of 1 mg/L (i.e. one dilution above the ECOFF). In 2024, lower resistance levels in *Salmonella* from poultry were reported when compared to those reported in 2022. Nevertheless, the percentage of tigecycline-resistant isolates with a MIC of 1 mg/L remained consistent with previous years. Specifically, 280 out of 334 (83.8%), 43 out of 47 (91.5%) and 29 out of 30 (96.7%) from broilers, fattening turkeys and laying hens, respectively, had a MIC of 1 mg/L. Tigecycline resistance showed considerable variation across reporting MSs for all food-producing animals (Annex A.2, tables 1, 6, 10, 14 and 18). Resistance levels varied most in *Salmonella* from broilers (0%–42.5%).

Resistance levels to **colistin** were very low in *Salmonella* isolates from pigs, low in poultry and moderate in calves (Table 8). The smaller overall sample size of *Salmonella* isolates from calves (*N* = 80) compared to the other animal groups (i.e. broilers, *N* = 2059; pigs, *N* = 1474; laying hens, *N* = 1093; and turkeys, *N* = 563) should be taken into consideration when interpreting these results. Across all targeted food-producing animals, most individual countries reported no resistance or very low levels of resistance to colistin. However, some exceptions occurred for MSs reporting > 10 isolates. High resistance levels were reported by the Netherlands (29.5%, *N* = 112) in isolates from laying hens, Portugal (23.1%, *N* = 13) in isolates from calves and Poland (20.8%, *N* = 212) in isolates from broilers. Moderate resistance levels were reported by Poland

(18.8%, *N* = 80) and Belgium (18.2%, *N* = 22) in isolates from laying hens, and by Portugal (11.1%, *N* = 36) in isolates from fattening turkeys (Annex A.2, tables 1, 6, 10, 14 and 18).

2.4.3 | Tigecycline and colistin resistance in *Salmonella* serovars

Tigecycline resistance in *Salmonella* spp.

The number and percentage of tigecycline-resistant *Salmonella* isolates detected by MSs from targeted food-producing animals and the predominant serovars accounting for this resistance are shown in Figure 9. Certain serovars displayed resistance to tigecycline, which could reflect the dissemination of this resistance within these serovars.

In **2024**, ***S.* Infantis** was the predominant serovar among tigecycline-resistant isolates recovered from broilers, laying hens and fattening turkeys (Figure 9). The second most common serovar among the tigecycline-resistant isolates in broilers and fattening turkeys was ***S.* Newport** and ***S.* Agona**, respectively (Figure 9). In **2023**, most of the tigecycline-resistant isolates recovered from pigs were ***S.* Rissen** and **monophasic *S.* Typhimurium**, while in calves, ***S.* Typhimurium** was more prevalent (Figure 9).

MDR was often a feature among tigecycline-resistant isolates. For instance, 93.6% of tigecycline-resistant isolates from fattening turkeys (*n* = 44), 91.9% from broilers (*n* = 307) and 83.3% from laying hens (*n* = 25) were multidrug-resistant.

Among broilers, 97.9% of all tigecycline-resistant ***S.* Infantis** (*n* = 274) were multidrug-resistant. Most of these isolates (*n* = 271), as well as all tigecycline-resistant *S.* Infantis isolates from laying hens and fattening turkeys, were resistant to ciprofloxacin, nalidixic acid, sulfamethoxazole and tetracycline (CIP-NAL-SUL-TGC-TET), either alone or in combination with additional resistances. This resistance profile is characteristic of certain MDR broiler clones of ***S.* Infantis** (Alba et al., 2020; Alvarez et al., 2023; Nógrády et al., 2012).

In pigs, 74.8% of all tigecycline-resistant *Salmonella* isolates were multidrug-resistant (*n* = 80), with 84.0% exhibiting resistance to at least ampicillin, sulfamethoxazole and tetracycline (AMP-SUL-TGC-TET). ***S.* Rissen** (*n* = 25) and **monophasic *S.* Typhimurium** (*n* = 17) were the most frequent serovars with the above-mentioned resistance profile. Among the tigecycline-resistant isolates from calves, three ***S.* Typhimurium** isolates and one ***S.* Rissen** were also MDR.

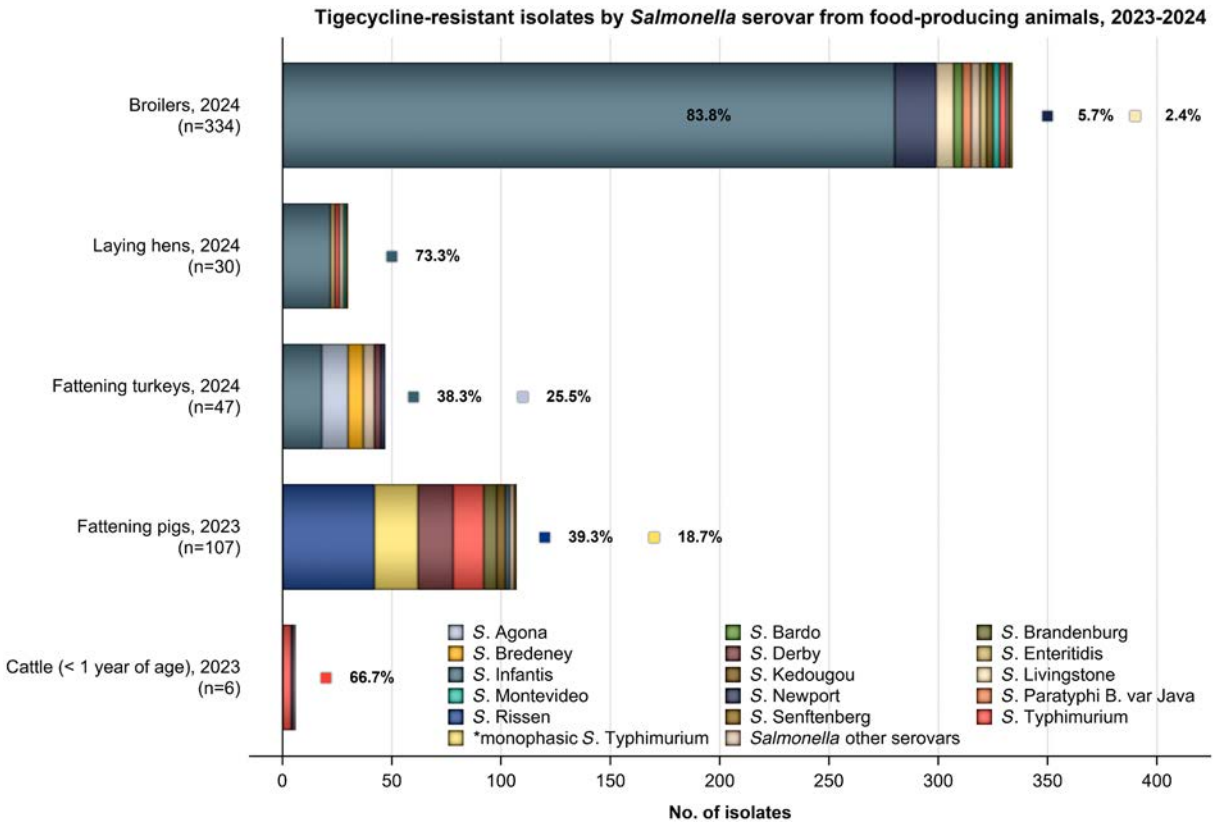


FIGURE 9 Breakdown of the number of tigecycline-resistant *Salmonella* isolates by serovar from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
n, Total number of tigecycline-resistant isolates reported by MSs; predominant serovars are also expressed as a percentage; *Monophasic *S.* Typhimurium includes all antigenic formulas;
Notes: Salmonella serovars in the legend are listed by alphabetical order. The ECOFF used to determine tigecycline resistance was MIC > 0.5 mg/L.

Colistin resistance in *Salmonella* spp.

The number and percentage of colistin-resistant *Salmonella* isolates detected from targeted food-producing animals and the predominant serovars accounting for this resistance are presented in Figure 10. Resistance to colistin was generally observed in S. *Enteritidis*, representing the 93.2%, 84.6% 37.5% and 28.6% of colistin-resistant isolates from laying hens, broilers, pigs and turkeys, respectively, while in calves, resistance to this antimicrobial was mainly found in *S*. Dublin (81.8%). Notably, ***S.* Enteritidis** and ***S.* Dublin** are **group D salmonellas** (serogroup O9). *Salmonella* belonging to group D tend to show decreased susceptibility to colistin without having any known acquired or mutational colistin resistance mechanisms (Agersø et al., 2012; Ricci et al., 2020a, 2020b). This is exemplified by the proportion of colistin-resistant isolates belonging to ***S.* Enteritidis** in poultry and ***S.* Dublin** in calves in both reporting years. The remaining serovars listed in the figure do not belong to group D (serogroup O9).

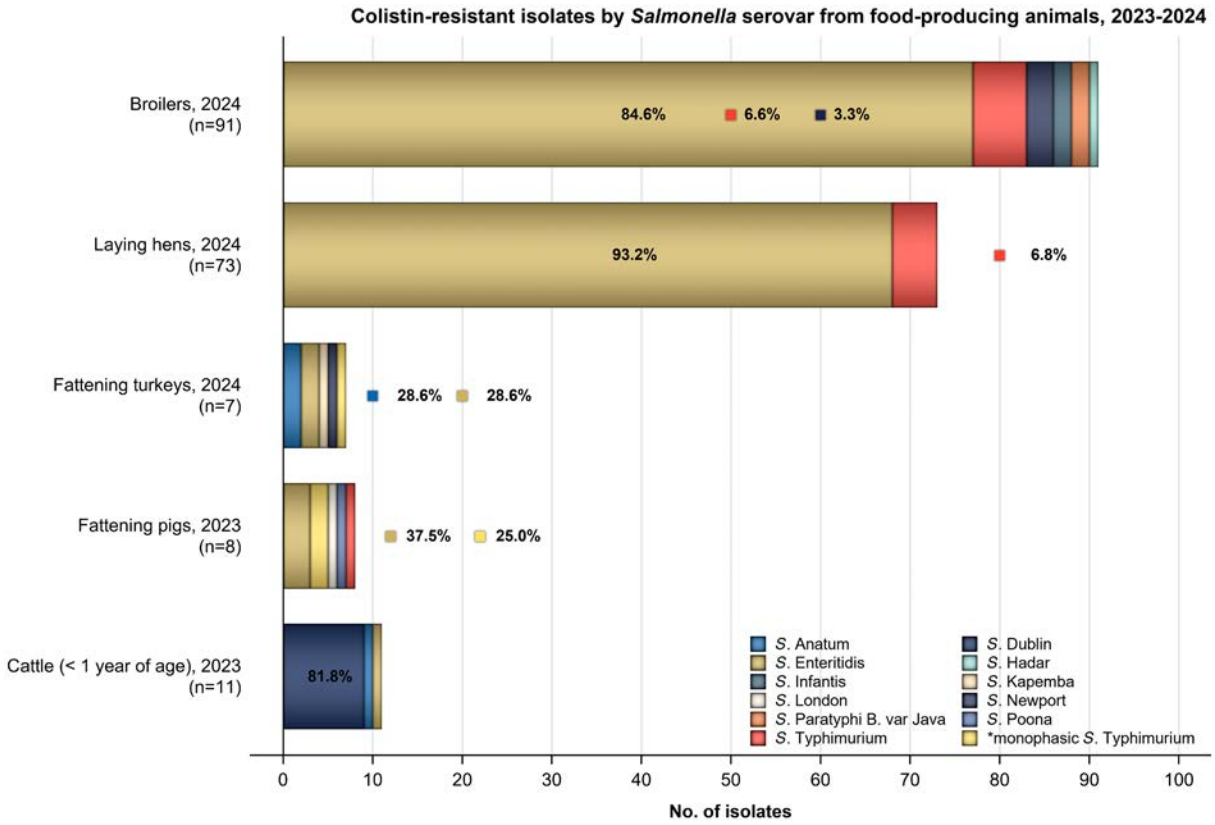


FIGURE 10 Breakdown of the number of colistin-resistant *Salmonella* isolates by serovar from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
n, Total number of colistin-resistant isolates reported by the MSs; predominant serovars are expressed as a percentage. *Monophasic *S*. Typhimurium includes all antigenic formulas;
Notes: Salmonella serovars in the legend are listed by alphabetical order.

2.4.4 | Complete susceptibility and multidrug resistance

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 (Appendix A – Materials and methods). **CS** is defined as complete susceptibility to the selected antimicrobial classes listed above. **MDR** is defined as resistance to three or more antimicrobial classes listed above.

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 country-specific MDR and CS.

Overall **MDR** at the MS level was observed at high levels in isolates from pigs (43.3%, median = 38.8%), broilers (35.1%, median = 29.8%), calves (25.0%, median = 23.1%) and fattening turkeys (22.9%, median = 15.2%; Figure 15). Few countries reported zero MDR in any of these food-producing animal populations. In contrast, MDR was reported at a low level in isolates from laying hens (6.0%, median = 0.0%).

Conversely, overall **CS** at the MS level was observed at extremely high levels in laying hens (72.4%, median = 90.0%), very high levels in fattening turkeys (56.7%, median = 63.3%) and in calves (56.3%, median = 50.0%), and at high levels in broilers (38.1%, median = 40.0%) and pigs (36.9%, median = 41.0%; Figure 15 and Annex A.2, tables 1, 6, 10, 14 and 18).

The **spatial distribution of CS** across all reporting countries can be seen in Figure 11. CS levels varied widely among reporting countries, particularly in broilers and fattening pigs (Figure 11). Of note are the extremely high CS levels in *Salmonella* isolates from broilers reported by France (90.7%, *N* = 172) and Portugal (81.0%, *N* = 42). In contrast, several central and eastern European countries reported low to moderate levels (Figure 11A). For laying hens, all countries reported very high to extremely high CS levels, except for Italy (36.1%, *N* = 169) and Romania (27.0%, *N* = 74). Most countries reported very high to extremely high CS levels in fattening turkeys, except for Hungary (13.3%, *N* = 75) and Portugal (25.0%, *N* = 36; Figure 11C). For pigs, CS rates were generally higher in Central and Northern Europe, when compared to parts of Southern and Eastern Europe (Figure 11D).

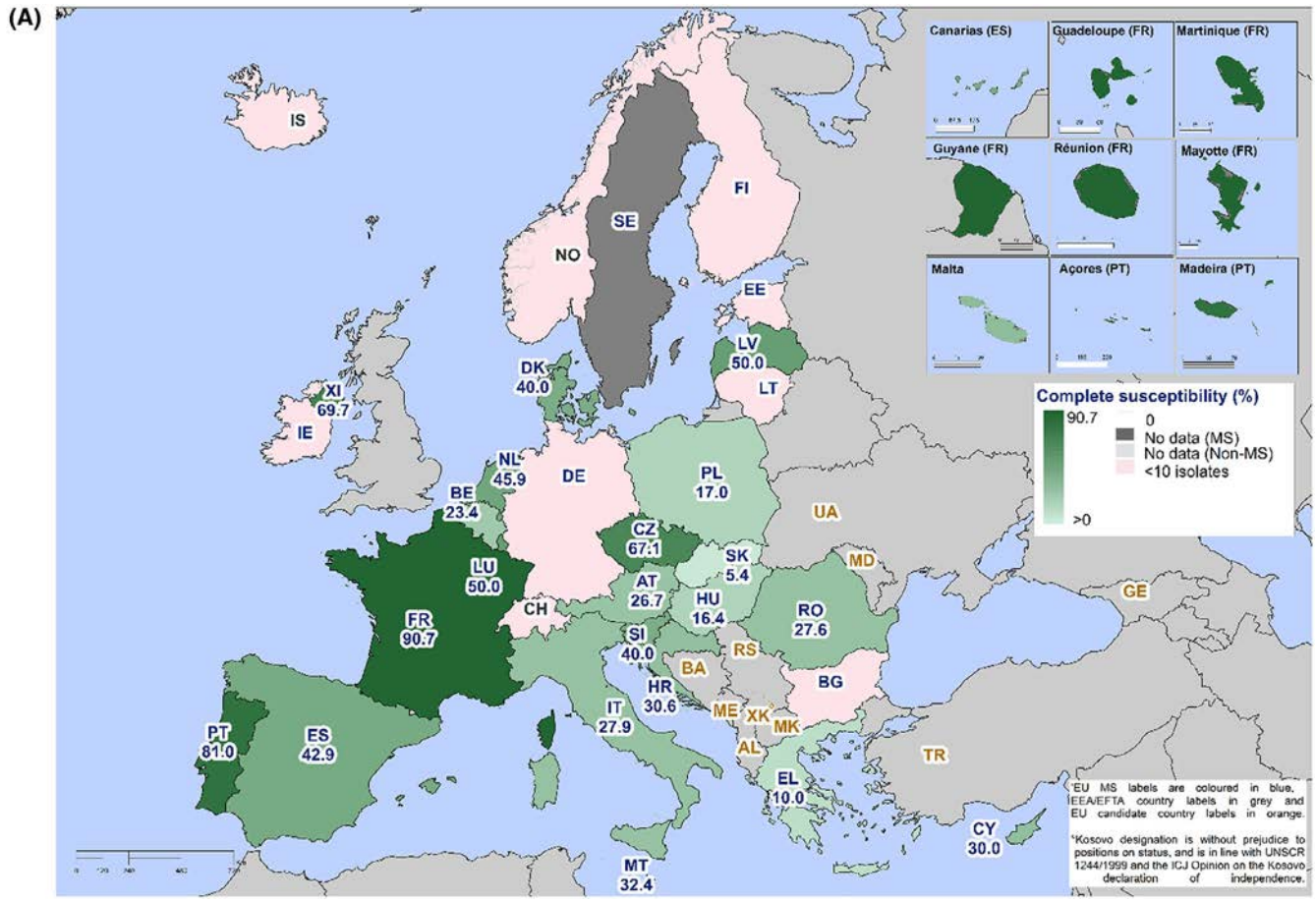


FIGURE 11 (Continued)

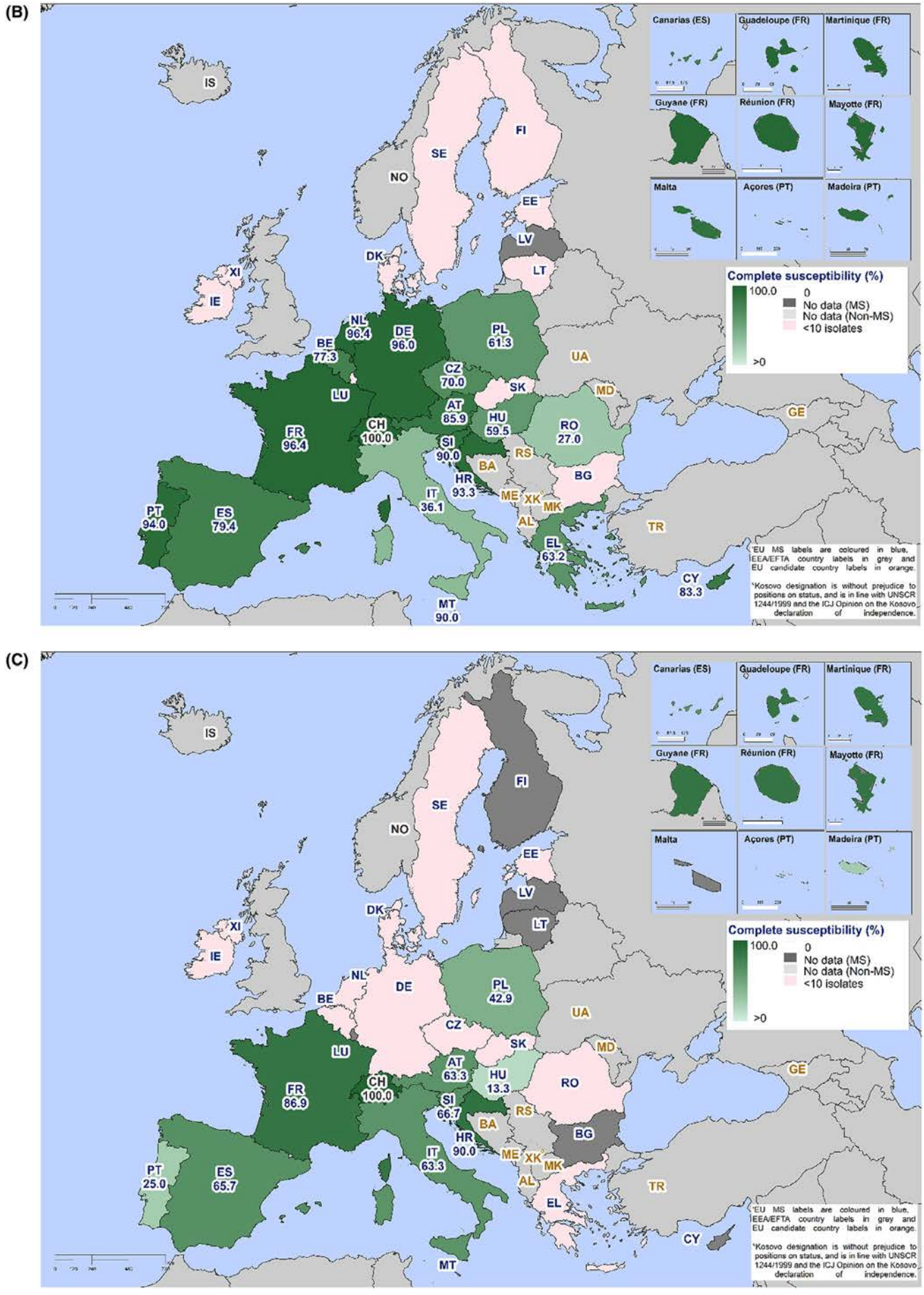


FIGURE 11 (Continued)

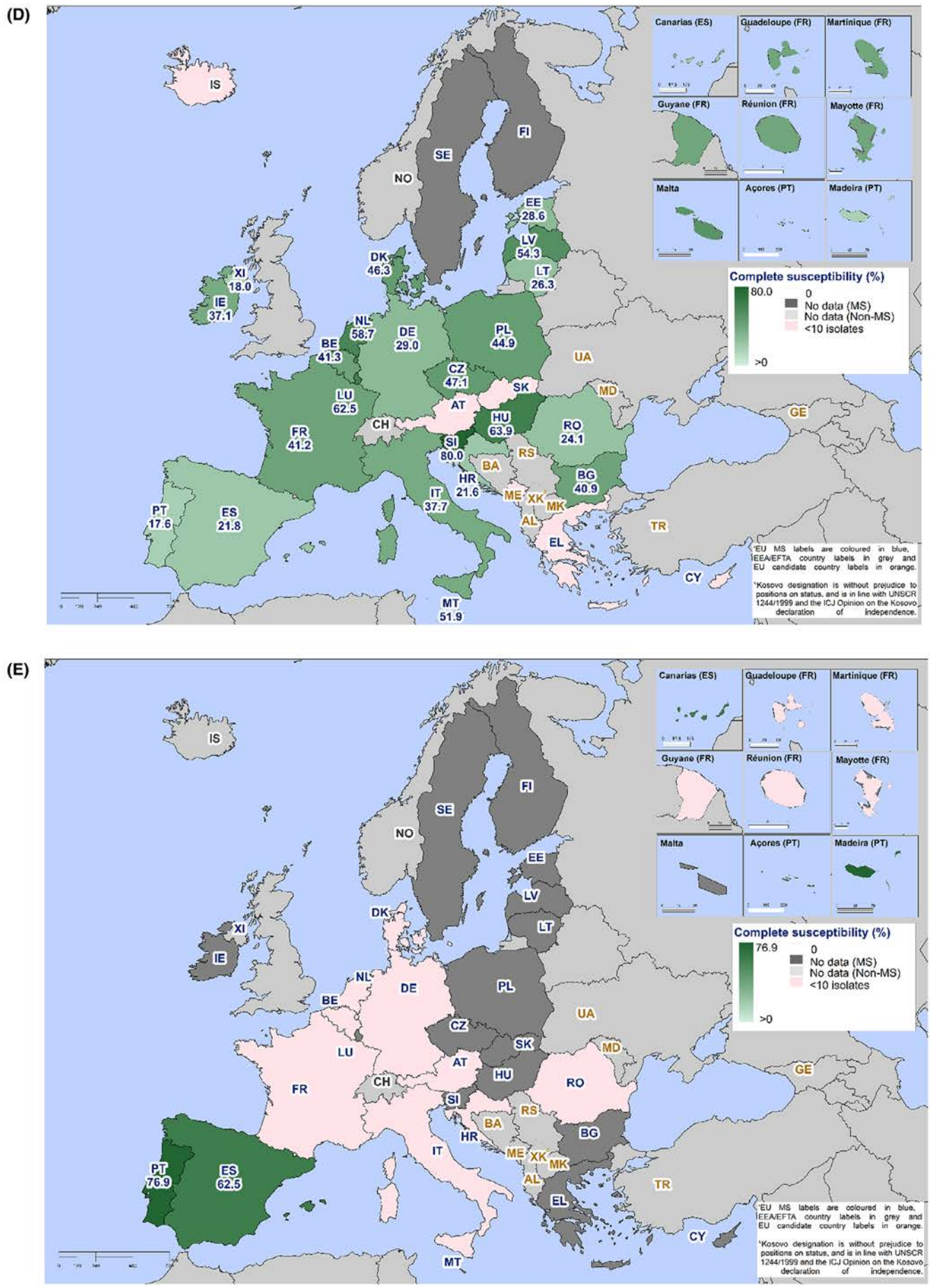


FIGURE 11 Spatial distributions of complete susceptibility to the selected antimicrobials tested among *Salmonella* spp. from (A) broilers and (B) laying hens, (C) fattening turkeys, (D) fattening pigs and (E) calves, using harmonised ECOFFs, 2023–2024.
Maps are presented only when at least four Member States (MSs) 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 **multidrug-resistant** among particular *Salmonella* serovars within the different food-producing animal species are presented in Figure 12. As in previous years, in **2024**, ***S.* Infantis** contributed most to MDR in all poultry populations. **Monophasic *S.* Typhimurium** (13.6%) and ***S.* Agona** (16.3%) were the second largest contributors to MDR in laying hens and turkeys, respectively (Figure 12). In **2023**, **monophasic *S.* Typhimurium** and ***S.* Typhimurium** contributed most to multidrug resistance in *Salmonella* isolates from pigs and calves (Figure 12).

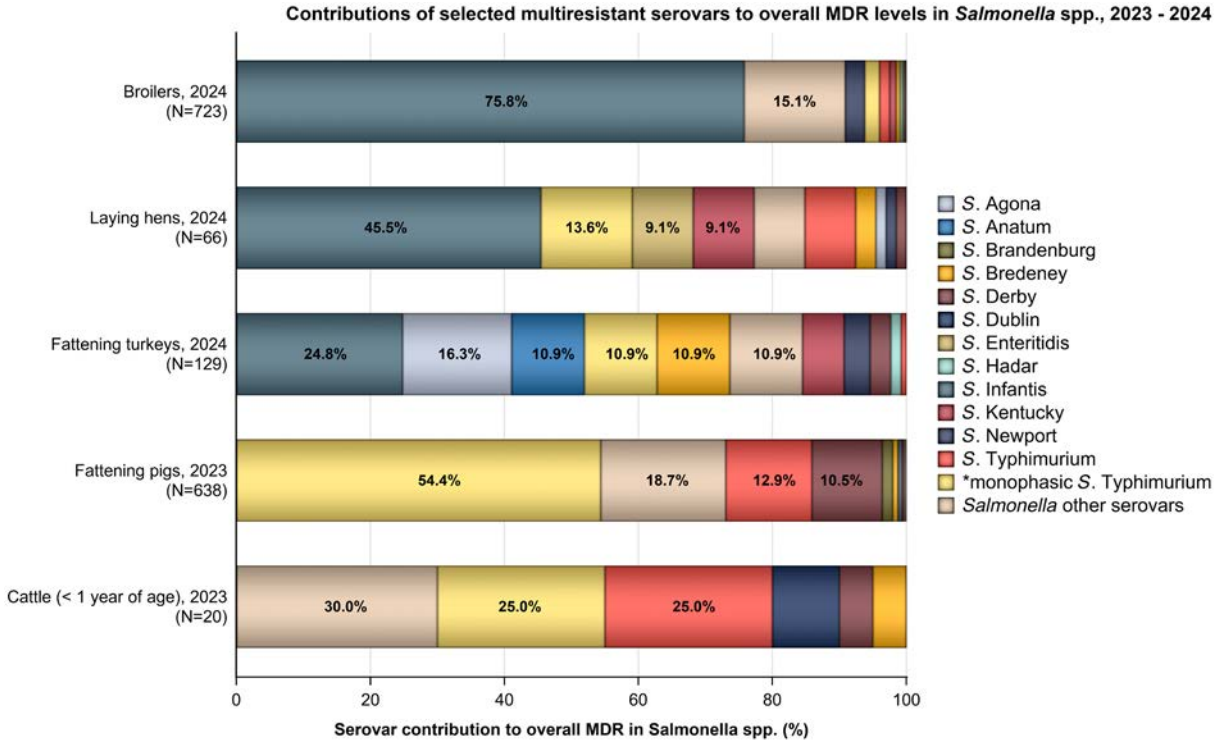


FIGURE 12 Proportions of certain serovars exhibiting multidrug resistance to overall MDR levels in *Salmonella* spp. recovered from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
Notes: Salmonella serovars in the legend are listed by alphabetical order.
Abbreviations: *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.

2.4.5 | Temporal trends in resistance

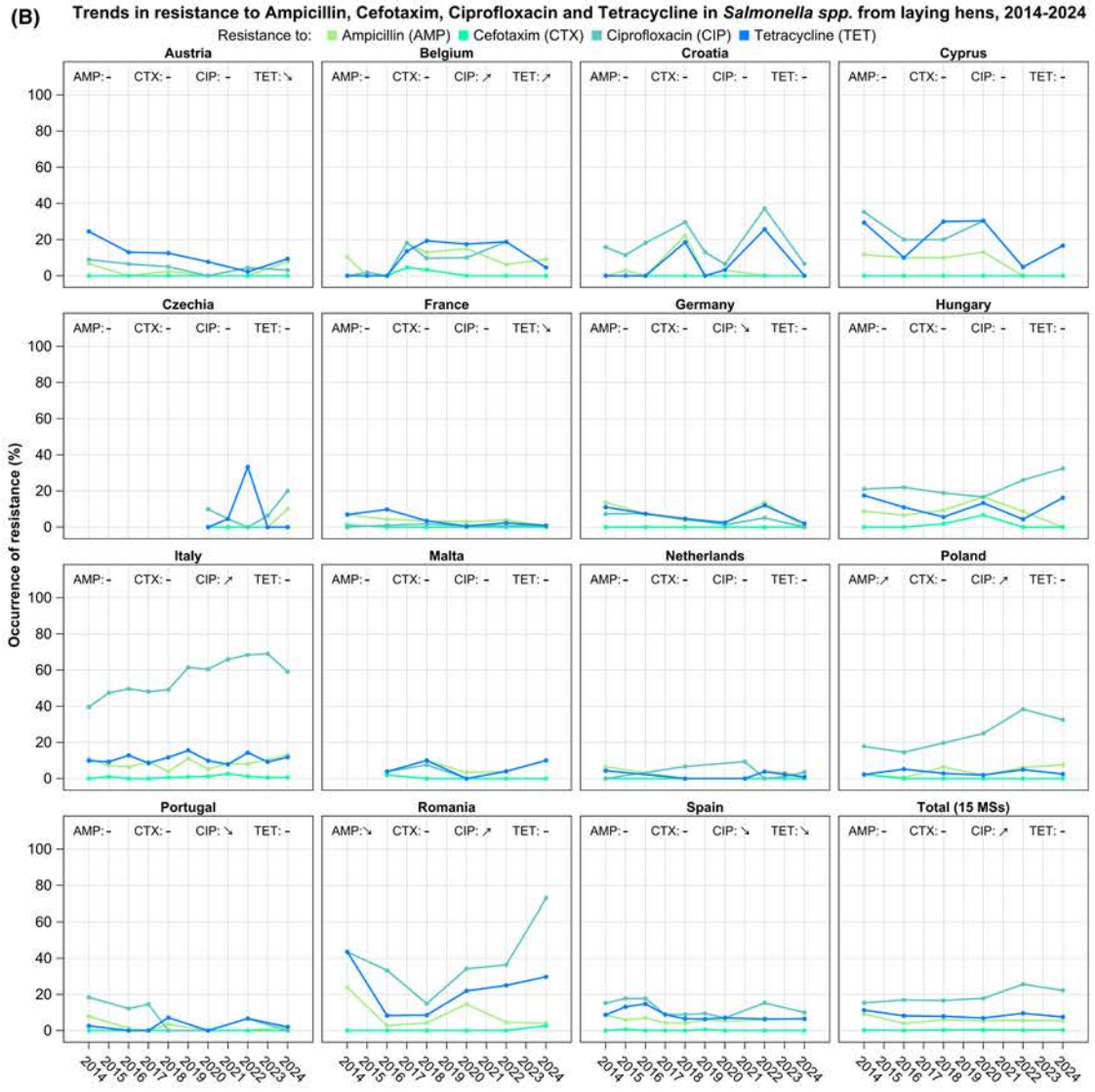
Temporal trends in antimicrobial resistance were assessed using logistic regression for countries reporting data for poultry populations for at least three consecutive years over the period 2014–2025 (Appendix A – Materials and methods). Resistance trends by country and serovar for each selected antimicrobial varied (Figure 13 and Table 9; Annex A.3). Overall, at the **MS-group level**, a statistically significant **decreasing trend** in **tetracycline** resistance was observed in *Salmonella* isolates from broilers. In isolates from fattening turkeys, resistance to **ampicillin**, **ciprofloxacin** and **tetracycline** also showed a significant **decrease**. Conversely, in laying hens, a statistically significant **increasing** trend in ciprofloxacin resistance was registered (Figure 13). Notably, Belgium, Italy and Spain have shown a **decrease** in **cefotaxime** resistance over the past decade in broilers. In contrast, Belgium, Italy, Poland and Romania show an increase in ciprofloxacin resistance in isolates from laying hens, which has contributed to the overall increasing trend seen at the MS-group level (Figure 13).

TABLE 9 Summary of countries with significantly increasing or decreasing trends in resistance to selected antimicrobials in *Salmonella* spp. from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2014–2024.

	AMP		CTX		CIP		TET	
Animal population	↓	↑	↓	↑	↓	↑	↓	↑
Broilers, 2024 16 MSs	4 (ES, FR, IT, RO)	5 (AT, BE, HU, PL, SI)	3 (BE, ES, IT)	1 (MT)	4 (ES, PT, RO, SI)	5 (AT, BE, CZ, PL, SK)	4 (ES, HU, RO, SI)	4 (AT, BE, PL, SK)
Laying hens, 2024 15 MSs	1 (RO)	1 (PL)	–	–	3 (DE, ES, PT)	4 (BE, IT, PL, RO)	4 (AT, DE, ES, FR)	1 (BE)
Fattening turkeys, 2024 5MSs	4 (ES, FR, HU, IT)	–	–	1 (IT)	–	–	3 (ES, FR, IT)	–

Note: ↓, statistically significant decreasing trends; ↑, statistically significant increasing trends.
Abbreviations: AMP, ampicillin; COL, colistin; CIP, ciprofloxacin; CTX, cefotaxime; TET, tetracycline; Abbreviations for reporting countries can be found here.

FIGURE 13 (Continued)



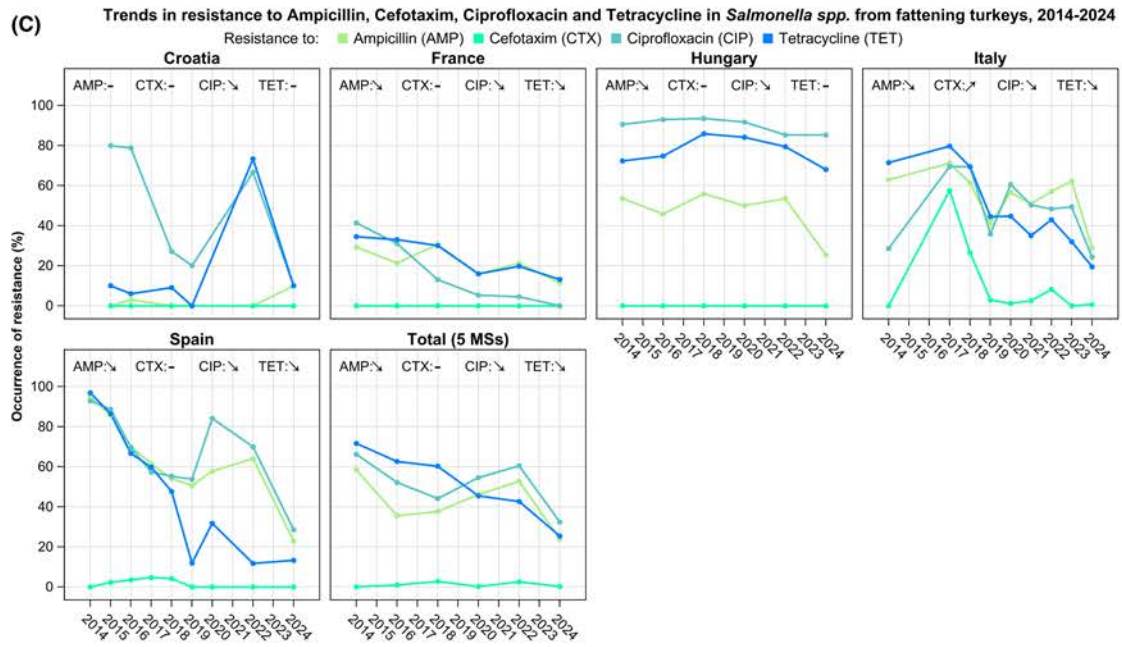


FIGURE 13 Trends in resistance to ampicillin, ciprofloxacin, cefotaxime and tetracycline in *Salmonella* spp. from broilers (A), laying hens (B) and turkeys (C), EU MSs and the United Kingdom (Northern Ireland), 2014–2024.

Notes: Only countries reporting > 10 isolates in a given year and reporting data for at least 3 years in the period between 2014 and 2024 by no more than a 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.

2.4.6 | High-level resistance to ciprofloxacin (CIP)

The distribution of ciprofloxacin-resistant isolates displaying levels of microbiological resistance or high-level resistance (isolates with a MIC ≥ 4 mg/L) within each food-producing animal species is illustrated in Figure 14. The serovars displaying **high-level resistance** to fluoroquinolones are of interest from both the epidemiological and the public/animal health perspectives. In **2024**, ***S.* Infantis**, ***S.* Newport** and ***S.* Kentucky** accounted for most of the isolates from **broilers** exhibiting high-level ciprofloxacin resistance. Noteworthy, ***S.* Kentucky** was the most reported serovar exhibiting high-level ciprofloxacin resistance in **laying hens**, **fattening turkeys** and **pigs**. A detailed analysis of the high-level resistance to ciprofloxacin in *S.* Kentucky and other *Salmonella* serovars is presented in Annex A.3.

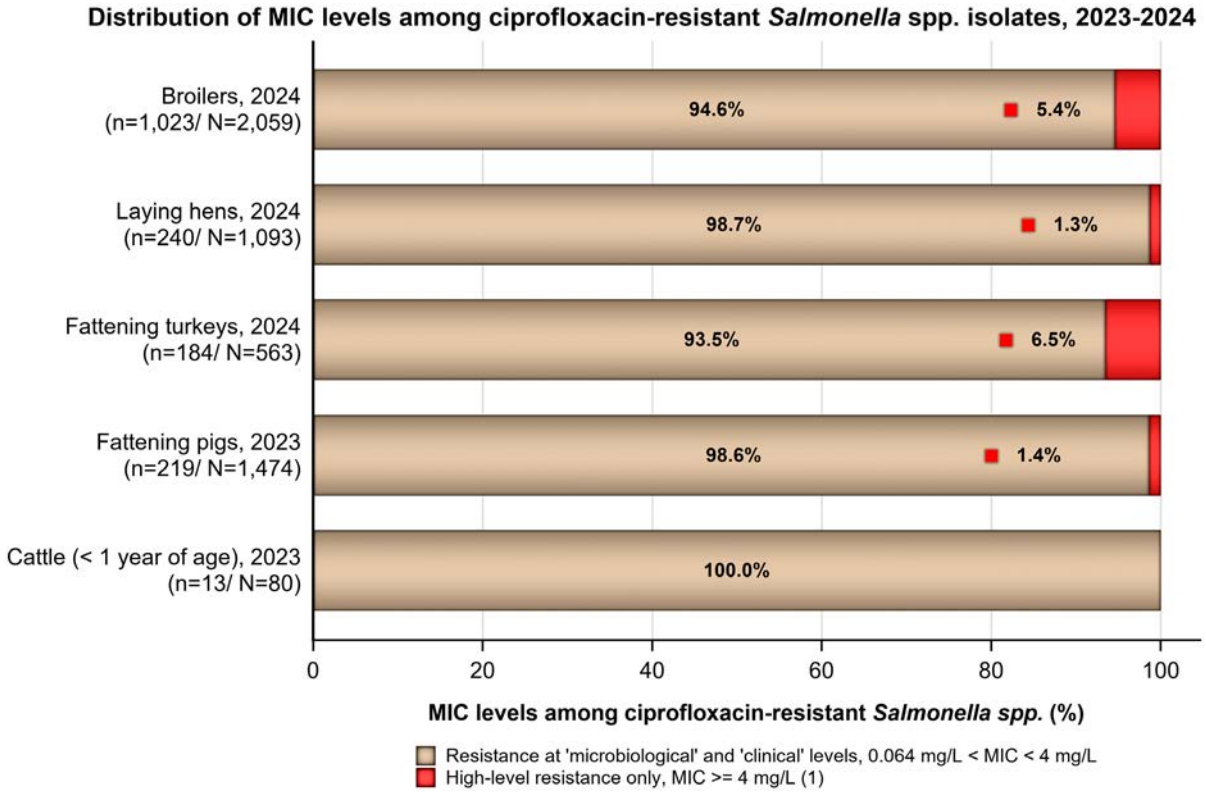


FIGURE 14 Distribution of MIC levels among ciprofloxacin-resistant *Salmonella* spp. isolates from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
Abbreviations: *N*, Total number of *Salmonella* spp. isolates reported by MSs; *n*, number of ciprofloxacin-resistant *Salmonella* isolates.

2.4.7 | 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, 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 (Appendix A – Materials and methods).

The proportion of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. at the MS level was generally very low or low in 2023 and 2024 (ranging between 0% and 2.2%, Annex A.2, tables 1, 6, 10, 14, 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 2024 was 1.2% in broilers, 0.3% in laying hens and 0.2% in turkeys, and in **2023** was 0.8% in pigs and 1.3% in calves. Detailed data per country and matrix are presented in Annex A.2 (Table 22–25). An overview of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. reported in 2023 and 2024 is given in Tables 10 and 11.

In **2024**, WGS data for *Salmonella* spp. were reported by three MSs (Germany, Italy and the Netherlands). Italy reported ***S.* Infantis** ($n = 11$) and ***S.* Senftenberg** ($n = 1$) from **broilers** and *S.* Infantis ($n = 1$) from **laying hens** carrying the $\boldsymbol{bla_{CTX\text{-}M\text{-}1}}$ gene. Italy also reported $\boldsymbol{bla_{TEM\text{-}106}}$ in one ***S.* Anatum** isolate from **fattening turkeys**. In **2023**, 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. Germany and the Netherlands also reported WGS data for imported meat sampled at BCPs (see specific textbox at the end of Chapter 4).

TABLE 10 Summary of presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. from targeted food-producing animals collected within the routine monitoring by serovar, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

Year	Animal population	Serovar	*n*	ESBL[a]	AmpC[b]	ESBL + AmpC[c]	Genotype (*n*)
2024	Broilers (*n* = 23)	*S.* India	1	–	1	–	bla_{CMY-2} (1)
		S. Infantis	17	16	1	–	$bla_{CTX-M-1}$ (11)
		S. Kentucky	1	1	–	–	–
		S. Livingstone	1	–	1	–	–
		S. Paratyphi B	1	1	–	–	–
		S. Rissen	1	1	–	–	–
		S. Strathcona	1	1	–	–	$bla_{CTX-M-1}$ (1)
	Fattening turkeys (*n* = 1)	*S.* Anatum	1	1	–	–	$bla_{TEM-106}$
	Laying hens (*n* = 3)	*S.* Derby	1	1	–	–	$bla_{CTX-M-1}$ (1)
		S. Infantis	1	1	–	–	–
		S. Kedougou	1	1	–	–	
2023	Calves (*n* = 1)	*S.* Dublin	1	1	–	–	–
	Fattening pigs (*n* = 12)	*S.* Bredeney	1	1	–	–	–
		S. enterica subs. Enterica*	1	1	–	–	$bla_{CTX-M-1}$ (1)
		S. Kedougou	7	6	1	1	–
		S. Kentucky	1	1	–	–	–
		S. Typhimurium, monophasic	2	2	–	–	$bla_{CTX-M-1}$ (1)

Abbreviations: AmpC, AmpC beta-lactamase; CP, carbapenemase; ESBL, extended-spectrum beta-lactamase; *n*, number of presumptive ESBL-/AmpC-/CP-producing isolates.

**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.

[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.

Carbapenem resistance in* Salmonella *spp.

Carbapenems are categorised as authorised for use in humans only (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 2023 and 2024, none of the *Salmonella* isolates recovered from any of the targeted food-producing animal populations exhibited microbiological resistance to meropenem. This is consistent with data from animal origins since 2020.

2.4.8 | 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 markedly influence the overall resistance levels in *Salmonella* spp., as the proportion of completely susceptible and multidrug-resistant isolates may vary significantly among serovars recovered from each of the studied food-producing animal populations. The analysis of antimicrobial resistance 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 are from clinical cases, while animal data come from healthy animals.

All of these factors may introduce a source of variation in results when comparing the 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 assessment of CS and MDR in *Salmonella* spp. isolates from humans is described in Section 2.3.5. Not all MSs test human 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 for 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 a 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 2024 and targeted food-producing animals for 2023–2024 in *Salmonella* spp. isolates and the serovars *S.* Infantis, *S.* Enteritidis and *S.* Kentucky, *S.* Typhimurium and its monophasic variant, and *S.* Derby, are summarised in Figure 15.

In **2024**, **MDR** was overall moderate (18.7%, *N* = 10,511) among ***Salmonella* spp**. reported in **human cases** in the EU, ranging from low levels among *S.* Enteritidis (3.2%, *N* = 3615) to very high among *S.* Kentucky (67.8%, *N* = 245) and monophasic *S.* Typhimurium (64.6%, *N* = 1492), while MDR in *S.* Infantis was reported at high levels (47.3%, *N* = 372).

MDR was observed at high levels in *Salmonella* spp. recovered from **pigs** (43.3%), **broilers** (35.1%), **turkeys** (22.9%) and **calves** (25.0%), while in **laying hens**, a markedly lower MDR level (6.0%) was observed.

The highest levels of MDR among all animal populations were observed in *S.* Infantis isolates, followed by monophasic *S.* Typhimurium and *S.* Kentucky. MDR in ***S.* Infantis** isolates from **broilers** (82.2%, *N* = 667) and **turkeys** (80.0%, *N* = 40) was reported at extremely high levels, showing considerably higher MDR values than that serovar recovered from humans (47.3%). In contrast, MDR levels in *S.* Infantis from **laying hens** (28.8%, *N* = 104) and pigs (9.8%, *N* = 41) were lower than those in humans.

In general, ***S.* Enteritidis** isolates from pigs and poultry populations showed a similar occurrence of MDR to those from humans (Figure 15). This was not the case in the occurrence of MDR levels in ***S.* Kentucky**, where differences were evident when comparing isolates from humans and turkeys to other animal origins. MDR levels in *S.* Kentucky from humans and turkeys reached very high and extremely high levels, respectively. While in monophasic *S.* typhimurium, MDR levels ranged from high to very high in poultry populations and humans, and reached extremely high levels in fattening pigs. (Figure 15).

Overall, in 2024, **CS** in ***Salmonella* spp**. isolates from humans was 57.9%. For animals, CS was high for pigs (36.8%) and broilers (38.1%), very high in turkeys (56.7%) and calves (56.3%) and extremely high in laying hens (72.4%). 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 (53.5%, *N* = 284) and humans (63.0%) to extremely high levels in turkeys (84.4%, *N* = 32) laying hens (81.6%, *N* = 380) and pigs (72.7%, *N* = 22).

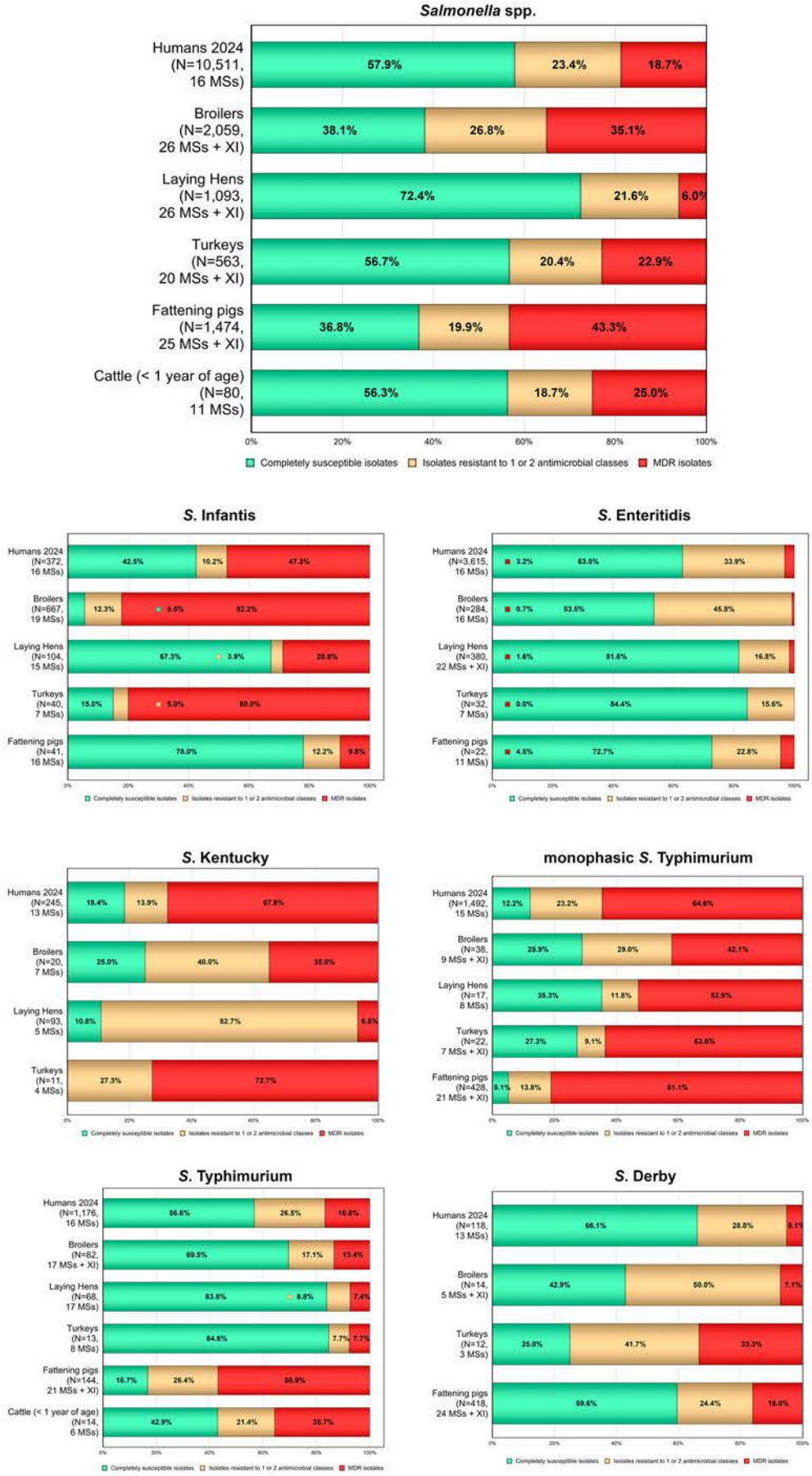


FIGURE 15 Multidrug resistance (MDR) and complete susceptibility (CS) in *Salmonella* spp. and selected serovars recovered from humans and targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
Abbreviations: MSs, Member States; *N*, total number of isolates belonging to a specific serovar reported by the MSs; XI, United Kingdom (Northern Ireland).

Resistance to selected antimicrobials

Overall resistance to **ampicillin**, **sulfonamides** and **tetracyclines** was observed at high levels in ***Salmonella* spp.** isolates from humans in 2024 and ranged from moderate to very high in isolates from targeted food-producing animals, except in laying hens, where low levels of resistance were reported (Figure 16). **Ciprofloxacin** resistance was observed at moderate levels in fattening pigs and calves, high levels in humans (21.8%), laying hens (22.0%) and turkeys (32.7%) and at very high levels in broilers (49.7%) in 2024 (Figure 16). Overall, **cefotaxime** resistance was noted at very low levels in human isolates in 2024 (1.6%) and was seldomly detected in food-producing animals in 2023–2024 (Figure 16).

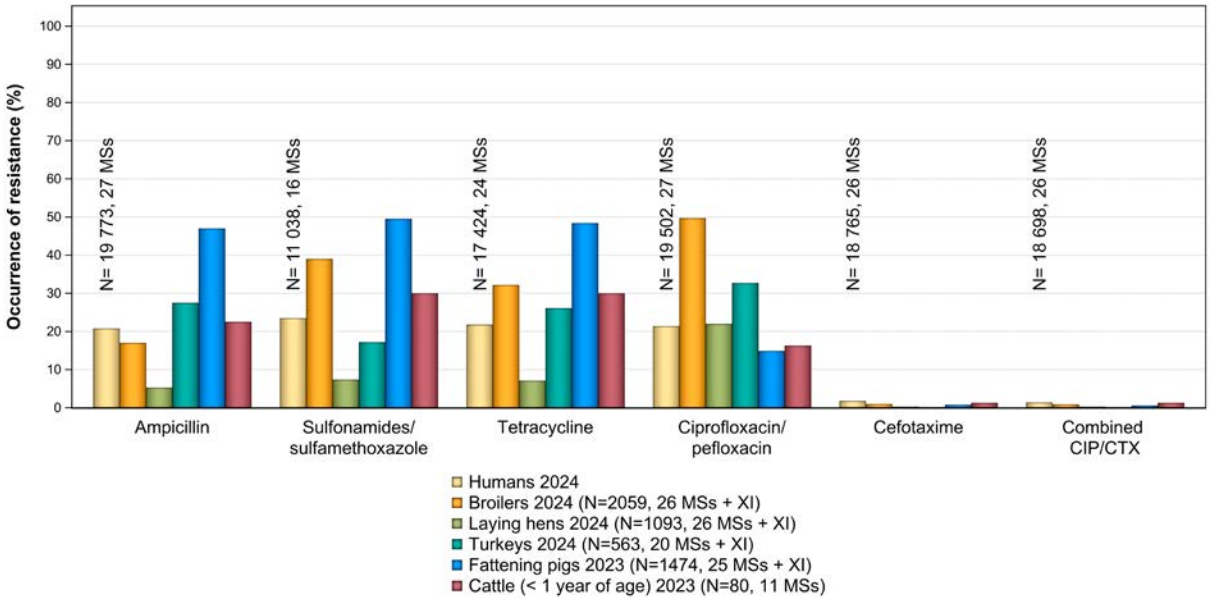


FIGURE 16 Occurrence of resistance to selected antimicrobials in ***Salmonella* spp.** from humans (2024) and targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

Resistance to selected antimicrobials by serovar

***S.* Infantis** was the fourth most common serovar identified in human cases in 2024, with 1689 cases reported in the EU/EEA, the most common serovar reported in broilers and the second and third in laying hens and turkeys, respectively. Resistance to ciprofloxacin in humans and laying hens was high (37.4% and 31.7%, respectively), while extremely high levels were reported in isolates from both broiler (93.4%) and turkey flocks (82.5%; Figure 17). Generally, resistance levels to sulfonamides and tetracycline were moderate in pigs, reaching high levels in humans and laying hens and extremely high levels in broilers (81.7% and 81.4%, respectively) and turkeys (72.5% and 80.0%, respectively; Figure 17). 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).

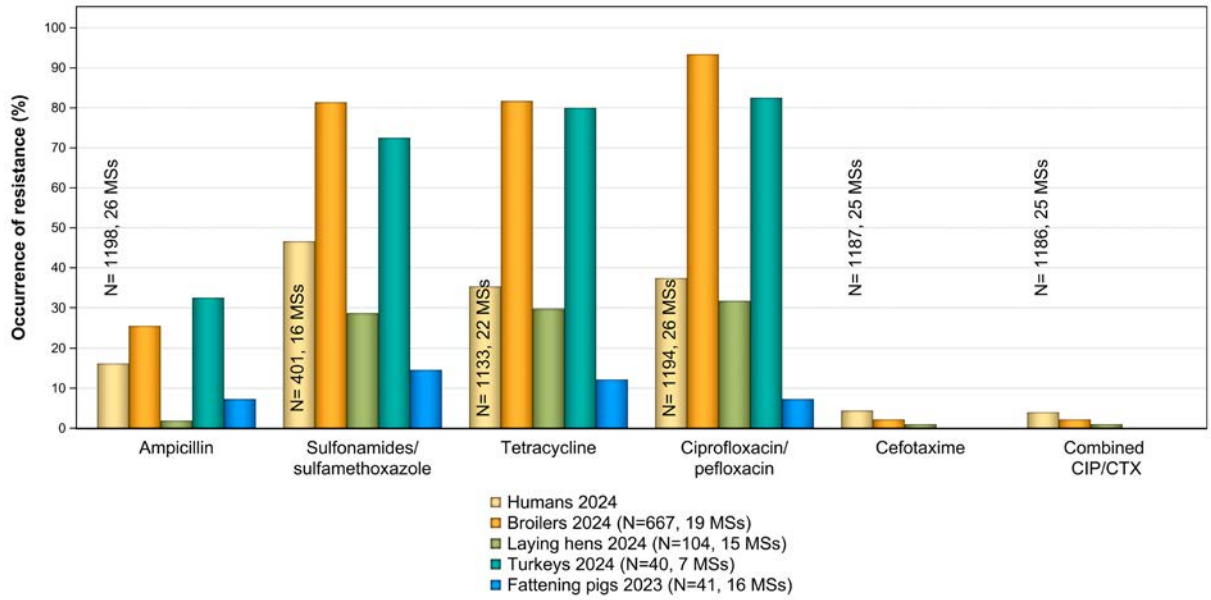


FIGURE 17 Occurrence of resistance to selected antimicrobials in ***S.* Infantis** from humans (2024) and targeted food-producing animals (≥ 10 isolates), EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

***S.* Enteritidis** was the most common *Salmonella* serovar identified in human cases in 2024, with 29,761 cases reported in the EU/EEA. It was also the most common serovar reported in laying hens in 2024 and the second one in broilers. While MDR was uncommon among *S.* Enteritidis isolates from both humans and poultry populations (Figure 18), resistance levels in *S.* Enteritidis from humans were high for ciprofloxacin and moderate for colistin. Similar resistance levels to these AMs were reported in *S.* Enteritidis isolated from laying hens and pigs, with the highest levels reported in isolates from broilers (Figure 18). 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., 2020a, 2020b).

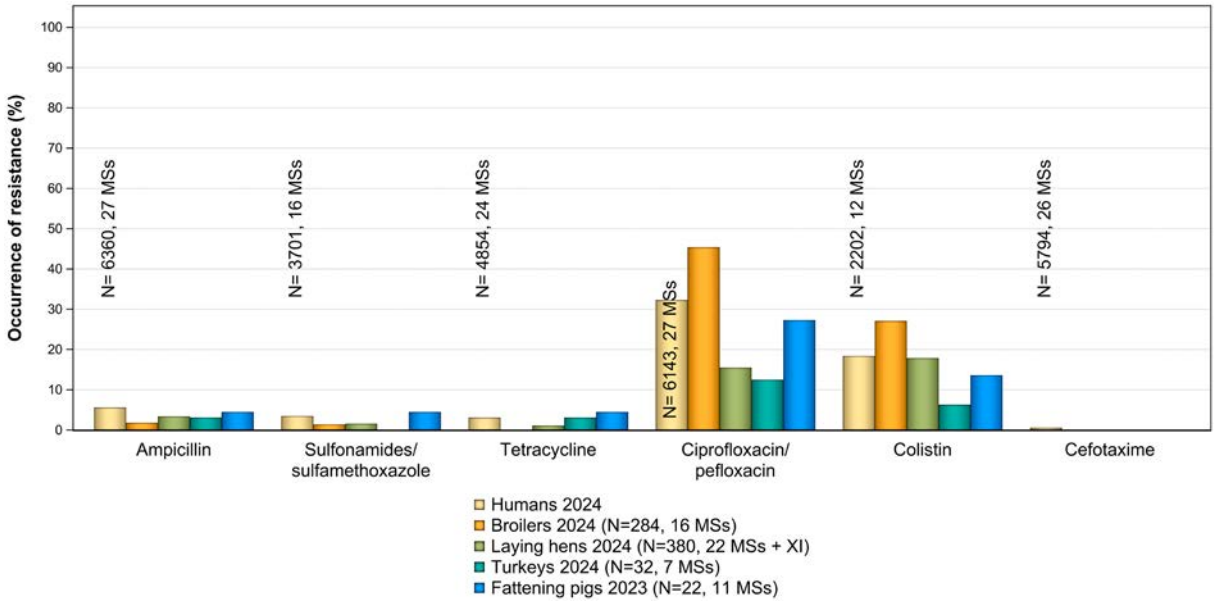


FIGURE 18 Occurrence of resistance to selected antimicrobials in ***S.* Enteritidis** from humans (2024) and targeted food-producing animals (≥ 10 isolates), EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

***S.* Kentucky** was the ninth most reported serovar from human cases in 2024, with 441 cases reported in the EU/EEA. Extremely high levels of resistance to ciprofloxacin were reported in human cases and all targeted food-producing animal populations (Figure 19). Additionally, *S.* Kentucky accounted for most (77.1%) of the *Salmonella* isolates recovered from poultry exhibiting high-level resistance to ciprofloxacin (Annex A.3). Similarly, in *Salmonella* isolates from humans in 2024, *S.* Kentucky accounted for 90.0% of the 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).

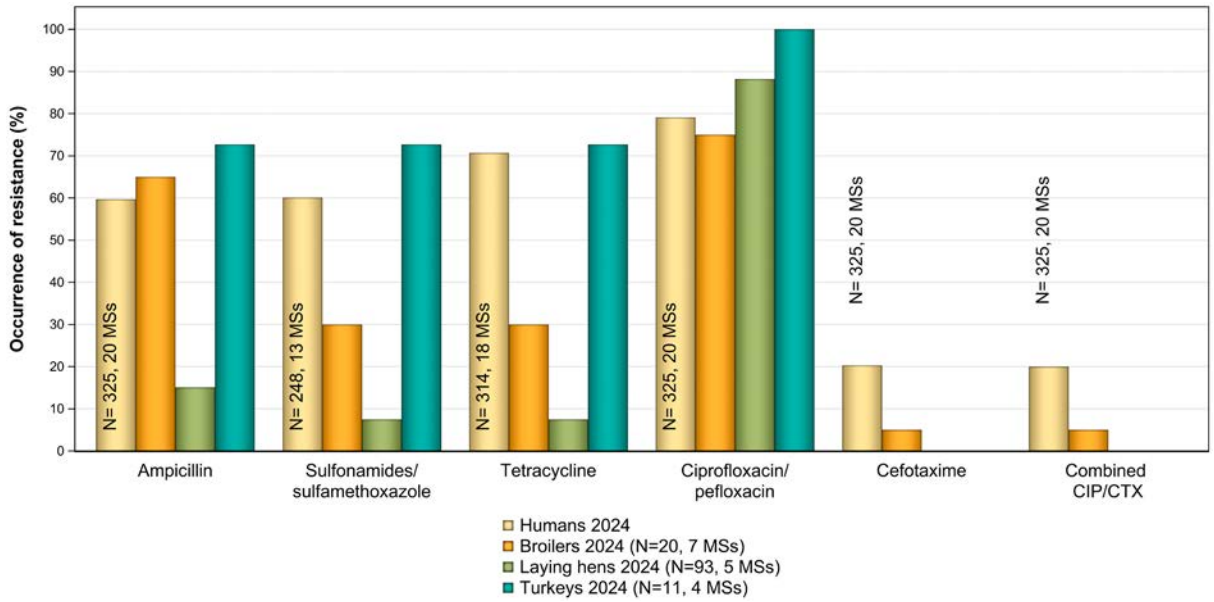


FIGURE 19 Occurrence of resistance to selected antimicrobials in ***S.* Kentucky** from humans (2024) and targeted food-producing animals (≥ 10 isolates), EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

***S.* Typhimurium** was the second most common *Salmonella* serovar identified in human cases in 2024, with 6804 cases reported in the EU/EEA and the second, third and fourth most common serovar identified in calves, pigs and laying hens, respectively. Considering all reporting MSs, considerably higher resistance levels to ampicillin, sulfonamides and tetracycline were observed in pigs and calves when compared to human cases. On the other hand, isolates from laying hens ($N=68$) and broilers ($N=82$) exhibited lower resistance levels to these AMs (Figure 20). Resistance to cefotaxime was only reported in human isolates (0.6%).

