Critical Reviews in Microbiology

ISSN: 1040-841X (Print) 1549-7828 (Online) Journal homepage: www.tandfonline.com/journals/imby20

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To cite this article: Carlos Bastidas-Caldes, Fernanda Hernández-Alomía, Francisco Bolaños, Emily Cisneros-Vásquez & Daniel Romero-Alvarez (10 Aug 2026): Antimicrobial resistance in Ecuador, 2000–2024: a systematic review within a One Health framework, Critical Reviews in Microbiology, DOI: 10.1080/1040841X.2026.2709521

To link to this article: https://doi.org/10.1080/1040841X.2026.2709521

CRITICAL REVIEWS IN MICROBIOLOGY
https://doi.org/10.1080/1040841X.2026.2709521

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REVIEW ARTICLE

Antimicrobial resistance in Ecuador, 2000–2024: a systematic review within a One Health framework

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ABSTRACT

Antimicrobial resistance (AMR) is a major global public health threat, particularly in low- and middle-income countries. In Ecuador, AMR research has expanded during the last two decades, but evidence remains fragmented and largely restricted to the human health sector. We systematically reviewed studies reporting laboratory-confirmed bacterial resistance in Ecuador between 2000 and 2024, including evidence from human, animal, food, and environmental sources. Eighty studies met the inclusion criteria. Most were hospital-based and conducted in urban areas, with limited evidence from rural, Amazonian, and insular regions. Gram-negative bacteria accounted for the greatest resistance burden, particularly Escherichia coli (56.6%), Klebsiella pneumoniae, Salmonella spp. (22.3%), the Acinetobacter baumannii complex, and Pseudomonas aeruginosa, together with resistant Staphylococcus aureus and Mycobacterium tuberculosis. Resistance to beta-lactams and fluoroquinolones predominated, whereas carbapenem resistance was especially notable among WHO priority pathogens. Evidence from animal, food, and environmental sectors was scarce and heterogeneous, and molecular characterization was inconsistently reported. These findings highlight important surveillance gaps beyond hospital settings and underscore the need for integrated multisectoral surveillance to strengthen public health policy, antimicrobial stewardship, and AMR prevention in Ecuador.

ARTICLE HISTORY
Received 29 January 2026
Revised 9 July 2026
Accepted 21 July 2026

KEYWORDS
Surveillance; Stewardship; Epidemiology; Bacteriology; Public health

Introduction

Antimicrobial resistance (AMR) represents one of the most pressing challenges to global health, undermining decades of medical progress and jeopardizing the efficacy of life-saving therapies. In 2019, AMR was estimated to be directly responsible for 1.27 million deaths and associated with nearly five million fatalities worldwide, with the highest burden concentrated in low- and middle-income countries (Murray et al. 2022). Recognizing its cross-cutting impact, the World Health Organization (WHO) has consistently placed AMR among its global health threats, calling for robust national action plans, integrated surveillance systems, and stewardship interventions (WHO 2016, 2025). The Global Action Plan on AMR and the Global Antimicrobial Resistance and Use Surveillance System (GLASS) emphasizes the need for systematic evidence collection across human, animal, and environmental domains to guide policy and mitigate risk (WHO 2025).

In 2024, WHO released the updated Bacterial Priority Pathogens List (BPPL), refining its original 2017 prioritization by integrating new data on resistance trends, burden, and transmission dynamics (Sati et al. 2025). The 2024 BPPL confirmed that carbapenem-resistant *K. pneumoniae* and *Escherichia coli*, carbapenem-resistant *Acinetobacter baumannii*, rifampicin-resistant *Mycobacterium tuberculosis*, and methicillin-resistant *Staphylococcus aureus* remain critical or high-priority pathogens. Additionally, fluoroquinolone-resistant *Salmonella enterica*, *Shigella spp.*, and *Neisseria gonorrhoeae* were highlighted as emerging resistant bacteria in low- and middle-income countries. This updated prioritization provides a straightforward framework for research, policy, and public health strategies against AMR.

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Supplemental data for this article can be accessed online at https://doi.org/10.1080/1040841X.2026.2709521.

In the Americas, the Pan American Health Organization (PAHO) has urged member states to operationalize One Health multisectoral strategies, acknowledging persistent barriers such as fragmented health systems, limited laboratory capacity, and insufficient stewardship implementation (PAHO 2025). Regional reports highlight a sustained increase in resistance to extended-spectrum beta-lactams, carbapenems, and fluoroquinolones across both clinical and veterinary contexts (Rodríguez-Baño et al. 2018). Yet, despite growing awareness, comprehensive and integrative AMR surveillance remains scarce across Latin America.

Ecuador epitomizes these regional challenges. National AMR surveillance, coordinated by the Ministry of Public Health through the Integrated Epidemiological Surveillance System (SIVE) and WHONET (https://whonet.org/), has expanded in recent years generating valuable hospital- and outpatient-based resistance data (MSP 2023). *E. coli*, *K. pneumoniae*, and *S. aureus* dominate among isolates with alarming levels of extended-spectrum beta-lactamase production, carbapenemase-mediated resistance, and methicillin resistance, respectively (Satán et al. 2023). However, surveillance activities remain largely restricted to the human health sector. Data on antimicrobial use and resistance in livestock production, foodborne pathogens, and environmental reservoirs are fragmented and limited to isolated academic reports, creating a landscape of fragmented evidence.

The 2019–2023 Ecuadorian National Plan on AMR achieved notable advances in hospital surveillance and infection prevention. Nonetheless, its final evaluation revealed substantial gaps in intersectoral governance, incorporation of animal and environmental data, and stewardship initiatives (MSP 2025). Accordingly, we developed a systematic review consolidating published AMR academic literature in Ecuador as evidence synthesis. We used One Health framework to (i) map the distribution of resistant bacteria across human, animal, foodborne, and environmental contexts, (ii) identify geographic and sectoral evidence gaps, and (iii) provide a robust evidence-base landscape on antibiotic resistance bacteria to strengthen surveillance and policymaking.

Objective

This is a One Health study that systematically reviews and synthesizes published evidence on antimicrobial resistance in Ecuador, integrating findings from human, animal, environmental, and foodborne sources to inform surveillance, policy, and research priorities.

Methodology

Eligibility criteria

Original peer-reviewed studies reporting AMR in bacterial isolates collected from any geographic region of Ecuador were eligible for inclusion. Studies involving human clinical and community sources, animals, food, or environmental samples were considered. Eligible study designs included cross-sectional studies, surveillance reports, and case series with at least 10 laboratory-confirmed bacterial isolates. Studies employing phenotypic antimicrobial susceptibility testing (AST), genotypic methods (e.g. PCR, sequencing, or other molecular approaches), or a combination of both were eligible for inclusion, provided they reported original AMR data from bacterial isolates collected in Ecuador.

Articles published in English or Spanish between January 2000 and June 2024 were considered.

Exclusion criteria included duplicate publications or studies with overlapping datasets, studies conducted outside Ecuador, studies including fewer than 10 laboratory-confirmed bacterial isolates, reviews, editorials, conference abstracts, theses, institutional reports, and other non-peer-reviewed literature, as well as studies without extractable primary antimicrobial resistance data or without laboratory-confirmed bacterial isolates.

Information sources and search strategy

Between July and August 2024, a systematic search was conducted in PubMed and Scielo. The search strategy combined Medical Subject Headings (MeSH) and free-text terms in English and Spanish, including combinations of "antimicrobial resistance," "antibiotic resistance," "antimicrobial resistant," and "antibiotic resistant," together with their Spanish counterparts (i.e. *resistencia antimicrobiana, resistencia bacteriana, antimicrobiano resistente, antibiótico resistente, antimicrobiano*, and *antibiótico*), always linked with the country descriptor "Ecuador". This strategy was iteratively refined to ensure both sensitivity and specificity in the retrieval of relevant studies (Walpole 2019). All references were imported into Rayyan QCRI (Qatar Computing Research Institute) where duplicates were removed, and titles and abstracts were independently screened by reviewers prior to full-text assessment.

Study selection and inclusion criteria

A total of 156 records were initially identified from PubMed ($n = 129$) and Scielo ($n = 27$). After importing

all records into Rayyan QCRI, duplicates were removed and 150 unique articles remained for screening. Two independent reviewers (FH-A and EC) screened titles and abstracts, followed by full-text assessment. Any discrepancies were resolved by a third reviewer (CB-C). The inclusion of studies was evaluated independently by two reviewers, focusing on three main domains: (i) clarity and representativeness of the sampling strategy, (ii) completeness and standardization of AST methods, and (iii) transparency in reporting interpretative guidelines (e.g. CLSI or EUCAST).

Following study selection, a structured methodological robustness assessment was performed for all included studies using variables extracted during the review process. The assessment considered completeness of epidemiological reporting (GEO, SRC), bacterial identification (ID), phenotypic antimicrobial susceptibility testing (PHENO), molecular characterization (MOL), sample-size support (N), and reporting completeness (DATA). The complete assessment is provided in Supplementary Table S7.

Of the 150 screened articles, 55 were excluded, leading to 95 full-text reports being assessed for eligibility. Reasons for exclusion during this stage included: lack of available data ($n=4$), duplicates ($n=5$), case-study design ($n=3$), background-only content ($n=2$), or data overlap with other studies ($n=1$). Ultimately, 80 studies were included in the review. The detailed selection process is illustrated in the PRISMA flow diagram (Figure 1).

Data extraction

We used a standardized template to extract the following variables: author, year of publication, and study design. We also noted the sample type and source (clinical, community, animal, food, or environment). For human studies, clinical sources included hospital-based, healthcare-associated, and outpatient healthcare settings, whereas community sources referred to non-clinical community populations. Bacterial species, AST methodology, and interpretative guidelines (CLSI or EUCAST) were also recorded. When available, we recorded reported resistance profiles and genetic determinants of resistance. If essential data were missing or in inaccessible supplementary files, we contacted the corresponding authors for information.

Statistical analysis and data visualization

Data was extracted into a standardized spreadsheet and double-checked for accuracy. Resistance data were aggregated separately for each bacterial species–antimicrobial combination by summing resistant isolates (n) and total isolates tested (N) across all eligible studies, and overall resistance proportions were calculated as cumulative n/N with corresponding 95% confidence intervals.

To summarize resistance frequencies, descriptive analyses were performed by bacterial species, antimicrobial class, sample source (clinical, community, animal, food, or environment), and bacterial group (Gram-positive, Gram-negative, and acid-fast bacteria). Descriptive analyses included the distribution of antimicrobial resistance genes (ARGs), classification of priority pathogens according to the WHO Bacterial Priority Pathogens List (BPPL 2024), and visualization of pathogen–antimicrobial–source relationships using alluvial diagrams and other graphical approaches.

