



OPEN ACCESS

EDITED BY

Windell L. Rivera,
University of the Philippines Diliman,
Philippines

REVIEWED BY

Chelea Matchawe,
Institute of Medical Research and Studies of
Medicinal Plants (IMPM), Cameroon
Elizabeth M. Parker,
The Ohio State University, United States

*CORRESPONDENCE

Jenny J. Chaparro-Gutiérrez
✉ jenny.chaparro@udea.edu.co

RECEIVED 19 April 2025

ACCEPTED 08 August 2025

PUBLISHED 03 September 2025

CITATION

Barrientos-Villegas S, García-Álvarez MI,
Vidal JL, Gómez-Osorio LM,
López-Osorio S and
Chaparro-Gutiérrez JJ (2025) Systematic
review: genotypic and phenotypic resistance
of fluoroquinolone-resistant *Salmonella* in
livestock in South America (2020–2024).
Front. Vet. Sci. 12:1614486.
doi: 10.3389/fvets.2025.1614486

COPYRIGHT

© 2025 Barrientos-Villegas, García-Álvarez,
Vidal, Gómez-Osorio, López-Osorio and
Chaparro-Gutiérrez. This is an open-access
article distributed under the terms of the
[Creative Commons Attribution License](#)
(CC BY). The use, distribution or reproduction
in other forums is permitted, provided the
original author(s) and the copyright owner(s)
are credited and that the original publication
in this journal is cited, in accordance with
accepted academic practice. No use,
distribution or reproduction is permitted
which does not comply with these terms.

Systematic review: genotypic and phenotypic resistance of fluoroquinolone-resistant *Salmonella* in livestock in South America (2020–2024)

Stefany Barrientos-Villegas, María Isabel García-Álvarez,
Juana L. Vidal, Luis M. Gómez-Osorio, Sara López-Osorio and
Jenny J. Chaparro-Gutiérrez*

CIVAB Research Group, Faculty of Agricultural Sciences, University of Antioquia (UdeA), Medellín, Colombia

Objective: To determine the frequency of phenotypic and genotypic resistance to quinolones and fluoroquinolones in *Salmonella* spp. isolated from production animals (pigs, poultry, cattle) and rodents in South America between 2020 and 2024, with the goal of providing key information on resistance in these countries for public health and food safety.

Methods: A systematic review was conducted following the PRISMA guidelines, using databases such as Scopus, PubMed, SciELO, and Latindex. Studies on *Salmonella* spp. resistant to quinolones and fluoroquinolones in production animals, meat products, and rodents in South America during 2020–2024 were included.

Results: Of the 83 initial results, 27 studies were selected. 70.4% of the studies were conducted in Brazil. 88% of the studies ($n = 24/27$) used phenotypic methods, with the disk diffusion technique being the most common. Ciprofloxacin was the most studied antibiotic, with an overall resistance of 32.5%, followed by nalidixic acid (60.6%) and enrofloxacin (23.7%). The average multidrug resistance (MDR) was 62%. 44% of the studies ($n = 12/27$) employed genotypic methods, with whole genome sequencing (WGS) being the most notable technique. Mutations were reported in *parC* (58%), *gyrA* (50%), *gyrB* (8%), and the presence of *qnr* genes (75%) and *aac(6′)-Ib-cr* (8%). No studies on rodents were found.

Conclusion: Resistance to quinolones and fluoroquinolones in *Salmonella* spp. in South America endangers public health and food safety. To address antimicrobial resistance, monitoring and control measures must be implemented, regional research should be promoted, and stronger restrictions should be enforced.

KEYWORDS

quinolones, fluoroquinolones, antimicrobial resistance, *Salmonella*, South America

1 Introduction

Salmonella spp. belongs to the Enterobacteriaceae family, with over 2,600 serotypes reported, affecting a wide range of animals, including humans (1). The *Salmonella* genus consists of two species: *enterica* and *bongori* (2). *S. enterica* is classified into six subspecies: *enterica* (subsp. I), *salamae* (subsp. II), *arizonae* (subsp. IIIa), *diarizonae* (subsp. IIIb), *houtenae*

(subsp. IV), and *indica* (subsp. VI). Subspecies I is associated with more than 99% of the diseases caused by *Salmonella* in warm-blooded animals, including gastroenteritis and enteric fever (3).

Nontyphoidal salmonellosis has been the most commonly reported zoonotic disease in humans (4). It is acquired through three main routes: food, animal handling on farms or carcass handling in slaughterhouses, contact with pets (dogs and cats), and exotic animals (birds, ferrets, lagomorphs, mustelids, reptiles, and rodents) (5). *Salmonella* transmission has been primarily linked to contaminated water and food sources, including eggs, meats, and vegetables (6). In this context, the prevention and control of pathogens are ongoing challenges, which is why antimicrobials are frequently used in veterinary medicine to treat and prevent diseases (7). However, there is growing concern that the use of these in animal production may compromise human health through the zoonotic transfer of resistant bacteria via contaminated animal-derived food, direct contact, and their spread in the environment (8).

Nontyphoidal salmonellosis mainly causes self-limiting gastroenteritis in both humans and animals (9). However, when this infection becomes invasive, it requires antibiotic treatment. If the pathogens show resistance, it limits the therapeutic options available for the patient (10). Fluoroquinolones (FQ) have been widely used in clinical practice for the treatment of salmonellosis in both humans and animals (11) and Ciprofloxacin is the first-line antibiotic used to treat both typhoidal and nontyphoidal salmonellosis in humans (9, 12). However, the emergence of resistance or multidrug resistance (MDR) to these antibiotics has become a critical issue in the clinical treatment of the disease (13). This is why the World Health Organization (WHO) classifies fluoroquinolone-resistant *Salmonella* as a high-priority pathogen to support research and the development of new antibiotics (12, 14).

Resistance to fluoroquinolones in *Salmonella* can occur due to mutations in the quinolone resistance-determining regions (QRDR) of the chromosomal *gyr* and *par* genes, resulting in a reduced binding affinity of the topoisomerase enzymes to quinolones (15). Secondly, plasmid-mediated quinolone resistance (PMQR) involves the acquisition of (i) *qnr* genes (*qnrA*, *qnrB*, *qnrS*, *qnrC*, *qnrD*), which encode topoisomerase-binding proteins that provide physical protection against quinolones, (ii) the *aac(6′)-Ib-cr* gene, which encodes a modifying enzyme that reduces the activity of fluoroquinolones, and (iii) *oqxAB* and *qepA*, which encode quinolone efflux pumps. Finally, the negative and positive regulation of porins encoded by chromosomal genes or the efflux pumps of multiple drugs (AcrAB-TolC), respectively, reduce intracellular concentrations of fluoroquinolones (14).

In South America, the dynamics of antimicrobial resistance (AMR) in *Salmonella* within the animal sector—particularly in production animals and across the food supply chain—are poorly characterized. Countries such as Venezuela, Guyana, French Guiana, and Suriname reported very limited research between 2020 and 2024, highlighting significant gaps in AMR surveillance and data. Understanding the current status of fluoroquinolone-resistant *Salmonella* is especially critical, given the scarcity and fragmentation of existing evidence. This study aims to consolidate available data on phenotypic and genotypic resistance to quinolones and fluoroquinolones in *Salmonella* isolated from pigs, poultry, cattle, and rodents. The inclusion of rodents is supported by their established role as reservoirs and amplifiers of zoonotic pathogens in agricultural

environments. By providing a unified analysis, this review contributes to a clearer understanding of the regional AMR landscape and supports the development of targeted public health strategies, including improved biosecurity and responsible antibiotic use on farms.

2 Materials and methods

2.1 Study search

The study was conducted following the guidelines established in the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA)(16). The study populations included *Salmonella* isolates from production animals such as cattle, poultry, pigs, meat products from these animals, and rodents. The primary outcome of interest was the reported frequencies of phenotypic and genotypic resistance to FQ: non-susceptibility to nalidixic acid (Nal ns), non-susceptibility to ciprofloxacin (Cip ns), non-susceptibility to enrofloxacin (Enr ns), frequency of mutations in QRDR genes, and the presence or absence of PMQR genes. The secondary outcomes included MDR, reported serotypes and sequence types (ST), amino acid substitutions in mutated genes, and the phenotypic and genotypic techniques used. MDR was defined as resistance to three or more drugs.

A literature search was conducted in English, Spanish, Portuguese, and French using Boolean logic tools with the operators “AND” and “OR” to search for relevant articles in the PubMed, Scopus, SciELO, and Latindex databases. The search aimed to identify pertinent articles published from January 1, 2020, to August 24, 2024. The search string that allowed for the identification of most studies was as follows: *Salmonella* AND (quinolone OR fluoroquinolone OR ciprofloxacin OR nalidixic acid OR enrofloxacin) AND (livestock OR cattle OR swine OR pig OR poultry OR rodent OR rat OR beef OR chicken OR pork OR meat) AND (Peru OR Brazil OR Colombia OR Ecuador OR Chile OR Venezuela OR Argentina OR Uruguay OR Bolivia OR Guyana OR Paraguay OR French Guiana OR Suriname). The search was conducted on August 24, 2024. Additional articles were also included, manually located in the Scopus, PubMed, SciELO, and Latindex databases. Additional articles were also included through manual searches of reference lists from selected studies and relevant journals.