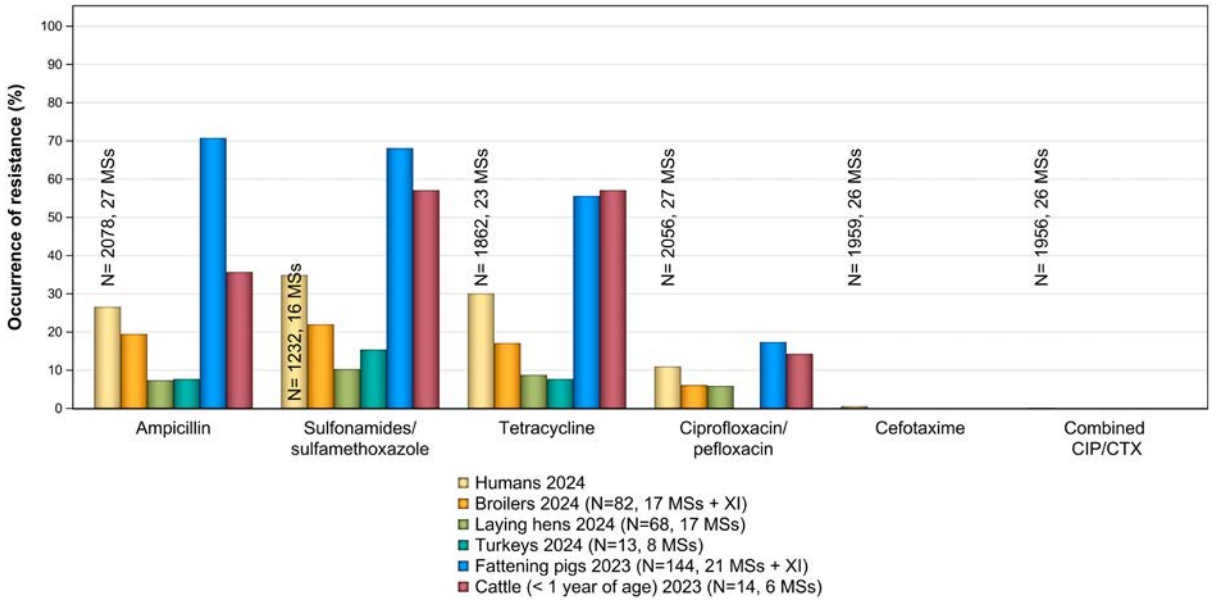


FIGURE 20 Occurrence of resistance to selected antimicrobials in ***S.* Typhimurium** from humans (2024) and targeted food-producing animals (≥ 10 isolates), EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

Monophasic *S.* Typhimurium was the third most common serovar reported from human cases in 2024, with 6073 registered cases in the EU/EEA, the most common serovar reported in pigs. Considering all reporting MSs, the highest levels of resistance in monophasic *S.* Typhimurium from humans were observed for ampicillin, sulfonamides and tetracycline, as were also for isolates from pigs and poultry populations (Figure 21). 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 poultry populations) to extremely high levels of resistance (in humans and pigs). This resistance pattern (together with resistance to streptomycin) is typical of the pandemic monophasic *S.* Typhimurium ST34 (Charity et al., 2022; Hopkins et al., 2010).

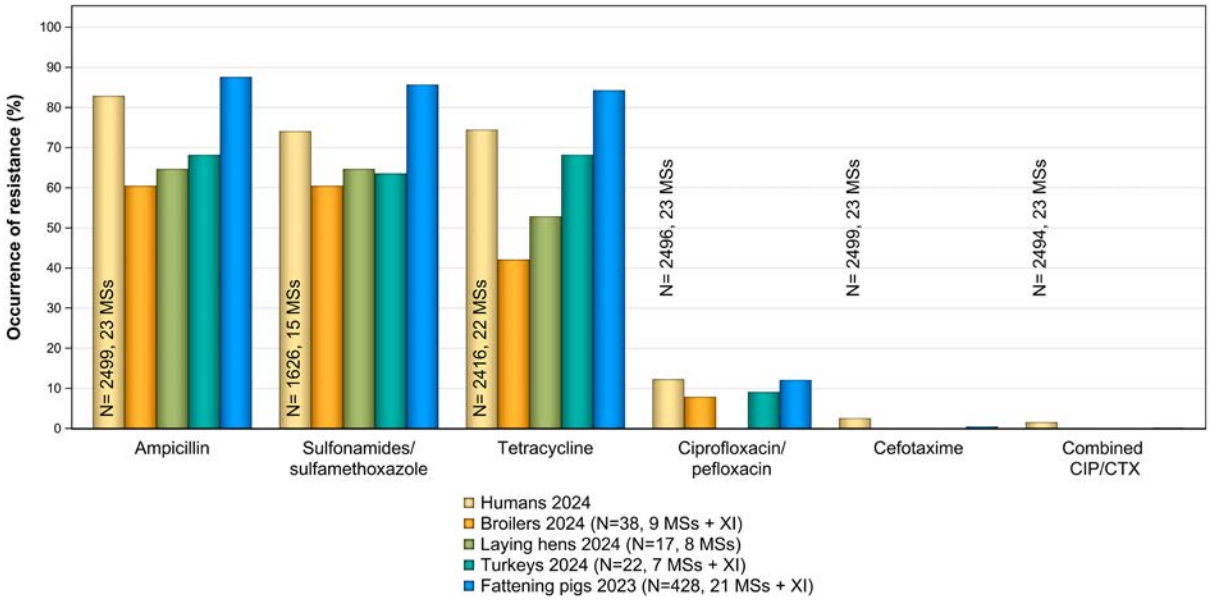


FIGURE 21 Occurrence of resistance to selected antimicrobials in **monophasic *S.* Typhimurium** from humans (2024) and targeted food-producing animals (≥ 10 isolates), EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

***S.* Derby** was the sixth most common serovar reported from human cases in 2024, with 596 cases registered by EU/EEA countries and the second in pigs. Although MDR was less frequently observed among *S.* Derby isolates from humans and animals in comparison to *S.* Typhimurium and its monophasic variant (Figure 15), resistance to ampicillin, sulfonamides and tetracycline was relatively common in *S.* Derby isolates from human cases, fattening turkeys, pigs and broilers (Figure 22).

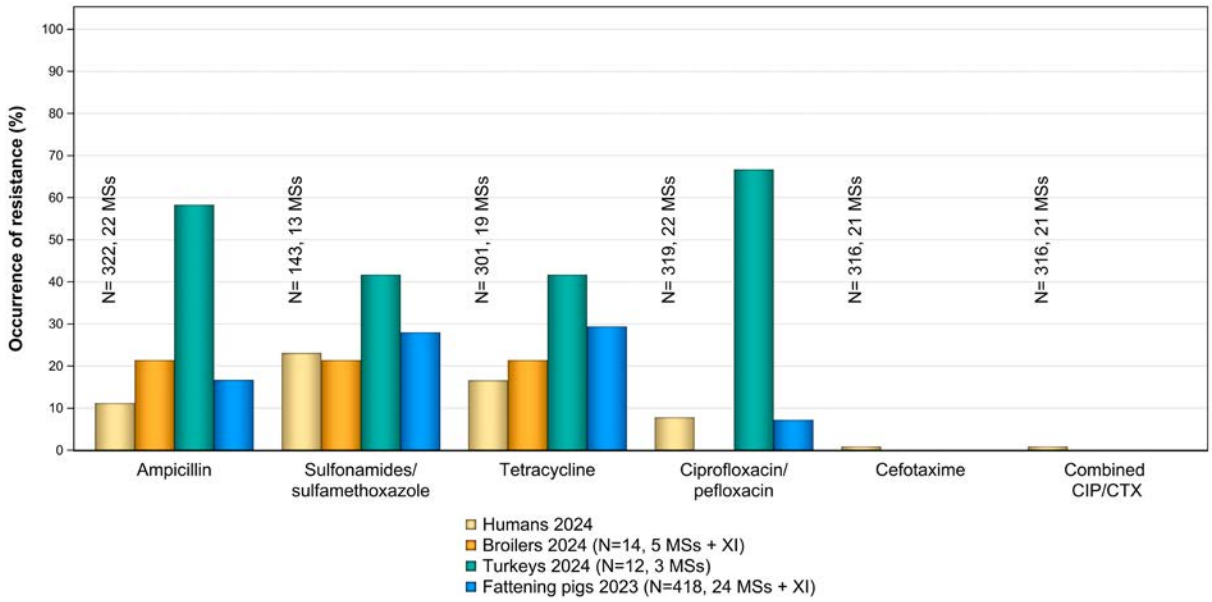


FIGURE 22 Occurrence of resistance to selected antimicrobials in ***S.* Derby** from humans (2024) and targeted food-producing animals (≥ 10 isolates), EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

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

The overall proportion of presumptive ESBL-/AmpC-producing *Salmonella* spp. at the MS level was generally very low or low in 2023 and 2024 among all targeted food-producing animal populations and very low in isolates from human cases (Table 6). In 2023 and 2024, no *Salmonella* spp. isolates recovered from animal origins were microbiologically resistant to meropenem. Similar to 2023, meropenem resistance in 2024 was reported in *Salmonella* spp. isolates from humans (< 0.1%, Table 6), with three countries reporting one to three resistant isolates each.

TABLE 11 Summary of the presumptive ESBL-, AmpC- or CP-producing *Salmonella* spp. from humans and targeted food-producing animals, subjected to supplementary testing (panel 2) or whole genome sequencing, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

	ESBL and/or AmpC[a]	ESBL[b]	AmpC[c]	ESBL + AmpC[d]	CP[e]
Population	**% R (*n*)**	**% R (*n*)**	**% R (*n*)**	**% R (*n*)**	**% R (*n*)**
Humans 2024 (*N* = 18,128, 27 MSs)	1.1 (203)	0.9 (171)	0.1 (27)	< 0.1 (5)	< 0.1 (5)
Humans 2023 (*N* = 18,459, 26 MS)	0.9 (162)	0.8 (141)	0.1 (21)	0 (0)	< 0.1 (6)
Broilers, 2024 (*N* = 2059, 26 MSs + XI)	1.2 (24)	1.0 (20)	0.1 (3)	< 0.1 (1)	0 (0)
Laying hens, 2024 (*N* = 1093, 26 MSs + XI	0.3 (3)	0.3 (3)	0 (0)	0 (0)	0 (0)
Fattening turkeys, 2024 (*N* = 563, 21 MSs)	0.2 (1)	0.2 (1)	0 (0)	0 (0)	0 (0)
Fattening pigs, 2023 (*N* = 1474, 25 MSs + XI)	0.8 (12)	0.7 (11)	0 (0)	0.1 (1)	0 (0)
Cattle under 1 year of age, 2023 (*N* = 80, 11 MSs)	1.3 (1)	1.3 (1)	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; *n*, number of presumptive ESBL- and/or AmpC–/CP-producing isolates; *N*, total number of isolates tested.

[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).

[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 the CP-encoding gene reported.

2.6 | Discussion

Salmonella spp. has consistently been the second most reported food-borne zoonotic agent in the EU over the past decade. Although most salmonellosis cases are self-limiting, rarely leading to clinical conditions that require antimicrobial treatment, the emergence of *Salmonella* strains resistant to clinically-relevant antimicrobials may compromise treatment efficacy and result in a higher disease burden, thus representing an important public health concern.

In 2023 and 2024, the detection of resistant *Salmonella* isolates varied markedly based on their animal origins, serovars and reporting countries. These factors may introduce variability in the results when considering data from all reporting countries; therefore, results should be interpreted cautiously.

Regarding data from humans, resistance predicted from WGS has been an accepted test method since 2019 and for 2024, five 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 2023–2025. 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

As in previous years, *Salmonella* isolates recovered from targeted animal populations in 2023–2024 showed high resistance to **tetracyclines**, **sulfonamides** and **ampicillin**, with overall lower levels in laying hen flocks. **Temporal trends** at the MS level in *Salmonella* spp. reveal decreasing trends in ampicillin and ciprofloxacin (turkeys) and tetracycline resistance (broilers and turkeys). **Monophasic *S.* Typhimurium** continues to be the serovar registering the highest resistance levels to these antimicrobials, a characteristic of the most frequent clone (Sequence Type (ST) 34) circulating within the EU (Sun et al., 2020). Due to the recent implementation of Commission Implementing Decision 2020/1729, data from pigs and calves are not yet available to statistically estimate temporal trends. Although these antimicrobials are commonly used in veterinary medicine, associations between antimicrobial consumption and resistance in *Salmonella* spp. are inconsistent (ECDC, EFSA, EMA, 2021, 2024), most likely due to the limited number of isolates (especially when comparing with other more ubiquitous bacteria, such as *E. coli* and *C. jejuni*), combined with the diversity of serovars. Still, based on trend analysis of serovar specific data from humans, where many more isolates are available, we could observe that resistance to both ampicillin and tetracycline declined significantly in a large proportion of reporting countries over the period 2014–2024. The decline was primarily driven by a reduction in resistance in *S*. Typhimurium and for tetracycline, also in monophasic *S*. Typhimurium. Both these serovars are most commonly associated with pigs and calves. However, the lack of genotypic data from food-producing animals limits the understanding of the contribution of the spread of resistant clones and/or the influence of antimicrobial usage, both at the human and veterinary levels.

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) and as AMEG category B antimicrobials for veterinary medicine, whose use in animals should be restricted to mitigate the risk to public health (EMA, 2019). 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 2023 and 2024. In *Salmonella* spp. isolated from human cases in 2024, resistance levels to cefotaxime and ceftazidime were also low.

In 2024, most ESBL phenotypes in food-producing animals were associated with *S*. Infantis from broilers, with 11 isolates harbouring $\boldsymbol{bla_{\text{CTX-M-1}}}$. Fourteen *S*. Infantis from humans also carried this ESBL gene. A dominant cluster of *S*. Infantis strains isolated from the environment, animals, food and humans, and harbouring pESI-like plasmids carrying $bla_{\text{CTX-M-1}}$ genes has been identified in Italy (Russo et al., 2024), suggesting clonal spread among animal populations and humans. In 2023, Germany reported a monophasic *S*. Typhimurium harbouring $\boldsymbol{bla_{\text{CTX-M-1}}}$ from a pig isolate. In monophasic *S*. Typhimurium from humans, this ESBL gene was also the most common in 2024, detected in 17 of the 18 isolates from one country (Slovenia), although without any indication of cases being linked to a single source outbreak. 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 pigs, but also cattle and sheep) (Rodríguez et al., 2012; Sun et al., 2020).

Moreover, both in 2023 and 2024, no *Salmonella* spp. isolates recovered from animal/meat origins were microbiologically resistant to **meropenem**. Similarly to 2023, *Salmonella* spp. isolates from humans resistant to meropenem were recovered in a few countries in 2024; however, at the MS level, the occurrence of meropenem resistance was < 0.1%.

Ciprofloxacin/nalidixic acid resistance was highest among *Salmonella* isolates recovered from poultry populations, especially broilers. *S*. Infantis from broilers 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 high levels of resistance to these antimicrobials. This likely reflects the spread of resistant clones belonging to these serovars.

From human data reported in 2024, *S*. Kentucky, followed by *S*. Infantis and *S*. Enteritidis, also showed the highest resistance to these substances. Resistance to ciprofloxacin/nalidixic acid, sulfamethoxazole and tetracycline is typical of a clone of *S*. Infantis prevalent in broilers across Europe (Alba et al., 2020). Ciprofloxacin resistance was observed at very similar levels to nalidixic acid resistance in food-producing animals. However, isolates exhibiting ciprofloxacin resistance and nalidixic acid susceptibility were also observed and most frequently identified in turkeys, indicating the involvement of plasmid-mediated quinolone resistance (PMQR) mechanisms. Several isolates from broilers and pigs were also reported with this same profile, predominantly originating from Spain. Ciprofloxacin resistance increased significantly in 2014–2024 in *Salmonella* isolated from humans in more than half of the reporting countries, mainly due to an increase in resistance in *S*. Enteritidis but several countries also observed an increased resistance in monophasic *S*. Typhimurium.

In both reporting years, the overall **combined resistance to ciprofloxacin and cefotaxime** in *Salmonella* isolates from human cases 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 and *S*. Kentucky isolates from human cases in 2024, with several countries reporting moderate levels of combined resistance and in *S*. Kentucky, two countries reporting high and very high levels of combined resistance. ESBL was reported in 13.0% of *S*. Kentucky from humans in 2024. Combined resistance was not seen in *S*. Kentucky nor *S*. Infantis in laying hens or turkey flocks. In *Salmonella* isolates from broilers, only Malta reported combined resistance in a single *S*. Kentucky. *S*. Kentucky ST198 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 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 2024, as many as four mutations in the QRDR were identified in nine of 10 ciprofloxacin-resistant *S*. Kentucky, all ST198. The tenth carried a *qnr*-gene.

Regarding *S*. Infantis isolated from humans, two ESBL types dominated in 2024 – $bla_{\text{CTX-M-1}}$, which was identified in 14 *S*. Infantis isolates from four countries, of which nine from Italy, and $bla_{\text{CTX-M-65}}$, identified in 17 isolates from six countries, of which six from Spain and five from Germany. Regarding *S*. Infantis in broiler flocks, Malta and Italy reported moderate and low levels of combined microbiological resistance to ciprofloxacin and cefotaxime. Several scientific publications in Europe highlight the involvement of plasmids, which appear to be responsible for resistance in many European MDR *S*. Infantis isolates from food-producing animals, meat and humans (Alba et al., 2020; Alvarez et al., 2023; Franco et al., 2015; Nógrády et al., 2012).

High-level resistance to ciprofloxacin

In 2024, high-level resistance to ciprofloxacin was observed in several isolates from poultry. *S*. Newport and *S*. Infantis were the most prevalent serovars exhibiting high-level resistance among broilers, with *S*. Kentucky being the third most frequently reported. This is unlike findings from previous years, when *S*. Kentucky was the most commonly found serovar. In isolates from human cases in 2024 however, high-level ciprofloxacin resistance was still most commonly found in *S*. Kentucky (in 78.9% 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, which was also confirmed by the sequencing data available on resistant *S*. Kentucky isolates from humans. All 10 *S*. Kentucky predicted to be resistant to ciprofloxacin were ST198, and nine of these had two mutations each in *parC* and *gyrA*, while the tenth carried a qnrB19-gene. Sequence typing is not performed on isolates from food-producing animals in the framework of the EU AMR monitoring, and further studies are needed to conclude on the presence of the ST198 clone among the food-producing animals monitored.

Occurrence of resistance to last resort antimicrobials

Tigecycline resistance in poultry was mostly found in *S*. Infantis, while in pigs was primarily detected in *S*. Rissen and monophasic *S*. Typhimurium. In 2024, *S*. Infantis was the serovar exhibiting the highest tigecycline resistance in humans. Multidrug resistance was a common feature among tigecycline-resistant *Salmonella* serovars from animal populations. The recent revision of the ECOFF for tigecycline in the current legislation lowered the threshold from MIC > 1 mg/L to MIC > 0.5mg/L. This change has led to higher than expected levels of tigecycline resistance in previous years (EFSA, 2024, 2025), with most isolates now classified as tigecycline-resistant having a MIC one dilution above the new ECOFF. Under the previous ECOFF, these isolates would have been considered susceptible. Still, 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). In 2024, tigecycline resistance levels in *Salmonella* from poultry populations were lower when compared to those reported in 2022, while the percentage of tigecycline-resistant isolates with a MIC of 1 mg/L remained consistent. This suggests a true decrease in tigecycline resistance at the EU level, despite the ECOFF revision. 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 meat) in China (Bai et al., 2019; He et al., 2019). Two human isolates of *S*. Kentucky ST198, from two different countries, carried *tet*(X4) in 2024 – these were the first findings ever of this gene in the European *Salmonella* 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 13 of the 27 reporting MSs. EUCAST has temporarily removed the *Salmonella*-specific ECOFF until more comprehensive data are 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 five countries reporting sequences for AMR in humans in 2024, none of the 1603 isolates carried resistance mechanisms to colistin. Only one isolate harboured an *mcr-9* gene, which usually does not confer phenotypic resistance to colistin.

Multidrug resistance (MDR)

In 2023 and 2024, high MDR levels were observed among *Salmonella* spp. from food-producing animals, except in laying hens (6.0%). MDR levels varied across serovars, which may exhibit distinct MDR patterns. Therefore, when comparing MDR levels across animal populations and countries, it is essential to consider the relative contribution of a particular serovar. For example, the overall lower MDR levels in laying hens likely reflects the predominance of *S*. Enteritidis, the most frequently reported serovar by MSs, which showed extremely high complete susceptibility levels (81.6%). In contrast, the high MDR levels observed in broilers reflect the high occurrence of *S*. Infantis and its extremely high MDR level (82.2%).

In *Salmonella* spp. strains from human cases, MDR was detected in 18.7% 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, *S*. Kentucky isolates from turkeys exhibited extremely high MDR levels, 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 imported or consumed while travelling (Tate et al., 2022). Similar studies at the EU level are needed to elucidate these differences.

3 | ANTIMICROBIAL RESISTANCE IN *CAMPYLOBACTER* SPP.

3.1 | Key findings

- In 2024, 23 MSs and two non-MSs reported **data on AMR in *C. jejuni* and *C. coli*** isolates from humans. In the same year, data from broilers were reported for *C. jejuni* by 27 MSs, the United Kingdom (Northern Ireland) and three non-MSs, and for *C. coli* by 24 MSs, the United Kingdom (Northern Ireland) and one non-MS. Additionally, in 2024, data from fattening turkeys were reported by 10 MSs for *C. jejuni* and by 11 MSs for *C. coli*.
- The **occurrence of resistance** differed widely between reporting countries, across different antimicrobials and between the two *Campylobacter* species, with overall resistance levels higher in *C. coli* than in *C. jejuni*.
- In 2023–2024, resistance to **ciprofloxacin** ranged from high or very high to extremely high, in *C. jejuni* and *C. coli* isolates, recovered from humans and food-producing animals in the EU. In 2024, levels of resistance to ciprofloxacin in human isolates ranged from 33.2% to 97.0% in *C. jejuni*, while for *C. coli* isolates, 12 out of 18 countries reporting at least 10 *C. coli* isolates found levels of ciprofloxacin resistance higher than 70% (extremely high). 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 85.1% in fattening turkeys, although very high levels were also observed in *C. jejuni* from poultry.
- Resistance to **erythromycin** varied from rare to low in *C. jejuni* from humans and food-producing animals but was higher in *C. coli*, ranging from overall 5.1% in humans to 31.6% in calves.
- **WGS** results for erythromycin-resistant *C. jejuni* and *C. coli* isolates from food-producing animals in 2023–2024 revealed a predominant presence of the A2075G mutation in the 23S rRNA gene. The transferable *erm*(B) gene was only detected in one *C. coli* isolate from calves in 2023 and two *C. coli* isolates from fattening turkeys in 2024. No *erm*(B) genes were detected among WGS results reported for *Campylobacter* from humans in 2024.
- 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, and higher in *C. coli* isolates, varying from overall low levels observed in humans (5.0%) and broilers (7.8%), to high levels in calves (30.3%), which 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 calves in 2023, and the moderate to very high levels of resistance to ertapenem in *C. jejuni* and *C. coli* isolated from poultry in 2024

might be a cause for public health concern, as those antimicrobials are recommended for treatment of severe invasive *Campylobacter* infections in humans.

- **Gentamicin** resistance in *C. jejuni* and *C. coli* from humans was observed at very low and low levels, respectively, 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 broilers and from fattening turkeys between 2022 and 2024.
- The **prevalence of resistance** to selected antimicrobials in *C. jejuni* and *C. coli* from broilers in 2024 showed high between-country variability for ciprofloxacin and tetracycline, ranging from 0% to high or very high levels. A narrower variability range, from low to high levels, was observed in the prevalence of ciprofloxacin and tetracycline resistance in *C. jejuni* from fattening turkeys. Notably, a more limited between-country variability and lower levels of prevalence of resistance were found for erythromycin and gentamicin, in both *C. jejuni* and *C. coli*, although moderate and high prevalence of erythromycin resistance were found in *C. coli* from broilers and fattening turkeys, respectively, in few reporting countries.
- Overall, **complete susceptibility** (CS), defined as susceptibility to ciprofloxacin, erythromycin, tetracycline and gentamicin, was higher in *C. jejuni* than in *C. coli* isolates. In humans, in 2024, the overall CS level was 28.0% in *C. jejuni* and 12.7% in *C. coli*. In food-producing animals, CS was least common in *C. coli* isolates from calves (4.5%) and fattening turkeys (5.3%), and most common in *C. jejuni* from pigs (51.1%).
- **Multidrug resistance** (MDR), defined as resistance to at least three antimicrobials among ciprofloxacin, erythromycin, tetracycline and gentamicin, was generally very low for *C. jejuni* isolated from humans (0.7%) and ranged from very low to low in the animal species considered. Compared to *C. jejuni*, MDR was markedly higher in *C. coli*, occurring in 7.5% of the isolates from humans, and at low to high levels in isolates from food-producing animals, with the highest values in calves (34.8%) and the lowest in broilers (7.6%). These results are in line with the higher levels of resistance to selected antimicrobials seen in *C. coli* isolates.
- **Over the period 2014–2024**, **resistance to ciprofloxacin in *C. jejuni*** increased significantly in humans in 11 MSs and one non-MS, and in broilers in seven MSs. In the same period, resistance to ciprofloxacin in *C. coli* increased significantly in humans in four MSs, in broilers in two MSs and in fattening pigs in two non-MSs.
- **Over the period 2014–2024, erythromycin resistance** in *C. jejuni* decreased significantly in humans in 10 countries (nine MSs and one non-MS), in broilers in seven countries (six MSs and one non-MS), and in fattening turkeys in two MSs. Erythromycin resistance in *C. coli* also decreased in humans in eight MSs and in fattening pigs in four countries (three MSs and one non-MS). An increasing trend in erythromycin resistance in *C. jejuni* was observed in humans in two MSs and in broilers in one MS, as well as in *C. coli* in broilers in one MS.

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

The two main *Campylobacter* species responsible for human infections are *C. jejuni*, which is the 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.

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 2024. Data from 2023 are presented in the 2022–2023 report (EFSA and ECDC, 2025b).

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 calves 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 calves and fattening turkeys, respectively. This chapter includes data on *C. jejuni* and *C. coli* in broilers and fattening turkeys in 2024, and in calves and fattening pigs in 2023 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, calves, fattening pigs and other animal species) performed in 2023 and 2024 is available as supporting documentation on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17950222.

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, is 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, 2025). Further consideration on the data used and the methodology applied in the analysis can be found in Appendix A – Materials and methods.

Information on the classification of antimicrobials according to their use in animals and their importance in treating human infections is provided in the Introduction and in the text box below.

Classification of antimicrobials according to AMEG and WHO

The mandatory antimicrobials to be reported for *Campylobacter* isolates are categorised as indicated below under the AMEG and the WHO frameworks (for additional information, refer to the Introduction):

Antimicrobial	WHO classification	AMEG classification
Ciprofloxacin	HPCIA	B – restrict
Chloramphenicol	HIA	C – caution
Ertapenem	Authorised in humans only	A – avoid
Erythromycin	CIA	C – caution
Gentamicin	CIA	C – caution
Tetracycline	HIA	D – prudence

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

3.3.1 | Data reported

For 2024, 23 MSs and two non-MS (Iceland and Norway) reported data on AMR from *C. jejuni* and *C. coli* isolated from human cases of campylobacteriosis. The 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.

Sixteen 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 (Bulgaria, Latvia and Romania providing sequences that were interpreted by ECDC, and Ireland and the Netherlands providing already interpreted data) (Appendix A – Materials and methods, table A.33). Not all countries reported results for all antimicrobials in the harmonised panel (ECDC, 2016).

The reported data represented 22.2% and 25.9% of the confirmed human cases with *C. jejuni* and *C. coli*, respectively, reported in the EU/EEA in 2024.

3.3.2 | Occurrence of resistance

In 2024, high to extremely high levels of resistance to **ciprofloxacin** were reported in *C. jejuni* isolated from humans, with levels below 40% in Ireland (38.6%) and Norway (33.2%), and over 90% in Cyprus, Lithuania, Bulgaria, Greece and Portugal (range 90.4%–97.0%) (Annex B.1, table 1). The overall resistance level of ciprofloxacin in the EU was extremely high (72.0%) (Figure 23; Table 12). The overall ciprofloxacin resistance level in *C. coli* in the EU was at a similar level (76.5%) however, the median level in *C. coli* was higher due to all countries – except for one – reporting very high to extremely high ciprofloxacin resistance levels (Figure 23; Table 12; Annex B.1, table 2). The highest ciprofloxacin resistance levels in *C. coli* isolates were reported by Lithuania and Portugal (100% and 91.5%, respectively). The lowest ciprofloxacin resistance levels in *C. coli* were reported by Ireland (42.9%) and the Netherlands (60.0%).

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 0.6% (Figure 23; Table 12). The highest levels were reported by Estonia, Malta and Luxembourg (5.7%, 4.6%, 2.4%, respectively). Erythromycin resistance was generally higher in *C. coli* compared to *C. jejuni*, with an overall EU resistance in *C. coli* of 5.1% and ranging from rare to moderate by country. The highest erythromycin resistance was reported in Spain, Portugal and Finland (15.6%, 14.9% and 14.7%, respectively) (Figure 23 and Annex B.1, table 2).

In 2024, overall, MSs reported high **tetracycline** resistance in human *C. jejuni* (45.9%, Figure 23; Table 12) with levels ranging from moderate (13.3%, Iceland) to extremely high (75.0%–83.8% in Malta, Latvia, Lithuania and Cyprus) (Annex B.1, table 1). The overall level of tetracycline resistance in human *C. coli* in the EU was very high (62.3%) with resistance levels varying from high (35.7%, Ireland) to extremely high (90.0% in Lithuania; 83.7% in Spain and 79.8% in Portugal). Nine out of 18 countries reporting at least 10 isolates obtained extremely high tetracycline resistance levels (Annex B.1, table 2).

Seventeen and 11 MSs reported data on **gentamicin** resistance from more than 10 isolates in *C. jejuni* and *C. coli* respectively (Annex B.1, tables 1 and 2). For *C. jejuni*, resistance levels in the EU were very low in general (0.4%, table 12) with eight

countries reporting 0.0% resistance, and the highest resistance reported by Estonia (2.1%). Overall gentamicin resistance levels in *C. coli* were somewhat higher in the EU, but still considered low (1.9%). All countries reporting resistance in *C. coli* in at least 10 isolates reported rare to low levels of resistance.

Only a few countries reported at least 10 isolates tested in relation to **co-amoxiclav** resistance (eight for *C. jejuni* and three for *C. coli*). For *C. jejuni* and *C. coli*, the overall EU resistance level was low (7.7% and 6.2%, respectively) (Annex B.1, tables 1 and 2), though two countries reported high and one country reported very high levels of resistance to co-amoxiclav in *C. jejuni* and two countries reported high levels in *C. coli* (Annex B.1, tables 1 and 2).

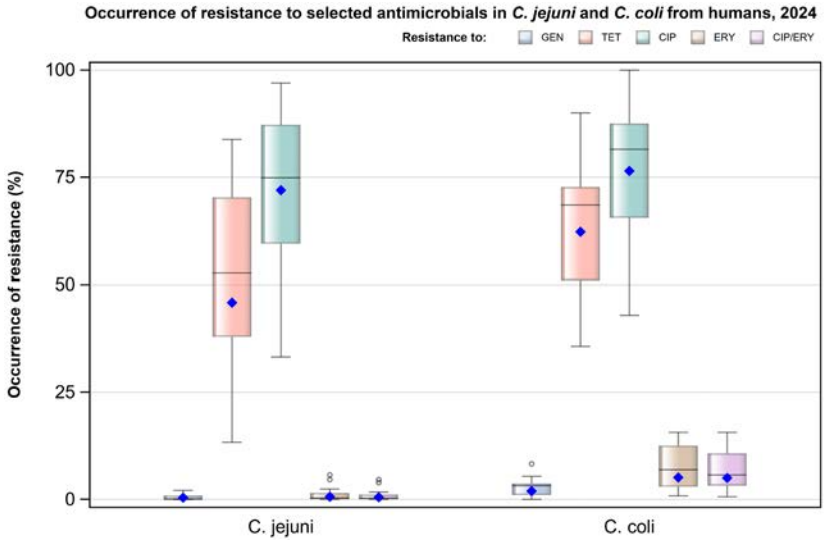


FIGURE 23 Boxplot of the occurrence of resistance to a selection of antimicrobials in *Campylobacter jejuni* and *C. coli* isolated from humans, 2024.
Notes: Only MSs reporting data for 10 or more isolates are shown in the graph; however, all isolates are included in the calculation of resistance at the reporting MS-group level. Blue diamond, Resistance at the reporting MS-group level.
Abbreviations: CIP/ERY, combined resistance to ciprofloxacin and erythromycin; CIP, ciprofloxacin; ERY, erythromycin; GEN, gentamicin; Horizontal lines represent median; Lower and upper box boundaries, 25th and 75th percentiles, respectively; TET, tetracycline.

TABLE 12 Overall resistance levels in the European Union in *Campylobacter jejuni* and *C. coli* isolated from humans, 2024.

	Ciprofloxacin		Erythromycin		Tetracycline		Gentamicin		Combined CIP/ERY	
***Campylobacter* species**	***N***	**% res**	***N***	**% res**	***N***	**% res**	***N***	**% res**	***N***	**% res**
C. jejuni (23 MSs)	20,012	**72.0**	20,466	**0.6**	18,317	**45.9**	9959	**0.4**	19,824	**0.5**
C. coli (23 MSs)	3268	**76.5**	3374	**5.1**	3069	**62.3**	1665	**1.9**	3231	**5.0**

Abbreviation: 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 in humans, was very low at the EU level in *C. jejuni* (0.5%) and low (5.0%) in *C. coli* (Table 12 and Annex B.1, tables 1 and 2). These percentages were similar to the proportions reported in 2023. The levels of combined resistance to both ciprofloxacin and erythromycin in human *C. jejuni* isolates ranged from 0.0% to 4.6%, with the highest levels reported by Malta and Estonia. The levels of combined resistance to both ciprofloxacin and erythromycin in human *C. coli* isolates ranged from 0.6% to 15.6%, with the highest level reported by Spain (Figure 24; Annex B.1, tables 1 and 2).

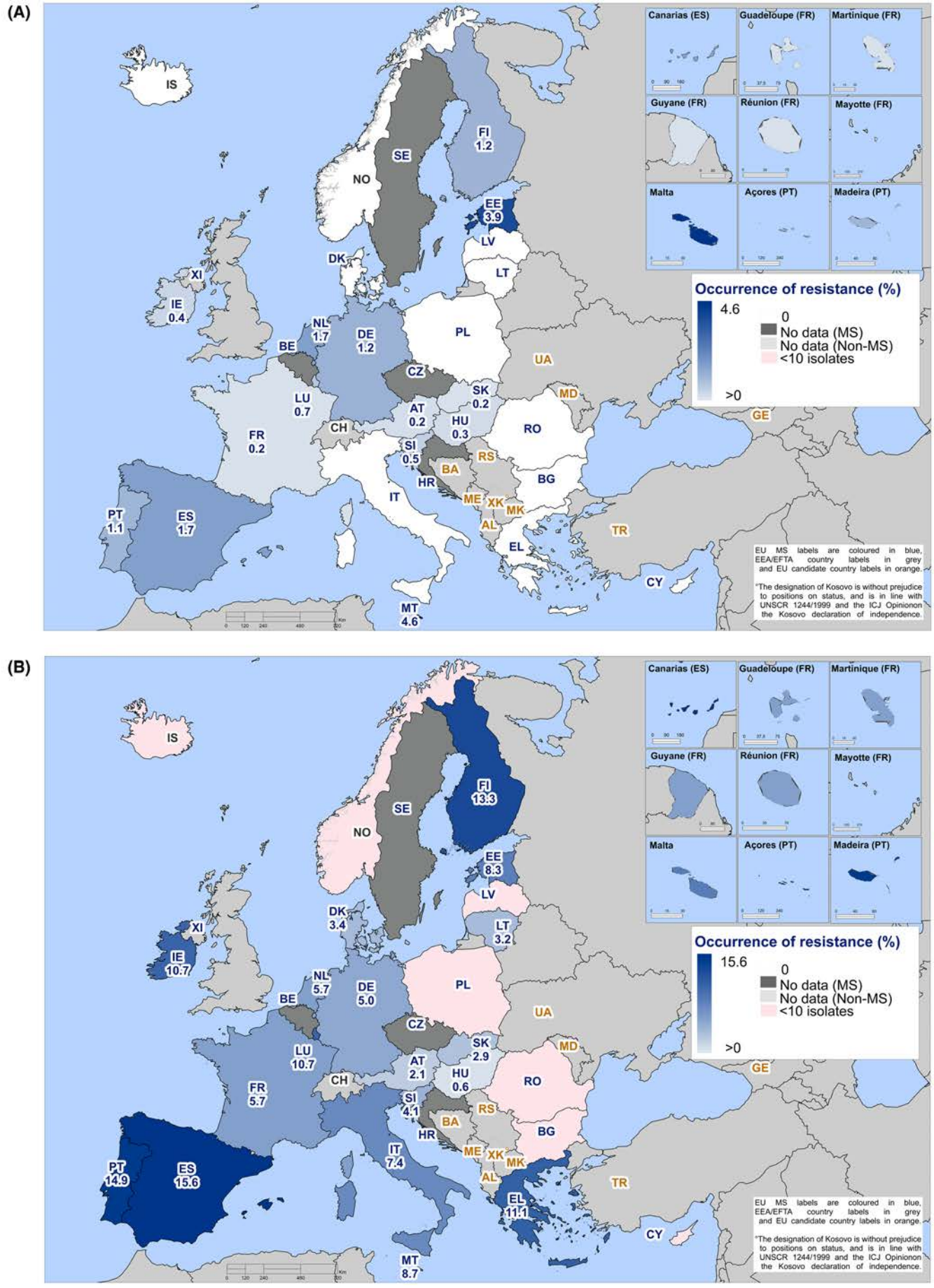


FIGURE 24 Spatial distribution of combined resistance to ciprofloxacin and erythromycin in (A) *Campylobacter jejuni* and (B) *C. coli* isolates from humans, 2024.
The designation of Kosovo is without prejudice to positions on status, and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

3.3.4 | Complete susceptibility and multidrug resistance

Analyses of CS and 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 in resistance

Temporal trends were analysed for countries reporting data for at least 3 years over the period 2014–2024 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 13); Figures 25 and 26). Statistically significant ($p < 0.05$) increasing trends of **ciprofloxacin** resistance were observed in *C. jejuni* isolates from 12 EU MSs and in *C. coli* isolates from Hungary, The Netherlands, Slovakia and Slovenia. In the case of the Netherlands, data from ciprofloxacin resistance in *C. coli* for 2022 and 2023 has been excluded in the trends analysis, as the country had some methodological problems during those years after shifting from phenotypic susceptibility testing (with 71.7% resistance reported in 2021) to genotypic (no resistant isolated detected in 2022 or 2023). Statistically significant decreasing trends in ciprofloxacin resistance in *C. jejuni* were found for four MSs and for Norway, while decreasing trends were found in *C. coli* for Spain. Only two countries (Estonia and Luxembourg) showed a significant increase in **erythromycin** resistance in *C. jejuni* isolates, and none in *C. coli*. Statistically significant decreases in erythromycin in *C. jejuni* and *C. coli* were respectively noted in 10 (including non-MS Norway) and 8 countries. Finally, **tetracycline** resistance in *C. jejuni* significantly increased for six MSs and decreased for five countries. For *C. coli*, statistically increasing trends in time were seen for one country (France) and decreasing trends in seven countries.

TABLE 13 Number of countries with significantly* increasing or decreasing trends in resistance to selected antimicrobials for *Campylobacter jejuni* and *C. coli* in humans, 2014–2024.

***Campylobacter* species**	**Ciprofloxacin**		**Erythromycin**		**Tetracycline**	
	↑	↓	↑	↓	↑	↓
C. jejuni (20 MSs + 2 non-MS)	12 (AT, BG, CY, DE, DK, IS, FR, LT, MT, PL, SI, SK)	5 (EE, ES, FI, NO, PT)	2 (EE, LU)	10 (DE, DK, FI, FR, IT, LT, NL, NO, PT, SK)	6 (AT, BG, DE LT, NL, SK)	5 (ES, FI, FR, LU, PT)
C. coli (20 MSs)	4 (HU, NL, SI, SK)	1 (ES)	0	8 (AT, EE, ES, FI, FR, IT, PT, SK)	1 (FR)	7 (AT, DE, FI, IT, ES, PT, SI)

Note: ↓, statistically significant decreasing trends; ↑, statistically significant increasing trends;
*$p < 0.05$, logistic regression. Abbreviations for reporting countries can be found here.

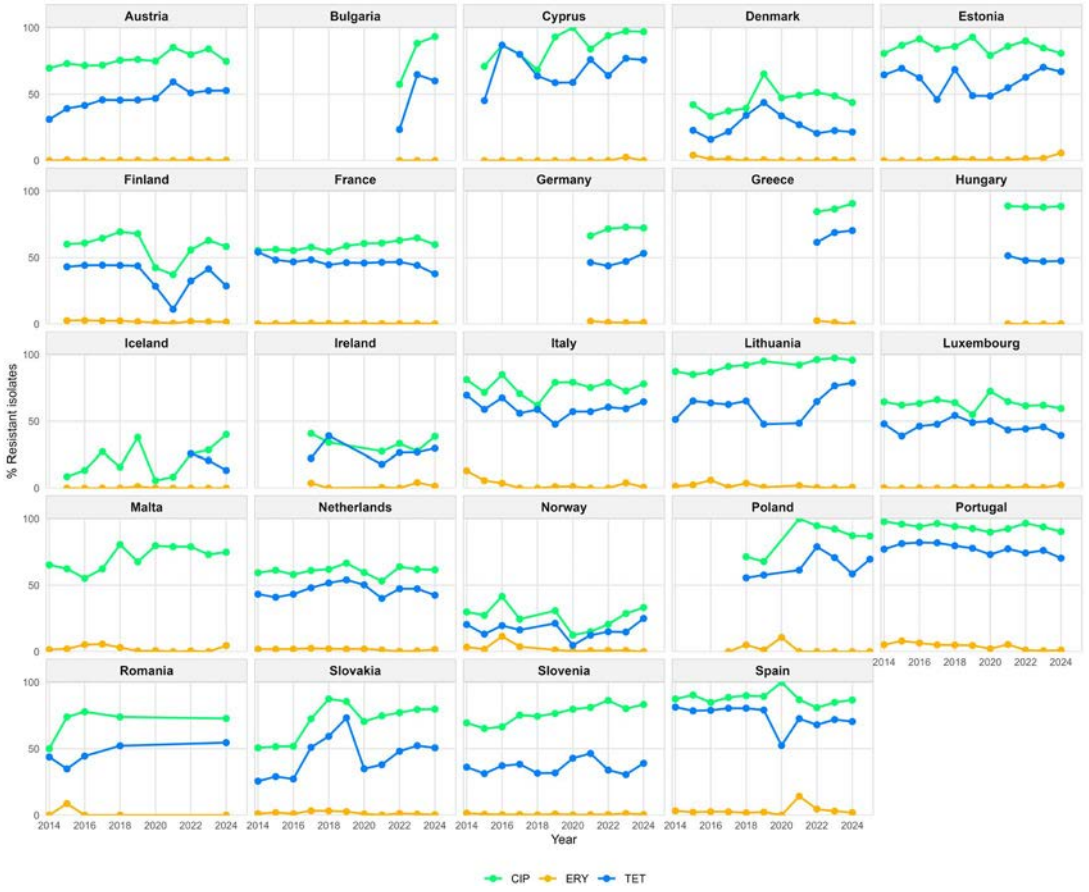


FIGURE 25 Trends in ciprofloxacin, erythromycin and tetracycline resistance in *Campylobacter jejuni* from humans in 24 reporting countries, 2014–2024.

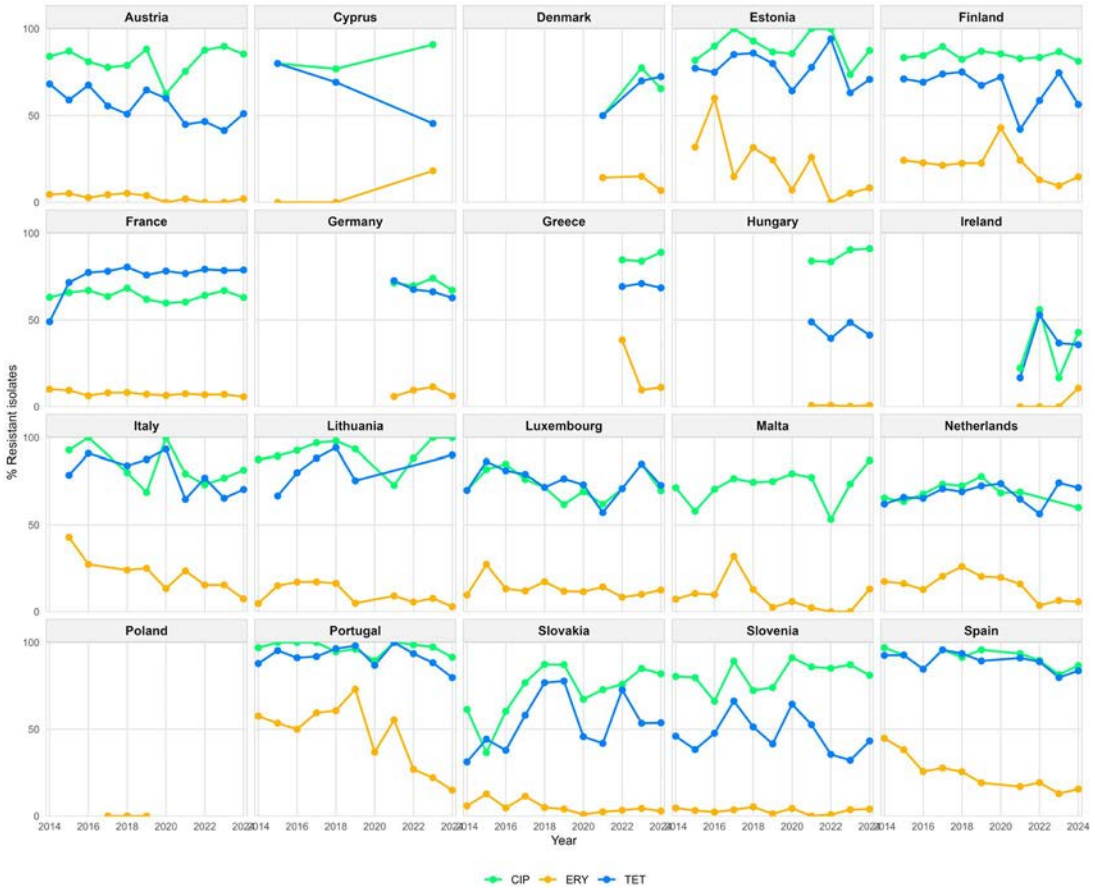


FIGURE 26 Trends in ciprofloxacin, erythromycin and tetracycline resistance in *Campylobacter coli* from humans in 20 reporting countries, 2014–2024.

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* = 2987, seven MSs and one non-MS) 0.2% showed MIC values > 128 mg/L while for *C. coli* the percentage was higher, 4.4% (*N* = 472, six MSs and one non-MS). No *erm*(B) genes were detected among the 118 *Campylobacter* sequences reported by three countries as their AMR data for 2024.

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

3.4.1 | Data reported

In the present report, the 2023 resistance data on *Campylobacter* from fattening pigs and calves are considered for comparison with 2024 data on *Campylobacter* isolates from broilers and fattening turkeys. Information on the reported mandatory data on *C. jejuni* and *C. coli* isolates from the different animal populations in 2023 and 2024 is presented in Table 14.

Resistance data concerning food-producing animals, reported in 2023 and 2024, 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 2023 and 2024, is available as supporting documentation on the EFSA Knowledge Junction community on Zenodo (https://doi.org/10.5281/zenodo.17950222).

According to the EU rules for the AMR monitoring in *Campylobacter*, which have been 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 resistance

Data on the occurrence of resistance in *C. jejuni* and *C. coli* in caecal samples from fattening pigs (2023), calves (2023), broilers (2024) and fattening turkeys (2024) are presented in Table 14 and Figure 27. The detailed country-level information on the occurrence of resistance is presented in Annex B.2 (Tables 1–2, 7–8, 13–16).

Resistance to **tetracycline** in *C. jejuni* isolates ranged from 38.3 to 65.6% among MSs and from 19.6% to 35.1% in non-MSs, while in *C. coli* it ranged from 68.4 to 88.6% among MSs and from 23.3% to 50% in non-MSs. The highest levels were found in *C. coli* from calves (88.6% in 11 MSs; 50% in one non-MS) and fattening turkeys (83.1%; 11 MSs). Within each species, *C. coli* showed higher resistance than *C. jejuni* (Table 14).

Resistance to **ciprofloxacin** ranged from 34.0% to 76.4% in *C. jejuni* isolates among reporting MSs, with non-MSs reporting levels between 39.2% (in broilers) and 54.5% (in calves). In *C. coli* MSs reported from 54.3% to 85.1%, while non-MSs reported between 44.9% and 58.1%. Highest levels were observed in *C. coli* from fattening turkeys (85.1% in 11 MSs) and calves (80.4% in 11 MSs). For *C. jejuni*, the highest levels were observed among isolates from broilers (69.2%; data from 26 MSs and the United Kingdom [Northern Ireland]) and fattening turkeys (76.4% in 10 MSs). Fattening pigs showed the lowest levels for both *Campylobacter* species (34.0% for *C. jejuni*; 54.3% and 44.9% in MSs and non-MSs, respectively, for *C. coli*) (Table 14).

Resistance to **gentamicin** ranged from 0.2% to 4.3% in *C. jejuni* isolates and from 1.5% to 10.5% in *C. coli*. Non-MSs reported absent or very low levels of gentamicin resistance in both *Campylobacter* species. Highest levels were observed in *C. coli* isolates from calves (10.5% in 11 MSs), while resistance remained low or absent in other groups (Table 14).

Resistance to **erythromycin** in *C. jejuni* was low (0.4%–2.1% in MSs; absent in non-MSs), but higher in *C. coli* (range: 8.7%–31.6% in MSs and 0%–4.7% in non-MSs). Highest levels occurred in *C. coli* isolates from calves (31.6% in 11 MSs), followed by *C. coli* from fattening turkeys and fattening pigs (13.0%). Notably high occurrences were reported in Portugal in *C. coli* isolates from fattening turkeys (42.2%) and fattening pigs (52.7%), in Cyprus in *C. coli* from fattening pigs (62.8%) and in *C. coli* from calves in Belgium (75.9%). Among non-MSs, occurrence was highest in C. coli from broilers in Switzerland (4.7%) (Table 14).

Resistance to **chloramphenicol** across all populations was absent to very low (0.0%–0.4%), except for *C. coli* from calves (1.7% in 11 MSs) (Table 14).

Resistance to **ertapenem** in *C. jejuni* ranged from 0.0 to 22.1%, with the highest values in fattening turkeys (22.1% in 10 MSs) and broilers (18.4% in 27 MSs and the United Kingdom (Northern Ireland); 0.8% in non-MSs). Resistance to ertapenem in *C. coli* ranged from 3.4% to 66.5%, with the highest resistance in isolates from fattening turkeys (66.5% in 11 MSs), broilers (53.9% in 24 MSs and the United Kingdom (Northern Ireland); 32.6% in one non-MS) and calves (35.5% in 11 MSs; 25% in one non-MSs) (Table 14).

TABLE 14 Occurrence of resistance (%) to selected antimicrobials in *C. coli* and *C. jejuni* in caecal samples from targeted food-producing animals using harmonised ECOFFs, 2023–2024, 27 MSs and the United Kingdom (Northern Ireland).

Campylobacter species	Categories	Year	No. of isolates	Reporting countries (*N*)	CHL	CIP	ETP	ERY	GEN	TET	CIP/ERY
C. jejuni	Broilers	2024	3323	AT, BE, BG, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HR, HU, IE, IT, LT, LU, LV, MT, NL, PL, PT, RO, SE, SI, SK, XI (28)	0.1	69.2	18.4	1.6	0.2	54.1	1.5
	Fattening turkeys	2024	946	AT, DE, ES, FR, HR, IE, IT, PL, PT, RO (10)	0.0	76.4	22.1	0.4	0.2	60.2	0.4
	Calves	2023	1470	AT, BE, DE, DK, ES, FR, HR, IT, NL, PT, RO (11)	0.0	57.6	2.4	1.1	1.1	65.6	0.8
	Fattening pigs	2023	47	AT, BG, CY, CZ, DE, EE, FI, HU, IE, IT, LV, LU, NL (13)	0.0	34.0	0.0	2.1	4.3	38.3	2.1
C. coli	Broilers	2024	1743	AT, BE, BG, CY, CZ, DE, DK, ES, FI, FR, GR, HR, IE, IT, LT, LU, MT, NL, PL, PT, RO, SE, SI, SK, XI (25)	0.2	77.7	53.9	8.7	1.5	71.0	7.8
	Fattening turkeys	2024	1461	AT, DE, ES, FR, HR, HU, IE, IT, PL, PT, RO (11)	0.1	85.1	66.5	13.0	2.8	83.1	12.7
	Calves	2023	465	AT, BE, DE, DK, ES, FR, HR, IT, NL, PT, RO (11)	1.7	80.4	35.5	31.6	10.5	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)	0.4	54.3	3.4	13.0	2.3	68.4	10.6

Note: The shades of blue indicate different levels of antimicrobial resistance. From rare to extremely high. A blank cell represents no resistance. The correspondence between colour and resistance level categories can be found in the 'Definitions' section.

Abbreviations for reporting countries can be found here.

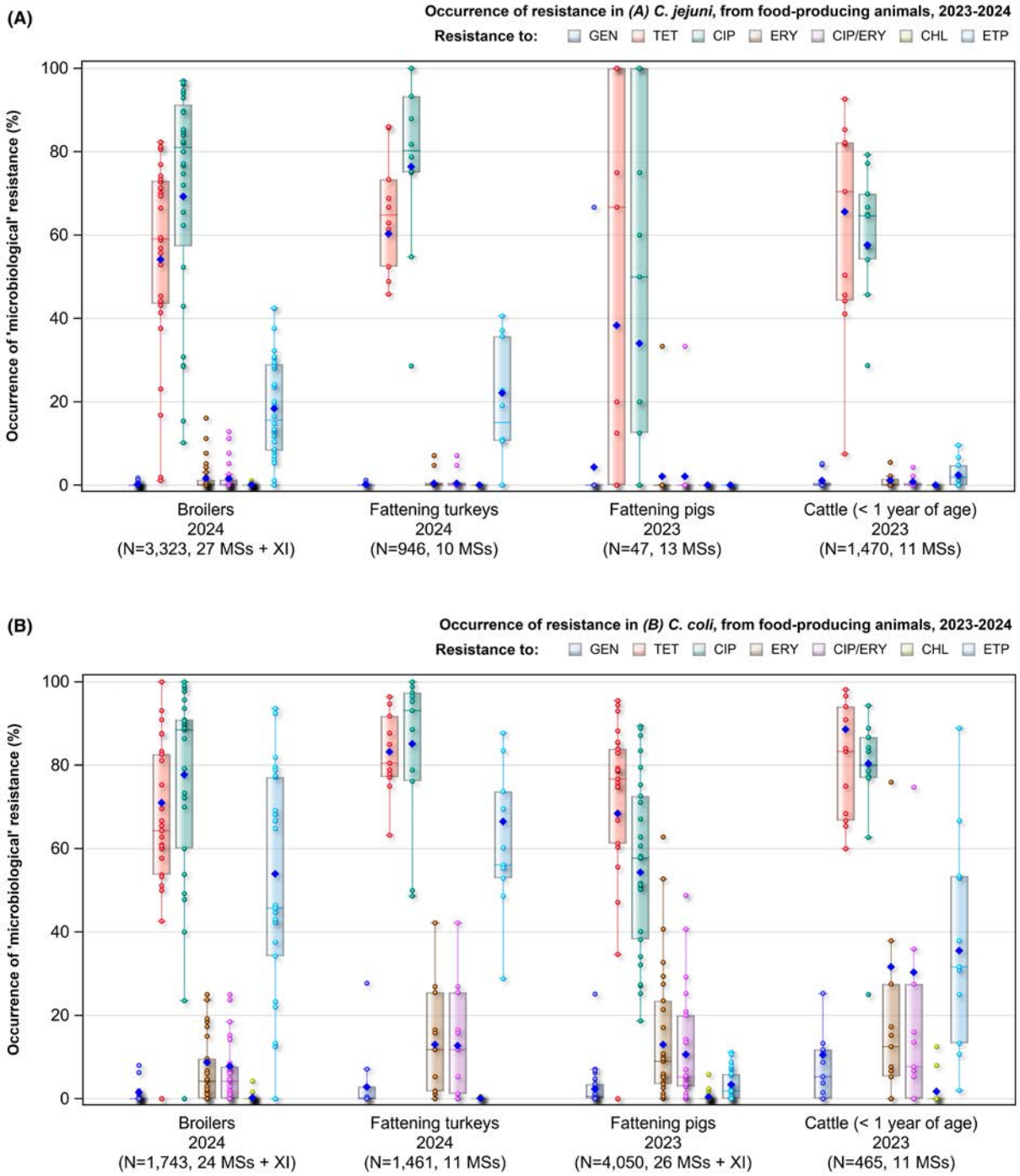


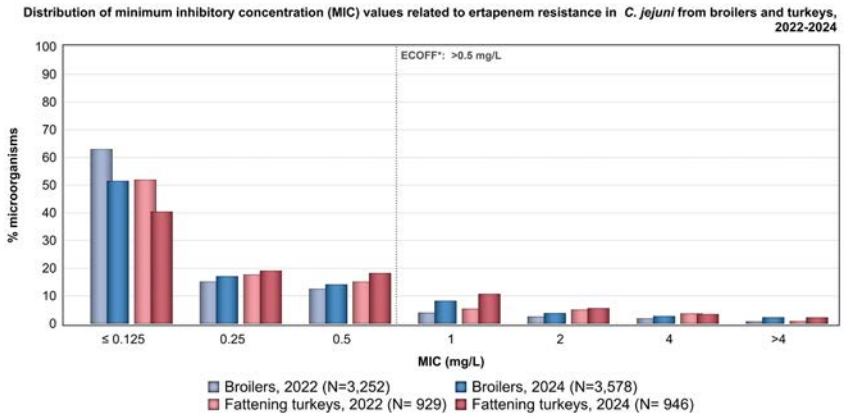
FIGURE 27 Occurrence of resistance to antimicrobials in (A) *C. jejuni* and (B) *C. coli* from targeted food-producing animals, in EU MSs and the United Kingdom (Northern Ireland), 2023–2024.
Abbreviations for reporting countries can be found here.
Abbreviations: CHL, chloramphenicol; CIP/ERY, combined resistance to ciprofloxacin and erythromycin; CIP, ciprofloxacin; ERY, erythromycin; ETP, ertapenem; GEN, gentamicin; TET, tetracycline.

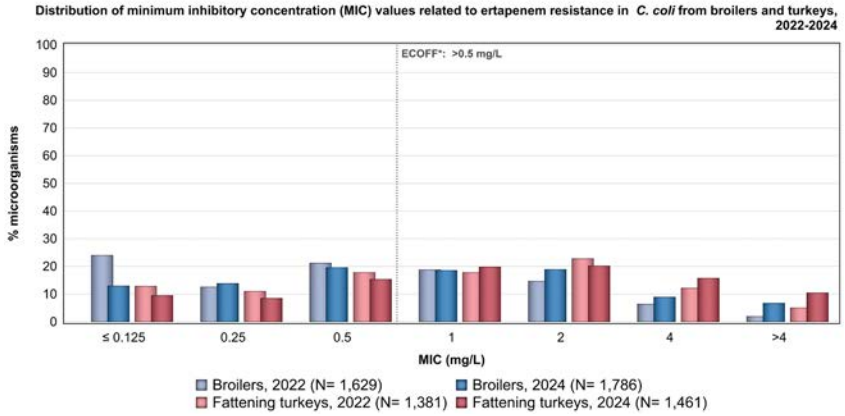
Further considerations regarding the levels of ertapenem resistance in *Campylobacter jejuni* and *C. coli* from broilers and fattening turkeys

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, 2025), for the monitoring of ertapenem resistance following the requirements of Commission Implementing Decision (EU) 2020/1729.

In 2024, minimum inhibitory concentration (MIC) values were reported for the second mandatory year for *C. jejuni* and *C. coli* from broilers and fattening turkeys. Considering the data reported by all reporting countries, the occurrence of ertapenem resistance increased from 2022 to 2024 among *C. jejuni* from broilers (from 9.2% to 17.1%) and fattening turkeys (from 15.1% to 22.1%), and in *C. coli* from broilers (from 42.1% to 53.4%) and fattening turkeys (from 58.1% to 66.5%).

MIC distribution (%) in ertapenem-resistant and susceptible *C. coli* and *C. jejuni* isolates from broilers and fattening turkeys in 2022 and 2024, reported by MSs and non-MSs, is presented below.





*ECOFF, Epidemiological cut-off.

The observed increases in the occurrence of ertapenem resistance are a result of shifts in the ertapenem MIC distributions towards higher values in 2024, as shown in the figure above. Both *C. jejuni* and *C. coli* isolates from broilers and fattening turkeys, presented an increased occurrence of higher MIC values in 2024 compared to 2022. Notably, in 2024, *C. coli* from both animal species presented higher occurrence of MIC values above the ECOFF, and particularly of values equal to or greater than 4 mg/L, which translates into a higher overall occurrence of ertapenem-resistant *C. coli* isolates. Among *C. jejuni* isolates, although there was a shift towards higher MIC values in 2024 compared to 2022, the increase occurred most notably for MIC values of 0.25 and 0.5 mg/L, which are observed in ertapenem-susceptible isolates, and for the MIC value 1 mg/L, right above the ECOFF.

3.4.3 | Combined resistance to ciprofloxacin and erythromycin

Under the AMEG framework, fluoroquinolones are classified under Category B – Restrict. They are among the highest priority critically important antimicrobials in human medicine, and their use in animals should be restricted to exceptional cases and be based on antimicrobial susceptibility testing, wherever possible. Macrolides are considered critically important antimicrobials in human medicine. According to the AMEG classification, these fall under Category C – Caution, and their use in animals should only be considered when no clinically effective alternatives from Category D – Prudence are available.

Since resistance to fluoroquinolones (including ciprofloxacin) is common in *C. jejuni* and *C. coli*, macrolides (including erythromycin) are often the treatment choice for *Campylobacter* infections in humans. Hence, 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).

Combined resistance to ciprofloxacin and erythromycin was consistently higher in *C. coli* than in *C. jejuni* across all tested animal populations (Table 14, Figure 27; detailed country-level data in Annex B.2, tables 1, 2, 7, 8, 13–16). The spatial distribution of co-resistance occurrence is shown in Figures 28 and 29 for animal populations with data from more than four reporting countries.

Low average levels of co-resistance were observed in *C. jejuni* from calves (0.8% in 11 MSs; 0% in 1 non-MS) and fattening pigs (2.1% in 13 MSs) in 2023, and from broilers (1.5% in 27 MSs and the United Kingdom [Northern Ireland]) and fattening turkeys (0.4%; 10 MSs) in 2024. In contrast, *C. coli* showed higher co-resistance: calves (30.3% in 11 MSs; 0% in 1 non-MS) in 2023, turkeys (12.7% in 11 MSs; 0% in 1 non-MS) in 2024, fattening pigs (10.6% in 27 MSs; 0.5% in 3 non-MSs) in 2023 and broilers (7.8% in 24 MSs and the United Kingdom (Northern Ireland); 4.7% in 1 non-MS) in 2024.