Data visualization was employed as an analytical tool to detect hidden patterns. RAWGraphs was used to construct interactive Sankey diagrams linking pathogens, antibiotic classes, and sample sources. Flourish was implemented to generate circular plots mapping the distribution of resistance genes. Both packages were used through R and R Studio (version 4.3.2; https://cran.r-project.org/bin/windows/base/) for reproducible analysis and custom plotting. All visualizations were cross validated against the raw data to ensure consistency.

Classification of priority pathogens

Priority categories for the bacterial pathogens identified in this review were assigned according to the World Health Organization Bacterial Priority Pathogens List (WHO 2024). Under this framework, carbapenem-resistant Enterobacterales, carbapenem-resistant non-fermenting Gram-negative bacteria, and rifampicin-resistant mycobacteria were classified as *critical priority pathogens*. Likewise, methicillin-resistant Gram-positive staphylococci, vancomycin-resistant enterococci, fluoroquinolone-resistant enteric bacteria, and carbapenem-resistant non-fermenting rods were categorized as *high-priority pathogens*.

Results

Study characteristics

A total of 80 studies published between 2000 and 2024 met the inclusion criteria (Figure 1; Tables S1–S3). The number of studies increased notably after 2015. Most were conducted in urban hospital settings, mainly in the largest cities in the country, namely Quito–its

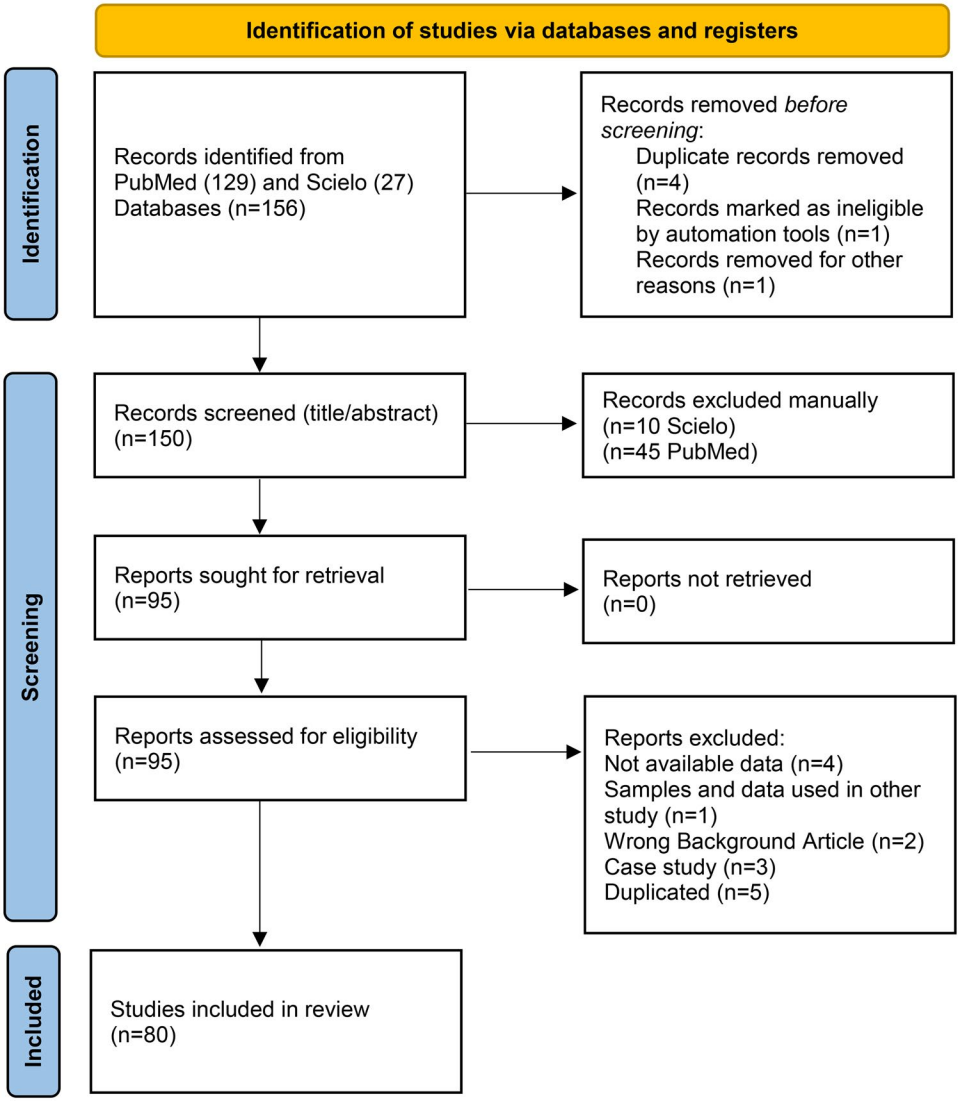

Figure 1. PRISMA 2020 flow diagram. We identified a total of 156 studies that were filtered with our inclusion criteria to obtain a total of 80 studies for analysis in this systematic review.

capital–and Guayaquil. The majority focused on human health, while a smaller proportion investigated animal, foodborne, or environmental sources.

The included studies covered the four major ecoregions of Ecuador (Figure 2). A total of 56 studies were conducted in the Andean region, while 24 studies originated from the Coastal region. In the Amazon basin, 12 studies were identified, and in the Galapagos Islands three studies were reported. Two of the included studies lacked information of sample origin. The provincial distribution was markedly uneven, with over half of the province-level records concentrated in Pichincha ($n = 53$), followed by Imbabura and Loja ($n = 13$ each), whereas Carchi had no eligible studies.

Among the 80 studies, 59 reported the use of antibiogram-based susceptibility testing, 55 employed PCR, and 15 included sequencing techniques. Whole-genome sequencing (WGS) was applied in only one study. Automated systems were less frequently reported, with Vitek mentioned in seven studies and microdilution in six studies. Other approaches included E-test (three studies), agar dilution (three studies), double-disk synergy testing (two studies), and proportion methods (three studies; Tables S2-S3).

Regarding host origin, 40 studies investigated human-derived isolates. Among animal sources, 19 studies focused on poultry, seven on swine, and five on dogs. Other hosts were less frequently studied, including cattle (three studies), cats (one study), guinea pigs (two studies), shrimp (one study), ducks (one study), and wild animals (one study). Eleven studies lacked data on the origin of host data.

Human clinical samples were the most common. Fifteen studies analyzed urine samples and 15 other

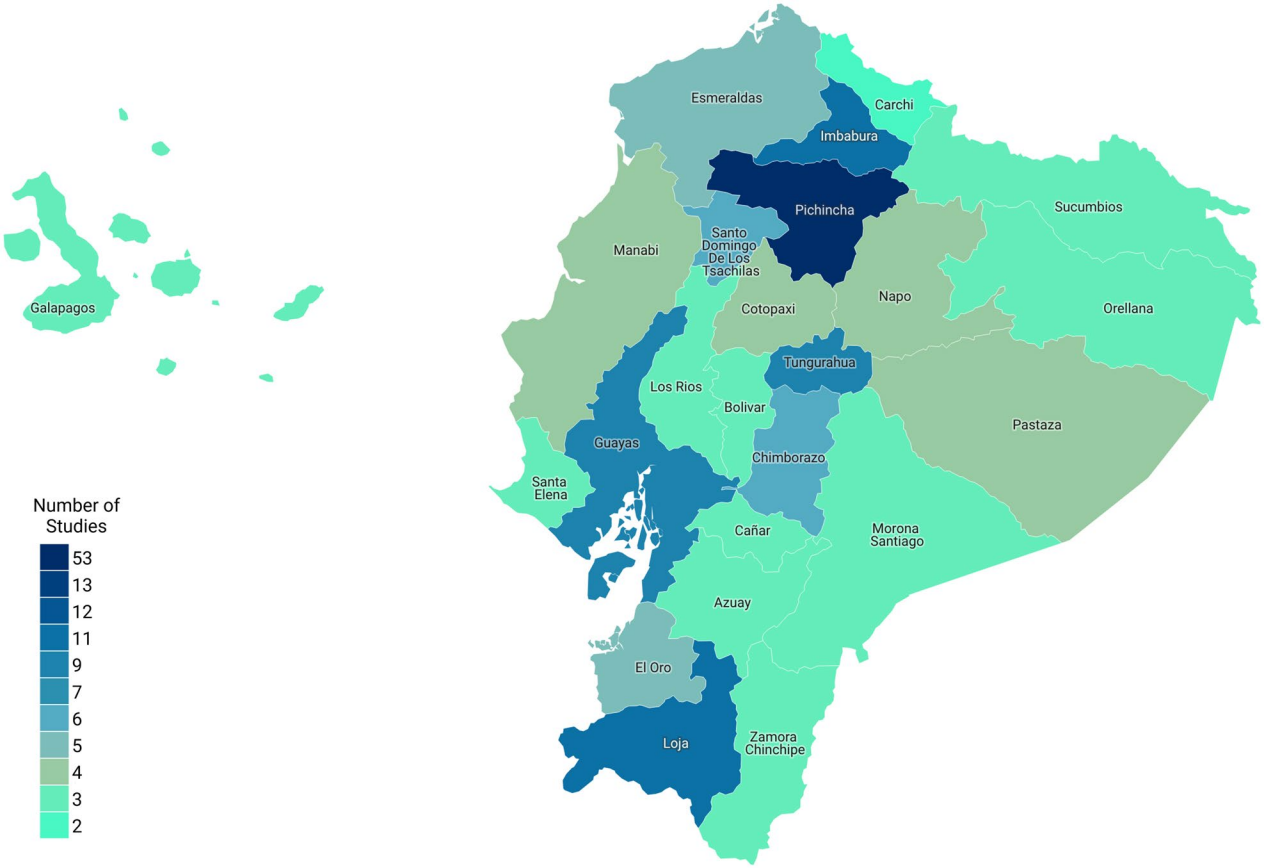

Figure 2. Geographic distribution of the included studies across the provinces of Ecuador. Color intensity represents the number of included studies conducted in each province. Carchi had no eligible studies. Two included studies were not mapped because the province of sample origin was not reported.

blood samples. Other frequently reported specimens were respiratory (11 studies), wound exudates (nine studies), and stool samples (eight studies). Additional clinical sources included catheters (four studies), cerebrospinal and brain–spinal fluids (three studies), abscesses (three studies), rectal swabs (three studies), and skin samples (three studies). Less common were pleural fluid (two studies), pericardial fluid (two studies), food matrices (four studies), and environmental water (two studies). Single reports described isolates from bone, ulcers, sediment, sputum, ICU devices, milk, tracheal aspirates, and meat. Nine studies lacked information of sample type (Tables S2 and S3).

