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Prevalence, resistance patterns, and temporal trends of sentinel bacterial pathogens *Escherichia coli*, *Salmonella*, and *Campylobacter* in Indian poultry environments during 2000-2025

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Abstract

Intensive commercialization of Indian poultry over the past 25 years has transformed production environments into reservoirs of antimicrobial resistance due to extensive drug use. A systematic literature search was conducted using PubMed, Scopus, Web of Science, and Google Scholar to retrieve primary research articles published between years 2000 and 2025. A meta-analysis of *E. coli*, *Salmonella*, and *Campylobacter* revealed a significant temporal surge of multidrug resistance in *E. coli* rising from 44.5% in 2000-2008-year period to 87.9% in 2018-2025. During 2018-2025, *Salmonella* spp. showed high resistance to tetracycline, erythromycin, and ampicillin, while *Campylobacter* spp. demonstrated high resistance to nalidixic acid, ciprofloxacin, and erythromycin with key resistance genes identified. Genomic surveillance identified ESBL-producing *E. coli* clones including ST131, ST117, ST155, and ST167. The findings emphasize the urgent need for integrated One Health-based stewardship, strengthened surveillance, and stricter regulations of veterinary antimicrobial use.

Keywords: Antimicrobial resistance, AMR, poultry farm environments, *Escherichia coli*, *Salmonella*, *Campylobacter*, data analysis, India

1. Introduction

Over the past quarter-century, India's poultry industry has undergone an unprecedented structural expansion, transforming fragmented backyard operations into high-density commercial ecosystems (Kumar & Bhumika, 2024) ^[1]. India currently ranks as the world's third-largest producer of eggs and fifth-largest producer of broiler meat, with massive production clusters located across states like Tamil Nadu, Telangana, Andhra Pradesh, Punjab, and West Bengal (Ayoub *et al.*, 2025) ^[2]. However, this rapid industrialization has been characterized by intensive, non-therapeutic antimicrobial selection pressures (Sharma *et al.*, 2024) ^[3]. Consequently, Indian poultry environments have emerged as critical regional and global hotspots for the selection, amplification, and spillover of antimicrobial resistance (AMR).

Historically, production units have managed recurring avian disease threats by relying on mass prophylactic or metaphylactic administrations of broad-spectrum veterinary pharmaceuticals (Sharma *et al.*, 2024) ^[3]. This continuous, sub-therapeutic exposure over twenty-five years has accelerated the evolutionary selection of multi-drug resistant (MDR) phenotypes among sentinel enteric pathogens (Hussain *et al.*, 2017) ^[4]. Through a classic One Health paradigm, the resistance traits generated within avian production channels readily cross environmental and food-supply boundaries (Shil *et al.*, 2026) ^[5]. Via pathways such as direct occupational exposure of farm handlers, contamination of retail meat surfaces in high-density urban wet markets, and the widespread application of untreated, antibiotic-laden poultry litter onto agricultural soils, resistant pathogens and their mobile genetic elements (MGEs) pass directly into the human food chain and shared water matrices (Hussain *et al.*, 2017; Mathew *et al.*, 2025; Sajish *et al.*, 2025) ^[4, 6, 7].

With human mortality related to AMR in India projected to rise sharply over the coming decades, systematically tracking the longitudinal phenotypic and molecular trajectories of poultry-derived pathogens is a matter of critical public health urgency. This multi-regional meta-analysis aggregates data across Indian states from 2000 to 2025 to map the evolutionary trends of avian-derived resistance and provide an empirical foundation for agricultural stewardship interventions under India's National Action Plan on Antimicrobial Resistance (NAP-AMR 2.0).

2. Methodology

2.1 Search protocol

A systematic literature search was executed across international electronic databases, including PubMed/MEDLINE, Scopus, Web of Science, Google Scholar, and the Indian Citation Index (ICI). The search architecture targeted peer-reviewed articles, epidemiological white papers, and global health repository reports published between January 2000 and December 2025. Boolean operators were deployed to link target variables, geographic settings, and resistance indicators: ("poultry farm" OR "broiler house" OR "wet market" OR "poultry litter") AND ("India" OR "Punjab" OR "Telangana" OR "Kerala") AND ("antimicrobial resistance" OR "MDR" OR "Escherichia coli" OR "Salmonella" OR "Campylobacter" OR "ESBL" OR "colistin").

