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Review

Antimicrobial Resistance in Romanian Meat Production Systems (2010–2025): A Critical Review of Pathogen-Specific Evidence and Surveillance Gaps

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Abstract

Antimicrobial resistance (AMR) in foodborne bacteria remains a major public health concern in the European Union (EU) and globally. Romania represents a relevant setting due to the coexistence of intensive livestock production, small- and medium-sized holdings, and backyard farming systems. This review synthesizes evidence published between 2010 and 2025 on the occurrence and AMR of *Salmonella* spp., *Campylobacter* spp., *Listeria monocytogenes*, and *Escherichia coli* along the Romanian meat production chain, considering national studies within the broader EU surveillance context. Particular attention is given to multidrug resistance (MDR), resistance determinants, and potential selective pressures associated with antimicrobial use and production environments. The evidence indicates recurrent detection of resistant bacteria, with marked pathogen- and sector-specific differences. High quinolone/fluoroquinolone resistance was consistently documented in *Campylobacter* spp., while *Salmonella* spp. showed diverse resistance phenotypes and substantial multiple/MDR, with longitudinal poultry data indicating increased MDR in specific populations. *E. coli* exhibited complex MDR and extensively drug-resistant (XDR) phenotypes and diverse resistance determinants, whereas multidrug-resistant *L. monocytogenes* was documented in meat-processing environments. Methodological heterogeneity precludes inference of a uniform national temporal increase in AMR. Standardized longitudinal surveillance integrating phenotypic, molecular, and genomic data within a One Health framework is needed to improve AMR monitoring and control across the farm-to-fork continuum.

Keywords: antimicrobial resistance; foodborne pathogens; Romania; meat products; MDR; *Salmonella*; *Campylobacter*; *E. coli*; *Listeria monocytogenes*; One Health

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1. Introduction

Antimicrobial resistance (AMR) in foodborne and indicator bacteria remains a major public health challenge in the EU, with European Food Safety Authority (EFSA) and European Centre for Disease Prevention and Control (ECDC) surveillance documenting persistent and, for several bacteria–antimicrobial combinations, high levels of resistance in *Salmonella* spp., *Campylobacter* spp., and commensal *Escherichia coli* from food-producing animals across Member States [1,2]. Romania provides a relevant setting for examining

AMR because its meat production sector encompasses heterogeneous livestock production systems, ranging from vertically integrated farms to small- and medium-sized holdings and backyard production. This structural diversity creates different epidemiological contexts for pathogen circulation, antimicrobial exposure, biosecurity, and the potential maintenance and dissemination of antimicrobial-resistant bacteria.

Romanian studies have documented multiple and multidrug resistance among *Salmonella* isolates from poultry and pork [3,4], elevated levels of fluoroquinolone resistance in *Campylobacter* from poultry [5,6], and MDR/XDR phenotypes and resistance determinants, including extended-spectrum β-lactamase and AmpC β-lactamase-associated resistance (ESBL/AmpC), among *Escherichia coli* isolates from food-producing animals [7–9]. *Listeria monocytogenes* with antimicrobial-resistant phenotypes have also been recovered from meat-processing environments [10]. Together, these findings indicate that AMR occurs at different stages of Romanian meat production, although the available evidence differs considerably among pathogens, animal species, production stages, study periods, and methodological approaches.

At the European level, reductions in antimicrobial use in food-producing animals and the containment of AMR are major components of current One Health strategies [11,12]. However, interpreting the Romanian evidence over time remains challenging because most available studies are cross-sectional and differ in sampling design, bacterial populations, antimicrobial panels, susceptibility-testing methods, and definitions of multiple or multidrug resistance. Consequently, differences among studies cannot necessarily be interpreted as temporal changes in AMR.

This narrative review critically synthesizes evidence published between 2010 and 2025 on the occurrence and antimicrobial resistance of major foodborne bacterial pathogens along the Romanian meat production chain, evaluates the extent to which temporal changes can be identified from the available evidence, contextualizes national findings within the broader EU framework, and identifies priorities for future integrated One Health surveillance and research.

2. Materials and Methods

2.1. Literature Search

A structured literature search was conducted across four major databases: PubMed, Web of Science Core Collection, Scopus, and Google Scholar. Searches were performed using combinations of predefined keywords and Boolean operators. Search terms included: "Romania," "antimicrobial resistance," "AMR," "foodborne pathogens," "meat," "poultry," "swine," "beef," "*Salmonella*," "*Campylobacter*," "*E. coli*," "*Listeria*," "multidrug resistance," "MDR," "extended-spectrum β-lactamase," "ESBL," "AMR trends," "slaughterhouse," "processing environment," and "One Health." Selection was based on targeted searches and expert assessment rather than a formal systematic screening protocol; record counts for each screening step were not prospectively tracked.

The search covered the period 1 January 2010 to 31 December 2025 and was used to identify the primary Romanian evidence included in the review; the literature search was completed on 31 March 2026. Publications appearing after the search date were used only where relevant to provide updated contextual or EU-level information and were not considered part of the primary evidence base.

To provide a broader European context, supplementary targeted searches were conducted during manuscript revision to identify relevant original studies from Romania's neighboring countries and other European regions. Relevant EFSA/ECDC surveillance reports and accompanying datasets were also consulted to identify harmonized European antimicrobial resistance indicators. International studies published between 2010 and 2025

were prioritized, while the EFSA/ECDC report published in 2026 was used to contextualize surveillance data collected in 2023–2024.

2.2. Eligibility Criteria

Studies were screened according to predefined inclusion and exclusion criteria. Studies were eligible if they *(i)* were conducted in Romania; *(ii)* investigated *Salmonella* spp., *Campylobacter* spp., *Escherichia coli*, or *Listeria monocytogenes* in food-producing animals, meat, carcasses, slaughterhouses, processing environments, or other relevant stages of the meat production chain; and *(iii)* reported pathogen occurrence and/or antimicrobial resistance data. Peer-reviewed journal articles constituted the primary Romanian evidence base. Selected international studies, reviews, EU surveillance reports, and policy documents were used separately to provide mechanistic, epidemiological, and policy context; these sources were not included in the Romanian primary-evidence synthesis. Studies were excluded if they focused exclusively on human clinical isolates, were unrelated to food-producing animals or the meat production chain, or did not provide information relevant to pathogen occurrence or AMR. The grey literature, theses, and non-peer-reviewed reports were excluded from the primary evidence synthesis.

International comparator studies were selected according to their relevance to Romanian meat-production systems, considering bacterial species or serovar, animal population, food-chain stage, sampling matrix, and availability of antimicrobial susceptibility data. Priority was given to original studies reporting isolate denominators, AST methods, interpretive criteria, MDR definitions, and molecular resistance determinants. Studies involving representative or routine surveillance populations were distinguished from those examining clinically affected animals, selected resistant isolates, or molecularly characterized subsets. The latter were retained where they contributed relevant mechanistic evidence but were not considered directly comparable for resistance prevalence estimates. These international studies were used exclusively for contextual comparison and were not incorporated into the primary Romanian evidence synthesis.

2.3. Data Extraction

For each eligible Romanian study, information was extracted for publication year, study period, animal species or food matrix, food-chain stage, sample size, bacterial species or serovar, pathogen occurrence, antimicrobial susceptibility testing method, resistance phenotype, MDR/XDR classification where reported, and resistance determinants where available. Literature screening and study selection were conducted by one reviewer without independent duplicate screening. Data extraction was performed by one reviewer and subsequently verified by a second reviewer to ensure accuracy and consistency.

For selected international studies, additional information was extracted on country, sampling period, animal population, bacterial species or serovar, sample matrix, number of isolates subjected to AST, testing method, interpretive criteria, antimicrobial-specific resistance frequencies, MDR definition, and available molecular findings. Particular attention was given to distinguishing microbiological resistance based on epidemiological cut-off values (ECOFFs) from resistance determined using clinical breakpoints.

2.4. Data Synthesis

Because the included studies varied substantially in study design, sampling strategy, food-chain stage, animal species, sample size, antimicrobial susceptibility testing (AST) panels, and interpretive criteria, the evidence was synthesized qualitatively rather than through direct quantitative comparisons or meta-analysis. Data were organized separately for the four bacterial groups considered in this review (*Salmonella* spp., *Campylobacter*

spp., *Escherichia coli*, and *Listeria monocytogenes*) and summarized by pathogen occurrence, antimicrobial resistance profiles, multidrug resistance (MDR), and, where available, resistance determinants.

The terminology used in the original studies was retained. Because definitions of MDR differed among studies, the operational definition reported by each study was considered where available, and MDR frequencies based on different definitions were not treated as directly comparable. Study quality and comparability were considered qualitatively across four domains: sampling representativeness, geographical coverage, isolate-selection criteria, and validity of antimicrobial susceptibility testing, including the interpretive standards applied. Particular attention was given to studies involving restricted sampling populations, geographically limited datasets, selected bacterial isolates, or incompletely specified susceptibility criteria. Findings affected by these limitations were interpreted within their original study context rather than extrapolated to the national level.