Across different sources, *E. coli* was the most dominant and consistently detected bacteria, with frequencies ranging from five studies in food to 16 in animal sources. Clinical sources exhibited the highest variety of bacteria species isolated with moderate frequencies (five–eight studies). In contrast, community and environmental sources showed the lowest variety of isolated bacterial species, with most reporting only once or twice. Animal and food sources displayed similar patterns, primarily characterized by the repeated detection of *E. coli* (16 and four studies, respectively) and *Salmonella* (six and five studies; Figure 3 and Table S3).

Bacterial prevalence

Among Gram-positive organisms, *S. aureus* accounted for 45.4% of isolates ($n = 7{,}506/16{,}529$; [44.28–46.54] 95% CI), coagulase-negative Staphylococci (CoNS) for 42.8% ($n = 6{,}125/14{,}322$; [41.53–44.01] 95% CI), and *Streptococcus* spp. for 2.1% ($n = 276/13{,}168$; [0.41–3.79] 95% CI). Other less common Gram-positive bacteria detected in our review included *Listeria monocytogenes* at 28.9% ($n = 15/52$; [5.92–51.77] 95% CI), *Vibrio parahaemolyticus* at 80.8% ($n = 185/229$; [75.11–88.46] 95% CI), and *Campylobacter* spp. (Toledo et al. 2017; Vinueza-Burgos et al. 2017; Simaluiza et al. 2018; Toledo et al. 2018) at 39.0% ($n = 440/1{,}129$; [34.42–43.53] 95% CI). Other microorganisms (Zhou et al. 2022) reported sporadically included *N. gonorrhoeae* (9.0%; $n = 18/200$; [0–22.22] 95% CI), *Chlamydia trachomatis* (15.5%; $n = 31/200$; [2.76–28.24] 95% CI), *Mycoplasma genitalium* (8.5%; $n = 17/200$; [0–21.76] 95% CI), and *M. tuberculosis* (28.4%; $n = 2{,}350/8{,}287$; [26.54–30.18] 95% CI; Figure 4).

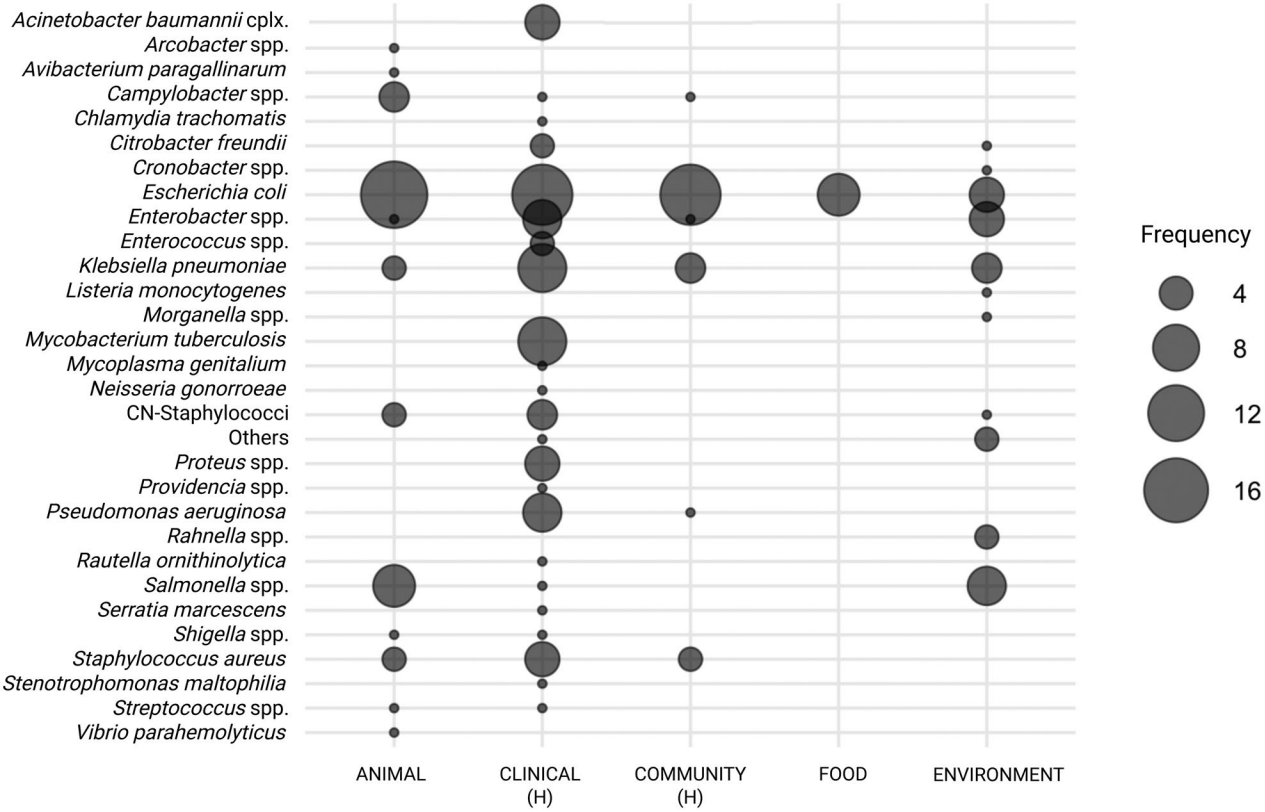

Figure 3. Bubble plot showing the number of studies conducted in Ecuador reporting bacterial pathogens 2000–2024. Each bubble represents the frequency of studies identifying a given bacterial genus or species (y-axis) within each defined category (x-axis), namely human clinical or community, animal, food, and environment. Bubble size is proportional to study count. Bacterial taxa are presented in alphabetical order.

Across the included studies, Gram-negative bacteria showed to be the most prevalent. *E. coli* was the most frequently recovered organism, isolated in 56.6% of processed samples ($n = 42{,}691/75{,}380$ [56.16–57.10] 95% CI). *K. pneumoniae* were isolated in 22.3% ($n = 10{,}347/46{,}428$ [21.48–23.08] 95% CI). *Salmonella* spp. were recovered in 2.3% of samples ($n = 1{,}083/47{,}382$ [1.40–3.18] 95% CI), *Enterobacter* spp. in 4.3% ($n = 1{,}954/46{,}010$ [3.35–5.14] 95% CI), *Proteus* spp. in 4.1% ($n = 1{,}829/44{,}382$ [3.21–5.03] 95% CI), and the *A. baumannii* complex in 3.5% ($n = 1{,}587/45{,}333$ [2.60–4.41] 95% CI). *Pseudomonas aeruginosa* accounted for 8.5% ($n = 3{,}822/45{,}068$; [7.60–9.36] 95% CI; Figure 4). Other microorganisms reported sporadically (Luna-Galaz et al. 2016; Rosa et al. 2020; Calero-Cáceres 2022a; Villacís et al. 2023).

Resistance in gram-positive bacteria

For Gram-positive bacteria, resistance of *S. aureus* and negative-coagulase Staphylococci (CoNS) were strongly linked to penicillins, cephalosporines, macrolides and sulfonamides, with the majority of flows directed toward hospital clinical sources (Reyes et al. 2009; Zurita et al. 2016; Zambrano-Mila et al. 2020). Community-associated isolates appeared less frequently but remained visible, particularly involving *S. aureus* connected to quinolones and lincosamide resistance, reflecting outpatient skin and soft tissue infections. Animal sources contributed only marginal flows, involving *Enterococcus* spp. and *Streptococcus* spp., while food and environment-derived isolates were rare and contributed to negligible connections (Figure 5 and Table S4).

In *S. aureus*, resistance was 39.9% for penicillins including oxacillin ($n = 2{,}999/7{,}506$ [38.85–41.06] 95% CI), 28.9% for cephalosporins ($n = 2{,}175/7{,}506$ [27.95–30.00] 95% CI), 22.1% for lincosamides ($n = 1{,}664/7{,}506$ [21.23–23.11] 95% CI), 40.3% for macrolides ($n = 3{,}028/7{,}506$ [39.23–41.45] 95% CI), and 34.8% for sulfonamides ($n = 2{,}611/7{,}506$ [33.71–35.86] 95% CI) (Supplementary Table S5).

In CoNS, resistance was 71.8% for penicillins including oxacillin ($n = 4{,}397/6{,}125$ [70.66–72.91] 95% CI), 65.5% for cephalosporins ($n = 4{,}012/6{,}125$ [64.31–66.69] 95% CI), 42.8% for quinolones ($n = 2{,}626/6{,}125$ [41.63–44.11] 95% CI), 49.9% for lincosamides ($n = 3{,}057/6{,}125$ [48.66–51.16] 95% CI), 66.8% for macrolides

