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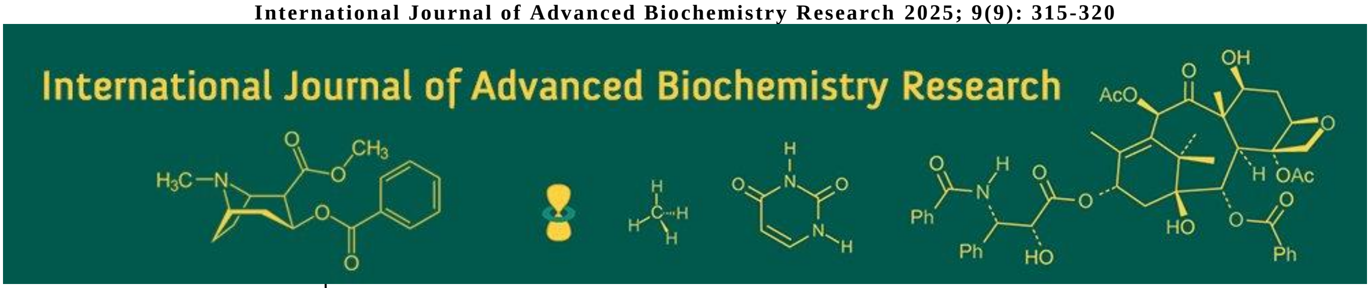

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Meta-analytic assessment of antimicrobial resistance in animals in India across five priority bacterial pathogens

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Abstract

Antimicrobial resistance (AMR) has emerged as a critical global health concern, threatening both human and animal health, and undermining the effectiveness of available treatment options. In veterinary medicine, the problem is particularly alarming in countries like India, where livestock, poultry, and companion animals constitute a significant part of the agricultural and domestic ecosystem and serve as potential reservoirs of resistant bacterial pathogens. The indiscriminate and often unregulated use of antibiotics for therapeutic, prophylactic, and growth-promoting purposes has further accelerated the selection pressure, contributing to the widespread dissemination of resistant strains. This meta-analytic study was conducted to systematically estimate the pooled prevalence of AMR among five priority bacterial pathogens of veterinary importance, namely *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Salmonella enterica*, and *Pseudomonas aeruginosa*, isolated from different animal sources across India. A comprehensive search of published literature was carried out using electronic databases and institutional repositories to identify relevant studies reporting resistance patterns. The findings of this study highlight considerable variation in resistance levels across bacterial species and antibiotic categories, with multidrug resistance (MDR) emerging as a major concern in veterinary pathogens. Overall, this study provides robust pooled evidence of the burden of AMR in animal-associated bacterial pathogens in India.

Keywords: Antimicrobial resistance, meta-analysis, MDR, veterinary medicine

Introduction

Antimicrobial resistance (AMR) is widely recognized as one of the greatest threats to global health, food security, and sustainable development in the 21st century. The World Health Organization (WHO) has identified AMR as one of the top ten global public health threats, with profound implications for both human and veterinary medicine (Kumari *et al*., 2021) [10]. The growing ineffectiveness of antimicrobial drugs jeopardizes the ability to treat common infections, increases morbidity and mortality, and imposes significant economic burdens on healthcare and agricultural systems worldwide (Singh *et al*., 2019; Kumar *et al*., 2021) [15, 9]. In the veterinary sector, the consequences of AMR are twofold: reduced therapeutic efficacy in animals, leading to poor clinical outcomes, production losses, and compromised animal welfare, and heightened risk of zoonotic transmission to humans, either through direct animal contact or indirectly via the food chain (Patel *et al*., 2025; EFSA, 2025) [13, 7]. These challenges are particularly acute in low-and middle-income countries (LMICs), such as India, where surveillance systems are fragmented, regulatory enforcement is weak, and antibiotic stewardship is insufficient (Chakraborty *et al*., 2024) [5].

India represents a unique and urgent case study in veterinary AMR for several reasons. First, it is one of the world's largest producers and consumers of antibiotics in food animals, with particularly high usage reported in the poultry and dairy sectors (Chakraborty *et al*., 2024) [5]. Antimicrobials are widely employed not only for therapeutic purposes but also for prophylaxis, meta-phylaxis, and growth promotion (Thakur and Panda, 2017) [20]. Such practices have generated substantial selective pressure for the emergence and persistence of resistant bacterial populations in animal hosts. Second, India has one of the highest livestock densities globally, further increasing opportunities for bacterial transmission within and between herds, flocks, and human populations (Sonavale *et al*., 2020) [16].