2.2 Study selection

The study selection was carried out by two independent reviewers (SBV and MIG), and the references were exported to the Rayyan online application software for screening and selection. In the first phase of review (screening), titles and abstracts were evaluated to identify studies related to the primary outcomes of interest. At this stage, exclusion criteria were applied to discard studies whose titles and/or abstracts were not relevant. Discrepancies between reviewers were resolved through discussion or, if necessary, by consulting a third reviewer.

In the second phase (eligibility), a full-text review of the selected articles was conducted, with detailed assessment based on the following eligibility criteria: (i) publication in English, Spanish,

Portuguese, or French; (ii) inclusion of phenotypic and/or genotypic determinants of fluoroquinolone resistance; (iii) isolation of *Salmonella* from production animals, meat products, or rodents; (iv) exclusion of incomplete or unclear studies; (v) exclusion of studies conducted outside South America; and (vi) inclusion of studies published before August 24, 2024.

Duplicate references were identified and removed using EndNote software prior to the screening process. Additionally, data extraction was performed by one reviewer and independently validated by a second reviewer to minimize errors or inconsistencies. To assess the risk of bias and methodological quality of the included studies, we used the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for prevalence studies. Two independent reviewers (SBV and MIG) performed the quality assessment, and disagreements were resolved by consensus or by involving a third reviewer. Studies were not excluded based on quality, but the appraisal results were considered when interpreting the findings.

2.3 Data extraction

The following data were considered and extracted: (i) study identifier: Title, authors, year of publication, country, species (production animals, meat animals, or rodents); (ii) Methods: sample type, sample size, identification method, antimicrobial susceptibility testing (fluoroquinolones or quinolones), breakpoint/interpretive standard level, and gene detection (phenotype-based/genotype-based); (iii) Results: number of isolates, number of isolates tested for susceptibility, number of MDR strains, number of strains resistant to nalidixic acid (Nal ns), number of strains resistant to ciprofloxacin (Cip ns), number of strains resistant to enrofloxacin (Enr ns), number of strains examined for mutation detection (*gyrA*, *gyrB*, *parC* y *parE*), number of mutants, mutation positions, substituted amino acids, number of strains examined for plasmid-mediated quinolone resistance genes (PMQR) (*qnrA*, *qnrB*, *qnrC*, *qnrD*, *qnrS*, *aac(6')-Ib-cr*, *qepA*, *oqxA/B*) and number of strains with PMQR genes.

2.4 Data analysis

Data were analyzed using descriptive statistics in Microsoft Excel (Microsoft 365®). Additionally, GIS software (QGIS 3.16.15) was used to generate maps illustrating the distribution of resistance patterns across South America.

Inferential statistical analyses were not applied in this study due to the high heterogeneity among the included articles in terms of study design, sample sizes, animal species, sampling matrices, and laboratory methodologies. As a result, quantitative synthesis through meta-analysis was not feasible. A descriptive approach was used instead, in line with the exploratory nature of this review.

3 Results

Our search strategy yielded a total of 83 results, with 57 found in PubMed, 18 in Scopus, and 8 in SciELO. After excluding 46 articles based on their title and abstract, 37 were selected for full-text reading, and of these, only 10 were excluded, resulting in a total of 27 articles

included in this study. The main reason for excluding articles during the selection process was that they did not analyze the *Salmonella* agent or did not focus on relevant animal matrices of interest (Figure 1).

According to our results, 70.4% ($n = 19/27$) of the studies were conducted in Brazil, followed by Argentina and Colombia with 7.4% ($n = 2/27$) each. Next, Paraguay, Uruguay, Chile, and Ecuador each represented 3.7% ($n = 1/27$).

Regarding the species studied, 40.74% of the articles focused on swine and its products ($n = 11/27$), a percentage equal to that of poultry and its products ($n = 11/27$). Cattle and their products were investigated in 3.7% ($n = 1/27$), while 14% ($n = 4/27$) involved a combination of matrices from different species (swine, cattle, and poultry). No published research was found regarding rodents.

3.1 Phenotypic resistance to quinolone and fluoroquinolone in *Salmonella*

Of the 27 studies, 88% ($n = 24/27$) employed phenotypic methods to detect fluoroquinolone resistance in *Salmonella* isolates the most commonly method used to assess AMR was disk diffusion (17), in 75% ($n = 18/24$) of the studies, followed by broth microdilution (18) in 25% ($n = 6/24$) of the studies, according to CLSI guidelines. The most studied fluoroquinolone was ciprofloxacin, present in 91.6% ($n = 22/24$) of the studies, with an overall resistance of 32.53%. It was followed by nalidixic acid, studied in 15 of the 24 studies, which showed an overall resistance of 60.6%. In contrast, enrofloxacin was the least evaluated, being analyzed in 10 of the 24 studies, with an overall resistance of 23.74%. MDR was assessed in 17 of the 24 studies ($n = 17/24$), with an overall percentage of 62%.

3.1.1 Poultry isolates

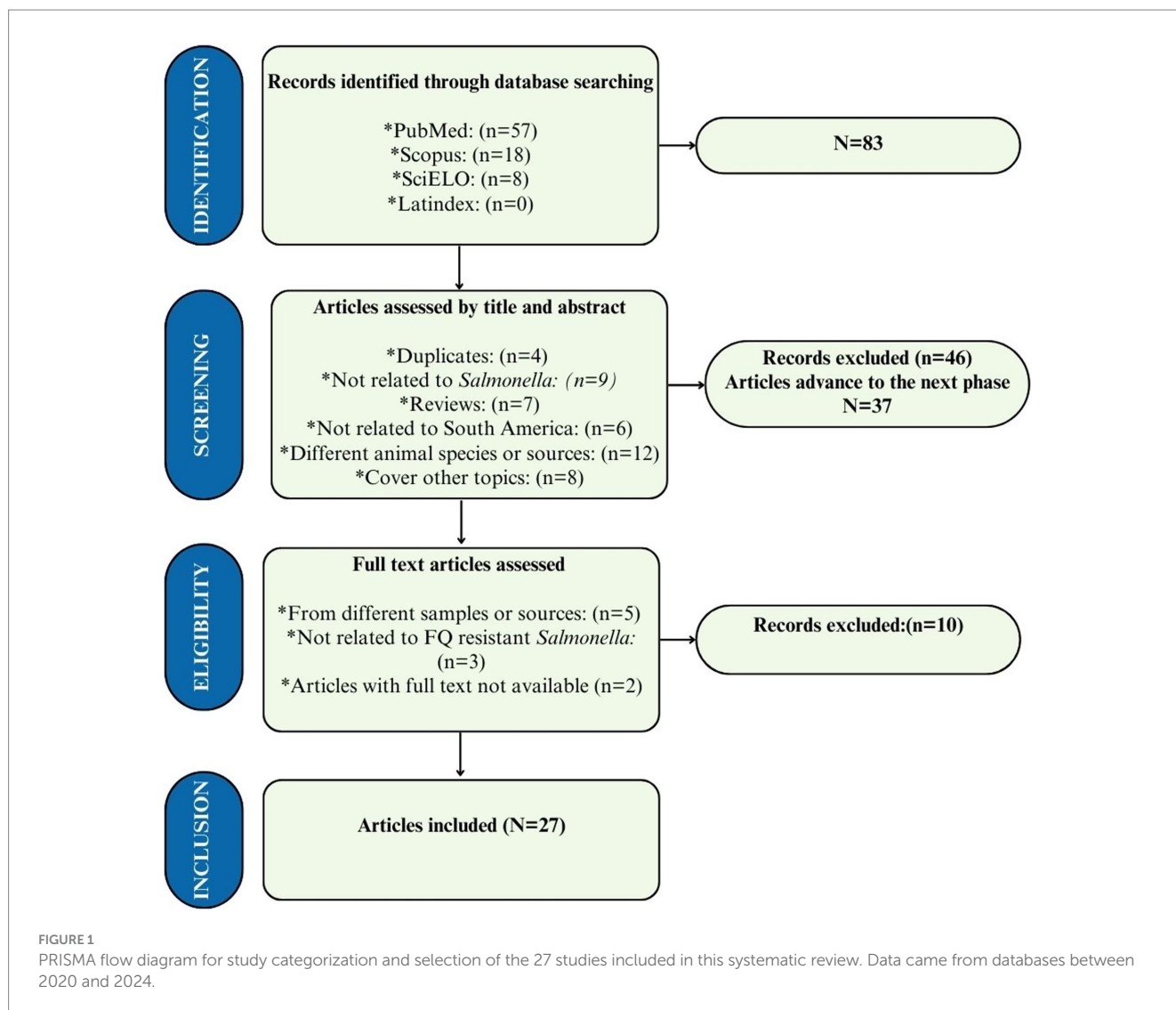
The most used sample type in poultry studies was a combination of matrices from various sources, accounting for 37.5% ($n = 3/8$), followed by feces and chicken meat. The most frequently isolated serotype was *Salmonella* Heidelberg, reported in 62.5% of the studies ($n = 5/8$), with average resistances in chicken meat of 96.3, 38.9% to nalidixic acid and ciprofloxacin, respectively. In feces, resistances of 54% to ciprofloxacin were found (Table 1).