Temporal patterns were evaluated descriptively and only when sufficiently comparable data were available. Greater weight was assigned to longitudinal within-study observations than to comparisons between independent cross-sectional studies. Owing to methodological heterogeneity, differences in prevalence or resistance frequencies between studies conducted in different years were not interpreted as evidence of temporal increases or decreases unless supported by directly comparable data. Romanian findings were then compared with available EU-level surveillance data to assess similarities and differences in pathogen distribution and antimicrobial resistance patterns and to identify areas where national surveillance remains limited.

International comparisons were conducted qualitatively, with quantitative contrasts restricted to sufficiently comparable bacterial species or serovars, animal populations, sampling matrices, and AST interpretation systems. Harmonized EFSA/ECDC surveillance was considered separately from independently conducted studies because differences in sampling design, antimicrobial panels, interpretive criteria, and MDR definitions may substantially influence reported resistance frequencies. Molecular investigations and studies based on selected resistant populations were used to contextualize resistance mechanisms rather than to estimate background resistance frequencies.

For the cross-country comparison, data were extracted from the EFSA/ECDC 2023–2024 surveillance annexes covering *Salmonella* spp., *Campylobacter* spp., and indicator *Escherichia coli*. Selected indicators were visualized in a heat map generated using Python (version 3.11.8), incorporating Romania and nine other EU Member States. Surveillance data corresponded to 2023 for pigs and 2024 for poultry. Reported resistance percentages and corresponding isolate denominators were retained without pooling results from independent studies. The pooled European reporting category was presented separately and includes Romanian observations; for some indicator *E. coli* populations, it also includes Northern Ireland. Missing data and estimates derived from very small isolate collections were identified in the figure. No statistical comparisons between countries or meta-analytical pooling were performed.

3. Results

To contextualize the outcomes related to pathogen-specific antimicrobial resistance, it is essential to outline the general structural and functional characteristics of Romania's livestock and meat production systems. The organization of this sector influences pathogen exposure, biosecurity practices, antimicrobial use, and the conditions under which resistant bacteria may emerge and disseminate throughout the food chain.

3.1. Romania's Livestock and Meat Production Context (2010–2025)

3.1.1. Structural Dualism in Animal Production

Romania's livestock sector remains marked by structural dualism. A substantial proportion of animals, most notably pigs, are still raised in non-professional or backyard production systems, where biosecurity and management practices may differ substantially from those of intensive production systems. These units may be less consistently represented in antimicrobial-use monitoring and may provide conditions favorable to the maintenance and dissemination of antimicrobial-resistant microorganisms [13,14]. Romanian livestock production is characterized by the coexistence of small-scale and family-operated holdings with larger commercial and vertically integrated production systems, particularly in the swine sector [13–15]. This structural heterogeneity has important implications for biosecurity, antimicrobial stewardship, and the conditions under which antimicrobial-resistant bacteria may be maintained or disseminated. Traditional small-ruminant farming systems form part of this heterogeneous production landscape, and antimicrobial-resistant bacteria have also been documented in such Romanian settings [16].

3.1.2. The Poultry Sector

Poultry production, particularly broiler production, is characterized by relatively high levels of production integration and standardization in some Romanian production systems. These characteristics may facilitate the implementation of biosecurity, performance monitoring, and standardized production practices. At the same time, high stocking densities and repeated production cycles may facilitate pathogen transmission, while antimicrobial exposure can provide selective pressure favoring resistant bacterial populations [17,18]. Recent Romanian studies have reported ESBL/AmpC-producing *E. coli* in poultry and multidrug-resistant *Salmonella* isolates from poultry meat and other food-chain settings [3,8,19]. These findings align with EU surveillance data showing persistent resistance in poultry-associated pathogens [2].

3.1.3. The Swine Sector

Romania's swine sector has been substantially affected by African swine fever (ASF) since its emergence in 2017, with recurrent outbreaks continuing to affect domestic pig production and requiring sustained surveillance and control measures [20]. Many small and medium farms were depopulated, contributing to changes in the structure and management of pig production in affected areas [21]. Repeated production cycles, pathogen reintroduction, and exposure to selective pressures, including certain biocides and antimicrobial residues, may contribute to the persistence and co-selection of antimicrobial resistance within intensive livestock production environments [22]. Studies from Romania and neighboring Eastern European regions have documented colistin resistance genes (*mcr*), ESBL/AmpC phenotypes, and MDR *E. coli* in swine production systems [7,23–26].

3.1.4. Cattle and Small Ruminants

Although less intensively farmed than poultry and swine, cattle and sheep may serve as reservoirs of foodborne pathogens and transmission points for foodborne pathogens in Romania's animal production sector. Surveillance data and targeted regional studies demonstrate that bovine and ovine meat products, particularly beef, veal, and mutton, harbor a range of zoonotic bacteria with public health significance. Romanian investigations have documented the presence of *Salmonella* spp., Shiga toxin-producing *Escherichia coli* (STEC), and *Listeria* spp. in carcasses, retail cuts, and processing environments, underscoring the contribution of ruminant-derived foods to the national antimicrobial resistance landscape [27–29].

3.2. Pathogen and AMR Dissemination Along the Romanian Meat Production Chain

The structure and operational dynamics of Romania's meat production chain create multiple biological interfaces at which foodborne pathogens and antimicrobial-resistant bacteria may be introduced, selected, maintained, or redistributed. From farm-level microbial reservoirs to processing environments and retail distribution, different stages involve antimicrobial exposure, animal contact, environmental contamination, and food-handling processes that may influence the occurrence and distribution of resistant bacterial populations. Understanding these interfaces is important for contextualizing the Romanian AMR evidence reported during the 2010–2025 period.

3.2.1. Farm-Level Reservoirs and Preharvest Transmission Nodes

Romanian livestock farms, characterized by structural heterogeneity and variable biosecurity, represent potential sources of foodborne bacteria entering the meat production chain, including *Salmonella* spp., *Campylobacter* spp., *Escherichia coli*, and *Listeria* spp. [27,28,30]. Intensive poultry and swine operations can support high animal and microbial densities [31], while smallholder and backyard systems frequently exhibit environmental commingling, informal husbandry, and inconsistent antimicrobial stewardship [14,32,33]. Together, antimicrobial exposure, animal density, environmental contamination, and variable biosecurity may create conditions favoring the selection or maintenance of resistant bacterial populations. Manure management practices and contaminated housing surfaces may additionally contribute to environmental contamination and bacterial circulation between animals and their surroundings.

3.2.2. Slaughter and Carcass Contamination

Transport, loading, and lairage conditions substantially influence the microbial load introduced into slaughterhouses. Stress, crowding, and the mixing of animals from different holdings may increase pathogen shedding and opportunities for cross-contamination [24,34–36]. Slaughterhouses also represent an occupational interface between animals, bacteria, and humans. Studies of pig slaughterhouse workers have demonstrated carriage of antimicrobial resistance determinants, including *tetW* and *ermB*, highlighting the relevance of occupational exposure within a One Health framework [37]. Once animals enter processing facilities, several operational stages, such as hide or feather removal, scalding and defeathering, carcass dressing, and evisceration, create opportunities for the transfer of microorganisms from the animal surface or intestinal contents onto equipment and carcasses.

Salmonella spp. and *Listeria monocytogenes* can survive in processing environments, particularly in niches where sanitation is difficult or where biofilms develop [38–41]. The slaughter environment itself can sustain contamination when sanitation routines are inconsistent or when biofilms form on wet or hard-to-access surfaces [10,42–45]. However, environmental detection or biofilm-forming capacity alone should not be interpreted as evidence of long-term persistence unless repeated isolation or molecularly related strains are demonstrated over time.

Knives, hooks, conveyor belts, transport crates, and other inadequately cleaned equipment can contribute to microbial redistribution within processing facilities. Process water and wastewater resulting from slaughtering operations may also represent routes for microbial contamination [46]. Genes associated with reduced susceptibility to disinfectants have also been described in foodborne bacteria, although the presence of these determinants alone does not establish bacterial persistence or failure of routine sanitation procedures [47,48].

In poultry and swine plants, mechanical processes and high line speeds can increase opportunities for microbial spread [9,34], while chilling and carcass-handling steps may

permit survival of *L. monocytogenes* and other cold-tolerant organisms [48–50]. Overall, animal-related factors and facility-level conditions shape microbial contamination during slaughter and influence both immediate carcass hygiene and downstream contamination risks within the meat production chain.

3.2.3. Processing and Meat Handling

Manual cutting and deboning involve repeated contact between workers and carcasses, and frequent contact between carcasses and equipment surfaces increases opportunities to redistribute pathogens already present on carcasses or within the processing environment. Grinding and mixing steps can homogenize localized contamination events, enabling resistant *E. coli* or *Salmonella* spp. to become distributed across larger product batches. Romanian studies have documented antimicrobial-resistant bacteria in meat products and carcass-associated biofilms, including isolates recovered from pork, beef, and poultry matrices [14,25,51]. These findings demonstrate the presence of resistant bacteria in finished meat products but, in the absence of longitudinal or strain-level tracking, do not establish that individual isolates originated from contamination events documented at earlier production stages.