Among the 13 MSs providing data on *C. jejuni* from pigs in 2023, none reported more than 10 isolates (precluding spatial mapping); co-resistance was detected in only one isolate, from Italy. In *C. coli* from pigs, co-resistance was reported by 24 MSs and 2 non-MSs (Norway and Switzerland) out of 30 countries, ranging from 0.4% (Netherlands, Norway) to 48.8% (Cyprus, Portugal).

For cattle in 2023, co-resistance in *C. jejuni* was found in Belgium, Germany, Italy and the Netherlands (range: 0.5%–4.3%), while co-resistance in *C. coli* was seen in eight MSs (Belgium, Croatia, France, Germany, Italy, Netherlands, Portugal and Spain), ranging from 5.3% (Spain) to 74.7% (Belgium).

In broilers in 2024, *C. jejuni* co-resistance was found in 9 MSs (Belgium, Bulgaria, Cyprus, Czechia, Germany, Hungary, Malta, Portugal, Romania) and the United Kingdom (Northern Ireland), ranging from 0.5% (Czechia) to 12.9% (Malta); *C. coli* co-resistance was reported by 17 MSs, the United Kingdom (Northern Ireland) and Switzerland, ranging from 1% (United Kingdom (Northern Ireland) to 25% (Portugal).

Co-resistance in *C. jejuni* from fattening turkeys in 2024 was reported in four MSs (Ireland, Italy, Poland and Portugal; 0.6%–7.1%), and in *C. coli* in nine out of 11 reporting MSs (Austria, Germany, Hungary, Ireland, Italy, Poland, Portugal, Romania, Spain), ranging from 1.1% (Hungary) to 42.2% (Portugal).

Compared to 2022, in 2024, the occurrence of co-resistance mostly decreased, except in *C. jejuni* from broilers, where the average co-resistance rose from 1.1% to 1.5% (27 MSs and United Kingdom [Northern Ireland]). In *C. jejuni* from fattening turkeys, it decreased from 1.6% to 0.4% (10 MSs). In *C. coli*, co-resistance in broilers also declined slightly in 2024 (from 8.2% to 7.8%; 24 MSs and United Kingdom [Northern Ireland]), while in fattening turkeys it decreased from 17.4% to 12.7% (11 MSs).

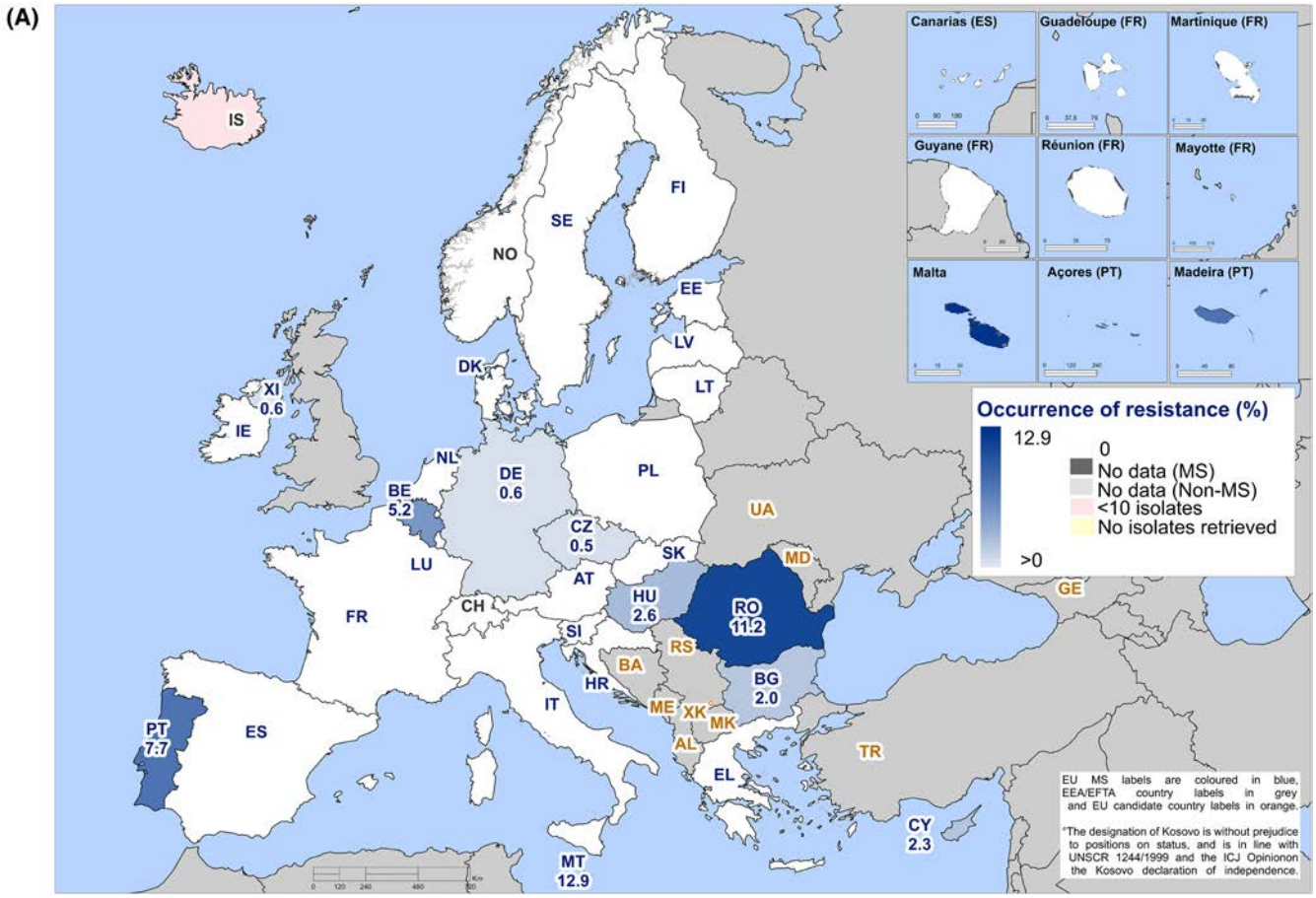


FIGURE 28 (Continued)

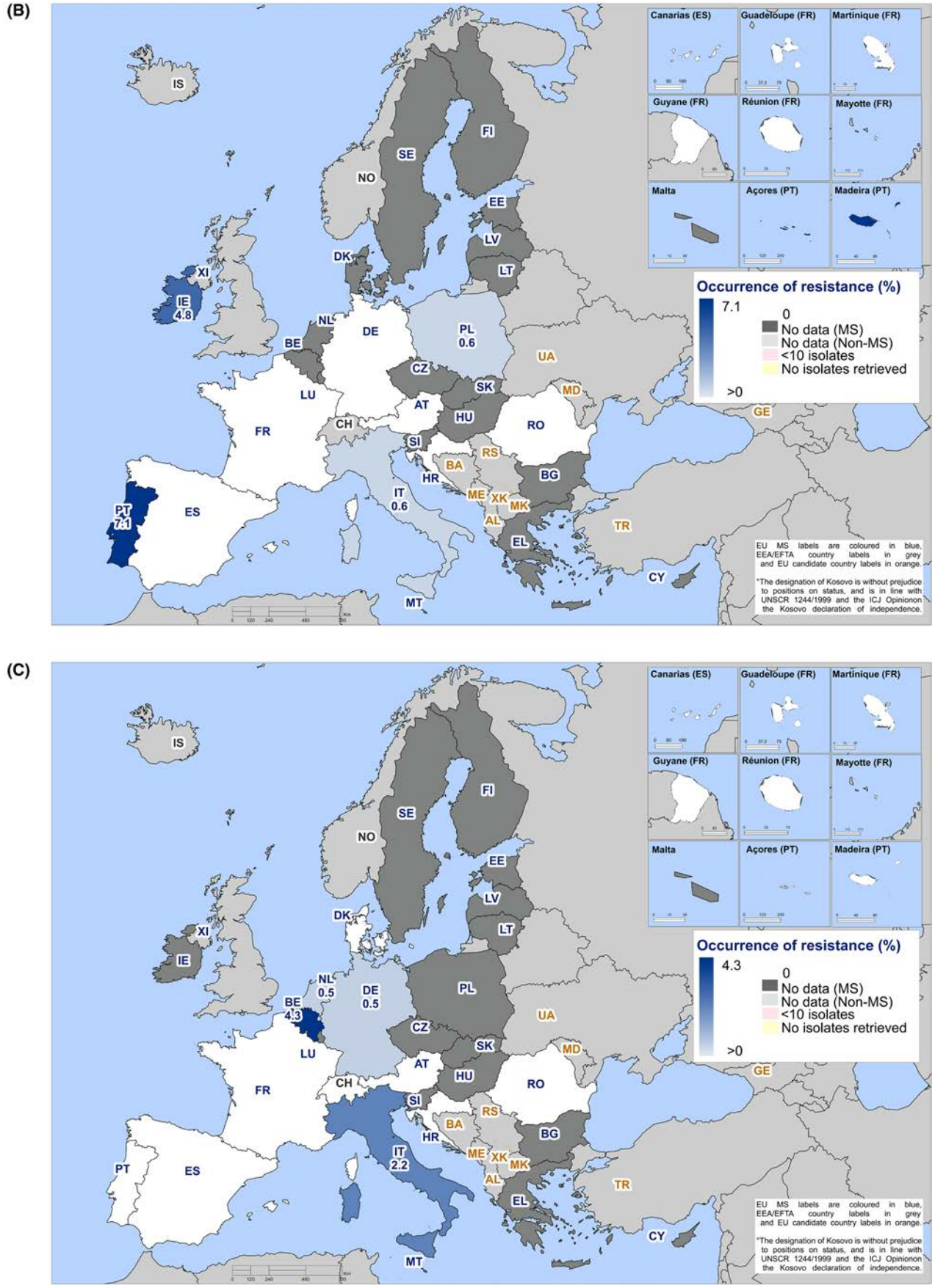


FIGURE 28 Spatial distribution of combined resistance to ciprofloxacin and erythromycin in *C. jejuni* isolates from (A) broilers (27 MSs, the United Kingdom [Northern Ireland] and 3 non-MSs, 2024), (B) fattening turkeys (10 MSs, 2024), (C) calves (11 MSs and 1 non-MS, 2023).
Notes: Maps are presented 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.

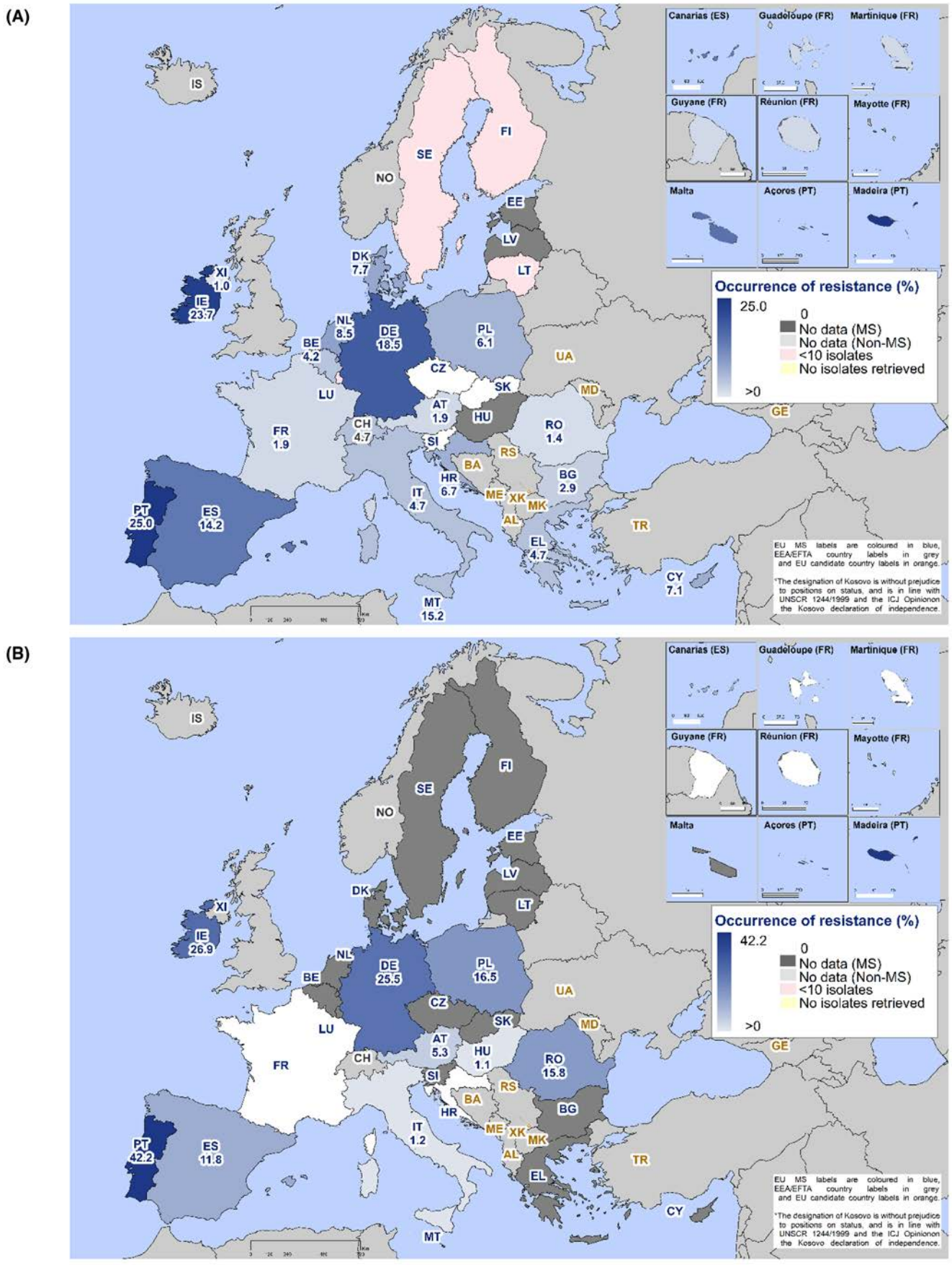


FIGURE 29 (Continued)

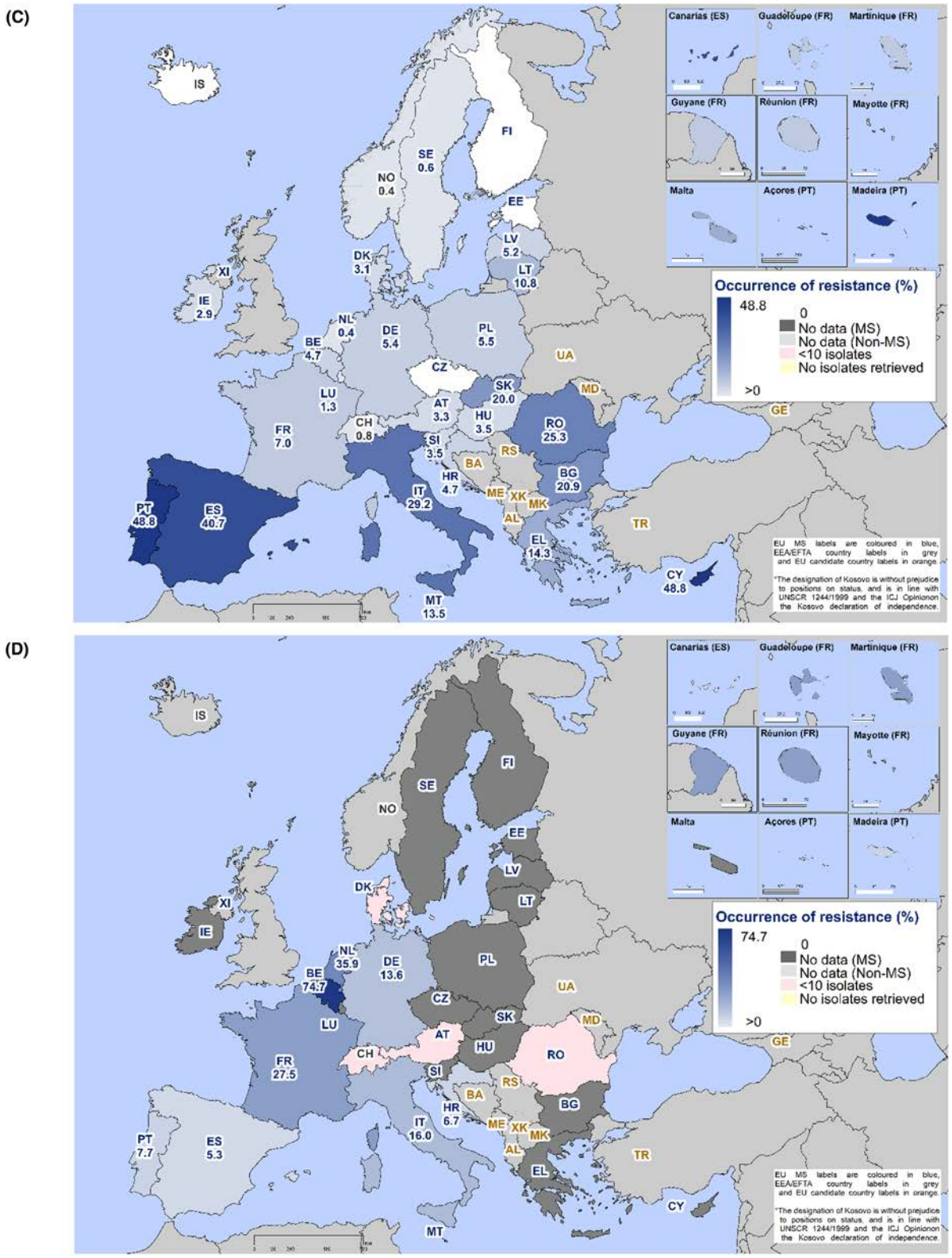


FIGURE 29 Spatial distribution of combined resistance to ciprofloxacin and erythromycin in *C. coli* isolates from (A) broilers (24 MSs, the United Kingdom [Northern Ireland] and 1 non-MS, 2024), (B) fattening turkeys (11 MSs, 2024), (C) fattening pigs (27 MSs and 3 non-MSs, 2023), (D) calves (11 MSs and 1 non-MS, 2023).
Notes: 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** is estimated as the product of the occurrence of *C. jejuni* or *C. coli* in caecal samples from the given animal species (Annex B.2, tables 3, 4, 9 and 10) and the percentage occurrence of resistance in the corresponding

isolates (Annex B.2, tables 1, 2, 7 and 8). Monitoring the prevalence of resistant *Campylobacter* enables addressing 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. Further information on the prevalence of resistance in *Campylobacter* can be found in a dedicated EFSA story map (available online here). The country-level estimates of the prevalence of resistance to selected antimicrobials in *C. jejuni* and *C. coli* from caecal samples of broilers and fattening turkeys in 2024 are presented in Annex B.2 (Tables 5, 6, 11 and 12) and Annex B.3 (Figures 4 to 7), and can be visualised on the EFSA dashboard on AMR in *Campylobacter* (available online here). The results of the prevalence of resistance to ciprofloxacin, tetracycline, erythromycin and gentamicin in *C. jejuni* and *C. coli* isolates from broilers and fattening turkeys are addressed below. Details on the prevalence of resistance to chloramphenicol and ertapenem can be found in Annexes B.2 and B.3.

In 2024, for broilers, 27 MSs, the United Kingdom (Northern Ireland), and 3 non-MSs reported the occurrence of *C. jejuni*, with values among MSs ranging from 4.8% (Sweden) to 62.7% (Lithuania) and two non-MSs reported the lowest levels (0.7% in Iceland and 3.4% in Norway). The occurrence of *C. coli* in broilers was reported by 25 MSs, the United Kingdom (Northern Ireland) and 1 non-MS, ranging from 0.1% (Sweden and Finland) to 73.5% (Malta) among MSs and with 6.6% reported in Switzerland. In the same reporting year, for fattening turkeys, the occurrence of *C. jejuni* was reported for 10 MSs with values ranging from 0% (in six MSs) to 7.1% (Portugal). The occurrence of *C. coli* was reported for 11 MSs, with values ranging from 0% (Croatia and France) to 42.2% (Portugal).

Between-country variability in the prevalence of resistance in *C. jejuni* from broilers ranged from absent to high for ciprofloxacin resistance, varying between 0.0% and 0.7% in Iceland, Norway, Finland and Sweden, and 49.9%, 51.7% and 60.2% in Poland, Romania and Lithuania, respectively. The same was observed for the prevalence of tetracycline resistance, which ranged from 0.0% in Iceland and 0.1% in Sweden, Finland and Norway to 45.6% in Lithuania and 45.8% in the United Kingdom (Northern Ireland). The prevalence of erythromycin resistance varied from absent to low (from 0% in 18 MSs and 3 non-MSs to 6% in Romania). Resistance to gentamicin was detected only in six MSs, with prevalence ranging from 0.1% (Denmark) to 0.7% (Slovenia). Notably, in three MSs (Belgium, Czechia and Romania) both gentamicin and erythromycin resistance were detected among *C. jejuni* from broilers. In a single reporting country (Iceland), *C. jejuni* from broilers did not show resistance to any of the tested antimicrobials.

Among *C. jejuni* from fattening turkeys, the prevalence of resistance to ciprofloxacin and tetracycline presented somewhat narrower variability, although ranging from low to high (7.8% in Ireland to 38.6% in Spain for ciprofloxacin; 10% in Portugal to 32.7% in Romania for tetracycline). The prevalence of resistance to erythromycin varied from absent (in six MSs) to low (1.3% in Ireland), and gentamicin resistance was only observed in one MS (0.3% in Italy).

The prevalence of resistance in *C. coli* from broilers showed high between-country variability for ciprofloxacin (from 0% in Finland and 0.1% in Sweden to 63.5% in Malta) and for tetracycline (from 0% in Finland and Sweden to 51.2% in Malta). Prevalence of erythromycin resistance among the same isolates varied from absent (in 7 MSs) to 7.2% in Portugal, and 14.1% in Malta, while prevalence of gentamicin resistance varied from absent (in 18 MSs, the United Kingdom (Northern Ireland) and Switzerland) to 5.9% in Malta. Six MSs (Cyprus, France, Italy, Malta, Portugal and Spain) reported both erythromycin and gentamicin resistance among *C. coli* from broilers, with Malta reporting the highest prevalence levels.

In *C. coli* from fattening turkeys the between-country variability for the prevalence of resistance was also high, especially for ciprofloxacin (from 9.4% in Austria to 65.1% in Portugal) and tetracycline (9.4% in Austria to 63.5% in Portugal). Resistance to erythromycin was reported in all but one MS (0% in Croatia), and the prevalence of resistance was highest in Portugal (27.8%), while gentamicin resistance was only detected in four MSs (Italy, Poland, Portugal and Spain), with prevalence ranging from 0.2% (Poland) to 18.3% (Portugal).

3.4.5 | Complete susceptibility and multidrug resistance

Analyses of **CS** and **MDR** focus on antimicrobials important for treatment of animals and humans, belonging to groups B (Restrict), C (Caution) and D (Prudence) of the AMEG classification, and to groups HIA (highly important), CIA (critically important) and HPCIA (highest priority critically important) of the WHO classification. The target substances that EFSA and ECDC agreed to include in the CS and MDR analyses are ciprofloxacin (fluoroquinolone –classes B and HPCIA), erythromycin (macrolide – classes C and CIA), gentamicin (aminoglycoside – classes C and CIA) and tetracycline (classes D and HIA). 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 1–2, 7–8, 13–16).

3.4.6 | Temporal trends in resistance

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 criteria for trend analysis require data from at least three distinct years within the 2014–2024 period, with no more than a 1 year gap between each data point during the period 2020–2024. Furthermore, each data point must include a minimum of 10 isolates. 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 a few data points leading to unexpected findings (e.g. the 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 (2014–2024), 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.

3.4.6.1 | *Temporal trends in resistance in* C. jejuni *isolates from broilers*

The results from the analysis of temporal trends in resistance in *C. jejuni* from broilers were obtained using data from 23 MSs and 2 non-MSs (Figure 30; Table 16; see also Annex B.2, table 17). A significant decreasing trend in resistance was observed for ciprofloxacin in three MSs (Finland, France and Latvia), for erythromycin in six MSs (Bulgaria, Germany, Italy, Portugal, Romania and Slovakia) and one non-MS (Switzerland), and for tetracycline in four MSs (Finland, France, Italy and Spain). A significant increase in resistance was detected for ciprofloxacin in seven MSs (Croatia, Cyprus, Denmark, Germany, Romania, Slovenia and Sweden), for tetracycline in nine MSs (Austria, Croatia, Denmark, Germany, Ireland, Latvia, Poland, Slovakia and Sweden) and for erythromycin in a single MS (Belgium).

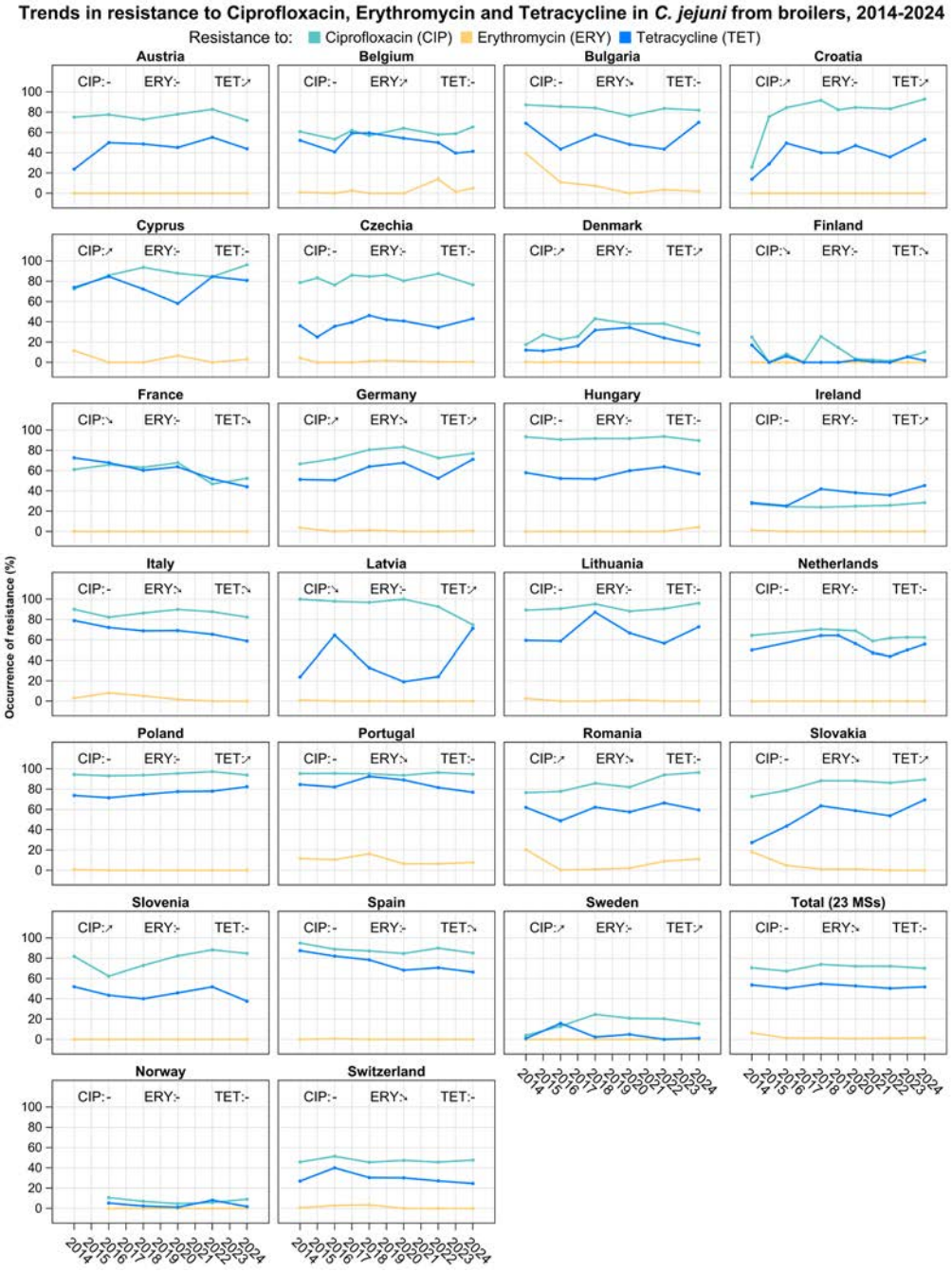


FIGURE 30 Trends in ciprofloxacin (CIP), erythromycin (ERY) and tetracycline (TET) resistance in *C. jejuni* from broilers, 2014–2024.
Notes: Only countries that reported data fulfilling all inclusion criteria explained in the text are shown. Overall temporal trend (shown in box 'Total (23 MSs)') is presented only for Member States and for even years when the monitoring of AMR in the EU in broilers is mandatory according to Decision (EU) 2020/1729.

3.4.6.2 | *Temporal trends in resistance in* C. coli *isolates from broilers*

The results from the analysis of temporal trends in resistance in *C. coli* from broilers were obtained using data from five MSs and one non-MS (Figure 31; Table 16; see also Annex B.2, table 17). A significant decreasing trend in resistance in *C. coli* from broilers was observed for tetracycline in two MSs (Czechia and the Netherlands), while no decrease in ciprofloxacin resistance was detected among any of the nine MSs individually. Significantly increasing trends in resistance were observed for erythromycin and tetracycline in one MS (Ireland), and for ciprofloxacin in two MSs (Ireland, Netherlands).

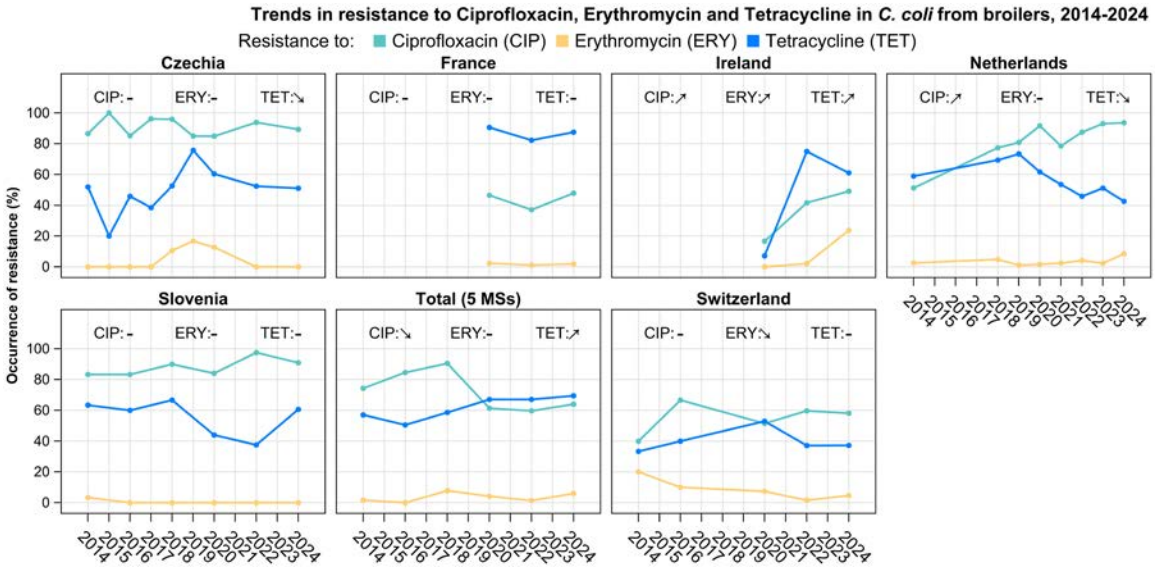


FIGURE 31 Trends in ciprofloxacin (CIP), erythromycin (ERY) and tetracycline (TET) resistance in *C. coli* from broilers, 2014–2024.
Notes: Only countries that reported data fulfilling all inclusion criteria explained in the text are shown. Overall temporal trend (shown in box 'Total (five MSs)') is presented only for Member States and for even years when the monitoring of AMR in the EU in broilers is mandatory according to Decision (EU) 2020/1729.

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

The results from the analysis of temporal trends in resistance in *C. jejuni* from fattening turkeys were obtained using data from seven MSs (Figure 32; Table 16; see also Annex B.2, table 17). No increasing trends in resistance to the selected antimicrobials (ciprofloxacin, erythromycin and tetracycline) were detected either in the period considered or among the seven reporting countries included in the analysis. A significant decreasing trend in resistance to tetracycline was observed in one MS (France), while two MSs (Italy and Spain) showed significant decreasing trends in resistance to all three antimicrobial substances.

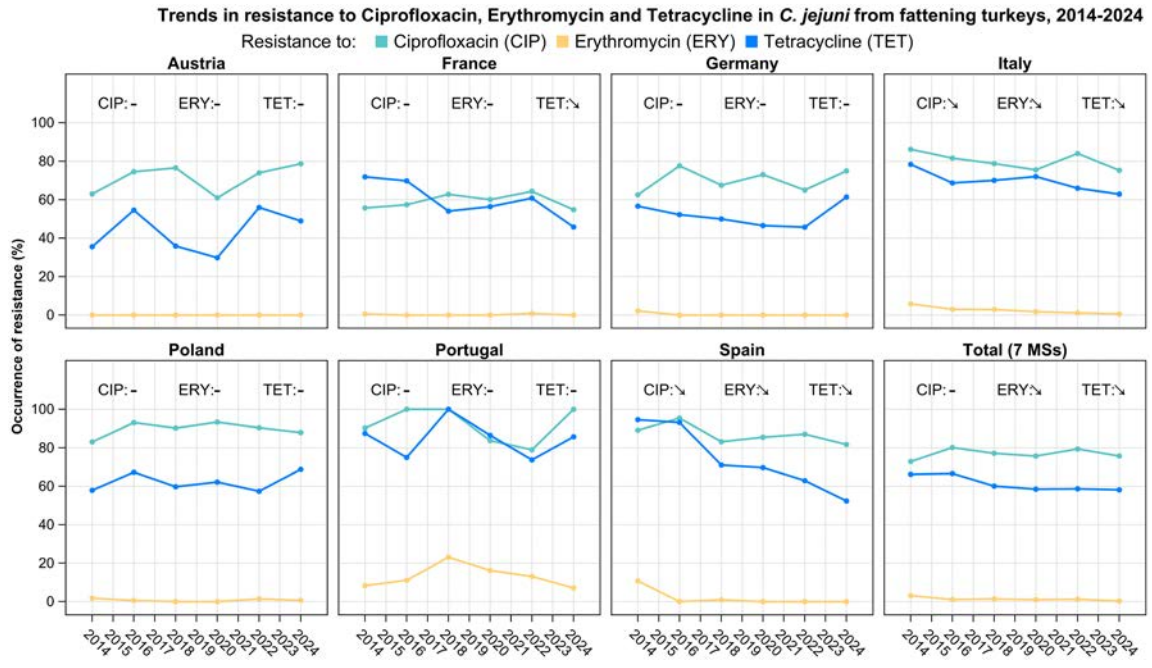


FIGURE 32 Trends in ciprofloxacin (CIP), erythromycin (ERY) and tetracycline (TET) resistance in *C. jejuni* from fattening turkeys, 2014–2024.
Notes: Only countries that reported data fulfilling all inclusion criteria explained in the text are shown. Overall temporal trend (shown in box 'Total (seven MSs)') is presented only for Member States and for even years when the monitoring of AMR in the EU in fattening turkeys is mandatory according to Decision (EU) 2020/1729.

3.4.6.4 | *Temporal trends in resistance in* C. coli *isolates from fattening turkeys*

Due to the scarcity of comparable historical data on *C. coli* from fattening turkeys, the temporal trends in resistance to selected antimicrobials was not analysed. 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.

3.4.6.5 | *Temporal trends in resistance* Campylobacter *isolates from fattening pigs*

Due to the scarcity of comparable historical data on *C. jejuni* from fattening pigs, the temporal trends in resistance to selected antimicrobials were not analysed. Comparable data may become available in the coming years due to the implementation of the monitoring requirements laid down in Commission Implementing Decision (EU) 2020/1729.

Temporal trends in resistance to selected antimicrobials in *C. coli* from fattening pigs obtained using data from 10 MSs and 2 non-MS, for the period 2014–2024, are shown in Table 16; Annex B.2, table 17; Annex B.3, figure 1. Significant increasing trends in resistance were observed for ciprofloxacin in two non-MSs (Norway and Switzerland) and for tetracycline in one MS (Estonia). Decreasing trends in resistance were shown by two MSs (Luxembourg and Spain) for ciprofloxacin, by three MSs for tetracycline (Belgium, Spain and Sweden), and by three MSs (Ireland, Luxembourg and Spain) and one non-MS (Switzerland) for erythromycin.

3.4.6.6 | *Temporal trends in resistance in* Campylobacter *isolates from calves*

Temporal trends in resistance to selected antimicrobials in *C. jejuni* and *C. coli* from calves obtained using data from 2 MSs (Belgium and the Netherlands), for the period 2014–2024, are shown in Annex B.2, table 17; Annex B.3, figure 2. In *C. jejuni*, a significant decreasing trend in ciprofloxacin resistance was observed in one MS (Belgium), while no significant trends were detected among *C. coli*.

3.4.7 | High-level resistance to erythromycin

The distribution of MIC values of **erythromycin resistance** in *Campylobacter* recovered from caecal samples of food-producing animals following legislative requirements in 2023 and 2024 is 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 33 (see also Annex B.2, table 18) 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. These data display isolates with 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.

Among *C. coli*, high MIC values were particularly frequent in resistant isolates from calves (16.3% with MIC between 128 and 512 mg/L; 76.2% with MIC > 512 mg/L), followed by *C. coli* from fattening turkeys (44.7% with MIC between 128 and 512 mg/L; 41.1% with MIC > 512 mg/L) and *C. coli* from fattening pigs (47.2% of isolates with MIC between 128 and 512 mg/L; 39.1% of isolates with MIC > 512 mg/L).

Notably, very high MIC levels were also observed in erythromycin-resistant *C. jejuni* from calves, although only a few isolates ($n = 16$) were resistant to erythromycin. Erythromycin-resistant *C. jejuni* from broilers showed the next highest occurrence of high MIC values (28.3% with MIC between 128 and 512 mg/L; 37.7% with MIC> 512 mg/L).

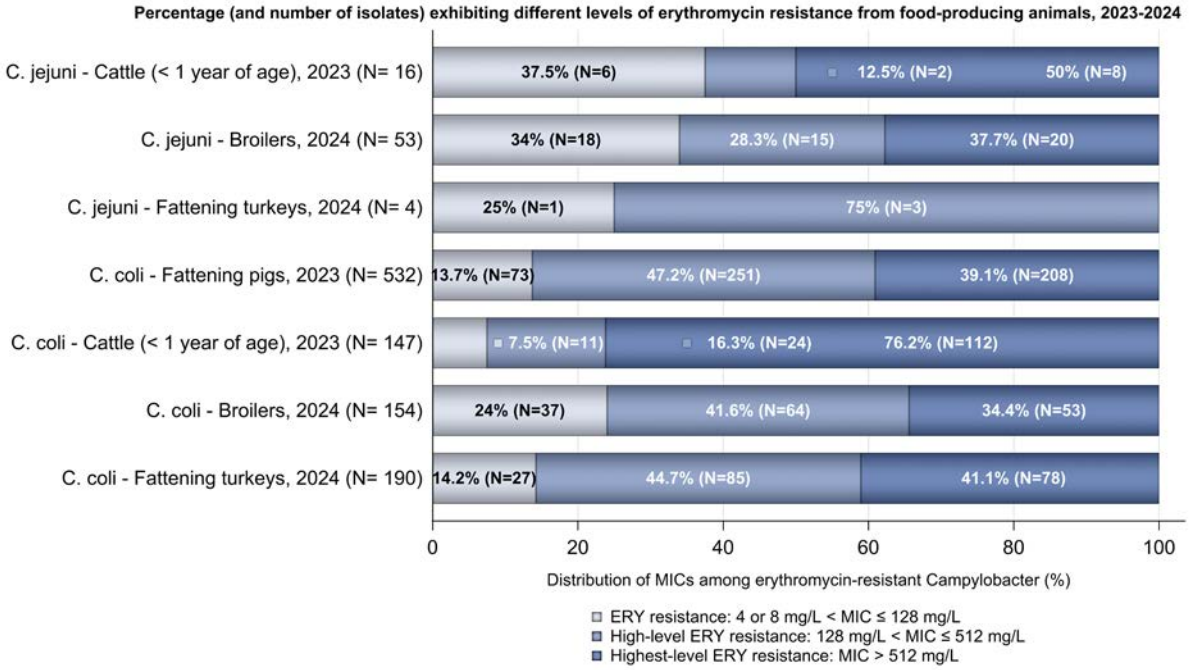


FIGURE 33 Percentage (and number) of *C. jejuni* and *C. coli* isolates exhibiting different levels of erythromycin resistance in targeted food-producing animals, in reporting MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.

3.4.8 | Summary of voluntary whole genome sequencing reporting

In 2023 and 2024, WGS information was reported on voluntary basis by some MSs 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 15.

In 2023, 56 erythromycin-resistant *C. coli* isolates (nine from calves and 47 from fattening pigs), and 2 erythromycin-resistant *C. jejuni* isolates (from calves) were whole genome sequenced to determine their erythromycin resistance genotype. Among *C. coli* from calves, the A2075G mutation in the 23S rRNA ribosomal gene was detected in seven out of nine isolates, while one isolate presented the rplV mutation 103A>V and the *erm*(B) gene was detected in another isolate (from the Netherlands), where presence of the 23S 2075A>G mutation and the gentamicin resistance gene *aph(2′)-Ic* were also reported. Among *C. coli* from fattening pigs, 45 of the 47 sequenced isolates presented a mutation in the 23S rRNA ribosomal gene (A2075G in all isolates except for one with a 2059A>G mutation), one showed the rplV mutation 103A>V and the *erm(N)* gene was detected in a single isolate (from Italy). The two *C. jejuni* isolates from calves sequenced in 2023 presented an A2075G mutation in the 23S rRNA ribosomal gene.

In 2024, the erythromycin resistance genotype was reported for 38 *C. coli* erythromycin-resistant isolates (23 from broilers and 15 from fattening turkeys), and 6 erythromycin-resistant *C. jejuni* (five from broilers and one from fattening turkeys). Among *C. coli* from broilers, the A2075G mutation in the 23S rRNA ribosomal gene was detected in all sequenced isolates. Among *C. coli* from fattening turkeys the same mutation was present in 13 out of 15 isolates, while the *erm*(B) gene was detected in the remaining two isolates (from Romania). The erythromycin-resistant *C. jejuni* from broilers and fattening turkeys showed the presence of the A2075G mutation in the 23S rRNA ribosomal gene.

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 in 2023 for 19 *C. coli* isolates from calves, 46 *C. coli* isolates from fattening pigs, 7 *C. jejuni* isolates from calves and 2 *C. jejuni* isolates from fattening pigs. In 2024, gentamicin resistance genes were reported for two and four *C. coli* isolates from broilers and fattening turkeys, respectively, and for two *C. jejuni* isolates from fattening turkeys. Among the reported gentamicin resistance genes, the most common ones were *aph(2″)-If* and *aph(2″)-Ii*, reported in 35 and 32 isolates, respectively, followed by the gene *aph(2″)-Ic*, detected in 10 isolates. The *aph(3′)-IIIa* gene was only detected among poultry *C. coli* isolates (one from broilers and one from fattening turkeys). The gene *apmA*, which confers broad-spectrum resistance to aminoglycosides, including gentamicin, was reported in a single *C. coli* isolate from calves. Finally, the spectinomycin resistance gene *aad9* was detected in a single *C. coli* isolate from pigs and in two *C. coli* isolates from calves.

TABLE 15 Antimicrobial resistance genes and mutations conferring resistance to erythromycin and gentamicin reported for *C. jejuni* and *C. coli* from targeted food-producing animals, 2023–2024.

Species	Animal population, year	ERY-resistant isolates	GEN-resistant isolates
C. coli	Calves, 2023	23S mutation 2075A>G (**IT(9)**, **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)**)
		erm(*N*) (**IT(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, 2024	23S mutation 2075A>G (**IT (8), IE(13), RO(2)**)	*aph(2′′)-If*; (**IT(1)**)
		–	*aph(3′)-IIIa*; (**IT(1)**)
	Fattening turkeys, 2024	23S 2075A>G mutation (**IE(9), IT(3), RO(1)**)	*aph(2′′)-Ii* (**IT(2)**)
		erm(B) (**RO(2)**)	*aph(2′′)-Ih* (**IT(2)**)
C. jejuni	Calves, 2023	23S 2075A>G mutation (**IT(3)**)	*aph(2′)-Ii* (**IT(7)**);
		rplV mutation 103A>V (**IT(1)**)	*aph(2′)-If* (**IT(2)**)
	Fattening pigs, 2023	23S 2075A>G mutation (**IT(1)**)	*aph(2′)-If* (**IT(2)**)
		–	*aph(2′)-Ii* (**IT(1)**)
	Broilers, 2024	23S 2075A>G mutation (**RO(5)**)	–
	Fattening turkeys, 2024	23S 2075A>G mutation (**IT(1)**)	*aph(2′′)-If* (**IT(1)**)
		–	*aph(3′)-IIIa*; (**IT(1)**)

Notes: 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.

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 (2024) and food-producing animals (2023 and 2024) is presented in Figures 34 and 35, respectively.

High to extremely high levels of resistance to **ciprofloxacin** were observed in isolates from humans (72.0% in *C. jejuni* by 23 MSs; 76.5% in *C. coli* by 23 MSs) and from high to extremely high in food-producing animals (ranging from 34.0% in *C. jejuni* from fattening pigs to 85.1% 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 2024 (85.1%), followed by *C. coli* from calves in 2023 (80.4%). However, isolates of *C. jejuni* from broilers (69.2%) and fattening turkeys (76.4%) 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 very low to low levels for *C. jejuni* from both humans (0.6%) and food-producing animals (ranging from 0.4% in fattening turkeys to 2.1% in fattening pigs). Higher levels of resistance were observed in *C. coli* isolates from both humans (5.1%) and food-producing animals (ranging from 8.7% in broilers to 31.6% in calves). Overall, erythromycin resistance among animals was observed at the highest levels in *C. coli* isolates recovered from calves in 2023, followed by fattening turkeys in 2024 and fattening pigs in 2023 (13.0%), and broilers (8.7%) in 2024. Country-level variation was notable: in 2024, Spain and Portugal reported 15.6% and 14.9% erythromycin resistance in *C. coli* from humans, and among the highest levels in pigs (40.7% and 52.7%, respectively). Belgium reported 75.9% resistance in *C. coli* from calves but no human data.

Overall resistance to **gentamicin** was either absent or detected at low levels among *Campylobacter* isolated from food-producing animals (range from 0.2% in *C. jejuni* from broilers and fattening turkeys to 4.3% in *C. jejuni* from fattening pigs), except for moderate occurrence in *C. coli* from calves in 2023 (10.5%). Similarly, overall resistance to gentamicin was very low in human *C. jejuni* isolates (0.4%) and low in *C. coli* isolates from humans (1.9%).

The overall levels of resistance to **tetracycline** were high to very high in *C. jejuni* isolates from both humans (45.9%) and food-producing animals (ranging from 38.3% in fattening pigs to 65.6% in calves). Very high to extremely high levels of resistance to tetracycline were detected in *C. coli* isolates from humans (62.3%) and food-producing animals (ranging from 68.4% in fattening pigs to 88.6% in calves in 2023).

Overall levels of **combined resistance to ciprofloxacin and erythromycin** in *C. jejuni* were very low to low in both humans (0.5%) and food-producing animals (ranging from 0.4% in fattening turkeys to 2.1% in fattening pigs). Conversely, higher levels of co-resistance were observed in *C. coli* from both humans (5.0%) and animals, with the highest levels

reported in isolates from calves (30.3%) in 2023, followed by fattening turkeys (12.7%) in 2024, fattening pigs (10.6%) in 2023 and broilers (7.8%) in 2024.

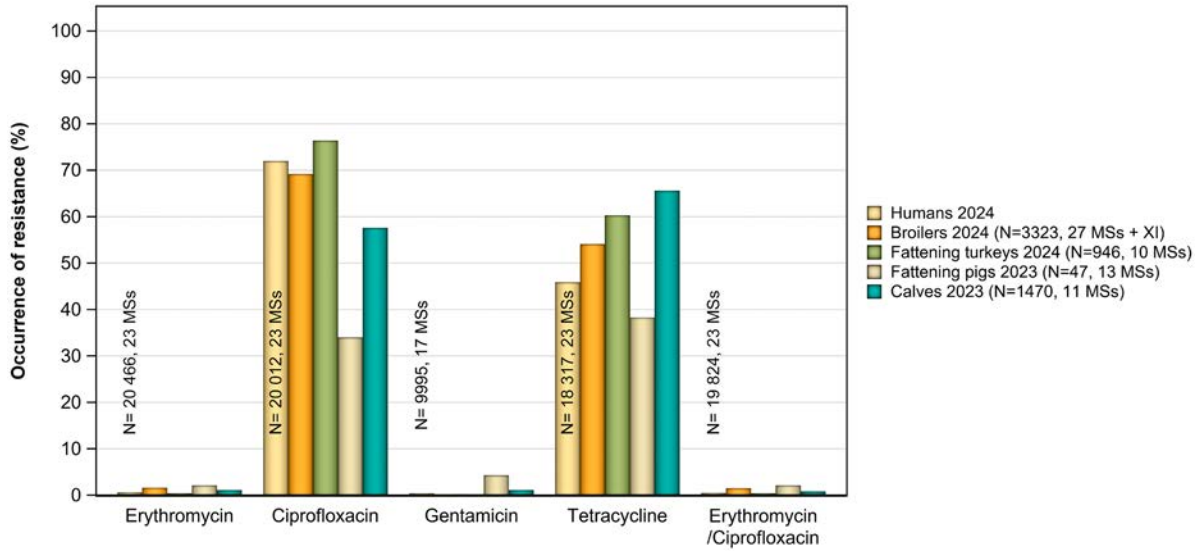


FIGURE 34 Comparison of *Campylobacter jejuni* occurrence of resistance between humans and food-producing animals, EU MSs, 2023–2024.

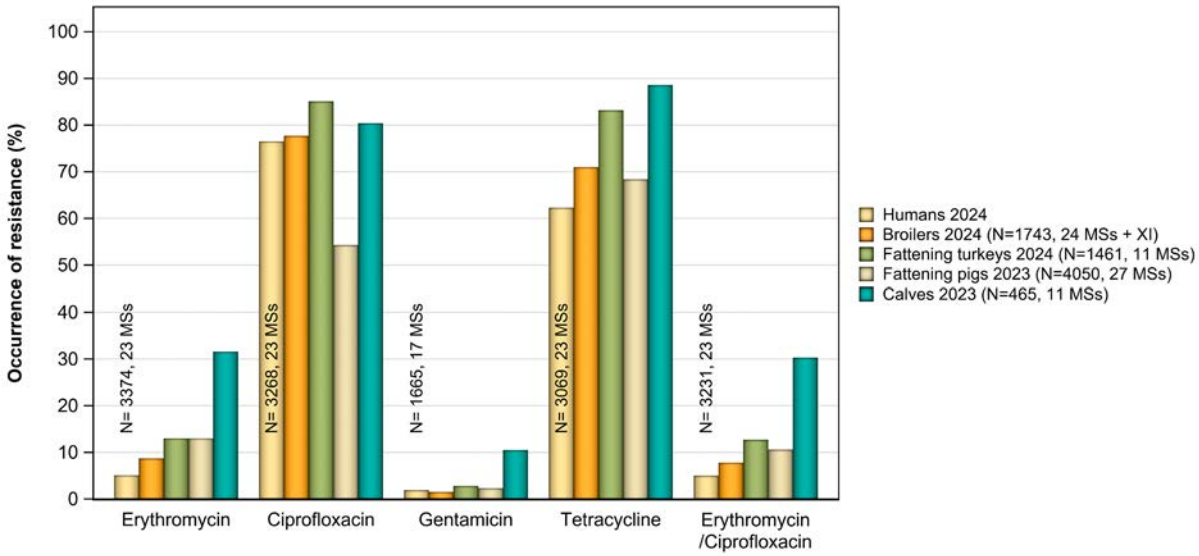


FIGURE 35 Comparison of *Campylobacter coli* occurrence of resistance between humans and food-producing animals, EU MSs, 2023–2024.

The analyses of CS and MDR in both humans and food-producing animals focus on critically important antimicrobials for human and animal treatment. For this reason, the target substances were agreed by EFSA and ECDC and include ciprofloxacin, erythromycin, gentamicin and tetracycline. Levels of CS and MDR in *Campylobacter* isolates recovered from humans in 2024 and from food-producing animals in 2023–2024 by EU MSs are displayed in Figure 36. 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 3 and 4) and Annex B.2 (Tables 1–2, 7–8, 13–16), respectively.

Complete susceptibility to the four target antimicrobials in humans was reported at levels of 28.0% in *C. jejuni* isolates and at 12.7% in *C. coli* isolates (Figure 36). Similarly, in food-producing animals, the observed overall CS was higher in *C. jejuni* than in *C. coli*. In *C. jejuni* isolates, the highest levels of CS were observed in fattening pigs (51.1%) in 2023, followed by broilers (25.5%) in 2024, calves (21.2%) in 2023 and fattening turkeys (17.7%) in 2024. The overall CS level in *C. coli* was low for isolates from calves (4.5%) in 2023 and fattening turkeys (5.3%) in 2024, but higher for broilers (10.0%) in 2024 and fattening pigs (19.7%) in 2023. The average CS observed in *C. jejuni* and *C. coli* from broilers and fattening turkeys were slightly higher than those observed in 2022, except for *C. coli* from broilers, where it decreased from 13.1% to 10.0%.

Multidrug resistance, defined as resistance to at least three antimicrobials among the four target substances, was reported at levels of 0.7% in *C. jejuni* isolates and 7.5% in *C. coli* isolates from humans in 2024 (Figure 36). Similarly, in food-producing animals, the observed overall MDR was higher in *C. coli* than in *C. jejuni* isolates. MDR was observed at low levels in *C. jejuni* isolates from fattening turkeys (0.6%) and broilers (1.1%) in 2024, and from calves (1.6%) and fattening pigs

(4.3%) in 2023. The highest levels of MDR were reported in *C. coli* isolates from calves (34.8%), followed by fattening turkeys (12.4%), fattening pigs (10.7%) and broilers (7.6%). The MDR levels observed in *C. jejuni* and *C. coli* from broilers and fattening turkeys in 2024 were mostly lower than the levels reported in 2022, except for MDR in *C. jejuni* from broilers, which has remained at a similar level.

Interestingly, as previously observed with the 2022 reported data, in 2024 the proportions of CS and MDR among *C. jejuni* and *C. coli* isolates recovered from humans continued to show most similarity to the proportions observed with isolates from broilers, followed by isolates from calves and fattening turkeys for *C. jejuni* and by isolates from fattening pigs for *C. coli*.

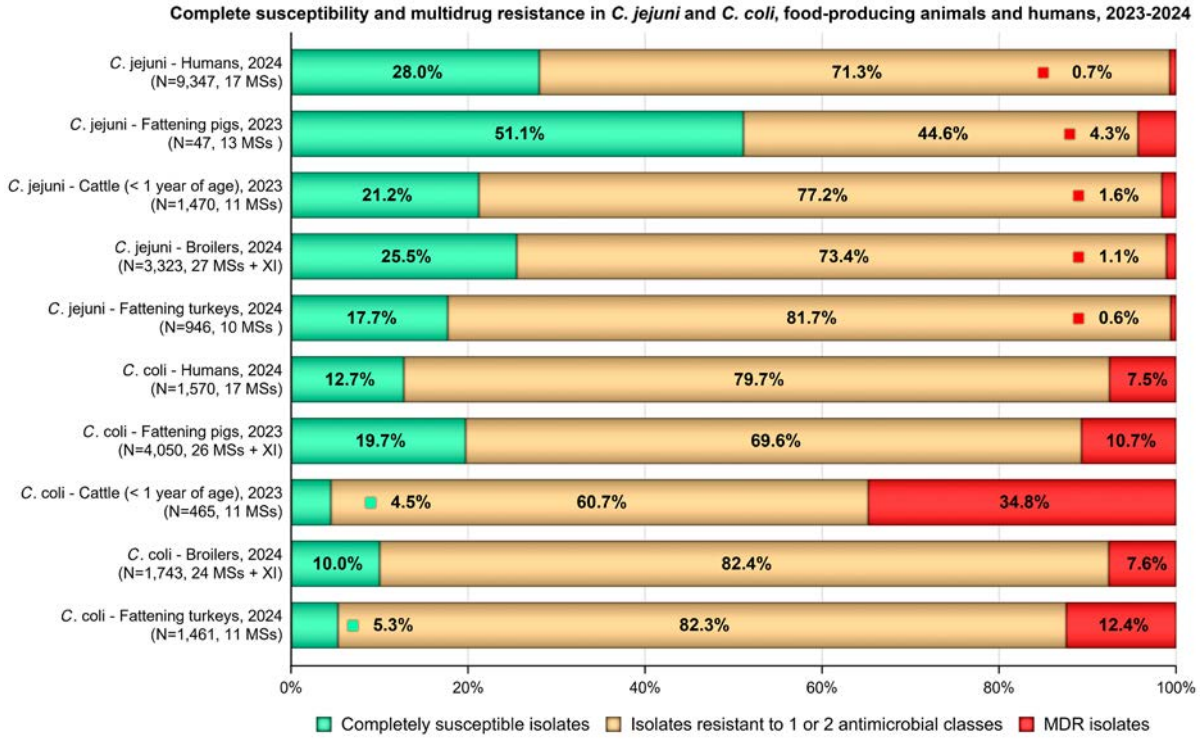


FIGURE 36 Proportion of isolates completely susceptible, resistant to one or two antimicrobial classes and multidrug-resistant (MDR) among *Campylobacter jejuni* and *C. coli* from humans, fattening pigs, calves, broilers and fattening turkeys, in reporting EU MSs, 2023–2024.

Table 16 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 2014–2024. 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 and 1 non-MS for humans and 7 MSs for broilers) and the decrease in erythromycin resistance (9 MSs and 1 non-MS for humans, 6 MSs and 1 non-MS 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 eight MSs and from fattening pigs in three MSs and one non-MS. Significant decrease of ciprofloxacin resistance or increase of erythromycin resistance were less commonly detected among the reporting countries included in the temporal trend analysis.

TABLE 16 Number of countries with significantly increasing or decreasing trends in resistance to selected antimicrobials for *Campylobacter jejuni* and *C. coli* from humans and from targeted food-producing animals (2014–2024).

		CIP		ERY		TET	
Campylobacter	**Population**	↓	↑	↓	↑	↓	↑
C. jejuni	**Humans, 2024** 20 MSs + 2 non-MSs	5 (EE, ES, FI, NO, PT)	12 (AT, BG, CY, DE, DK, FR, IS, LT, MT, PL, SI, SK)	10 (DE, DK, FI, FR, IT, LT, NL, NO, PT, SK)	2 (EE, LU)	5 (ES, FI, FR, LU, PT)	6 (AT, BG, DE, LT, NL, SK)

(Continues)

TABLE 16 (Continued)

		CIP		ERY		TET	
Campylobacter	**Population**	↓	↑	↓	↑	↓	↑
	Broilers, 2024 23 MSs + 2 non-MSs	3 (FI, FR, LV)	7 (CY, DE, DK, HR, RO, SE, SI)	7 (BG, CH, DE, IT, PT, RO, SK)	1 (BE)	4 (ES, FI, FR, IT)	9 (AT, DE, DK, HR, IE, LV, PL, SE, SK)
	Fattening turkeys, 2024 7 MSs	2 (ES, IT)	–	2 (ES, IT)	–	3 (ES, FR, IT)	–
C. coli	**Humans, 2024** 20 MSs	1 (ES)	4 (HU, NL, SI, SK)	8 (AT, EE, ES, FI, FR, IT, PT, SK)	–	7 (AT, DE, FI, IT, ES, PT, SI)	1 (FR)
	Broilers, 2024 6 MSs	–	2 (IE, NL)	–	1 (IE)	2 (CZ, NL,)	1 (IE)
	Fattening pigs, 2023 10 MSs + 2 non-MSs	2 (ES, LU)	2 (CH, NO)	4 (CH, ES, IE, LU)	–	3 (BE, ES, SE)	1 (EE)

Notes: ↓, statistically significant decreasing trends; ↑, statistically significant increasing trends.
Abbreviations: CIP, ciprofloxacin; ERY, erythromycin; TET, tetracycline; Abbreviations for reporting countries can be found here.

3.6 | Discussion

Campylobacter is a major food-borne zoonotic pathogen and its presence in food-producing animals poses a risk for transmission to humans. Antibiotic-resistant strains complicate treatment of human campylobacteriosis and are a public health concern (Garcia & Heredia, 2013; Moore et al., 2006). The primary species causing human infections is *C. jejuni*, prevalent in poultry, followed by *C. coli*, more common in fattening pigs (Jehanne et al., 2020).

The EU-wide harmonised monitoring of AMR in *C. jejuni* and *C. coli*, under Commission Implementing Decision (EU) 2020/1729, has enhanced integrated reporting and analysis of AMR occurrence and temporal trends. However, the number of reporting countries and isolate numbers may vary considerably, reflecting differences in national meat production.

Resistance in human isolates has been associated with resistance in bacteria from food-producing animals and antimicrobial use in both sectors. The fourth JIACRA report (ECDC, EFSA, EMA, 2024) found significant associations between resistance to fluoroquinolones, macrolides and tetracycline in *Campylobacter* from animals and humans across the EU.

AMR data from 2023–2024 showed high to extremely high fluoroquinolone resistance (**ciprofloxacin**) in *C. jejuni* and *C. coli* from humans and animals. Between 2014 and 2024, an increase in ciprofloxacin resistance in *C. jejuni* was observed in isolates from humans in 12 countries, and in isolates from broilers in seven countries. Similar trends were noted in *C. coli* isolates from humans in four countries, from broilers in two and from fattening pigs in two non-EU states. These findings are consistent with global patterns of increasing fluoroquinolone-resistant *Campylobacter* and highlight its zoonotic transmission potential (Inglis et al., 2021; Ortega-Sanz et al., 2025; Yang et al., 2019).

A genomic study conducted in Spain (Ortega-Sanz et al., 2025) found widespread fluoroquinolone resistance in *C. jejuni* and *C. coli* across the poultry supply chain and in human clinical isolates. Notably, resistance determinants were more diverse in human isolates from hospitals and isolates from samples collected at retail than in those collected at farm level, suggesting that resistance may not originate exclusively from farms. Nevertheless, the high resistance at farm level points to continued use of fluoroquinolones in poultry production, where flock-wide treatments affect large numbers of animals.

Ciprofloxacin resistance in *Campylobacter* is concerning, as fluoroquinolones are commonly used to treat human diarrhoea (Espinoza et al., 2020). Although treatment is generally discouraged due to the disease's self-limiting nature, it may be necessary for immunocompromised or patients with comorbidities (Yang et al., 2019). High resistance levels make ciprofloxacin less suitable for treatment unless susceptibility is confirmed.

The main mechanism of quinolone and fluoroquinolone resistance in *Campylobacter* is the C257T mutation in the *gyrA* gene (Elhadidy et al., 2020; Espinoza et al., 2020; Garcia-Fernandez et al., 2024a, 2024b). Changes in the *CmeABC* multidrug efflux pump expression increase MICs of several antimicrobials and enhance survival in bile salts and host colonisation (Lekshmi et al., 2023). Highly resistant isolates with a transferable *RE-CmeABC* 'super' efflux pump, first identified in China (Yao et al., 2016), show elevated MICs to ciprofloxacin, florfenicol, chloramphenicol, erythromycin and tetracycline. Recent studies have detected *RE-CmeABC* in *Campylobacter* from poultry and human cases (Gao Fen et al., 2023; Gharbi et al., 2024; Ortega-Sanz et al., 2025). Additionally, plasmid-mediated quinolone resistance genes (*qnrB*, *qnrS*, *qepA*) were found in *C. coli* from poultry (Gharbi et al., 2024), raising concerns about horizontal gene transfer.

As the use of fluoroquinolones are discouraged for treatment of severe human campylobacteriosis in Europe, macrolides are now the first-line treatment, making monitoring resistance to these antimicrobials critical. Resistance to **erythromycin** was low or absent in *C. jejuni* from humans, poultry, and calves, but higher and highly variable between countries in *C. coli* from humans and all targeted animals, with highest levels observed in calves. From 2014 to 2024, erythromycin resistance in *C. jejuni* declined in humans (10 countries), broilers (7 countries) and turkeys (2 countries). *C. coli* showed

decreasing resistance in humans (eight countries) and pigs (four countries). Increasing trends within this period were rare. Many resistant isolates had very high MICs (> 512 mg/L), especially in calves.