3.1.2 Pigs isolates

The most commonly used sample type in swine studies was a combination of matrices from various sources, representing 45% ($n = 5/11$) of the cases. The most frequently reported serotype was *S. typhimurium*, found in 81.8% ($n = 9/11$) of the isolates, followed by *S. Derby*, which appeared in 63.6% ($n = 7/11$). On average, in the mesenteric lymph nodes, the most studied individual matrix, resistances of 44, 40, and 37% were observed for nalidixic acid, ciprofloxacin, and enrofloxacin, respectively (Table 2).

3.1.3 Cattle isolates

According to a study conducted in Uruguay isolates with non-susceptibility to fluoroquinolones were reported, with 77.3% ($n = 58/75$) of the isolates being non-susceptible to ciprofloxacin, which is a second-generation fluoroquinolone. Additionally, in this group, 6.6% ($n = 5/75$) were non-susceptible to enrofloxacin. 56% ($n = 42/75$) were MDR (Table 3).



3.1.4 Combined matrices

Of the 24 studies that used phenotypic methods, 4 of them used matrices involving a mixture of different species, primarily from their meat products. The average resistance to nalidixic acid was 75%, and to ciprofloxacin was 35% (Table 4).

3.2 Genotypic resistance to quinolone and fluoroquinolone in *Salmonella*

Of the 27 studies reviewed, 44% ($n = 12/27$) employed genotypic techniques to detect resistance genes in *Salmonella*. The most commonly used methodology was WGS, with the Illumina MiSeq platform being the most widely used, employed in 71% ($n = 5/7$) of the studies that applied Whole Genome Sequencing (WGS), followed by Illumina HiSeq. In comparison, the PCR technique was used in a smaller number of studies, as shown below. In all of the studies that used these techniques, mutations were found in *gyrA* 50% ($n = 6/12$), *parC* 58% ($n = 7/12$), *gyrB* 8% ($n = 1/12$), *qnr* genes 75% ($n = 9/12$), and *aac(6')-Ib-cr* 8% ($n = 1/12$).

3.2.1 Polymerase chain reaction (PCR) techniques

PCR involves DNA extraction, amplification with specific primers, and thermal cycling, followed by detection via gel electrophoresis or real-time PCR (19). This rapid and sensitive technique enables precise detection of microorganisms and resistance genes, even in low-DNA samples (20). Of the 27 studies, only 19% ($n = 5/27$) used PCR techniques or molecular identification of resistance genes, and all of them correspond to different South American countries. Among the most commonly investigated genes are PMQR genes, highlighting *qnrB*, which was present in 100% of the studies that employed molecular methods, where the most commonly used primer sequences were: *qnrB*-F GATCGTGAAAGCCAGAAAGG and *qnrB*-R ACGATGCCTGGTAGTTGTCC (21).

In two of these five studies, QRDRs (quinolone resistance-determining regions) genes were identified, which are chromosomal and result from mutations in the *gyr* and *par* genes. Of these mutations, the most frequently investigated was in the *gyrA* gene, which was analyzed in two of the five studies that used these techniques and primarily presented mutations at position 83. The *parC* gene was only investigated in one study, where mutations T57S were found (Table 5).

TABLE 1 Phenotypic resistance to FQ into *Salmonella* in poultry isolates in South America (2020–2024).

Author	Country	<i>Salmonella</i> isolation	Sample type	Serotypes	Nal ns		Cip ns		Enr ns		MDR
Souza et al. (26)	Brazil	<i>n</i> = 62	Cloacal swabs, drag swabs, feeders, drinkers and Poultry meat	<i>S. Heidelberg</i>	Meat 20/20 Poultry 9/10 Farm 21/32	(80.65%)	Meat <i>n</i> = 0/20 Poultry <i>n</i> = 0/10 Farm <i>n</i> = 1/32	(1.61%)	Meat <i>n</i> = 4/20 Poultry <i>n</i> = 2/10 Farm <i>n</i> = 12/32	(29.03%)	41/62
Lucca et al. (30)		<i>n</i> = 22	Carcasses broilers	<i>S. Pullorum</i> , <i>S. Heidelberg</i> <i>S. Corvalis</i>	-	-	18/22	(81.82%)	2/22	(9.09%)	14/22
Monte et al. (32)		<i>n</i> = 108	Poultry production: Surfaces Transport Processing Final product	<i>S. Enteritidis</i>	-	-	1/108	(0.93%)	20/108	(18.52%)	-
Perin et al. (28)		98/300	Chicken meat	<i>S. Typhimurium</i> , <i>S. Heidelberg</i> , <i>S. Ndolo</i> , <i>S. Minnesota</i> , O:4,5, <i>S. Thompson</i> , <i>S. Schwarzengrund</i> , <i>S. Abani</i> , o:3,10:e,h	93/98	(94.90%)	74/78	(75.51%)	-	-	84/98
Moreira et al. (25)		<i>n</i> = 25	Poultry feces	<i>S. Minnesota</i>	7/25	(28%)	4/25	(16%)	-	-	16/25
Grossi et al. (31)		<i>n</i> = 96	Chicken carcasses, bird cages/transport boxes, and end cuts	<i>S. Heidelberg</i> , <i>S. Schwarzengrund</i> , <i>S. Anatum</i> , O:4,5	-	-	2/96	(2.08%)	-	-	6/96
Herrera-Sánchez et al. (24)	Colombia	<i>n</i> = 39	Broiler feces	<i>S. Heidelberg</i> , <i>S. paratyphi</i> B.	-	-	36/39	(92.31%)	19/39	(48.72%)	-
Lapierre et al. (27)	Chile	87/360	Chicken meat	<i>S. Infantis</i>	85/87	(97,70%)	2/87	(2.30%)	3/87	(3.45%)	82/87

Phenotypic resistance in *Salmonella*, broken down by country and matrix. The ex: *n* = 65 in the “*Salmonella* Isolation” column refers to previously isolated strains, while the fractions indicate the proportion of the agent isolated in the analyzed samples. The symbol “-” denotes concepts not studied in that specific analysis, allowing for easy identification of areas lacking information.

TABLE 2 Phenotypic resistance to FQ into *Salmonella* in pig isolates in South America (2020–2024).

Author	Country	<i>Salmonella</i> isolation	Sample type	Serotypes	Nal ns		Cip ns		Enr ns		MDR
Azevedo et al. (42)	Brazil	29/100	Porcine mesenteric lymph nodes	S. Derby. S. Cerro, S. Give	19/29	65.5%	23/29	79.3%	16/23	69.6%	23/29
de Quadros et al. (63)		19/90	Pig carcass swabs	S. Typhimurium, S. Derby, S. Infantis	-	-	-	-	<i>n</i> = 0/90	0%	9/25
Simoni et al. (46)		<i>n</i> = 140	Environment, pig carcass, lymph nodes, intestinal content, and pork	S. Derby isolates collected over a 10-year	13/140	9.29%	0/140	0%	-	-	-
Viana et al. (54)		<i>n</i> = 41	Swines samples from lairage, barn floors, mesenteric lymph nodes, tonsils, swine carcasses and knives	S. Typhimurium S. I 4,[5],12:i:- S. Bredeney S. Brandeburgo S. Panama S. Londres S. Mbandaka S. Derby S. Bovismorbificans	-	-	21/41	51.22%	-	-	30/41
Possebon et al. (43)		91/250	Swine mesenteric lymph nodes	S. Typhimurium, S. I.4,5,12:i:- S. Infantis y S. Havana	37/91	40.66%	-	-	-	-	64/91
Pissetti et al. (45)		<i>n</i> = 413	Intestinal swine content, lymph nodes, carcasses and products of swine origin.	S. Typhimurium S. Derby isolates from 2000 to 2015	-	-	77/413	18,64%	-	-	-
Cabral et al. (52)		<i>n</i> = 29	Intestinal faeces, mesenteric and submandibular lymph nodes, jowl, ham and from the water for cleaning the carcasses in swine slaughterhouses	S. Typhimurium	19/29	65.52%	19/29	0.41%	14/29	48.28%	17/29
Kich et al. (64)	Colombia	65/378	Pig carcasses	S. Typhimurium, <i>S. infantis</i>	28/61	45.90%	1/61	1.6%	-	-	32/61
Vidal et al. (67)		149/653	Pigs fecal samples	S. Typhimurium, S.I.4,12:i:-, S. Enteritidis, S. Virchow, S. Bovismorbificans, S. Edinburg, S. Heidelberg, S. Infantis, S. Manhattan,	-	-	76/139	54.68%	-	-	61/139
Parada et al. (38)		<i>n</i> = 55	Organs, feces and mesenteric nodes from pigs	S. Anatum, Brandenburg, Bredeney, Choleraesuis, Derby, Glostrup, Heidelberg, Infantis, Livingstone, Montevideo, Oranienburg, Panama, Rissen, Typhimurium.	<i>n</i> = 29/55	52.73%	10/55	18.18%	-	-	31/55
Vico et al. (66)	Argentina	241/580	Swine mesenteric lymph nodes	S. Anatum, Typhimurium, Panama, I 1,3,19: Z10:-, I 4,5,12: I:-, 4,5,12:d:-, Lexington, Westhampton, Derby, Adelaide, Bredeney, Corvallis, Javiana, Minnesota, Mbandaka	13/50	26.00%	0/50	0.00%	2/50	4%	43/50

Phenotypic resistance in *Salmonella*, broken down by country and matrix. The ex: *n* = 65 in the “*Salmonella* Isolation” column refers to previously isolated strains, while the fractions indicate the proportion of the agent isolated in the analyzed samples. The symbol “-” denotes concepts not studied in that specific analysis, allowing for easy identification of areas lacking information.