3.2.4. Packaging, Storage, Distribution, and Retail

Although packaging generally reduces direct environmental exposure, microorganisms acquired during earlier production stages may remain viable on meat products. Romanian studies have documented *Salmonella* spp. and antimicrobial-resistant bacteria in meat products sampled at retail and other downstream stages of the production chain [3,19,52]. Their detection at retail confirms contamination at the point of sampling but does not, by itself, identify the stage at which contamination occurred.

Selected foodborne bacteria can survive during chilled storage and under low-oxygen conditions such as vacuum or modified-atmosphere packaging depending on the organism, product characteristics, and storage conditions [53,54]. Cold-chain storage exposes bacterial populations to environmental stresses including refrigeration, nutrient limitation, oxidative stress, and low-oxygen conditions. Although these conditions can influence bacterial survival and stress responses, recovery of resistant bacteria from refrigerated retail products should not, by itself, be interpreted as evidence that refrigeration specifically selects for antimicrobial resistance.

Romanian analyses of food-contact surfaces have also identified biofilm-forming *E. coli* with resistance to β-lactams, quinolones, and tetracyclines [51], supporting the potential role of processing and retail environments as secondary contamination sources.

3.3. Pathogen-Specific Evidence and Temporal Patterns

3.3.1. *Salmonella* spp.

Salmonella spp. have been detected at several stages of the Romanian meat production chain, particularly in poultry and pork (Table 1). Mihaiu et al. [4] identified *Salmonella* spp. in 149 of 650 poultry and pork meat samples (22.92%), while Morar et al. [25] reported 26 positive samples among 108 samples collected from pork, packaged pork products, and the slaughterhouse environment (24.1%). The latter included 12/47 (25.5%) pork samples, 7/44 (15.9%) packaged pork products, and 7/17 (41.2%) environmental samples. These findings demonstrate the occurrence of *Salmonella* spp. at different stages of pork and poultry production, although differences in study design and sampling prevent direct comparison of prevalence estimates between studies.

Table 1. Occurrence, antimicrobial resistance, and multidrug resistance of *Salmonella* spp. along the Romanian meat chain.

Food-Chain Stage	Sample/Source	Isolates/Serovars	Occurrence/Study Population	Antimicrobial Resistance Profile	Resistance Determinants/MDR	References
Production units and retail	Chicken and pork meat	13 serovars, predominant: *S.* Infantis, *S.* Typhimurium, *S.* Derby, *S.* Colindale	149/650 (22.92%)	Disk diffusion, CLSI: SMX 87.25%; STR 81.21%; TET 80.53%; NAL 65.10%; CIP 42.95%; AMP 20.81%; CHL 16.78%; CAZ 11.41%	83.22% classified as MDR; (standardized MDR definition not specified)	Mihaiu et al. [4]
Slaughterhouse/ pork-processing chain	Pork, packaged pork products, slaughterhouse environment	*Salmonella* spp.	Overall: 26/108 (24.1%): • pork: 12/47 (25.5%); • packaged pork products: 7/44 (15.9%); • slaughterhouse environment: 7/17 (41.2%)	VITEK 2, CLSI: TET 61.5%; AMP 50%; PIP 50%; TMP-SMX 34.6%; AMC 26.9%; NIT 23.1%; CFZ 15.4%; PIP/TAZ 7.7%; CIP/NOR/IMI 3.8%;	MDR strains reported; frequency and operational definition not specified	Morar et al. [25]
Pork/traditional slaughter	Pork carcass meat	8 serovars: *S.* Infantis, *S.* Typhimurium, *S.* Derby; *S.* Virchow; *S.* Brandenburg; *S.* Ruzizi, *S.* Muenchen, *S.* Bredeney	48/208 (23.07%)	Disk diffusion; CLSI: STR 91.66%; TET 83.33%; SMX 68.7%; NAL 56.25%	93.75% classified as MDR (≥3 antimicrobials)	Tăbăran et al. [14]
Slaughterhouse/ retail	Chicken carcasses, retail chicken meat	8 serovars: *S.* Infantis, *S.* Bredeney, *S.* Virchow, *S.* Djugu, *S.* Grampian, *S.* Brandenburg, *S.* Derby, *S.* Ruzizi	42/317 (13.2%); • slaughterhouse 12.8%; • retail 17.8%	Broth microdilution; CLSI TET 66.6%; NAL 64.3%; SMX 64.3%; CIP 61.9%; STR 59.5%; TMP 33.3%, AMP 9.5%; CHL 7.1%; GEN 2.4%; no resistance to CTX, CAZ.	71.4% classified as MDR (≥2 antimicrobials)	Tîrziu et al. [52]
Laboratory-based surveillance	Raw poultry meat products	*S.* Enteritidis, *S.* Typhimurium	112 isolates	Disk diffusion; CLSI: 2011–2015: TET 74%; SFN 54%; STR 34%; AMP 32%; CEP 8%; QUI 4% 2016–2021: TET 84%; NAL 78%; AMP 78%	MDR increased from 24% (2011–2015) to 56% (2016–2021); (≥3 antimicrobials)	Forgaciu et al. [3]
Retail/raw and RTE foods	Raw pork; chicken carcasses; fresh retail chicken meat; RTE meat products (sausages, ham, salami)	11 serovars, predominant: *S.* Infantis, *S.* Typhimurium, *S.* Rissen, *S.* Derby, *S.* Enteritidis.	raw pork 33/146 (22.6%), raw chicken 12/132 (9.1%) RTE meat products 3/62 (4.8%)	Broth microdilution; CLSI: AZM 88.2%; TET 54.9%; SMX 54.9%; CIP 45.1; NAL 43.1%; AMP 35.3%; CHL 33.3%; TGC 25.5%; CTX/CST 13.7%; TMP 7.8%; GEN 2%	68.6% classified as MDR (≥1 agent in ≥3 antimicrobial classes)	Tîrziu et al. [19]
Farm/ cattle slaughterhouse	Cattle fecal	*S.* Typhimurium, *S.* Enteritidis	14/50 (28%)	Not reported	Not reported	Brătfelan et al. [27]
	Cattle carcasses	Not detected	0	-	-	

Note: AMC, amoxicillin/clavulanic acid; AMP, ampicillin; AZM, azithromycin; CAZ, ceftazidime; CEP, cephalosporins; CFZ, cefazolin; CHL, chloramphenicol; CIP, ciprofloxacin; CLSI, Clinical and Laboratory Standards Institute; CST, colistin; CTX, cefotaxime; GEN, gentamicin; IMI, imipenem; NAL, nalidixic acid; NIT, nitrofurantoin; NOR, norfloxacin; PIP, piperacillin; PIP/TAZ, piperacillin/tazobactam; QUI, quinolones; SFN, sulfonamides; SMX, sulfamethoxazole; STR, streptomycin; TET, tetracycline; TGC, tigecycline; TMP, trimethoprim; TMP-SMX, trimethoprim–sulfamethoxazole; MDR, multidrug resistance; RTE, ready to eat. MDR definitions follow those reported in the original studies and differ according to the number of antimicrobial agents or classes considered.

In poultry, Tîrziu et al. [52] detected *Salmonella* spp. in 42/317 (13.2%) samples, with occurrence of 12.8% at the slaughterhouse level and 17.8% in retail chicken meat. In a subsequent investigation of raw and ready-to-eat (RTE) foods, Tîrziu et al. [19] detected *Salmonella* spp. in 33/146 (22.6%) raw pork samples, 12/132 (9.1%) raw chicken samples, and 3/62 (4.8%) RTE meat products. More recently, Tăbăran et al. [14] recovered 48 isolates from 208 traditionally obtained pork samples, corresponding to an occurrence of 23.07%.

Evidence from cattle is more limited and illustrates the importance of distinguishing intestinal carriage from carcass contamination. Brătfelan et al. [27] detected *Salmonella* spp. in 14/50 (28%) cattle fecal samples, whereas no *Salmonella* spp. was detected in the 100 corresponding carcass samples examined. These findings document fecal carriage in the investigated cattle population but do not demonstrate transfer to carcasses during slaughter.

Overall, the available studies demonstrate heterogeneous occurrence of *Salmonella* spp. across animal species, sample types, and stages of the meat production chain. Because these investigations differ substantially in design, geographical coverage, sampling strategy, and study population, their prevalence estimates should not be interpreted as a continuous national temporal trend.

High-resistance frequencies to several antimicrobial classes have been reported among Romanian *Salmonella* isolates. Mihaiu et al. [4] reported resistance to sulfamethoxazole (87.25%), streptomycin (81.21%), tetracycline (80.53%), nalidixic acid (65.10%), ciprofloxacin (42.95%), ampicillin (20.81%), chloramphenicol (16.78%), and ceftazidime (11.41%). Of the 149 isolates, 124 (83.22%) were reported as multiple resistant, with 35 distinct resistance patterns. This terminology should be retained because the study reported multiple resistance rather than applying the same MDR definition used in all subsequent studies.