The cause of high erythromycin resistance in *C. coli* isolates from calves is unclear but may involve group treatments with macrolides – used as a second-line antimicrobial in veal farms (Mallioris et al., 2024) – or cross-selection from other antimicrobials. For example, the use of enrofloxacin significantly alters calves' gut microbiota and resistome, with high doses potentially driving clonal expansion and AMR gene transfer (Beyi et al., 2021).

High macrolide resistance in *Campylobacter* is primarily driven by mutations in the 23S rRNA gene (e.g. A2074G, A2074C, A2075G) (Hull et al., 2021; Hurtado et al., 2025). The transferable *erm*(B) gene, often found on MDR islands or plasmids, also confers high resistance to macrolides, in addition to lincosamides and streptogramin B (Wang et al., 2014). Mutations in *rplD* or *rplV* genes encoding 50S ribosomal proteins have also been reported in connection to erythromycin resistance in *Campylobacter* (Mouftah et al., 2021), although often only when occurring together with a 23S rRNA gene mutation (Bolinger & Kathariou, 2017).

Since 2021, susceptibility testing includes erythromycin concentrations up to 512 mg/L (Commission Implementing Decision (EU) 2020/1729), allowing differentiation between low-level resistance (likely due to ribosomal mutations or efflux pump activity) and high-level resistance (possibly linked to *erm*(B)). WGS of isolates from 2023 to 2024 revealed that most carried the A2075G mutation. The *erm*(B) gene was identified in one *C. coli* isolate from pigs in the Netherlands and two *C. coli* isolates from fattening turkeys in Romania. Additional notable mutations were detected in isolates from turkeys in Spain and fattening pigs in Portugal. These findings support existing literature indicating that 23S rRNA mutations can confer resistance levels comparable to those mediated by *erm*(B), particularly when combined with the activity of the *CmeABC* efflux pump (Bejaoui et al., 2022; Wei & Kang, 2018).

Tetracycline resistance was high to extremely high in *Campylobacter* isolates from humans and food-producing animals in 2023–2024, with the highest levels observed in both *C. jejuni* and *C. coli* from calves. A decade-long review of AMR in *Campylobacter* isolates from animals and humans in Europe has reported 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 particularly high levels of resistance observed in calves.

The **prevalence of resistance** to selected antimicrobials in *Campylobacter* isolates from food-producing animals in 2023 and 2024 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 affect true prevalence. Considerable between-country variability was observed in the prevalence of ciprofloxacin and tetracycline resistance in *C. jejuni* and *C. coli* from broilers and fattening turkeys. Comparably lower levels and lower between-country variability was observed in the prevalence of erythromycin resistance, with the exception of *C. coli* from fattening turkeys. This may pose a significant public health concern in the event of zoonotic transmission, given the increasing reliance on macrolides as the first-line treatment of human campylobacteriosis.

MDR, defined as resistance to at least three antimicrobials among ciprofloxacin, erythromycin, tetracycline and gentamicin, was generally lower in *C. jejuni* than *C. coli*. MDR levels ranged from very low in *C. jejuni* from fattening turkeys to high in *C. coli* from calves. Similar **CS**, defined as susceptibility to ciprofloxacin, erythromycin, tetracycline and gentamicin, and MDR occurrence in *C. jejuni* and *C. coli* in humans and broilers suggest that broilers may also be a reservoir for resistant *C. coli*, consistent with studies identifying chicken as a major source of human campylobacteriosis caused by both *Campylobacter* species in France, the United Kingdom and the United States (FSA, 2021; Hudson et al., 2021; Jehanne et al., 2020; Pascoe et al., 2024).

Chloramphenicol resistance was absent or very low in most animal isolates, except for *C. coli* from young cattle (1.7% in 2023). **Ertapenem** resistance varied among *Campylobacter* isolates from different animal species. In 2024, moderate levels were reported in *C. jejuni* isolates from broilers and turkeys, and very high levels were reported in *C. coli* from the same animal species. In 2023, resistance ranged from absent to low in *C. jejuni* and from high to low in *C. coli* isolates from calves and pigs, respectively. Despite no EUCAST cut-off, rising MICs in *Campylobacter* from broilers and fattening turkeys between 2022 and 2024 are concerning, as carbapenems like ertapenem are used to treat invasive human *Campylobacter* infections (Dai et al., 2020; EFSA, 2019).

WGS is strongly recommended for isolates with MDR, high-level erythromycin or ciprofloxacin resistance, or resistance to gentamicin or ertapenem. It helps identify AMR genes, their origins and potential for horizontal transfer. Moreover, WGS can contribute to the detection of prevalent resistant lineages or subtypes (Garcia-Fernandez et al., 2024a, 2024b; 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

- In 2023–2024, resistance to **ampicillin, sulfamethoxazole, trimethoprim** or **tetracycline** was common, with median[3] resistance levels ranging from high to very high across all food-producing animal populations targeted, except calves, where median levels remained low. Resistance to quinolones was common in broilers and turkeys, with high median levels. Resistance to other antimicrobials was less common.
- For the WHO highest priority critically important and critically important antimicrobials **colistin, azithromycin** and **third-generation cephalosporins** (cefotaxime or ceftazidime) resistance was uncommon, with median resistance levels ranging from rare to low in all animal populations. Whereas median levels of resistance to **ciprofloxacin** were low in pigs and calves but high in turkeys and very high in broilers. Combined resistance to third-generation cephalosporins and fluoroquinolones remained generally uncommon across all animal populations.
- Resistance to **meropenem** was not detected in any isolates in 2023–2024.
- A large variation in antimicrobial resistance (AMR) levels was recorded among countries, with lower levels typically reported in Northern Europe.
- **Complete susceptibility** (CS) was more frequently observed in isolates from pigs and calves, whereas **Multidrug resistance** (MDR) was more common in isolates from broilers and turkeys. Marked inter-country differences were recorded in both CS and MDR. MDR patterns most involved tetracycline, ampicillin, sulfamethoxazole and trimethoprim, with quinolones additionally frequent in broiler and turkey isolates.
- The **KOI_{CS}**, which adjusts for the relative sizes of the different food-producing animal populations, varied widely across countries, ranging from less than 10% to more than 80%. The highest KOI_{CS} values were typically observed in Northern Europe.
- In several reporting countries, statistically significant decreasing **trends** in resistance to ampicillin, ciprofloxacin, cefotaxime, tetracycline and colistin, along with increasing trends in CS and KOI_{CS}, reveal progress in reducing AMR. The most pronounced improvements have occurred in broilers and turkeys in recent years.
- At the EU MS level, statistically significant decreasing **trends** in resistance were observed for ciprofloxacin and tetracycline in broilers and turkeys, and for colistin and tetracycline in pigs and calves. No combinations showed statistically significant increasing trends. KOI_{CS} has increased significantly over the last 10 years.
- At the EU level and in certain MSs, some previously declining resistance trends or increasing susceptibility trends in indicator *E. coli* from broilers and turkeys, and KOI_{CS}, have stabilised and plateaued. Although based on recent data points and requiring further investigation, these changes highlight the ongoing need for strengthened efforts to combat AMR.

4.2 | Monitoring antimicrobial 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 using antimicrobials in food-producing animals, clonal spread of resistant organisms, dissemination of resistance determinants and the effects of co-selection in bacteria exhibiting MDR. Further information on AMR in *E. coli* 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.

Since 2014, the EU legislation[4] 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. Data can be further visualised interactively using the EFSA dashboard on AMR in *E. coli*.

[3]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.

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

4.3 | Food-producing animals: Occurrence of antimicrobial resistance in indicator commensal *E. coli*

4.3.1 | Data reported

All EU Member States reported AMR data for indicator commensal *E. coli* from broilers in 2024 and from pigs in 2023. Member States with significant turkey and calf production submitted data for these species in 2024 and 2023, respectively, in accordance with EU legislative requirements. Furthermore, some countries reported such data on a voluntary basis. A detailed summary of the number of countries reporting data per targeted food-producing animal category, and the number of isolates per category, is presented in Table 17.

This chapter presents summary data on the occurrence of AMR to substances used in veterinary and/or human medicine, including combined resistance to ciprofloxacin and cefotaxime. It also includes analyses of MDR patterns and complete susceptibility (CS). Annex C provides detailed aggregated data on AMR, MDR, CS and combined resistance in *E. coli* from broilers and turkeys (2024), and from pigs and cattle (2023), at both individual MS and MS-group levels. Additionally, resistance in indicator *E. coli* isolates recovered from imported fresh meat sampled at BCPs in 2023 and 2024 is presented in a dedicated textbox at the end of the chapter. Moreover, the findings of the specific monitoring of ESBL-, AmpC- or CP-producing *E. coli* using selective culturing methods, including data on their prevalence and occurrence, are presented in Chapter 5.

TABLE 17 Overview of countries reporting indicator commensal *E. coli* and number of isolates per targeted food-producing animal population in 2023 and 2024.

		EU member states and the United Kingdom (Northern Ireland)		Non-member states	
Year	Animal population	Number of countries	Number of isolates	Number of countries	Number of isolates
2024	Broilers	27 + 1	4451	4	620
	Fattening turkeys	12[a]	1653	0	–
2023	Fattening pigs	27 + 1	4368	5	683
	Calves	11[b]	1964	2[b]	210

[a]Austria, Croatia, France, Germany, Hungary, Ireland, Italy, Poland, Portugal, Romania, Spain and Sweden.

[b]Austria, Belgium, Croatia, Denmark, France, Germany, Italy, Netherlands, Portugal, Romania and Spain as well as the Republic of North Macedonia and Switzerland.

4.3.2 | Occurrence of resistance

Resistance to antimicrobials commonly used in veterinary medicine

Resistance to **ampicillin**, **sulfamethoxazole**, **trimethoprim** and **tetracycline** was common among all four targeted food-producing animal populations, with high to very high median levels of resistance reported by EU MSs and the United Kingdom (Northern Ireland) (Figure 37, Table 2; Annex C). An exception was trimethoprim in calves, where the median level was low. Large inter-country variation was observed for all four antimicrobials in all animal populations, with resistance levels ranging from 2.9% to 90.6% for ampicillin, 3.4% to 92.9% for sulfamethoxazole, 2.4% to 60.0% for trimethoprim and 0.0% to 82.4% for tetracycline (Figure 37; Annex C, tables T.1–T.4).

For **chloramphenicol**, the overall median resistance level across all reporting MSs was low to moderate in all animal populations (8.5%–13.8%). Some countries, however, reported high to very high resistance, and one country reported an extremely high level of resistance among isolates from turkeys (Annex C, tables T.1–T.4).

The overall median resistance to **gentamicin** was very low to low across all animal populations (1.8%–4.6%), though some countries reported moderate resistance levels (Annex C, tables T.1–T.4). For **amikacin**, occurrence of resistance was generally rare based on median values, although some countries reported up to low levels of resistance (Annex C, tables T.1–T.4).

Resistance to highest priority critically important antimicrobials

Resistance to **ciprofloxacin** and **nalidixic acid** was common in poultry, with high/very high median levels observed in broilers (median: ciprofloxacin 52.1%; nalidixic acid 46.8%) and high median levels observed in turkeys (median: ciprofloxacin 39.4%; nalidixic acid 22.9%) (Figure 37, Table 18; Annex C, tables T.3 and T.4). Substantial inter-country variations were noted, with resistance levels ranging from 0.0% to 90.6% for ciprofloxacin and 0.0% to 84.7% for nalidixic acid (Figure 37; Annex C). In contrast, pigs and calves showed low median resistance levels to both antimicrobials (pigs: median 8.1% and 4.9%; calves: 6.3% and 3.2%, respectively) (Figure 37, Table 18; Annex C, tables T.1 and T.2). Furthermore, most countries reported higher levels of ciprofloxacin resistance than nalidixic acid resistance, indicating the presence of transmissible genes mediating quinolone resistance (Jacoby et al., 2014).

Across all targeted animal populations, the overall median resistance to third-generation cephalosporins (**cefotaxime** and/or **ceftazidime**) was undetected or very low, ranging from 0.0% to 0.8% (Figure 37, Table 18; Annex C, tables T.1–T.4). In countries reporting resistant isolates, resistance levels were generally either very low or low. All isolates exhibiting resistance to third-generation cephalosporins (and/or carbapenems) were further phenotypically characterised to identify presumptive production of ESBL-, AmpC- and/or CP-enzymes using a secondary panel. The results of these investigations are presented in Chapter 5 – Extended-spectrum beta-lactamase (ESBL)-, AmpC- and /or carbapenemase (CP)-producing *E. coli*. None of the indicator *E. coli* isolates from the targeted food-producing animal populations exhibited microbiological resistance to carbapenems (**meropenem**) in 2023–2024 (Annex C, tables T.1–T.4).

The median resistance to **colistin** and **tigecycline** was rare across all targeted animal populations, although some countries reported resistance up to the low range. Notably, Poland reported a moderate level of tigecycline resistance in pigs and a high level of colistin resistance in turkeys (Annex C, tables T.1–T.4). The median resistance to **azithromycin** was rare in calves, very low in broilers and turkeys, and low in pigs, with some countries reporting resistance levels up to the low range for all populations (Annex C, tables T.1–T.4).

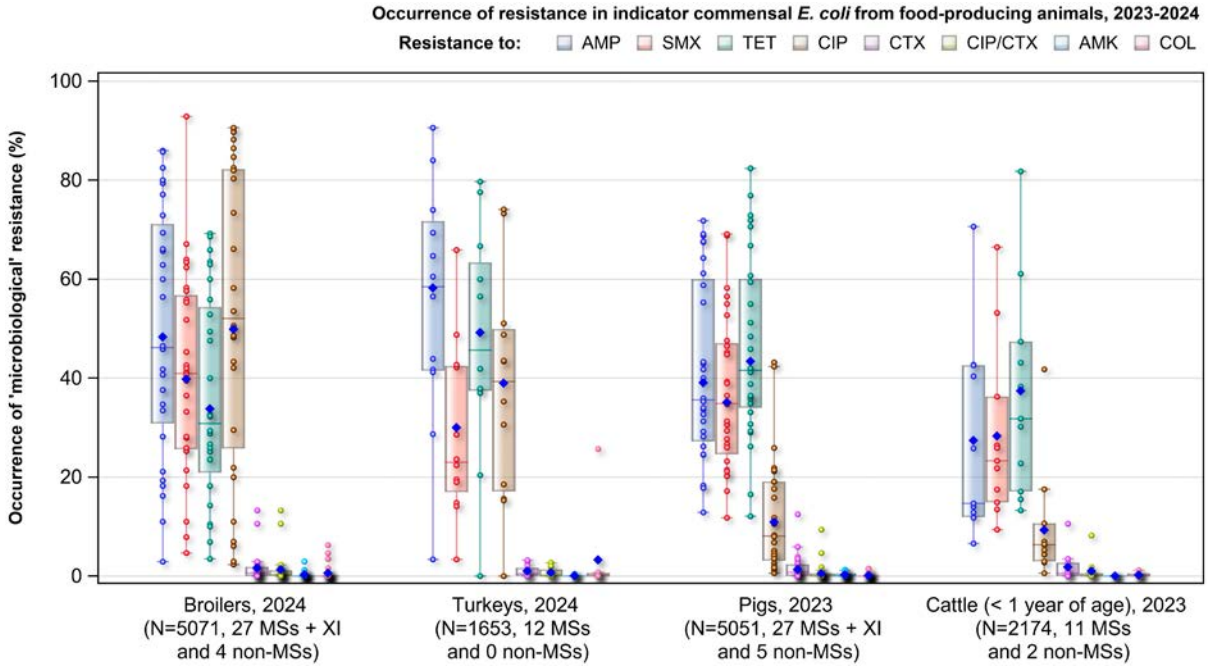


FIGURE 37 Distribution of the occurrence of resistance to selected antimicrobials in indicator commensal *E. coli* isolates recovered from targeted animal populations, 2023–2024. EU MSs, the United Kingdom (Northern Ireland) and non-MSs.

Notes: 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.

Abbreviations: 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, sulfamethoxazole; TET, tetracycline; XI, the United Kingdom (Northern Ireland).

TABLE 18 Median level of microbiological resistance to first- and second-line antimicrobials in *E. coli* isolates from targeted food-producing animals, EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

Year	Animal population	AMP %R	SMX %R	TET %R	CIP %R	CTX %R	CIP/CTX %R	AMK %R	COL %R
2024	Broilers (N = 4451)	46.2	40.9	30.8	52.1	0.6	0.3[a]	0.0	0.3
	Turkeys (N = 1653)	58.5	23.0	45.7	39.4	0.5	0.0	0.0	0.0
2023	Pigs (N = 4638)	35.6	34.8	41.5	8.1	0.8	0.0	0.0	0.0
	Calves (N = 1964)	14.7	23.3	31.8	6.3	0.6	0.0	0.0	0.0

Notes: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. A blank cell represents no resistance. The correspondence between colour and resistance level categories can be found in the 'Definitions' section.

Abbreviations: AMP, ampicillin; AMK, amikacin; AZT, azithromycin; CHL, chloramphenicol; GEN, gentamicin; ; N, total number of isolates tested; %R, percentage of resistant isolates; SMX, sulfamethoxazole; TET, tetracycline; TMP, Trimethoprim.

[a]Using clinical breakpoints to interpret resistance, the median combined resistance to ciprofloxacin and cefotaxime was 0.0.

Combined resistance to fluoroquinolones and 3rd-generation cephalosporins

In most reporting countries, microbiological[5] **combined resistance** to **ciprofloxacin** and **cefotaxime** was either undetected or detected at very low levels across all targeted animal populations (Figure 38; Table 19; Annex C, tables T.1–T.4). The median level of **combined resistance** was rare in pigs, calves and turkeys, and very low in broilers. Some countries reported, however, higher levels. **Clinical**[6] **combined resistance** was not detected in isolates from any of the targeted populations in most countries; where present, it was low to very low, except in broilers from Cyprus, which reported moderate levels (Annex C, tables T.1–T.4).

TABLE 19 Combined resistance to ciprofloxacin and cefotaxime in indicator commensal *E. coli* from targeted food-producing animals applying ECOFFs and clinical breakpoints, as issued by EUCAST, EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.

	Microbiological combined resistance to CIP & CTX using ECOFFs			Clinical combined resistance to CIP & CTX using clinical breakpoints		
Food-producing animal population	***N***	**% *R***	**95% CI**	***N***	**% *R***	**95% CI**
Pigs, 2023[a]	24	0.5	0.3, 0.7	5	0.1	0.0, 0.2
Calves, 2023[b]	25	1.1	0.8, 1.7	7	0.3	0.2, 0.7
Broilers, 2024[c]	59	1.2	0.9, 1.5	39	0.8	0.6, 1.1
Turkeys, 2024[d]	12	0.7	0.4, 1.3	3	0.2	0.1, 0.5

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

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

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

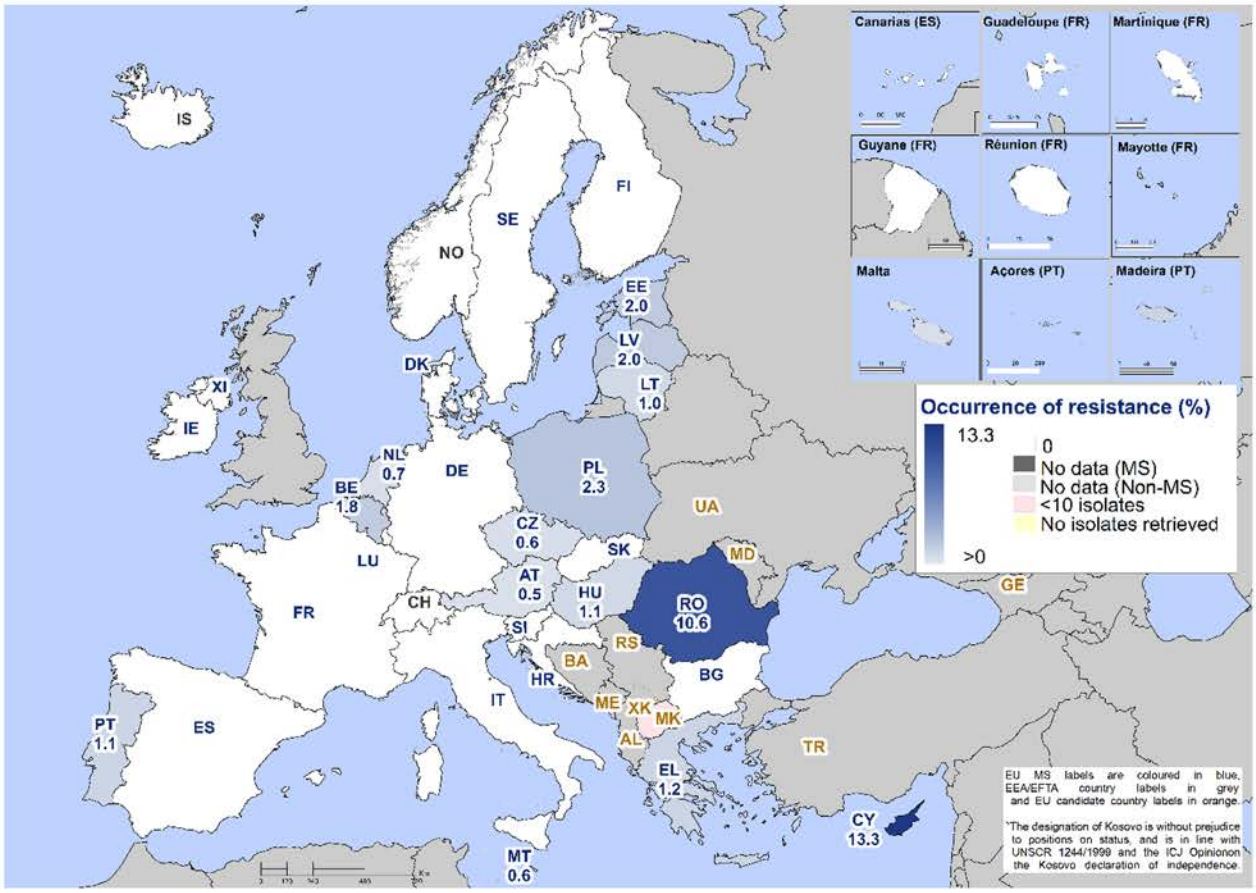
[c]27 MSs, the United Kingdom (Northern Ireland), 4 non-MSs; 5071 isolates investigated.

[d]12 MSs; 1653 isolates investigated.

[5]That is defining resistance by epidemiological cut-off value (ECOFF). See Appendix A for the definition.

[6]That is defining resistance by clinical breakpoint. See Appendix A for the definition.

(A)



(B)

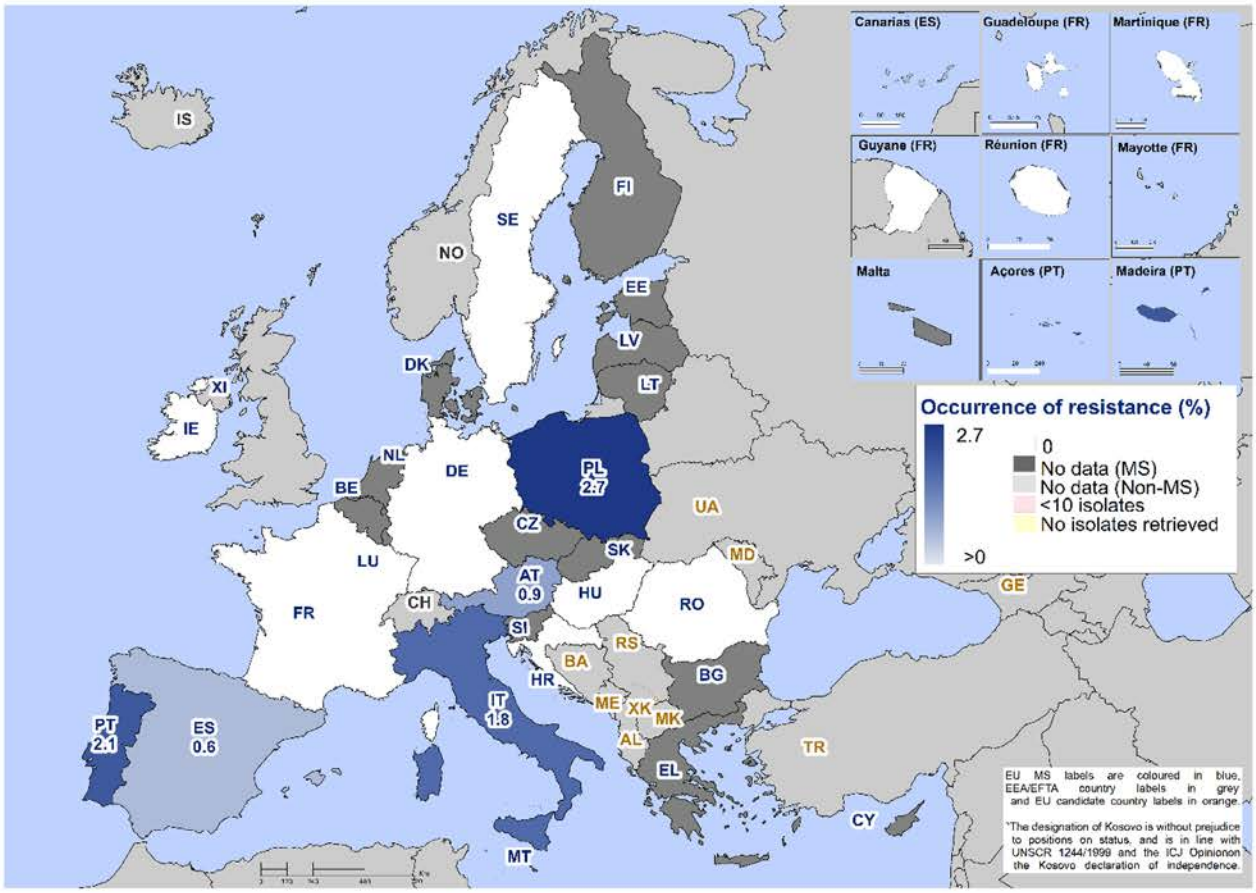


FIGURE 38 (Continued)

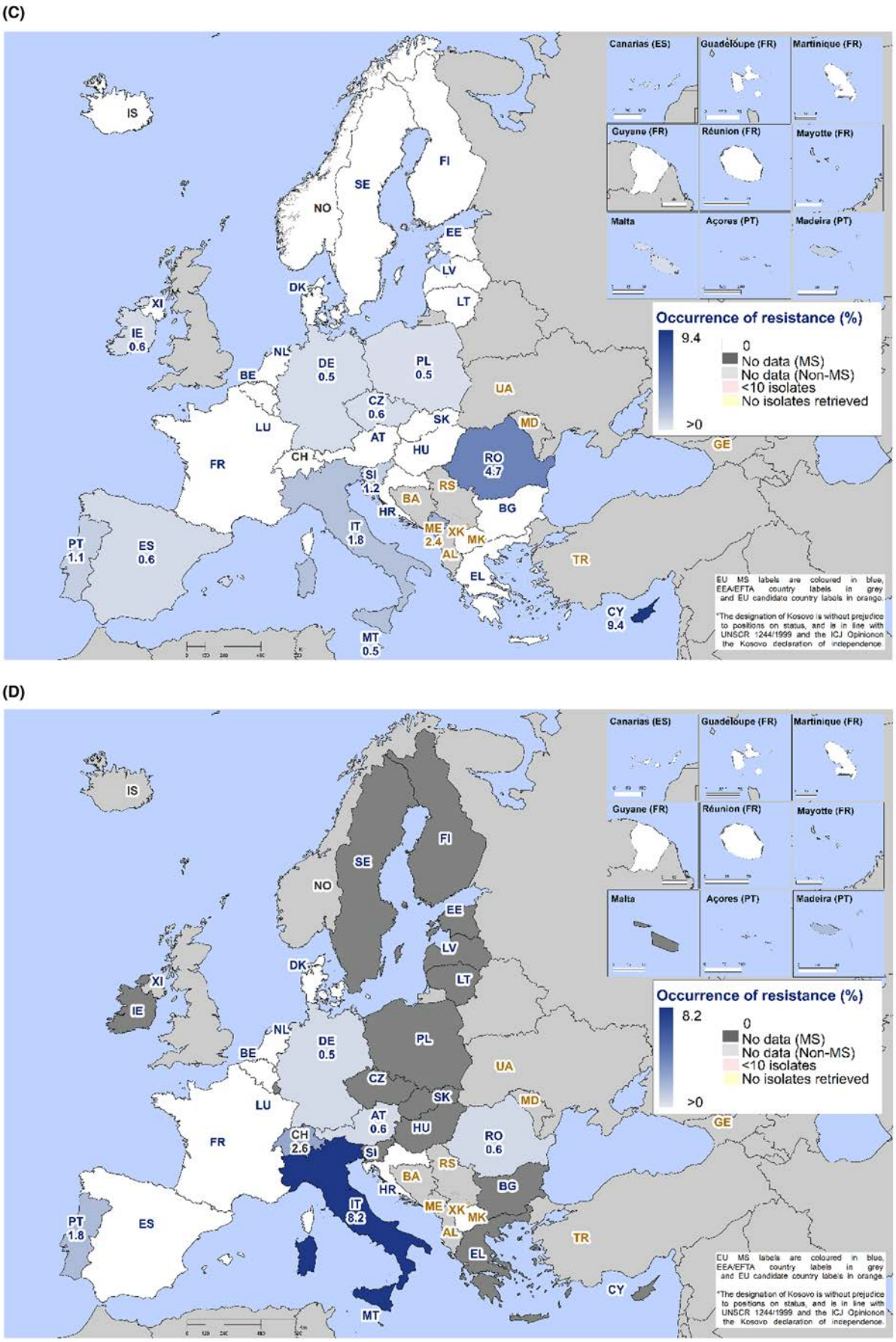


FIGURE 38 Spatial distribution of microbiological combined resistance to cefotaxime and ciprofloxacin in indicator commensal *E. coli* from broilers (A), turkeys (B), pigs (C), calves (D) EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.
Notes: The designation of Kosovo is without 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 | Temporal trends in resistance

Temporal trends in resistance to ampicillin, cefotaxime, ciprofloxacin, colistin and tetracyclines in indicator *E. coli* from food-producing animals were assessed for countries that provided data for at least 3 years between 2014 and 2024. Aminopenicillin (e.g. ampicillin) and tetracycline are the most widely sold antimicrobials for use in food-producing animals in Europe (EMA, 2025), making resistance trends particularly relevant, as reductions in resistance are primarily attributed to decreased usage (ECDC, EFSA, EMA, 2024). Trends in resistance to WHO highest priority critically important antimicrobials – cefotaxime, ciprofloxacin and colistin – were also addressed due to their potential impact on human health. Statistical significance ($p < 0.05$) was assessed using logistic regression (see Appendix A – Materials and methods for details on the methodological approach).

Overview of the statistically significant trends at the MS level

Sufficient data to assess temporal trends were available from 31 countries for pigs, 29 for broilers, 12 for calves and 11 for turkeys (Table 20). In total, 415 animal/substance combinations were analysed for statistically significant trends in resistance to **ampicillin**, **cefotaxime**, **ciprofloxacin**, **colistin** and **tetracyclines**. Of these, 114 combinations (28%) showed statistically significant ($p < 0.05$) decreasing trends, while 29 combinations (7%) showed statistically significant increasing trends (Table 20). The highest proportion of decreasing trends was observed in turkeys (45%) and broilers (39%), while broilers also showed the highest proportion of increasing trends (11%). In several countries, resistance levels remained consistently low over time, limiting the potential for further reduction.

TABLE 20 Overview of statistically significant trends in resistance to ampicillin, cefotaxime, ciprofloxacin, colistin and tetracyclines in indicator commensal *E. coli* from targeted food-producing animals over 2014–2024, EU MSs and non-MSs.

	AMP			CTX			CIP			COL			TET			Total		
Animal population	↓	↑	↔	↓	↑	↔	↓	↑	↔	↓	↑	↔	↓	↑	↔	↓	↑	↔
Broilers[a]	13	7	9	14	1	14	14	2	13	4	1	24	13	2	14	58	13	74
Pigs[b]	5	2	24	2	2	27	2	5	24	1	0	30	14	0	17	24	9	122
Turkeys[c]	7	0	4	2	0	9	5	0	6	5	1	5	8	0	3	25	2	28
Calves[d]	3	1	8	0	1	11	2	0	10	1	0	11	5	1	6	11	3	46
Total	28	10	45	18	3	61	23	7	53	11	2	70	40	3	40	118	27	270

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

[a]26 MSs, 3 non-MSs.

[b]27 MSs, 4 non-MSs.

[c]10 MSs, 1 non-MS.

[d]9 MSs, 3 non-MSs.

Overview of the statistically significant trends at the EU MS-group level

At the EU MS-group level, a multi-country weighted mean using population size (expressed by PCU) was calculated, as the weighting factor provides a more realistic and population-representative summary of regional patterns. By giving greater influence to larger countries, it reflects the true scale of impact across. This approach also limits distortion from potential country outliers, whose extreme values could otherwise disproportionately affect the unweighted total. The trend analysis revealed statistically significant decreasing trends for 10 combinations: ampicillin, cefotaxime, ciprofloxacin and tetracyclines in broilers, ciprofloxacin and tetracyclines in turkeys, and colistin and tetracyclines in pigs and calves (Figures 6–9). No combinations with statistically significant increasing trends were detected.

Overview of Trends in Broilers

At the EU MS-group level, statistically significant decreasing trends for ciprofloxacin and tetracyclines were also revealed. Among the 29 countries reporting data from broilers, 58 decreasing and 13 increasing trends were statistically significant (Table 20; Figure 39). Italy and Portugal reported decreasing trends for all five antimicrobials assessed, while five countries showed decreasing trends for four[7] out of the five. In contrast, three countries[8] exhibited increasing trends for more than one antimicrobial, and in three countries, no statistically significant trends were observed.

[7]Ampicillin, cefotaxime, ciprofloxacin and tetracycline in Belgium, France, Ireland, Latvia, the Netherlands and Spain; ampicillin, ciprofloxacin, colistin and tetracycline in Romania.

[8]Cyprus, Denmark and Slovakia.

Overview of Trends in Turkeys

At the EU MS-group level, statistically significant decreasing trends were observed for ciprofloxacin and tetracyclines. Among the 11 individual countries reporting data for turkeys, 25 statistically decreasing trends and 2 increasing trends were revealed (Table 20; Figure 40). Spain reported decreasing trends for all five antimicrobials, while four countries reported decreases for four[9] of the five antimicrobials. No statistically significant trends were observed in Norway and Romania.

Trend slope changes identified

At the EU level, trend slope changes were identified for tetracycline resistance in *E. coli* from broilers and for tetracycline and ampicillin resistance in *E. coli* from turkeys using a change-point logistic model.[10] The previously declining EU-level resistance trends for these antimicrobials have stabilised and plateaued between 2022 and 2024. This pattern aligns with recent trend changes reported in several Member States, where stable or increasing resistance to ampicillin, ciprofloxacin and/or tetracyclines in *E. coli* from broilers[11] and turkeys[12] has been observed, underscoring the influence of country-specific dynamics on EU-wide patterns. However, these EU-level trend changes are based solely on 2022 and 2024 data, and further follow-up is needed to determine whether the plateau reflects a short-term fluctuation or a sustained interruption of the previous decreasing trend.

[9]Ampicillin, ciprofloxacin, colistin and tetracycline in France, Italy and Portugal; ampicillin, cefotaxime, ciprofloxacin and tetracycline in Hungary.

[10]Further information on change-point logistic model is presented in material and methods.

[11]Ampicillin, ciprofloxacin and tetracycline in Bulgaria, France and Italy.

[12]France, Italy, Poland and Romania.

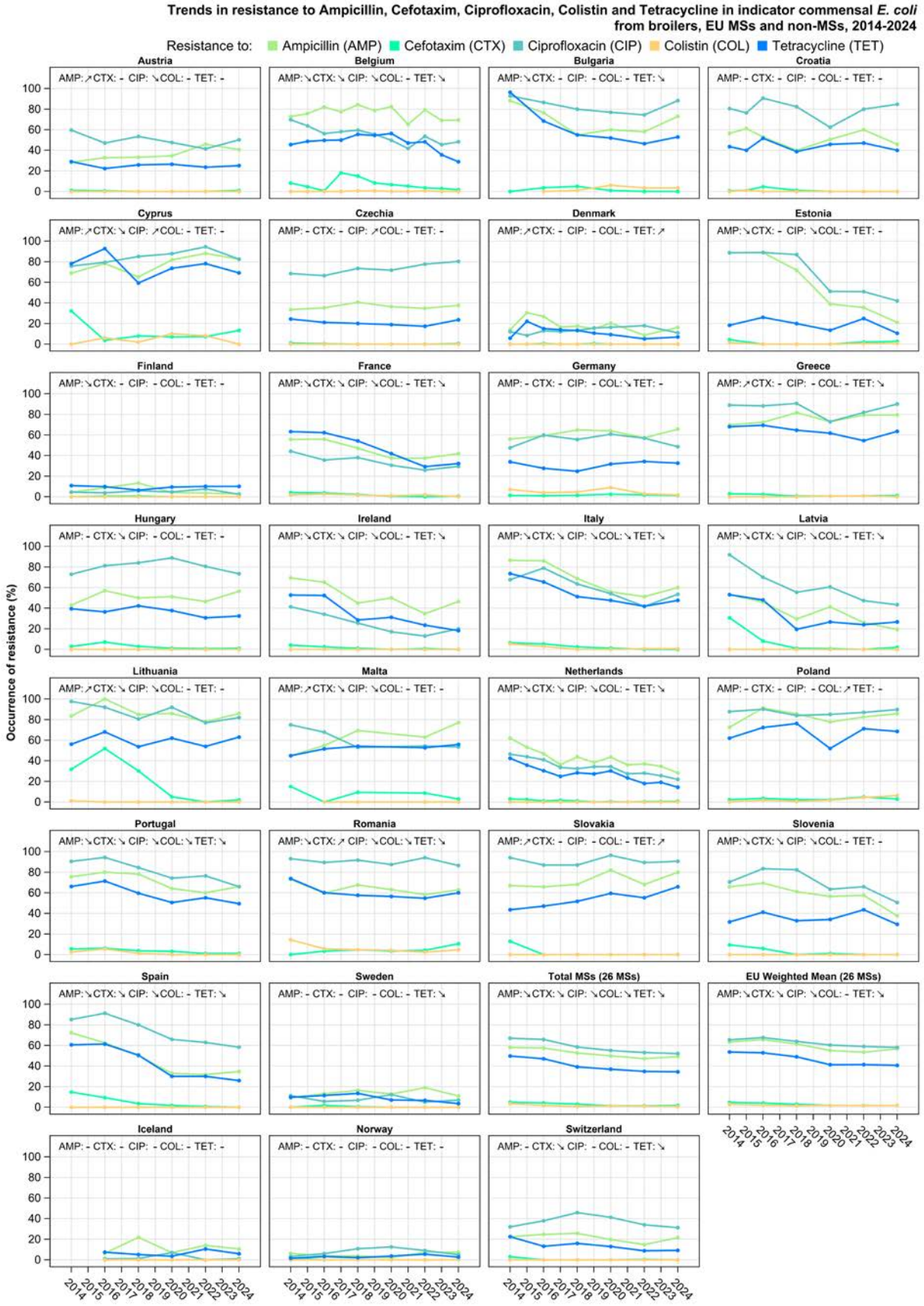


FIGURE 39 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, colistin and tetracycline in *E. coli* from broilers, EU MSs and non-MSs, 2014–2024.

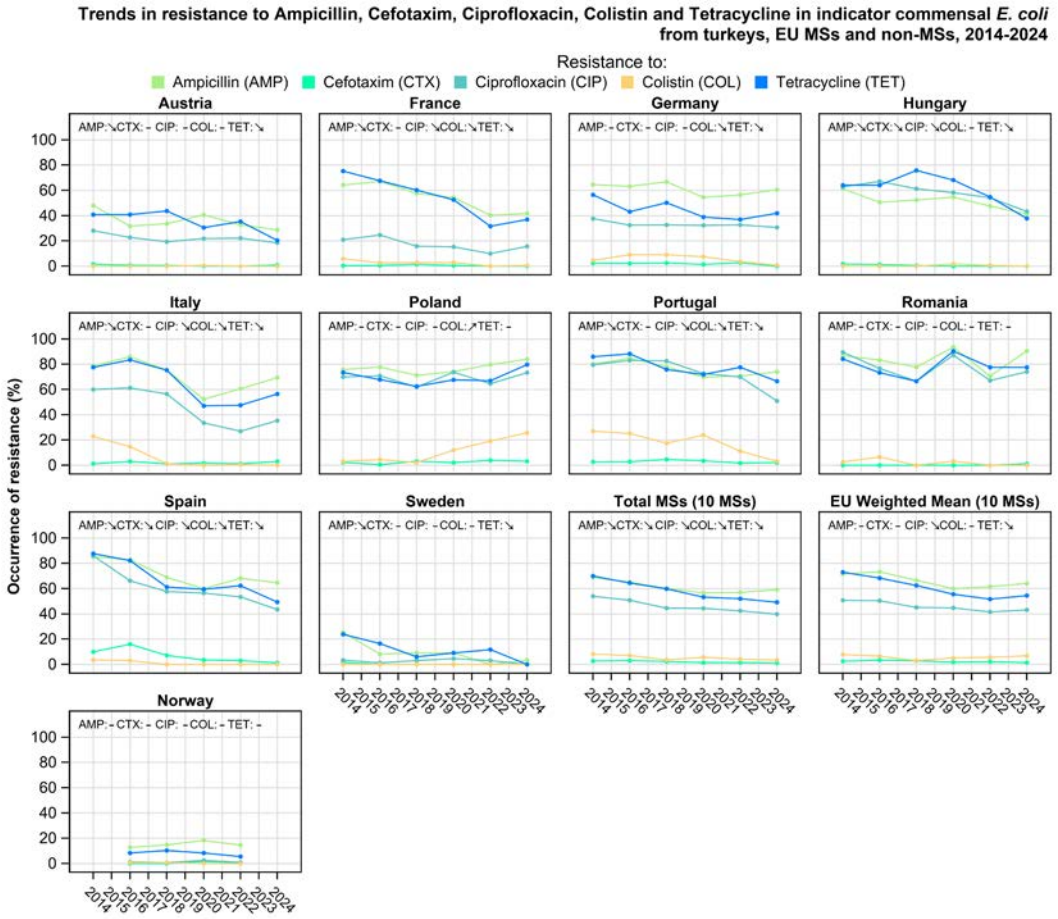


FIGURE 40 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, colistin and tetracycline in *E. coli* from turkeys, EU MSs and non-MSs, 2014–2024.

Pigs

At the EU MS-group level, statistically significant decreasing trends were revealed for colistin and tetracyclines. Among the 31 countries reporting data from pigs, 24 decreasing trends and 9 increasing trends were statistically significant (Table 20; Figure 41). Four countries reported significant decreases in resistance to three[13] of the five antimicrobials. Romania was the only country to register statistically significant increases for more than one substance. Notably, tetracycline resistance declined in 14 countries and increased in none. In 13 countries, no statistically significant trends were observed.

Calves

At the EU MS-group level, a statistically significant decreasing trends were revealed for colistin and tetracycline. Among the 12 individual countries reporting data from calves, 11 statistically significant decreasing trends and 3 increasing trends were identified (Table 20; Figure 42). Switzerland registered decreasing trends for three[14] of the five antimicrobials. In four countries, no statistically significant changes in resistance were observed.

[13]Ampicillin, cefotaxime and tetracycline in Belgium; ampicillin, ciprofloxacin and tetracycline in Cyprus and the Republic of North Macedonia; ampicillin, colistin and tetracycline in Spain.

[14]Ampicillin, ciprofloxacin and tetracycline.

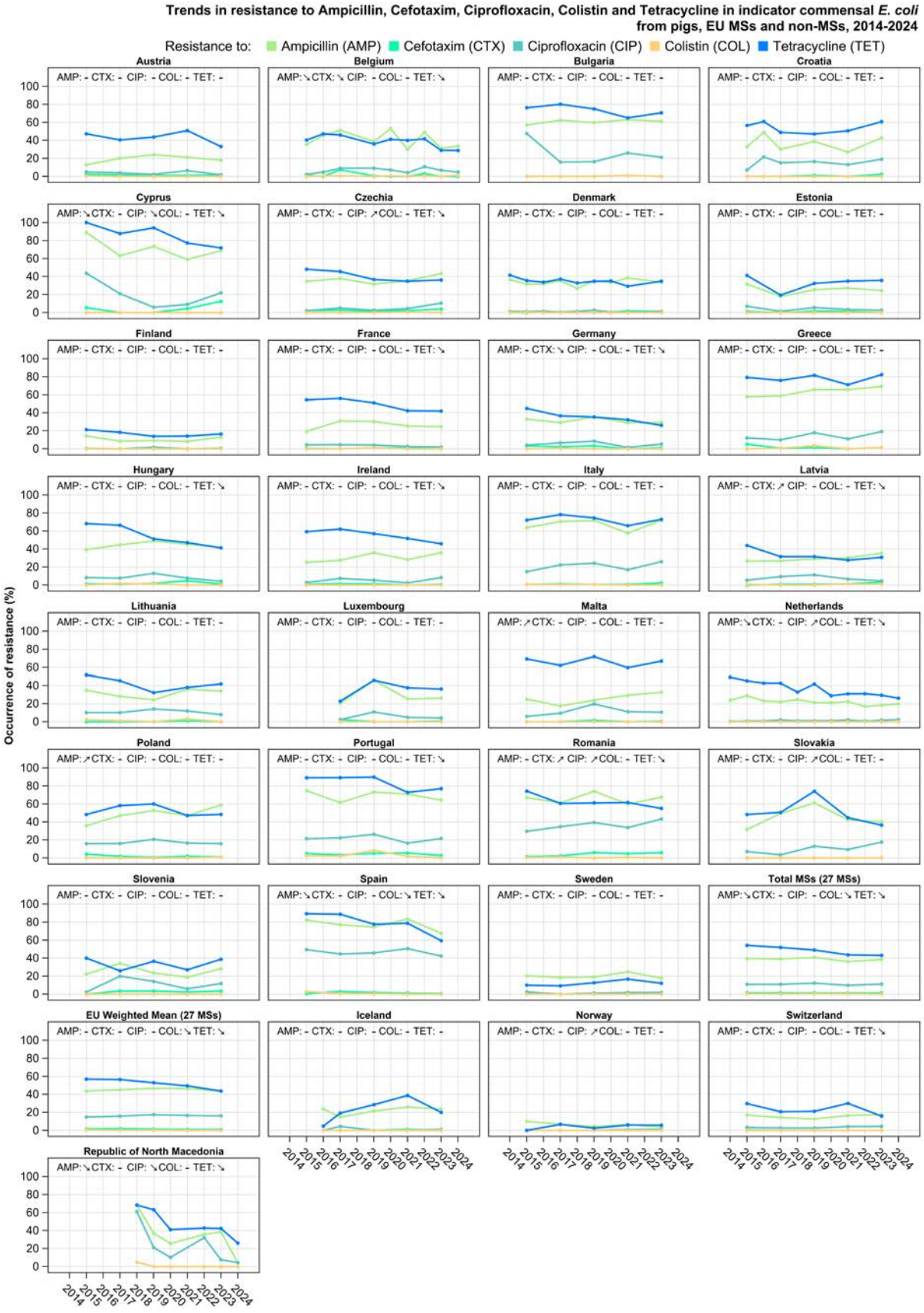


FIGURE 41 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, colistin and tetracycline in *E. coli* from pigs, EU MSs and non-MSs, 2014–2024.

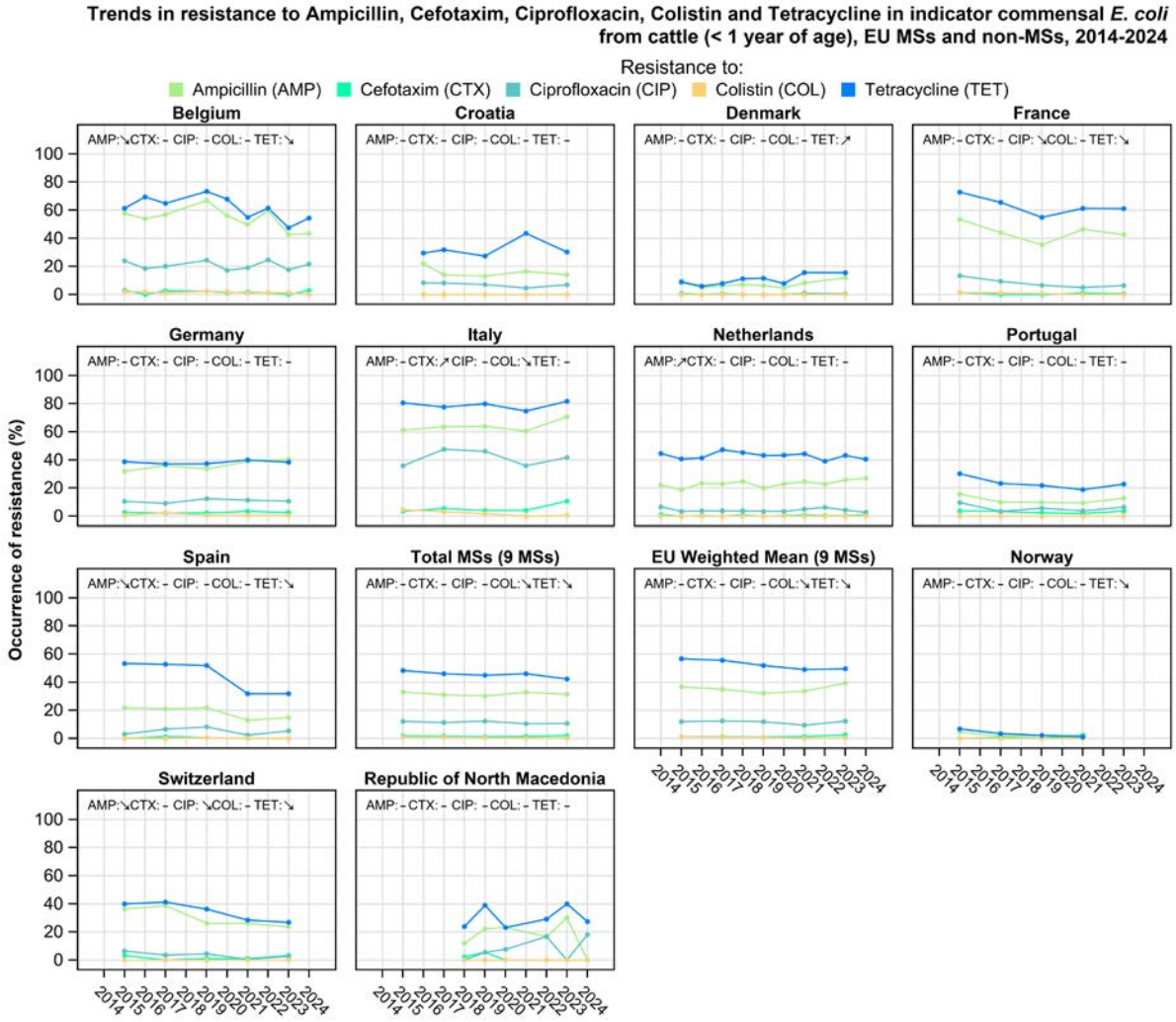


FIGURE 42 Trends in resistance to ampicillin, cefotaxime, ciprofloxacin, colistin and tetracycline in *E. coli* from calves, EU MSs and non-MSs, 2014–2024.

4.3.4 | Multidrug resistance

Multidrug-resistant isolates

MDR is defined as microbiological resistance to three or more antimicrobial classes within the harmonised testing panel. Across all reporting EU MSs and the United Kingdom (Northern Ireland), the median MDR in *E. coli* isolates was 41.2% in broilers, 33.6% in turkeys, in 2024, and 30.6% in pigs and 22.9% in calves, in 2023 (Annex C, tables T.1–T.4). For all targeted animal populations, MDR varied widely between reporting countries, ranging from 1.2% to 82.0% in broilers, 0.0% to 83.5% in turkeys, 6.5% to 68.8% in pigs and 6.6% to 72.4% in calves (Figure 43; Annex C, tables T.1–T.4).

Multidrug resistance patterns

A wide variety of resistance patterns was observed among the MDR isolates recovered from all targeted animal populations. The most common MDR pattern among isolates from broilers included ampicillin, ciprofloxacin, nalidixic acid, sulfamethoxazole, trimethoprim and tetracycline. The 10 most common MDR patterns contained various combinations of these substances, with two patterns also including chloramphenicol. These 10 patterns accounted for over 50% of the MDR isolates. Additionally, nine isolates showed resistance to eight or more antimicrobial classes.

The predominant MDR pattern among isolates from turkeys was ampicillin, ciprofloxacin and tetracycline, with or without nalidixic acid resistance. The 10 most common MDR patterns contained various combinations of these antimicrobials, often alongside chloramphenicol, sulfamethoxazole and/or trimethoprim. These 10 patterns accounted for over 50% of the MDR isolates. Additionally, nine isolates showed resistance to eight antimicrobial classes.

The most common MDR pattern among isolates from pigs was ampicillin, sulfamethoxazole, trimethoprim and tetracycline. The 10 most common MDR patterns included various combinations of these substances, with the addition of chloramphenicol, ciprofloxacin and/or nalidixic acid. These 10 patterns accounted for 65% of the MDR isolates. Additionally, five isolates showed resistance to eight or more antimicrobial classes.

The predominant MDR pattern among isolates from calves consisted of ampicillin, sulfamethoxazole, trimethoprim and tetracycline. The 10 most common MDR patterns included various combinations of these substances, often with chloramphenicol, ciprofloxacin, nalidixic acid and/or gentamicin. These 10 patterns accounted for 65% of MDR isolates. Additionally, three isolates showed resistance to nine different substances.

None of the MDR-resistant patterns included resistance to azithromycin, meropenem or tigecycline. Resistance to amikacin was present in 15 isolates (eight from pigs and seven from broilers). Colistin resistance was observed in a small number of MDR isolates from broilers ($n = 28$), pigs ($n = 3$) and calves ($n = 3$), but was more frequent in MDR isolates from turkeys, constituting 7.4% of cases ($n = 51$).

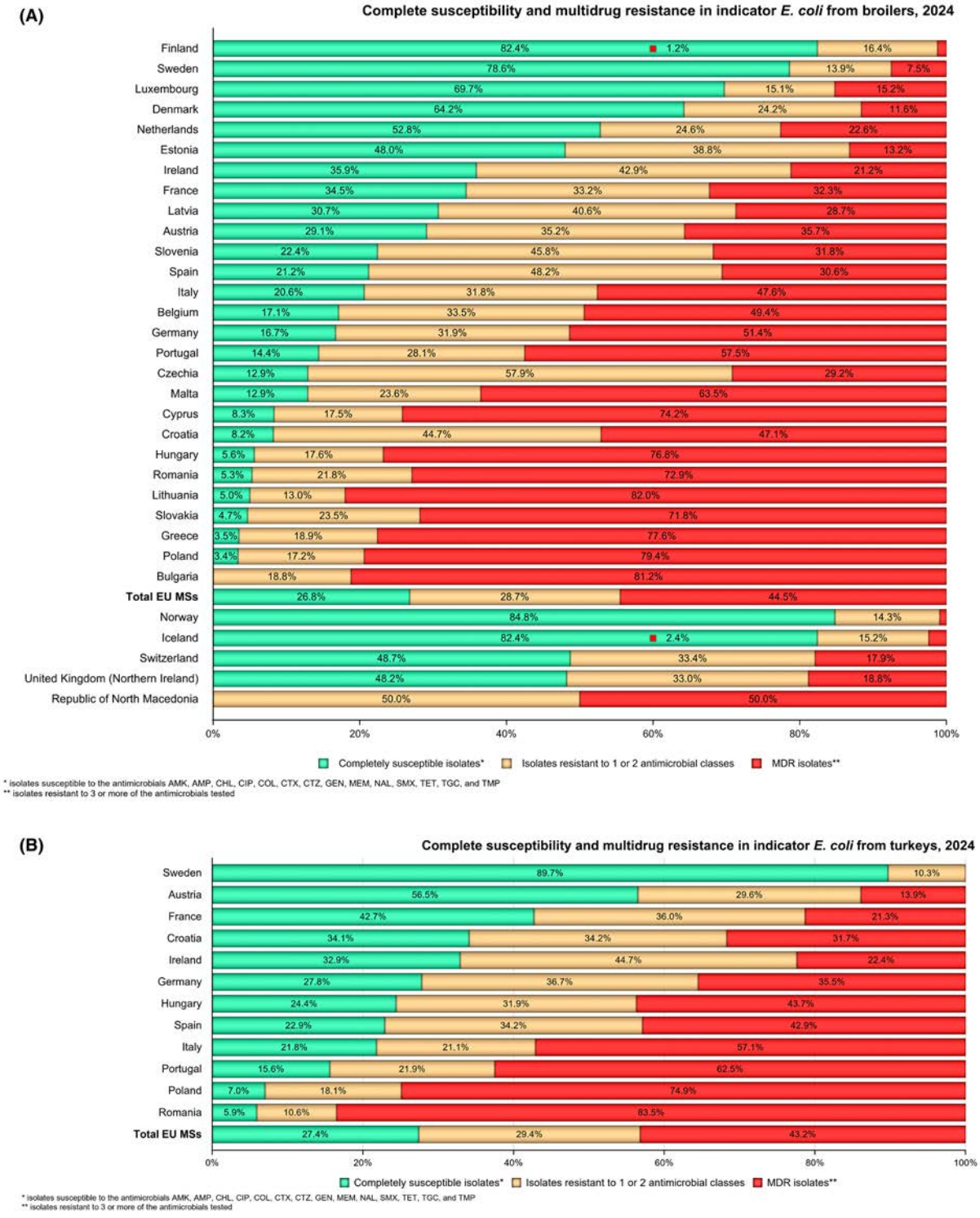


FIGURE 43 (Continued)

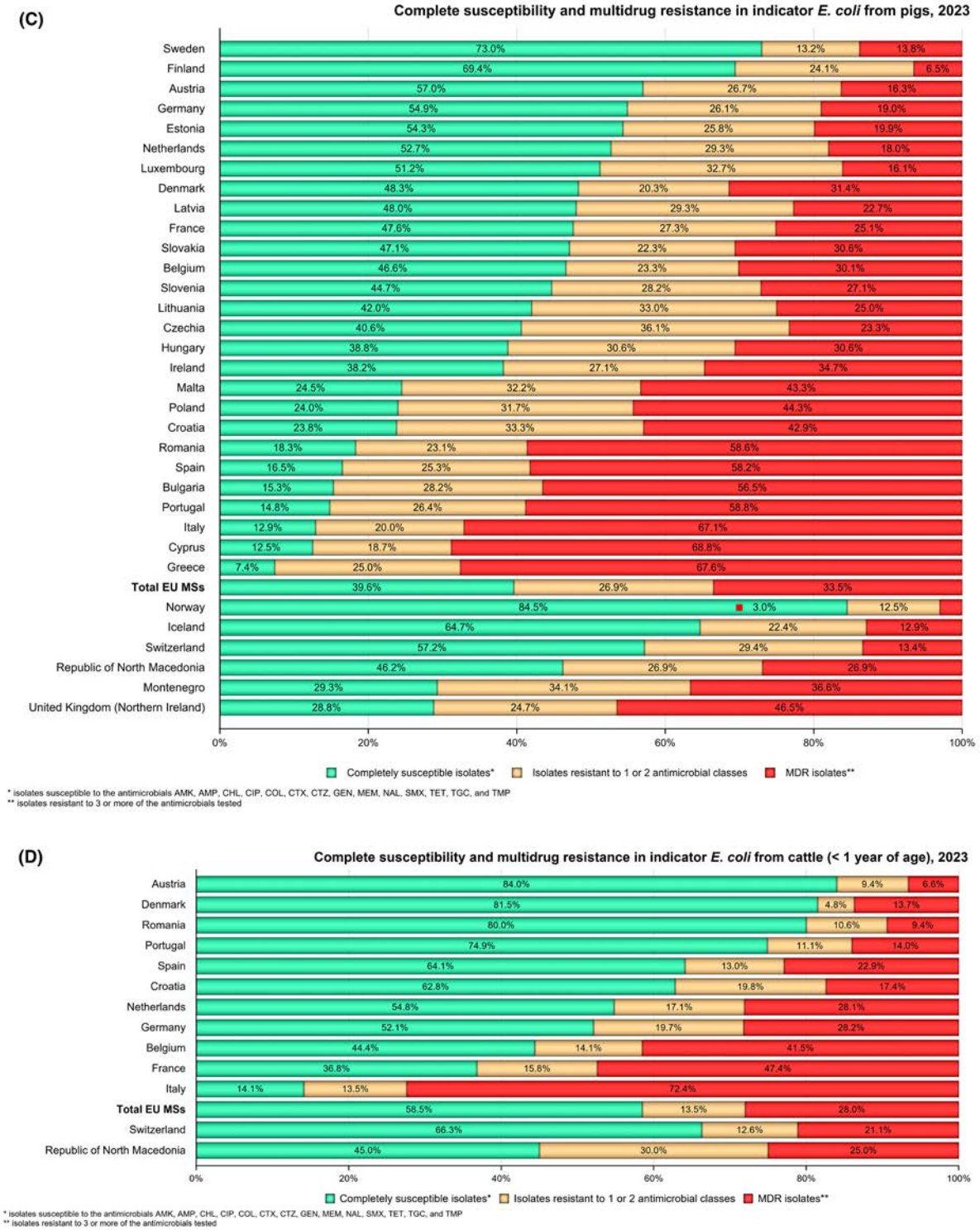


FIGURE 43 Occurrence of complete susceptibility to the antimicrobials tested, resistance to one or two substances or multidrug resistance in indicator commensal *E. coli* from targeted animal populations EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.

4.3.5 | Complete susceptibility

Completely susceptible isolates

Resistance can be assessed by evaluating the proportion of indicator *E. coli* isolates exhibiting susceptibility to all of a predefined set of antimicrobials, using ECOFFs for interpretation. Here, isolates susceptible to the antimicrobials AMK, AMP, CHL, CIP, COL, CTX, CTZ, GEN, MEM, NAL, SMX, TET, TGC and TMP are here referred to as CS.

Across all reporting EU MSs and the United Kingdom (Northern Ireland), the median proportion of CS *E. coli* isolates was 18.8% in broilers, 29.8% in turkeys, 41.3% in pigs and 62.8% in calves (Annex C, tables T.1–T.4). CS varied considerably between MSs and the United Kingdom (Northern Ireland), ranging from 0.0% to 82.4% in broilers, 5.9% to 89.7% in turkeys, 7.4% to 73.0% in pigs and 14.1% to 84.0% in calves. (Figure 43 and Figure 44; Annex C, tables T.1–T.4).