TABLE 3 Phenotypic resistance to FQ *Salmonella* in cattle isolates in South America (2020–2024).

Author	Country	<i>Salmonella</i> isolation	Sample type	Serotypes	Nal ns		Cip ns		Enr ns		MDR
Casaux et al. (41)	Uruguay	<i>n</i> = 75	Calves, cows, heifer, organs, samples from environment, food sample, udder swab, drinking water, bovine fetus autopsy.	<i>S.</i> Typhimurium, <i>S.</i> Newport, <i>S.</i> Anatum, <i>S.</i> Dublin, <i>S.</i> Agona, <i>S.</i> Montevideo y IIIb 61:i:z53	-	-	58/75	77.33%	5/75	6.67%	42/75

Phenotypic resistance in *Salmonella*, broken down by country and matrix. The ex: *n* = 65 in the “*Salmonella* Isolation” column refers to previously isolated strains, while the fractions indicate the proportion of the agent isolated in the analyzed samples. The symbol “–” denotes concepts not studied in that specific analysis, allowing for easy identification of areas lacking information.

3.2.2 Whole genome sequencing (WGS)

WGS involves DNA extraction, library preparation, sequencing (Illumina/Nanopore), genome assembly, and bioinformatics analysis to detect genetic variants and resistance genes (22). This high-resolution technique enhances epidemiological surveillance and pathogen control by identifying resistance mechanisms and phylogenetic relationships (23).

Of the 27 studies analyzed, only 25.9% (*n* = 7/27) implemented WGS, mostly in poultry isolates. Mutations in QRDR genes were identified in all the studies, with the *gyrA* gene being involved in 71% of the cases. The most frequent mutation in this gene occurred at position 83, reported in 57% of the studies, with changes in various amino acids. On the other hand, mutations in the *parC* gene were observed in 71% of the studies, with the most common being the one at position 57, where in all cases, a threonine to serine change was detected. Regarding PMQR-mediated resistance genes, the *qnrB19* gene was the most reported, present in 43% of the studies. Additionally, different associated plasmid replicons were identified (Table 6).

These findings reveal a recurring pattern of specific chromosomal mutations (*gyrA* S83 and *parC* T57) and plasmid-mediated resistance (*qnrB19*) in isolates, which may indicate clonal spread or horizontal gene transfer in the food production chain. The frequent detection of these markers underscores the need for routine WGS-based surveillance in high-risk reservoirs to guide more targeted interventions in antimicrobial resistance control.

As previously mentioned, resistance to ciprofloxacin is of great importance, as it is the most studied antibiotic in this study and the first-line treatment for both typhoidal and non-typhoidal *Salmonella* spp. infections in humans. Between 2020 and 2024 in South America, a total of 490 *Salmonella* strains were found to be resistant to the antibiotic through phenotypic antibiogram testing, out of 1,781 tested strains, resulting in an overall resistance rate of 27.5%. Specifically, 307 resistant strains were reported in Brazil, 112 in Colombia, 58 in Uruguay, 10 in Argentina, 2 in Chile, and 1 in Paraguay (Figure 2).

4 Discussion

4.1 Phenotypic resistance and variability between countries and species

Phenotypic resistance to quinolones and fluoroquinolones in *Salmonella* from poultry and swine in South America reveals an

alarming trend of antimicrobial resistance that varies between countries and production systems. This is particularly concerning, as fluoroquinolones are classified as “highest priority” by the World Health Organization (WHO) (12), they play a crucial role in the treatment of serious bacterial infections in humans and animals. Their prioritization is due to the fact that, in many cases, they are the only or few therapies available to treat severe non-human-origin infections (24).

Phenotypic resistance in *Salmonella* from poultry fecal samples is widely documented. In Brazil, resistance to nalidixic acid was reported at 90% in cloacal swabs and 28% in other samples, while ciprofloxacin resistance ranged from 0 to 16% (25, 26). In Colombia, resistance to ciprofloxacin (92.3%), levofloxacin (57%), and enrofloxacin (48.7%) was observed in poultry feces (24). Serotypes such as *S. Paratyphi* B, *S. Minnesota*, and *S. Heidelberg* have been identified, with the latter two showing multidrug resistance (MDR) rates of 64–66% (24–26).

In Chile, *Salmonella* isolates from chicken meat show 97% resistance to nalidixic acid, with 94% classified as MDR (27). Similar trends are observed in Brazil, where resistance to nalidixic acid ranges from 94.9 to 100%, likely due to the selective pressure from extensive antibiotic use in poultry production (28, 29). In Brazil, chicken carcass isolates also exhibit high FQ resistance, with ciprofloxacin resistance reaching 81.82% and MDR rates at 63.64% (30). However, other studies report significantly lower ciprofloxacin resistance (0.93–2.08%), suggesting possible methodological differences or evolving resistance patterns over time (31, 32).

In Colombia, older studies reported low resistance in poultry farms to levofloxacin, 2.3% in Cundinamarca, 0% in Santander (33), but more recent data show a sharp increase in resistance, likely due to continued antibiotic use (24). Genetic studies highlight *Salmonella* Heidelberg (ST15) as a major concern due to its high morbidity, resistance, and outbreak potential, posing a significant public health risk (34–37).

4.2 Genotypic resistance and key mutations

Genotypic studies identified key mutations in *gyrA* and *parC*, along with the *qnrB19* gene, as major contributors to fluoroquinolone resistance (34, 35). Many ciprofloxacin-resistant strains carried both *gyrA* mutations and the *qnrB* gene, enhancing resistance (38). A study on *S. Heidelberg* from Brazilian poultry meat imported to the Netherlands found *parC* mutations in all 122

TABLE 4 Phenotypic resistance in *Salmonella* in combined matrices in South America (2020–2024).

Author	Country	<i>Salmonella</i> isolation	Sample type	Serotypes	Nal ns		Cip ns		Enr ns		MDR
Ortiz et al. (65)	Paraguay	<i>n</i> = 98	Food animals	<i>S. Heidelberg</i> , <i>S. Tennessee</i> , <i>S. Anatum</i>	80/98	81.63%	1/98	1%	-	-	-
Gomes et al. (48)	Brazil	57/780	Chicken and Pork	<i>S. Heidelberg</i> , <i>S. Typhimurium</i> and Give, <i>S. Schwarzengrund</i>	Chicken 48/58 Pork <i>n</i> = 23/60	60.17%	Chicken 43/58 Pork <i>n</i> = 18/60	51.69%	-	-	Chicken 46/58 Pork <i>n</i> = 30/60
Vilela et al. (68)		<i>n</i> = 5	Swine gallbladder, Chicken spleen, gallbladder and ileum	<i>S. choleraesuis</i> isolates	3/5	60%	4/5	80%	-	-	-
Vilela et al. (29)		<i>n</i> = 11	Chicken meat, bovine meat, animal feed, and a drag swab.	<i>S. Heidelberg</i>	11/11	100%	1/11	9%	-	-	-

Phenotypic resistance in *Salmonella* spp. broken down by country and matrix. The ex: *n* = 65 in the “*Salmonella* Isolation” column refers to previously isolated strains, while the fractions indicate the proportion of the agent isolated in the analyzed samples. The symbol “-” denotes concepts not studied in that specific analysis, allowing for easy identification of areas lacking information.

TABLE 5 Genes conferring resistance to quinolones and fluoroquinolones identified in *Salmonella* spp. using PCR techniques in South America between 2020 and 2024.

Author	Country	Type of samples	Number of samples	Target genes	Number of mutations	Point mutations (QRDR)
Parada et al. (38)	Argentina	Organs, feces and mesenteric nodes from pigs	30	*Amino acid substitutions of QRDRs: <i>gyrA</i> *PMQR: <i>qnrB</i>	30/30 had a <i>gyrA</i> mutation 16/30 had a <i>qnrB</i> gene	<i>gyrA</i> : (S83Y, S83F, D87G, (S83Y + D72E))
Herrera-Sánchez et al. (24)	Colombia	Broiler feces	39	*PMQR: <i>qnrA,B,C, D,S</i>	24/39 had a <i>qnrB</i> gene 1/39 <i>aac(6′)-Ib-cr</i> gen	-
Lapierre et al. (27)	Chile	Chicken meat	87	*PMQR: <i>qnrB</i>	2/3 had a <i>qnrB</i> gene	-
Grossi et al. (31)	Brazil	Chicken carcasses, bird cages/transport boxes, and end cuts	96	*Amino acid substitutions of QRDRs: <i>gyrA</i> and <i>parC</i> *PMQR: <i>qnrB,S</i>	0/96 had a <i>gyrA</i> mutation 96/96 had a <i>parC</i> mutation 94/96 had a <i>qnrB</i> gene 0/96 had a <i>qnrS</i> gene	<i>parC</i> : (T57S)
Ortiz et al. (65)	Paraguay	Food animals	41	*PMQR: <i>qnrA,B,S</i>	13/41 had a <i>qnrB</i> gene 1/41 had <i>qnrS</i> + <i>qnrS</i> genes	-

(–) In this study, no QRDR mutations are reported.

isolates, with 96.7% also carrying *gyrA* mutations (39). Similarly, *qnrB19* was detected in *S. Minnesota* from Brazilian poultry meat (35, 37). The *aac(6′)-Ib-cr* gene, linked to fluoroquinolone resistance, was found in one *S. Heidelberg* isolate from Colombian broiler farms, which showed resistance to ciprofloxacin and levofloxacin (24, 40).