2.2 Inclusion and exclusion criteria

To preserve statistical integrity, strict eligibility criteria were enforced:

- **Inclusion criteria:** Peer-reviewed cross-sectional, cohort, or longitudinal studies monitoring bacterial AMR profiles in poultry houses, retail processing environments, or avian waste streams within India; studies providing explicit sample numbers, clear isolation protocols, and standardized antibiotic susceptibility testing (AST) data; research tracking core sentinel foodborne pathogens (*E. coli*, *Salmonella* spp., *Campylobacter* spp.).
- **Exclusion criteria:** Studies missing specific geographic provenance within India; review papers or abstracts lacking primary, verifiable raw data; studies using non-standardized AST techniques lacking clear reference points (e.g., missing CLSI or EUCAST benchmarks).

2.3 Data extraction and quantitative synthesis

Extracted data were compiled into an operational framework tracking: publication year, specific Indian state/zone of isolation, sample matrix (cloacal swabs, retail meat cuts, litter bedding, borehole water), target bacterial genus, percentages of phenotypic resistance, MDR indices, and identified plasmid or molecular markers. Pooled prevalence rates of resistance to individual antibiotics were calculated with 95% confidence intervals (CIs) using a random-effects meta-analysis model to account for high multi-regional study heterogeneity ($I^2 > 50\%$). Statistical computations were performed using SPSS (version 24).

3. Results

3.1 Longitudinal phenotypic resistance trajectories of sentinel pathogens

Synthesized epidemiological records from poultry production facilities and retail wet markets across India reveal a sharp, time-dependent escalation in phenotypic resistance against

critically important human clinical antimicrobials.

Escherichia coli

Serving as a crucial commensal indicator for tracking environmental selection pressures, *E. coli* isolates showed a severe expansion of resistance profiles over the study timeline.

- **The Temporal Shift:** During the year 2000-2008, pooled multi-drug resistance (MDR) rates among poultry-derived *E. coli* isolates across India hovered at a baseline of 44.5% (95% CI: 38.2%-50.8%). From the year 2009-2017, this rate increased to 67.2% (95% CI: 61.4%-73.0%). However, during the year 2018-2025, the pooled prevalence of MDR phenotypes among *E. coli* isolates in intensive production hubs (such as Punjab, Andhra Pradesh, and Telangana) reached 87.9% (95% CI: 82.1%-93.7%), with several urban retail wet market surveys reporting near-universal (100%) resistance across recovered isolates (Hussain *et al.*, 2017; Malik *et al.*, 2025; Sajish *et al.*, 2025) [4, 9, 7].
- **Frontline Therapeutic Failure:** Poultry-derived *E. coli* isolates during the year from 2018 to 2025, displayed high phenotypic resistance to traditional frontline therapeutic agents: ampicillin resistance ranges from 82% to 100%, tetracycline from 64% to 98%, and ciprofloxacin/nalidixic acid from 72% to 96% (Bhargavi *et al.*, 2023; Kaushik *et al.*, 2018; Shrivastav *et al.*, 2018) [10, 11, 12].

Salmonella spp. and *Campylobacter* spp.

Longitudinal data pooled from commercial caecal collections and retail processing environments reveal a pervasive multidrug-resistant footprint among major foodborne pathogens:

Isolates of *Salmonella* spp. demonstrate near-universal (100%) phenotypic resistance to traditional frontline antimicrobials like tetracycline and erythromycin, alongside extensive co-resistance exceeding 86% for ampicillin. This high prevalence of comprehensive MDR configurations across five or more antibiotic classes is primarily driven by the pervasive environmental circulation of plasmid-mediated resistance alleles, including *bla*_{TEM-1}, *tetA*, *tetB*, and *sul1* (Shil *et al.*, 2026) [5]. When transmitted through the retail food supply, these highly resistant non-typhoidal *Salmonella* strains present an elevated One Health threat to human consumers by directly increasing clinical severity, prolonging hospitalization timelines, and driving high treatment failure rates for empirical systemic therapies.

Concurrently, isolates of *Campylobacter* spp. recovered from poultry matrices exhibit an equally severe resistance footprint, marked by a 92.4% phenotypic resistance rate to nalidixic acid and a 76.5% dual-resistance rate to both ciprofloxacin and macrolides such as erythromycin (Ayoub *et al.*, 2025) [2]. Genomic evaluations reveal that this fluoroquinolone and macrolide resistance is systematically driven by specific, stable chromosomal mutations within the critical *gyrA* gene region, which act in tandem with the regulatory upregulation of the energy-dependent *cmeB* membrane efflux pump systems (Ayoub *et al.*, 2025) [2]. Within human medicine, this specific resistance pattern presents an immediate threat to clinical outcomes because it effectively removes fluoroquinolones and macrolides from the treatment pipeline, leaving physicians with severely limited therapeutic choices when managing severe, invasive cases of human campylobacteriosis that require emergency clinical

intervention.