Morar et al. [25] also identified resistant *Salmonella* spp. in the pork production chain. Resistance was most frequent to tetracycline (61.5%), ampicillin (50%), and piperacillin (50%), followed by trimethoprim–sulfamethoxazole (34.6%), amoxicillin/clavulanic acid (26.9%), nitrofurantoin (23.1%), and cefazolin (15.4%). Lower resistance frequencies were reported for piperacillin/tazobactam, ciprofloxacin, norfloxacin, and imipenem, while no resistance was detected to cefotaxime, ceftazidime, cefepime, amikacin, or gentamicin. MDR isolates were also reported [25].

In poultry, Tîrziu et al. [52] reported resistance to tetracycline (66.6%), nalidixic acid and sulfamethoxazole (64.3% each), ciprofloxacin (61.9%), and streptomycin (59.5%). Resistance to trimethoprim, ampicillin, chloramphenicol, and gentamicin occurred at lower frequencies, while no resistance to cefotaxime or ceftazidime was detected. The authors classified 30/42 isolates (71.4%) as MDR, using an operational definition of resistance of at least two antimicrobials. Because this differs from commonly used MDR definitions based on resistance across three or more antimicrobial classes, this percentage should not be directly compared with MDR frequencies reported using other definitions.

More recent evidence from traditionally obtained pork also demonstrates substantial resistance. Tăbăran et al. [14] reported resistance to streptomycin in 91.66% of isolates, tetracycline in 83.33%, sulfamethoxazole in 68.7%, and nalidixic acid in 56.25%. MDR, defined in that study as resistance to at least three antimicrobials, was identified in 45/48 isolates (93.75%).

The available Romanian studies demonstrate considerable serovar diversity. Earlier investigations identified *S.* Infantis, *S.* Typhimurium, *S.* Derby, and *S.* Colindale among the predominant serovars in poultry and pork [4]. Poultry studies subsequently continued to identify *S.* Infantis, together with *S.* Enteritidis, *S.* Typhimurium, *S.* Bredeney, *S.* Virchow, and several less frequently detected serovars [3,52].

The available poultry studies therefore indicate the occurrence of several epidemiologically relevant serovars, particularly *S.* Infantis, *S.* Enteritidis, and *S.* Typhimurium, rather than demonstrating replacement by a single dominant serovar over time.

The pork chain shows broader serovar diversity. In Tîrziu et al. [19], *S.* Typhimurium was the most frequently identified serovar in raw pork, with nine isolates, followed by *S.* Rissen with eight and *S.* Infantis with six. *S.* Derby, *S.* Bredeney, *S.* Brandenburg, *S.* Enteritidis, *S.* Gloucester, *S.* Goldcoast, *S.* Kottbus, and *S.* Ruzizi occurred at lower frequencies. All *Salmonella* isolates recovered from chicken meat in that study were *S.* Infantis, while isolates from RTE sausages included *S.* Typhimurium and *S.* Derby.

Tăbăran et al. [14] identified eight serovars among 48 isolates from traditionally obtained pork, with *S.* Infantis and *S.* Typhimurium each accounting for 15/48 isolates (31.25%), followed by *S.* Derby with 11/48 (22.91%). *S.* Virchow and *S.* Brandenburg each represented 4.16%, while *S.* Ruzizi, *S.* Muenchen, and *S.* Bredeney were each detected at 2.08%. Rather than demonstrating a temporal shift, these findings show that *S.* Typhimurium, *S.* Infantis, and *S.* Derby accounted for a substantial proportion of the pork-associated isolates in this particular study. The available evidence does not support a uniform temporal increase or decrease in *Salmonella* occurrence in Romania. Differences among studies reflect variation in animal species, meat matrices, geographical areas, production systems, sampling stages, and methodological approaches, which limits direct temporal comparison. *Salmonella* spp. has been detected in pork and poultry at slaughter, processing, and retail stages, while recent cattle data demonstrate fecal carriage without detectable carcass contamination in the population examined. The strongest evidence for temporal change in antimicrobial resistance comes from the longitudinal poultry study of Forgaciu et al. [3], which compared isolates collected during 2011–2015 and 2016–2021. Resistance to tetracycline increased from 74% to 84%, while substantial differences were also observed for several other antimicrobials. Most importantly, MDR increased from 24% during 2011–2015 to 56% during 2016–2021. Because these observations were generated within the same longitudinal study, they provide stronger evidence of temporal change than comparisons between independent cross-sectional investigations.

3.3.2. *Campylobacter* spp.

Campylobacter spp. have been detected at different stages of the Romanian poultry meat chain, although reported occurrence varies considerably according to the sampling matrix and food-chain stage (Table 2). Popa et al. [6] reported the highest occurrence, detecting *Campylobacter* spp. in 276/324 (85.2%) broiler cecal samples collected during slaughter. Among the recovered isolates, *C. coli* predominated (63.4%), whereas *C. jejuni* accounted for 36.6%, indicating substantial intestinal carriage of thermophilic *Campylobacter* spp., in slaughtered broilers.

Detection frequencies were considerably lower in chicken meat. Tîrziu et al. [19] detected *Campylobacter* spp. in 10/34 (29.4%) retail raw chicken samples, with *C. coli* again predominating (70%) over *C. jejuni* (30%). More recently, Popa et al. [5] reported an overall prevalence of 27.7% across slaughterhouse and retail poultry samples, including 13/40 (32.5%) chicken neck-skin samples collected at slaughter and 23/90 (25.5%) retail poultry meat samples. These results should not be interpreted as evidence of lower *Campylobacter* spp. occurrence over time because cecal samples measure intestinal carriage, whereas neck-skin and retail meat samples reflect contamination at subsequent stages of the production chain.

Table 2. Occurrence, antimicrobial resistance, and multidrug resistance of *Campylobacter* spp. along the Romanian meat chain.

Food-Chain Stage	Sample/Source	Species/Isolates	Occurrence/Study Population	Antimicrobial Resistance Profile	Resistance Determinants/ MDR/Limitations	Reference
Broilers/slaughter	Broiler caecal samples	*C. coli*	276/324 (85.2%)/ 175/276 isolates (63.4%).	Not tested	Not reported.	Popa et al. [6]
		C. jejuni	138/182 (75.8%)/ 101/276 isolates (36.6%).	Broth microdilution (EUCAMP): CIP 79.2%; NAL 78.2%; TET 49.5%; STR 7.9%; ERY/GEN 0%.	6.9% MDR (≥3 classes)	
Turkeys/slaughter	Turkey caecal samples	*C. jejuni*	75/138 isolates (54.3%).	Broth microdilution (EUCAMP): CIP 70/75 (93.3%); TET 58/75 (77.3%); ERY 14/75 (18.7%); ETP 11/75 (14.7%); CHL/GEN 0%.	Not reported.	Popa et al. [55]
		C. coli	63/138 isolates (45.7%).	Broth microdilution (EUCAMP): CIP 54/63 (85.7%); TET 59/63 (93.7%); ERY 18/63 (28.6%); ETP 8/63 (12.7%); CHL/GEN 0%.		
Pigs/slaughter	Pig caecal samples	*C. coli*	36/39 positive samples (92.3%).	EURL: TET 27/36 (75.0%); CIP 25/36 (69.4%); ERY 3/36 (8.3%); GEN and ETP 1/36 (2.8%) each; CHL 0%.	19.5% MDR (≥3 classes)	Popa et al. [36]
Cattle/slaughter	Cattle caecal samples	*C. jejuni*	5/17 positive samples (29.4%).	EURL: CIP 3/5 (60.0%); TET 1/5 (20.0%); ERY/ETP/GEN/CHL 0%.	Not reported.	Popa et al. [36]
Poultry/slaughter	Chicken carcasses	*C. jejuni*	22/144 positive carcasses (15.3%).	E-test: TET 31.8%; sulfonamides 13.6%; CIP/NAL/CHL 9.1% each; AMP 4.5%.	40.9% MDR (≥3 antimicrobials)	Dan et al. [9]
Slaughterhouse/ retail	Chicken neck skin; retail fillets, backs and necks	*Campylobacter* spp.	36/130 (27.7%): overall 13/40 (32.5%) slaughterhouse 23/90 (25.5% retail).	Disk diffusion: CIP 41.6%; TET 25.0%; CHL 16.6%; GEN 11.1%; ETP 5.6%; ERY 2.8%.	Not reported.	Popa et al. [5]
Retail/poultry	Raw retail chicken meat	*C. jejuni*	3/10 isolates.	Pooled AST for all 10 *C. jejuni* + *C. coli* isolates: CIP/NAL 80%; TET 40%; STR/ERY 10% each; GEN 0%.	100% MDR (≥3 classes)	Tîrziu et al. [19]
		C. coli	7/10 isolates.		14.3% MDR (≥3 classes)	

Note: AMP, ampicillin; AST, antimicrobial susceptibility testing; CHL, chloramphenicol; CIP, ciprofloxacin; ERY, erythromycin; ETP, ertapenem; EUCAMP, *Campylobacter* antimicrobial susceptibility testing microdilution panel; EURL, European Union Reference Laboratory (testing protocol); GEN, gentamicin; NAL, nalidixic acid; STR, streptomycin; TET, tetracycline; MDR, multidrug resistance; E-test, antimicrobial gradient diffusion test; n, number of isolates tested.