Several studies from India illustrate the extent of the problem. *Escherichia coli* and *Staphylococcus aureus* isolates from bovine mastitis cases frequently exhibit multidrug resistance (MDR), limiting treatment options for dairy farmers (Kumari *et al*., 2021; Kumar *et al*., 2021) [10, 9]. In poultry, *Salmonella enterica* is increasingly reported as resistant to fluoroquinolones and cephalosporins, which are categorized as critically important antimicrobials (CIAs) for human medicine (Inbaraj *et al*., 2022) [8]. *Klebsiella pneumoniae*, particularly from companion animals, has emerged as a reservoir of extended-spectrum β-lactamase (ESBL)-producing strains (Banerjee *et al*., 2020) [3], while the detection of carbapenemase-producing *Enterobacterales* in dogs and cats signals a worrying overlap with resistance profiles observed in human clinical pathogens (Bandyopadhyay *et al*., 2021) [2] Additionally, *Pseudomonas aeruginosa*, a common opportunistic pathogen in animals, demonstrates resistance to multiple drug classes, further complicating treatment (Sowmya *et al*., 2024) [17].

When viewed globally, India's AMR situation in animals reflects trends observed in other LMICs, yet with distinctive challenges. The European Food Safety Authority (EFSA) reports high levels of resistance in commensal *E. coli* from poultry flocks across Europe, but unlike India, stringent antimicrobial stewardship policies and routine surveillance programs are in place (EFSA, 2025) [6]. In contrast, countries in Africa and Southeast Asia show patterns of widespread, unregulated antimicrobial use similar to India (Malik *et al*., 2023) [12]. The United States has restricted the use of medically important antimicrobials in food-producing animals through the U.S. Food and Drug Administration (FDA), demonstrating the impact of policy interventions in reducing selection pressure (Malik *et al*., 2023) [12]. These global comparisons underscore the urgent need for India to adopt harmonized AMR surveillance systems, promote rational antimicrobial use, and implement One Health-based strategies.

Against this backdrop, the present study undertakes a systematic literature and meta-analysis of AMR in veterinary pathogens in India over the past two decades (2000-2025). Specifically, the analysis focuses on five priority bacterial pathogens of veterinary and public health significance—*Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Salmonella enterica*, and *Pseudomonas aeruginosa*. These organisms are consistently associated with important animal diseases such as mastitis, colibacillosis, salmonellosis, wound infections, and systemic opportunistic infections, while also posing a substantial risk of zoonotic spillover to humans (Rao *et al*., 2023) [14]. By synthesizing existing evidence, this meta-analysis aims to generate pooled prevalence estimates of AMR in animal-origin bacteria in India, thereby providing an evidence base for veterinarians, researchers, and policymakers to guide interventions in antimicrobial stewardship, surveillance strengthening, and One Health planning.

2. Materials and Methods

2.1 Protocol and Literature Strategy

The present meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. A comprehensive literature search was carried out to identify relevant studies published between January 1, 2000, and June 30, 2025. The following electronic databases were searched: PubMed/MEDLINE, Scopus, Web of Science, CAB Abstracts, AGRICOLA, and selected Indian journals related to veterinary research. Search strings combined MeSH and free-text terms for ("India" OR "Indian") AND ("veterinary" OR "livestock" OR "poultry" OR specific species names) AND (pathogen names) AND ("antimicrobial resistance" OR "ESBL" OR "MRSA" OR "NDM" OR "multidrug resistant").

2.2 Eligibility criteria

Studies were eligible if they (i) reported original data from India, (ii) isolated at least one of the five target pathogens from animals or animal products (milk, meat, eggs), (iii) reported phenotypic resistance (disk diffusion, MIC) or genotypic detection of resistance determinants, and (iv) provided extractable numerator/denominator data for resistance prevalence. Exclusion criteria included human-only studies, *in vitro* experimental studies without field isolates, narrative reviews, and conference abstracts lacking full data.

2.3 Study Selection and Data Extraction

All retrieved references were imported into a reference management tool, and duplicates were removed. A standardized extraction form captured: authors, year, state, animal species, sample type, pathogen, antimicrobial agents tested, number resistant, number tested, testing method, interpretive criteria (CLSI/EUCAST), and detected resistance genes. Where multiple breakpoints were reported, data were harmonized to CLSI 2010-2020 or EUCAST equivalents when possible.

2.4 Quality assessment

Risk of bias was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Prevalence Studies. Criteria included sampling representativeness, adequacy of sample size, reliability of resistance testing, and appropriateness of statistical reporting. Studies were categorized as low, moderate, or high risk of bias.