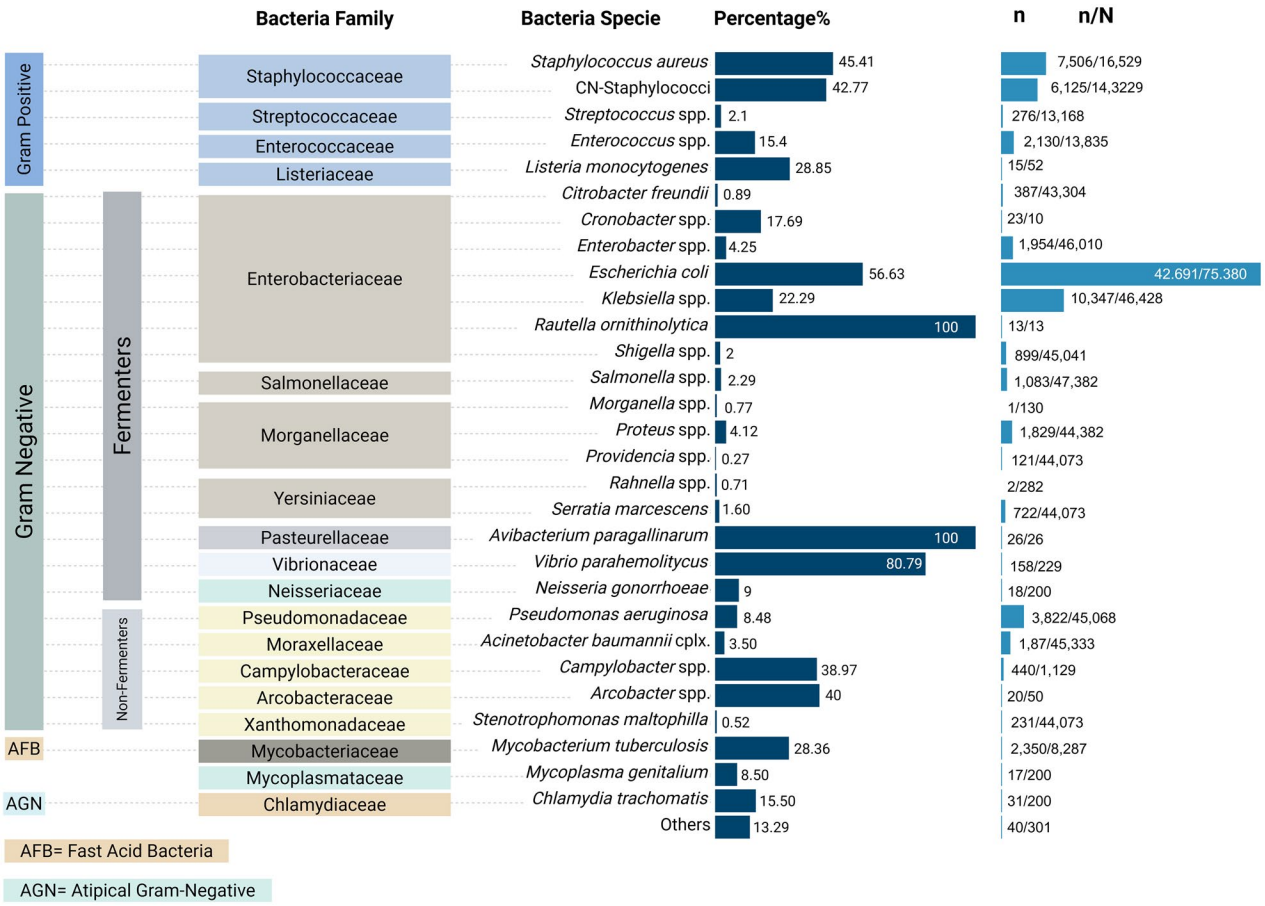

Figure 4. Distribution and prevalence of bacterial pathogens reported across Ecuador 2000–2024. Gram-positive, Gram-negative fermenters and non-fermenters, fast-acid bacteria (AFB), and atypical Gram-negative organisms (AGN) are displayed on the left. Prevalence bars (middle) reflect the proportion of isolates reported in the included studies, while counts (n/N) on the right illustrate the raw counts for proportion calculation.

(*n* = 4,096/6,125 [65.69–68.05] 95% CI), 52.2% for sulfonamides (*n* = 3,200/6,125 [50.99–53.50] 95% CI), and 1.3% for glycopeptides tested for vancomycin (*n* = 83/6,125 [1.07–1.64] 95% CI). In *Enterococcus* spp., resistance was 35.9% for aminoglycosides (*n* = 765/2,130 [33.88–37.95] 95% CI) and 30.2% for quinolones (*n* = 643/2,130 [28.24–32.14] 95% CI; Supplementary Table S5).

Resistance in gram-negative bacteria

The data revealed broad connections between *E. coli* and *Klebsiella* spp. with penicillins, cephalosporins, carbapenems, and fluoroquinolones (Armas-Freire et al. 2015; Salgado Yepez et al. 2017), most of which flowed directly into hospital clinical sources (Garrido et al. 2017; Soria Segarra et al. 2018; Zurita et al. 2019b, 2023). These flows indicate that resistant isolates from clinical samples represent the dominant contribution to AMR surveillance data for Gram-negative organisms in Ecuador. In contrast, community-acquired isolates were mainly linked to *E. coli* and *Salmonella* spp. (Eisenberg et al. 2012; Hedman et al. 2019a), particularly with quinolones, reflecting their role in outpatient and enteric infections (Tables S5-S6).

Animal-derived isolates contributed to narrow streams, primarily involving *Salmonella* spp. (Mejia et al. 2021; Amancha et al. 2023; Vinueza-Burgos et al. 2023)and *Campylobacter* spp. (Ochoa et al. 2016; Toledo et al. 2018), associated with resistance to quinolones and tetracyclines, consistent with their importance in zoonotic transmission. Food-related isolates were infrequent but showed connections with *E. coli* (Zurita et al. 2020; Barragán-Fonseca et al. 2022)and *Vibrio parahaemolyticus* (Sperling et al. 2015), while environmental isolates contributed sporadic but detectable flows, mainly linked to *Enterobacter* spp. and *A. baumannii* cplx. (Figure 6).

In *E. coli*, resistance was highest for ampicillin (15.1%; *n* = 6,433/42,691 [14.76–15.44] 95% CI) and ampicillin–sulbactam (28.7%; *n* = 12,255/42,691 [28.27–29.13] 95% CI) among penicillins. Cephalosporins showed considerable variability, with resistance reaching 21.6% for ceftriaxone (*n* = 9,237/42,691 [21.21–21.99] 95% CI), 14.8% for

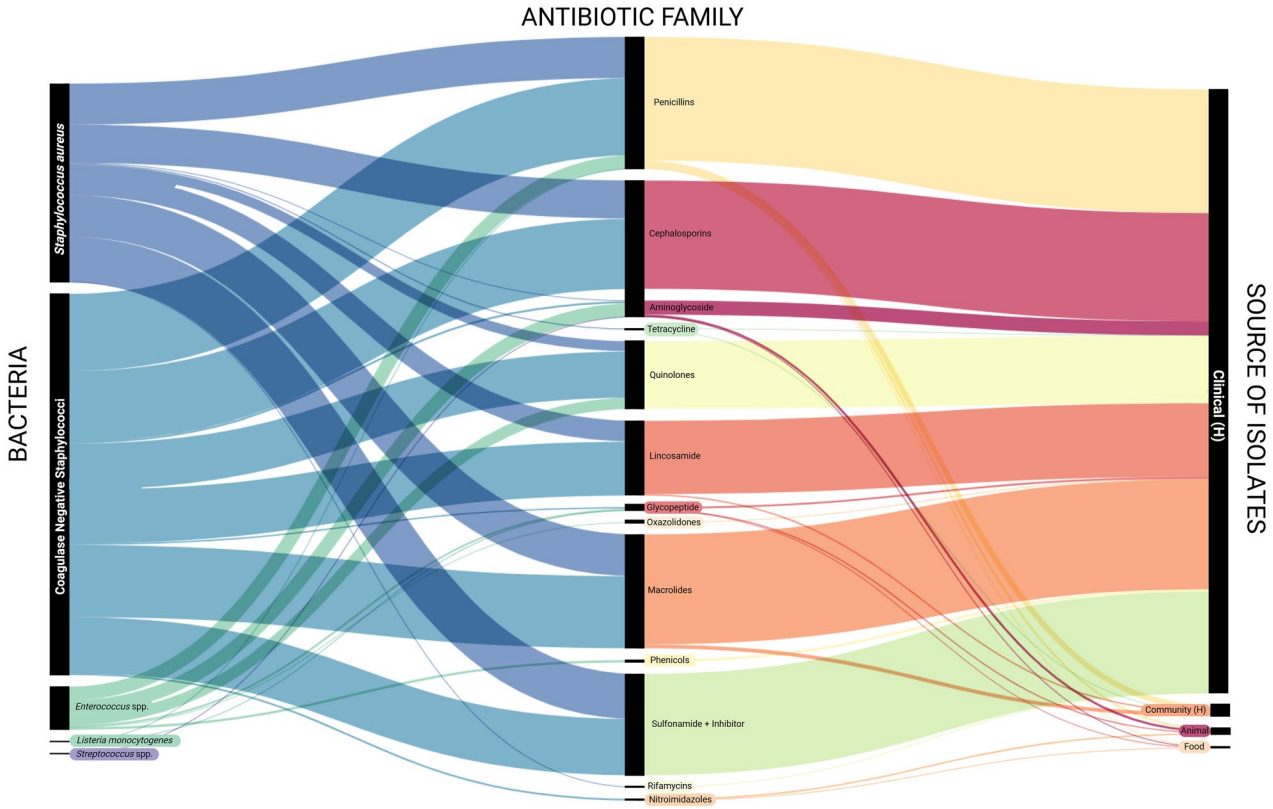

Figure 5. Antimicrobial resistance patterns in Gram-positive bacteria from Ecuador, 2000–2024. Alluvial diagram illustrating the relationship between Gram-positive bacteria species, antibiotic families, and sources of isolation. Flow widths are proportional to the aggregated counts of resistant isolates (n) for each bacterial taxon, antimicrobial family and sample source association across the included studies. Antimicrobial families were positioned on the Central axis to facilitate visualization of the relationships between bacterial taxa and sample sources across the included studies. Flow widths represent the number of studies reporting each association and do not reflect resistance prevalence or isolate frequency.

ceftazidime (*n* = 6,310/42,691 [14.46–15.14] 95% CI), and 13.2% for cefepime (*n* = 5,618/42,691 [12.88–13.52] 95% CI). Ciprofloxacin exhibited the highest resistance among quinolones at 34.8% (*n* = 14,846/42,691 [34.35–35.25] 95% CI;). Tetracycline resistance remained notable at 14.7% (*n* = 6,256/42,691 [14.36–15.04] 95% CI), while gentamicin showed 4.1% resistance (*n* = 1,738/42,691 [3.91–4.29] 95% CI). Carbapenem resistance remained low, with meropenem, imipenem, and ertapenem all ≤0.7%. Resistance was also low for chloramphenicol (2.8%), trimethoprim–sulfamethoxazole (11.6%), and nitrofurantoin (0.4%), while vancomycin, azithromycin, and colistin showed resistance levels below 0.1% (Supplementary Tables S5).

In *Klebsiella* spp., resistance was between 1 and 69.9% for penicillins, 0.8-64% for cephalosporins, and 0.3-37% for carbapenems. In *Salmonella* spp., resistance was 93.26% for aminoglycosides (*n* = 1,010/1,083 [91.77–94.75] 95% CI), 56.2% for tetracyclines (*n* = 609/1,083 [53.28–59.19] 95% CI), 61.59% for quinolones (*n* = 667/1,083 [58.69–64.49] 95% CI), 38.13% for phenicols (*n* = 413/1,083 [35.24–41.03] 95% CI), and 33.8% for sulfonamides (*n* = 366/1,083 [30.98–36.61] 95% CI; Supplementary Table S5).