Antimicrobial resistance in *Salmonella* from swine varies across countries, influenced by production practices, antibiotic use, and regulations. In Brazil, de Quadros et al. (63) found that only 16% of *Salmonella* strains were fully susceptible, yet enrofloxacin inhibited 100% of them. This is notable, as enrofloxacin was widely used before 2017. However, stricter fluoroquinolone regulations in pork

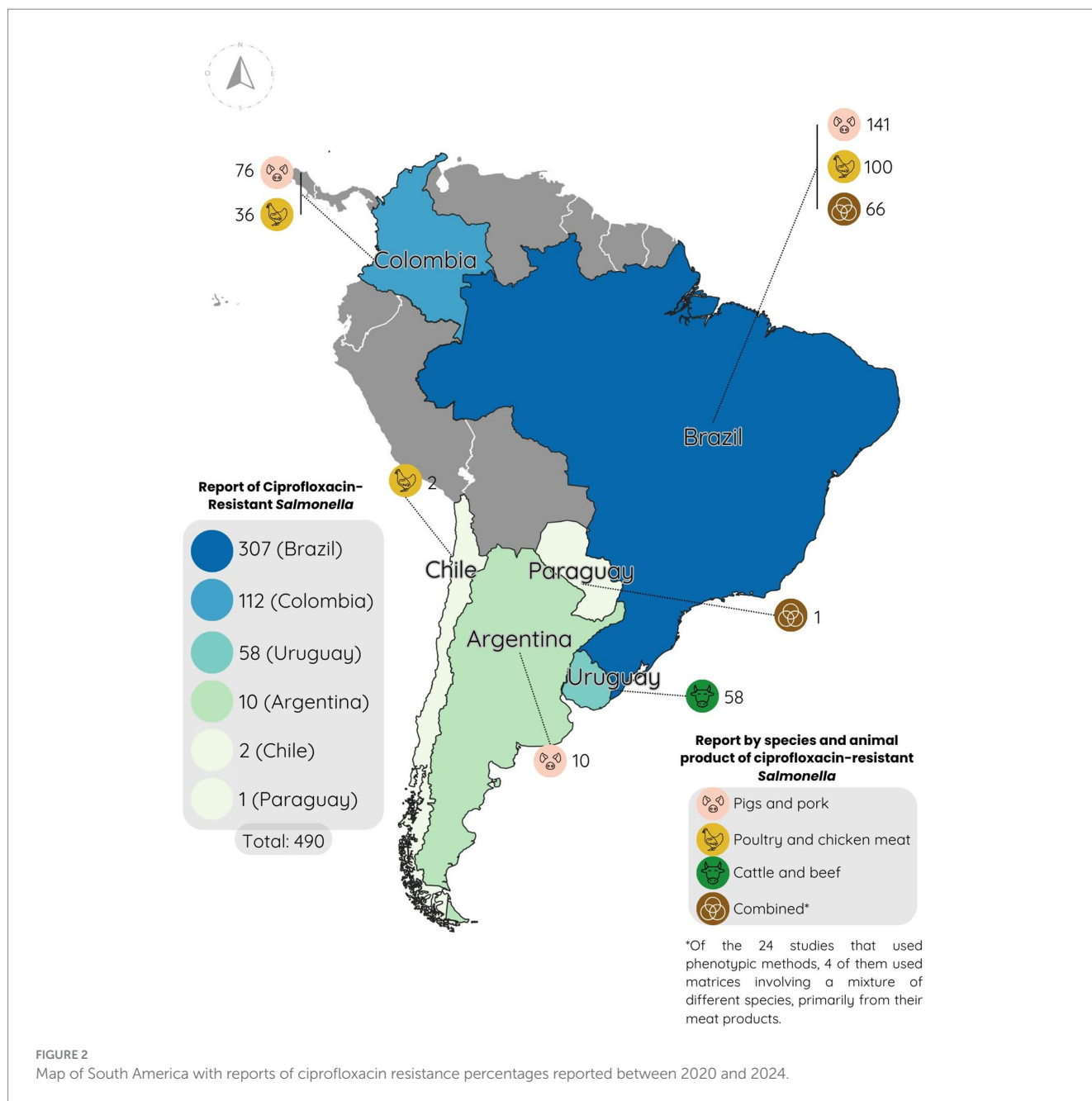
production appear to have reduced resistance, indicating a positive impact of recent policies (41).

However, Kich et al. (64) reported high nalidixic acid resistance (45.9%) in carcasses, while studies on mesenteric lymph nodes found resistance rates of 40.6–65.5% and MDR rates of 70.3–79% (42, 43). In Argentina, Vico et al. (66) observed 52% resistance to fluoroquinolones in mesenteric lymph nodes and 86% MDR. Resistance in *S. Typhimurium* and *S. Derby*, a key serotype in swine and pork products worldwide, is particularly concerning (44–46). The role of *S. Derby*, which is one of the most frequently reported serotypes in swine and pork products, both in Brazil and other regions such as the European Union and China (46, 47). In Colombia,

TABLE 6 Genes conferring resistance to quinolones and fluoroquinolones identified in *Salmonella* spp. using WGS Techniques in South American countries between 2020 and 2024.

Author	Country	Type of sample	Sequence Type (Number of samples)	Gene: Number of mutations	Chromosomal point mutations (QRDR)	PMQR Genes	Plasmids
Saidenberg et al. (37)	Brazil	Asymptomatic broiler chicken feces	<i>S. Heidelberg</i> ST15 (<i>n</i> = 10) <i>S. Minnesota</i> ST548 (<i>n</i> = 4)	<i>gyrA</i> : <i>n</i> = 10/10 <i>parC</i> : <i>n</i> = 14/14	<i>gyrA</i> (S83F) <i>parC</i> (T57S)	<i>qnrB19</i> (ColRNAI): <i>n</i> = 3/14	ColRNAI, IncX1, IncC, IncI1 y ColpVC, Col156, IncX4, IncFII
Viana et al. (54)		Swines samples from lairage, barn floors, mesenteric lymph nodes, tonsils, swine carcasses and knives	<i>S. Typhimurium</i> ST19 (<i>n</i> = 16) <i>S. I</i> 4,[5],12:i:- ST19 (<i>n</i> = 5) <i>S. Bredeney</i> ST241 (<i>n</i> = 9) <i>S. Brandeburgo</i> ST65 (<i>n</i> = 4) <i>S. Panama</i> ST48 (<i>n</i> = 2) <i>S. Londres</i> ST155 (<i>n</i> = 2) <i>S. Mbandaka</i> ST413 (<i>n</i> = 1) <i>S. Derby</i> ST40 (<i>n</i> = 1) <i>S. Bovismorbificans</i> ST150 (<i>n</i> = 1)	<i>gyrA</i> : <i>n</i> = 24/41 <i>parC</i> : <i>n</i> = 16/41 <i>gyrB</i> : <i>n</i> = 1/41	<i>gyrA</i> (D87N) (S83F) (S83Y) <i>parC</i> (T57S) <i>gyrB</i> (E466D)	<i>qnrE1</i> : <i>n</i> = 6/41 <i>qnrS1</i> : <i>n</i> = 9/41 <i>qnrB19</i> : <i>n</i> = 2/41 <i>oqxA</i> : <i>n</i> = 2/41 <i>oqxB</i> : <i>n</i> = 2/41	ColRNAI, INCr, Incl 1, incA/C2, IncX4, TrfA, IncHI2, inCHI2A, IncFIA(HI1), IncFII(S), IncFIB(S), IncFIC(FII), incY, Col(MGD2), IncFII(Pcry), IncHI1A, IncHI1B(R27), p0111
Vilela et al. (68)		Swine gallbladder, Chicken spleen, gallbladder and ileum	<i>S. Choleraesuis</i> ST145 (<i>n</i> = 5)	<i>gyrA</i> : <i>n</i> = 4/5 <i>parC</i> : <i>n</i> = 5/5	<i>gyrA</i> (S83Y) <i>parC</i> (T57S)	-	IncX4; IncFIB(S), IncFII(S), IncHI2, IncHI2A, IncFIA(HI1), IncHI1A, IncHI1B(R27), IncFII(S)
Vilela et al. (29)		Chicken meat, bovine meat, animal feed, and a drag swab.	<i>S. Heidelberg</i> ST15 (<i>n</i> = 11)	<i>gyrA</i> and <i>parC</i> : <i>n</i> = 11/11	<i>gyrA</i> (S83F) <i>parC</i> (T57S)	-	ColpVC, IncC, IncX1, and IncI1-I(Alpha)
Benevides et al. (61)		Caecal content laying hens and a laying quail	<i>S. Mbandaka</i> ST413 (<i>n</i> = 6)	<i>parC</i> : <i>n</i> = 6/6	<i>parC</i> (T57S)	-	IncHI2A, IncN
Casaux et al. (41)	Uruguay	Calves, cows, heifer, organs, samples from environment, food sample, udder swab, drinking water, bovine fetus autopsy.	<i>S. Dublin</i> ST10 (<i>n</i> = 6) <i>S. Typhimurium</i> ST19 (<i>n</i> = 31) <i>S. Newport</i> ST45 (<i>n</i> = 24) <i>S. Anatum</i> ST64 (<i>n</i> = 11) <i>S. Agona</i> ST13 (<i>n</i> = 1) <i>S. Montevideo</i> ST138 (<i>n</i> = 1) <i>S. IIIb</i> 61:i:z53 ST430 (<i>n</i> = 1)	<i>parC</i> : <i>n</i> = 38/75	<i>parC</i> (T57S)	<i>qnrB19</i> (ColE1): <i>n</i> = 5/75	IncFII, IncFII(S), IncFIB, IncFIB(S), Col440I, IncI1, IncX1, IncHI2A, IncQ1, IncI2, IncI2(Delta) IncFIC(FII)
Burnett et al. (62)	Ecuador	Poultry	<i>S. Infantis</i> ST32 (<i>n</i> = 5) <i>S. Schwarzengrund</i> ST96 (<i>n</i> = 2)	<i>gyrA</i> : <i>n</i> = 5/7	<i>gyrA</i> (D87Y)	<i>qnrB19</i> (Col440II): <i>n</i> = 2/7	IncFIB, Col440II

(–) In this study, no QRDR mutations are reported.