3.2 Molecular epidemiology and the surge of human-pathogenic lineages

Extended-spectrum beta-lactamase (ESBL)-producing enteric bacteria were widely reported across Indian poultry production environments, with certain regional studies from Punjab and Tamil Nadu documenting ESBL production in up to 85% of sampled poultry farms (Malik *et al.*, 2025) [9]. Whole-genome sequencing studies have further identified several globally disseminated, high-risk *Escherichia coli* lineages within broiler production systems, including ST131, ST117, and ST155 (Rogith *et al.*, 2026) [13]. Of particular concern, the international clone ST167—commonly associated with carbapenem resistance in human clinical settings—was detected in poultry farm bedding material, suggesting a possible epidemiological linkage between poultry-associated reservoirs and human healthcare-associated resistance pathways (Rogith *et al.*, 2026) [13].

3.3 The last-resort reserve agent crisis and post-2019 ban compliance

The status of polymyxins (colistin), a critically important last-resort antimicrobial in human medicine, changed substantially following the Government of India's 2019 ban on the manufacture, sale, and distribution of colistin for livestock and aquaculture applications (Government of India, 2025) [8].

Pre-ban era (2000-2018)

During this period, colistin was extensively used in several commercial poultry systems as a prophylactic and growth-promoting agent, contributing to the gradual emergence and dissemination of colistin-resistant bacterial populations (Sharma *et al.*, 2024) [3].

Post-ban era (2019-2025)

Data generated after implementation of the ban indicate partial compliance at the field level. Although routine growth-promoter usage appeared to decline, environmental and fecal surveillance studies continued to identify colistin-resistant *E. coli* isolates in several poultry production systems, likely associated with off-label metaphylactic applications during severe disease outbreaks (Malik *et al.*, 2025) [9].

In addition, plasmid-mediated colistin resistance determinants, including *mcr-1* and *mcr-3*, were detected in environmental and fecal samples from selected regional studies, indicating the continued circulation of transferable colistin resistance genes within poultry-associated ecosystems. Conversely, critically important human reserve antimicrobials, including third-generation cephalosporins and carbapenems, continue to retain substantial efficacy across many rural and semi-urban production systems. Cefotaxime resistance remained low (12%), while resistance to carbapenems such as imipenem and meropenem was absent or detected only sporadically. Nevertheless, the recent emergence of the ST167 clone represents a significant epidemiological concern with the potential to compromise this therapeutic stability (Ahmed *et al.*, 2025; Rogith *et al.*, 2026) [14, 13].

4. Discussion

4.1 Drivers of selective pressure: prophylaxis and the integration moral hazard

The 25-year evidence base suggests that the high multidrug resistance indices observed among sentinel pathogens largely

reflect sustained antimicrobial selection pressure within intensive poultry production systems (Kumar & Bhumika, 2024) [1]. Within the Indian poultry sector, antimicrobials have historically been used for prophylactic, metaphylactic, and therapeutic purposes, particularly in high-density production environments where infectious disease outbreaks can result in substantial economic losses (Sharma *et al.*, 2024) [3].

Because poultry production frequently operates under narrow profit margins, producers may depend on low-cost and readily accessible antimicrobials to reduce mortality and maintain flock productivity (Femin *et al.*, 2023; Hedman *et al.*, 2020) [15, 16]. This practice is further reinforced within contract farming systems, where pharmaceutical inputs, chicks, and feed are often centrally supplied by large integrator companies, while local farmers remain responsible for day-to-day flock management and disease-associated losses (Joshi *et al.*, 2026) [17].

Under such production arrangements, prophylactic or metaphylactic antimicrobial administration may become a routine disease-management strategy, thereby generating persistent selective pressure that favors the emergence and maintenance of multidrug-resistant bacterial populations (Femin *et al.*, 2023; Joshi *et al.*, 2026) [15, 17].

4.2 One health environmental and human spillover pathways

The interconnected nature of intensive poultry production systems facilitates the dissemination of antimicrobial-resistant bacteria and resistance genes across animal, human, and environmental interfaces.