Trends in complete susceptibility

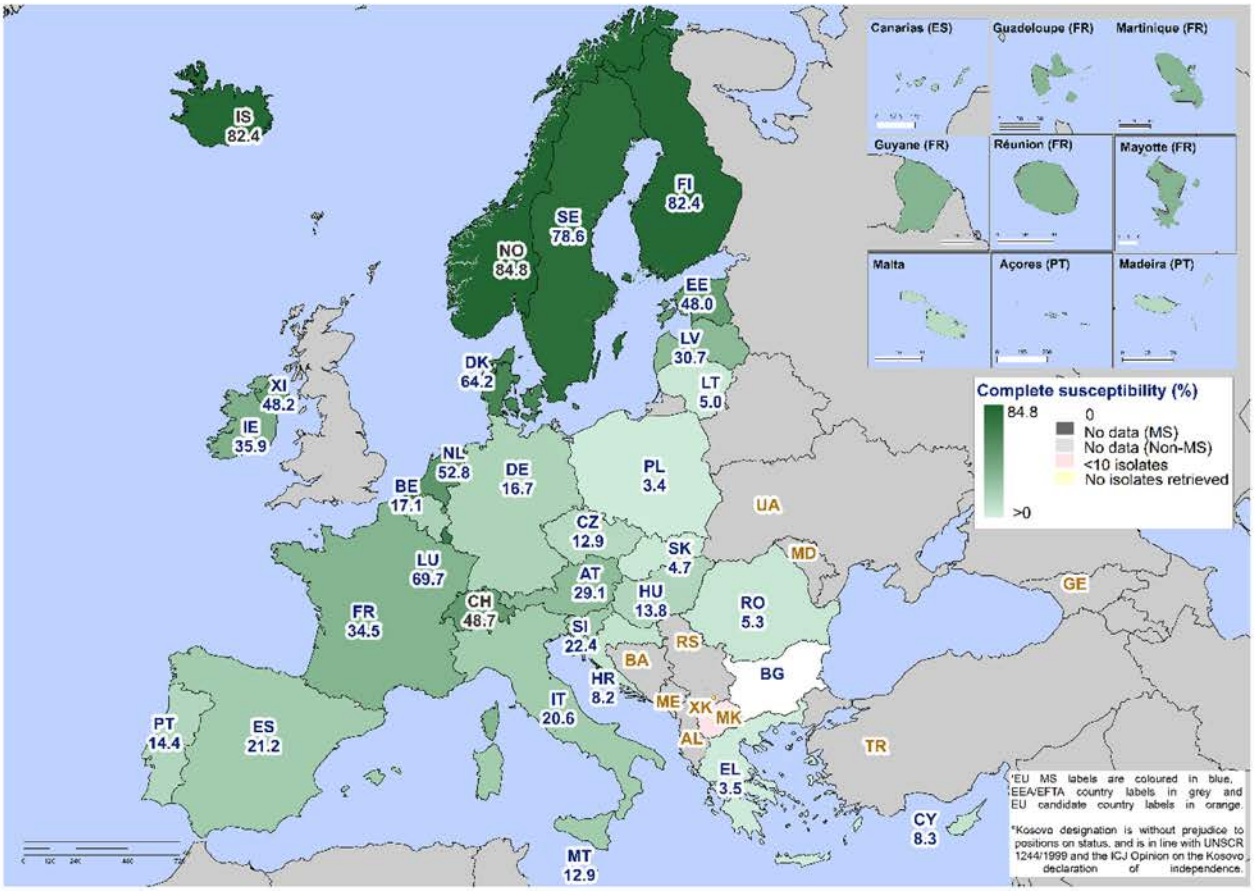
Temporal trends in CS in indicator *E. coli* from broilers, turkeys, pigs, and calves were assessed at both the EU MS-group level and for individual countries reporting data for at least 3 years between 2014 and 2024. At the EU MS-group level, resistance data were weighted by the size of national domestic animal populations to account for differences in population size, ensuring that each country contributes to the overall resistance estimate in proportion to its production.

Across the targeted animal populations, 32 statistically significant increasing trends and 3 decreasing trends in CS were identified among reporting countries (Figure 45). France, Portugal and Spain reported increasing trends in all four animal populations, while Ireland showed increases in both populations for which data were available. In several countries, CS levels have remained consistently high, limiting the potential for further improvement. At the EU MS-group level, statistically significant increasing trends were observed for all four animal populations.

In recent years, several MSs have reported stable or even decreasing levels of CS. Given the size of the animal populations and their relative contribution to the overall EU production, these national trends have substantially influenced the aggregated EU-level data. As a result, the previously increasing EU trend in CS has plateaued, highlighting the influence of country-specific dynamics on European resistance patterns.

At the EU level, change-point logistic models identified shifts in CS trends in *E. coli* from broilers and turkeys, with previously increasing trends plateauing between 2020 and 2024 for broilers and 2022–2024 for turkeys. As these observations are based on recent data points, further analysis is needed to determine whether the plateau reflects a short-term fluctuation or a sustained change in the underlying trend.

(A)



(B)

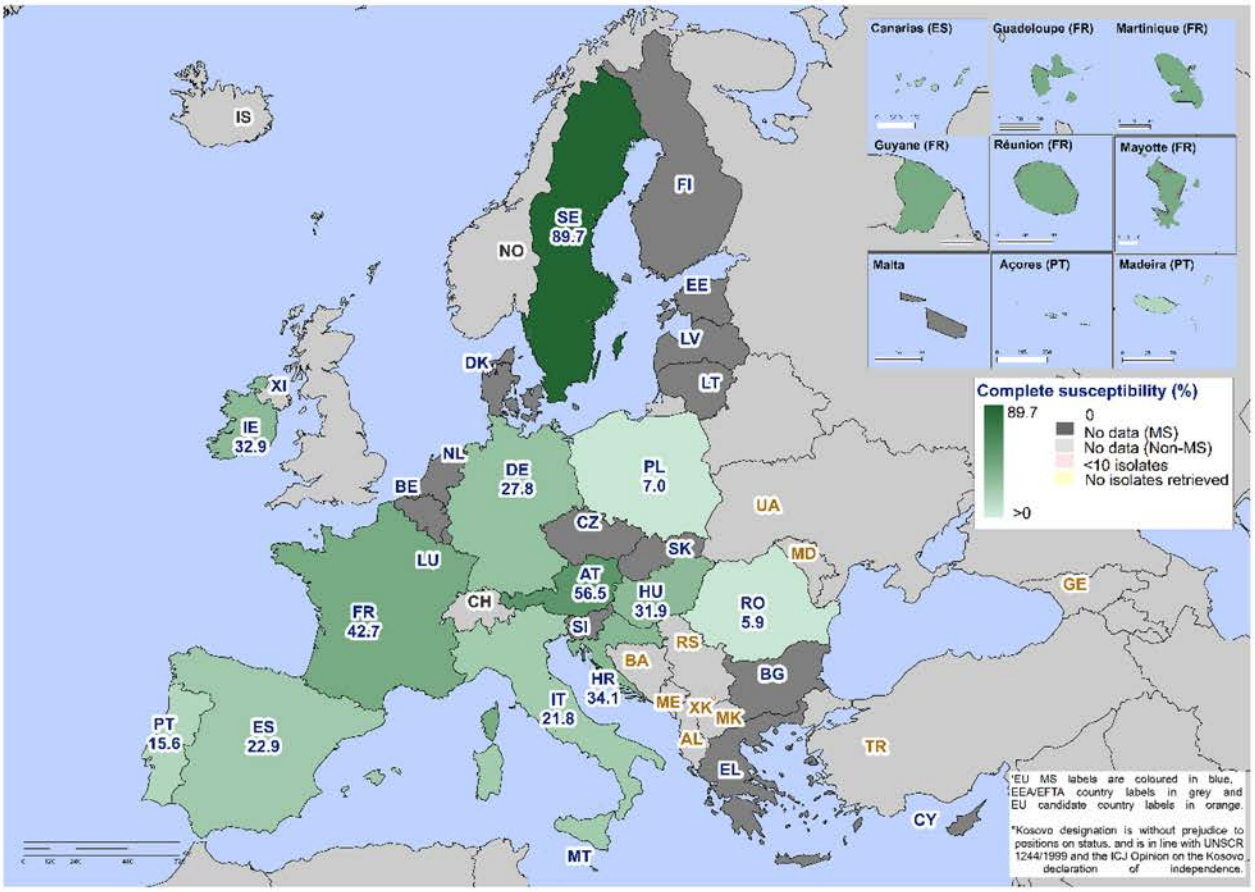
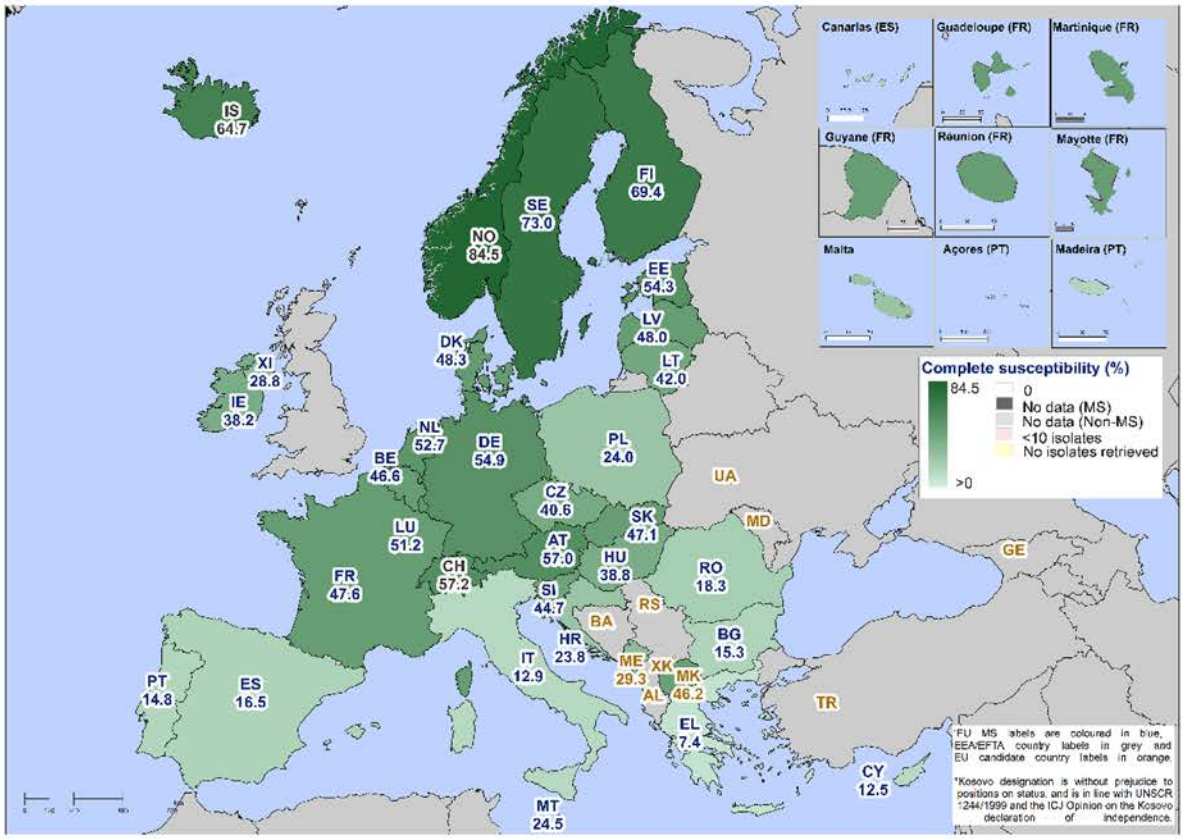


FIGURE 44 (Continued)

(C)



(D)

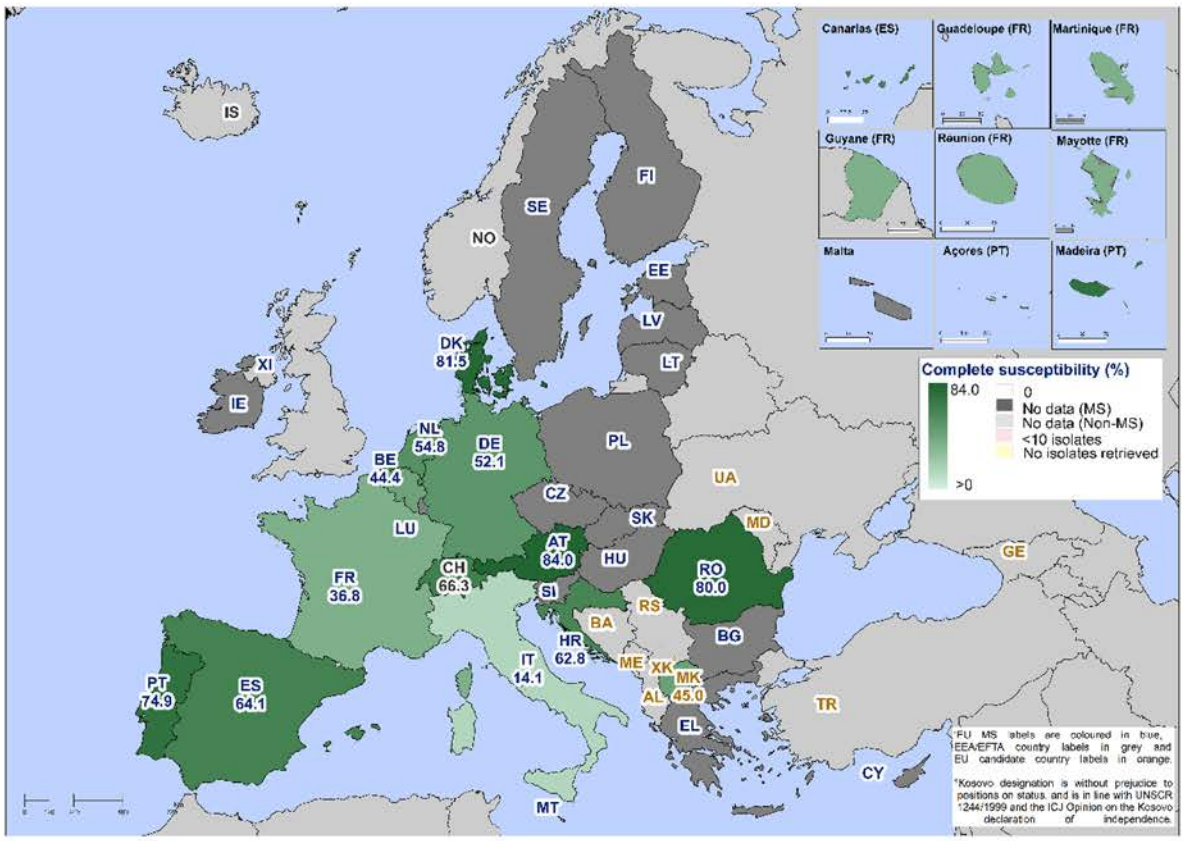


FIGURE 44 Spatial distribution of complete susceptibility to the antimicrobials tested in indicator commensal *E. coli* from broilers (A), turkeys (B), pigs (C), calves (D) EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.
The designation of Kosovo is without prejudice to positions on status and is in line with UNSCR 1244/1999 and the ICJ Opinion on the Kosovo declaration of independence.

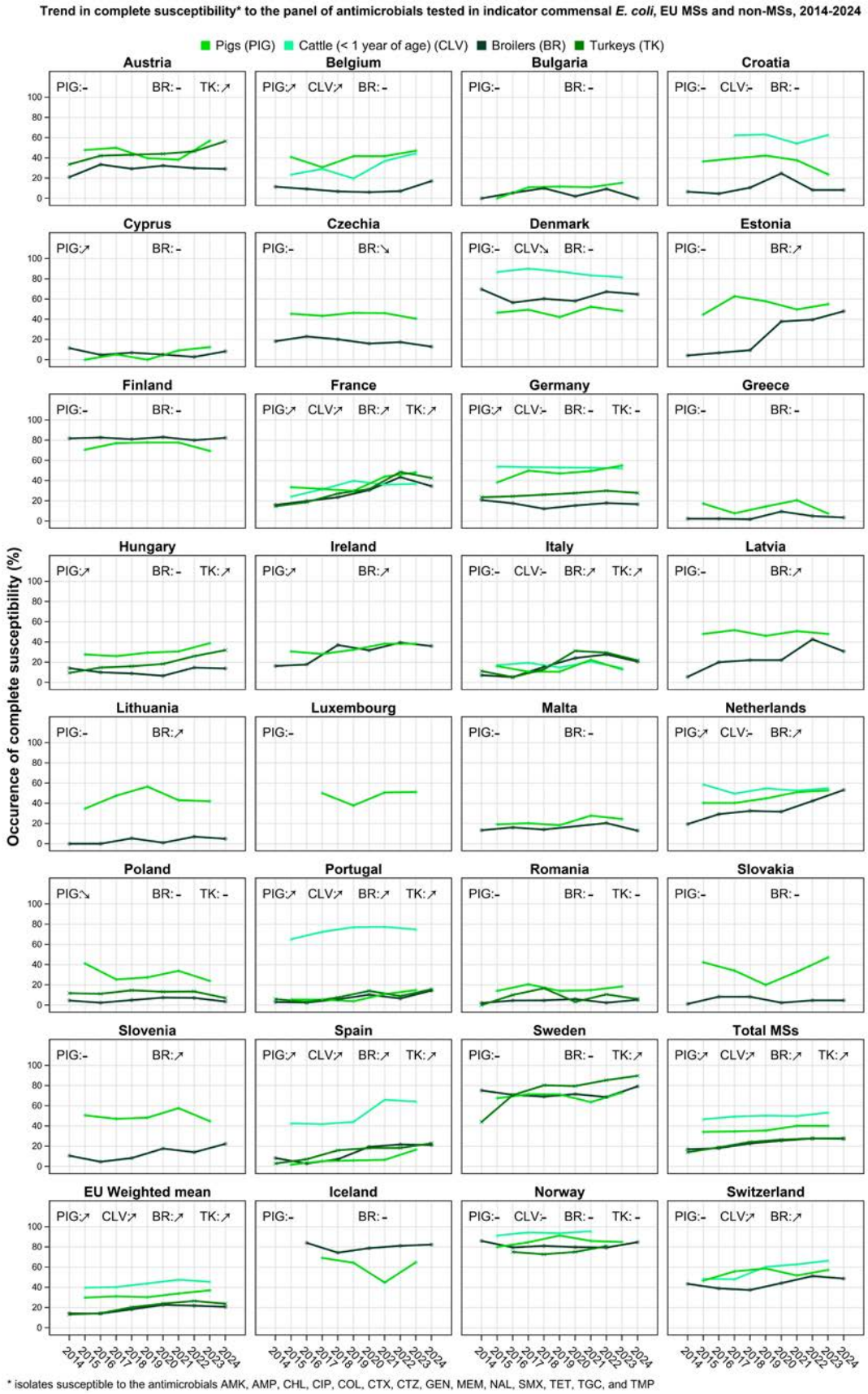


FIGURE 45 Trends in the occurrence of complete susceptibility to the panel of antimicrobials tested in indicator commensal *E. coli* from targeted animal populations, EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2014–2024.

4.3.6 | Key outcome indicator of complete susceptibility

The proportion of completely susceptible indicator *E. coli* isolates from targeted food-producing animals serves as a KOI_{CS} for the overall AMR situation in a country's food-producing animals. To account for differences in population size in a

country, KOI_{CS} was calculated as the weighted mean of the proportions of completely susceptible indicator *E. coli* isolates across animal populations, with weights based on the relative population sizes using the 'population correction unit' (PCU) established by EMA (2011).

KOI_{CS} were calculated using data reported over two consecutive years. Specifically, CS data from broilers and turkeys reported in even-numbered years were combined with data from fattening pigs and calves reported in the adjacent odd-numbered years. Data from broilers and pigs were included for all countries, while data from turkeys and calves were included only for countries that reported them. See also, Appendix A – Materials and methods as well as information about PCU from EMA (EMA, 2025).

The KOI_{CS} for EU MSs was 44.9% in 2023–2024, representing a statistically significant increase of 48% over the past decade. Marked variation in KOI_{CS} was observed among the 30 countries that reported consistently over the study period (Figure 46). In 2023–2024, KOI_{CS} levels were below 10% in 2 countries, 10%–20% in 5 countries, 20%–40% in 10 countries, 40%–60% in 9 countries, 60%–80% in 3 countries (Finland, Iceland and Sweden) and above 80% in 1 country (Norway).

Furthermore, a statistically significant increasing trend in KOI_{CS} was observed in 11 countries, with several showing substantial improvements. No country reported a statistically significant decreasing trend in KOI_{CS}. However, the increasing EU-level trend in KOI_{Cs} has plateaued between the 2022–2023 and 2023–2024 data points, as indicated by a change-point logistic model. This aligns with similar plateaus or even decreases reported in CS for broilers and turkeys, as well as for several Member States—including France, Spain, Poland, Latvia, Italy, Germany and Bulgaria – underscoring the influence of country-specific dynamics on the overall European pattern.

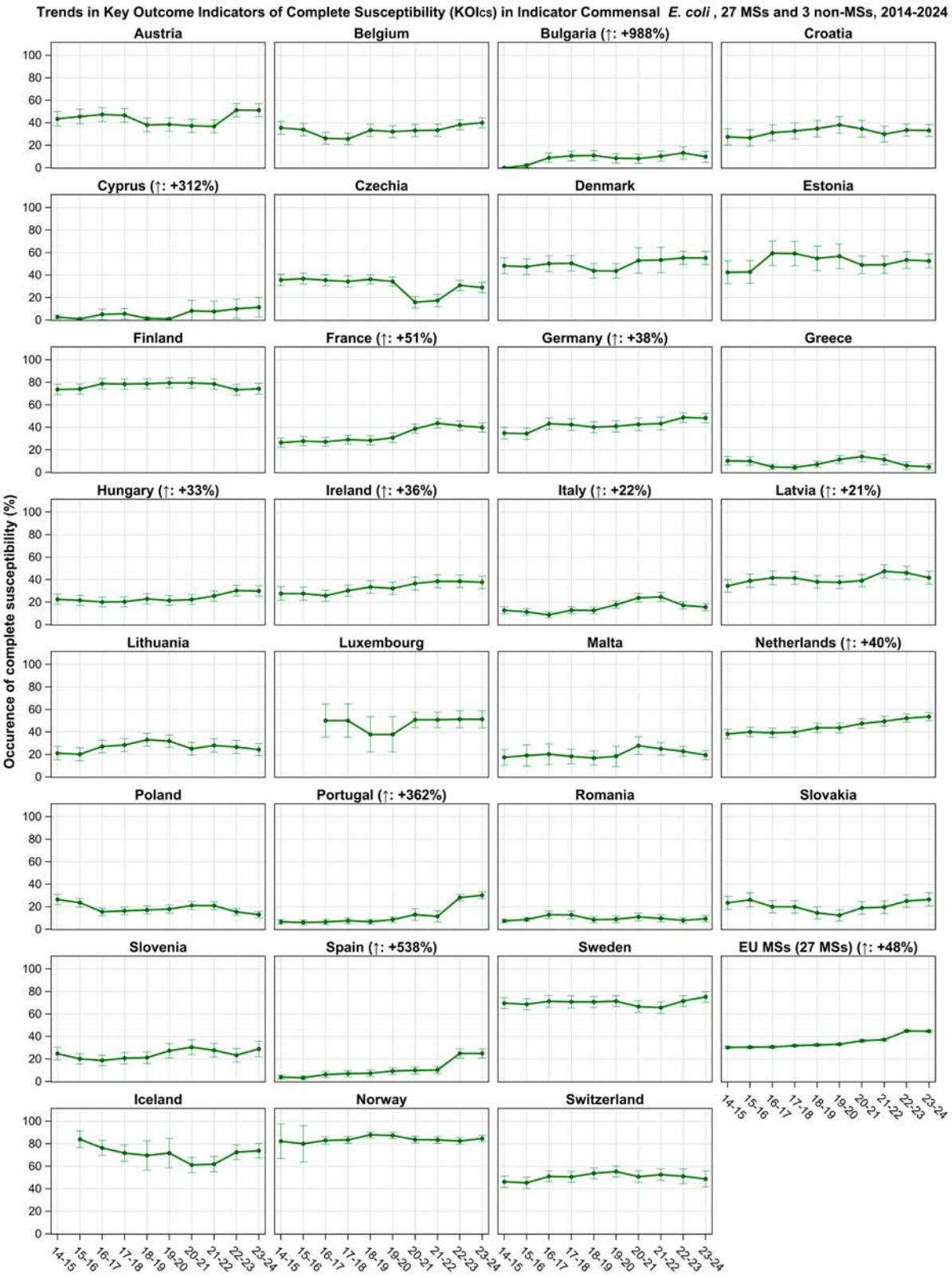


FIGURE 46 Trends in the key outcome indicator of complete susceptibility (KOI_{CS}) in indicator commensal *E. coli* from targeted animal populations EU MSs and non-MSs, 2014–2024.

4.4 | Discussion

E. coli, an abundant and ubiquitous commensal bacterial species, has been selected as a reporting organism due to its relevance in reflecting the overall antimicrobial resistance situation, including transmissible genes, in food-producing animals. As *E. coli* is ubiquitous, the data is more stable than what can be the case for less abundant zoonotic bacterial species. Given the ubiquitous presence of commensal *E. coli* in the intestinal tract of healthy animals included in the monitoring, potential differences in isolation frequency across countries or animal species are considered highly unlikely to impact the occurrence of resistance in the isolates analysed.

Resistance to antimicrobials classified as **WHO highest priority critically important** and critically important antimicrobials is of particular concern due to the potential risk of transmission to humans via the food chain. At the EU level, no significant differences were observed in the **low-level occurrence of resistance** to cefotaxime, ceftazidime, azithromycin and colistin across the four animal populations monitored. Meropenem resistance was not identified in any isolates of indicator *E. coli*. Carbapenem resistance remains uncommon in commensal *E. coli* from food-producing animals in Europe, based on non-selective culturing methods of isolates assessing resistance to third-generation cephalosporins (cefotaxime and ceftazidime) and carbapenems. Additionally, caecal samples are cultured on selective media specifically targeting *E. coli* resistant to third-generation cephalosporins and carbapenems, facilitating detection of carbapenem-resistant strains, which have been detected particularly in pigs. Detailed results from selective monitoring are presented in Chapter 5 – Extended-spectrum beta-lactamase (ESBL)-, AmpC- and /or carbapenemase (CP)-producing *E. coli*.

At the EU level, median resistance levels to **ciprofloxacin** and **nalidixic acid** in commensal *E. coli* were low in pigs and calves, but high in turkeys and high/very high in broilers. Notably, a substantial proportion of isolates across all animal populations exhibited resistance to ciprofloxacin without concurrent resistance to nalidixic acid; a resistance pattern which generally indicates the presence of transmissible genes mediating quinolone resistance (Jacoby et al., 2014).

The median levels of **azithromycin** resistance were rare, very low or low in all targeted animal populations. However, higher resistance levels were reported in some countries for all targeted animal populations. Although azithromycin, an azalide within the macrolide class, is not used in animals, the use of other related macrolides in food-producing animals may exert selective pressure, contributing to the emergence of azithromycin resistance. Across all reporting MSs, the median level of resistance to **colistin** was rare in all targeted animal populations, although some countries reported higher levels.

At the MS-group level, resistance to antimicrobials commonly used, **ampicillin**, **sulfamethoxazole**, **trimethoprim**, as well as **tetracyclines**, was generally common in indicator *E. coli* for all targeted animal populations, apart from trimethoprim resistance in isolates from calves, where levels were lower.

The occurrence of resistance to most antimicrobials varied markedly between reporting countries. In pigs and broilers, the situation was generally more favourable in Northern Europe than in Southern and Eastern Europe. A similar, though less pronounced, pattern was discerned for turkeys.

The frequent occurrence of resistance to these substances in indicator *E. coli* likely reflects both historical and ongoing widespread use of these antimicrobials in food-producing animals across several MSs (ECDC, EFSA and EMA, 2024; Queenan et al., 2016). Disparities in the levels of consumption of antimicrobials across animal populations, but also possibly the modes of administration, are likely mirrored in the differences in resistance observed between animal species. In poultry, flock treatment is almost exclusively practised, whereas in some countries, pigs and calves are typically treated individually.

The frequent occurrence of tetracycline, ampicillin, sulfamethoxazole and trimethoprim as core components of MDR patterns in *E. coli* across all animal populations, along with the common inclusion of (fluoro)quinolones (ciprofloxacin/nalidixic acid) in MDR profiles from broilers and turkeys, likely reflects their extensive and prolonged use in several countries. Additionally, the co-localisation of resistance genes conferring resistance to these substances on mobile genetic elements facilitates co-selection, further contributing to the persistence and dissemination of MDR.

In several countries and at the EU MS-group level, statistically **significant decreasing trends** in resistance in indicator *E. coli*, notably in broilers and turkeys, were revealed. For several antimicrobials and countries, statistically significant associations were demonstrated between trends in antimicrobial use in food-producing animals and the corresponding levels of resistance in indicator *E. coli* isolates (ECDC, EFSA and EMA, 2024). These reductions in resistance are considered to be largely attributable to the sustained overall decline in sales of antimicrobials for animal use, as documented in the ESUAvet report (EMA, 2025).

To address the challenges posed by co-selection and co-resistance in AMR monitoring and in assessing the relationship between antimicrobial consumption (AMC) and resistance, the occurrence of CS in indicator *E. coli* has been consistently included in the harmonised AMR monitoring in food-producing animals. The levels of CS vary markedly across countries' animal populations. In general, higher proportions of completely susceptible isolates from pigs, broilers and to a lesser extent, turkeys were more commonly observed in Northern Europe compared to Southern and Eastern regions. Contrastingly, at the individual country level, the picture was more complex. For example, Austria, Denmark, Portugal and Romania recorded CS levels exceeding 70%, indicating that resistance can differ markedly between animal production sectors within the same country. Given the demonstrated association between overall AMC and CS (ECDC, EFSA and EMA, 2024), the findings suggest that AMC varies not only between countries but also across different animal populations within the same country. The ongoing implementation of Regulation (EU) 2019/6 on veterinary medicinal products will enable future analyses to directly compare resistance levels with antimicrobial usage by animal species, providing further insights into AMR variations within and between countries.

Trends in CS at the level of individual animal populations serve as a valuable complement to KOIcs, ensuring that any positive or negative developments in animal populations of smaller relative sizes are not unnoticed. KOIcs has been retained as the primary indicator for assessing AMR in food-producing animals. It is particularly relevant for evaluating overall AMR-related risks in food-producing animals, as it accounts for differences in the relative size of food animal populations within each country.

Marked variations in KOIcs were registered, ranging from < 10% in two MSs to > 80% in one country (Norway). The KOIcs has been used to assess the development of AMR in relation to the overall AMC in food-producing animals (ECDC, EFSA and EMA, 2024; Queenan et al., 2016), and a statistically significant negative association has been demonstrated between KOIcs

and overall AMC. A reduction in AMC in food-producing animals is expected to improve KOIcs, a trend already observable in several countries alongside decreasing overall AMC (ECDC, EFSA and EMA, 2024).

Statistically significant decreases in resistance to individual substances indicate progress in several countries, corroborated by significant increases in CS and KOIcs at both the national and EU MS-group levels. However, trends appear to stagnate among broilers and turkeys in some countries, leading to a plateau in EU-level KOIcs between 2022–2023 and 2023–2024. This coincides with a 5% rise in antimicrobial consumption (AMC) in food-producing animals from 2023 to 2024, interrupting a long-term downward trend (2010–2022) (EMA, 2025). While it remains unclear whether this reflects a temporary fluctuation or a new pattern, it needs further attention in the upcoming years. Continued monitoring and efforts are warranted to sustain these favourable conditions and, where possible, achieve further reductions in resistance.

Monitoring AMR in imported fresh meat sampled at BCP

***Salmonella* spp.**

In 2024, *Salmonella* isolates from imported fresh meat from broilers sampled at the BCPs were reported by seven MSs: France (*N* = 1), Germany (*N* = 5), Ireland (*N* = 1), the Netherlands (*N* = 28), Poland (*N* = 3), Romania (*N* = 1), Spain (*N* = 2) and the United Kingdom (Northern Ireland) (*N* = 1). Overall, isolates exhibited very high levels of resistance to tetracyclines (64.3%), sulfonamides (64.3%), and ampicillin (59.5%). In contrast, resistance to amikacin (2.4%), chloramphenicol (4.8%), colistin (2.4%) and trimethoprim (7.1%) was low, and no resistance to gentamicin and azithromycin was detected. Very high resistance was also observed for ciprofloxacin (61.9%), nalidixic acid (57.1%) and the same occurred when looking at resistance to third-generation cephalosporins (57.1% for cefotaxime and ceftazidime). No resistance to meropenem was reported; however, tigecycline resistance in *Salmonella* isolates from imported fresh meat from broilers was reported at a high level (26.2%). Germany and the Netherlands reported WGS data and identified $\boldsymbol{bla_{CMY\text{-}2}}$ in two and 15 *Salmonella* isolates, respectively. No *Salmonella* data from imported fresh turkey meat were reported in 2024.

Indicator commensal E. coli

Occurrence of resistance

In total, 14 MSs reported data on 1075 indicator commensal *E. coli* isolates from imported fresh meat across the four monitored animal categories. The majority were derived from broiler meat (*N* = 378), cattle meat (*N* = 349) and pig meat (*n* = 298), with fewer isolates (*N* = 50) from turkey meat (Table; Annex C, tables 5–8).

Among *E. coli* isolates from imported **fresh broiler meat**, resistance was high to very high for **ampicillin, ciprofloxacin, nalidixic acid, sulfamethoxazole, trimethoprim** and **tetracycline**. Moderate resistance levels were observed for **gentamicin**, **cefotaxime** and **ceftazidime**. A similar pattern was noted among isolates from imported **fresh turkey meat**, with high to very high resistance to ampicillin, chloramphenicol, ciprofloxacin, nalidixic acid, sulfamethoxazole and trimethoprim, and extremely high resistance to tetracyclines. Resistance to trimethoprim was moderate. However, resistance to cefotaxime and ceftazidime was low. In isolates from imported **fresh bovine meat**, resistance was generally uncommon, with median levels of resistance classified as rare, very low or low. In contrast, isolates from imported **fresh pig meat** showed high median resistance to tetracyclines, and moderate median resistance to ampicillin, sulfamethoxazole and trimethoprim (Table 21).

Resistance to **meropenem** was not detected in any isolates from imported fresh meat. Resistance to **amikacin**, **colistin** and **azithromycin** was observed only in a few isolates across the different meat categories, with occurrence ranging from 0.0% to 2.0% (Annex C, tables 5–8).

Overall resistance to **nalidixic acid** and **ciprofloxacin** was very low to low in isolates from imported cattle meat and low in those from imported pig meat (Annex C, tables 5–6). In contrast, resistance levels to both substances were high in isolates from imported fresh broiler and turkey meat, ranging from 31.7% to 40.0% (Annex C, tables 7–8).

Overall resistance for **cefotaxime** and **ceftazidime** was moderate in isolates from imported broiler meat, but very low to low in isolates from imported bovine, pig and turkey meat (Annex C, tables 5–8).

Combined resistance to ciprofloxacin and cefotaxime

Microbiological combined resistance to ciprofloxacin and cefotaxime was low in *E. coli* isolates from imported fresh broiler meat (7.4%) and fresh turkey meat (2.0%), whereas it remained very low in isolates from fresh pig and cattle meat (Table 1; Annex C, tables 5–8).

TABLE 21 Combined resistance to ciprofloxacin and cefotaxime in indicator *E. coli* from imported fresh meat from broilers, turkeys, pigs and cattle, applying ECOFFs and clinical breakpoints, as issued by EUCAST, EU MSs and non-MSs, 2023–2024.

	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**
Pig meat, 2023[a]	2	0.7	0.2, 2.4	1	0.3	0.1, 1.9
Cattle meat, 2023[b]	1	0.3	0.1, 1.6	0	0.0	0.0, 1.1
Broiler meat, 2024[c]	28	7.4	5.2, 10.5	15	4.0	2.4, 6.4
Turkey meat, 2024[d]	1	2.0	3.5, 10.5	1	2.0	3.5, 10.5

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

[a]4 MSs and the United Kingdom (Northern Ireland); 298 isolates investigated.

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

[c]13 MSs and the United Kingdom (Northern Ireland); 378 isolates investigated.

[d]4 MSs; 50 isolates investigated.

Complete susceptibility and multidrug resistance.

Across all reporting MSs and the United Kingdom (Northern Ireland), the proportion of CS *E. coli* isolates from imported fresh meat was 29.9% for broiler meat, 12.0% for turkey meat, 55.7% for pig meat and 88.0% for cattle meat (Annex C, tables 5–8).

The level of MDR among indicator *E. coli* isolates from imported broiler and turkey meat was high, at 36.0% and 58.0%, respectively. In contrast, MDR levels were low in isolates from imported bovine meat (4.0%), and moderate in those from fresh pig meat was moderate (20.8%), (Annex C, tables 5–8).

The MDR patterns in *E. coli* isolates from imported fresh broiler meat were most frequently included ampicillin, sulfamethoxazole and trimethoprim, often combined with tetracycline. Resistance to ciprofloxacin and nalidixic acid was also a common among MDR isolates, occasionally without sulfamethoxazole and trimethoprim. In isolates from imported turkey meat, MDR patterns predominantly involved ampicillin, sulfamethoxazole, trimethoprim and tetracycline. For pig meat isolates, sulfamethoxazole, trimethoprim and tetracycline were most common, often in combination with ampicillin. Similarly, MDR isolates from cattle meat frequently exhibited resistance to ampicillin, sulfamethoxazole, trimethoprim and tetracycline.

None of the MDR patterns included resistance to amikacin or azithromycin. Resistance to tigecycline was observed in only two isolates from pig meat. Colistin resistance was present in two isolates from fresh broiler meat and one from bovine meat but was absent in isolates from fresh pig or turkey meat.

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

In 2024, 24 presumptive ESBL-/AmpC-/CP-producing *Salmonella* spp. isolates were detected in imported broiler meat, including 19 $\boldsymbol{bla_{CMY-2}}$ carrying isolates reported by Germany (2 *S*. Minnesota, 2 *S*. Typhimurium (4,12)) and the Netherlands (13 *S*. Minnesota, 2 *S*. Heidelberg) (Table 22, see also EFSA and ECDC, 2025b).

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

In 2023 and 2024, 43 presumptive ESBL-/AmpC-/CP-producing *E. coli* isolates were detected in imported broiler, turkey, pig and bovine meat sampled at BCPs (Table 22). Consistent with meat sampled at retail, these ESBL-/AmpC-/CP-producing *E. coli* were more frequently identified in imported poultry meat than in imported meat from pigs and bovines (Annex D.1 – Table 1).

In 2024, Germany and the Netherlands reported WGS data for 20 isolates recovered from imported broiler meat, with no isolates detected from imported turkey meat. The most common gene was $\boldsymbol{bla_{CTX-M-55}}$ ($n = 12$), followed by $\boldsymbol{bla_{CTX-M-8}}$ ($n = 5$), $\boldsymbol{bla_{CTX-M-2}}$ ($n = 2$) and $\boldsymbol{bla_{CMY-2}}$ ($n = 1$). In 2023, the Netherlands reported WGS data for isolates from imported pig meat, identifying one isolate harbouring $\boldsymbol{bla_{CTX-M-14}}$ and another carrying $\boldsymbol{bla_{CTX-M-15}}$ (Annex D.3 – Table 1).

TABLE 22 Summary of presumptive ESBL-, AmpC- or CP-producing *Salmonella* spp. and *E. coli* from imported fresh meat sampled at border control posts, routine monitoring, EU MSs, the United Kingdom (Northern Ireland), 2023-2024.

	ESBL and/or AmpC[a]	ESBL[b]	AmpC[c]	ESBL+ AmpC[d]	CP[e]
Matrix	**% *R* (*n*)**	**% *R* (*n*)**	**% *R* (*n*)**	**% *R* (*n*)**	**% *R* (*n*)**
***Salmonella* spp.**					
Broiler meat at BCP, 2024 (*N* = 25, 5 MSs)	96 (24)	0 (0)	88 (22)	8 (2)	0 (0)
Indicator commensal *E. coli*					
Broiler meat at BCP, 2024 (*N* = 39, 8 MS)	97,4 (38)	79,5 (31)	15,4 (6)	2,6 (1)	0 (0)
Turkey meat at BCP, 2024 (*N* = 2, 1 MS)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Pig meat at BCP, 2023 (*N* = 4, 3 MSs)	100 (4)	75 (3)	25 (1)	0 (0)	0 (0)
Bovine meat at BCP, 2023 (*N* = 2, 2 MSs)	50 (1)	50 (1)	0 (0)	0 (0)	0 (0)

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

[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).

[b]All 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 genes.

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

In 2023, 15 countries (Belgium, Denmark, Estonia, France, Germany, Ireland, Italy, Malta, the Netherlands, Portugal, Romania, Spain, Sweden, Switzerland and the United Kingdom (Northern Ireland)) collected samples of imported pig and bovine meat at BCPs. In 2024, 14 countries (Belgium, Estonia, France, Germany, Ireland, Italy, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Spain and United Kingdom (Northern Ireland) reported sampling of broiler and turkey meat.

In 2024, 56.5% of broiler meat isolates (191/338) and 60% of turkey meat isolates (24/40) tested positive for presumptive ESBL-/AmpC-/CP-producing *E. coli*. In contrast, positivity rates were lower in 2023 for pig and bovine meat samples, with 4.7% (12/254) from pig meat and 0.4% (3/742) from bovine meat (Annex D.1 – Table 22).

In 2024, five countries (Belgium, Germany, Italy, the Netherlands and the United Kingdom (Northern Ireland)) reported WGS data from isolates collected during the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* in imported meat, compared to only two countries (Germany and the Netherlands) in 2023 (Annex D.3 – Table 16). In imported broiler meat, $\boldsymbol{bla_{\text{CTX-M-55}}}$ was the most commonly reported gene ($n = 47$), followed by $\boldsymbol{bla_{\text{CTX-M-8}}}$ ($n = 14$), $\boldsymbol{bla_{\text{CMY-2}}}$ ($n = 9$), $\boldsymbol{bla_{\text{CTX-M-2}}}$ ($n = 9$), $\boldsymbol{bla_{\text{CTX-M-65}}}$ ($n = 3$), $\boldsymbol{bla_{\text{CTX-M-15}}}$ ($n = 2$), $\boldsymbol{bla_{\text{DHA-1}}}$ ($n = 2$), $\boldsymbol{bla_{\text{CTX-M-14}}}$ ($n = 1$) and $\boldsymbol{bla_{\text{SHV-2}}}$ ($n = 1$). Co-carriage was observed in Germany ($\boldsymbol{bla_{\text{CTX-M-8}}}$ & $\boldsymbol{bla_{\text{CTX-M-55}}}$, $n = 1$) and the Netherlands ($\boldsymbol{bla_{\text{CMY-2}}}$ & $\boldsymbol{bla_{\text{CTX-M-55}}}$, $n = 1$; $\boldsymbol{bla_{\text{SHV-12}}}$ & $\boldsymbol{bla_{\text{CMY-2}}}$, $n = 1$).

In imported turkey meat, all findings originated from the Netherlands. The most frequently reported gene was $\boldsymbol{bla_{\text{CTX-M-55}}}$ ($n = 11$), followed by, $\boldsymbol{bla_{\text{CTX-M-65}}}$ ($n = 4$), $\boldsymbol{bla_{\text{CTX-M-8}}}$ ($n = 2$), $\boldsymbol{bla_{\text{CTX-M-15}}}$ ($n = 2$), $\boldsymbol{bla_{\text{SHV-12}}}$ ($n = 2$) and $\boldsymbol{bla_{\text{CMY-2}}}$ ($n = 2$). Co-carriage of $\boldsymbol{bla_{\text{CTX-M-164}}}$ & $\boldsymbol{bla_{\text{CTX-M-55}}}$ was identified in one isolate in the Netherlands.

In 2023, the Netherlands reported $\boldsymbol{bla_{\text{CTX-M-15}}}$ ($n = 3$) and $\boldsymbol{bla_{\text{CTX-M-1}}}$ ($n = 2$) in imported pig meat, while Germany reported $\boldsymbol{bla_{\text{CTX-M-55}}}$ ($n = 1$) in imported bovine meat.

The ESBL-encoding genes identified in *E. coli* from imported broiler and turkey meat at BCPs differed from those at retail. At retail, $\boldsymbol{bla_{\text{SHV-12}}}$ and $\boldsymbol{bla_{\text{TEM12}}}$ predominated in broiler meat, while $\boldsymbol{bla_{\text{CTX-M-1}}}$ and $\boldsymbol{bla_{\text{CTX-M-15}}}$ were most frequent in turkey meat. In contrast, $\boldsymbol{bla_{\text{CTX-M-55}}}$ and $\boldsymbol{bla_{\text{CTX-M-8}}}$ were dominant in both broiler and turkey meat at BCPs. These ESBL-encoding genes are commonly reported in Brazil, the main origin of the imported poultry meat samples (Egervärn et al., 2014; Casella et al., 2018; Adur et al., 2022; Soncini et al., 2022).

***Specific monitoring of CP-producing* E.coli**

In 2023, 16 countries (Belgium, Denmark, Estonia, France, Germany, Ireland, Italy, Lithuania, Luxembourg, Malta, Portugal, Romania, Spain, Sweden, Switzerland and the United Kingdom – Northern Ireland) collected 199 samples of imported pig meat and 685 samples of imported bovine meat as part of the specific monitoring of CP-producing *E. coli*.

In 2024, 14 countries (Belgium, Estonia, France, Germany, Hungary, Ireland, Italy, Malta, Poland, Portugal, Romania, Slovakia, Spain and the United Kingdom – Northern Ireland) collected 2523 broiler meat samples and 10 turkey meat samples. Notably, no presumptive CP-producing *E. coli* were detected in any samples.

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

5.1 | Key findings

- In indicator commensal *E. coli* collected in routine monitoring, the occurrence of ESBL-/AmpC-/CP-producing isolates remained consistently low to very low in 2023 and 2024.
- In 2023 and 2024, 10 countries[15] in total reported **WGS** data each year, however the set of reporting countries varied across animal populations and meat categories.
- In 2023 and 2024, diverse **ESBL- and AmpC-encoding genes** were identified. The most frequent ESBL genes were $\boldsymbol{bla}_{\textbf{CTX-M-1}}$ and $\boldsymbol{bla}_{\textbf{CTX-M-15}}$ in *E. coli* from pigs, calves, turkeys and their derived meat. In broilers and broiler meat, $\boldsymbol{bla}_{\textbf{SHV-12}}$ was highly prevalent, with $\boldsymbol{bla}_{\textbf{CTX-M-1}}$ and $\boldsymbol{bla}_{\textbf{TEM-52}}$ also frequently detected. The **C-42T mutation** in the chromosomal AmpC gene, associated with the AmpC phenotype, was the most frequently detected in almost all animal populations (turkeys, pigs and calves) and their derived meat, followed by $\boldsymbol{bla}_{\textbf{CMY-2}}$. The exception was in broiler and broiler meat at retail, where the pattern was reverse, and $\boldsymbol{bla}_{\textbf{CMY-2}}$ was more prevalent than the **C-42T mutation**.
- Overall, a high degree of **correspondence** was observed between MIC-based phenotypes and genotypic predictions for isolates with both data types available.
- 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* remained high in some countries, while several others showed statistically significant decreases across both animal populations and meat categories. Overall, the ESBL phenotype was consistently more prevalent than the AmpC phenotype across all tested animal populations and food categories, based on both phenotypic and genotypic data.
- Statistically significant decreases in the key outcome indicator of prevalence of ESBL- and/or AmpC-producing *E. coli* (KOI_{ESC}) were observed in seven MSs and one non-MS, while one MS showed a statistically significant increase; no significant trends were discerned in the remaining countries.
- In the **specific monitoring of ESBL-/AmpC-/CP-producing *E. coli***, one broiler isolate carried the $\boldsymbol{bla}_{\textbf{VIM-1}}$ gene in 2024. In 2023, $\boldsymbol{bla}_{\textbf{OXA-181}}$ was identified in three pig isolates; one pig isolate harboured both $\boldsymbol{bla}_{\textbf{OXA-181}}$ and $\boldsymbol{bla}_{\textbf{NDM-5}}$, whereas $\boldsymbol{bla}_{\textbf{NDM-5}}$ and $\boldsymbol{bla}_{\textbf{VIM-1}}$ were detected in single isolates from different calves.
- In the **specific monitoring of CP-producing *E. coli***, one broiler isolate carried $\boldsymbol{bla}_{\textbf{OXA-244}}$ gene in 2024. In 2023, $\boldsymbol{bla}_{\textbf{OXA-181}}$ was detected in 24 pig isolates and four calf isolates; $\boldsymbol{bla}_{\textbf{OXA-48}}$ appeared in 21 pig isolates and one calf isolate; $\boldsymbol{bla}_{\textbf{NDM-5}}$ was found in five pig isolates; and $\boldsymbol{bla}_{\textbf{OXA-244}}$ was identified in one pig isolate. Additionally, one isolate from pig meat was also reported, carrying the $\boldsymbol{bla}_{\textbf{NDM-5}}$ gene.
- In 2023, five isolates from pigs were reported to simultaneously **co-harbour** the CP-encoding genes $\boldsymbol{bla}_{\textbf{OXA-181}}$ and $\boldsymbol{bla}_{\textbf{NDM-5}}$, with four detected through the specific CP-producer monitoring and one through the specific ESBL-/AmpC-/CP-producing *E. coli* monitoring.

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

Under Commission Implementing Decision (EU) 2020/1729, the routine monitoring of indicator *E. coli* in caecal samples from broilers, turkeys, pigs and calves is mandatory to be performed on a biennial basis following a rotating scheme. In addition, specific monitoring of ESBL-, AmpC- and/or CP-producing *E. coli* must be carried out in caecal samples and retail meat from the same animal populations. Since 2021, AMR data from imported fresh meat sampled at BCPs must also be reported. Moreover, in 2021, WGS was introduced as an alternative to phenotypic testing for indicator *E. coli* and *Salmonella* isolates resistant to extended-spectrum cephalosporins (ESC) and/or carbapenems (Panel 1), and for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* (Annex D.3). Harmonised protocols developed by the EURL-AR ensure data

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

comparability across countries. WGS reporting enhances understanding of the potential contribution of food-producing animals and derived food to the human AMR burden (EFSA, 2019). Accordingly, this chapter describes 2024 AMR data, on *E. coli* isolates from caecal samples collected from broilers and turkeys, as well as from broiler and turkey meat at retail, and 2023 data from caecal samples collected from pigs and cattle (< 1 year) and their derived meat. The overview of the number of EU MSs, the United Kingdom (Northern Ireland) and non-MSs reporting phenotypic and/or WGS data for the different animal and food categories (at retail or BCPs) in 2023 and 2024 is presented in Table 23.

TABLE 23 Overview of countries reporting AMR data from the **specific monitoring of ESBL-, AmpC- and/or CP-producing *E. coli*** with phenotypic and/or genotypic results, 2023–2024.

Year	Animal population/ meats categories	Number of isolates tested	Countries reporting phenotypic data (*N*)	Countries reporting WGS data (*N*)
2024	Broilers	9652	BG, CH, CY, DK, EE, ES, FR, GR, HR, HU, IE, IS, LT, LU, LV, MT, PL, PT, RO, SI, SK, XI (22)	AT, BE, CZ, DE, FI, IT, NL, SE, NO (9)
	Turkeys	3118	ES, FR, HR, HU, IE, PL, PT, RO, SE (9)	AT, DE, IT (3)
	Broiler meat (Retail)	7616	BG, CH, CY, DK, EE, ES, FR, GR, HR, HU, IE, IS, LT, LU, LV, MK, MT, PL, PT, RO, SI, SK (22)	AT, BE, CZ, DE, FI, IT, NL, SE, XI, NO (10)
	Turkey meat (Retail)	4774	BG, CH, DK, EE, ES, FI, FR, GR, HR, HU, IE, LT, LU, LV, MT, PL, PT, RO, SE, SI, SK, XI (22)	AT, BE, CZ, DE, IT, NL XI, NO (8)
	Broiler meat (BCPs)	338	EE, ES, FR, IE, MT, PL, PT, RO, SK, XI (10)	BE, DE, IT, NL (4)
	Turkey meat (BCPs)	40	FR, IE (2)	NL (1)
2023	Pigs	8356	BG, CH, CY, DK, EE, ES, FR, GR, HR, HU, IE, IS, LT, LU, LV, MT, PL, PT, RO, SI, SK, XI (22)	AT, BE, CZ, DE, FI, IT, NL, SE, NO (9)
	Calves	3747	CH, DK, ES, FR, HR, PT, RO, SE (8)	AT, BE, DE, IT, NL (5)
	Pig meat (Retail)	7059	BG, CH, CY, DK, EE, ES, FI, FR, GR, HR, HU, IE, LT, LU, LV, MT, PL, PT, RO, SE, SI, SK (22)	AT, BE, CZ, DE, IT, NL, XI, NO (8)
	Bovine meat (Retail)	7112	BG, CH, CY, DK, EE, ES, FR, GR, HR, HU, IE, LT, LU, LV, MT, NO, PL, PT, RO, SE, SI, SK (22)	AT, BE, CZ, DE, FI, IT, NL, XI (8)
	Pig meat (BCPs)	254	DK, EE, FR, IE, IT, RO, SE, XI (8)	NL (1)
	Bovine meat (BCPs)	742	BE, CH, DK, ES, FR, IE, IT, MT, NL, PT, RO, SE, XI (13)	DE (1)

Abbreviations: BCPs, border control posts; MSs, EU Member States; N, number of countries reporting data; non-MSs, non-EU Member States; WGS, whole genome sequencing;) Abbreviations for reporting countries can be found here.

All prevalence and occurrence tables on ESBL-, AmpC- and/or CP-producing *E. coli* from the 2023 to 2024 monitoring, along with resistance data referenced in this chapter, are available in Annexes D.1 and D.3 and documents on Zenodo (https://doi.org/10.5281/zenodo.17950222). Details on materials and methods are provided in Appendix A. Interactive data visualisation is available via the EFSA AMR dashboard (here). Results from imported meat sampled at BCPs are presented in the textbox '**Monitoring AMR in imported fresh meat at BCP**'.

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

Presumptive ESBL-, AmpC- and/or CP-producing indicator *E. coli* collected within the framework of the **routine monitoring** were tested for antimicrobial susceptibility using Panel 2 of antimicrobials or WGS, following the EU legislation.[16]

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

In 2023 and 2024, the proportion of extended-spectrum cephalosporin-resistant (ESC-resistant) indicator commensal *E. coli* was generally low. Among reporting MSs, ESC resistance ranged from 0% to 13.3% in broilers, 0% to 3.5% in turkeys, 0% to 12.5% in pigs and 0% to 10.6% in calves. At the MS-group level, the occurrence of presumptive ESBL-/AmpC-/CP-producing *E. coli* was 1.5% in broilers, 0.8% in turkeys, 1.1% in pigs and 1.6% in calves. Across targeted food-producing animal, the ESBL phenotype was more common than the AmpC phenotype (Table 24). Detailed data per country are presented in Annex D.1 – tables T1–T4.

[16]According to Commission Implementing Decision **2020/1729**, all 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 beta-lactams and beta-lactam inhibitors (Panel 2) to infer the presence of potential resistance mechanisms (See **Appendix A – Materials and methods**).

TABLE 24 Summary of presumptive ESBL-, AmpC- and/or CP-producing *E. coli* subjected to supplementary testing (Panel 2) or whole genome sequencing in EU MSs and the United Kingdom (Northern Ireland), 2023–2024.

	ESBL and/or AmpC[a]	ESBL[b]	AmpC[c]	ESBL+ AmpC[d]	CP[e]
Animal population/ meats categories	***% R (n)***	***% R (n)***	***% R (n)***	***% R (n)***	***% R (n)***
Broilers, 2024 (*N* = 4451; 27 MSs + XI)	1.5 (67)	1.1 (51)	0.3 (12)	0.1 (4)	< 0.1 (1)
Turkeys, 2024 (*N* = 1653; 12 MSs)	0.8 (13)	0.7 (12)	0.1 (1)	0 (0)	0 (0)
Pigs, 2023 (*N* = 4368; 27 MSs + XI)	1.1 (50)	0.9 (38)	0.3 (12)	0 (0)	0 (0)
Calves, 2023 (*N* = 1964; 11 MSs)	1.6 (32)	1.1 (22)	0.5 (9)	0.1 (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.

[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 2024, a total of 10 indicator *E. coli* isolates collected under the routine monitoring were identified, based on WGS analysis, as carrying ESBL-, AmpC- or carbapenemase-encoding genes. These included broiler isolates from Germany ($n = 3$) and the Netherlands ($n = 2$) and turkey isolates from Italy ($n = 6$). In 2023, 29 such isolates were identified: from calves by Germany ($n = 3$), Italy ($n = 18$) and the Netherlands ($n = 1$), and from pigs by Germany ($n = 2$), Italy ($n = 4$) and Norway ($n = 1$). The complete list of all genes reported under the routine monitoring is presented in Annex D.3 – tables T1. Genes identified in imported fresh meat sampled at BCPs are presented in the textbox **'Monitoring AMR in imported fresh meat at BCP'**.

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

5.4.1 | Prevalence of ESBL- and/or AmpC-producing *E. coli*

The **specific monitoring** of ESBL-, AmpC- or CP-producing *E. coli* includes the selective culturing of samples on media containing 1 mg/L cefotaxime, as recommended by EUCAST, enabling the detection of very low numbers of resistant isolates in a sample.[17]

The prevalence of presumptive ESBL- or AmpC-producing *E. coli* in all animal populations and food categories tested in 2023 and 2024, at the MS level is presented in Table 25. Detailed information regarding prevalence and occurrence per country and animal/food category is presented in tables available online at Zenodo (https://doi.org/10.5281/zenodo.17950222), Annex D.1 – tables T5 to T20. CP-producing isolates detected on the specific monitoring of ESBL- and/or AmpC-producing *E. coli* are presented in **Section 5.5.3**.

A high **overall prevalence** of presumptive ESBL- and/or AmpC-producing *E. coli* at the MS level was observed across all targeted food-producing animals: 34.2% in broilers, 27.0% in turkeys, 40.9% in pigs and 41.4% in calves. In retail meat, prevalence was similarly high in broiler meat (29.4%) and turkey meat (23.7%), but notably lower in pig meat (5.4%) and bovine meat (4.4%) (Table 25).

[17]The method is described in detail in **Appendix A – Materials and methods** and protocols are available at: https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols.

TABLE 25 Summary of the presumptive ESBL–/ and/or AmpC-producing *E. coli* isolates from targeted food-producing animals and derived meat through **specific monitoring** in EU MSs, the United Kingdom (Northern Ireland), 2023–2024.

Animal population/ meats categories	ESBL and/or AmpC[a]			ESBL[b]			AmpC[c]			ESBL + AmpC[d]		
	n	Occ %	Prev%	*n*	Occ %	Prev%	*n*	Occ %	Prev%	*n*	Occ %	Prev%
Broilers, 2024 (Ns = 8859; *N* = 3027; 27 MSs + XI)	2993	98.9	34.2	2379	78.6	27.2	518	17.1	5.9	98	3.2	1.1
Turkeys, 2024 (Ns = 3118; *N* = 842; 12 MSs)	839	99.6	27.0	737	87.5	23.8	69	8.2	2.2	33	3.9	1.1
Pigs, 2023 (Ns = 7572; *N* = 3120; 27 MSs + XI)	3081	98.8	40.9	2320	74.4	30.8	683	21.9	9.1	80	2.6	1.1
Calves, 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
Broiler meat at retail, 2024 (Ns = 6848; *N* = 2027; 27 MSs + XI)	1996	98.5	29.4	1571	77.5	23.2	368	18.2	5.4	59	2.9	0.9
Turkey meat at retail, 2024 (Ns = 4501; *N* = 1062; 26 MSs + XI)	1057	99.5	23.7	918	86.4	20.6	109	10.3	2.5	30	2.8	0.7
Pig meat at retail, 2023 (Ns = 6467; *N* = 351; 27 MSs + XI)	351	100	5.4	263	74.9	4.1	77	21.9	1.2	11	3.1	0.2
Bovine meat 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

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, the 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*.

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

[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 (**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.

When considering only countries that reported more than 10 presumptive ESBL- and/or AmpC-producing isolates, the **prevalence** in **food-producing animals** varied widely across reporting countries in 2023–2024. Based on MIC data, prevalence in broilers ranged from 2.9% (Denmark) to 85.3% (Malta); in turkeys, from 6.4% (France) to 56.9% (Portugal); in pigs, from 6.8% (France) to 81.8% (Spain); and in calves, from 4.2% (Denmark) to 54.1% (Portugal) (Figure 47).

Prevalence also varied among **MSs reporting WGS data:** in broilers, from 14.6% (Netherlands) to 57.4% (Belgium); in turkeys, from 19.0% (Austria) to 32.3% (Germany); in pigs, from 3.3% (Sweden) to 71.0% (Italy); and in calves, from 27.9% (Austria) to 88.7% (Italy). Substantial differences between MSs were also observed when ESBL- and AmpC-producing *E. coli* were analysed separately (Figure 47; Annex D.1 – tables T5 to T8).

In **meat sampled at retail**, the **prevalence** of presumptive ESBL- and/or AmpC-producing *E. coli* also varied considerably between reporting countries. Among those reporting MIC data, prevalence ranged from 6.6% (Denmark) to 68.0% (Lithuania) in broiler meat; 9.4% (France) to 53.3% (Spain) in turkey meat; 4.0% (Ireland) to 21.5% (Slovakia) in pig meat; and 3.7% (Spain) to 24.9% (Hungary) in bovine meat (Figure 48).

Among **MSs reporting WGS data**, **prevalence** ranged from 3.7% (Sweden) to 37.9% (Germany) in broiler meat; 13.3% (Czechia) to 36.4% (Austria) in turkey meat; 3.2% (Germany) to 8.8% (Czechia) in pig meat; and 9.7% (Czechia) to 10.0% (Italy) in bovine meat (Figure 48; Annex D.1 – Tables T9 to T12).