Regarding antimicrobial resistance, fluoroquinolone resistance represents the most consistent finding across the available Romanian poultry studies. Popa et al. [6] reported ciprofloxacin resistance in 79.2% and nalidixic acid resistance in 78.2% of *C. jejuni* isolates from broiler ceca. Tetracycline resistance was also frequent (49.5%), whereas streptomycin resistance was substantially lower (7.9%), and no resistance to erythromycin or gentamicin was detected. MDR was reported in 7/101 (6.9%) *C. jejuni* isolates.

A different resistance profile was reported in the more recent slaughterhouse and retail investigation by Popa et al. [5]. Among the 36 *Campylobacter* isolates recovered across both sampling stages, resistance was highest to ciprofloxacin (41.6%), followed by tetracycline (25.0%), chloramphenicol (16.6%), gentamicin (11.1%), ertapenem (5.6%), and erythromycin (2.8%). These resistance percentages refer to the complete set of 36 isolates and should therefore not be attributed separately to the slaughterhouse or retail groups. Although ciprofloxacin and tetracycline resistance frequencies in this study were lower than those reported previously, the difference cannot be interpreted as a temporal decline in resistance. The studies differed in sampling matrices, food-chain stage, isolate composition, and methodological context. Species composition represents an additional source of heterogeneity because resistance patterns may differ between *C. jejuni* and *C. coli*, making aggregate *Campylobacter* resistance frequencies dependent partly on the species represented in each study. Evidence from other livestock species also indicates substantial antimicrobial resistance. In turkeys, Popa et al. [55] reported ciprofloxacin resistance of 93.3% in *C. jejuni* and 85.7% in *C. coli*, while investigations in pigs identified ciprofloxacin and tetracycline resistance of 69.4% and 75.0%, respectively, among *C. coli* isolates; cattle-associated *C. jejuni* showed lower resistance frequencies, although only five isolates were examined [36].

Overall, the available Romanian evidence identifies quinolone and fluoroquinolone resistance as the most consistently reported AMR feature of poultry-associated *Campylobacter*. Tetracycline resistance has also been repeatedly documented, whereas erythromycin and gentamicin resistance were absent or comparatively uncommon in most of the investigated populations. MDR has been reported, including in 6.9% of *C. jejuni* isolates in the study by Popa et al. [6], but the limited number and heterogeneity of available studies do not allow a reliable temporal trajectory for MDR to be established.

3.3.3. *Escherichia coli*

Escherichia coli has been detected at several stages of the Romanian meat production continuum, from food-producing animals to slaughterhouses and meat products (Table 3). However, its reported occurrence varies considerably according to animal species, sample type, and the *E. coli* population targeted. Earlier surveillance of meat products by Zaulet et al. [29] indicated a relatively low occurrence of *E. coli* Biotype I, with detection in 1/501 (0.2%) raw meat samples and 125/10,548 (1.2%) ground or mechanically processed meat samples, while VTEC O157 was not detected. In contrast, Dan et al. [9] recovered *E. coli* from 18/144 (12.5%) poultry carcasses, demonstrating their presence at the slaughter and processing stage.

Cattle studies provide further evidence of *E. coli* occurrence at the animal and slaughterhouse levels, particularly for pathogenic strains. Tăbăran et al. [28] identified 29/164 (17.7%) *E. coli* isolates carrying virulence markers among isolates recovered from cattle intestinal samples collected during evisceration. More recently, Brătfelan et al. [27] detected pathogenic *E. coli* in 7/50 (14%) cattle fecal samples and 5/100 (5%) carcass samples. The lower occurrence on carcasses than fecal samples indicates that intestinal carriage was more frequent than carcass contamination in the population examined. Detection on carcasses confirms the presence of pathogenic *E. coli* after slaughter, although the study design does not establish the precise route or timing of contamination.

Table 3. Occurrence, antimicrobial resistance, and resistance determinants of *Escherichia coli* along the Romanian meat chain.

Food-Chain Stage	Sample/Source	*E. coli* Type/ Serogroup	Occurrence/Study Population	Antimicrobial Resistance Profile	MDR/Resistance Determinants	Reference
Farm/swine production	Rectal fecal samples from piglets from grower farms	*E. coli*	76/140 (54.3%)	MicroScan WalkAway MIC: AMP 100%; MEZ 100%; PIP 76.3%; TET 59.2%; PIP/TAZ 10.5%; TGC 3.9%; MEM 0%	MDR not reported using a comparable isolate-level definition; *ampC*, *blaZ*, *blaTEM*, and *tetK* detected;	Lungu et al. [7]
Farm/poultry production	Fecal samples from broilers and turkeys	*E. coli*	60/102 (59%) presumptive ESBL/AmpC; • turkeys 55%; • broilers 61%	Broth microdilution: • broilers: NAL 85%; AMP/CIP 73%; CTX 61%; CAZ 59%; FEP 56%; TET 39%. • turkeys: AMP 81%; TET 77%; CHL/SMZ 74%; NAL 71%; CIP 68%; CTX/CAZ 54%; FEP 55%.	Overall: MDR 44% (≥3 classes); XDR 50% (all but ≤2 classes) Broilers: 55% MDR, 39% XDR Turkeys: 19% MDR; 74% XDR *ampC* 44.2%; *blaZ* 72.7%; *blaTEM* 58.1%	Rus et al. [8]
Farm/cattle reservoir → slaughterhouse	Cattle intestinal contents collected during evisceration	*E. coli*	164 isolates recovered from 170 samples	Disk diffusion, CLSI: NAL 58%; TET 54%; CIP 49%; cephalosporin resistance also detected	68.9% classified as MDR (≥3 drugs); 17.7% virulence-gene-positive isolates: *tet(A)/tet(B)* 64%; *sul1/aadA1* 52.3%; *blaTEM* 23.8%; *blaSHV* 2.3% (pooled results Romania–France)	Tăbăran et al. [28]
Slaughterhouse/ beef processing	Cattle carcasses, post-evisceration and cooling	*E. coli*; O101 and O26	5/100 carcasses (5%); 7/50 fecal (14%)	Not reported	Not reported	Brătfelan et al. [27]
Poultry meat/retail	Poultry carcasses/meat	*E. coli*	18/144 carcasses (12.5%)	Agar dilution MIC (CLSI) TET 66.7%; QUI 55.5%; NAL 44.4%; CIP 33.3%; AMP 27.7%; SMX 22.2%; SMX/TMP 22.2%; STR 11.1%; GEN 11.1%	52% MDR (>3 drugs); resistance genes detected: *blaTEM*, *tetA*, *dfrIa*, *sul/sul1*	Dan et al. [9]
Retail/meat products	Raw and ground meat, various animal species	*E. coli*	raw meat 1/501 (0.2%); ground meat 125/10,548 (1.2%);	Not reported	Not reported	Zaulet et al. [29]

Note: AMP, ampicillin; AmpC, AmpC β-lactamase; CAZ, ceftazidime; CHL, chloramphenicol; CIP, ciprofloxacin; CLSI, Clinical and Laboratory Standards Institute; CTX, cefotaxime; ESBL, extended-spectrum β-lactamase; FEP, cefepime; GEN, gentamicin; MDR, multidrug resistance; MEM, meropenem; MEZ, mezlocillin; MIC, minimum inhibitory concentration; NAL, nalidixic acid; PIP, piperacillin; PIP/TAZ, piperacillin/tazobactam; QUI, quinolones; SMX, sulfamethoxazole; SMX/TMP, sulfamethoxazole/trimethoprim; SMZ, sulfamethoxazole; STR, streptomycin; TET, tetracycline; TGC, tigecycline; CLSI, Clinical and Laboratory Standards Institute; MIC, minimum inhibitory concentration; MDR, multidrug resistance: XDR, extensively drug-resistant.

The available studies also indicate considerable heterogeneity among pathogenic *E. coli* populations. Earlier meat surveillance did not detect VTEC O157 in the matrices examined by Zaulet et al. [29]. However, subsequent cattle studies demonstrated that surveillance targeting O157 alone cannot capture the full diversity of pathogenic *E. coli*. Tăbăran et al. [28] detected cattle-associated isolates carrying major virulence determinants, including *stx1*, *stx2*, and *eaeA*, while Brătfelan et al. [27] identified pathogenic isolates belonging to non-O157 serogroups, including O101 and O26. The detection of non-O157 pathogenic *E. coli* is particularly relevant from a surveillance perspective because it indicates that pathogenic populations in Romanian food-producing animals are heterogeneous. Therefore, surveillance strategies restricted to O157:H7 may underestimate the diversity of pathogenic *E. coli* occurring along the meat chain, supporting the inclusion of non-O157 serogroups and virulence markers in future monitoring programs.

Antimicrobial resistance has also been documented in several of the investigated *E. coli* populations. In poultry carcasses, Dan et al. [9] reported resistance to tetracycline (66.7%), the quinolone category tested (55.5%), nalidixic acid (44.4%), ciprofloxacin (33.3%), and ampicillin (27.7%), while resistance to other tested antimicrobials occurred at lower frequencies. These findings demonstrate that resistance to tetracyclines and quinolone or fluoroquinolone antimicrobials was already present among poultry-associated *E. coli* during the earlier part of the reviewed period.