Vidal et al. (67) reported 44% MDR in *Salmonella* from swine feces, with 55% ciprofloxacin resistance, emphasizing the impact of antibiotic overuse in pig farming.

Recent studies reveal distinct resistance patterns between poultry and swine. Pigs show higher resistance to azithromycin, ampicillin, and chloramphenicol, while poultry exhibit greater resistance to quinolones and sulfonamides, reflecting differences in antibiotic use between both industries (48).

Antimicrobial resistance data for cattle is limited. In Uruguay, high non-susceptibility to FQ has been reported, with 77.3% of isolates non-susceptible to ciprofloxacin and 6.6% to enrofloxacin (41). Additionally, 56% of isolates exhibited MDR particularly in serotypes like *S. Typhimurium*, *S. Newport*, and *S. Anatum* are notably prevalent in intensive cattle production, causing both enteric and invasive diseases such as septicemia (49).

Genotypic studies identify ST19 (*S. Typhimurium*) and its monophasic variant as key serovars in swine, commonly detected in Brazil and the European Union (50–54). *S. Typhimurium* is the second most common cause of salmonellosis outbreaks in the EU, with pork as the main source in 2014 (55).

The Ser83Phe mutation is frequently reported in pigs strains with reduced susceptibility to CIP, which has been detected in clinical cases in Peru (56). PMQR genes of the *qnr* alleles, such as the *qnrB19* gene, are associated with the spread of *Salmonella* strains resistant to CIP in the United States (57). The Thr57Ser mutation has been described as relevant for reducing susceptibility to ciprofloxacin (58). The frequent detection of *gyrA* (position 83) and *parC* (position 57) mutations highlights their critical role in fluoroquinolone resistance. These findings underscore the need for targeted surveillance and intervention strategies to mitigate the spread of resistant strains.

4.3 One Health implications and need for coordinated surveillance

The antimicrobial resistance observed to quinolones and fluoroquinolones reflects the selective pressure generated by the use of antibiotics in intensive animal production systems. This resistance can vary considerably between different matrices, such as meat, feces and carcass swabs, highlighting the importance of sampling multiple sources within the production system. Although antibiotics remain a crucial tool for treating bacterial diseases, the increase in antimicrobial resistance has reduced their effectiveness (59). Resistance to fluoroquinolones is particularly concerning, as they are commonly used to treat severe human infections, such as systemic salmonellosis in immunocompromised individuals (60).

These findings underscore the urgency of adopting a coordinated One Health approach that integrates surveillance, policy, and intervention strategies across human, animal, and environmental sectors to effectively mitigate the spread of antimicrobial resistance in South America.

4.4 Limitations

This study has several limitations that should be considered when interpreting the results. First, not all South American countries published research on quinolone- and fluoroquinolone-resistant *Salmonella* between 2020 and 2024, which limits the representativeness of the data for the entire region. In addition, there was considerable variability in the types of samples or matrices used in the included studies—ranging from feces, tissues, food, and in some cases pooled samples from different animal species—making it difficult to isolate *Salmonella*-specific information.

Although the study initially sought to include data on fluoroquinolone-resistant *Salmonella* from rodents, no eligible studies were found from South America during the selected period. However, in veterinary medicine, rodents are recognized as important reservoirs and amplifiers of zoonotic infections, including *Salmonella*. Their absence in the published literature highlights a relevant knowledge gap that should be addressed in future research.

Finally, although a predefined protocol was used to guide the review process, it was not formally registered in a database such as PROSPERO. This omission is acknowledged as a limitation in the transparency of the study methodology.

Future studies should aim to include a broader range of countries and matrices, and explore the role of rodents in the dissemination of antimicrobial-resistant *Salmonella*.

5 Conclusion

The antimicrobial resistance to quinolones and fluoroquinolones in *Salmonella* from poultry, swine, and cattle in South America shows a concerning trend, with high rates of resistance and multidrug resistance across several countries. The indiscriminate use of antibiotics in animal production systems appears to be a key factor in the accelerating pressure of the problem, which could undermine the effectiveness of treatments

in both humans and animals. Furthermore, resistance varies significantly across different matrices, highlighting the need for more comprehensive surveillance and the use of more standardized diagnostic techniques. The findings of this study highlight the urgent need for coordinated regional efforts to monitor and control antimicrobial resistance in *Salmonella*. Policymakers, researchers, and industry stakeholders must collaborate to implement effective strategies that safeguard public health and ensure food safety.

Author contributions

SB-V: Investigation, Data curation, Writing – original draft, Formal analysis. MG-Á: Writing – review & editing, Investigation, Data curation. JV: Writing – review & editing. LG-O: Writing – review & editing. SL-O: Writing – review & editing. JC-G: Writing – review & editing, Funding acquisition.

Funding

The author(s) declare that financial support was received for the research and/or publication of this article. This project was funded by Group CIBAV, Strategy of sustainability 2023–2025, Faculty of Agrarian Sciences at the University of Antioquia, Medellin, Colombia.

Acknowledgments

We would like to thank the reviewers and collaborators who provided valuable feedback and support throughout this study.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The authors declare that Gen AI was used in the creation of this manuscript. The authors acknowledge the use of ChatGPT, an artificial intelligence (AI) model developed by OpenAI, as a tool to support translation and enhance the clarity and coherence of the manuscript's writing. However, the authors declare that this AI model was not used for the creation of the manuscript's content, the formulation of ideas, or the generation, analysis, or interpretation of the results presented.

Any alternative text (alt text) provided alongside figures in this article has been generated by Frontiers with the support of artificial intelligence and reasonable efforts have been made to ensure accuracy, including review by the authors wherever possible. If you identify any issues, please contact us.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated

References

- Oludairo OO, Kwaga JKP, Kabir J, Abdu PA, Gitanjali A, Perrets A, et al. A review on *salmonella* characteristics, taxonomy, nomenclature with special reference to non-Typhoidal and Typhoidal salmonellosis. *Zagazig Vet J.* (2022) 50:160–71. doi: 10.21608/zvjz.2022.137946.1179
- Moura EAGO, DGD S, Turco CH, Sanches TVC, Storino GY, Almeida HMS, et al. *Salmonella* bacterin vaccination decreases shedding and colonization of *Salmonella* Typhimurium in pigs. *Microorganisms.* (2021) 9:1163. doi: 10.3390/microorganisms9061163
- Chen HM, Wang Y, Su LH, Chiu CH. Nontyphoid *salmonella* infection: microbiology, clinical features, and antimicrobial therapy. *Pediatr Neonatol.* (2013) 54:147–52. doi: 10.1016/j.pedneo.2013.01.010
- European Centre for Disease Prevention and Control (ECDC). The European Union one health 2022 zoonoses report. *EFSA J.* (2023) 21:e8442. doi: 10.2903/j.efsa.2023.8442
- Márquez RJA. Sanidad animal y salud pública: el paradigma de la salmonella. New York: Amazing Books (2023).
- Dudhane RA, Bankar NJ, Shelke YP, Badge AK. The rise of non-typhoidal *salmonella* infections in India: causes, symptoms, and prevention. *Cureus.* (2023) 15:e46699. doi: 10.7759/cureus.46699
- Ayala-Romero C, Ballen-Parada C, Rico-Gaitán M, Chamorro-Tobar I, Zambrano-Moreno D, Poutou-Piñales R, et al. Prevalencia de *Salmonella* spp., en ganglios mesentéricos de porcinos en plantas de beneficio Colombianas. *Rev MVZ Córdoba.* (2018) 23:6474–86. doi: 10.21897/rmvz.1242
- Gouvêa R, Santos F, Aquino M, Pereira VL. Fluoroquinolones in industrial poultry production, bacterial resistance and food residues: a review. *Braz. J Poultr Sci.* (2015) 17:1–10. doi: 10.1590/1516-635x17011-10
- Eng SK, Pusparajah P, Ab Mutalib NS, Ser HL, Chan KG, Lee LH. *Salmonella*: A review on pathogenesis, epidemiology and antibiotic resistance. *Front Life Sci.* (2015) 8:284–93. doi: 10.1080/21553769.2015.1051243
- Mulvey MR, Boyd DA, Olson AB, Doublet B, Cloeckert A. The genetics of *salmonella* genomic island 1. *Microbes Infect.* (2006) 8:1915–22. doi: 10.1016/j.micinf.2005.12.028
- Martinez M, McDermott P, Walker R. Pharmacology of the fluoroquinolones: a perspective for the use in domestic animals. *Vet J.* (2006) 172:10–28. doi: 10.1016/j.tvjl.2005.07.010
- World Health Organization. Critically important antimicrobials for human medicine. Geneva: World Health Organization (2019).
- Gu Y, Huang L, Wu C, Huang J, Hao H, Yuan Z, et al. The evolution of fluoroquinolone resistance in *salmonella* under exposure to sub-inhibitory concentration of enrofloxacin. *Int J Mol Sci.* (2021) 22:12218. doi: 10.3390/ijms222112218
- Cuyppers WL, Jacobs J, Wong V, Klemm EJ, Deborggraeve S, Van Puyvelde S. Fluoroquinolone resistance in *salmonella*: insights by whole-genome sequencing. *Microb Genom.* (2018) 4:e000195. doi: 10.1099/mgen.0.000195
- Correia S, Poeta P, Hébraud M, Capelo JL, Igrejas G. Mechanisms of quinolone action and resistance: where do we stand? *J Med Microbiol.* (2017) 66:551–9. doi: 10.1099/jmm.0.000475
- Page MJ, Moher D, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. PRISMA 2020 explanation and elaboration: updated guidance and exemplars for reporting systematic reviews. *BMJ.* (2021) 372:n160. doi: 10.1136/bmj.n160
- Biemer JJ. Antimicrobial susceptibility testing by the Kirby-Bauer disc diffusion method. *Ann Clin Lab Sci.* (1973) 3:135–40.
- Wiegand I, Hilpert K, Hancock REW. Agar and broth dilution methods to determine the minimal inhibitory concentration (MIC) of antimicrobial substances. *Nat Protoc.* (2008) 3:163–75. doi: 10.1038/nprot.2007.521
- Mullis KB, Faloona FA. Specific synthesis of DNA in vitro via a polymerase-catalyzed chain reaction. *Methods Enzymol.* (1987) 155:335–50. doi: 10.1016/0076-6879(87)55023-6
- Huggett J, Dheda K, Bustin S, Zumla A. Real-time RT-PCR normalisation; strategies and considerations. *Genes Immun.* (2005) 6:279–84. doi: 10.1038/sj.gene.6364190
- Robicsek A, Strahilevitz J, Sahn DF, Jacoby GA, Hooper DC. qnr prevalence in Cefazidime-resistant Enterobacteriaceae isolates from the United States. *Antimicrob Agents Chemother.* (2006) 50:2872–4. doi: 10.1128/AAC.01647-05
- Quainoo S, Coolen JPM, van Hijum SAFT, Huynen MA, Melchers WJG, van Schaik W, et al. Whole-genome sequencing of bacterial pathogens: the future of nosocomial outbreak analysis. *Clin Microbiol Rev.* (2017) 30:1015–63. doi: 10.1128/CMR.00016-17
- Köser CU, Bryant JM, Becq J, Török ME, Ellington MJ, Marti-Renom MA, et al. Whole-genome sequencing for rapid susceptibility testing of *M. tuberculosis.* *N Engl J Med.* (2013) 369:290–2. doi: 10.1056/NEJMc1215305
- Herrera-Sánchez MP, Castro-Vargas RE, Fandiño-de-Rubio LC, Rodríguez-Hernández R, Rondón-Barragán IS. Molecular identification of fluoroquinolone resistance in *salmonella* spp. isolated from broiler farms and human samples obtained from two regions in Colombia. *Vet World.* (2021) 14:1767–73. doi: 10.14202/vetworld.2021.1767-1773
- Moreira JPFF, do Monte DFM, Lima C d A, de Oliveira CJB, da Silva Martins NR, Berchieri Junior A, et al. Molecular genotyping reveals inter-regional relatedness among antimicrobial resistant *salmonella* Minnesota strains isolated from poultry farm and humans, Brazil. *Braz J Microbiol.* (2022) 53:503–8. doi: 10.1007/s42770-021-00666-1
- Souza AIS, Saraiva MMS, Casas MRT, Oliveira GM, Cardozo MV, Benevides VP, et al. High occurrence of β -lactamase-producing *salmonella* Heidelberg from poultry origin. *PLoS One.* (2020) 15:e0230676. doi: 10.1371/journal.pone.0230676
- Lapierre L, Cornejo J, Zavala S, Galarce N, Sánchez F, Benavides MB, et al. Phenotypic and genotypic characterization of virulence factors and susceptibility to antibiotics in *salmonella* Infantis strains isolated from chicken meat: first findings in Chile. *Animals.* (2020) 10:1049. doi: 10.3390/ani10061049
- Perin AP, Martins BTF, Barreiros MAB, Yamatogi RS, Nero LA, dos Santos Bersot L. Occurrence, quantification, pulse types, and antimicrobial susceptibility of *salmonella* sp. isolated from chicken meat in the state of Paraná, Brazil. *Braz J Microbiol.* (2020) 51:335–45. doi: 10.1007/s42770-019-00188-x
- Vilela FP, dos Prazeres Rodrigues D, Allard MW, Falcão JP. Genomic analyses of drug-resistant *Salmonella enterica* serovar Heidelberg strains isolated from meat and related sources between 2013 and 2017 in the south region of Brazil. *Curr Genet.* (2023) 69:141–52. doi: 10.1007/s00294-023-01264-4
- Lucca V, Borges KA, Furian TQ, Chitolina GZ, Streck AF, da Rocha DT, et al. Phenotypic and molecular characterisation of *salmonella* spp. isolates in healthy poultry. *Br Poultr Sci.* (2024) 65:415–23. doi: 10.1080/00071668.2024.2337180
- Grossi JL, Yamatogi RS, Call DR, Nero LA. High prevalence of intermediate resistance to ciprofloxacin in *Salmonella enterica* isolated from a Brazilian poultry production chain, located in Minas Gerais state. *Int J Food Microbiol.* (2023) 394:110180. doi: 10.1016/j.jifoodmicro.2023.110180
- Monte DFM, Andriheto C, Ribeiro VB, Landgraf M, Destro MT. Highly clonal relationship among *Salmonella Enteritidis* isolates in a commercial chicken production chain, Brazil. *Braz J Microbiol.* (2020) 51:2049–56. doi: 10.1007/s42770-020-00372-4
- Donado-Godoy P, Clavijo V, León M, Tafur MA, Gonzales S, Hume M, et al. Prevalencia de *Salmonella* en canales de carne de pollo de engorde al por menor en Colombia. *J Food Prot.* (2012) 75:1134–8. doi: 10.4315/0362-028X.JFP-11-513
- de Melo RT, dos Reis CT, Peres PABM, Braz RF, Monteiro GP, Rossi DA. *Salmonella enterica* Serovar Minnesota biofilms, susceptibility to biocides, and molecular characterization. *Pathogens.* (2021) 10:581. doi: 10.3390/pathogens10050581
- Monte DF, Lincopan N, Beriman H, Cerdeira L, Keelara S, Thakur S, et al. Genomic features of high-priority *Salmonella enterica* Serovars circulating in the food production chain, Brazil, 2000–2016. *Sci Rep.* (2019) 9:11058. doi: 10.1038/s41598-019-45838-0
- Koutsoumanis K, Allende A, Alvarez-Ordóñez A, Bolton D, Bover-Cid S, Chemaly M, et al. *Salmonella* control in poultry flocks and its public health impact. *EFSA J.* (2019) 17:e05596. doi: 10.2903/j.efsa.2019.5596
- Saidenberg ABS, Franco LS, Reple JN, Hounmanou YMG, Casas MRT, Cardoso B, et al. *Salmonella* Heidelberg and *salmonella* Minnesota in Brazilian broilers: genomic characterization of third-generation cephalosporin and fluoroquinolone-resistant strains. *Environ Microbiol Rep.* (2023) 15:119–28. doi: 10.1111/1758-2229.13132
- Parada J, Galas M, Faccone D, Tamiozzo P, Carranza A. Antibiotic resistance and associated resistance determinants in different *Salmonella enterica* serovars isolated from pigs in Argentina. *Vet World.* (2022) 15:1215–20. doi: 10.14202/vetworld.2022.1215-1220
- van den Berg RR, Dissel S, Rapallini MLBA, van der Weijden CC, Wit B, Heymans R. Characterization and whole genome sequencing of closely related multidrug-resistant *Salmonella enterica* serovar Heidelberg isolates from imported poultry meat in the Netherlands. *PLoS One.* (2019) 14:e0219795. doi: 10.1371/journal.pone.0219795
- Vetting MW, Park CH, Hegde SS, Jacoby GA, Hooper DC, Blanchard JS. Mechanistic and structural analysis of aminoglycoside N-acetyltransferase AAC (6')-Ib and its bifunctional, fluoroquinolone-active AAC (6')-Ib-cr variant. *Biochemistry.* (2008) 47:9825–35. doi: 10.1021/bi800664x