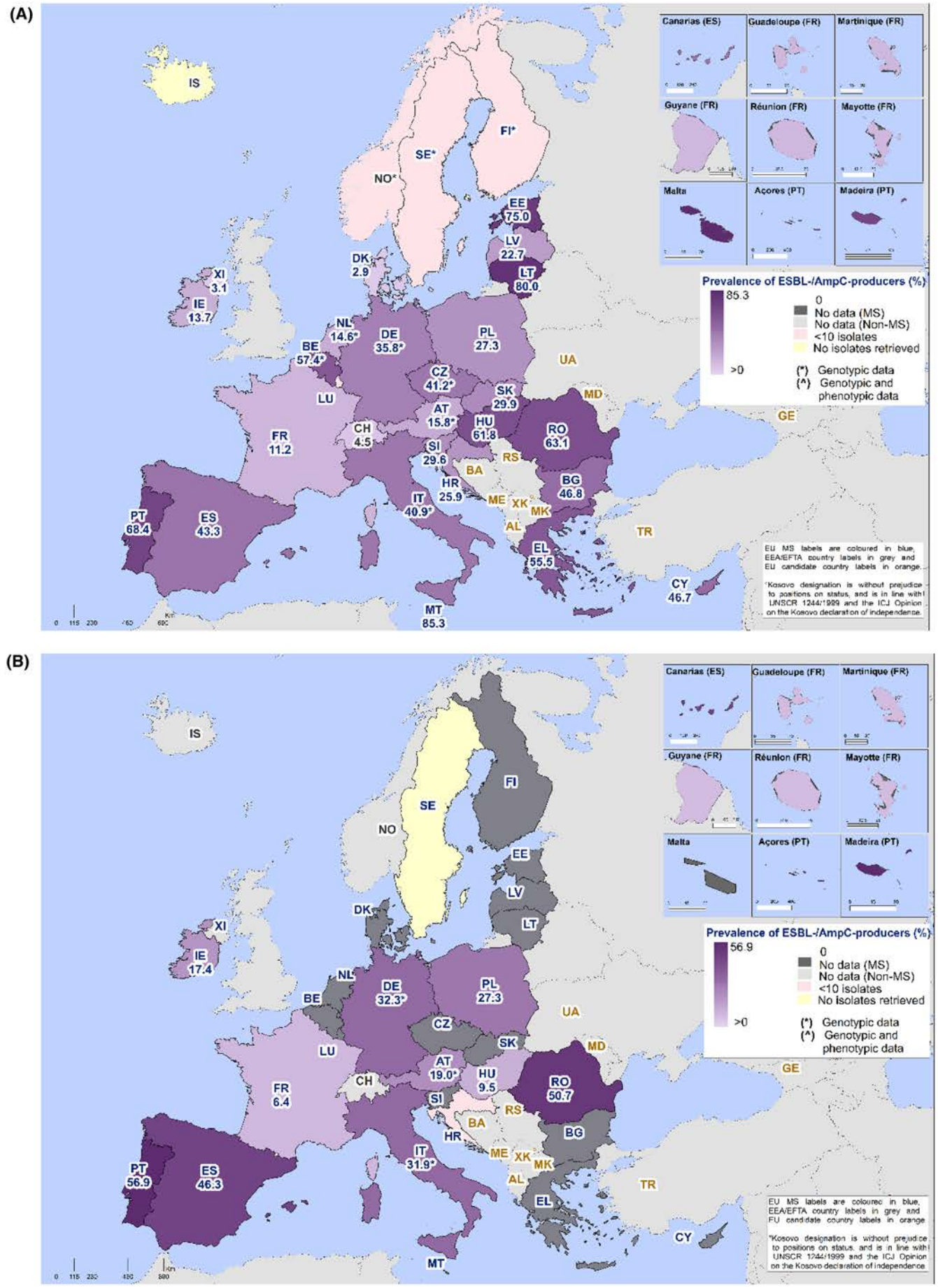


FIGURE 47 (Continued)

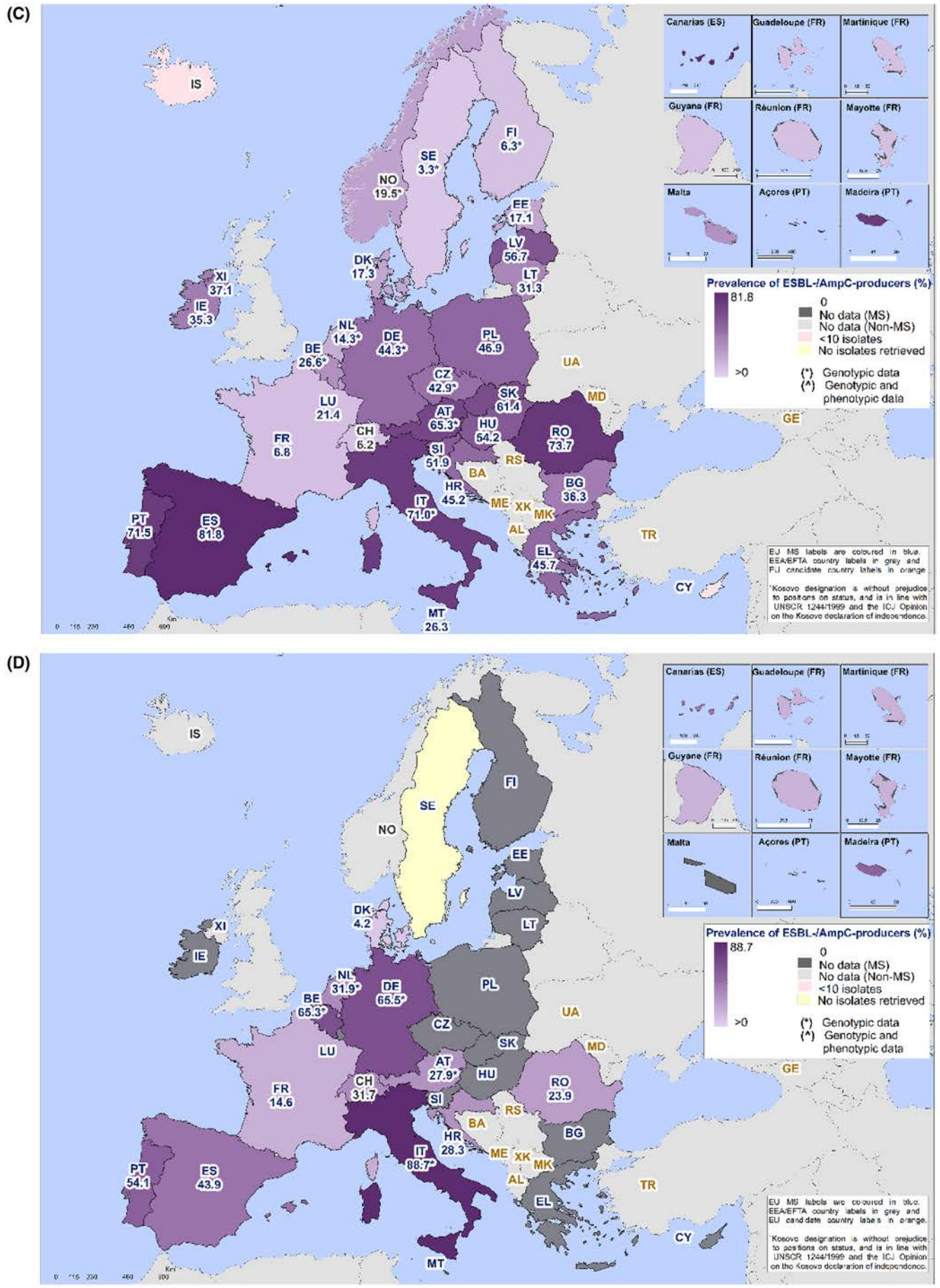
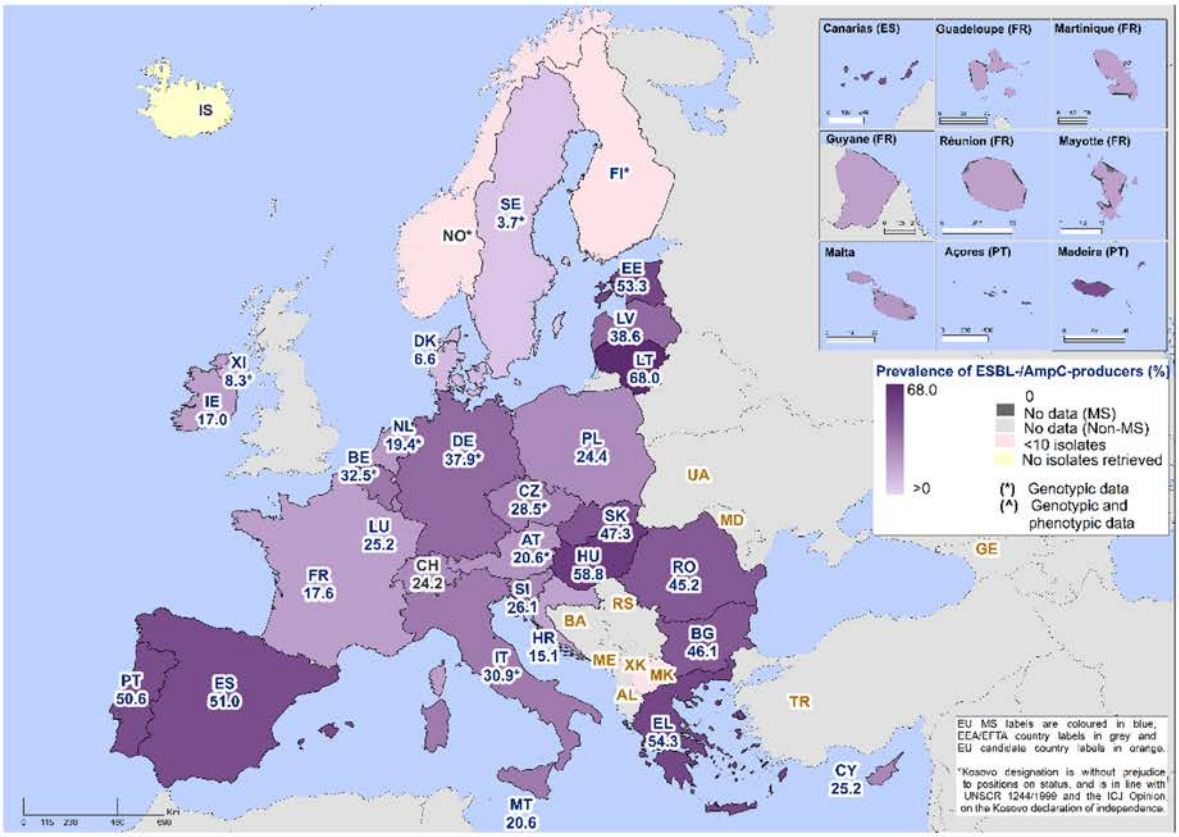


FIGURE 47 Spatial distribution of the prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* from (A) broilers in 2024, (B) turkeys in 2024, (C) pigs in 2023 and (D) calves in 2023, in EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.

Notes: '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 ESBL-and/or AmpC- producing E. 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.

(A)



(B)

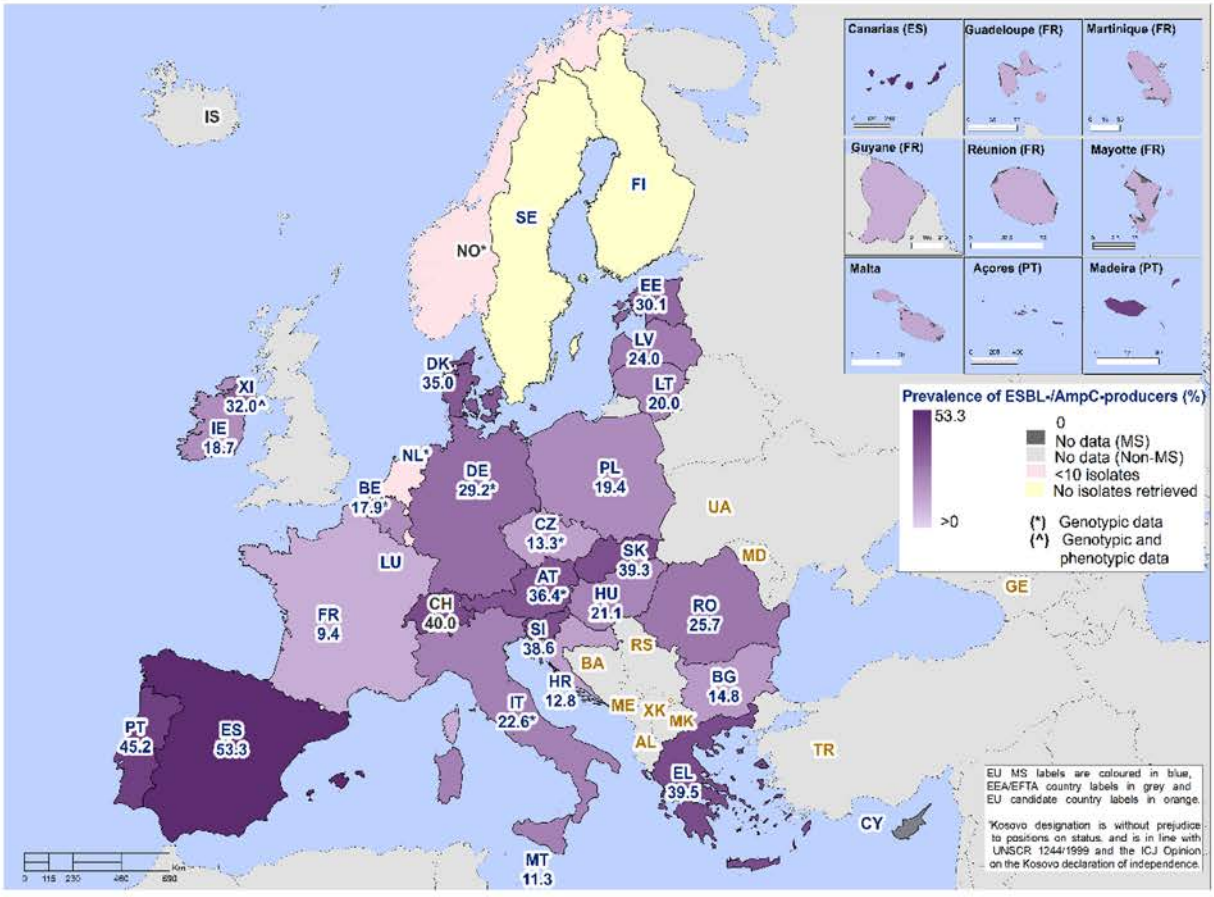


FIGURE 48 (Continued)

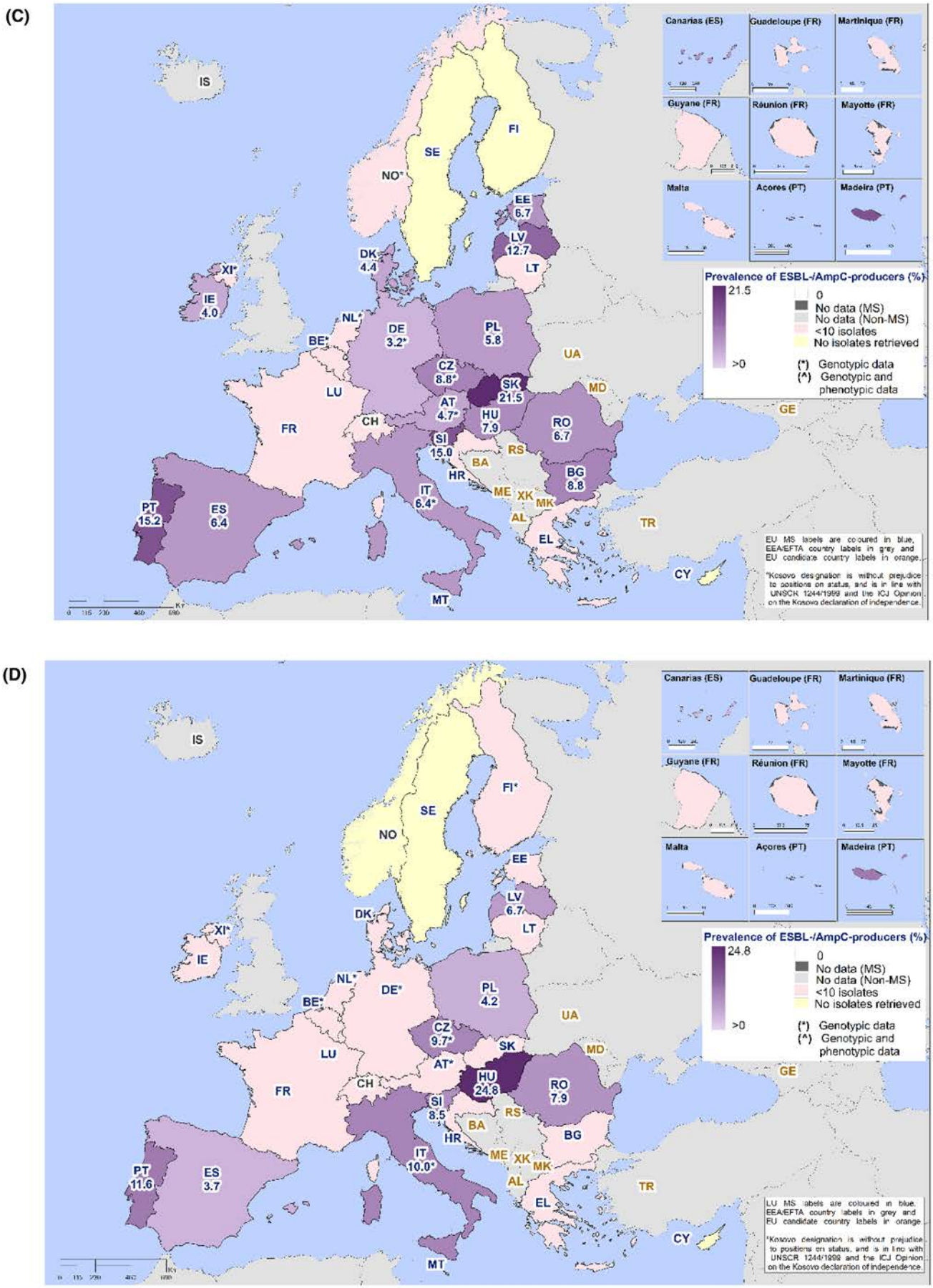


FIGURE 48 Spatial distribution of the prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* from (A) broiler meat in 2024, (B) turkey meat in 2024, (C) pig meat in 2023 and (D) bovine meat in 2023, in EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.
Notes: 'No data' refers 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 ESBL-and/or AmpC- producing E. 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.

5.4.2 | ESBL- and AmpC-encoding resistance genes

In 2023 and 2024, 10 countries reported WGS data for the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*: Austria, Belgium, Czechia, Finland, Germany, Italy, Sweden, The Netherlands, Norway and the United Kingdom (Northern Ireland).

In 2024, WGS data were submitted for isolates from broilers ($n = 739$), turkeys ($n = 263$), broiler meat ($n = 612$) and turkey meat ($n = 121$). In 2023, data were provided for isolates from pigs ($n = 928$), calves ($n = 871$), pig meat ($n = 86$) and bovine meat ($n = 79$). Detailed data on ESBL-, AmpC- and/or CP-encoding **genes** reported are available in Annex D.3 (Tables T2–T5). A summary of CP-encoding genes identified in 2023–2024 is provided in **Section 5.5**, **Monitoring of carbapenemase-producing *E. coli***.

ESBL-encoding genes were more frequently reported than AmpC-encoding genes, consistent with phenotypic data indicating a higher occurrence of ESBL than AmpC phenotypes across all matrices. In addition, Annex D.2 provides an integrated overview of the ESBL-, AmpC- and CP-encoding genes identified through both the specific monitoring of ESBL-/AmpC-/CP-producing *E. coli* and the specific monitoring of CP-producing *E. coli* isolates using whole genome sequencing.

A variety of **ESBL-encoding** genes were detected, as shown in Figure 49 (a and b). Frequencies reported refer exclusively to isolates carrying a single ESBL gene; isolates co-harbouring two or more ESBL genes were excluded to prevent double-counting and are presented separately under the 'More than one ESBL gene' category in Figure 49. Additional details on such cases are provided in the Figure 49 note and in the Annex D.3 **(Tables T2 and T3)**. In broilers and broiler meat, $\boldsymbol{bla_{\text{SHV-12}}}$ was the most frequently reported gene ($n = 200$ and $n = 175$, respectively), followed by $\boldsymbol{bla_{\text{CTX-M-1}}}$ ($n = 139$) in broilers and $\boldsymbol{bla_{\text{TEM-52}}}$ ($n = 114$), in broiler meat. Of note, $\boldsymbol{bla_{\text{TEM-52}}}$ was also detected in broilers, but ranking third ($n = 117$). In turkeys and turkey meat, $\boldsymbol{bla_{\text{CTX-M-1}}}$ ($n = 101$ and $n = 84$, respectively) predominated, followed by $\boldsymbol{bla_{\text{CTX-M-15}}}$ ($n = 40$ and $n = 70$, respectively). A similar pattern was observed in pigs, calves, pig meat and bovine meat, where $\boldsymbol{bla_{\text{CTX-M-1}}}$ was the most frequent gene detected ($n = 423$, $n = 301$, $n = 42$ and $n = 35$, respectively), followed by $\boldsymbol{bla_{\text{CTX-M-15}}}$ ($n = 66$, $n = 274$, $n = 6$ and $n = 17$, respectively).

The various **AmpC resistance** mechanisms identified are presented in Figure 49 (c and d). As for ESBL, the frequencies reported refer only to isolates with a single resistance gene; additional details are available in Annex D.3 (Tables T4 and T5). In broilers and broiler meat, $\boldsymbol{bla_{\text{CMY-2}}}$ was the most frequently reported gene ($n = 91$ and 72, respectively), followed by the **C-42T mutation** ($n = 59$ and 15, respectively). In turkeys and turkey meat, the **C-42T mutation** predominated ($n = 30$ and 27, respectively), followed by $\boldsymbol{bla_{\text{CMY-2}}}$ ($n = 2$ and 7, respectively). A similar pattern was observed in pigs, pig meat, calves and bovine meat, where the **C-42T mutation** was the most frequent ($n = 202$, 12, 31 and 6, respectively), followed by $\boldsymbol{bla_{\text{CMY-2}}}$ ($n = 33$, 6, 6 and 1).

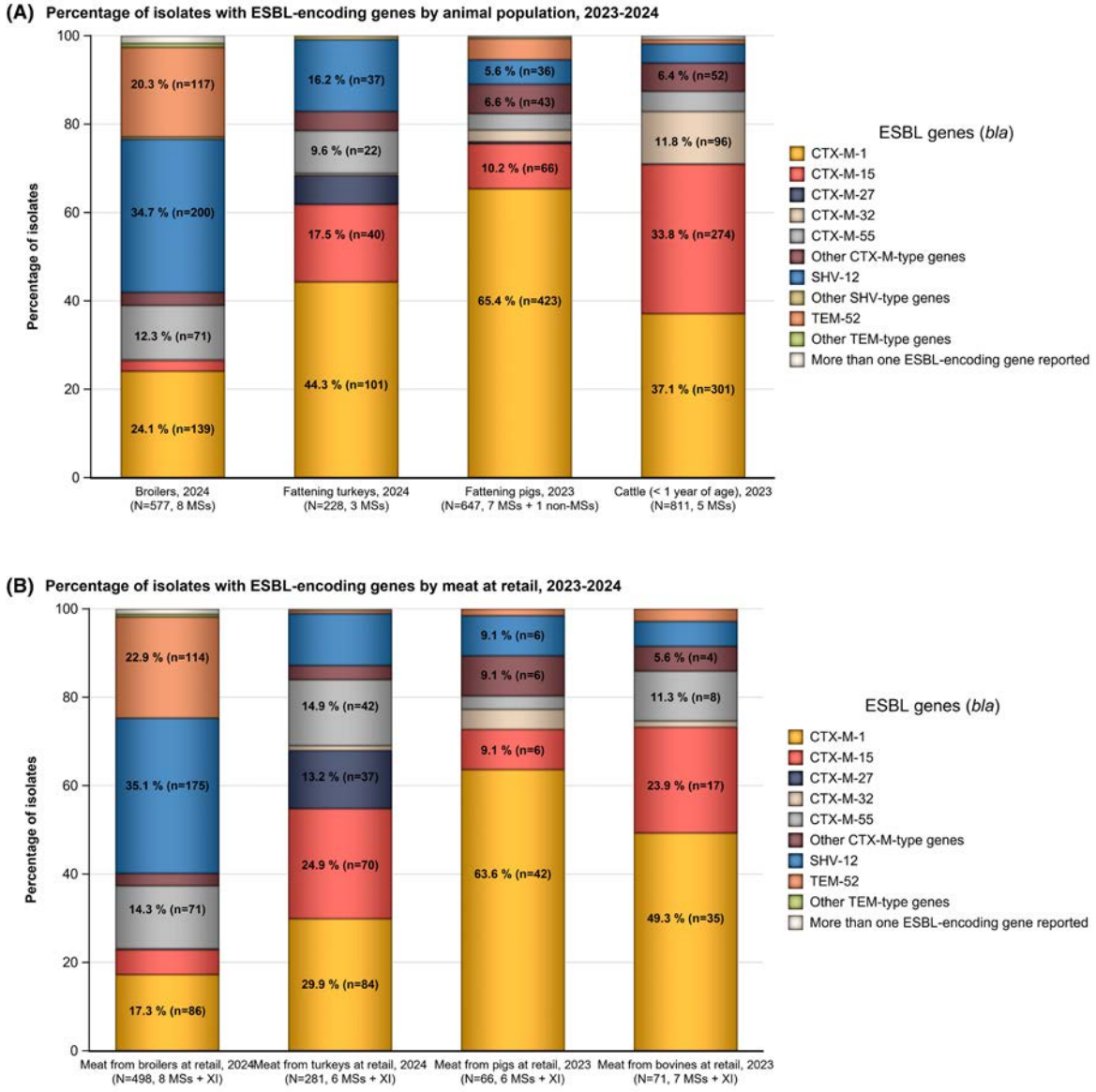


FIGURE 49 (Continued)

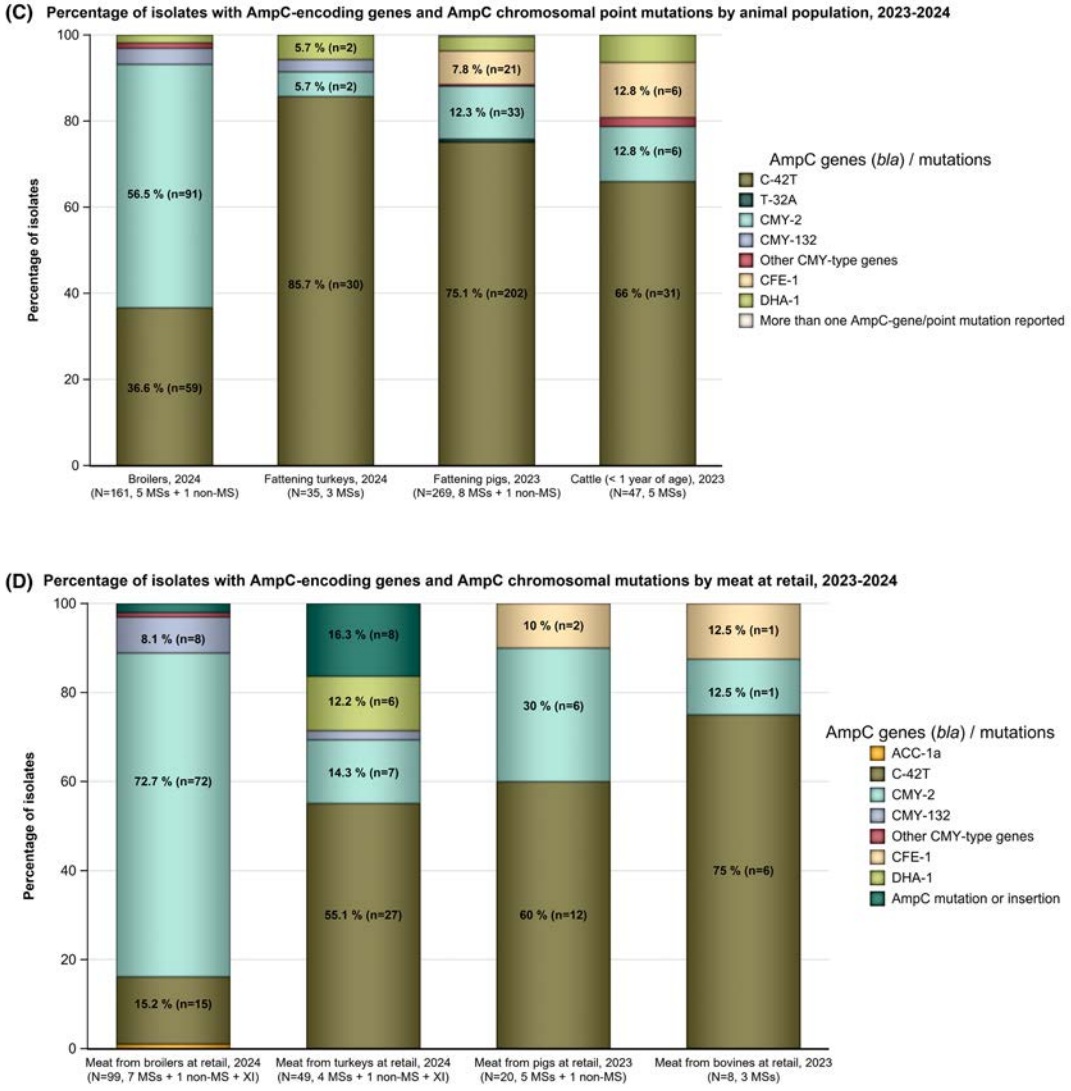


FIGURE 49 Detection of *E. coli* isolates harbouring (A) ESBL-encoding genes in targeted food-producing animals, (B) ESBL-encoding genes in retail meat, (C) AmpC-encoding genes and chromosomal point mutations in targeted food-producing animals and (D) AmpC-encoding genes and chromosomal point mutations in retail meat, in EU MSs, United Kingdom (Northern Ireland) and non-EU MSs, 2023–2024.
Notes: 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. 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/point mutation; non-MS, non-EU Member States; XI, the United Kingdom (Northern Ireland). The category ***bla*$_{\text{TEM-52}}$** also includes isolates with the variants ***bla*$_{\text{TEM-52B}}$** and ***bla*$_{\text{TEM-52C}}$**. The category '**More than one ESBL gene (*bla*) reported**' includes 3 isolates from pigs, carrying ***bla*$_{\text{CTX-M-1}}$** + ***bla*$_{\text{CTX-M-14}}$** ($n=1$), ***bla*$_{\text{CTX-M-32}}$** + ***bla*$_{\text{SHV-12}}$** ($n=1$) or ***bla*$_{\text{CTX-M-55}}$** + ***bla*$_{\text{CTX-M-65}}$** ($n=1$); 7 isolates from cattle under 1 year of age carrying ***bla*$_{\text{CTX-M-14}}$** + ***bla*$_{\text{CTX-M-55}}$** ($n=1$), ***bla*$_{\text{CTX-M-15}}$** + ***bla*$_{\text{CTX-M-55}}$** ($n=1$), ***bla*$_{\text{CTX-M-15}}$** + ***bla*$_{\text{SHV-12}}$** ($n=2$), ***bla*$_{\text{CTX-M-189}}$** + ***bla*$_{\text{CTX-M-55}}$** ($n=2$) or ***bla*$_{\text{CTX-M-32}}$** + ***bla*$_{\text{TEM-52}}$** ($n=1$); 10 isolates from broilers carrying ***bla*$_{\text{CTX-M-55}}$** + ***bla*$_{\text{TEM-124}}$** ($n=1$), ***bla*$_{\text{CTX-M-55}}$** + ***bla*$_{\text{TEM-131}}$** ($n=1$), ***bla*$_{\text{CTX-M-55}}$** + ***bla*$_{\text{TEM-187}}$** ($n=1$), ***bla*$_{\text{SHV-12}}$** + ***bla*$_{\text{TEM-52}}$** ($n=2$), ***bla*$_{\text{TEM-15}}$** + ***bla*$_{\text{TEM-52}}$** ($n=5$); 7 isolates from broiler meat ***bla*$_{\text{CTX-M-1}}$**+***bla*$_{\text{TEM-187}}$** ($n=1$), ***bla*$_{\text{SHV-12}}$** + ***bla*$_{\text{TEM-52}}$** ($n=2$), ***bla*$_{\text{TEM-15}}$** + ***bla*$_{\text{TEM-52}}$** ($n=2$), ***bla*$_{\text{CTX-M-1}}$** + ***bla*$_{\text{TEM-207}}$** ($n=1$) or ***bla*$_{\text{CTX-M-1}}$** + ***bla*$_{\text{TEM-106}}$** + ***bla*$_{\text{TEM-126}}$** ($n=1$) and 2 isolates from turkey meat carrying ***bla*$_{\text{CTX-M-1}}$** + ***bla*$_{\text{TEM-106}}$** + ***bla*$_{\text{TEM-126}}$** ($n=1$) or ***bla*$_{\text{CTX-M-55}}$** + ***bla*$_{\text{TEM-126}}$** + ***bla*$_{\text{TEM-207}}$** ($n=1$) The category 'More than one AmpC gene (***bla***) /point mutation reported' includes one isolate from pigs, carrying ***bla*$_{\text{CMY-2}}$** + C-42T point mutation.

Correspondence between MIC values and reported genes

In 2024, both phenotypic and genotypic data for ESBL-, AmpC- and CP-producing *E. coli* were reported by four countries (Finland, the Netherlands, Sweden and the United Kingdom (Northern Ireland)), and in 2023 by seven countries (Finland, the Netherlands, Portugal, Spain, Sweden, the United Kingdom (Northern Ireland) and Iceland). Overall, a high level of correspondence (i.e. ≥ 90% of the isolates carrying the gene also exhibited the expected phenotype) was observed between the presence of ESBL-, AmpC- or CP-encoding genes and the phenotype predicted based on MIC data. However, for some genes, the overall correspondence was < 90%. The reported genes, associated phenotypes and a summary of genotype–phenotype concordance for genes detected in are provided in Annex D.3 – Tables T14 and T15. In addition, concordance between phenotypic and genotypic results was evaluated using Cohen's kappa. In 2024, the kappa value was 0.76 (95% CI: 0.66, 0.85), reflecting a good agreement between the two methods. Observed discrepancies may partly reflect the presence of resistance genes detected by WGS but not phenotypically expressed.

5.4.3 | Comparing the prevalences of ESBL-producing *E. coli* and AmpC-producing *E. coli*

According to monitoring protocols, only one isolate per positive sample is characterised. Consequently, when both ESBL- and AmpC-producing *E. coli* are present, the probability of detecting either phenotype depends on their relative abundance within the sample. In most countries and across the food-producing animal populations monitored and their derived meat, presumptive ESBL-producing isolates were more frequently detected than presumptive AmpC-producing isolates.

The **prevalence of presumptive ESBL- or AmpC- producing *E. coli*** across the targeted food-producing animals and derived meat samples tested in 2023 and 2024 is shown in Figure 50.

A high overall prevalence of presumptive **ESBL-producing** *E. coli* at the MS level was observed across all targeted food-producing animals: 27.2% in broilers, 23.8% in turkeys, 30.8% in pigs and 37.0% in calves. In retail meat, prevalence was similarly high in broiler meat (23.2%) and turkey meat (20.6%), but notably lower in pig meat (4.1%) and bovine meat (3.9%) (Figure 50A – Annex D.1 – Tables T5–T12).

Conversely, the **overall prevalence** of presumptive **AmpC-producing** *E. coli* at the MS level was **very low** across all targeted food-producing animals and their derived meats: 5.9% in broilers, 2.2% in turkeys, 9.1% in pigs, 3.6% in calves, 5.4% in broiler meat, 2.5% in turkey meat 1.2% in pig meat and 0.5% in bovine meat (Figure 50B – Annex D.1 – Tables T5–T12).

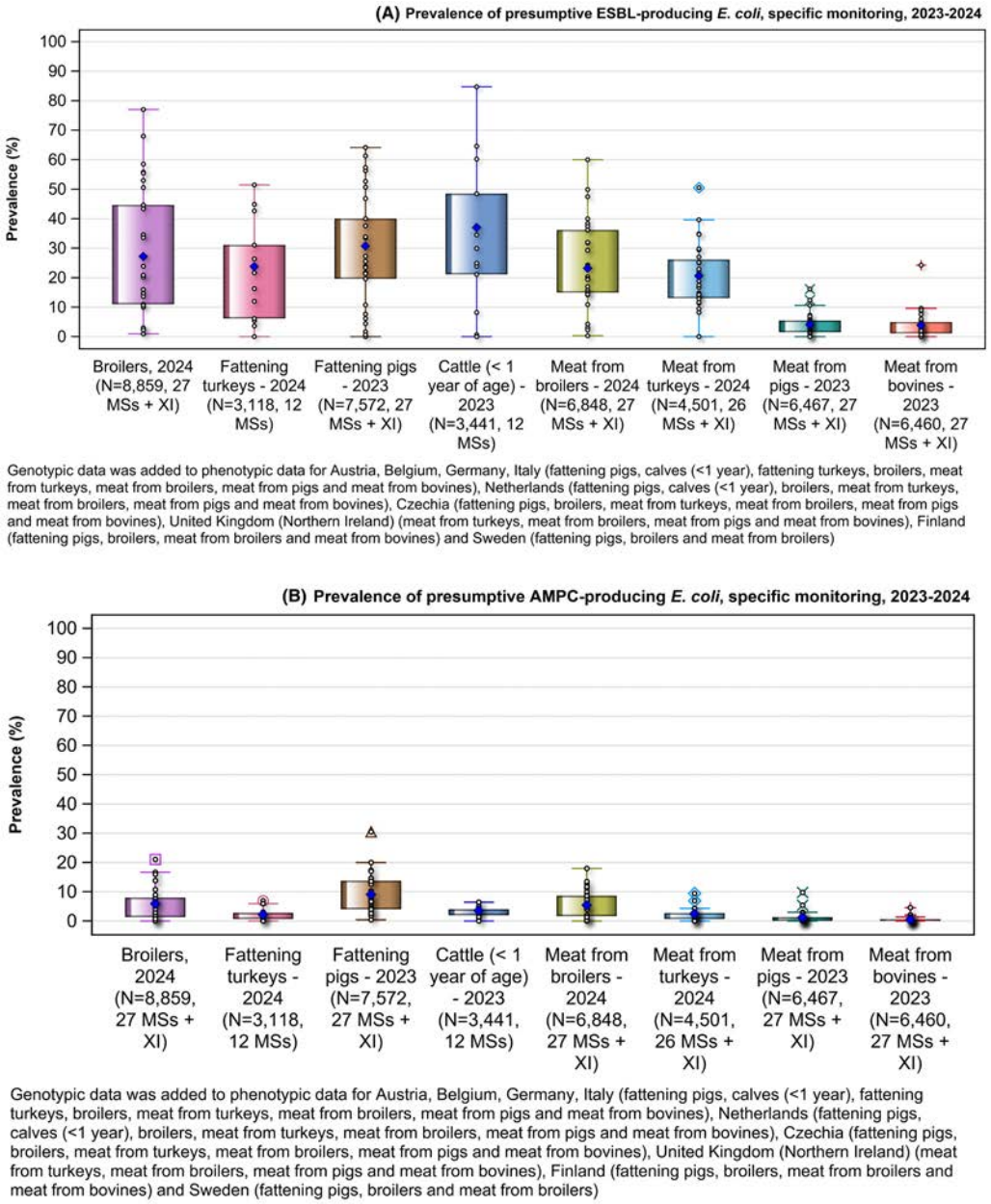


FIGURE 50 Prevalence of presumptive (A) ESBL-producing and (B) AmpC-producing *E. coli* through specific monitoring, in EU MSs, the United Kingdom (Northern Ireland), 2023–2024.

Notes: 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 75th percentile) are visualised using a different symbol for each matrix (i.e. circle for turkeys). MSs, EU Member States; XI, The United Kingdom (Northern Ireland).

In most countries and across the food-producing animal populations monitored, presumptive ESBL-producing isolates were more frequently detected than presumptive AmpC-producing isolates (**Figures 51**, **52**). The spatial distribution maps provided in Annex D.2 further illustrate the heterogeneous geographic patterns of occurrence across countries (Annex D.2 – Figure T1–T4).

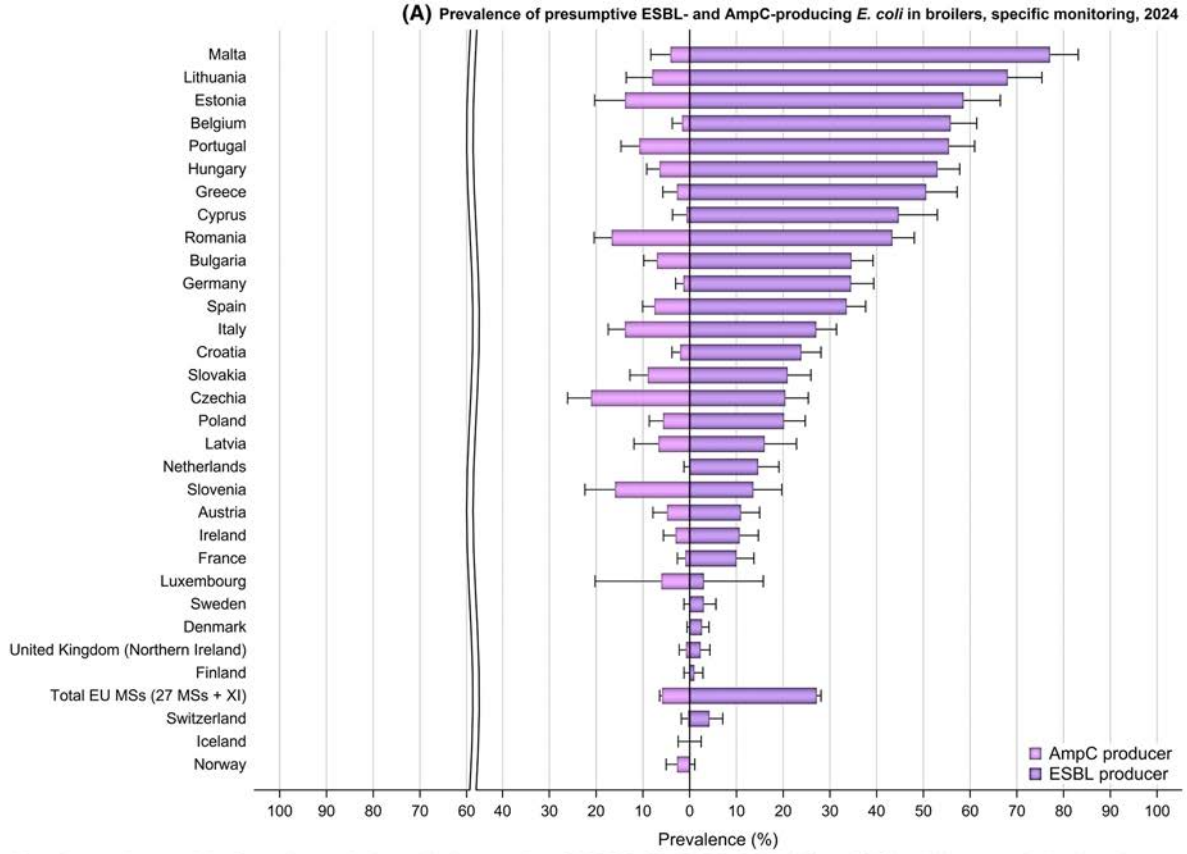
Marked variations in the prevalence of different phenotypes were observed across reporting in MSs. Excluding those with fewer than 10 presumptive ESBL- and/or AmpC-producing isolates, the prevalence of **ESBL-producing** *E. coli* in broilers ranged from 2.3% (United Kingdom – Northern Ireland) to 77.1% (Malta); in turkeys, from 5.5% (France) to 51.5% (Portugal); in pigs, from 1.7% (Denmark) to 64.2% (Spain); and in calves, from 0.7%(Denmark) to 84.7% (Italy) (Figure 51).

In meat at retail, the prevalence of **ESBL phenotype** ranged from 2.3% (Sweden) to 60.0% (Lithuania) in broiler meat; from 8.2% (France) to 50.5% (Spain) in turkey meat; from 1.0% (Ireland) to 16.1% (Slovakia) in pig meat; and from 3.0% (Spain) to 24.2% (Hungary) in bovine meat (Figure 52).

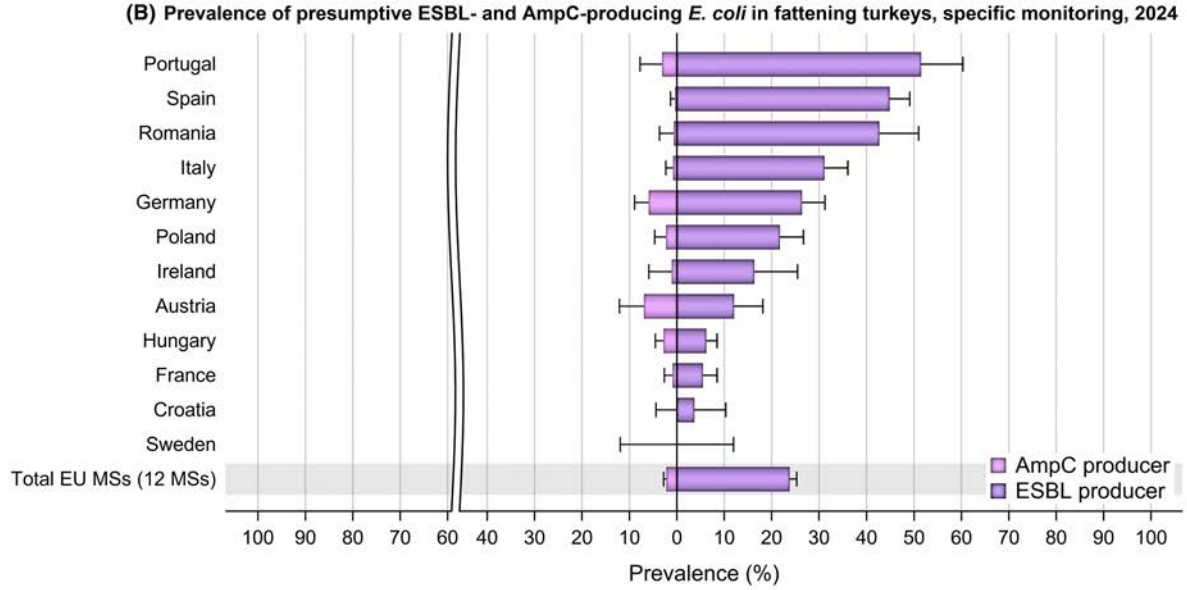
As monitoring of turkey and cattle matrices is not mandatory in countries with limited production, data were reported by only a subset of countries. Overall, greater variability was observed in food-producing animals than in meat at retail, with the highest prevalence generally reported in broilers and calves (Annex D.1 – Table T13 to T20 – Annex D.2 Figures 1–4).

Compared with the ESBL phenotype, the prevalence of **AmpC-producing** *E. coli* isolates was generally lower and exhibited less variability between reporting countries. Across monitored food-producing animal populations, prevalence ranged from 0.0% (Denmark and The Netherlands) to 21.1% (Czechia) in broilers, 0.4% (Spain) to 7.0% (Austria) in turkeys, 0.5% (Malta) to 30.5% (Slovenia) in pigs and 0.9% (Germany) to 6.4 (France) in calves (Figure 51).

In meat at retail, the prevalence of **AmpC-producing** *E. coli* ranged from 0.0% (Ireland) to 18.0% (Slovakia) in broiler meat, 0.0% (Czechia, Croatia and Malta) to 9.5% (Slovakia) in turkey meat, 0.0% (Bulgaria) to 9.8% (Slovenia) in pig meat and 0.0% (Spain) to 4.6% (Slovenia) in bovine meat (Figure 52; Annex D.1 – Table T13 to T20; Annex D.2 Figures 1–4).

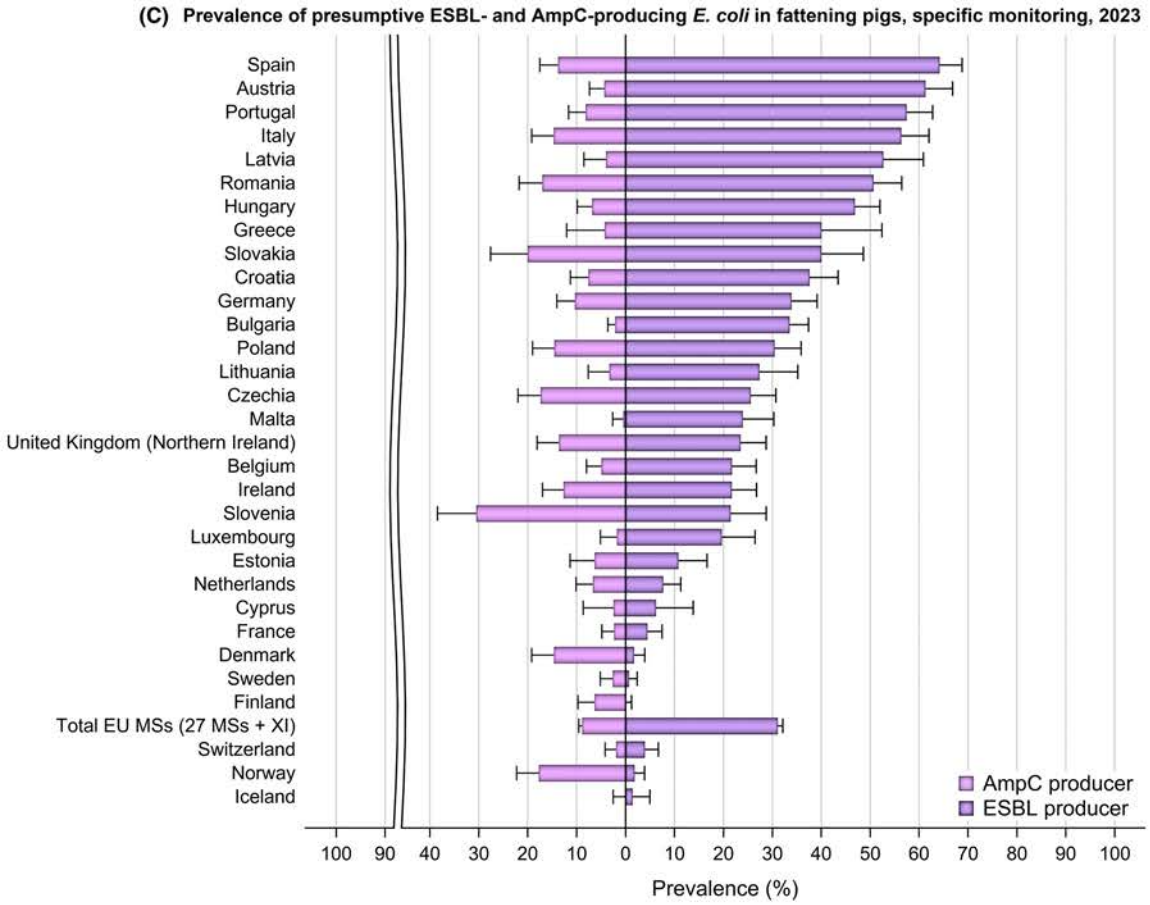


Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, FI, IT, NL, NO and SE for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing *E. coli* are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

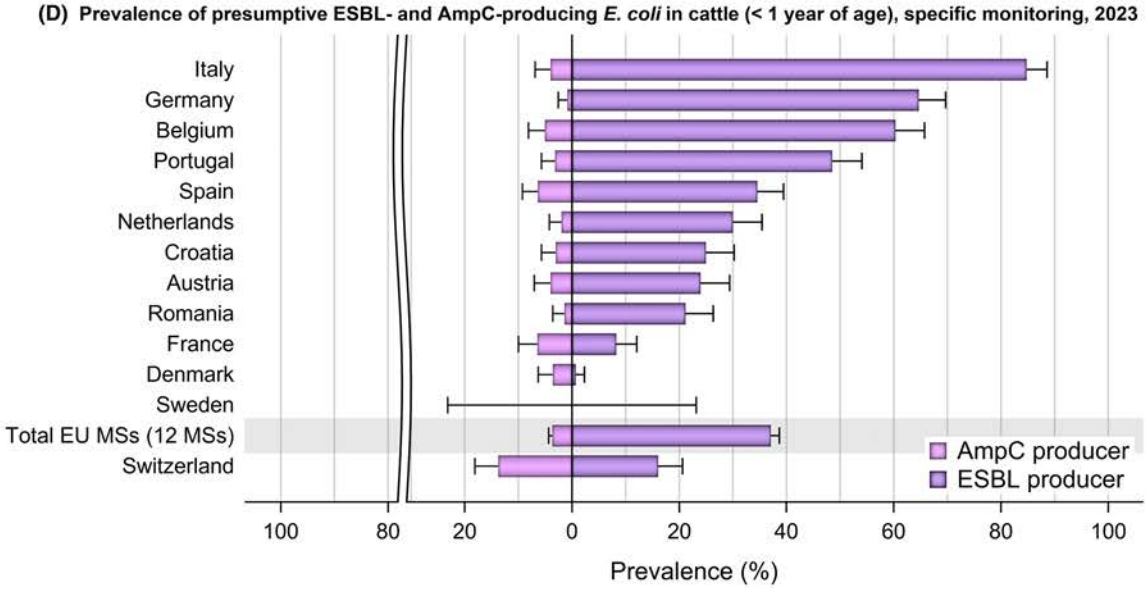


Prevalence estimates derive from phenotypic data, with the exception of AT, DE and IT for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing *E. coli* are also indicated. Please note the different scales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

FIGURE 51 (Continued)

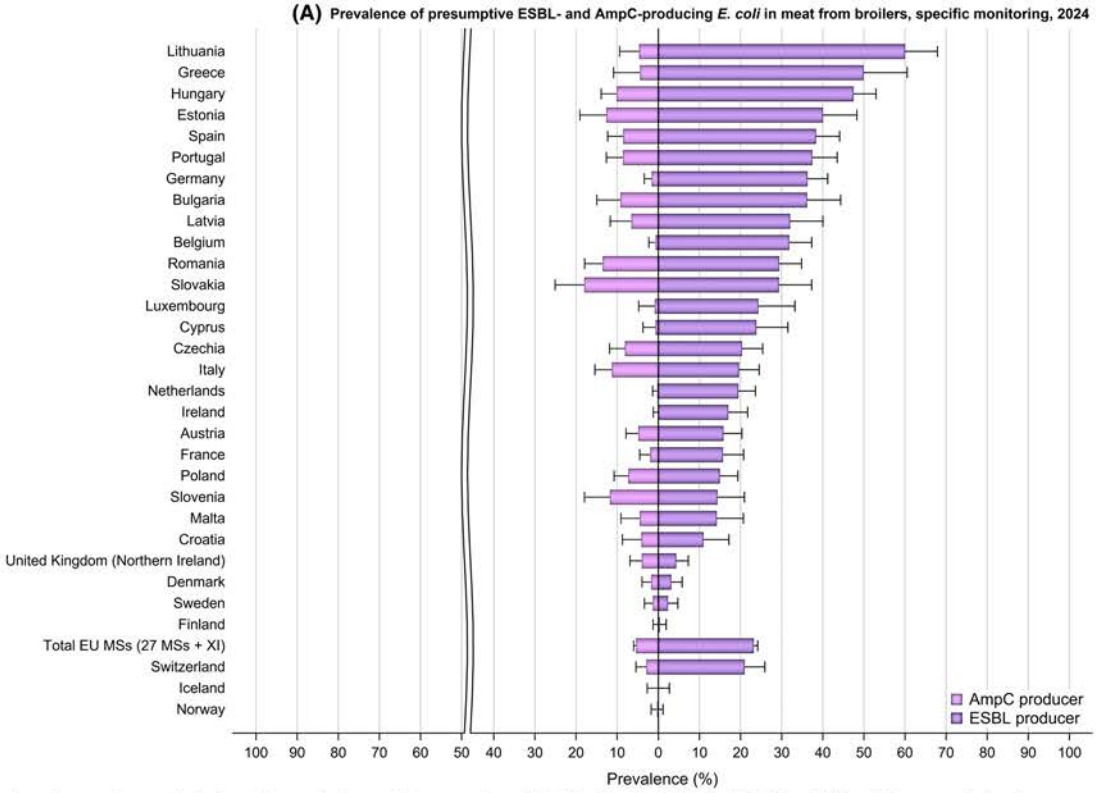


Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, FI, IT, NL, NO and SE for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing *E. coli* are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

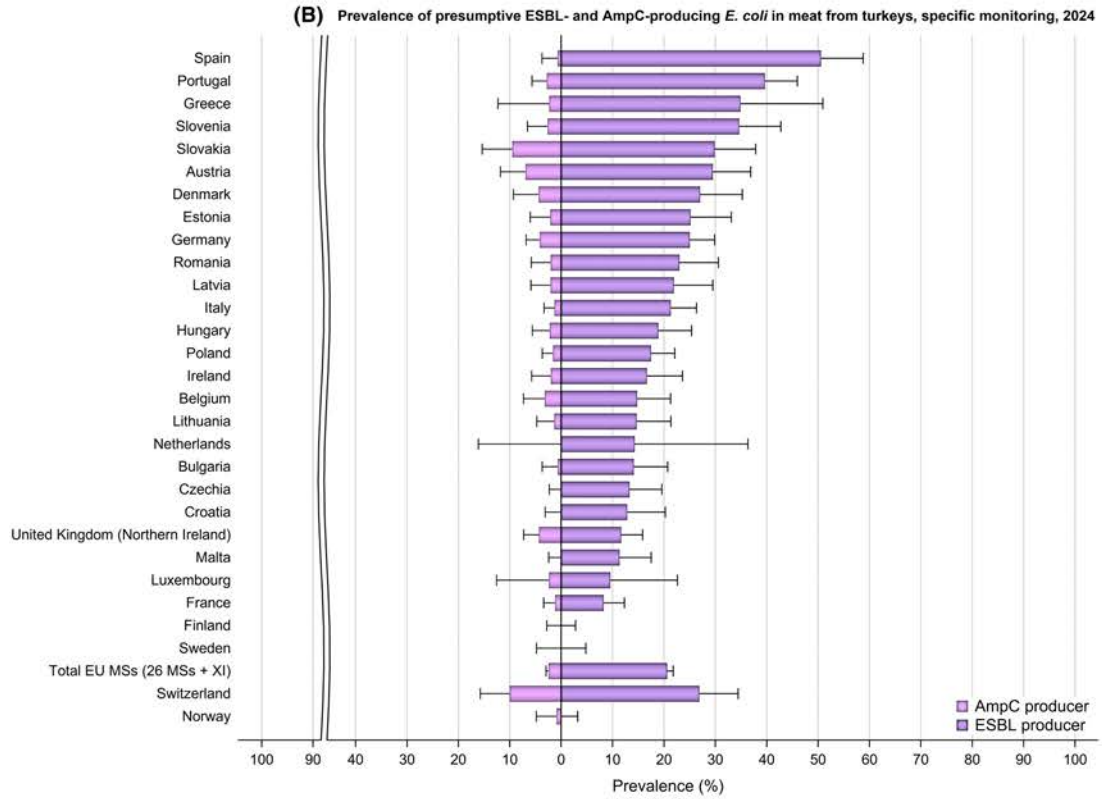


Prevalence estimates derive from phenotypic data, with the exception of AT, BE, DE, IT, and NL for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing *E. coli* are also indicated. Please note the different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

FIGURE 51 Prevalence of presumptive ESBL-producing versus AmpC-producing *E. coli* from targeted food-producing animals, in EU MSs, United Kingdom (Northern Ireland) and non-EU MSs, 2023–2024.

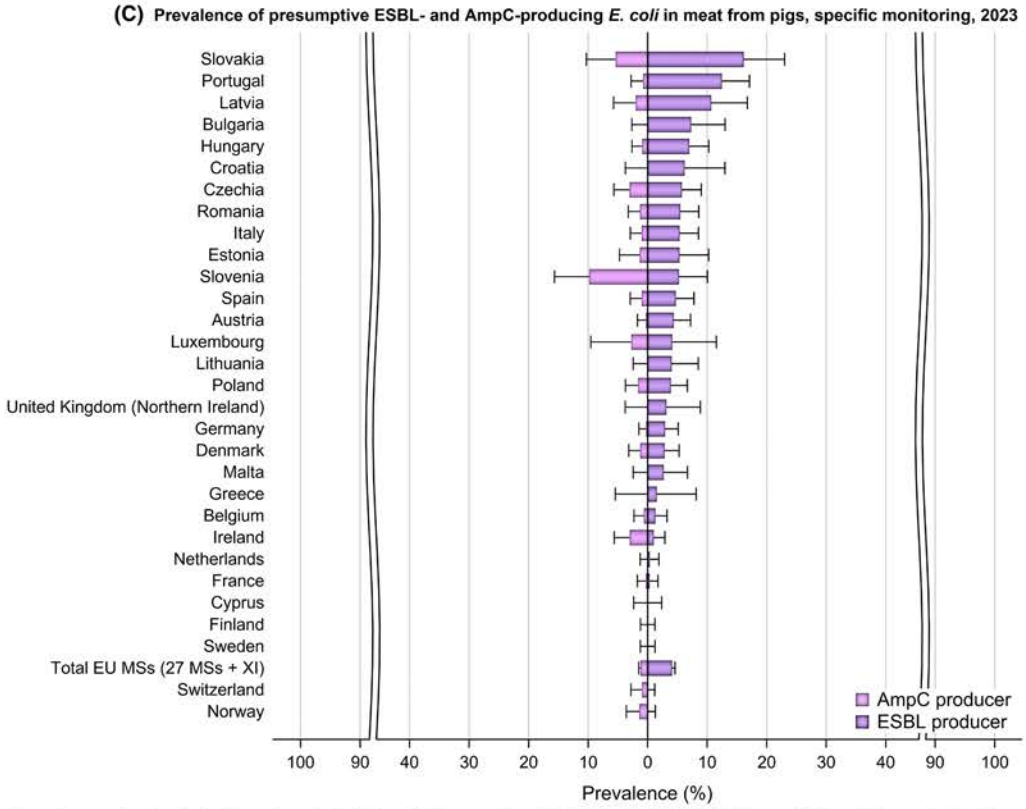


Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, FI, IT, NL, NO, SE and XI for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing *E. coli* are also indicated. Please note the different scales used for the x-axis in the subfigures to improve the visibility of the variations among countries

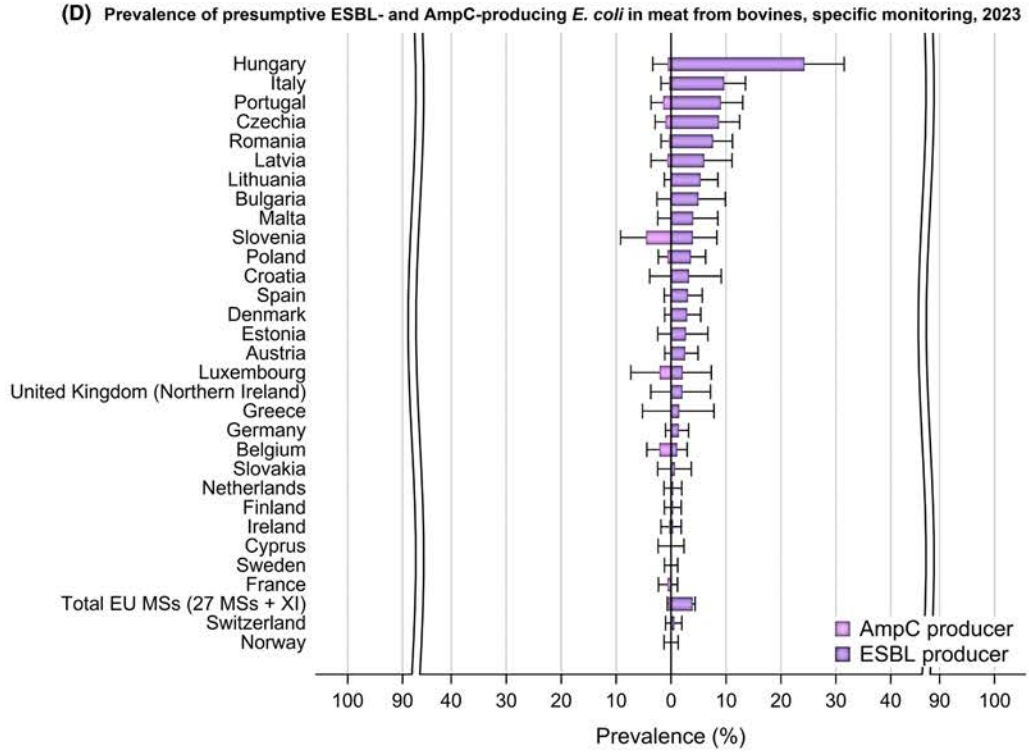


Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, IT, NL, NO and XI for which genotypic data have been used to assess prevalence
The upper bounds of the 95% confidence interval of the prevalence of ESBL- and/or AmpC-producing *E. coli* are also indicated. Please 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 AT, BE, CZ, DE, IT, NL, NO and XI 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



Prevalence estimates derive from phenotypic data, with the exception of AT, BE, CZ, DE, FI, IT, NL and XI 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 *E. coli* from targeted food-producing animals, in EU MSs, United Kingdom (Northern Ireland) and non-EU MSs, 2023–2024.

5.4.4 | Relative abundance of ESBL- and AmpC-producing *E. coli*

According to monitoring protocols, one isolate per positive sample is characterised. As a result, when both ESBL- and AmpC-producing *E. coli* are present, detection of either phenotype reflects their relative abundance within the sample. Overall, across most countries and the monitored food-producing animal populations and their derived meat, presumptive ESBL-producing isolates were more frequently detected than presumptive AmpC-producing isolates, providing useful insights into the prominent resistance patterns (Annex D.1 – Tables T13–T20).

At the MS level, the overall occurrence of presumptive ESBL-producing *E. coli* was high across all targeted food-producing animals and their derived meats: 78.6% in broilers, 87.5% in turkeys, 74.4% in pigs and 88.3% in calves. In retail meat, occurrence remained high in broiler meat (77.5%) and turkey meat (86.4%) but was slightly lower in pig meat (74.9%) and bovine meat (86.7%). In contrast, presumptive AmpC-producing *E. coli* showed low overall occurrence across the same populations and meat types: 17.1% in broilers, 8.2% in turkeys, 21.9% in pigs, 8.7% in calves, 18.2% in broiler meat, 10.3% in turkey meat, 21.9% in pig meat and 10.7% in bovine meat.

5.4.5 | Trends in prevalence of ESBL- and/or AmpC-producing *E. coli*

This section presents data on temporal trends in the prevalence of ESBL- and/or AmpC-producing *E. coli* across reporting countries. Several countries consistently reported high prevalence. Detailed prevalence data by country, targeted food-producing animal species and derived meat for 2023 and 2024 are presented in Figures 53 and 54 (Annex D.1 – Table T5–T12). Historical data are available in previously published reports.

At the MS-group level, **the prevalence** of presumptive ESBL-, AmpC- and/or CP-producing *E. coli* decreased significantly in broilers (−44%) and broiler meat (−41%) between 2016 and 2024. Statistically significant decreasing trends in broilers were reported by 25 MSs[18] and three non-MSs,[19] with Estonia being the only country showing a significant increase. For broiler meat, 20 MSs[20] and two non-MSs[21] reported significant decreases, while Belgium and Malta recorded increases. In turkeys, prevalence also declined significantly (−42%) over the same period, with significant decreases reported by eight MSs.[22] At the MS-group level, **prevalence** in pigs remained stable, while pig meat showed a 40% reduction between 2015 and 2023. Nine MSs[23] and two non-MSs[24] reported significant decreases in pigs, while seven countries[25] reported increases. For pig meat, seven countries[26] showed significant decreases and three reported[27] increases. In calves, a modest but significant decrease (−2%) was observed at the MS-group level, with bovine meat showing a larger decline (−50%) over the same period. For calves, only France, Spain and Norway reported significant decreases, while Croatia showed an increase. For bovine meat, eight countries[28] recorded significant decreases and three reported[29] increases.

[18]Austria, Belgium, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain and Sweden.

[19]Iceland, Norway and Switzerland.

[20]Austria, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Finland, France, Germany, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Poland, Romania, Slovenia, Spain and Sweden.

[21]Norway and Switzerland.

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

[23]Belgium, Bulgaria, Denmark, Estonia, France, Italy, Luxembourg, Spain and Sweden.

[24]Iceland and Switzerland.

[25]Austria, Czechia, Finland, Malta, Romania, Slovakia and Slovenia.

[26]Austria, Belgium, Bulgaria, Cyprus, Czechia, Malta and Romania.