Resistance was also reported among cattle-associated pathogenic *E. coli*. Tăbăran et al. [28] documented MDR in 20/29 (68.9%) Romanian pathogenic isolates, while 9/29 (31%) were resistant to cefotaxime and/or ceftazidime. Resistance determinants included *tet(A)/tet(B)* (64%), *sul1/aadA1* (52.3%), *blaTEM* (23.8%), and *blaSHV* (2.3%); however, these gene frequencies were calculated from the combined Romanian and French isolates (n = 42), rather than the Romanian subset alone. These findings demonstrate the co-occurrence of phenotypic resistance and multiple resistance determinants among pathogenic cattle-associated *E. coli*.

Swine-associated *E. coli* also showed substantial antimicrobial resistance. Lungu et al. [7] characterized 76 *E. coli* isolates from piglets in grower farms in western Romania and reported resistance to ampicillin and mezlocillin in all isolates, followed by piperacillin (76.3%) and tetracycline (59.2%). Resistance was considerably lower to piperacillin/tazobactam (10.5%) and tigecycline (3.9%), while no meropenem resistance was detected. Molecular analysis identified *ampC*, *blaZ*, *blaTEM*, and *tetK* [7]. These findings extend the Romanian evidence of antimicrobial-resistant *E. coli* beyond poultry and cattle to swine production.

More recent poultry data demonstrated extensive phenotypic resistance. Rus et al. [8] reported high resistance among broiler isolates to nalidixic acid (85%), ampicillin and ciprofloxacin (73%), cefotaxime (61%), ceftazidime (59%), cefepime (56%), and tetracycline (52%). Turkey isolates showed high resistance to ampicillin (81%), tetracycline (77%), chloramphenicol/sulfamethoxazole (74%), nalidixic acid (71%), and ciprofloxacin (68%), together with resistance to third- and fourth-generation cephalosporins. The simultaneous occurrence of resistance to β-lactams, quinolones or fluoroquinolones, tetracyclines, and other antimicrobial classes indicates a broad resistance spectrum in the poultry-associated *E. coli* population investigated.

Rus et al. [8] also documented substantial MDR and XDR. Among broiler isolates, 55% were classified as MDR and 39% as XDR, whereas among turkey isolates, 19% were classified as MDR and 74% as XDR. Across all 102 poultry isolates, 44% were MDR and 50% were XDR. The high frequency of phenotypic resistance was accompanied by reported prevalences of the investigated β-lactam resistance determinants of 44.2% for ampC, 72.7% for *blaZ*, and 58.1% for *blaTEM*. The presence of presumptive ESBL/AmpC-producing

isolates in both broilers and turkeys further demonstrates complex β-lactam resistance in poultry-associated *E. coli* populations.

Dan et al. [9] also detected resistance determinants among the investigated poultry-associated *E. coli*, including *blaTEM*, *tetA*, *dfrIa*, and *sul/sul1*, associated with β-lactam, tetracycline, trimethoprim, and sulfonamide resistance, respectively. The authors reported MDR in 52% of *E. coli* isolates, whereas the overall MDR frequency of 23% referred to all bacterial species investigated in the study. However, differences in MDR definitions and susceptibility-testing approaches limit direct comparison with the species-specific MDR and XDR frequencies reported in subsequent studies.

From a temporal perspective, the available evidence demonstrates that antimicrobial-resistant *E. coli* has been identified in Romanian food-producing animals and meat throughout the reviewed period. Resistance to tetracyclines and quinolone or fluoroquinolone antimicrobials was already documented in earlier poultry isolates, while subsequent studies identified MDR pathogenic *E. coli* in cattle, extensive β-lactam and tetracycline resistance with multiple resistance determinants in swine, and MDR/XDR populations with presumptive ESBL/AmpC phenotypes and multiple β-lactam resistance determinants in poultry. However, these findings should not be interpreted as demonstrating a quantitative temporal increase in AMR, MDR, or XDR. The studies were not longitudinally linked and differed in animal populations, sampling matrices, selection criteria, antimicrobial panels, and MDR/XDR definitions. In particular, Rus et al. [8] specifically investigated *E. coli* in the context of ESBL/AmpC characterization, whereas earlier studies addressed broader bacterial populations or different epidemiological objectives.

The broader spectrum of resistance mechanisms described in recent studies may also reflect increasingly detailed phenotypic and molecular characterization rather than the emergence of these mechanisms during the study period. Therefore, the availability of more extensive molecular data in recent investigations should not itself be interpreted as evidence of increasing AMR over time.

Overall, the available evidence demonstrates the occurrence of *E. coli*, including pathogenic and antimicrobial-resistant populations, at different stages of the Romanian meat production chain and in several food-producing animal populations. Resistance to tetracyclines and quinolones or fluoroquinolones has been repeatedly documented, while subsequent investigations have additionally identified resistance to extended-spectrum cephalosporins, MDR/XDR phenotypes, and diverse resistance determinants in cattle, swine, and poultry. However, differences in study design, bacterial populations, sampling matrices, antimicrobial panels, and molecular methods prevent inference of a uniform national temporal increase in AMR.

3.3.4. *Listeria monocytogenes*

Listeria monocytogenes has been detected at different stages of the Romanian meat production chain, although its occurrence varies considerably according to the investigated matrix (Table 4). Sala et al. [10] documented substantial environmental contamination in a pig slaughterhouse and raw-processing facility, recovering *L. monocytogenes* from 25/97 (25.8%) environmental samples. Detection occurred on both food-contact surfaces, 14/60 (23.3%), and non-food-contact surfaces, 11/37 (29.7%). These findings demonstrate that *L. monocytogenes* was widely distributed across the investigated processing environment. Its detection on both food-contact and non-food-contact surfaces identifies potential environmental sources of contamination, although the cross-sectional study design does not establish long-term persistence within the facility.

Table 4. Occurrence and antimicrobial resistance of *Listeria* spp. reported along the Romanian meat production chain.

Food-Chain Stage/Source	Sample/Matrix	*Listeria* Isolates	Occurrence	Antimicrobial Resistance Profile	MDR/Resistance Determinants	References
Slaughter-house/processing environment	Food-contact and non-food-contact surfaces in a pig slaughterhouse/raw-processing plant	*L. monocytogenes*	Overall: 25/97 (25.8%); food-contact: 14/60 (23.3%); non-food-contact: 11/37 (29.7%)	VITEK 2 (CLSI): PEN 100%; IMI 100%; FA 100%; OXA 92%; FOS 92%; CLI 88%; RIF 56%; SXT 48%; TET 44%; CIP 4%;	100% classified as MDR (resistance to 4–9 drugs)	Sala et al. [10]
Poultry slaughter/processing	Chicken carcasses	*L. monocytogenes*	19/144 (13.2%)	Agar dilution MIC (CLSI) TET 31.6%; CHL 21.1%; QUI 21.1%; AMP 10.5%; CIP 10.5%; NAL 10.5%; SFN 5.3%; SMX 5.3%; SXT 5.3%	Species-specific MDR not reported	Dan et al. [9]
Retail/mixed animal-origin foods	RTE meat products, pork, snails and dairy products	*L. monocytogenes*	Overall: 17/221 (7.7%); RTE meat: 8/130 (6.2%); raw-food group: 6/47 (12.8%); dairy: 3/44 (6.8%).	VITEK 2 (EUCAST): PEN/FA 100%; OXA 88.2%; FOS 82.4%; CLI 76.5%; IMI 52.9%; CIP/RIF 41.2%; SXT/TET 29.4%.	100% classified as MDR (≥3 classes)	Tîrziu et al. [56]
Retail/meat products	Bovine, ovine, caprine, pork, chicken and turkey meat products	*L. monocytogenes*	Overall: 7/1841 (0.38%); raw pork: 2/292 (0.7%); mechanically processed red meat: 4/374 (1.1%); RTE meat products: 1/1146 (0.1%)	Not reported	Not reported	Zaulet et al. [29]
Retail/RTE foods	RTE pork, poultry and beef products; fish and dairy foods	*L. monocytogenes*	Across all food types: 26/8151 (0.32%); meat-associated isolates: 22/26 (84.6%);	Disk diffusion (EUCAST and CLSI): SXT 26.9%; OXA 23.1%; AMP/TET 19.2%; CIP/LEV/MXF 0%.	23.1% classified as MDR (≥3 drugs); *tet(C)*, *tet(M)*, *tet(K)*, *ampC* and *dfrD* detected	Duma et al. [57]
Cattle sampled at slaughter	Cattle fecal and carcass samples	*Listeria* spp.;	Fecal: 2/50 positive for *Listeria* spp.; carcasses: 0/100;	Not applicable	Not reported	Brătfelan et al. [27]

Note: AMP, ampicillin; CHL, chloramphenicol; CIP, ciprofloxacin; CLI, clindamycin; FA, fusidic acid; FOS, fosfomycin; IMI, imipenem; LEV, levofloxacin; MXF, moxifloxacin; NAL, nalidixic acid; OXA, oxacillin; PEN, benzylpenicillin; QUI, quinolones; RIF, rifampin; SFN, sulfonamides; SMX, sulfamethoxazole; SXT, trimethoprim-sulfamethoxazole; TET, tetracycline; CLSI, Clinical and Laboratory Standards Institute; EUCAST, European Committee on Antimicrobial Susceptibility Testing; MDR, multidrug resistance; MIC, minimum inhibitory concentration; RTE, ready-to-eat.