41. Casaux ML, D'Alessandro B, Vignoli R, Fraga M. Phenotypic and genotypic survey of antibiotic resistance in *Salmonella enterica* isolates from dairy farms in Uruguay. *Front Vet Sci.* (2023) 10:1055432. doi: 10.3389/fvets.2023.1055432
42. de Azevedo EC, Martins BTF, Tiba Casas MR, Possebon FS, Araújo Junior JP, Nero LA, et al. Multidrug resistance and virulence profiles of *salmonella* isolated from swine lymph nodes. *Microb Drug Resist.* (2021) 27:562–70. doi: 10.1089/mdr.2020.0120
43. Possebon FS, Tiba Casas MR, Nero LA, Yamatogi RS, Araújo JP, Pinto AN. Prevalence, antibiotic resistance, PFGE and MLST characterization of *salmonella* in swine mesenteric lymph nodes. *Prev Vet Med.* (2020) 179:105024. doi: 10.1016/j.prevetmed.2020.105024
44. Hsueh PR, Teng LJ, Tseng SP, Chang CF, Wan JH, Yan JJ, et al. Ciprofloxacin-resistant *Salmonella enterica* Typhimurium and Choleraesuis from pigs to humans, Taiwan. *Emerg Infect Dis.* (2004) 10:60–8. doi: 10.3201/eid1001.030171
45. Pissetti C, de Freitas Costa E, Zenato KS, de Itapema Cardoso MR. Critically important antimicrobial resistance trends in *salmonella* Derby and *Salmonella* Typhimurium isolated from the pork production chain in Brazil: a 16-year period. *Pathogens.* (2022) 11:905. doi: 10.3390/pathogens11080905
46. Simoni C, de Campos Ausani T, Laviniki V, Lopes GV, de Itapema Cardoso MR. *Salmonella* derby from pig production chain over a 10-year period: antimicrobial resistance, biofilm formation, and genetic relatedness. *Braz J Microbiol.* (2022) 53:2185–94. doi: 10.1007/s42770-022-00846-7
47. Cai Y, Tao J, Jiao Y, Fei X, Zhou L, Wang Y, et al. Phenotypic characteristics and genotypic correlation between *salmonella* isolates from a slaughterhouse and retail markets in Yangzhou, China. *Int J Food Microbiol.* (2016) 222:56–64. doi: 10.1016/j.jfoodmicro.2016.01.020
48. Gomes VTM, Moreno LZ, Silva APS, Thakur S, La Ragione RM, Mather AE, et al. Characterization of *Salmonella enterica* contamination in pork and poultry meat from São Paulo/Brazil: serotypes, genotypes and antimicrobial resistance profiles. *Pathogens.* (2022) 11:358. doi: 10.3390/pathogens11030358
49. Costa LF, Paixão TA, Tsois RM, Bäumler AJ, Santos RL. Salmonellosis in cattle: advantages of being an experimental model. *Res Vet Sci.* (2012) 93:1–6. doi: 10.1016/j.rvsc.2012.03.002
50. Biasino W, De Zutter L, Mattheus W, Bertrand S, Uyttendaele M, Van Damme I. Correlation between slaughter practices and the distribution of *salmonella* and hygiene indicator bacteria on pig carcasses during slaughter. *Food Microbiol.* (2018) 70:192–9. doi: 10.1016/j.fm.2017.10.003
51. Bonardi S. *Salmonella* in the pork production chain and its impact on human health in the European Union. *Epidemiol Infect.* (2017) 145:1513–26. doi: 10.1017/S095026881700036X
52. Cabral CC, Panzenhagen PHN, Delgado KF, Silva GRA, Rodrigues DDP, Franco RM, et al. Contamination of carcasses and utensils in small swine slaughterhouses by *salmonella* in the northwestern region of the state of Rio de Janeiro, Brazil. *J Food Prot.* (2017) 80:1128–32. doi: 10.4315/0362-028X.JFP-16-387
53. dos Santos Bersot L, Quintana Cavicchioli V, Viana C, Konrad Burin RC, Camargo AC, de Almeida Nogueira Pinto JP, et al. Prevalence, antimicrobial resistance, and diversity of *salmonella* along the pig production chain in southern Brazil. *Pathogens.* (2019) 8:204. doi: 10.3390/pathogens8040204
54. Viana C, Sereno MJ, Pegoraro K, Yamatogi RS, Call DR, dos Santos Bersot L, et al. Distribution, diversity, virulence genotypes and antibiotic resistance for *salmonella* isolated from a Brazilian pork production chain. *Int J Food Microbiol.* (2019) 310:108310. doi: 10.1016/j.jfoodmicro.2019.108310
55. EFSA. The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2016. *EFSA J.* (2017) 15:e05077.
56. García C, Lejon V, Horna G, Astocondor L, Vanhoof R, Bertrand S, et al. Intermediate Susceptibility to Ciprofloxacin among *Salmonella enterica* Serovar Typhi Isolates in Lima, Peru. *J Clin Microbiol.* (2014) 52:968–70. doi: 10.1128/JCM.02663-13
57. Enekave E, Hong SL, Lim S, Hayer SS, Boxrud D, Taylor AJ, et al. Circulation of plasmids harboring resistance genes to quinolones and/or extended-spectrum cephalosporins in multiple *Salmonella enterica* serotypes from swine in the United States. *Antimicrob Agents Chemother.* (2019) 63:e02602. doi: 10.1128/AAC.02602-18
58. Ling JM, Chan EW, Lam AW, Cheng AF. Mutations in topoisomerase genes of fluoroquinolone-resistant *salmonellae* in Hong Kong. *Antimicrob Agents Chemother.* (2003) 47:3567–73. doi: 10.1128/AAC.47.11.3567-3573.2003
59. Ventola CL. The antibiotic resistance crisis. *P T.* (2015) 40:277–83.
60. Medalla F, Gu W, Mahon BE, Judd M, Folster J, Griffin PM, et al. Estimated incidence of antimicrobial drug-resistant nontyphoidal *salmonella* infections, United States, 2004–2012. *Emerg Infect Dis.* (2017) 23:29–37. doi: 10.3201/eid2301.160771
61. Benevides VP, Saraiva MMS, Nascimento CF, Delgado-Suárez EJ, Oliveira CJB, Silva SR, et al. Genomic features and phylogenetic analysis of antimicrobial-resistant *salmonella* Mbandaka ST413 strains. *Microorganisms.* (2024) 12:312. doi: 10.3390/microorganisms12020312
62. Burnett, E., Ishida, M., de Janon, S., Naushad, S., Duceppe, M.-O., Gao, R., et al. (2021). Whole-Genome Sequencing Reveals the Presence of the blaCTX-M-65 Gene in Extended-Spectrum β -Lactamase-Producing and Multi-Drug-Resistant Clones of *Salmonella* Serovar Infantis Isolated from Broiler Chicken Environments in the Galapagos Islands. *Antibiotics*, 10:3. doi: 10.3390/antibiotics10030267
63. de Quadros, C. L., Manto, L., Mistura, E., Webber, B., Ritterbusch, G. A., Borges, K. A., et al. (2020). Antimicrobial and Disinfectant Susceptibility of *Salmonella* Serotypes Isolated from Swine Slaughterhouses. *Current Microbiology*, 77, 1035–1042. doi: 10.1007/s00284-020-01904-9
64. Kich, J. D., Souza, A. I. A., Montes, J., Meneguzzi, M., Costa, E. F., Coldebella, A., et al. (2020). Investigation of *Listeria monocytogenes*, *Salmonella enterica* and *Yersinia enterocolitica* in pig carcasses in Southern Brazil. *Pesquisa Veterinária Brasileira*, 40, 781–790. doi: 10.1590/1678-5150-PVB-6628
65. Ortiz, F., Weiler, N., Álvarez, M., Orrego, V., Martínez, J., Melgarejo, N., et al. (2023). Mecanismos plasmídicos de resistencia a quinolonas, betalactámicos y colistina en *Salmonella enterica*. Paraguay 2020–2021. *Memorias del Instituto de Investigaciones en Ciencias de la Salud*, 21, 13. doi: 10.18004/mem.iics/1812-9528/2023.e21122313
66. Vico, J. P., Lorenzutti, A., Zogbi, A. P., Aleu, G., Sánchez, I. C., Caffer, M. I., et al. (2020). Prevalence, associated risk factors, and antimicrobial resistance profiles of nontyphoidal *Salmonella* in large scale swine production in Córdoba, Argentina. *Research in Veterinary Science*, 130. doi: 10.1016/j.rvsc.2020.03.003
67. Vidal, J. L., Clavijo, V., Castellanos, L. R., Kathiresan, J., Kumar, A. M. V., Mehta, K., et al. (2023). Multidrug-resistant *Salmonella* spp. In fecal samples of pigs with suspected salmonellosis in Antioquia, Colombia, 2019–2021. *Revista Panamericana de Salud Pública*, 47, 1. doi: 10.26633/RPSP.2023.46
68. Vilela, F. P., Rodrigues, D. d., Ferreira, J. C., Darini, A. L. d. C., Allard, M. W., Falcão, J. P., et al. (2020). Genomic characterization of *Salmonella enterica* serovar Choleraesuis from Brazil reveals a swine gallbladder isolate harboring colistin resistance gene mcr-1.1. *Braz. J. Microbiol.* 53, 1799–1806. doi: 10.1007/s42770-022-00812-3