[27]Estonia, Slovakia and Slovenia.

[28]Belgium, Bulgaria, Cyprus, Czechia, Germany, Malta, the Netherlands and Spain.

[29]Estonia, Hungary and Slovenia.

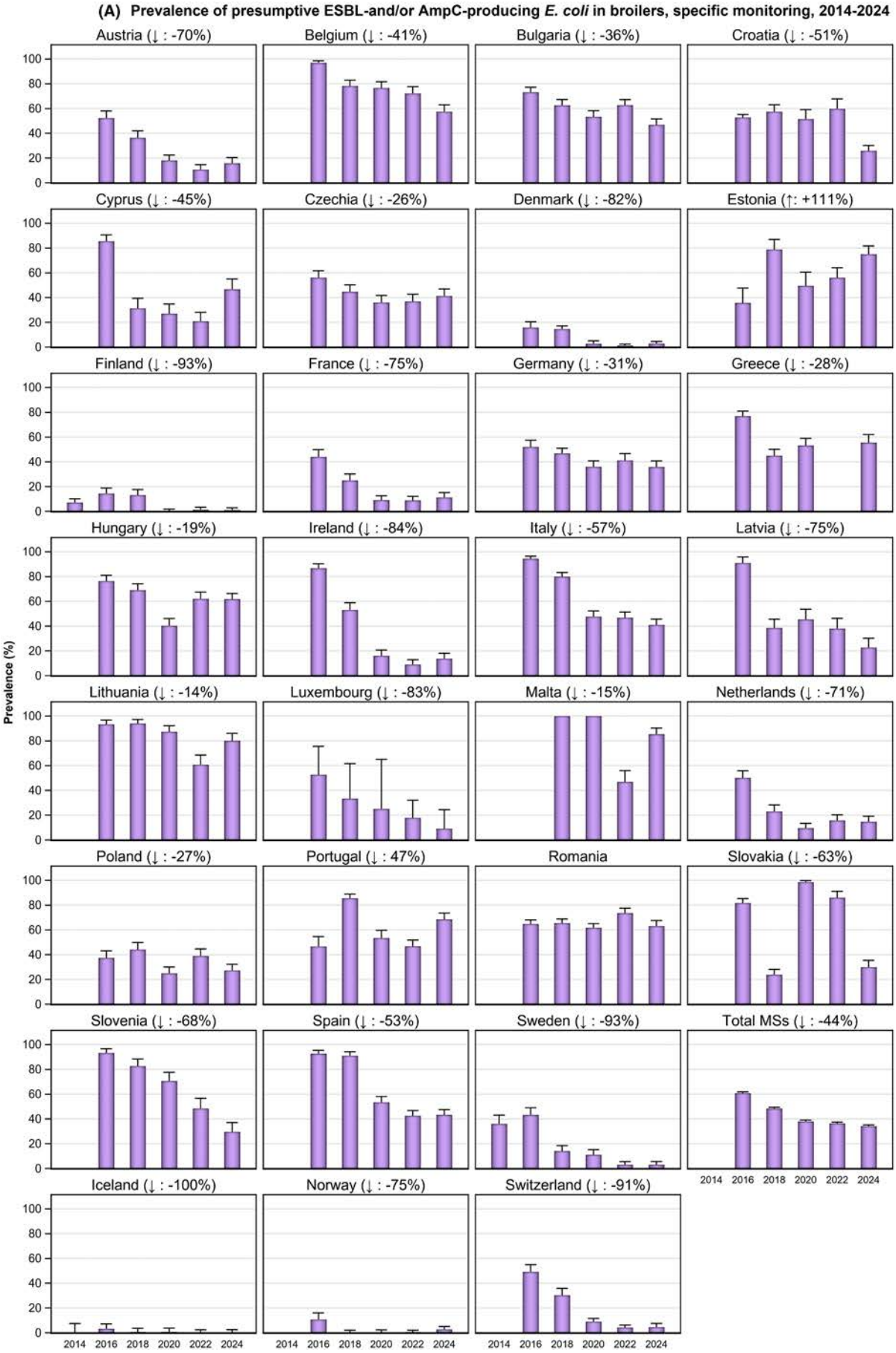


FIGURE 53 (Continued)

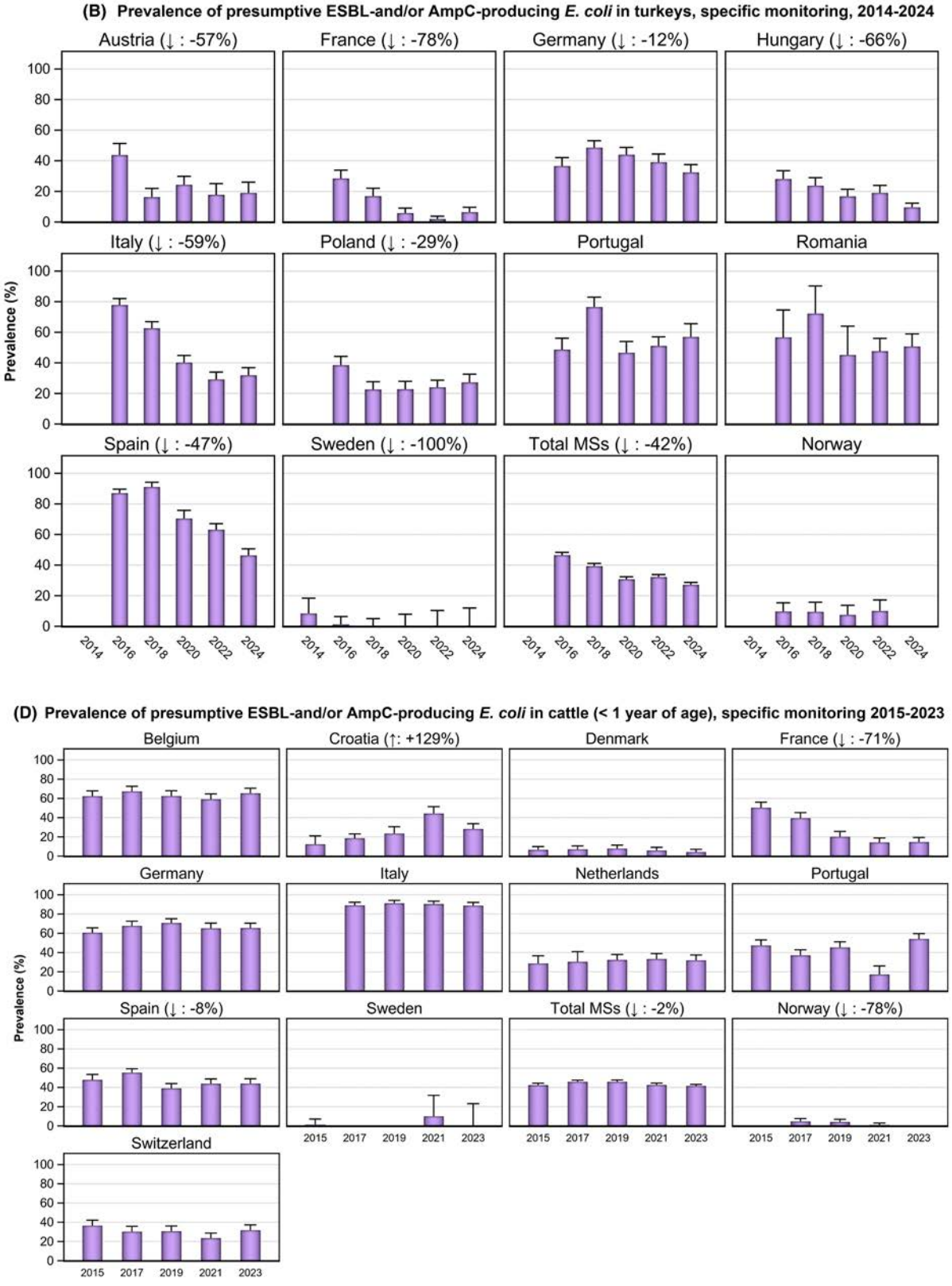


FIGURE 53 (Continued)

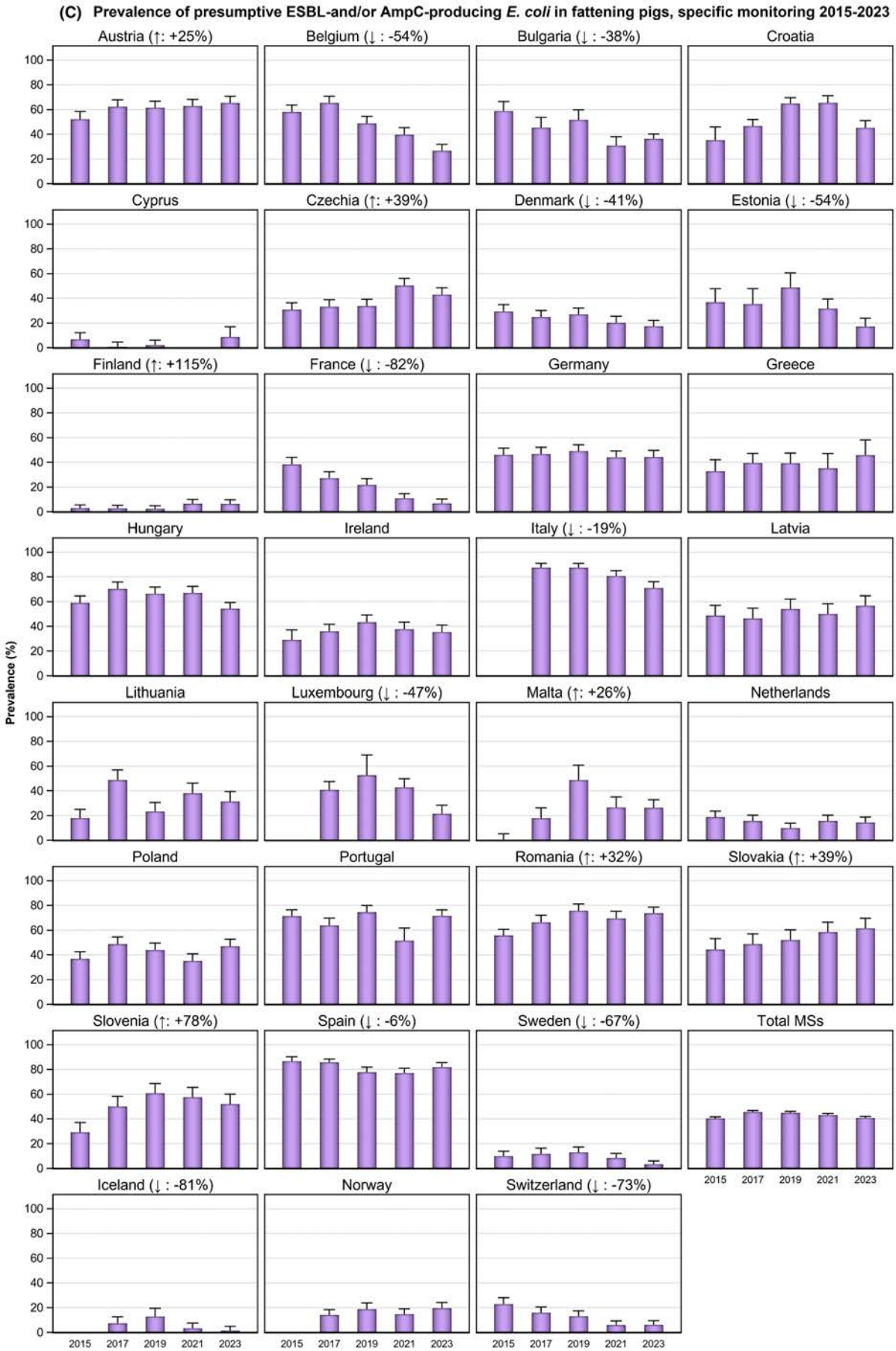


FIGURE 53 Trends in the prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* from targeted food-producing animals, in EU MSs, the United Kingdom (Northern Ireland) and non-EU MSs, 2014–2024.
Notes: Arrows indicate statistically significant decreasing/increasing trends over the period.

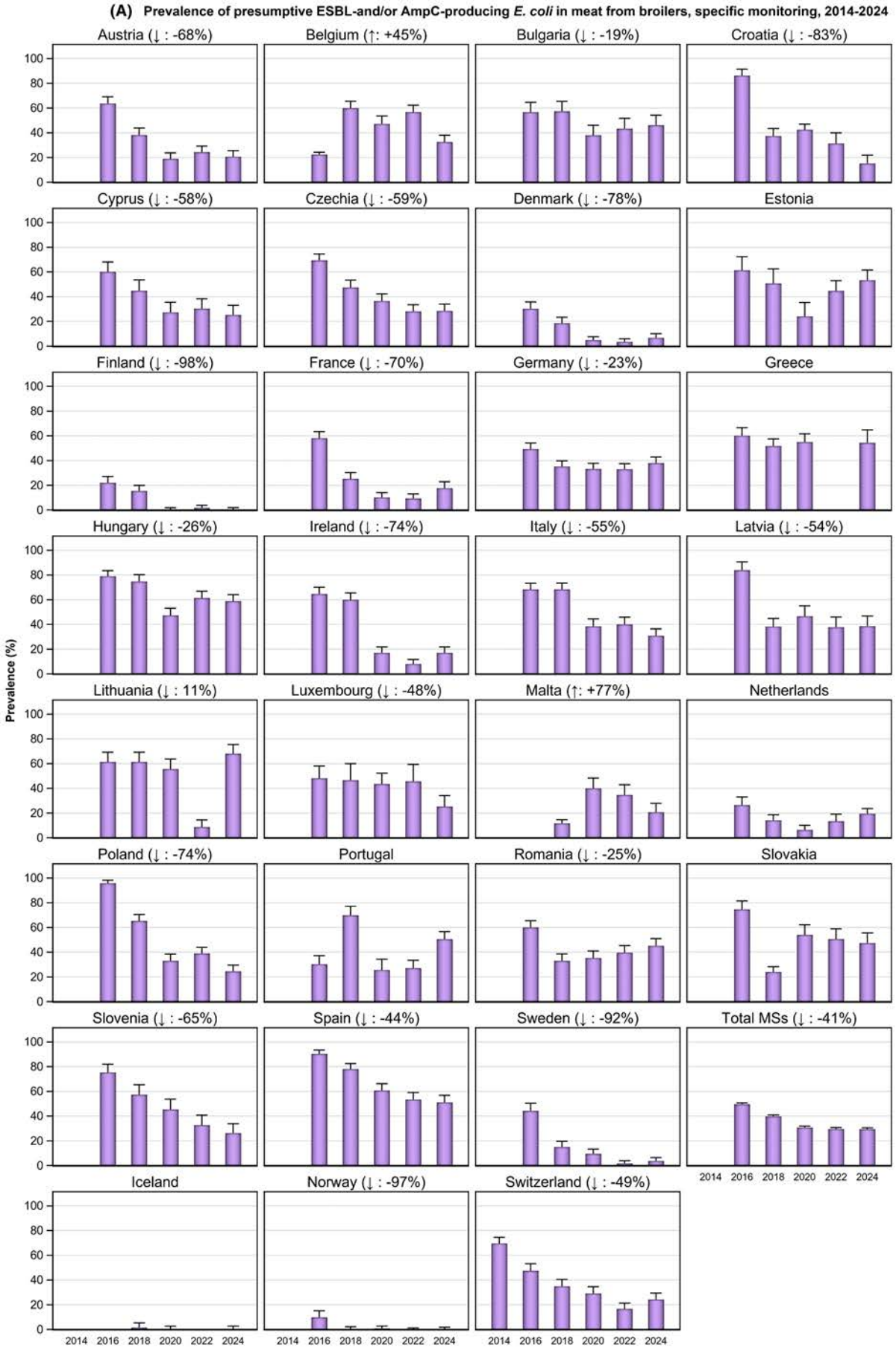


FIGURE 54 (Continued)

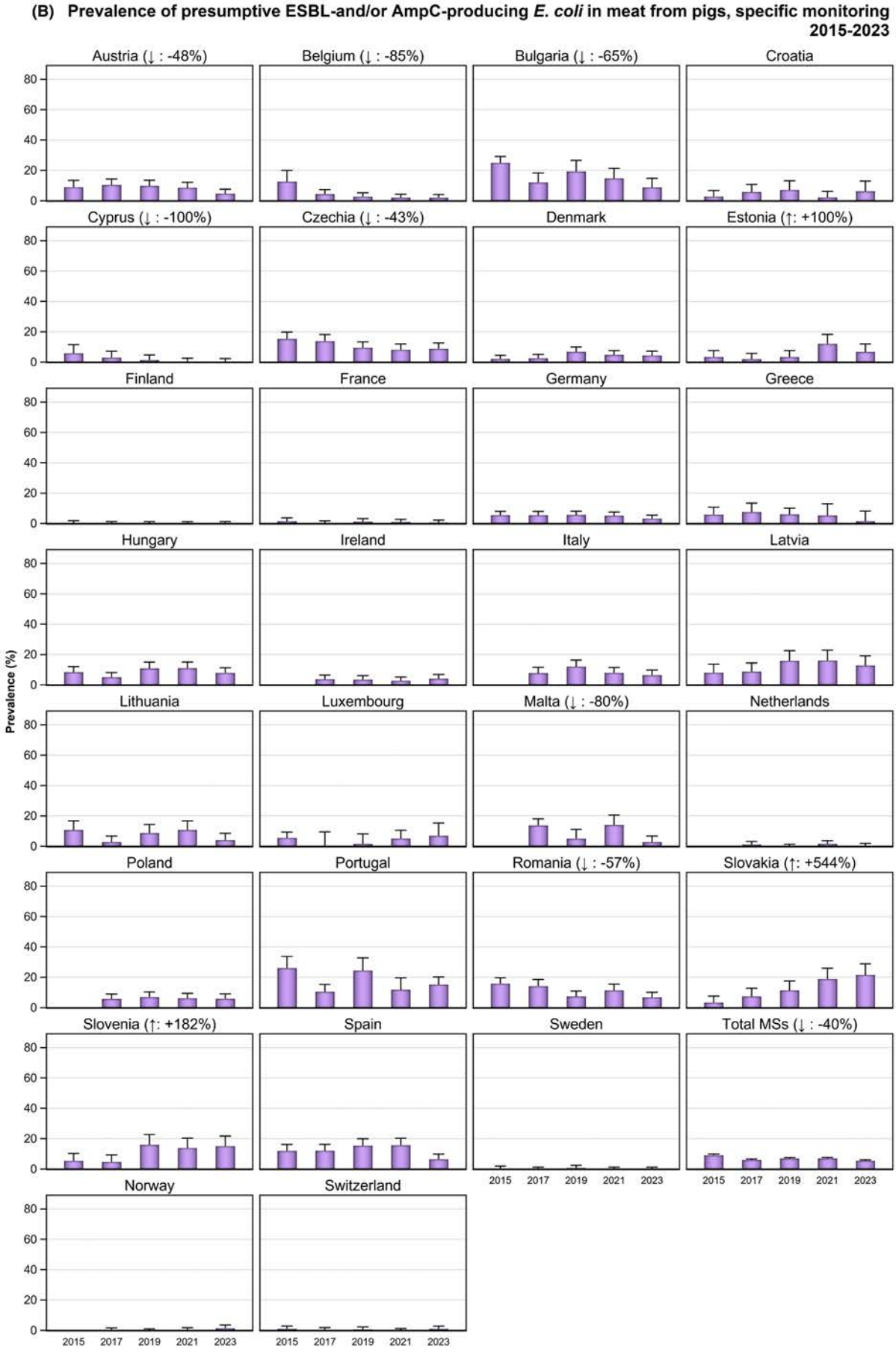


FIGURE 54 (Continued)

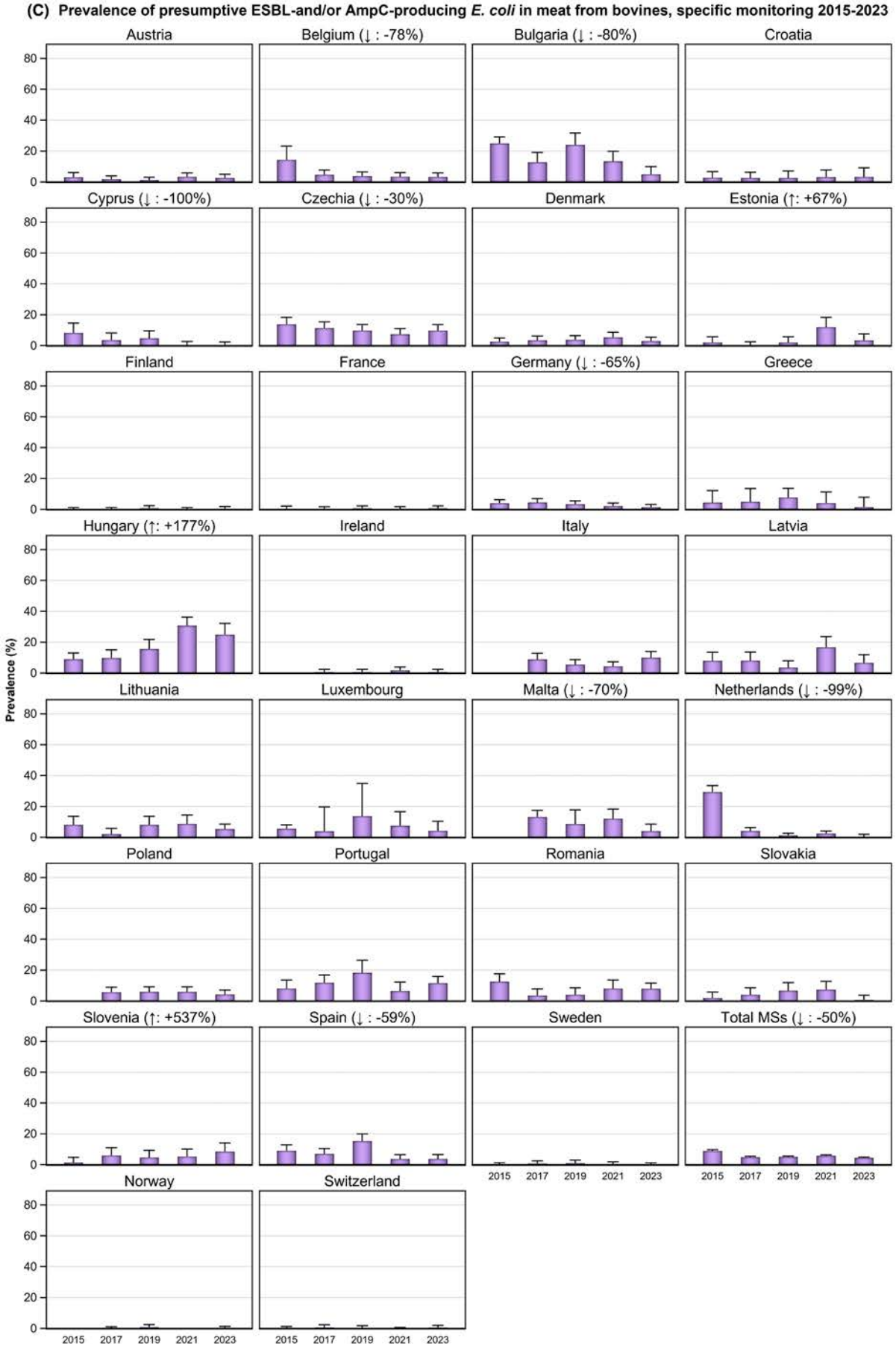


FIGURE 54 Trends in the prevalence of presumptive ESBL- and/or AmpC-producing *E. coli* in meat from targeted food-producing animals, in EU MSs, the United Kingdom (Northern Ireland) and non-EU MSs, 2014–2024.
Notes: Arrows indicate statistically significant decreasing/increasing trends over the period.

5.4.6 | KOI of prevalence of ESBL-/AmpC-producing *E. coli*

The proportion of samples from targeted food-producing animals tested positive for presumptive ESBL- and/or AmpC-producing *E. coli*, weighted by 'population correction unit' (PCU), has been retained as a Key Indicator.[30]

To account for differences in animal population sizes across countries, a weighted KOI_{ESC} was calculated. KOI_{ESC} represents the weighted mean prevalence of ESBL- and/or AmpC-producing *E. coli* across the four monitored animal populations in a country, with weights based on relative population size using the population correction unit (PCU). Developed by the European Medicines Agency (EMA), the PCU provides a technical measure of animal population size and is used to adjust antimicrobial sales data for population differences (EMA, 2011) (**Appendix A – Materials and methods**). KOI_{ESC} was calculated using data from two consecutive years to encompass all four populations. For example, 2023–2024 values combined pigs and calves from 2023 with broilers and turkeys from 2024.

Trends in KOI_{ESC} are shown in Figure 55 (Annex D.2 – Table 1). Nine countries[31] showed a decreasing trend, although some began from very high to extremely high levels. In 20 countries, KOI_{ESC} remained stable, while Romania exhibited a significant increase.

[30]According to Commission Implementing Decision 2020/1729/EU.

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

FIGURE 55 Changes in the key outcome indicator of ESBL- and/or AmpC-producing *E. coli* (KOI_{ESC}), 27 EU MSs and 3 non-EU MSs, 2015–2024.

5.4.7 | Discussion

The presence of ESBL-, AmpC- and/or CP-producing bacteria in animals poses a public health risk via direct contact or contaminated food. These bacteria serve as reservoirs of resistance genes that can be transferred to other bacteria, primarily through **horizontal gene transfer (HGT)** mediated by conjugative plasmids, transposons and insertion sequences (EFSA BIOHAZ Panel, 2021), facilitating rapid dissemination along the food chain. Although the latest JIACRA report (ECDC, EFSA, EMA, 2024) found no significant association between ESC resistance in animal-derived *E. coli* and invasive human *E. coli*, the complexity of the epidemiology highlights the need for strengthened integrated surveillance.

In 2023–2024, the overall proportion of ESBL-, AmpC- and/or CP-producing indicator *E. coli* detected through **routine monitoring** remained low.

In the **specific monitoring** of ESBL-/AmpC- producing *E. coli* across all animal populations monitored and their derived meat, the ESBL phenotype was more frequently reported than AmpC phenotype. Similarly, when providing WGS results, the main proportion of reported genes were ESBL-encoding, followed by AmpC-encoding genes. However, the prevalence of these phenotypes varied considerably between countries. For example, the **AmpC phenotype** was more common in **broilers** in Czechia, Slovenia, Luxembourg and Norway; in **calves** in Denmark; in **pigs** in Denmark, Finland, Slovenia, Sweden and Norway; in **broiler and turkey meat** in Norway; in **pig meat** in Ireland, Slovenia, Norway and Switzerland; and in **bovine meat** in Belgium, France and Slovenia.

In **pigs and calves**, the prevalence of ESBL- and/or AmpC- producing *E. coli* was higher in animals than in meat, whereas in **poultry**, prevalence levels were similar between meat and animals. This likely reflects differences in slaughter practices and the faster, more intensive production cycles typical of poultry production (EFSA and ECDC, 2025a, 2025b).

WGS analysis revealed that $\boldsymbol{bla}_{\textbf{SHV-12}}$, $\boldsymbol{bla}_{\textbf{CTX-M-1}}$ and $\boldsymbol{bla}_{\textbf{TEM-52}}$ were most frequently detected in **broilers** and **broiler meat**, whereas $\boldsymbol{bla}_{\textbf{CTX-M-1}}$ predominated in the remaining animal populations (**turkeys**, **pigs** and **calves**) and their **derived meat**, often followed by $\boldsymbol{bla}_{\textbf{CTX-M-15}}$.

$\boldsymbol{bla}_{\textbf{CTX-M-1}}$ was first identified in Germany in 1989, $\boldsymbol{bla}_{\textbf{CTX-M-15}}$ in India in 2001 and later in Poland in 2002, $\boldsymbol{bla}_{\textbf{SHV-12}}$ in Italy in 1991 and $\boldsymbol{bla}_{\textbf{TEM-52}}$ in France in 1998 (Baraniak et al., 2002; Bauernfeind et al., 1990; Laksai et al., 2000; Poyart et al., 1998). These genes are now well established in European food-producing animals and their meat, with $\boldsymbol{bla}_{\textbf{SHV-12}}$ predominantly reported in poultry (Day et al., 2016; Ewers et al., 2012, 2021; Käsbohrer et al., 2019).

Across all monitored animal populations and their derived meat, the AmpC phenotype was primarily associated with the **C-42T chromosomal mutation**, first reported in France in 2000 (Ewers et al., 2021). An exception was observed in **broilers and broiler meat**, where the $\boldsymbol{bla}_{\textbf{CMY-2}}$ gene predominated. This gene, initially described in Greece in 1990 (Bauernfeind et al., 1996) has persisted in European pig and broiler production, likely sustained by epidemic plasmids (Bevan et al., 2017; Mo et al., 2016).

Notably, in all other animal populations and meat categories (**turkeys, pigs, calves** and their **derived meat**) $\boldsymbol{bla}_{\textbf{CMY-2}}$ was consistently the second most frequently reported gene, following the **C-42T chromosomal mutation**.

In addition, $\boldsymbol{bla}_{\textbf{CFE-1}}$ was reported for the first time in EU monitoring in 2023, detected in **pigs, calves** and their **derived meat** in Italy. This gene was originally identified in Japan in 2004 (Nakano et al., 2004) and has since been reported in Italian dairy products, including cheese and salami (Crippa et al., 2024).

The dissemination of ESBL and plasmid-mediated AmpC genes in livestock is primarily driven by horizontal gene transfer, facilitated by **conjugative plasmids** (notably IncF, IncI, and IncA/C), as well as **integrons**, **insertion sequences** and **transposons**. These elements enable gene transfer between unrelated *E. coli* strains and even to *Salmonella* spp. Secondary transmission pathways include clonal expansion within farms, environmental contamination and in poultry, vertical transmission through hatching eggs (EFSA BIOHAZ Pane, 2021).

Since 2014, 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 remained stable in pigs and has slightly decreased in calves. In broilers and turkeys, a declining trend has been observed, likely associated with the phase-out of off-label use of extended-spectrum cephalosporin in poultry production (EMA/CVMP, 2018).

5.5 | Monitoring of carbapenemase-producing *E. coli*

5.5.1 | Routine monitoring of indicator *E. coli*

In the routine monitoring, no CP-producing isolates were detected in 2023 and 2024 (Table 26).

5.5.2 | Specific monitoring of ESBL-, AmpC- and/or CP-producing *E. Coli*

The use of selective media supplemented with 1 mg/L cefotaxime in the specific monitoring of ESBL-, AmpC- and/or CP-producing *E. coli* also allows for the detection of isolates with certain carbapenem resistance mechanisms. In 2024, one CP-producing *E. coli* isolate carrying blaVIM-1 was reported in broilers in Austria. In 2023, six CP-producing isolates were detected: two from calves, one reported by Germany harbouring blaVIM-1 and one by Italy carrying bla NDM-5, and four from fattening pigs. Among the pig isolates, three harboured blaOXA-181 (reported in Italy, Portugal and Spain) and one isolate from Portugal co-harboured blaOXA-181 and bla NDM-5 (Figure 56; Table 26; Annex D.3 – Tables T6–T9).

5.5.3 | Specific monitoring of carbapenemase-producing *E. coli*

Specific monitoring of CP-producing bacteria using selective media for the isolation of CP-producers, in accordance with the EURL-AR protocol[32,33] was made mandatory in 2021 (**Appendix A – Materials and methods**).

In 2023 and 2024, 27 MSs, the United Kingdom (Northern Ireland) and four non-MSs investigated: 9106 samples from broilers, 3091 from turkeys, 7725 from pigs, 3621 from calves, 7218 from broiler meat at retail, 4585 from turkey meat, 6692 from pig meat at retail and 6487 from bovine meat at retail (Annex D.1 – Table T21).

In 2024, although no CP-producing isolates were detected in turkeys or in broiler and turkey meat, one CP-producing isolate from a broiler was identified in the Netherlands, carrying ***bla*$_{\text{OXA-244}}$**. In addition, Iceland reported one presumptive CP-producing isolate from broilers, showing resistance to meropenem and ertapenem, for which no CP-encoding gene has been identified with the databases used for the resistant gene identification (Annex D – Tables 10 and 12).

In 2023, CP-producers were detected in pigs from Czechia ($n = 5$), Italy ($n = 19$), Portugal ($n = 7$), Romania ($n = 1$) and Spain ($n = 23$), in calves from Italy ($n = 4$) and Spain ($n = 1$). For two isolates from pigs (Spain, $n = 1$; Romania, $n = 1$) and one from in pig meat (from Spain) (Annex D.3 – Tables T11 and T13), the CP-encoding genes reported in 2023 and 2024 are summarised in Table 26 and Figure 56.

TABLE 26 Carbapenemase-encoding genes reported in ESBL-, AmpC- and/or CP-producing *E. coli* isolates from specific monitoring programmes, 2023–2024.

Year	Animal population/meats categories	Genes	Number of isolates	Countries detecting the isolates (*n*)
Specific monitoring of ESBL-/AmpC-/CP-producing *E. coli*				
2024	Broilers	*bla*$_{\text{VIM-1}}$	1	AT
2023	Calves	*bla*$_{\text{VIM-1}}$	1	DE
		bla$_{\text{NDM-5}}$	1	IT
	Fattening Pigs	*bla*$_{\text{OXA-181}}$	3	ES, IT, PT*
		bla$_{\text{OXA-181}}$ + *bla*$_{\text{NDM-5}}$	1	PT*
Specific monitoring of CP-producing *E. coli*				
2024	Broilers[a]	*bla*$_{\text{OXA-244}}$	1	NL
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*
	Calves	*bla*$_{\text{OXA-181}}$	4	IT (4)
		bla$_{\text{OXA-48}}$	1	ES
	Pig meat	*bla*$_{\text{NDM-5}}$	1	ES

Abbreviations: *n*, number of CP-producing isolates. Abbreviations for reporting countries can be found here.

[a]Iceland reported one presumptive CP-producing isolate from broilers, showing resistance to meropenem and ertapenem, for which no CP-encoding gene has been identified with the databases used for the resistant gene identification.

*These isolates co-carry a CP-encoding gene together with ESBL and/or AmpC genes.

The relationship between the investigated animal populations, the CP-encoding genes and the countries where CP-producing isolates were detected is illustrated in Figure 56. Among the isolates retrieved, most carbapenem- resistant *E. coli* isolates originated from fattening pigs mainly primarily carrying *bla*$_{\text{OXA-181}}$ (reported in Italy, Spain and Portugal), followed by *bla*$_{\text{OXA-48}}$ (Spain, Portugal and Romania) and *bla*$_{\text{NDM-5}}$ (Czechia). In addition, one *bla*$_{\text{NDM-5}}$ isolate was detected in pig meat from Spain. In calves, the *bla*$_{\text{OXA-181}}$ gene was also the most common CP-encoding gene detected (Italy). In broilers, *bla*$_{\text{VIM-1}}$ was identified in Austria, and *bla*$_{\text{OXA-244}}$ in the Netherlands. Notably, isolates co-harbouring bla$_{\text{OXA-181}}$ and *bla*$_{\text{NDM-5}}$ were reported in pigs from Portugal, raising particular concern.

[32]https://www.food.dtu.dk/english/-/media/institutter/foedevareinstituttet/temaer/antibiotikaresistens/eurl-ar/protocols/esbl-ampc-and-camrbapenemase-producing-e-coli/esbl_ampc_cpeprotocol_version_caecal_v9_17122024.pdf.

[33]https://www.food.dtu.dk/english/-/media/institutter/foedevareinstituttet/temaer/antibiotikaresistens/eurl-ar/protocols/esbl-ampc-and-camrbapenemase-producing-e-coli/esbl_ampc_cpeprotocol_version_meat_v9_17122024.pdf.

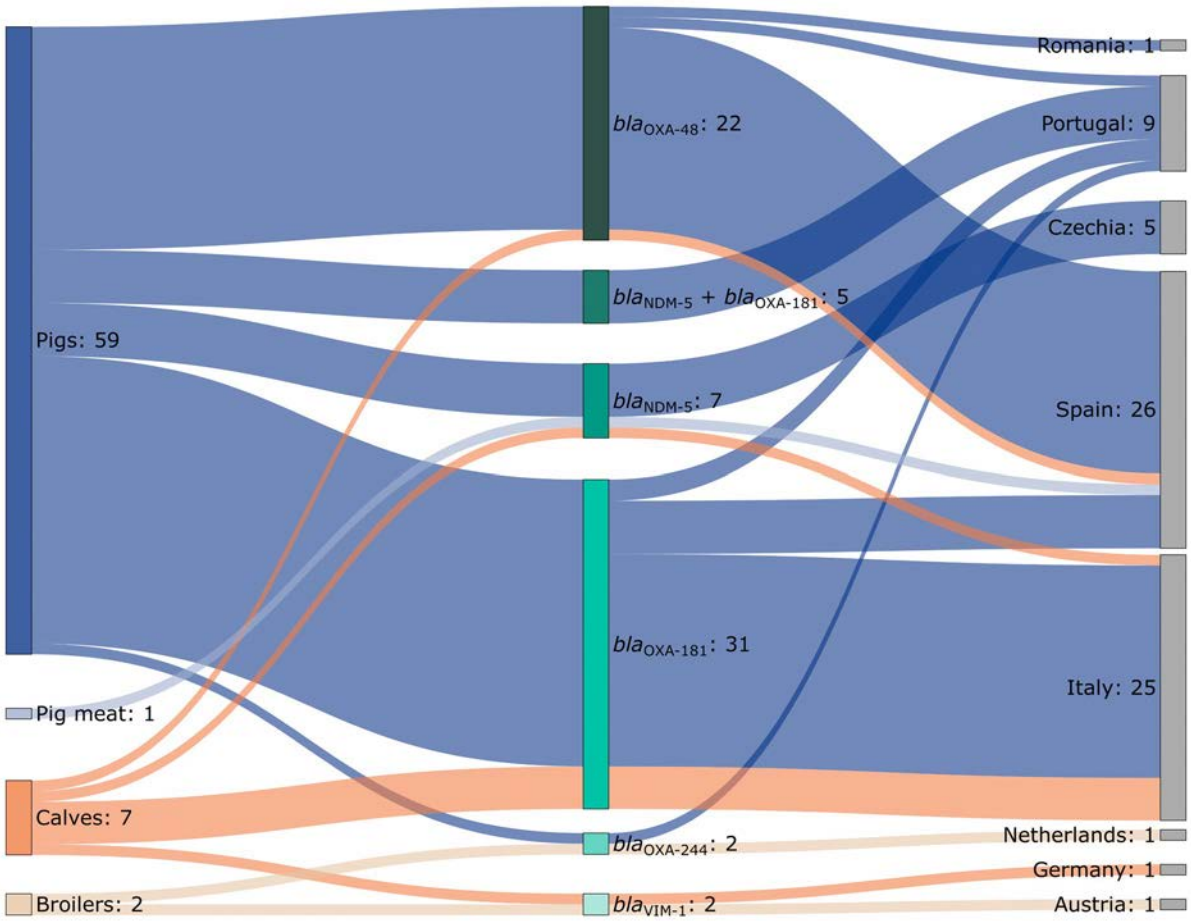


FIGURE 56 Distribution of carbapenemase-encoding genes (***bla*** genes) detected in *E. coli* from routine and specific monitoring of ESBL-, AmpC- and/or CP-producers, and from specific monitoring of CP-producers, in EU MSs, the United Kingdom (Northern Ireland) and non-MSs, 2023–2024.
Notes: The figure 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 1 year of age, seafood and pigs

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*$_{\text{NDM-5}}$** 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*$_{\text{NDM-1}}$** gene, was detected in a shrimp from India, through selective culturing (de Greeff et al., 2024).

In 2024, 10 carbapenem-resistant *E. coli* isolates carrying the ***bla*$_{\text{NDM-5}}$** gene were detected in pigs in Czechia through a targeted antimicrobial resistance monitoring, that was carried out following the positive findings in the previous year's monitoring. A total of 41 samples were tested from selected slaughterhouses and farms. In the Netherlands, one CP-producing *E. coli* isolate carrying the ***bla*$_{\text{OXA-244}}$** gene was also detected in pigs in 2024.

5.5.4 | Discussion

Carbapenems are critically important last resort antimicrobials reserved for treatment of severe human infections (WHO, 2024) and are placed in Category A ('Avoid') by EMA's AMEG categorisation, meaning they are not authorised in veterinary medicine in the EU (Commission Implementing Regulation (EU) 2022/1255[34]). In 2023 and 2024, 51,434 samples were tested under ESBL-/AmpC-/CP-specific monitoring, and 48,525 under dedicated CP-monitoring, confirming 70 CP-producing isolates. Seven isolates were detected via ESBL-/AmpC-/CP-monitoring and 63 via CP-specific monitoring.

One of the isolates detected through the CP-specific monitoring, has been confirmed as resistant to meropenem and ertapenem, for which no CP-encoding gene could be identified with the databases used for the resistance gene identification.

In 2023 and 2024, most CP-producing isolates originated from pigs ($n = 59$; predominantly harbouring $bla_{\text{OXA-181}}$, followed by $bla_{\text{OXA-48}}$, $bla_{\text{NDM-5 and }}$ $bla_{\text{OXA-244}}$) and calves ($n = 7$; which mainly carried $bla_{\text{OXA-181}}$ followed by $bla_{\text{OXA-48}}$, $bla_{\text{NDM-5}}$ **and** $bla_{\text{VIM-1}}$) while only two CP-producing isolates were detected in broilers ($bla_{\text{VIM-1}}$, $bla_{\text{OXA-244}}$). No isolates were reported from turkeys or poultry meat, whereas one isolate from pig meat carried $bla_{\text{NDM-5}}$. Notably, five pig isolates co-harboured $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$. For the first time in European livestock, $bla_{\text{OXA-244}}$ was reported in pigs in Portugal (2023) and broilers in the Netherlands (2024).

Since the start of harmonised AMR monitoring in the EU in 2014, and the inclusion of mandatory specific monitoring for carbapenemase-producing *E. coli* (CPE) in 2021, detections of CPE in food-producing animals have progressively increased. To date, 10 countries (Austria, Belgium, Czechia, Germany, Spain, Hungary, Italy, The Netherlands, Portugal, Romania) have reported positive findings in the animal populations covered in the mandatory AMR monitoring, with pigs representing the main reservoir, followed by bovines and, to a much lesser extent, poultry. CPE are thus more frequently detected in fattening pigs and calves and their derived meats than in poultry and poultry meat (EFSA, 2025).

Carbapenemase-encoding genes were first detected in 2015 and have since diversified. Gene distribution varied by source: pigs showed the greatest diversity (notably $bla_{\text{OXA-181}}$, $bla_{\text{OXA-48}}$, $bla_{\text{NDM-5}}$, $bla_{\text{VIM-1}}$), bovines mainly harboured $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$, and $bla_{\text{VIM-1}}$ predominated in poultry (EFSA, 2025).

Repeated detections across years and countries indicate persistence and possible dissemination: $bla_{\text{NDM-5}}$ in pigs in Czechia; $bla_{\text{OXA-181}}$ in pigs and bovines in Italy; $bla_{\text{OXA-48}}$ in pig in Spain; $bla_{\text{VIM-1}}$ in broilers in Austria and pig, pig meat and bovine in Germany. The highest number of detections occurred in 2021 and 2023, mainly linked to $bla_{\text{OXA-181}}$ and $bla_{\text{OXA-48}}$ in pigs from Italy and Spain, and multiple genes newly detected in Portugal. Several countries (e.g. Belgium, Romania, Hungary,) reported sporadic detections in single years, with the Netherlands reporting its first detection in 2024 ($bla_{\text{OXA-244}}$ in broilers). Overall, the increasing number of detections likely reflects both the expansion of monitoring activities and a genuine spread of carbapenemase-producing *E. coli* in European livestock (EFSA, 2025).

The $bla_{\text{OXA-181}}$ gene, a class D carbapenemase mainly associated with humans, was first detected in India in 2007 from a clinical sample (Castanheira et al., 2011) and since then, it has been reported in livestock, food and companion animals in the EU (Carfora et al., 2022; EFSA BIOHAZ Panel, 2025; EFSA and ECDC, 2025b; Ramírez-Castillo et al., 2023).

The $bla_{\text{NDM-5}}$ gene, a New Delhi Metallo-β-lactamase, was first reported in the United Kingdom in 2011 from a patient who had travelled from India (Hornsey et al., 2011) and has since become the most frequently detected carbapenemase in human *E. coli* in Europe (ECDC, 2018, 2023). Its increasing occurrence is linked to the global spread of specific *E. coli* sequence types (ST), posing a growing concern in EU/EEA countries (ECDC, 2023).

More recently, $bla_{\text{OXA-244}}$ was reported for the first time in livestock in Europe by the EU AMR monitoring in 2023 in Portugal. The gene was initially identified in humans in Spain in 2011, and it is of increasing concern due to several outbreaks and a sharp rise in detection in Europe since 2019 (ECDC, 2020, 2021; Falgenhauer et al., 2020; Izdebski et al., 2024; Kohlenberg et al., 2024; Lindemann et al., 2023; Peirano & Pitout, 2025; Welker et al., 2020). Because isolates carrying $bla_{\text{OXA-244}}$ are often difficult to detect (Hoyos-Mallecot et al., 2017; Peirano & Pitout, 2025), their occurrence in animals and food may currently be underestimated.

The co-occurrence of $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$ is worrisome and was detected for the first time in pig caecal samples in Portugal. Similar isolates, often linked to the high-risk clone ST410 in humans (Chudejova et al., 2021; Kim et al., 2021; Miller et al., 2017; Roer et al., 2018), raise concerns about possible transmission between animals and humans. Although sequence type information was not available, these findings highlight the need for genomic surveillance and further studies to clarify epidemiology and guide prevention strategies (Pitout et al., 2024).

The occurrence of CP-producing *E. coli* in livestock, food and companion animals reflects not only human-to-animal spill-over but also the potential for horizontal gene transfer via plasmids and other mobile genetic elements, as well as vertical transmission within animal populations (Carfora et al., 2022; EFSA, 2025; Irrgang et al., 2020; Madec et al., 2017). These findings highlight the importance of comprehensive surveillance, including both conventional phenotypic and genomic approaches, to monitor the spread of carbapenemase genes, identify emerging high-risk clones and support the development of targeted measures to prevent further dissemination along the food chain (Carfora et al., 2022; EFSA & ECDC, 2025b).

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

EFSA 2025 Scientific Opinion and EU Monitoring Findings on Carbapenemase-producing *E. coli*

The European Food Safety Authority (EFSA) recently published an updated scientific opinion on the occurrence and spread of carbapenemase-producing *Enterobacterales* (CPE) in food-producing animals and food within the EU and EFTA (EFSA BIOHAZ Panel, 2025a). This opinion provides an overview of data collected since 2011, highlighting that CPE remain rarely detected in the food chain but continue to emerge sporadically across countries and production sectors. The most frequently reported CP-eencoding genes include bla_{OXA-48}, $bla_{OXA-181}$, bla_{NDM-5} and bla_{VIM-1}, mainly in *E. coli* from pigs and calves. The opinion stresses the importance of harmonised monitoring and genomic characterisation to understand transmission pathways and prevent dissemination.

In this scientific opinion, EU-wide analysis of isolates recovered under the harmonised AMR monitoring (2015–2023) revealed an evolving CPE epidemiology in the food chain (Figure 57). Ten EU/EFTA countries reported positive findings, with **increasing detections in food-producing animals, particularly pigs**. Since the first detection of CP-encoding genes in 2015, several new genes have been identified over time: bla_{VIM-1} (2015), $bla_{OXA-162}$ (2016), bla_{OXA-48} and bla_{NDM-4}, (2019), $bla_{OXA-181}$ and bla_{NDM-5} (2021), and $bla_{OXA-244}$ (2023).

Repeated detections across years and countries indicate persistence and possible dissemination. bla_{VIM-1} has been recurrently detected in broilers in Austria, whereas in Germany it was identified across several matrices, including pigs, pig meat and bovines. Other genes show similar patterns: bla_{NDM-5} was reported in pigs in Czechia and in bovines in Italy, $bla_{OXA-181}$ in pigs and bovines in Italy and bla_{OXA-48} in pigs in Spain. Multiple genes (bla_{NDM-5}, bla_{OXA-48}, $bla_{OXA-181}$, bla_{VIM-1}) were detected across countries, most frequently in pigs, followed by bovines and poultry. An increase in detections was observed in 2021 and 2023 in pigs in Italy and Spain, and in 2023, Portugal reported the **first occurrence of the gene combination (bla_{NDM-5}+ $bla_{OXA-181}$)**. Some countries (e.g. Belgium, Hungary, Portugal, Norway) reported positive findings only in a single year, and trace-back investigations were performed in several cases to explore potential epidemiological links.

These findings confirm the **low but persistent occurrence of CPE** in the EU food chain and highlight the need for continued surveillance, including genomic characterisation, to track emerging resistance and potential dissemination. **Targeted monitoring in additional sources and bacterial species, combined with trace-back investigations, is recommended** to better understand CPE emergence and transmission.

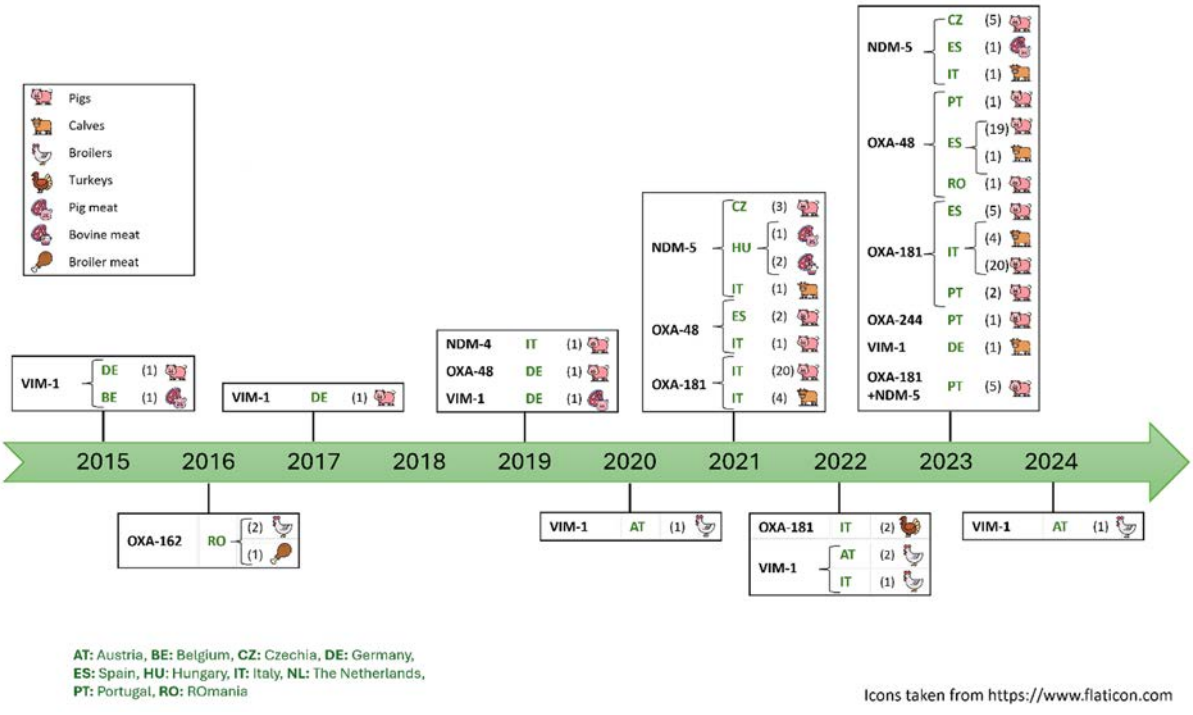


FIGURE 57 Temporal representation of the occurrence of CP-encoding genes present in CP-producing *E. coli* in targeted food-producing animals in EU MSs, the United Kingdom (Northern Ireland) and non-EU MSs, 2015–2024. Figure adapted from EFSA (2025).

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

6.1 | Key findings

- The voluntary monitoring of MRSA in food and food-producing animals in 2024 was reported by six countries. Although monitoring was not harmonised, the reported data provide useful information on the occurrence of MRSA. The results highlight the continued need for monitoring and molecular characterisation of MRSA isolates to follow the changing trends of MRSA in food-producing animals and food.
- Among MRSA isolates subjected to molecular typing in 2023 and 2024, livestock-associated (LA) clonal complex (CC) 398 remains the most reported in isolates from food and food-producing animals. Contrarily to 2023, in 2024 a few MRSA isolates from food did not carry *mecA* but *mecC*.
- Most MRSA isolates subjected to antimicrobial susceptibility testing were multidrug-resistant with high levels of erythromycin, tetracycline and tiamulin resistance reported.
- Resistance to vancomycin was not detected in 2024 but two isolates were reported to be resistant to linezolid (meat from turkey), one to rifampicin (meat from turkey) and one to mupirocin (meat from broiler chicken); these are all considered medically important antimicrobials for treatment of human infections.

6.2 | Data on MRSA addressed

Methicillin-resistant *Staphylococcus 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, antimicrobial resistance phenotype and molecular characterisation (i.e. SCC*mec* type), although 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 of human origin and are less frequently reported in food-producing animals. LA-MRSA have been detected in most food-producing animals, including those covered by the AMR monitoring performed according to Decision 2020/1729/EU. Introduction of a fourth category, wildlife-associated (WA) MRSA, has been discussed recently, 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.

In Europe, the monitoring of MRSA and related AMR in the veterinary sector is voluntary, and therefore only limited number of countries reported occurrence data in 2023 and 2024. Some countries also reported molecular data on *spa*- and/or sequence types, clonal complex and/or antimicrobial susceptibility. Therefore, the availability of comparable data on MRSA over time is limited and it is not possible to evaluate the temporal trends in occurrence of MRSA. There may also be differences in the sensitivity of detection methods used as well as sampling strategies, sample types collected and sampling stages which all should be considered when interpreting and comparing the results discussed below. A baseline study with the aim to estimate the prevalence of MRSA in fattening pigs in the EU population was performed in 2025, using healthy fattening pigs at slaughter as the target population. Details on sampling design and testing requirements are presented in Decision (EU) 2023/1017.

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 2024' published by ECDC (ECDC, 2025). Antimicrobial susceptibility in invasive *S. aureus* from humans is reported to EpiPulse Cases by the European Antimicrobial Resistance Surveillance Network (EARS-Net) hosted by ECDC. In 2025, these data were reported by all EU Member States and EEA countries. 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/EEA incidence of MRSA bloodstream infections decreased from 4.68 per 100,000 population in 2020 to 4.43 per 100,000 population in 2024 (2024 EU/EEA country range: 0.55–13.63). The EU/EEA population-weighted mean percentage of MRSA among invasive *S. aureus* isolates reported to EARS-Net decreased significantly from 16.7% in 2020 to 14.2% in 2024 (2024 EU/EEA country range: 1.9–46.0).

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 2024, the estimated total EU incidence of MRSA bloodstream infections was 20.4% lower than in 2019. As a result, the EU target for the incidence of MRSA bloodstream infections had already been reached by 2024. 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 Europe (ECDC, 2025).

6.3 | Food and animals: MRSA

Details of the occurrence of MRSA in food and food-producing animals in 2023 and 2024 are presented in Annex E and can be visualised interactively in the online EFSA dashboard on MRSA (here).

6.3.1 | Food: Monitoring of MRSA

In 2023, Austria, Germany, the Netherlands and Slovakia reported data. The occurrence of MRSA was investigated in meat from pigs (in all four countries) and meat from cattle (Austria, Germany and the Netherlands). Germany also investigated the occurrence of MRSA in shrimp, while the Netherlands also reported data from broiler, turkey, duck, deer (venison), farmed game, wild game (birds) and sheep meat (Annex E, Table 2). In 2024, Austria, Germany, Italy, the Netherlands, Norway and the Republic of North Macedonia reported data. The occurrence of MRSA was investigated in meat from broilers (in all six countries), cattle (Netherlands and the Republic of North Macedonia), venison (Netherlands), pork (Netherlands and the Republic of North Macedonia), sheep (Netherlands), turkey (Austria, Germany, Italy, the Netherlands and Norway), wild game birds (Netherlands) and crustaceans (Germany) (Annex E, Table 1).

Occurrence of MRSA in food reported from monitoring performed in 2023 and 2024 is presented in Figure 58. The number of samples collected for MRSA analysis in 2024 in Italy (broiler and turkey meat), the Republic of North Macedonia (broiler, bovine and pork meat), as well as from wild game birds in the Netherlands were insufficient to interpret the positive proportion, therefore are not included in the figure. In 2024, MRSA was frequently detected in meat from turkey: 16.2% of retail in Austria, 36.1% at retail and 56.5% at slaughter in Germany and 23.8% at retail in the Netherlands. Regarding meat from broilers, MRSA was detected in 4.6% of retail in Austria, 27.2% at slaughter in Germany, 2.4% and 6% of organic and conventional production meat in Germany, respectively, and 6.9% of retail in the Netherlands. No MRSA was detected in both retail turkey and broiler meat in Norway, as well as broiler meat samples collected at border control post in Germany. For other meat types, the Netherlands reported MRSA in 7.9% of retail pork meat, 7.6% of bovine meat (5.2% of retail beef meat and 11.3% of cattle carcasses at slaughter) and 4.5% of retail sheep meat. Germany also detected MRSA in 17.7% of crustacean retail sample.

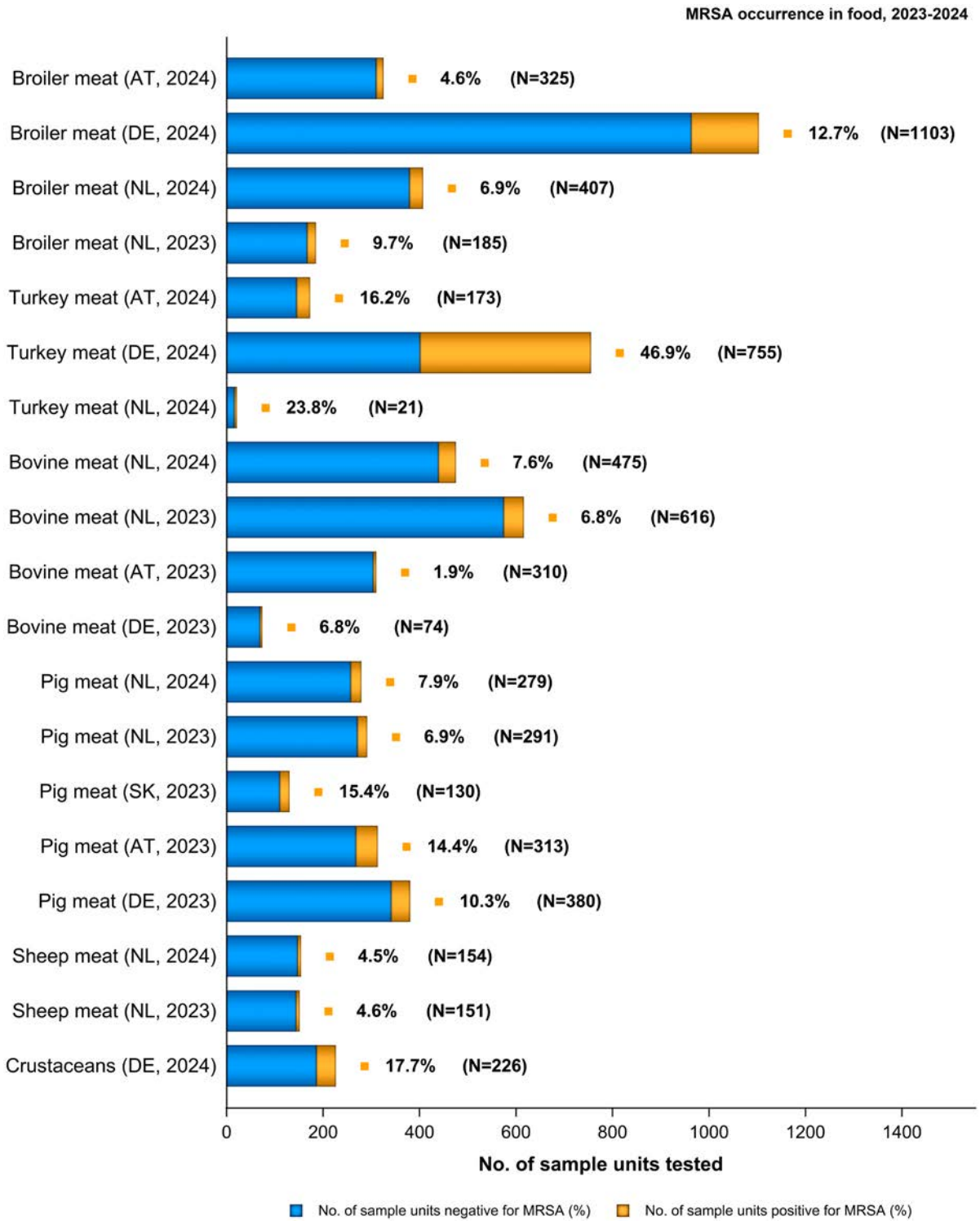


FIGURE 58 Methicillin-resistant *Staphylococcus aureus* in food, 2023 and 2024.
Notes: Only food categories where positive isolates were obtained and countries investigating > 10 samples are presented in this graph.
The isolation method used for detection of MRSA is not considered in this analysis.
Abbreviations: AT, Austria; Blue, Proportion of MRSA negative units (%); DE, Germany; *N*, Total number of sample units tested; NL, The Netherlands; NO, Norway; Orange, Proportion of MRSA positive units (%); SK, Slovakia.

6.3.2 | Animals: Monitoring of MRSA

6.3.2.1 | *Monitoring of MRSA in healthy animals*

In 2023, MRSA occurrence data in food-producing animals was 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 2024, MRSA data was reported by five MSs (Belgium, Germany, Italy, the Netherlands and Portugal) and two non-MSs (Norway and the Republic of North Macedonia). Monitoring was variable between countries and included cattle, pigs, poultry, small ruminants, horses, dogs, cats, veterinary clinics and zoos. Results of occurrence

of MRSA in food-producing animals for non-clinical investigations are detailed in Figure 59 and in Annex E – Tables 3 and 4. In 2024, MRSA occurrence was reported in fattening pigs in the Netherlands (71.1%), and in broilers from conventional farming in Germany (1.1%). MRSA was observed in different cattle categories in Belgium: in meat production animals (9.4%), dairy cows (9.5%) and calves under 1 year (44.1%). Portugal reported 11.7% and 5.4% MRSA positive samples in tested goats and sheep, respectively. No MRSA was reported in dairy cows (the Netherlands), cattle (the Republic of North Macedonia), organic broilers (Germany), broilers (Norway, the Republic of North Macedonia), pigs (Norway, the Republic of North Macedonia) and turkeys (Norway).