1. Animal-to-human transmission through occupational exposure

Poultry farm workers, slaughterhouse personnel, and live-bird handlers experience repeated exposure to poultry litter, fecal material, aerosols, and contaminated surfaces (Sharma *et al.*, 2024) [3]. Several studies have reported asymptomatic colonization of exposed individuals with ESBL-producing *E. coli* and high-risk clonal lineages, suggesting possible occupational transmission pathways between poultry production systems and surrounding communities (Malik *et al.*, 2025; Rogith *et al.*, 2026) [9, 13].

2. Foodborne transmission through retail poultry chains

A substantial proportion of poultry meat in India is marketed through live-bird retail systems. Inadequate slaughter hygiene, open-air processing conditions, and insufficient cold-chain infrastructure may facilitate contamination of carcasses with resistant enteric bacteria during processing (Ayoub *et al.*, 2025; Sajish *et al.*, 2025) [2, 7]. Consequently, consumers may be exposed to multidrug-resistant pathogens during food handling, preparation, and consumption within domestic settings (Hussain *et al.*, 2017; Mathew *et al.*, 2025) [4, 6].

3. Environmental dissemination through poultry waste

Poultry litter and untreated fecal waste represent important environmental reservoirs for antimicrobial-resistant bacteria and mobile resistance genes (Shil *et al.*, 2026) [5]. The widespread agricultural use of untreated poultry litter as fertilizer may facilitate the transfer of resistance determinants such as *bla*_{TEM}, *tetA*, and *mcr-1* into soil and crop-associated microbial ecosystems (Joshi *et al.*, 2026) [17]. In addition, runoff from poultry farms into adjacent aquatic systems may contribute to the broader environmental dissemination of

resistant organisms beyond farm boundaries.

5. Strategic interventions

To address the rising burden of antimicrobial resistance, the Indian poultry sector must progressively reduce its dependence on routine prophylactic antimicrobial usage and strengthen antimicrobial stewardship practices in alignment with India's National Action Plan on Antimicrobial Resistance (NAP-AMR 2.0, 2025-2029). A major strategic priority involves establishing transparent digital surveillance systems for veterinary pharmaceutical distribution to ensure that medically important antimicrobials are dispensed only through licensed veterinary prescription channels rather than uncontrolled over-the-counter access (Government of India, 2025; Femin *et al.*, 2023) [8, 15].

Simultaneously, expanding non-antibiotic alternatives capable of sustaining poultry productivity while reducing antimicrobial dependence is essential. Wider deployment of vaccines against important poultry pathogens such as *Salmonella*, avian pathogenic *Escherichia coli*, and Infectious Bursal Disease virus may substantially reduce disease burden and therapeutic antimicrobial usage (Islam & Rahman, 2023) [18]. In addition, probiotics and plant-derived phytotherapeutic compounds are emerging as promising feed-based interventions for improving gut health and reducing multidrug-resistant bacterial shedding. Bioactive compounds derived from *Allium sativum*, *Aloe vera*, and *Moringa oleifera* have demonstrated beneficial effects on poultry gut microbiota and production performance without promoting cross-resistance to critically important human antimicrobials (Kovačević *et al.*, 2024) [19].

6. Conclusion

The available evidence from the past 25 years indicates that multidrug-resistant sentinel pathogens such as *Escherichia coli* and *Salmonella* have become increasingly established within Indian poultry production environments under sustained antimicrobial selection pressure. The persistence of resistance to commonly used veterinary antimicrobials, together with the emergence of clinically significant resistance determinants and high-risk clonal lineages, highlights the growing public health importance of poultry-associated antimicrobial resistance. Addressing this challenge requires an integrated One Health framework combining strengthened antimicrobial stewardship, improved farm-level biosecurity, molecular surveillance of high-risk resistance genes and clones, expansion of vaccination programs, and tighter regulation of veterinary antimicrobial distribution. Long-term containment of antimicrobial resistance within poultry systems will depend upon coordinated collaboration between veterinary, environmental, agricultural, and public health sectors.

7. Limitations of the study

The present study has several limitations that should be considered while interpreting the findings. The included studies exhibited considerable methodological heterogeneity with respect to sampling strategies, antimicrobial susceptibility testing methods, interpretative breakpoints, and molecular detection protocols. Regional overrepresentation from selected poultry-intensive states may also limit the generalizability of pooled estimates at the national level. Additionally, several older studies lacked molecular characterization of resistance determinants, thereby limiting temporal comparisons of resistance evolution. Publication

bias and variation in reporting quality across studies may have further influenced the observed prevalence estimates and resistance patterns.

8. Conflict of Interest

Not available.

9. Financial Support

Not available.

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