In poultry, Dan et al. [9] detected *L. monocytogenes* in 19/144 (13.2%) chicken carcasses, demonstrating contamination at the slaughter and processing stage. In contrast, Zaulet et al. [29] reported considerably lower occurrence across a large meat-surveillance dataset, with *L. monocytogenes* detected in 7/1841 (0.38%) samples. Occurrence varied according to matrix, with detection in 2/292 (0.7%) raw pork samples, 4/374 (1.1%) mechanically processed red meat samples, and 1/1146 (0.1%) ready-to-eat meat products. These differences should not be interpreted as indicating higher or lower occurrence over time because the studies investigated different food matrices, production stages, and sampling populations.

More recently, Brătfelan et al. [27] detected *Listeria* spp. in two cattle fecal samples, while none of the 100 cattle carcasses examined were positive. Importantly, the isolates recovered from fecal samples were not confirmed as *L. monocytogenes*. Therefore, these findings provide evidence of *Listeria* spp. occurrence in the investigated cattle population but should not be used to estimate the occurrence of *L. monocytogenes* in cattle or beef carcasses.

Taken together, the available occurrence data demonstrate that *L. monocytogenes* was recovered from poultry carcasses, meat products, and processing environments in Romania, with particularly frequent detection on environmental surfaces in the facility investigated by Sala et al. [10]. However, detection in a processing environment should be distinguished from demonstrated persistence. Establishing persistent contamination would require repeated isolation over time, preferably supported by molecular or genomic evidence showing the recurrence of closely related strains. The available Romanian studies therefore demonstrate occurrence at several stages of the meat chain but do not establish a consistent temporal trend in prevalence.

Antimicrobial resistance was particularly pronounced among the *L. monocytogenes* isolates recovered from the pork-processing environment. Sala et al. [10] reported that all 25 isolates were resistant to benzylpenicillin, imipenem, and fusidic acid. Resistance to oxacillin and fosfomycin reached 92%, while 88% of isolates were resistant to clindamycin. Resistance was also reported to rifampin (56%), trimethoprim–sulfamethoxazole (48%), tetracycline (44%), and ciprofloxacin (4%). Conversely, no resistance was detected to gentamicin, erythromycin, moxifloxacin, linezolid, teicoplanin, vancomycin, or tigecycline. All 25 isolates were reported as resistant to four to nine antimicrobials and were classified as MDR in the original study. Susceptibility testing was performed using the VITEK 2 system. For 13 of the 17 tested antimicrobials, Sala et al. [10] applied CLSI interpretive criteria established for staphylococci rather than species-specific criteria validated for *L. monocytogenes*. Consequently, the unusually high resistance rates, particularly for resistance to imipenem, and the classification of all isolates as MDR should be interpreted cautiously.

Dan et al. [9] reported a different resistance profile among poultry-associated *L. monocytogenes*. Tetracycline resistance was detected in 31.6% of isolates, followed by chloramphenicol and quinolone resistance, both at 21.1%. Resistance to ampicillin, ciprofloxacin, and nalidixic acid was reported in 10.5% of isolates, while resistance to sulfonamides, sulfamethoxazole, and trimethoprim–sulfamethoxazole occurred in 5.3%. An *L. monocytogenes*-specific MDR frequency was not reported. Therefore, the overall MDR frequency of 23% reported by Dan et al. [9] across the bacterial isolates investigated in that study should not be attributed specifically to *L. monocytogenes*.

Direct comparison of the resistance frequencies reported by Sala et al. [10] and Dan et al. [9] is limited by differences in isolate source, antimicrobial panels, susceptibility-testing approaches, and study objectives. Consequently, the available evidence does not demonstrate an increase or decrease in *L. monocytogenes* antimicrobial resistance over the reviewed period. Rather, it confirms the occurrence of resistant *L. monocytogenes* in both poultry carcasses and a meat-processing environment, including isolates with resistance to multiple antimicrobials.

Overall, the Romanian evidence for *L. monocytogenes* is more limited than that available for *Salmonella* spp., *Campylobacter* spp., and *E. coli*. The available studies demonstrate contamination of poultry carcasses, meat products, and processing environments and document antimicrobial-resistant *L. monocytogenes*, including MDR isolates in one processing-environment study. However, the small number of studies, differences in sampled matrices and methods, and absence of longitudinal strain-level investigations prevent conclusions regarding national temporal trends or long-term persistence from being drawn. Continued surveillance combining food and environmental sampling with standardized antimicrobial susceptibility testing and molecular or genomic characterization would improve understanding of *L. monocytogenes* occurrence, resistance, and persistence within Romanian meat-production environments.

3.4. Critical Comparison with European and Neighboring-Country Evidence

Comparison with European surveillance and selected original studies reveals recurring AMR patterns alongside substantial differences among countries, bacterial populations, and animal-production sectors (Figure 1). The most consistent findings concern fluoroquinolone resistance in *Campylobacter* spp. and MDR in selected *Salmonella* serovars and indicator *E. coli* populations. However, differences in resistance frequencies cannot always be attributed to epidemiological factors independently of bacterial species, sampling populations, or AST methodology [2].

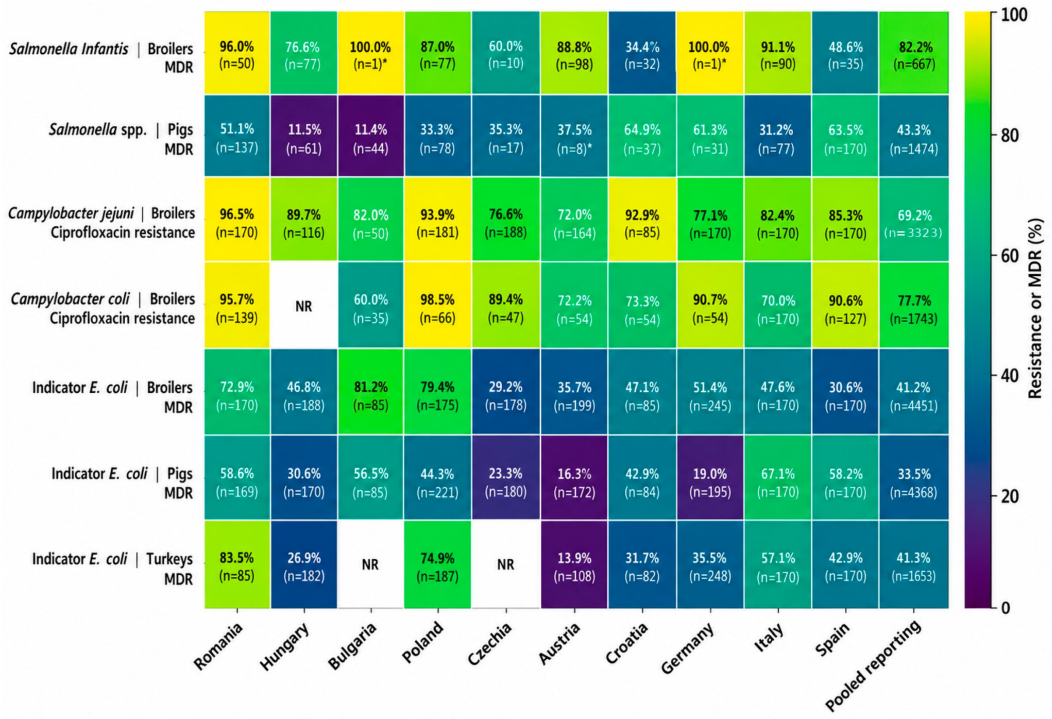


Figure 1. Cross-country comparison of antimicrobial resistance in food-producing animals based on EFSA/ECDC surveillance data (2023–2024). Colors range from dark purple (low resistance) to yellow (high resistance). Cells indicate percentages and tested isolates (n); white cells indicate unavailable data (NR). Pooled reporting includes Romania, and * indicates fewer than 10 isolates. Source: EFSA/ECDC [2], Annexes A.2, B.2, and C.

For *Salmonella*, serovar composition is particularly important when interpreting resistance patterns. In 2024 harmonized surveillance, MDR among broiler-associated *S.* Infantis reached 96.0% in Romania, compared with 76.6% in Hungary, 87.0% in Poland, and 82.2% across pooled European reporting isolates. In contrast, no MDR was reported among the

Romanian *S.* Enteritidis isolates examined, illustrating the considerable influence of serovar distribution on aggregate resistance estimates. Differences were also observed in fattening pigs, with MDR frequencies of 51.1% in Romania, 11.5% in Hungary, 11.4% in Bulgaria, and 33.3% in Poland [2]. Although these results indicate variation among monitored populations, they do not establish corresponding differences in national AMR burdens.