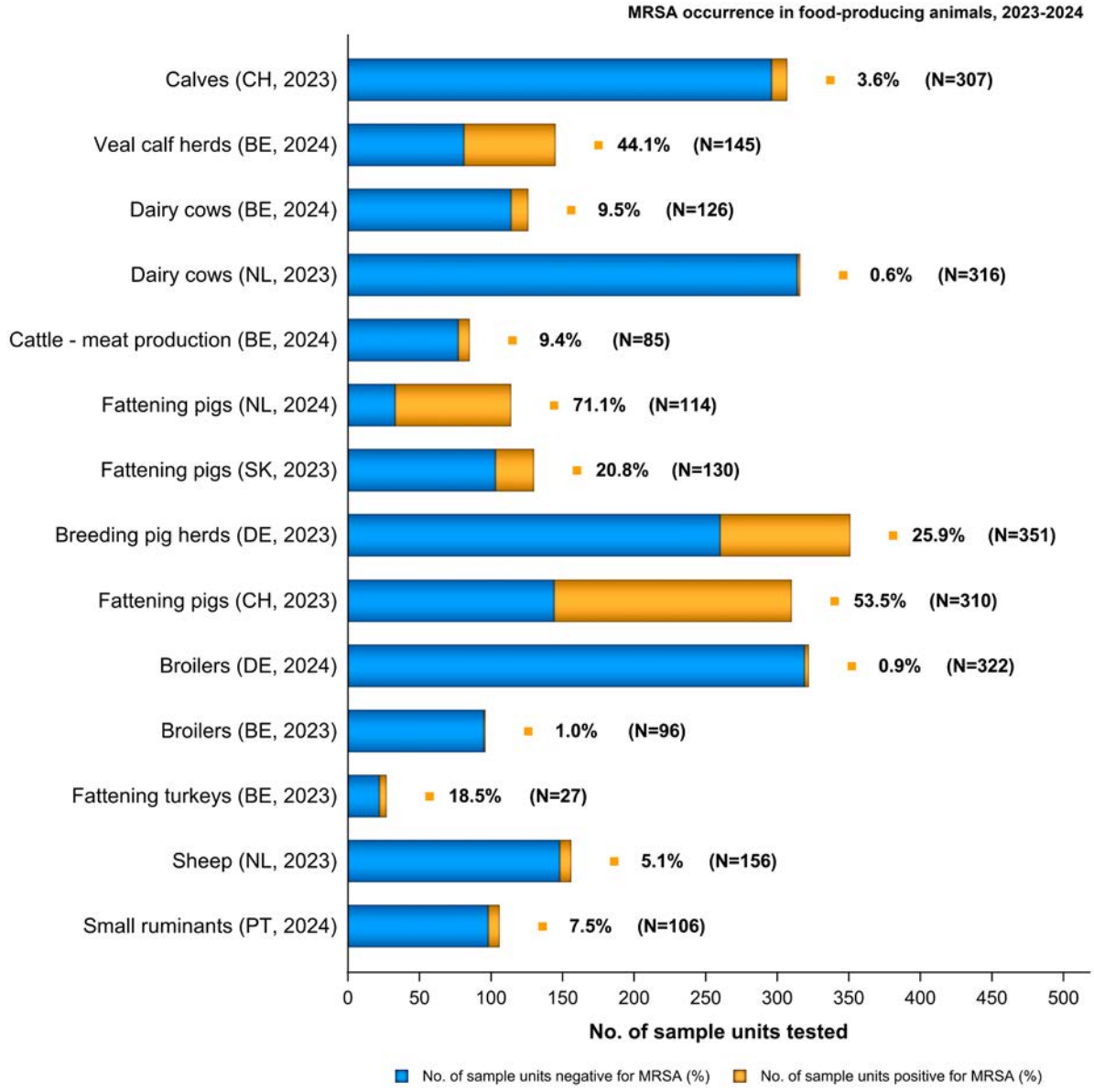


FIGURE 59 Methicillin-resistant *Staphylococcus aureus* in targeted food-producing animals, 2023 and 2024.
Notes: Only food-producing animal categories where positive isolates were obtained and countries investigating > 10 samples are presented in this graph. The isolation method used for detection of MRSA is not considered in this analysis.
Abbreviations: BE, Belgium; Blue, Proportion of MRSA negative units (%); CH, Switzerland; DE, Germany; *N*, Total number of sample units tested; NL, The Netherlands; NO, Norway; Orange, Proportion of MRSA positive units (%); PT, Portugal.

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

Clinical investigations differ from monitoring studies as the sampling is targeted to risk individuals, and selective culturing methods may not be used. Although it is relevant to recognise affected animal populations and MRSA occurrence, these data are not suited to infer prevalence or to be extrapolated to the population level but may give an indication of the occurrence of MRSA in each population. In 2024 for **food-producing animals** (Annex E – Table 5), a small number of pig samples from Norway were due to clinical investigations but resulted negative for MRSA. Following outbreak investigation, Norway also reported 29% MRSA positive samples in cattle. Italy reported one MRSA positive samples from pigs, and the Netherlands reported 14.3% MRSA occurrence in goats. For 2024 clinical investigations on **non-food-producing animals** (Annex E – Table 6), the Netherlands tested a very large number of samples with horses and zoo animals showing

the highest MRSA occurrence, i.e. 3.4% and 1.6%, respectively. Conversely, extensive dog and cat sampling resulted in extremely low occurrence (0.1%–0.2%). Norway's reporting on cats and dogs' data was negative for MRSA.

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

In 2024, molecular typing data were reported for 95 isolates from food-producing animals (poultry in Germany, small ruminants in Portugal and cattle in Belgium) and 723 isolates from food (meat from broilers and turkey in Austria and Germany, and crustaceans from Germany). *spa*-typing was reported for all isolates but one; molecular typing was reported by MLST ST for 141 isolates and by MLST CC for 372 isolates. In cases where only *spa*-type or ST were reported for an isolate, the CC was inferred based on reports in the literature. This is not an approximation of the membership to clonal complex since these are different typing methods and overlap in membership likely changes over time and origin of the isolates. The inferences made for this analysis are detailed in Annex E – Table 8. *spa*-type results can be explored interactively in the MRSA dashboard available here, while molecular typing results are presented in Tables 27, 28 and Figure 60. Isolates that were *spa* typed but not typed with MLST or with undefined clonal complex are not included in these tables and figure.

As in 2023, in 2024 the most frequently reported clonal complex was CC398, mostly associated with t899, t034 and t011 in food, and predominantly with t011 in food-producing animals (Table 27). In 2024, very few non-CC398 isolates were reported (CC1, CC5, CC8, CC22, CC30, CC45 and CC692), associated to a range of different *spa*-types (Table 28). The inferences made for this analysis are detailed in Annex E – Table 8. Among MRSA isolates subjected to molecular typing in 2024, livestock-associated (LA) – CC398 was the most reported CC in both isolates from food and food-producing animals (93%–98%); hospital-associated (HA) and community-associated (CA) non-CC398 were sparsely reported in food (0.4%–2.1%) (Figure 60). Regarding the characterisation of *mec* genes, contrarily to 2023 where all MRSA isolates carried *mecA*, in 2024, 10 isolates did not carry *mecA*. Of these, five carried the *mecC* gene and were resistant to cefoxitin (5/5), chloramphenicol (1/5), penicillin (5/5) and tetracycline (2/5) (Annex E – Table 8).

TABLE 27 *spa*-types of CC398 and their detection in animals and food, 2023 and 2024.

spa-type[§]	Year	Animals (*N*)	Total	Food (*N*)	Total
t034	2024	*Gallus gallus* (fowl) (3)	3	Crustaceans (1), Meat from broilers (*Gallus gallus*) (79), Meat from turkey (185)	265
	2023	Pigs (38)	38	Meat from bovine animals (3), Meat from pig (19)	22
t011	2024	Cattle (bovine animals) (66)	66	Meat from broilers (*Gallus gallus*) (34), Meat from turkey (56)	90
	2023	*Gallus gallus* (fowl) (1), Pigs (19), Turkeys (5)	25	Meat from bovine animals (3), Meat from pig (30)	33
t899*	2024		0	Meat from broilers (*Gallus gallus*) (6), Meat from turkey (68)	74
	2023	Pigs (6)	6	Meat from pig (8)	8
t2011	2024	Cattle (bovine animals) (5)	5		0
	2023	Pigs (6)	6	Meat from pig (6)	6
t1451	2024	Cattle (bovine animals) (2)	2	Meat from turkey (4)	4
	2023	Pigs (2)	2	Meat from pig (3)	3
t6575	2024		0	Meat from turkey (3)	3
	2023	Pigs (3)	3		0
t21298	2024		0	Meat from broilers (*Gallus gallus*) (1), Meat from turkey (3)	4
t8588	2024		0	Crustaceans (1), Meat from turkey (3)	4
t1344	2024	Cattle (bovine animals) (1)	1	Meat from broilers (*Gallus gallus*) (2)	2
t2970	2024	Cattle (bovine animals) (3)	3		0
t10485	2024		0	Meat from turkey (2)	2
t108	2024	Cattle (bovine animals) (1)	1		0
	2023	Pigs (1)	1		0
t1255	2024		0	Meat from turkey (2)	2
	2023		0	Meat from pig (1)	1
t1456	2024	Cattle (bovine animals) (1)	1		0
	2023	Pigs (1)	1		0
t2922	2023	Pigs (2)	2		0

(Continues)

TABLE 27 (Continued)

spa-type[§]	Year	Animals (*N*)	Total	Food (*N*)	Total
t12314	2024		0	Meat from broilers (*Gallus gallus*) (2)	2
t1580	2023		0	Meat from pig (1)	1
t1606	2024	Cattle (bovine animals) (1)	1	Meat from broilers (*Gallus gallus*) (1)	1
t16666	2023	Pigs (1)	1		0
t19248	2023	Pigs (1)	1		0
t22059	2024		0	Crustaceans (1)	1
t2346	2024	Cattle (bovine animals) (1)	1		0
t3075	2023	Pigs (1)	1		0
t3423	2024	Cattle (bovine animals) (1)	1		0
t4132	2024		0	Meat from broilers (*Gallus gallus*) (1)	1
t5524	2023		0	Meat from pig (1)	1
t588	2024	Cattle (bovine animals) (1)	1		0
t6606	2024		0	Meat from broilers (*Gallus gallus*) (1)	1
t6608	2023	Pigs (1)	1		0
t779	2024		0	Meat from broilers (*Gallus gallus*) (1)	1

Abbreviation: *N*, number of isolates.

[§]data retrieved from the prevalence data model.

*t899: *spa*-type t899 occurs both in Tables 1 and 2 since it has been identified in the current data in both clonal complex CC398 and CC1. Isolates of *spa*-type t899 where only *spa*-typing was available were inferred to be CC398.

TABLE 28 *spa*-types from clonal complexes other than CC398 and their detection in animals and food, 2023 and 2024.

spa-type[§¥]	Year	Animals (*N*)	Total	Food (*N*)	Total
t1430	2024		0	Meat from turkey (5)	5
	2023		0	Meat from pig (5)	5
t127	2024		0	Crustaceans (5), Meat from broilers (*Gallus gallus*) (1), Meat from turkey (2)	8
	2023		0	Meat from pig (1)	1
t002	2024		0	Meat from broilers (*Gallus gallus*) (2), Meat from turkey (1)	3
	2023		0	Meat from bovine animals (4)	4
t008	2024		0	Crustaceans (3)	3
	2023		0	Meat from bovine animals (1), Meat from pig (1)	2
t10204	2024		0	Meat from turkey (1)	1
	2023	Pigs (1)	1		0
t330	2024		0	Meat from broilers (*Gallus gallus*) (2)	2
t1419	2023		0	Meat from pig (1)	1
t1422	2024		0	Meat from turkey (1)	1
t177	2024	Cattle (bovine animals) (1)	1		0
t20072	2023		0	Meat from pig (1)	1
t023	2024		0	Meat from broilers (*Gallus gallus*) (1)	1
t309	2024		0	Crustaceans (1)	1
t3512	2023		0	Meat from pig (1)	1
t693	2023		0	Meat from pig (1)	1
t8425	2024		0	Meat from turkey (1)	1
t899*	2023		0	Meat from pig (1)	1

Abbreviation: *N*, number of isolates.

[§]Data retrieved from the prevalence data model.

[¥]Isolates that were *spa* typed but not typed with MLST or with undefined clonal complex are not included in this table.

*t899: *spa*-type t899 occurs both in Tables 1 and 2 since it has been identified in the current data in both clonal complex CC398 and CC1. Isolates of *spa*-type t899 where only *spa*-typing was available were inferred to be CC398 and reported in Table 27.

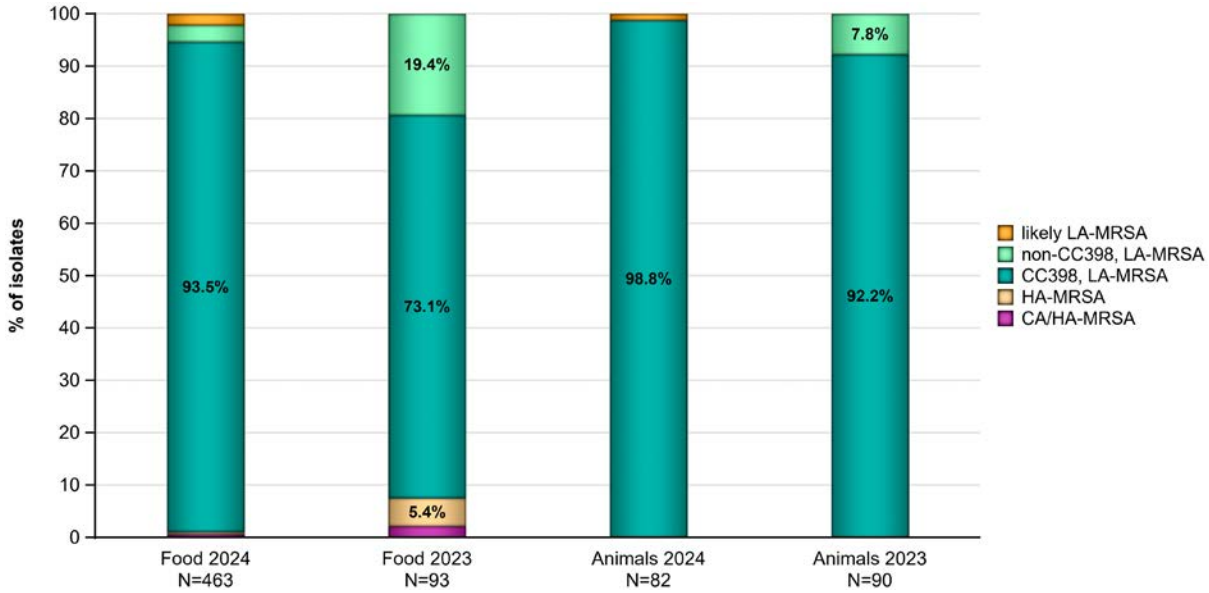


FIGURE 60 Methicillin-resistant *Staphylococcus aureus* types inferred from molecular typing data reported from food and animals, 2023 and 2024.
Abbreviations: CA-MRSA, community-associated MRSA; CC, clonal complex; HA-MRSA, hospital-associated MRSA; LA-MRSA, livestock-associated MRSA; *N*, Number of isolates with typing data (for some 2024 isolates it was not possible to infer molecular typing, therefore are not included).

6.4 | Summary data on the occurrence and susceptibility of MRSA

Antimicrobial susceptibility testing and monitoring of antimicrobial resistance (AMR) patterns in different MRSA lineages is important to monitor possible sources of resistance genes with potential to disseminate to other more virulent *S. aureus* strains (Haaber et al., 2017; Sahibzada et al., 2017). In 2024, antimicrobial susceptibility data were reported for 534 isolates from Germany ($n = 483$), Austria ($n = 43$) and Portugal ($n = 8$). Broth microdilution and EUCAST epidemiological cut-offs (ECOFFs) were used to determine the antimicrobial susceptibility of MRSA isolates from food-producing animals and meat. Detailed data on the occurrence of AMR in MRSA isolates from food-producing animals and food reported in 2023 and 2024 can be found in Annex E, Tables 10 and 11 and Figures 1 and 2.

Pertaining to medically important antimicrobials, no resistance to linezolid, vancomycin, nor fusidic acid was reported in 2023, while resistance to rifampicin was reported in a limited number of isolates. In 2024, no resistance to vancomycin was detected. Conversely, two isolates from Germany and Austria were reported as linezolid resistant (meat from turkey at slaughter and retail, respectively). The German isolate was classified as non-CC398 while the Austrian isolate as CC398 associated with *spa*-type t34. Additionally, one German isolate was resistant to rifampicin (meat from turkey) and another one to mupirocin (meat from broiler chicken); information on MLST and CC was not provided for these isolates, as analysis is not performed routinely. High levels of tiamulin (118/139) and tetracycline (128/139) resistance was also observed in isolates originating from meat from broilers. Similarly, high levels of resistance to tiamulin (269/350) and tetracycline (311/350) were found in isolates from meat from turkeys. As expected, nearly all isolates were resistant to penicillin (526/534) and cefoxitin (533/534), except for one German isolate from food susceptible to cefoxitin, and eight isolates from food or animal susceptible to penicillin (Germany and Portugal). For the remaining antimicrobial substances, the levels of resistance varied markedly between the different animal populations and food matrices tested.

Most MRSA isolates subjected to antimicrobial susceptibility testing in 2024 were multidrug-resistant (MDR) (523/534 = 97.9%), where MDR is defined as resistance to three or more antimicrobial classes. The most reported MDR pattern in both 2023 (12.2%) and 2024 (29.6%) was cefoxitin, clindamycin, erythromycin, penicillin, quinupristin/dalfopristin, tetracycline, tiamulin and trimethoprim (Annex E – Tables 12 and 13).

6.5 | Discussion

In 2024, the occurrence of MRSA was highly variable by country and sample origin. MRSA was detected in animal populations (food production and companion animals) and food sources. However, the limited and not harmonised monitoring does not provide comparable information on the occurrence of MRSA in food and food-producing animals.

Some countries reported molecular typing data on *spa*-types, STs and/or CCs. As in previous years, the most reported/inferred type for 2024 was LA-MRSA CC398 in animal populations and food matrices. LA-MRSA CC398 (Armand-Lefevre et al., 2005; Voss et al., 2005) has persisted in the European pig production since 2005. 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 associated mainly with *spa*-type t899. This *spa*-type 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) and has been linked to poultry with a sub-population that appears to be adapted to humans and poultry (Larsen et al., 2016; Tegegne et al., 2021).

In 2024, a few isolates did not carry *mecA* but *mecC* gene. The *mecC* gene has been detected in a limited number of isolates in previous years (EFSA and ECDC, 2021, 2022, 2023, 2024). Although the primary host for *mecC* is 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; Cui et al., 2021; Giacinti et al., 2017; Haenni et al., 2014; Schauer et al., 2018; Unnerstad et al., 2013) and in companion animals (Dewulf et al., 2025). Although rare, susceptibility to penicillin or cefoxitin in *mecA*–positive *S. aureus* has been reported as a combination of different mutations in the *mecA* promoter region (Harrison et al., 2019; Liang et al., 2022).

In 2024, resistance to the medically important antimicrobials vancomycin was not reported. However, sporadic resistance to linezolid, rifampicin and mupirocin was observed. All the above are considered medically important antimicrobials for treatment of human infections and should be avoided in veterinary medicine. Rifampicin 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, 2024); mupirocin is used for MRSA decolonisation (Deeny et al., 2015; Hetem & Bonten, 2013; Poovelikunnel et al., 2015) while linezolid is primarily used to treat infections by MRSA and vancomycin-resistant Enterococci (VRE) (Hashemian et al., 2018). Resistance to linezolid in the veterinary field has been attributed to the *cfr*-genes, responsible for resistance to oxazolidinones, phenicols, streptogamin 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; Timmermans et al., 2022). The use of tiamulin in food-producing animals has given rise to concerns regarding proliferation of the *cfr* gene (EMA/CVMP/AWP, 2014). Not surprisingly, tetracycline resistance was reported in high levels, since most isolates were typed as CC398, frequently carrying tetracycline resistance genes, especially *tet*(M) and sometimes *tet*(K) (Larsen et al., 2016). Tetracycline is still one of the most used antimicrobials in veterinary medicine (EMA, 2025) and various *tet* genes appear to have been integrated into SCCmec (Li et al., 2011; Price et al., 2012). Similarly, the high levels of tiamulin resistance are likely linked with the exclusive use of this class of antibiotics in veterinary settings (EMA/CVMP/AWP, 2014). MDR phenotypes were observed in most isolates subjected to susceptibility testing. It should be noted that the occurrence of resistance to antimicrobials used for treatment and control of human MRSA infections were overall rare or very low. Since the use of antimicrobials for food-producing animals in Europe has decreased in recent years, with a potential decrease in resistance including MRSA, the reason for the occurrence of MDR might be sought in potential MRSA reservoirs, like colonised veterinarians or farm workers, who could contribute to persistence of MRSA in the animal populations (Crespo-Piazuelo & Lawlor, 2021). Cross-contaminations could occur during transportation and lairage (Bangerter et al., 2016; Grøntvedt et al., 2016), or in general through the production pyramid (Höjgård et al., 2015; Olsen et al., 2018). High levels of biosecurity and hygiene at all levels of animal production (Grøntvedt et al., 2016; Komodromos et al., 2022) remain the best measure to minimise MRSA introduction and/or transmission and consequent MDR spread. The results of the MRSA prevalence baseline study in 2025 (Decision (EU) 2023/1017), will provide further insights thanks to harmonised data collection (EFSA, 2022) on the current prevalence of MRSA in pigs, the most common clonal types and the different antimicrobial-resistant profiles across the EU.

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 2023 and 2024 was performed in a limited number of MSs, ranging from three to seven reporting MSs depending on *Enterococcus* spp. and animal population.
- Occurrence of resistance differed greatly among *Enterococcus* spp., animal populations and reporting MSs.
- Resistance to clinically-relevant antimicrobials such as gentamicin, vancomycin, linezolid, daptomycin and tigecycline was either not detected or occurred in very low and low proportion of isolates, with the only exception of gentamicin resistance.
- Resistance to **gentamicin** was mainly observed in *E. faecalis* isolates from cattle under 1 year of age and fattening pigs, occurring in a moderate proportion of isolates (13.6% for cattle isolates and 11.6% for pig isolates). In contrast, gentamicin resistance in *E. faecium* from cattle and pigs, and in both enterococci species from poultry, was observed only in a very low and low proportion of isolates.
- Resistance to **vancomycin** was only observed among *E. faecium* isolates from cattle under 1 year of age and fattening pigs, ranging from very low (0.2% in pigs) to low (1.5% in cattle).
- Occurrence of resistance to **linezolid** was low in *E. faecalis* isolates from cattle under 1 year of age and fattening pigs (6.6% and 2.0%, respectively). In *E. faecalis* from poultry and in *E. faecium* from all animal populations monitored, linezolid resistance was not detected or occurred in very low (0.2%–0.6%) proportions of isolates.

7.2 | Data on *Enterococcus* spp. addressed

This section focuses on *E. faecalis* and *E. faecium* and summarises the occurrence of AMR in isolates recovered from food-producing animal populations. *E. faecalis* and *E. faecium* are commensals in the gut microbiota of humans and animals, and can also become opportunistic pathogens causing various types of localised and systemic infections (Gilmore et al., 2013). Additionally, *E. faecalis* and *E. faecium* have the ability to acquire and transfer AMR genes via horizontal gene transfer (Gilmore et al., 2013). For these reasons, enterococci are considered useful indicators for surveillance of AMR in food-producing animals.

In the framework of the Commission Implementing Decision (EU) 2020/1729 (European Commission, 2020) and EFSA Technical specifications (EFSA, 2019), the harmonised monitoring[35] and reporting of AMR in *Enterococcus* spp. from food-producing animals focuses on the species *E. faecalis* and *E. faecium* and is voluntary.

7.3 | Food-producing animals: Occurrence of antimicrobial resistance in *Enterococcus*

7.3.1 | Data reported

Data on *Enterococcus* spp. were reported by a small number of countries ranging from three to nine countries depending on the *Enterococcus* spp. and animal population (Table 29). The lowest number of countries reporting data was three for *E. faecalis* and *E. faecium* from fattening turkeys, whereas the highest number of countries reporting data was nine for *E. faecium* from broilers.

Countries reporting data on *Enterococcus* spp. provided information on both *E. faecalis* and *E. faecium* per each of the animal populations they examined, with the exceptions of Denmark that, in case of pigs, reported data only for *E. faecalis*, and North Macedonia that, in case of broilers, reported data only for *E. faecium*. There were notable differences in the numbers of isolates reported by the various countries for the different *Enterococcus* spp. and animal populations (Table 29).

TABLE 29 Overview of countries reporting antimicrobial resistance data for *Enterococcus* spp. from targeted food-producing animals, 2023–2024.

			Number of isolates per country									
***Enterococci* species**	**Year**	**Animal population**	**BE**	**DE**	**DK**	**ES**	**IT**	**NL**	**SI**	**Total MSs**	**MK**	**NO**
E. faecalis	2024	Broilers	184	122	17	80	17	98	43	561	–	100
		Fattening turkeys	–	165	–	119	23	–	–	307	–	–
	2023	Calves	90	87	–	2	19	–	–	198	4	–
		Fattening pigs	56	41	87	69	18	–	30	301	4	61
E. faecium	2024	Broilers	148	120	278	90	172	269	42	1119	1	312
		Fattening turkeys	–	133	–	51	170	–	–	354	–	–
	2023	Calves	138	92	–	8	170	–	–	408	11	–
		Fattening pigs	167	33	–	101	166	–	43	510	13	86

Abbreviations for reporting countries can be found here.

The data on occurrence of AMR in *E. faecalis* and *E. faecium* from food-producing animals reported by MSs and non-MSs in 2024 and 2023 are available in Annex F1 (Annex F1; Tables 1–4) as supporting documentation on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17950222

This chapter summarises the data reported by the MSs.

7.3.2 | Occurrence of antimicrobial resistance

Remarkable differences in the occurrence of resistance to the 12 antimicrobials included in the monitoring were observed among *Enterococcus* spp., animal populations and reporting MSs. Overall, when considering all animal populations and all MSs together, occurrence of resistance was highest for antimicrobials such as quinupristin-dalfopristin in *E. faecium*, and erythromycin and tetracycline in both enterococci species. Lowest occurrence of resistance was observed in both enterococci species for antimicrobials such as daptomycin, teicoplanin and vancomycin.

When considering all the animal populations monitored and the aggregated data from MSs, occurrence of resistance to **tetracyclines** (Tables 30 and 31 and Annex F1 – Tables 1–4) was extremely high (70.4%–82.8%) among *E. faecalis* isolates, and high to very high (34.6%–53.7%) among *E. faecium* isolates. 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 fattening turkeys (77.8%), broilers

[35]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.

(73.4%) and fattening pigs (70.4%). For ***E. faecium***, the highest level of resistance to tetracyclines was observed in isolates from fattening turkeys (53.7%), followed by cattle under 1 year of age (51.5%), fattening pigs (51%) and broilers (34.6%).

Occurrence of **erythromycin** resistance (Tables 30 and 31 and Annex F1 – Tables 1–4) was very high among *E. faecalis* (ranging from 50.8% to 62.0%) and high in *E. faecium* (ranging from 23.9% to 49.0%) isolates from all the animal populations, and when pooling data from all reporting countries. For ***E. faecalis***, the highest occurrence of erythromycin resistance was observed in isolates from broilers (62.0%), followed by cattle under 1 year of age (60.1%), fattening turkeys (58.6%) and fattening pigs (50.8%). For ***E. faecium***, the highest level of erythromycin resistance was observed in isolates from cattle under 1 year of age (49.0%), followed by fattening turkeys (38.4%), broilers (33.2%) and fattening pigs (23.9%).

Occurrence of resistance to **quinupristin/dalfopristin** (Tables 30 and 31 and Annex F1 – Tables 1–4) in ***E. faecium*** ranged from very high (65.2%) in broilers to extremely high (77.4%–82.8%) in the remaining animal populations monitored.

Resistance to **daptomycin, teicoplanin** and **vancomycin** (Tables 30 and 31 and Annex F1 – Tables 1–4) was not detected in ***E. faecalis*** isolates from almost all animal populations, with the exception of daptomycin resistance in fattening pigs (1.3%). In ***E. faecium*** isolates, no daptomycin resistance was detected in any animal population. A very low (0.1%) occurrence of teicoplanin resistance in *E. faecium* was observed in broilers, and very low (0.2%) and low (1.5%) occurrence of vancomycin resistance were reported in isolates from fattening pigs and calves, respectively.

Resistance to **ampicillin** (Tables 30 and 31 and Annex F1 – Tables 1–4) was not detected in ***E. faecalis*** from cattle under 1 year of age, fattening pigs and fattening turkeys and was very low (0.4%) in *E. faecalis* from broilers. Among ***E. faecium*** isolates, occurrence of ampicillin resistance was low in all animal populations from all countries (when analysing aggregated results), ranging from 5.7% in fattening pigs to 9.8% in cattle under 1 year of age.

Occurrence of resistance to **gentamicin** (Tables 30 and 31 and 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 (0.6%–4.2%). In both *E. faecalis* and *E. faecium*, the highest occurrence of gentamicin resistance was 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), whereas the lowest occurrence of gentamicin resistance was observed in isolates from broilers (0.5% and 0.6%, respectively). In isolates from fattening turkeys, occurrence of gentamicin resistance was very low (0.3%) for *E. faecalis* and low (1.7%) for *E. faecium*.

Occurrence of resistance to **linezolid** (Tables 30 and 31 and Annex F1 – Tables 1–4) ranged from very low to low among ***E. faecalis*** (0.2%–6.6%) across all animal populations. In ***E. faecium*** isolates, occurrence of resistance was very low (0.3%–0.6%) in all animal populations, except in fattening turkeys, where linezolid resistance was not detected. The highest levels of resistance were detected in *E. faecalis* from cattle under 1 year of age (6.6%) followed by fattening pigs (2.0%), whereas linezolid resistance was very low in *E. faecalis* from fattening turkeys and broilers (0.3% and 0.2%, respectively).

Resistance to **ciprofloxacin** (Tables 30 and 31 and Annex F1 – Tables 1–4) occurred in low proportion of ***E. faecalis*** (1.1%–5.2%) and ***E. faecium*** (2.3–%5.0%) isolates in all animal populations and all MSs, when considering aggregated results. In *E. faecalis*, lowest and highest occurrence of ciprofloxacin resistance was observed in isolates from broilers (1.1%) and fattening turkeys (5.2%), respectively. In *E. faecium*, lowest and highest occurrence of ciprofloxacin resistance was observed in isolates from fattening turkeys (2.3%) and broilers (5.0%), respectively.

Resistance to **tigecycline** (Tables 30 and 31 and Annex F1 – Tables 1–4) was not detected in ***E. faecalis*** and ***E. faecium*** from cattle under 1 year of age and fattening turkeys, respectively, when considering aggregated results from all MSs. In the remaining animal populations, and when analysing aggregated data from the reporting MSs, resistance to **tigecycline** ranged from very low to low both in ***E. faecalis*** (1.0%–3.3%) and ***E. faecium*** (0.8%–1.5%). For ***E. faecalis***, the highest occurrence (3.3%) of tigecycline resistance was reported in isolates from fattening turkeys. For ***E. faecium***, the highest occurrence (1.5%) of tigecycline resistance was observed in isolates from cattle under 1 year of age.

Occurrence of resistance to **chloramphenicol** (Tables 30 and 31 and Annex F1 – Tables 1–4) ranged from very low to low among ***E. faecium*** (0.5%–2.2%) isolates, and from low to high among ***E. faecalis*** isolates (1.1%–37.4%) from all the animal populations and all MSs, when considering aggregated results. For ***E. faecalis***, the highest occurrence of chloramphenicol resistance was observed in isolates from cattle under 1 year of age (37.4%) and fattening pigs (22.9%), whereas in isolates from fattening turkeys and broilers chloramphenicol resistance occurred in low proportions of isolates (3.3% and 1.1%, respectively). For ***E. faecium***, the highest occurrence of chloramphenicol resistance was reported among isolates from cattle under 1 year of age (2.2%) and fattening pigs (2.0%), while the lowest occurrence was observed in isolates from broilers and fattening turkeys, (0.5% and 0.6%, respectively).

7.3.3 | Discussion

Based on the data reported using harmonised sampling schemes and methods for monitoring of antimicrobial resistance, it is clear that occurrence of resistance differed greatly among *Enterococcus* spp., animal populations and reporting MSs. Resistance was mainly observed towards antimicrobials like erythromycin and tetracycline, belonging to antimicrobial classes listed in category C and D of the AMEG categorisation, which likely reflects the selective pressure to which gut bacteria in animal populations are exposed to. It is reassuring to observe that resistance to medically important antimicrobials such as gentamicin, vancomycin, linezolid, daptomycin and tigecycline was mostly not detected or occurred in very low and low proportions of isolates, with few exceptions described in this chapter. However, resistance to antimicrobials used in veterinary settings may represent a risk factor for co-selection of resistance to medically important antimicrobials, if the resistance determinants become genetically linked.

To improve our understanding of the epidemiology of antimicrobial-resistant enterococci in animal populations and to elucidate the potential contribution of enterococci from animals and food to public health problems, it would be interesting to obtain also genomic data to better define the clones, plasmids and genetic determinants associated with antimicrobial resistance in *E. faecalis* and *E. faecium* from animal populations.

TABLE 30 Occurrence of resistance to selected antimicrobials in *Enterococcus faecalis* isolates from targeted food-producing animals, EU MSs, 2023–2024.

Animal population	AMP %R	CHL %R	CIP %R	DPT %R	ERY %R	GEN %R	LZD %R	Q/D* %R	TEC %R	TET %R	TGC %R	VAN %R
Broilers, 2024 (*N* = 561; 7 MSs)	0.4	1.1	1.1	0.0	62.0	0.5	0.2	98.6	0.0	73.4	2.1	0.0
Fattening turkeys, 2024 (*N* = 307; 3 MSs)	0.0	3.3	5.2	0.0	58.6	0.3	0.3	97.4	0.0	77.8	3.3	0.0
Calves, 2023 (*N* = 198, 4 MSs)	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 (*N* = 301; 6 MSs)	0.0	22.9	4.0	1.3	50.8	11.6	2.0	98.3	0.0	70.4	1.0	0.0

Notes: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. A blank cell represents no resistance, except in Q/D in *E. faecalis*. The correspondence between colour and resistance level can be found in the 'Definitions' section.

**E. faecalis* has an expected phenotype of Q/D resistance. Of note, an ECOFF of 32 mg/L was established by EUCAST (www.eucast.org).

Abbreviations: AMP, ampicillin; CHL, chloramphenicol; CIP, ciprofloxacin; DPT, daptomycin; ERY, erythromycin; GEN, gentamicin; LZD, linezolid; *N*, Total number of isolates tested; Q/D, quinupristin/dalfopristin; %R, percentage of resistant isolates; TEC, teicoplanin; TET, tetracycline; TGC, tigecycline; VAN, vancomycin.

TABLE 31 Occurrence of resistance to selected antimicrobials in *Enterococcus faecium* isolates from targeted food-producing animals, EU MSs, 2023–2024.

Animal population	AMP %R	CHL %R	CIP %R	DPT %R	ERY %R	GEN %R	LZD %R	Q/D %R	TEC %R	TET %R	TGC %R	VAN %R
Broilers, 2024 (*N* = 1119; 7 MSs)	7.2	0.5	5.0	0.0	33.2	0.6	0.4	65.2	0.1	34.6	0.8	0.0
Fattening turkeys, 2024 (*N* = 354; 3 MSs)	6.5	0.6	2.3	0.0	38.4	1.7	0.0	77.4	0.0	53.7	0.0	0.0
Calves, 2023 (*N* = 408, 4 MSs)	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 (*N* = 510; 5 MSs)	5.7	2.0	4.1	0.0	23.9	1.6	0.6	82.8	0.0	51.0	1.0	0.2

Notes: The shades of blue indicate different levels of antimicrobial resistance, from rare to extremely high. A blank cell represents no resistance. The correspondence between colour and resistance level can be found in the 'Definitions' section.

Abbreviations: AMP, ampicillin; CHL, chloramphenicol; CIP, ciprofloxacin; DPT, daptomycin; ERY, erythromycin; GEN, gentamicin; LZD, linezolid; *N*, Total number of isolates tested; Q/D, quinupristin/dalfopristin; %R, percentage of resistant isolates; R, resistant; TEC, teicoplanin; TET, tetracycline; TGC, tigecycline; VAN, vancomycin.

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*; ESBL; extended-spectrum β-lactamase
% R	percentage of resistant isolates
%	percentage
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
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
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
WGS	whole genome sequencing
WHO	World Health Organization

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

MSs of the EU

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-Ms reporting countries

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

DEFINITIONS

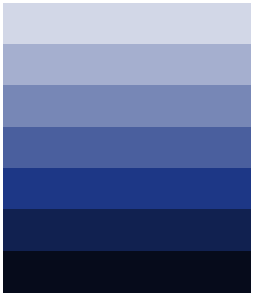
'Antimicrobial-resistant isolate' In the case of quantitative data, an isolate was defined as 'resistant' to a selected antimicrobial when its minimum inhibitory concentration (MIC) value (in mg/L) was above the cut-off value or the disc diffusion diameter (in mm) was below the cut-off value. The cut-off 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 2024

Data reported to EpiPulse Cases

EU Member states (MSs) report results from antimicrobial susceptibility testing of *Salmonella* spp. and *Campylobacter* spp. isolated from clinical cases in humans to the European Centre for Disease Prevention and Control (ECDC) on an annual basis. For the collection of 2024 data, ECDC had implemented a new surveillance system, EpiPulse Cases, which replaced The European Surveillance System, TESSy. Data can be submitted to the ECDC and EpiPulse Cases 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 raw or assembled sequences for analysis of resistance determinants and predicted phenotype in ECDC using ResFinder and PointFinder. The reporting of phenotypic quantitative data via 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 2024, 27 MSs, plus Iceland and Norway provided data on antimicrobial resistance (AMR) in human *Salmonella* isolates. Twenty-one countries reported measured values and three reported results interpreted as susceptible standard dosing regimen, susceptible increased exposure or resistant (SIR) according to the clinical breakpoints (CBPs) applied. Five 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 2024, 23 MSs, plus Iceland and Norway provided AMR data from human isolates. Sixteen 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*, seven 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. Five countries used sequencing (Table A.1). For *Campylobacter*, nine MSs and Iceland used only DDs for their AST, five MSs used DL, one MS and Norway used DLG and one 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 2024, all MSs except one 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, 2016). 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. Twelve MSs reported AST results on colistin, 16 and 1 non-MS on azithromycin and 14 on tigecycline for 2024.

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 2024, 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 2024 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 2024, all reporting countries tested the isolates against the three main antimicrobials ciprofloxacin, erythromycin and tetracycline. In relation to *Campylobacter jejuni* isolates, 18 reporting countries also tested for gentamicin and eight tested for co-amoxiclav. With regards to *Campylobacter coli* isolates, 18 reporting countries also tested these isolates for gentamicin and seven 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, 2025). 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, 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, except for meropenem, where the MIC for the non-susceptible category is substantially higher (+ 4 dilutions) than the ECOFF. For *Campylobacter*, there is full agreement across interpretive categories, except for the EUCAST ECOFF for tetracycline in *C. jejuni*, which is one dilution below the EUCAST CBP.

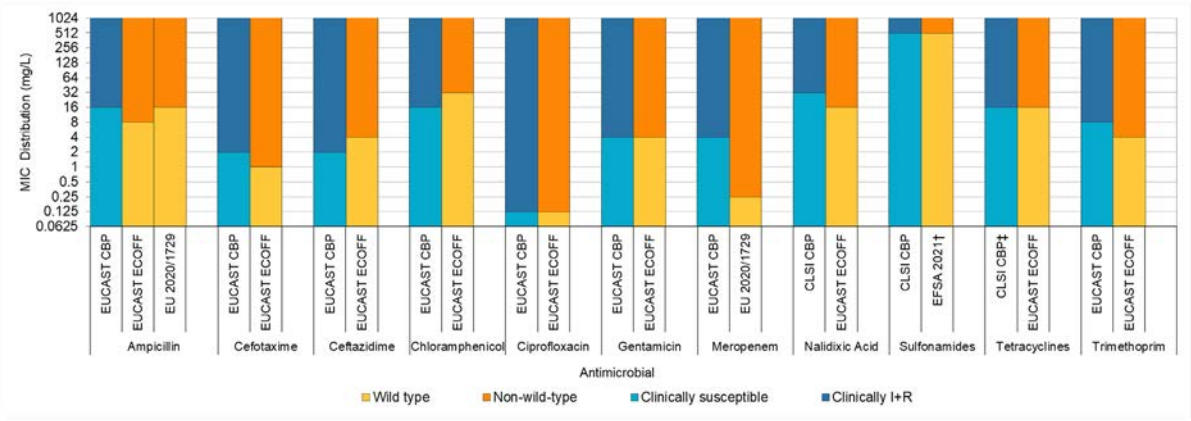

FIGURE A.1 Comparison of clinical breakpoints and epidemiological cut-off values used to interpret MIC data reported for *Salmonella* spp. from humans, animals or food. †EFSA Manual for reporting 2024 antimicrobial resistance data within the framework of Directive 2003/99/EC and Decision 2020/1729/EU. ‡Only R category included.

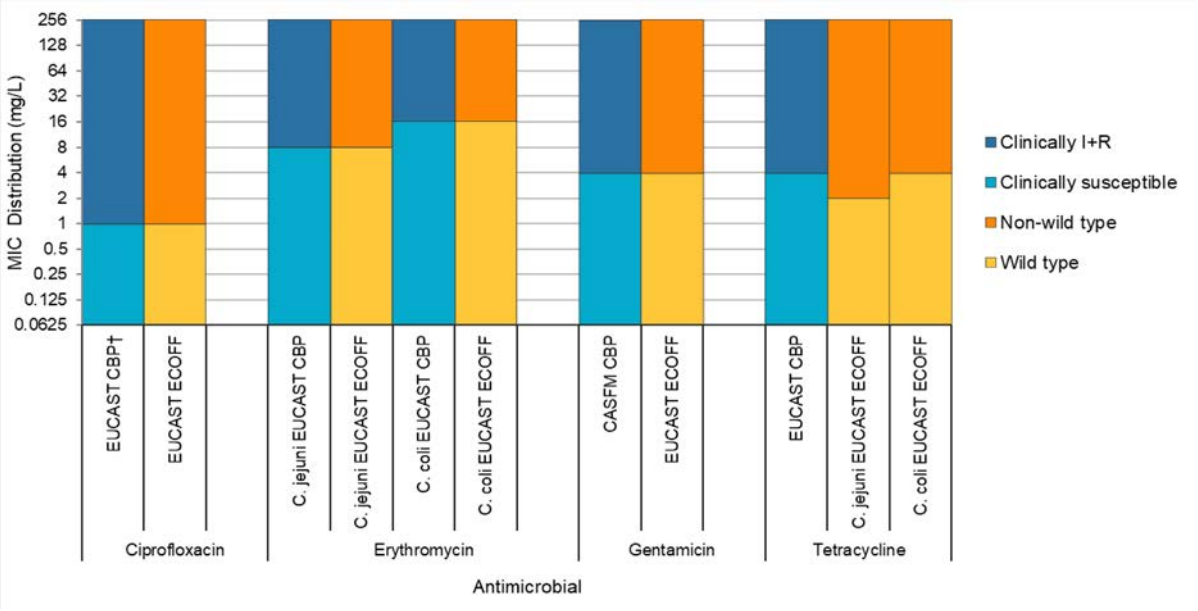

FIGURE A.2 Comparison of clinical breakpoints (CBPs) and epidemiological cut-off values (ECOFFs) used to interpret MIC data reported for *Campylobacter* spp. from humans and food-producing animals. †Only R category included.

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 it presents 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.

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 is 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.

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. The definitions of the susceptibility testing categories susceptible (S), intermediate (I) and resistant (R) 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 body tissues following administration, and assume that a clinical response will be obtained if the drug is given as recommended and no other adverse factors 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.

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 2014–2024 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 studied 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 and in *S.* Infantis was also presented in maps. 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 were presented for *C. jejuni* and *C. coli*.

Analysis of 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 2024. 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. Six countries (France, Germany, Italy, Poland, Slovakia and Spain) had not confirmed all presumptive ESBL/AmpC isolates, possibly due to clinical breakpoints being used in routine AST and not ECOFFs.

TABLE A.1 Antimicrobials reported, method used, type of data reported and interpretive criteria applied by MSs for *Salmonella* isolates from humans in 2024.

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.

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
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.
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	●	●	●	●	●	●	●	●	●	●	●	●	●		●	WGS	PWT/PNWT	Interpreted by ECDC using ResFinder and PointFinder

(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
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 2024.

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
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	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, plus CA-SFM CBP 2023 (AMC)
Greece	●	●	●	●	●	DD	Q	Interpreted by ECDC as for Germany
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 Germany
Lithuania			●	●	●	DD	SIR	EUCAST CBP
Luxembourg			●	●	●	DD	Q	Interpreted by ECDC, as for Austria.
Malta	●	●	●	●		DLG	Q	Interpreted by ECDC, as for Austria.
Netherlands	●		●	●	●	WGS	PWT/PNWT	Interpreted by NL using in-house pipeline based on PointFinder and Resfinder.
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	●	●	●	●	●	WGS	PWT/PNWT	Interpreted by ECDC, as for Bulgaria
Slovakia	●	●	●	●	●	No information	SIR	No information available.
Slovenia			●	●	●	DD	Q	Interpreted by ECDC, as for Austria.
Spain	●		●	●	●	DL	Q	Interpreted by ECDC, as for Austria.

Abbreviations: 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, 2024.

	Total *salmonella* tested	Travel-associated	Domestic	Unknown
Country	***N***	**%**	**%**	**%**
Austria	1401	1.6	68.2	30.2
Belgium	522	10.9	17.8	71.3
Bulgaria	36	0.0	0.0	100.0
Croatia	593	0.0	0.0	100.0
Cyprus	151	0.0	0.0	100.0
Czechia	200	0.0	100.0	0.0
Denmark	678	41.7	58.3	0.0
Estonia	134	14.2	51.5	34.3
Finland	79	5.1	94.9	0.0
France	1394	11.0	24.6	64.3
Germany	3113	2.4	97.6	0.0
Greece	441	0.0	0.0	100.0
Hungary	1427	0.4	99.6	0.0
Ireland	378	32.5	36.2	31.2
Italy	1203	0.0	0.0	100.0
Latvia	75	0.0	0.0	100.0
Lithuania	397	9.1	90.9	0.0
Luxembourg	195	39.5	38.5	22.1
Malta	75	0.0	0.0	100.0
Netherlands	1378	16.0	0.0	84.0
Poland	834	0.0	0.0	100.0
Portugal	851	0.1	6.6	93.3
Romania	135	0.0	100.0	0.0
Slovakia	2005	2.7	97.3	0.0
Slovenia	423	5.7	32.6	61.7
Spain	2134	1.0	54.6	44.4
Sweden	893	9.7	88.7	1.6
EU total (27 MSs)	**21,145**	**6.0**	**53.9**	**40.1**
Iceland	83	18.1	27.7	54.2
Norway	512	34.4	65.6	0.0

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

TABLE A.4 Proportion of tested *Campylobacter jejuni* and *Campylobacter coli* isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country in 2024.

	Total *C. Jejuni* & *C. Coli* tested	Travel-associated	Domestic	Unknown
Country	***N***	**%**	**%**	**%**
Austria	527	4.7	0.0	95.3
Bulgaria	20	0.0	0.0	100
Cyprus	40	0.0	0.0	100
Denmark	238	21.4	78.6	0.0
Estonia	264	2.7	48.5	48.9
Finland	1002	0.0	0.0	100
France	8159	0.0	0.0	100
Germany	1339	0.8	99.2	0.0
Greece	226	0.0	0.0	100
Hungary	4428	0.3	99.7	0.0
Ireland	297	0.7	5.1	94.3
Italy	199	2.0	13.6	84.4
Latvia	80	0.0	0.0	100
Lithuania	483	1.7	98.3	0.0
Luxembourg	481	0.0	0.0	100
Malta	198	4	96	0.0
Netherlands	355	7.3	0.0	92.7
Poland	82	0.0	0.0	100
Portugal	634	0.0	0.0	100
Romania	17	0.0	100	0.0
Slovakia	3639	1.3	98.7	0.0
Slovenia	856	0.0	0.0	100
Spain	609	0.2	45.3	54.5
Total (23 MSs)	**24,173**	**0.8**	**44.1**	**55.1**
Iceland	126	46	21.4	32.5
Norway	393	42.2	57.8	0.0

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

Antimicrobial susceptibility data from animals and food in 2023–2024

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

EU MSs reported mandatory data collected as part of AMR monitoring programmes during 2023 and 2024. '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 2023 and 2024, AMR data were collected from the bacteria listed above.

Countries may also report AMR data on other agents of public health importance, such as 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 2024 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, enterococci 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, 2020). 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 2024, 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 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 calves 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 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 pigs and of calves 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 2024, 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 2024. 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, 2021).

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 pigs and calves 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 2024, MSs collected indicator *E. coli* isolates based on random sampling of caecal samples gathered at slaughter from broilers and 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 (herd) 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, less than 100,000 tonnes of turkey meat or less than 50,000 tonnes of bovine 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 *E. coli*

In 2024, 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 also collected samples of fresh meat from broilers and turkeys gathered at retail and at border control posts. In 2023, MSs obtained caecal samples from fattening pigs and cattle (< 1 year) 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. 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 2023 and 2024. 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*.

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.

Enterococcus faecalis and *Enterococcus faecium*

E. faecalis and *E. faecium* isolates were collected by MSs on a voluntary basis as part of their national AMR monitoring programme, in accordance with Commission Implementing Decision (EU) 2020/1729 and EFSA Technical Specifications (EFSA, 2019). In 2024, MSs obtained enterococci isolates through random sampling of caecal samples at slaughter from broilers and fattening turkeys in countries producing over 10,000 tonnes of turkey meat annually (Annex Part A paragraph 1(e)(ii)). In 2023, isolates were collected from fattening pigs and cattle under 1 year of age in countries producing more than 10,000 tonnes of meat from these bovines annually (Annex Part A paragraph 1(e)(iv)). All isolates were tested for susceptibility to the antimicrobials specified in the Decision and EFSA Technical Specifications, with results interpreted using EUCAST epidemiological cut-off values.

Harmonised antimicrobial susceptibility testing

Routine monitoring of antimicrobial susceptibility

MSs followed Commission Implementing Decision (EU) 2020/1729 and recommendations from EFSA regarding the use of epidemiological cut-off values for AMR monitoring. MSs tested antimicrobials and interpreted the results using the ECOFFs and concentration ranges shown in Tables A.5 and A.6 to determine the susceptibility of the following microorganisms: *Salmonella* spp., *C. coli*, *C. jejuni* and indicator commensal *E. coli*.

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 A.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).[36] 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 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-lactam resistance phenotypes obtained (Figure A.3). WGS

[36]Available online:www.eurl-ar.eu.

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

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 (Table A.5 and Table A.7) are based on Commission Implementing Decision (EU) 2020/1729.

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 2023–2024 EUCAST ECOFF* (mg/L)	*E. coli* EU surveillance 2023–2024 EUCAST ECOFF* (mg/L)	Concentration range, mg/L (no. of wells)
Amikacin	> 4	> 8	4–128 (6)
Ampicillin	> 8	> 8	1–32 (6)
Azithromycin	NA[a]	NA[a]	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[b]	> 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[c]	> 64	8–512 (7)
Tetracycline	> 8	> 8	2–32 (5)
Tigecycline	NA[d]	NA[d]	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.

*EUCAST epidemiological cut-off values. '>' than the ECOFF, criteria used to determine microbiological resistance.

[a]EUCAST epidemiological cut-off (ECOFF) not available, > 16 mg/L was used.

[b]EUCAST epidemiological cut-off (ECOFF) value for *Salmonella* spp. not available, > 2 mg/L was used.

[c]EUCAST epidemiological cut-off (ECOFF) not available, > 256 mg/L was used.

[d]EUCAST epidemiological cut-off (ECOFF) not available, > 0.5 mg/L was used.

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 2023–2024 EUCAST ECOFF* (mg/L)	*C. coli* EU surveillance 2023–2024 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	> 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.

*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 2023–2024 EUCAST ECOFF* (mg/L)	*E. coli* EU surveillance 2023–2024 EUCAST ECOFF* (mg/L)	Concentration range, mg/L (no. of wells)
Cefepime	> 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)
Ertapenem[a]	> 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.

*EUCAST epidemiological cut-off values. '>' than the ECOFF, criteria used to determine microbiological resistance.

[a]EUCAST epidemiological cut-off (ECOFF) value for *E. coli* is tentative 0.03 mg/L.

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 and submitted to EFSA by the MSs and non-MSs consisted of a data review and 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 to request 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 of 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 330 isolates was made in 2023 and 100 isolates in 2024. 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.17950222). The tables also display complete susceptibility, multidrug resistance and co-resistance.

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.

The occurrence of resistance to a number of antimicrobials was determined for *Salmonella*, *Campylobacter* and indicator commensal *E. coli* isolates and is 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, the level or occurrence of AMR means the percentage of resistant isolates as a proportion of the isolates tested of that microorganism. The MSs reporting group refers to 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 in resistance to different antimicrobials are shown 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 9.4 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 a meaningful fit and resulted 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 (2014–2024), 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 a 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.

To detect potential shifts in AMR trends over time, a change-point logistic model was fitted using the PROC MCMC procedure in SAS 9.4. By estimating both the timing of the change point and the logistic trends before and after it, the model captures abrupt or gradual temporal shifts. This approach is particularly suited for analysing AMR trends, where the proportion of resistant isolates may change at varying rates across different periods.

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 2023 and 2024, 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; therefore, some apparent discrepancies between the colours and resistance levels may occur 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 multidrug-resistant bacteria. The intention was to focus mainly on multi–/co-resistance patterns involving important AMEG category A and B antimicrobials (EMA, 2019), such as cephalosporins, fluoroquinolones and macrolides. The occurrence of isolates with certain serotypes/resistance patterns of interest was studied at both the MS and EU levels, by grouping data for all MSs, and where relevant, also from 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.

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, turkeys, pigs and calves) 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 targeted animal populations. 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 trend graphs and 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). In the case of a statistically significant trend, the rate of change between the first and the latest data points was calculated and displayed alongside the graph.

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. 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/or carbapenems 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, the first condition for classifying isolates as presumptive ESBL/AmpC-producers related to their MIC for either cefotaxime or ceftazidime was the application of a screening breakpoint of MIC > 1 mg/L. Only isolates that presented MIC values fulfilling this criterion (as expected for most 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 or greater 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 underlined that some AmpC-enzymes (i.e. ACC-1) do not confer resistance to cefoxitin, and there are some other mechanisms including porin loss, presence of carbapenemases or 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 a negative synergy test for both cefotaxime and ceftazidime/clavulanic acid and 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 in combination with clavulanic acid, and a 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 the combination cefepime/clavulanic acid was unfortunately 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, 2012a, 2012b), 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 was chosen. It is known that other mechanisms (i.e. hyperproduction or combination of ESBLs and/or AmpC and porin loss) can also affect 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 reported carbapenem susceptibility testing data, 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 on 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 MIC > 0.125 mg/L 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 were 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 other mechanisms or technical issues in the MIC testing (i.e. MIC value close to the ECOFF) would probably 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 non-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.

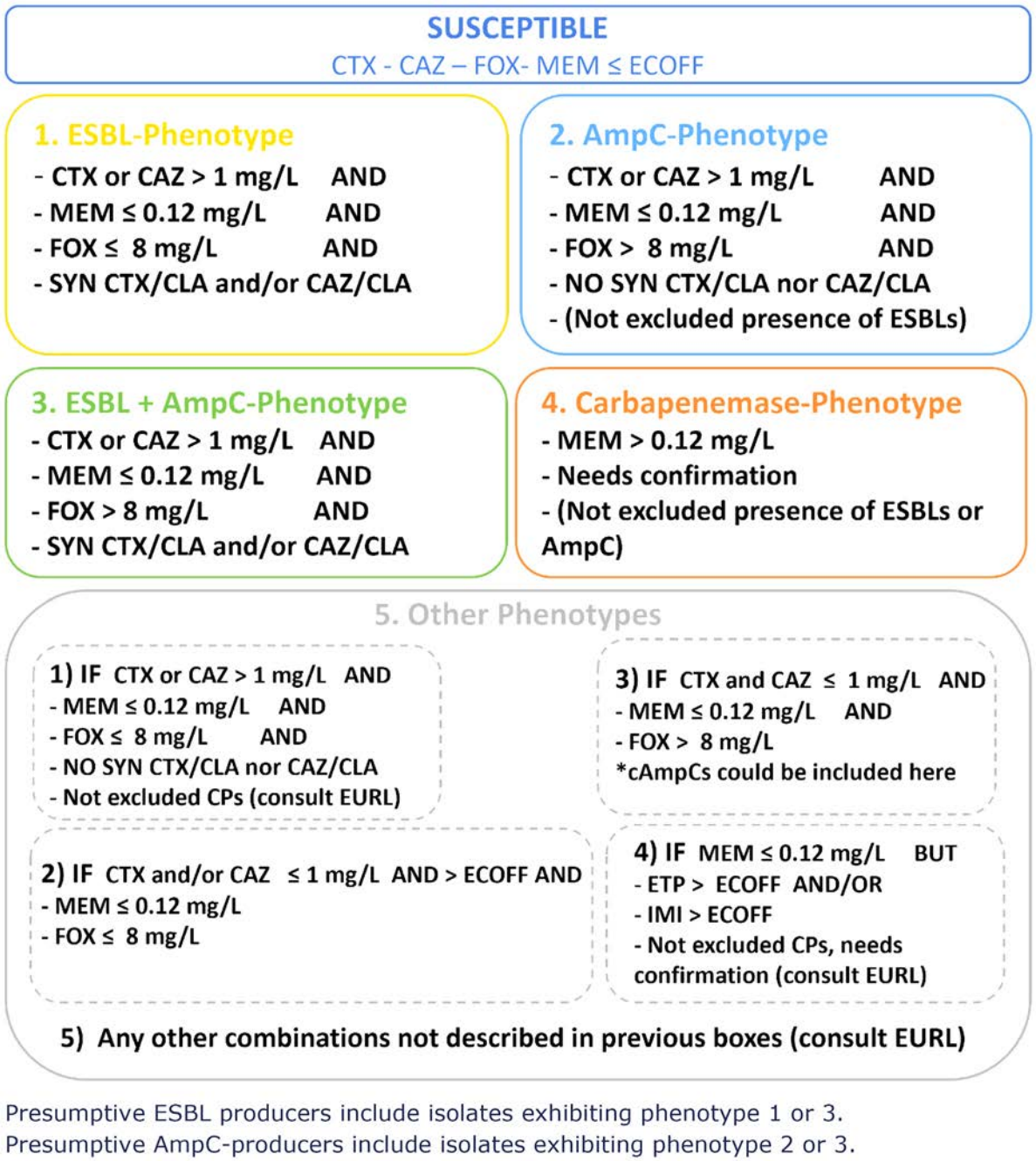

FIGURE A.3 Phenotypes inferred based on the resistance to the beta-lactams included in Panel 2. Presumptive ESBL-producers include isolates exhibiting phenotype 1 or 3. Presumptive AmpC-producers include isolates exhibiting phenotype 2 or 3.

Epidemiological cut-off values (ECOFFs) and clinical breakpoints (CBPs)

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 as 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 that present an ESBL and/or an 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.

Analysis of ESBL-/AmpC-/CP-genes

Countries 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 2023 and 2024 are listed below:

- Positive isolate is an isolate where at least one ESBL-, AmpC- or CP-gene was detected using WGS.
- Negative isolate is an isolate where no ESBL-, 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:

$$\text{Pr evalence} = \frac{\text{Number of positive samples}}{\text{Number of samples tested}} \times \frac{\text{Number of positive isolates}}{\text{Number of isolates tested}} \times 100$$

- 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-, 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:

$$\text{Correspondence} = \frac{\text{number of isolates with same phenotype predicted by both genotype and MIC}}{\text{Total number of isolates reported to harbour the specific gene}} \text{x100}$$

Correspondence was considered to be high if ≥ 90% of the isolates carrying a gene also exhibited the expected phenotype encoded by the gene.

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 a few MSs. MRSA occurrence data reported from clinical investigations of food-producing and/or companion animals in 2023–2024 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.17950222.

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, 2024, and trend graphs for individual serotypes for 2014–2024 period – Annex A.1;
- Occurrence of resistance to selected antimicrobials in *Salmonella* spp. from targeted food-producing animals, 2023–2024 - Annex A.2;
- Occurrence of resistance to selected antimicrobials in specific *Salmonella* serovars – Annex A.3.

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 *Campylobacter jejuni* and *C. coli* from humans, by country, in 2024 – Annex B1;
- Occurrence and prevalence of resistance to selected antimicrobials in *Campylobacter jejuni* and *C. coli* from targeted food-producing animals, for 2023–2024 – Annex B2;
- Trends of resistance in *Campylobacter jejuni* and *C. coli* in calves and in fattening pigs (2014–2024), Distribution of minimum inhibitory concentration (MIC) values related to erythromycin resistance in *Campylobacter jejuni* and *C. coli* from targeted food-producing animals (2023–2024), and Between-country variability in prevalence of resistance to selected antimicrobials in *Campylobacter jejuni* and *C. coli* from broilers and fattening turkeys (2024) – Annex B3.

Annex C: Data reported on antimicrobial resistance in indicator commensal *Escherichia coli* from targeted food-producing animals and derived meat

- The annex contains tables with the data reported on AMR in indicator commensal *Escherichia coli* from targeted food-producing animals and derived meat (data from pigs and calves from 2023 and data from poultry from 2024).

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 CP-producing *E. coli* from targeted food-producing animals and derived meat (data from pigs and calves from 2023 and from poultry from 2024), and on their resistance occurrence and prevalence (routine and specific monitoring programmes):

- Presumptive ESBL-, AmpC- and/or CP-producing indicator commensal *E. coli* – prevalence and occurrence tables from routine monitoring, targeted food-producing animals and derived meat, 2023–2024 – Annex D.1
- Presumptive ESBL-, AmpC- and/or CP-producing *E. coli* – prevalence and occurrence tables from specific monitoring, targeted food-producing animals and derived meat, 2023–2024 – Annex D.1
- Presumptive CP-producing *E. coli* – specific monitoring, targeted food-producing animals and derived meat, 2023–2024 – Annex D.1
- ESBL- and AmpC-producing isolates prevalence maps – targeted food-producing animals and derived meat, 2023–2024 – Annex D.2
- Key outcome indicators of prevalence – targeted food-producing animals, 2014–2024 – Annex D.2
- ESBL-, AmpC- and/or CP-encoding genes – WGS AMR MON, 2022–2023 – Annex D.3
- ESBL- and AmpC-encoding genes – WGS ESBL MON, 2022–2023 – Annex D.3
- CP-encoding genes – WGS CARBA MON, 2022–2023 – Annex D.3
- ESBL-, AmpC- and/or CP-encoding genes – AMR MON pnl2, ESBL MON pnl2, CARBA MON pnl2, 2022–2023 – Annex D.3
- Data include detected resistance genes and the concordance between genotype-predicted and MIC-based phenotypes.

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 2023 and 2024.

Annex F: Data reported on antimicrobial resistance in *Enterococci* from food-producing animals and derived meat

The annex contains tables with the data reported on the occurrence of resistance to selected antimicrobials in *Enterococcus faecalis* and *Enterococcus faecium* from food-producing animals (data from pigs and calves from 2023 and data from poultry from 2024).

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 2023–2024 are available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17950222.

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.17950222.The 2024 prevalence of MRSA aggregated dataset is also available on the Knowledge Junction at: https://doi.org/10.5281/zenodo.17950222.

A table showing ESBL-/AmpC-/CP-encoding genes and corresponding MIC data for cephalosporins and carbapenems reported in 2023 and 2024 is also available on the knowledge junction at: https://doi.org/10.5281/zenodo.17950222.

Country datasets

All country datasets containing the tables on the occurrence of antimicrobial resistance for 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 2023–2024 monitoring years are: the 27 EU Member States and the United Kingdom (Northern Ireland), three non-EU Member States (Iceland, Norway and Switzerland), as well as the Republic of North Macedonia as pre-accession countries.

Country	Link to the dataset
EU Member States	
Austria	https://doi.org/10.5281/zenodo.18020251
Belgium	https://doi.org/10.5281/zenodo.18015384
Bulgaria	https://doi.org/10.5281/zenodo.18017444
Croatia	https://doi.org/10.5281/zenodo.18016744
Cyprus	https://doi.org/10.5281/zenodo.18020152
Czechia	https://doi.org/10.5281/zenodo.18020579
Denmark	https://doi.org/10.5281/zenodo.18021468
Estonia	https://doi.org/10.5281/zenodo.18014532
Finland	https://doi.org/10.5281/zenodo.18021235
France	https://doi.org/10.5281/zenodo.18020342
Germany	https://doi.org/10.5281/zenodo.18021075
Greece	https://doi.org/10.5281/zenodo.18019903
Hungary	https://doi.org/10.5281/zenodo.18017343
Ireland	https://doi.org/10.5281/zenodo.18015712
Italy	https://doi.org/10.5281/zenodo.18021537
Latvia	https://doi.org/10.5281/zenodo.18623207
Lithuania	https://doi.org/10.5281/zenodo.18020463
Luxembourg	https://doi.org/10.5281/zenodo.18019732
Malta	https://doi.org/10.5281/zenodo.18015483
Netherlands	https://doi.org/10.5281/zenodo.18021830
Poland	https://doi.org/10.5281/zenodo.18014424
Portugal	https://doi.org/10.5281/zenodo.18021745
Romania	https://doi.org/10.5281/zenodo.18021304

Country	Link to the dataset
Slovakia	https://doi.org/10.5281/zenodo.18016907
Slovenia	https://doi.org/10.5281/zenodo.18020045
Spain	https://doi.org/10.5281/zenodo.18020871
Sweden	https://doi.org/10.5281/zenodo.18021987
United Kingdom (Northern Ireland)	https://doi.org/10.5281/zenodo.18016842
Non-EU countries	
Iceland	https://doi.org/10.5281/zenodo.18017273
Norway	https://doi.org/10.5281/zenodo.18015624
Republic of North Macedonia	https://doi.org/10.5281/zenodo.18016690
Switzerland	https://doi.org/10.5281/zenodo.18019783