For *V. parahaemolyticus*, resistance was registered as 96.2% for penicillins (*n* = 178/185 [93.47–98.97] 95% CI), 41.6% for aminoglycosides (*n* = 77/185 [34.52–29.88] 95% CI), and 51.3% for tetracyclines (*n* = 95/185 [44.15–58.55] 95% CI). In *Campylobacter* spp., resistance was 47.9% for tetracyclines (*n* = 211/440 [43.29–52.62] 95% CI) and 57%–70% for quinolones (Supplementary Table S5).

The *A. baumannii* cplx. (Rodríguez et al. 2016; Nuñez Quezada et al. 2017; Sotomayor et al. 2024) exhibited resistance between 54.1-67% for penicillins, 67.9% for cephalosporins (*n* = 1078/1587 [65.63–70.22] 95% CI), 56.1% for carbapenems (*n* = 890/1587 [53.64–58.52] 95% CI), 62.2% for aminoglycosides (*n* = 988/1,587 [59.87–64.64] 95% CI), and 61.8% for quinolones (*n* = 981/1,587 [59.42–64.21] 95% CI). In *P. aeruginosa* (Zurita et al. 2024), resistance was 35.7% for monobactams (*n* = 1,364/3,822 [34.17–37.21] 95% CI) and 32.9% for quinolones (*n* = 1257/3822 [31.40–34.38] 95% CI; Supplementary Table S5).

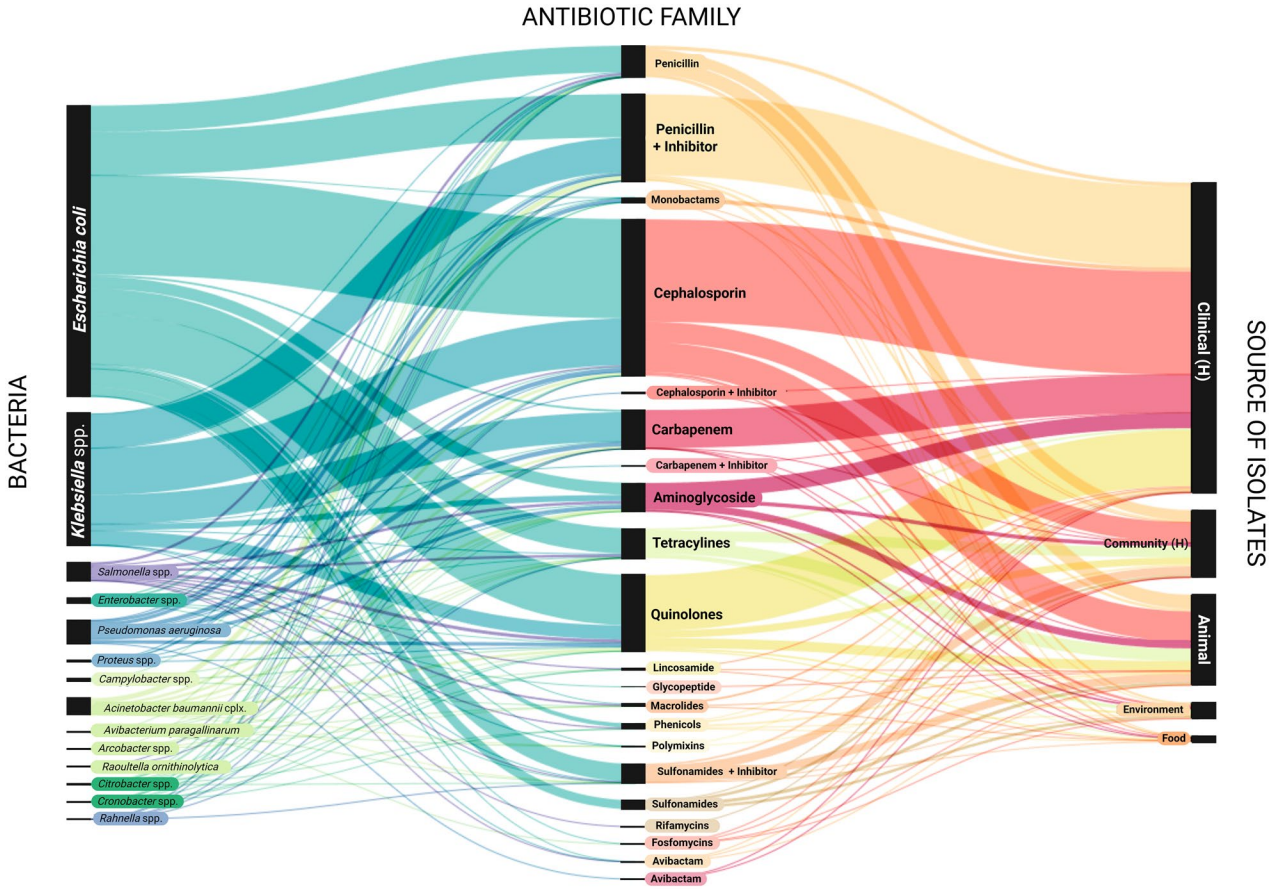

Figure 6. Antimicrobial resistance patterns in Gram-negative bacteria from Ecuador, 2000–2024. Alluvial diagram illustrates the relationships between Gram-negative species, antibiotic families, and sources of isolation. Flow widths are proportional to the aggregated counts of resistant isolates (n) for each bacterial taxon, antimicrobial family and sample source association across the included studies. Antimicrobial families were positioned on the Central axis to facilitate visualization of the relationships between bacterial taxa and sample sources across the included studies.

Resistance in acid-fast bacteria

In *M. tuberculosis* (Mertz et al. 2000; Giacomazzi et al. 2010; López et al. 2022; Morey-León et al. 2022), resistance was 9.4% for rifamycins ($n = 221/2,350$ [8.22–10.58] 95% CI) and 13.1% for first-line antituberculous drugs, including isoniazid, pyrazinamide, ethionamide, and ethambutol ($n = 308/2,350$ [11.74–14.47] 95% CI). Lower resistance was observed for aminoglycosides (0.8%; $n = 20/2,350$ [0.48–1.22] 95% CI) and cephalosporins (0.09%; $n = 2/2,350$ [0–0.2] 95% CI; Tables S5-S6).

Antimicrobial resistance in Ecuador under the WHO BPPL 2024

In our review, the highest resistance was observed in *Klebsiella* sp. to ceftazidime (CTX) and ceftriaxone (CRO) with values of 54.0% and 63.9%, respectively. Next higher values were seen in *A. baumannii* cplx. with 38.5% resistance for meropenem (MEM), *S. aureus* (MRSA) with 37.5% to oxacillin (OXA), and *Salmonella* spp. with 36.6% to ciprofloxacin (CIP). Other species had low frequency of resistant isolates in the categories analyzed with values ranging from 0.16% to 9.4% (Table 1).

Antimicrobial resistance genes (ARGs)

The diversity and frequency of ARGs varied markedly across bacterial species, reflecting both species-specific resistome breadth and the dominance of particular determinants (Figure 7 and Supplementary Table S6). *E. coli* exhibited the widest ARG repertoire, with 12 distinct genes detected. Most isolates carried $bla_{\text{CTX-M}}$, which accounted for 4.9% of the molecular screened population ($n = 1,688/34,051$ [3.92–5.99] 95% CI). In contrast, bla_{TEM} was present in 2.54% ($n = 864/34,051$ [1.49–3.59] 95% CI), while bla_{SHV} contributed only 0.3% ($n = 118/34,051$ [0–1.41] 95% CI). Quinolone resistance was rare, as *qnrB* mutations were identified in 0.1% ($n = 22/34,051$ [0–1.13] 95% CI). Tetracycline resistance was more frequent, with *tetA* detected in 1.7% ($n = 584/34,051$ [0.66–2.77] 95% CI) and *tetB* in 0.7%

Table 1. Resistance proportions, 95% confidence intervals, and WHO bacterial Priority pathogens list (BPPL 2024) classifications for key bacterial pathogens identified in Ecuador between 2000 and 2024.

Bacterial species	Antibiotic	Resistant n/N (%)	95% CI	WHO BPPL 2024 Category
Klebsiella spp.	Meropenem (MEM)	3,730/10,347 (36.0%)	[34.51–37.59]	Critical (carbapenem-resistant, 3GC-resistant)
	Imipenem (IPM)	3,828/10,347 (37.0%)	[35.47–38.53]	
	Ertapenem (ETP)	3,107/10,347 (30.0%)	[28.42–31.64]	
	Ceftriaxone (CRO)	6,619/10,347 (63.9%)	[62.81–65.13]	
	Cefotaxime (CTX)	161/10,347 (1.5%)	[0–3.47]	
	Ceftazidime (CTZ)	5,593/10,347 (54.0%)	[52.75–55.36]	
Escherichia coli	Ceftriaxone (CRO)	9,237/27,641 (33.4%)	[32.46–34.38]	Critical (carbapenem-resistant, 3GC-resistant)
	Cefotaxime (CTX)	4,536/27,641 (16.4%)	[15.33–17.49]	
	Ceftazidime (CTZ)	6,310/27,641 (22.8%)	[21.79–23.86]	
	Meropenem (MEM)	233/27,641 (0.8%)	[0–2.02]	
	Imipenem (IPM)	312/27,641 (1.1%)	[0–2.30]	
	Ertapenem (ETP)	240/27,641 (0.8%)	[0–2.04]	
Acinetobacter baumannii cplx.	Meropenem (MEM)	612/1,587 (38.5%)	[34.71–42.42]	Critical (carbapenem-resistant)
	Imipenem (IPM)	278/1,587 (17.5%)	[13.05–21.99]	
Mycobacterium tuberculosis	Rifampicin (RR)	221/2,350 (9.4%)	[5.56–13.25]	Critical (rifampicin-resistant)
Salmonella spp.	Ciprofloxacin (CIP)	397/1,083 (36.6%)	[31.92–41.40]	High (fluoroquinolone-resistant)
Enterococcus spp.	Vancomycin (VAN)	107/2,130 (5.02%)	[0.88-9.16]	High (vancomycin-resistant *E. faecium*)
Pseudomonas aeruginosa	Meropenem (MEM)	895/3,822 (23.4%)	[20.64–26.19]	High (carbapenem-resistant)
	Imipenem (IPM)	791/3,822 (20.7%)	[17.87–23.52]	
Enterobacter spp.	Cefepime (FEP)	13/1,954 (0.6%)	[0–5.08]	Critical (carbapenem-resistant, 4GC-resistant)
	Meropenem (MEM)	5/1,954 (0.2%)	[0–4.68]	
	Imipenem (IPM)	23/1,954 (1.2%)	[0–5.58]	
	Ertapenem (ETP)	2/1,954 (0.1%)	[0–4.53]	
Staphylococcus aureus	Oxacillin (OXA)	2,817/7,506 (37.5%)	[35.74–39.32]	High (MRSA)
Citrobacter spp.	Cefotaxime (CTX)	58/387 (15%)	[5.80–24.17]	Critical (3GC-resistant)
	Ceftazidime (CTZ)	18/387 (4.6%)	[0–14.38]	
Proteus spp.	Ceftriaxone (CRO)	3/1,829 (0.1%)	[0–4.74]	Critical (3GC-resistant)
	Cefotaxime (CTX)	58/1,829 (3.1%)	[0–7.68]	
	Ceftazidime (CTZ)	18/1,829 (0.9%)	[0–5.54]	

Abbreviations: WHO: World Health Organization; 95% CI: 95% confidence interval, calculated using the proportion method; n/N (%): number of resistant isolates (n) over total isolates tested (N), expressed as a percentage; CRO: ceftriaxone; MEM: meropenem; IPM: imipenem; OFL: oxacillin; VAN: vancomycin; CIP: ciprofloxacin; RR: rifampicin; MRSA: methicillin-resistant Staphylococcus aureus; 3GC: third-generation cephalosporins; cplx.: complex; GLASS: Global Antimicrobial Resistance Surveillance System; BPPL: Bacterial Priority Pathogens List (WHO 2024).