Independent European studies provide additional information on *Salmonella* spp. resistance mechanisms. In the Republic of Moldova, Burduniuc et al. [58], reported MDR in 10.4% of isolates from chicken meat preparations, whereas Serbian investigations identified colistin-nonsusceptible *S.* Infantis isolates subjected to genomic characterization [59]. Studies from Slovenia and Italy highlighted the importance of *S.* Infantis lineages carrying resistance-associated determinants, including pESI-like plasmids [60,61]. These findings provide relevant molecular context for Romanian investigations documenting resistant *S.* Infantis and other serovars in poultry and pork [3,4,14]. Nevertheless, similarities in resistance phenotypes or plasmid-associated determinants do not establish cross-border dissemination without evidence of genetic relatedness and epidemiological connections.

For *Campylobacter* spp., high fluoroquinolone resistance is consistently observed in Romania and several other European countries. In 2024 harmonized surveillance, ciprofloxacin resistance among broiler-associated *C. jejuni* reached 96.5% in Romania, compared with 89.7% in Hungary, 82.0% in Bulgaria, 93.9% in Poland, and 69.2% across pooled European reporting isolates. Similarly, resistance among *C. coli* reached 95.7% in Romania and 98.5% in Poland, compared with 77.7% in the pooled population [2]. These findings indicate that elevated fluoroquinolone resistance is not unique to Romanian poultry production, although its frequency varies among countries and bacterial species.

Independent studies further demonstrate the influence of animal host and bacterial species on *Campylobacter* spp. resistance. In Spain, López-Chavarrías et al. [62] identified substantial variation in erythromycin resistance across livestock-associated *C. jejuni* and *C. coli* populations. In Poland, Wieczorek et al. [63] reported high ciprofloxacin (71.0%), tetracycline (78.2%), and streptomycin (85.5%) resistance among *C. coli* recovered from pig and bovine carcasses. Earlier Hungarian investigations also documented species-related differences in resistance profiles [64]. These findings complement Romanian studies involving poultry, pigs, and cattle [5,6,36,55]. However, differences in host species and sampling matrices restrict direct comparison, emphasizing the importance of species-specific resistance reporting.

For *E. coli*, harmonized surveillance demonstrates considerable variation in MDR among European food-producing animal populations. In broilers, MDR frequencies reached 72.9% in Romania, 46.8% in Hungary, 81.2% in Bulgaria, and 79.4% in Poland, compared with 41.2% across pooled reporting isolates. Romanian surveillance also identified substantial MDR in pigs (58.6%) and turkeys (83.5%), with corresponding pooled frequencies of 33.5% and 41.3%, respectively [2]. These differences indicate that resistance varies not only between countries but also among livestock sectors. Nevertheless, harmonized indicator surveillance measures a specific commensal bacterial population and should not be directly equated with studies targeting pathogenic or resistance-selected isolates.

This distinction is particularly relevant when considering independent European investigations. De Jong et al. [65] examined commensal E. coli from food-producing animals using standardized MIC testing, although their clinical resistance criteria differed from those applied in harmonized ECOFF-based monitoring. Studies from Hungary and Bulgaria documented substantial resistance among turkey- and broiler-associated isolates, respectively, but differed in sampling populations and study design [66,67]. In Belgium, De Koster et al. [68] characterized ESBL-producing and ciprofloxacin-resistant isolates, providing valuable molecular evidence rather than estimates of background resistance.

Such investigations complement Romanian studies reporting MDR/XDR phenotypes and β-lactam resistance determinants in poultry, cattle, and swine [7,8,28].

For *Listeria monocytogenes*, European comparisons are particularly challenging because equivalent harmonized AMR surveillance data are unavailable in the selected EFSA/ECDC annexes. French genomic surveillance identified acquired resistance determinants in 2.23% of investigated isolates [69], whereas independent studies reported author-defined MDR frequencies of 87.4% in Italy and 2.9% in Spain [70,71]. These contrasting estimates should not be interpreted as differences in national resistance prevalence because they reflect distinct study populations, resistance measures, antimicrobial panels, and interpretive criteria. In particular, the Italian MDR classification included interpretations based on breakpoints established for other bacterial species [70]. Polish genomic investigations also identified resistance-associated and biocide-tolerance determinants in meat-associated isolates, although their detection does not establish phenotypic MDR or environmental persistence [72].

Overall, the European evidence confirms that several resistance patterns documented in Romanian meat-production systems are also encountered elsewhere, particularly fluoroquinolone resistance in *Campylobacter* spp. and MDR among selected *Salmonella* spp. and indicator *E. coli* populations [2]. However, the apparent magnitude of resistance depends on bacterial species or serovar, animal population, sampling stage, and AST interpretation. Harmonized surveillance provides the strongest basis for descriptive country-level comparisons, whereas independent studies offer complementary information on resistance mechanisms and local epidemiological characteristics. Together, these findings place Romanian AMR evidence within a broader European context without supporting conclusions about national temporal trends or cross-border dissemination.

4. Limitations and Future Directions

The Romanian evidence reviewed here remains fragmented across pathogens, animal species, geographical areas, and stages of the meat production chain. Although individual studies provide valuable information, relatively few datasets allow direct longitudinal comparison, and several animal-production sectors and food-chain stages remain less extensively investigated. Consequently, the available literature provides stronger evidence for the occurrence and characteristics of antimicrobial-resistant bacteria than for their evolution over time at the national level.

Furthermore, restricting the primary evidence synthesis to peer-reviewed publications may have excluded relevant information from governmental surveillance reports, theses, and other grey literature, while non-indexed or non-English-language publications may have been incompletely captured.

A further limitation is the limited integration of epidemiological and molecular information across the farm-to-retail continuum. Most studies characterize isolates from individual stages of production rather than following bacterial populations longitudinally through connected farms, slaughterhouses, processing facilities, and retail products. Consequently, detection of related bacterial species or resistance phenotypes at different stages cannot establish transmission pathways. Similarly, environmental detection alone cannot demonstrate persistence. Future studies should combine longitudinal sampling with strain-level molecular or genomic characterization to distinguish occurrence from persistence and epidemiologically supported dissemination. Where feasible, future investigations should also include epidemiologically linked environmental and human isolates to better characterize potential connections between animal production, food contamination, and human exposure within a One Health framework.

Future Romanian surveillance should prioritize geographically distributed and longitudinal studies, particularly in regions with limited published evidence and underrepresented animal-production sectors, including cattle, small ruminants, and non-intensive swine production. These studies should integrate sampling across farms, slaughterhouses, processing facilities, and retail, using harmonized AST methods, interpretive criteria, and MDR/XDR definitions. Greater use of whole-genome sequencing could complement phenotypic surveillance by resolving bacterial lineages, resistance determinants, plasmids and other mobile genetic elements, and relationships among isolates recovered from different stages of production.

Finally, integrating microbiological and genomic surveillance with antimicrobial-use data, farm-management characteristics, biosecurity practices, and other epidemiological information would provide a stronger basis for identifying factors associated with AMR selection and dissemination. Such integrated One Health surveillance would improve the ability to distinguish local observations from broader national patterns and support more targeted antimicrobial-stewardship and food-safety interventions.

5. Conclusions

This review demonstrates that antimicrobial-resistant foodborne bacteria are present across multiple components of the Romanian meat production chain, with important differences among pathogens, animal species, and production stages. The clearest recurring resistance patterns include quinolone and fluoroquinolone resistance in *Campylobacter* spp., multiple and multidrug resistance in *Salmonella* spp., and diverse MDR/XDR phenotypes and resistance determinants in *E. coli*. Antimicrobial-resistant *Listeria monocytogenes* has also been documented, including MDR isolates recovered from a meat-processing environment.

The available evidence does not support a uniform national increase in AMR during 2010–2025. The strongest evidence of temporal change comes from longitudinal *Salmonella* data in poultry, whereas temporal patterns for *Campylobacter* spp., *E. coli*, and *L. monocytogenes* remain less clearly defined. Accordingly, differences between independent studies conducted at different time points should not be interpreted as national temporal trends.

Overall, the Romanian evidence indicates that AMR is established across several food-producing animal populations and stages of meat production, but its temporal dynamics and pathways of dissemination remain incompletely resolved. Strengthening integrated surveillance across the meat production continuum will be important for improving the evidence base available for AMR control within a One Health framework.

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Abbreviations

The following abbreviations are used in this manuscript:

Abbreviation	Definition
AMR	Antimicrobial resistance
AmpC	AmpC β-lactamase
AST	Antimicrobial susceptibility testing
ASF	African swine fever
CLSI	Clinical and Laboratory Standards Institute
ECDC	European Centre for Disease Prevention and Control
ECOFF	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
ESBL	Extended-spectrum β-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
EU	European Union
MDR	Multidrug resistance
MIC	Minimum inhibitory concentration
RTE	Ready to eat
STEC	Shiga toxin-producing *Escherichia coli*
VTEC	Verotoxigenic *Escherichia coli*
XDR	Extensively drug-resistant

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