($n = 237/34,051$ [0–1.75] 95% CI), whereas sulfonamide resistance genes appeared sporadically (Figure 7 and Supplementary Table S6).

Klebsiella spp. carried nine distinct ARGs, with a markedly different profile. Carbapenem resistance was predominant, since bla_{KPC} was found in 8.5% of isolates ($n = 867/10,153$ [6.68–10.4] 95% CI). In contrast, bla_{OXA} variants appeared in 0.3% ($n = 34/10,153$ [0–2.28] 95% CI), and bla_{NDM} was limited to 0.07% ($n = 7/10,153$ [0–2.01] 95% CI). The *A. baumannii* cplx. harbored seven ARGs, and its profile was dominated by bla_{OXA}, present in 38.2% of isolates ($n = 605/1,583$ [34.35–42.09] 95% CI), while bla_{GES}, bla_{IMI}, and bla_{SPM} were only rarely detected. *Salmonella* spp. exhibited a narrower profile of four ARGs, with $bla_{CTX\text{-}M}$ universally present in 30.7% of isolates ($n = 283/920$ [25.58–36.14] 95% CI; Figure 7 and Supplementary Table S6).

S. aureus displayed a uniform profile characterized exclusively by *mecA,* which was detected in 9.9% of isolates under molecular characterization ($n = 728/7,335$ [7.75–12.10] 95% CI), consistent with widespread methicillin resistance.

Finally, *M. tuberculosis* showed the broadest mutational diversity, with 13 distinct ARGs identified. The most frequent determinants were *rpoB*, present in 5.9% of isolates ($n = 128/2,144$ [1.87–10.07] 95% CI), followed by *katG* in 5.0% ($n = 108/2,144$ [0.91–9.16] 95% CI). Mutations in the *inhA* promoter accounted for 0.9% ($n = 21/2,144$ [0–5.19] 95% CI). Other ARGs, such as *embB*, *pncA*, *kasA*, and *gid*, occurred at much lower frequencies (Figure 7 and Supplementary Table S6).

Discussion

This study is the first One Health systematic review that comprehensively synthesizes the nationwide evidence of antimicrobial resistance (AMR) in Ecuador, integrating evidence across human, animal, foodborne, and environmental sources. The increasing number of publications after 2015 reflects a growing national awareness of AMR and the gradual consolidation of diagnostic and research capacities. Nevertheless, evidence remains fragmented, heavily concentrated in urban hospital settings from Ecuadorian largest cities (Quito and Guayaquil), and limited by a pronounced underrepresentation of rural, Amazonian, and insular regions. This asymmetry likely reflects the distribution of tertiary-care hospitals, laboratory infrastructure, and research funding, rather than true epidemiological absence (Escobar et al. 2017). Such geographic bias masks potential emerging resistance hotspots in rural and ecologically sensitive zones, particularly where antimicrobials might be used for

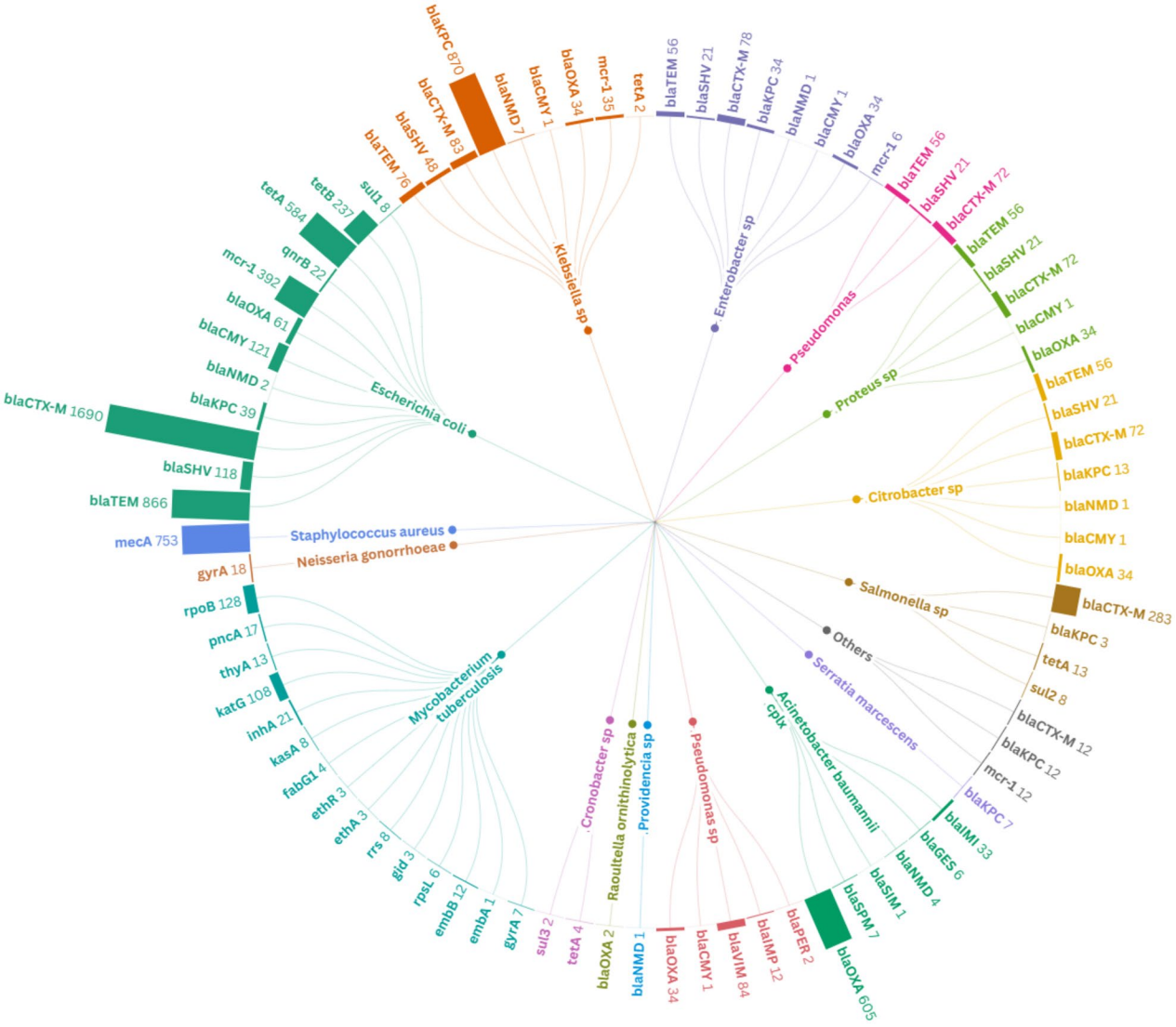

Figure 7. Network of antimicrobial resistance genes detected in bacterial isolates from Ecuador, 2000–2024. The circular layout links bacterial species (inner circle) with the antimicrobial resistance genes (outer circle) identified in the included studies. The barplot of each gene corresponds to the frequency of detection of that gene in the associated species. Numbers next to each gene indicate the count of isolates in which the gene was reported. Data derive from phenotypic–genotypic characterizations performed in clinical, community, animal, foodborne, and.

agriculture and aquaculture purposes that are, of course, poorly regulated (McKernan et al. 2021).

Most included studies focused on human health while animal, foodborne, and environmental sources accounted for less than one-third of the total available evidence in our review, highlighting the lack of integrated cross-sectoral surveillance. Within the human health sector, the predominance of *E. coli* as the most frequently studied organism shows its clinical importance and its utility as a sentinel species for AMR monitoring. Conversely, the limited number of studies addressing non-clinical or community-derived isolates restricts the understanding of transmission pathways between sectors and environments. The predominance of human clinical studies may partly reflect publication and database indexing bias, potentially underestimating evidence from the animal, food, and environmental sectors.

The methodological heterogeneity observed among the studies, where standard antibiogram-based testing predominated and molecular approaches were inconsistently applied, further constrains the comparability of results. Although 55 studies employed PCR, only one implemented whole-genome sequencing (WGS), evidencing a substantial technological gap that hampers the characterization of resistance mechanisms and the identification of genetic linkages across hosts and ecosystems. This methodological limitation is consistent with regional trends in Latin America, where WGS-based AMR surveillance remains scarce outside of pilot research projects (Calero-Cáceres et al. 2023). This

methodological and sectoral variability, further documented in the structured methodological robustness assessment (Supplementary Table S7), highlights the current fragmentation of AMR evidence in Ecuador and reinforces the need for greater methodological standardization in future One Health surveillance studies.

The distribution of sample types also reflects a strong clinical bias, dominated by urine and blood isolates, while food and environmental matrices were infrequently analyzed. This asymmetry reveals a surveillance system primarily focused on healthcare-associated pathogens rather than environmental or community reservoirs that sustain transmission dynamics (Lim et al. 2021). The recurrent detection of *E. coli* and *Salmonella* spp. in both animal and food sources reinforces the role of zoonotic and foodborne pathways in AMR dissemination (Vinueza-Burgos et al. 2016), yet the lack of longitudinal or genomic data prevents inferences about intersectoral connectivity.

The role of the bacterial source in AMR

Our alluvial plots revealed the overwhelming dominance of hospital-derived isolates, reflecting Ecuador's surveillance structure, and introducing a systematic bias toward urban settings with tertiary health centers. *E. coli*, *K. pneumoniae*, and *S. aureus* were the primary bacteria reported, strongly linked to beta-lactams, quinolones, and carbapenems (Zhang et al. 2015; Marusinec et al. 2021; Calderón et al. 2022). By contrast, community-level data remain scarce; however, outpatient infections—particularly urinary tract infections—have shown resistance levels comparable to those reported in urban hospital settings, as demonstrated in our study of ambulatory indigenous women from Otavalo, Imbabura Province (Bastidas-Caldes et al. 2024; Hernández-Alomía et al. 2025). Animal and foodborne sources were less frequent but demonstrated dense links with resistance classes (Moser et al. 2018; Vinueza-Burgos et al. 2019; Ortega-Paredes et al. 2019; Albán et al. 2020; Mitman et al. 2022; Tenea et al. 2023; Amato et al. 2023; Medina et al. 2024; Figures 5 and 6). Poultry isolates of *Salmonella* and *Campylobacter* clustered with quinolone/tetracycline resistance, reflecting historical use of growth promoters (Marusich et al. 1974; Iovine and Blaser 2004; Gouvêa et al. 2015). Multidrug-resistant *Salmonella infantis* in retail meat and resistant *Vibrio* sp. in shrimp highlight that foodborne sources represent underestimated contributors to the AMR burden (Vinueza-Burgos et al. 2016; Mejía et al. 2020).

Gram positive bacteria resistance

In terms of Gram-positive bacteria, our analysis shows that *S. aureus* ($N = 7506$) exhibits high resistance to beta-lactams and folate-pathway inhibitors, with rates of 39.95% to penicillins (including oxacillin), 28.98% to cephalosporins, and 34.79% to sulfonamides, as well as 40.34% to macrolides, and 22.17% lincosamides (Tables S5-S6). This pattern is consistent in magnitude with Ecuador's 2018 national data, showing >30% MRSA among *S. aureus* isolates, ~40% resistance to TMP-SMX and erythromycin, and ~20% to clindamycin, with no reports of vancomycin or linezolid resistance (Satán et al. 2023). Comparable levels have been documented in Argentina (37%; Togneri et al. 2017) and Brazil, where MRSA remains a major nosocomial pathogen driven by *mecA*-dependent beta-lactam resistance.

Community-associated MRSA (CA-MRSA) has been recognized in South America since the early 2000s, when *Panton-Valentine leukocidin* (PVL)-positive *S. aureus* carrying SCCmec IV was first reported in Brazil (Ribeiro et al. 2005). Subsequent studies confirmed CA-MRSA circulation in both hospital and outpatient settings, suggesting overlapping transmission chains between community and healthcare sectors. In Ecuador, accumulating evidence indicates that CA-MRSA is circulating across multiple non-hospital populations, including outpatients, medical students, and even healthcare workers (Bastidas et al. 2019; Baroja et al. 2021). MRSA has been detected in primary care and outpatient settings, as well as among asymptomatic carriers such as medical students and hospital staff, highlighting a blurring boundary between community and healthcare reservoirs and underscoring the need for integrated surveillance beyond hospital-based systems.

Beyond *mecA*, alternative *mec* homologs have emerged in animal reservoirs. The *mecC* gene—sharing ~69% nucleotide identity with *mecA*, was identified in livestock-associated MRSA (LA-MRSA) from dairy cattle in Brazil (Alves et al. 2020), with oxacillin-susceptible yet genotypically resistant (OS-MRSA) isolates. Sporadic reports of *mecB* and *mecC* in CoNS and food-chain isolates indicate a broader environmental reservoir.

Comparatively, CoNS ($N = 6125$) showed higher oxacillin resistance (69.1%), and similar resistance to macrolides (66.87%), lincosamides (49.91%), and sulfonamides (52.24%; Table S5), reflecting their role as reservoirs of transferable resistance determinants (*erm*, *msr*, *dfr*). Vancomycin resistance remains rare (1.36%), but the absence of molecular confirmation (*vanA/B*) in several studies limits the accuracy of prevalence estimates in Ecuador.

Enterococcus spp. presented a low but clinically relevant level of resistance to vancomycin (5%; $n = 107/2130$ [0.88–9.16] 95% CI), consistent with the emerging circulation of VRE in Ecuadorian hospitals (Satán et al. 2023). Although this prevalence remains below the rates reported in Brazil (~33%) and Argentina, where VRE has been described substantially higher frequencies (≥90% in outbreak-associated settings; (Corso et al. 2007), it likely reflects the early establishment of VRE in the country rather than its absence. Most Ecuadorian studies rely on non-standardized or purely phenotypic detection methods (Panesso et al. 2010; Resende et al. 2014), often lacking molecular confirmation of *vanA* or *vanB*, which may underestimate true prevalence. Similar limitations have been described in other Latin American hospital settings where reliance on phenotypic surveillance delayed the recognition of clonal VRE dissemination, which only became evident after the implementation of molecular typing and *vanA* detection during outbreak investigations (Rios et al. 2020). Regionally, *Enterococcus* spp. frequently displays resistance to beta-lactams and aminoglycosides, including high-level gentamicin resistance, particularly among *E. faecalis* lineages. In invasive infections from Argentina, high-level gentamicin resistance was detected in over 40% of *E. faecalis* isolates and in a subset of *E. faecium*, effectively compromising the bactericidal synergy of cell wall-active agents combined with aminoglycosides (Schell et al. 2020). Resistance to linezolid remains rare (1%–2%), but the recent detection of *optrA* and *poxtA* genes in Latin America (Saavedra et al. 2020) highlights the potential for cross-reservoir dissemination.

Gram negative bacteria resistance

Among Gram-negative pathogens, *E. coli* represented the bacterial taxon with the broadest resistance spectrum and ecological distribution across human, animal, and environmental (Braykov et al. 2016; Ortega-Paredes et al. 2020a; Calero-Cáceres et al. 2022a) compartments in Ecuador. Overall resistance reached 30.3% to fluoroquinolones, 18.8 % to third-generation cephalosporins, and sporadic resistance to carbapenems, reflecting patterns aligned with WHO-BBPL2024 reports for Latin America (WHO 2024). The dominance of ESBL-producing *E. coli*—principally mediated by $bla_{\text{CTX-M}}$ variants—was consistent across clinical, animal, and environmental isolates. Nationally, $bla_{\text{CTX-M-55}}$ and $bla_{\text{CTX-M-65}}$ emerged as the most frequent alleles, frequently co-occurring with bla_{TEM} and bla_{SHV} genes (Ortega-Paredes et al. 2020b; Montero et al. 2021). The first clinical detection of the pandemic *E. coli* O25-ST131 clone carrying $bla_{\text{CTX-M-15}}$ was reported in Quito, highlighting the local circulation of globally disseminated lineages (Chiluisa-Guacho et al. 2018). In semirural communities, *E. coli* isolates from humans and domestic animals shared indistinguishable $bla_{\text{CTX-M-55}}$ and $bla_{\text{CTX-M-65}}$ alleles and plasmid replicons, suggesting horizontal gene transfer rather than clonal expansion (Salinas et al. 2019, 2021). Environmental reservoirs amplify this connectivity: ESBL *E. coli* isolated from irrigation waters and fresh products displayed identical $bla_{\text{CTX-M}}$ profiles and multidrug phenotypes, reinforcing the link between wastewater use and foodborne exposure (Calero-Cáceres et al. 2022b; Montero et al. 2021). Parallel studies in small-scale poultry farming showed high cefotaxime resistance in broilers (66.1%) and rising $bla_{\text{CTX-M}}$ prevalence among backyard chickens without direct antibiotic exposure, evidencing farm-to-community spillover (Hedman et al. 2019b). Altogether, these findings position Ecuador as a hotspot of *E. coli*–mediated ESBL dissemination, where multiple $bla_{\text{CTX-M}}$ alleles and plasmid backbones circulate between clinical, animal, and environmental settings under sustained antimicrobial and ecological pressure, a pattern also shown across Latin America (Bastidas-Caldes et al. 2022).

Klebsiella spp. represented one of the major Gram-negative taxa with high multidrug resistance in Ecuador, showing resistance rates between 1% and 69.9% to penicillins, 0.8%–64% to cephalosporins, and 0.3%–37% to carbapenems. These findings align with national surveillance data, where *K. pneumoniae* was identified as the predominant carbapenemase producer, mainly associated with bla_{KPC} genes, followed by *E. coli* and *Enterobacter cloacae* cplx (Satán et al. 2023). Hospital outbreaks in Quito confirmed the endemic circulation of *K. pneumoniae* clones carrying $bla_{\text{KPC-2}}$, predominantly ST258 and ST25, associated with plasmids of the IncFIIK2 and IncR groups, indicating both horizontal and clonal dissemination (Reyes et al. 2021). Further studies from the same healthcare network detected $bla_{\text{KPC-5}}$ and $bla_{\text{KPC-9}}$ variants among ST25, ST258, and ST11 lineages, evidencing sustained multiclonal transmission (Prado-Vivar et al. 2019). These genotypic profiles mirror regional dynamics observed in South America, where *K. pneumoniae* ST258 and ST25 have become dominant epidemic lineages linked to $bla_{\text{KPC-2}}$ and $bla_{\text{KPC-3}}$ dissemination (Chen et al. 2014). Beyond clinical settings, plasmid-mediated colistin resistance (*mcr-1*) has been detected in 19.5% of *K. pneumoniae* isolates from humans and animal reservoirs, carried by IncI2 and IncX4 plasmids, reinforcing the zoonotic and environmental dimension of resistance spread (Bastidas et al. 2023a).

Other important gram-negative bacteria such as *Salmonella spp.* and *A. baumannii* cplx. represented two

key reservoirs of multidrug resistance (Tables S5-6). In *Salmonella spp.*, resistance to tetracyclines reached 56.2 %, suggesting a sustained antimicrobial pressure in animal production chains. These findings are consistent with the high occurrence of *S. infantis* in Ecuadorian poultry, where isolates frequently co-harbored $bla_{\text{CTX-M-65}}$, *tetA*, and *sul1* genes, conferring extensive drug resistant (XDR) phenotypes (Sánchez-Salazar et al. 2020). The predominance of MDR *S. infantis* across animal and environmental matrices supports its epidemiological relevance as a zoonotic and foodborne AMR vector.

In the *A. baumannii* cplx., resistance to penicillins was 54.1%–67%, indicating a broad-spectrum resistance phenotype. Genotypically, this complex harbored seven antimicrobial resistance genes, with a predominance of bla_{OXA} detected in 38.2% of isolates, confirming the central role of oxacillinase-type carbapenemases in regional resistance dynamics. These data align with national surveillance reports showing over 50% carbapenem resistance and the frequent detection of $bla_{\text{OXA-23}}$ and $bla_{\text{OXA-24}}$ among clinical isolates (Satán et al. 2023). The convergence of phenotypic multidrug resistance and bla_{OXA} dissemination in both clinical and environmental *Acinetobacter* populations highlight the environmental persistence of carbapenemase producers and their potential intersectoral spread.

P. aeruginosa remains one of the most clinically relevant non-fermenters due to its intrinsic and acquired multidrug resistance mechanisms. A multicentric study in Quito reported resistance levels above 70% for ciprofloxacin, amikacin, and imipenem/meropenem, and 100% for piperacillin-tazobactam among ICU isolates, far exceeding reference values from the CDC/NHSN network (72.7%–100% vs. 17%–42%; (Amer et al. 2018; Sánchez-Salazar et al. 2020). More recently, a national molecular survey detected bla_{VIM} as the predominant carbapenemase gene (72.7%) among *P. aeruginosa* isolates collected in six hospitals, accompanied by extensive co-resistance to aminoglycosides, fluoroquinolones, and beta-lactams, including ceftolozane/tazobactam (Soria-Segarra et al. 2024). The presence of bla_{VIM}-harboring clones reflects a well-established metallo-β-lactamase circulation pattern similar to that described in other Latin-American countries (Sader et al. 2005), but with a higher degree of multidrug and colistin co-resistance.

Fast acid resistance bacteria

In Ecuador, tuberculosis (TB) remains a major public health concern, with an estimated MDR-TB prevalence of 7%–9% among all TB cases (WHO 2024). Our systematic review found resistance to rifampicin and isoniazid in 5.2% [0.88–9.12] 95% CI of *M. tuberculosis* isolates, consistent with molecular surveys showing *rpoB* mutations in 92%–94% of rifampicin-resistant strains or *inhA* C(-15)T mutations in over 80% of isoniazid-resistant isolates (Franco-Sotomayor et al. 2019; Zurita et al. 2019a). The predominance of these canonical substitutions indicates a high degree of mutational convergence, similar to that reported across Latin America, yet novel variants such as *katG* Thr314Ala and Thr324Ser have also emerged locally, underscoring ongoing microevolutionary adaptation of Lineage 4 genotypes. Nationwide genotyping studies revealed that Lineage 4 accounts for ≈98% of Ecuadorian isolates, dominated by LAM (45%) and Haarlem (32%) sublineages, both significantly associated with MDR-TB, whereas the hypervirulent Beijing lineage remains rare (≤2%), in contrast to neighboring Colombia and Peru (Garzon-Chavez et al. 2019, 2020).

Despite the availability of molecular diagnostics (GeneXpert MTB/RIF), the persistence of MDR-TB hotspots and the detection of novel *katG* variants highlight diagnostic blind spots and the urgent need for expanded genomic surveillance integrating WGS and mutation tracking within the national TB control strategy. In recent years, TB incidence in Ecuador has shown a worrying resurgence, strongly linked to the structural weakening of the public health system, budgetary underfunding, and reduced access to diagnostic and treatment programs (Ortiz-Prado et al. 2024). In addition, the current security crisis and chronic prison overcrowding, conditions that favor transmission in confined environments, pose an imminent risk of amplifying the national TB burden and reversing previous control achievements.

One health implications

Antimicrobial resistance in Ecuador exemplifies the complexity of an ecosystem where clinical, agricultural, and environmental pressures converge (Yamamoto et al. 2019). High AMR values in foodborne and environmental isolates point to contamination gradients driven by agricultural runoff, waste mismanagement, and human effluents (Abosse et al. 2024; Ugoeze et al. 2024; Naznine et al. 2025). When interpreted alongside genotypic findings, such as the pervasive $bla_{\text{CTX-M}}$, *mcr-1*, and bla_{OXA} determinants, these data reveal an interconnected resistome shaped by overlapping anthropogenic activities rather than isolated clinical phenomena.

Eventhough having surveillance networks to track antibiotic resistance such as tertiary hospital network, Ecuador's AMR surveillance remains fragmented and

predominantly hospital-based, leaving major ecological and production systems underrepresented. The veterinary, food safety, and environmental sectors lack consistent monitoring frameworks and standardized reporting pipelines, resulting in substantial data asymmetry between human and non-human domains (Figures 3, 5 and 6). This fragmentation obscures early warning signals of emerging resistance, particularly at the human–animal–environment interface where genetic exchange is most active (Bengtsson-Palme et al. 2023; Al-Khalaifah et al. 2025).

The public health and economic implications are significant. Intensive poultry, shrimp, and swine production systems, key components of Ecuador's economy (Pacheco et al. 2018; Bastidas et al. 2023b), operate with limited antimicrobial stewardship and minimal laboratory oversight. The detection of resistant zoonotic pathogens within these industries, coupled with sporadic identification of ARGs in environmental reservoirs, signals the potential for silent amplification and feedback into human populations. Addressing these vulnerabilities requires expanded surveillance coverage and regulatory coordination across ministries of health, agriculture, and environment.

The forthcoming National AMR Plan (2025–2030) represents a critical opportunity to operationalize an integrated One Health architecture. Achieving this goal will depend on three complementary actions: (i) extending AMR surveillance beyond hospitals to include veterinary, aquaculture, and environmental laboratories; (ii) adopting genomic tools and harmonized AST methodologies; and (iii) establishing a centralized data-sharing platform that links clinical and non-clinical networks. Alignment with WHO GLASS standards would enhance Ecuador's regional comparability, while the prioritization of high-risk pathogens anchors national priorities within the global AMR agenda.

Limitation of the study

Despite the systematic search strategy and predefined inclusion criteria, publication bias is likely, as unpublished data and governmental surveillance reports were not always accessible, harmonized, or publicly available. In addition, substantial heterogeneity in laboratory methodologies may have affected the comparability of resistance estimates across studies. Antimicrobial susceptibility testing approaches ranged from disk diffusion to automated systems, with variable adherence to international standards such as CLSI or EUCAST. Importantly, interpretative criteria have evolved over time: breakpoints that were previously classified as "susceptible" under older guidelines may currently fall within intermediate or resistant categories, or vice versa, potentially influencing temporal comparisons.

While such methodological updates are more tightly controlled in clinical microbiology laboratories, our systematic review revealed that studies conducted in animal, environmental, and food matrices frequently employed non-standardized methodologies, including inappropriate antibiotic panels, disk concentrations, or interpretative criteria for specific microorganisms. These inconsistencies likely introduce additional bias and may lead to either over- or underestimation of resistance in non-clinical settings.

The methodological heterogeneity summarized in Supplementary Table S7 also limited direct quantitative comparisons across studies. While pathogen- or sector-specific analyses may provide additional insights, they require dedicated analytical frameworks and were beyond the predefined objectives and scope of the present nationwide One Health review. Such focused analyses represent an important direction for future research.

Furthermore, molecular analyses were applied inconsistently: only approximately half of the studies incorporated PCR-based confirmation of resistance determinants, and only one study employed whole-genome sequencing, limiting in-depth genetic characterization, clonal inference, and assessment of horizontal gene transfer. Geographically, the predominance of studies conducted in urban hospital settings resulted in underrepresentation of rural, Amazonian, and coastal–aquatic ecosystems, potentially masking resistance dynamics in ecologically and epidemiologically relevant reservoirs (Torres-Espín & Bastidas-Caldes, 2026). Finally, data spanning more than two decades were pooled, and this temporal breadth must be considered when interpreting the findings, as diagnostic capacities, laboratory standards, and epidemiological contexts have changed substantially over time. Despite these limitations, this synthesis provides a robust, transversal, and integrative overview of antimicrobial resistance in Ecuador, offering a comprehensive One Health perspective and identifying concrete priorities for future genomic, environmental, and community-based surveillance.

Conclusions

This systematic review demonstrates that antimicrobial resistance research in Ecuador remains overwhelmingly centered on the human health sector, with animal, foodborne, and environmental compartments markedly underrepresented. This imbalance constrains a

comprehensive understanding of AMR ecology and underscores the urgent need to expand surveillance across non-clinical reservoirs where resistance may emerge, persist, and spill back into human populations. Among the pathogens most frequently reported, *E. coli*, *K. pneumoniae*, *S. aureus*, *Salmonella* spp., *A. baumannii* cplx., *P. aeruginosa*, and *M. tuberculosis* accounted for the highest resistance burdens. Notably, several of these organisms such as carbapenem-resistant *K. pneumoniae*, third-generation cephalosporin–resistant *E. coli*, carbapenem-resistant *A. baumannii* cplx., fluoroquinolone-resistant *Salmonella* spp., and rifampicin-resistant *M. tuberculosis,* correspond to pathogens classified as critical or high priority in the WHO BPPL, highlighting their strategic relevance for national and regional AMR control. The recurrent detection of multidrug-resistant *Salmonella*, particularly *S. Infantis*, across animal, food, and environmental matrices reinforces its role as a zoonotic reservoir of resistance determinants, bridging production systems and human exposure pathways. Tuberculosis further exemplifies the genomic complexity of resistance in Ecuador, where multiple canonical and emerging mutations underpin MDR-TB persistence, emphasizing the need for expanded molecular and genomic surveillance. Similarly, the *A. baumannii* complex emerged as a major reservoir of broad-spectrum resistance, with widespread bla_{OXA} dissemination, reflecting its capacity to persist across clinical and environmental niches. Collectively, this One Health study reveals an interconnected resistome shaped by anthropogenic pressures across sectors and supports the adoption of an integrated surveillance strategy that prioritizes critical pathogens, strengthens non-human monitoring, and incorporates genomic tools to anticipate and mitigate AMR emergence in Ecuador.

Acknowledgments

The author acknowledges Universidad Espíritu Santo (UEES) for institutional support, including salary funding and support for article processing charges.

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CRediT: **Carlos Bastidas-Caldes**: Conceptualization, Formal analysis, Investigation, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing; **Fernanda Hernández-Alomía**: Formal analysis, Investigation, Methodology, Writing – original draft; **Francisco Bolaños**: Investigation, Methodology, Validation, Visualization; **Emily Cisneros-Vásquez**: Data curation, Formal analysis, Investigation; **Daniel Romero-Alvarez**: Investigation, Validation, Writing – original draft, Writing – review & editing.

Disclosure statement

The authors declare that there are no financial or non-financial competing interests associated with this work.

Funding

This research received no external funding.

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Data availability statement

No new data were generated or analyzed in this study. All data supporting the findings of this systematic review are available within the article and its supplementary materials.

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