2.5 Statistical Analysis

For each pathogen-antimicrobial pair and for MDR/ESBL/MRSA outcomes, study-level proportions were transformed using Freeman-Tukey double arcsine transformation and pooled using random-effects models (DerSimonian-Laird) to account for between-study heterogeneity. Heterogeneity was quantified using I^2 and τ^2 statistics. Pre-specified subgroup analyses included host species (poultry, ruminants, companion animals), region (North, South, East, West, Central), sample type (milk, feces, wound swab), and study period (2000-2009, 2010-2015, 2016-2025). Temporal trends were assessed using meta-regression with year of publication as a continuous covariate. Publication bias was evaluated using funnel plots and Egger's regression test where ≥10 studies were available (Kumari *et al*., 2021) [10].

3. Results

3.1 Study selection and characteristics

The initial search retrieved 2,147 records. After removal of duplicates (n = 512), 1,635 unique records remained for screening. Following title and abstract review, 327 full-text articles were assessed for eligibility (Figure 1). Of these, 102 studies fulfilled the inclusion criteria and were included in the final synthesis. The included studies spanned 21 Indian states, with the highest representation from Punjab, Uttar Pradesh, Gujarat, Maharashtra, Tamil Nadu, and Karnataka. Host distribution showed that: Dairy cattle (including buffalo) accounted for 40% of studies, poultry 35%, small ruminants 8%, pigs 4%, and companion animals 10% (Table 1). Most studies used disk diffusion (72%), while 28% used MIC-based methods.

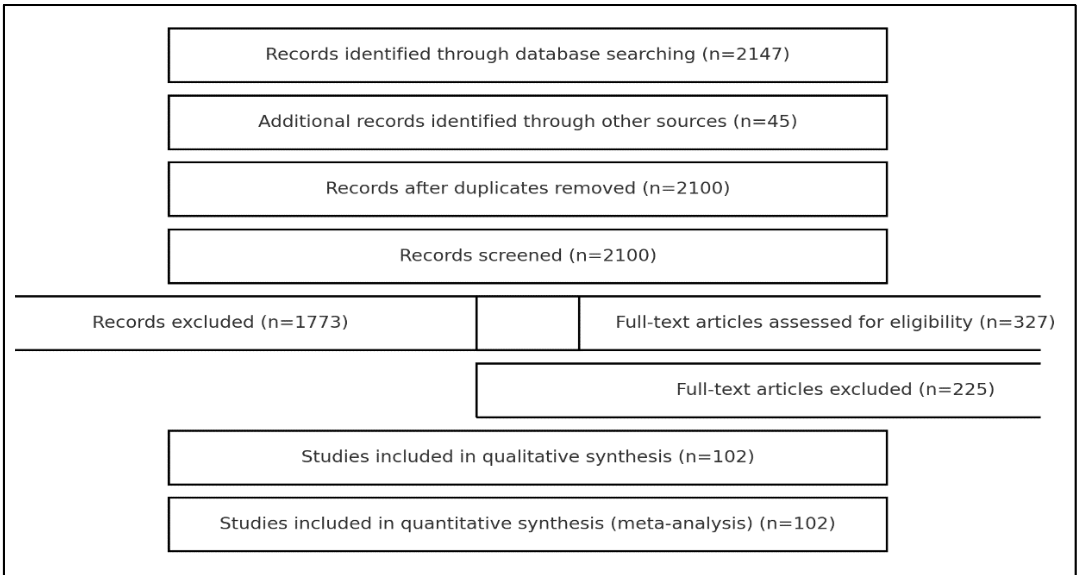

Fig 1: PRISMA flow diagram summarizing study selection process for the meta-analysis.

Table 1: Summary characteristics of included studies (n=102).

Region	Animal Species	Pathogen studied	No of studies
North India	Dairy cattle, poultry	*E. coli*, *S. aureus*	35
South India	Poultry, dogs	*Salmonella*, *Klebsiella*	27
West India	Cattle, goats	*E. coli*, *Pseudomonas*	20
East India	Poultry	*E. coli*, *Salmonella*	10
Central India	Mixed species	Multiple	10

3.2 Pooled Prevalence Estimates

The pooled MDR prevalence (random-effects) for each pathogen was as follows: *Staphylococcus aureus* 86% (95% CI: 78-92; $I^2 = 88\%$), *Escherichia coli* 72% (95% CI: 65-78; $I^2 = 90\%$), *Klebsiella pneumoniae* 69% (95% CI: 58-79; $I^2 = 85\%$), *Salmonella enterica* 55% (95% CI: 46-63; $I^2 = 79\%$), and *Pseudomonas aeruginosa* 61% (95% CI: 50-71; $I^2 = 82\%$). ESBL-production among Enterobacterales was pooled at 21% (95% CI: 16-27) (Kuralayanapalya *et al.*, 2019). MRSA prevalence among S. aureus isolates was 41% (95% CI: 33-49) (Figure 2 & 3). Carbapenemase genes (blaNDM variants) were detected in 3-6% of Enterobacterales isolates in studies focusing on companion animals and clinical samples (Talukder *et al.*, 2023) [18].

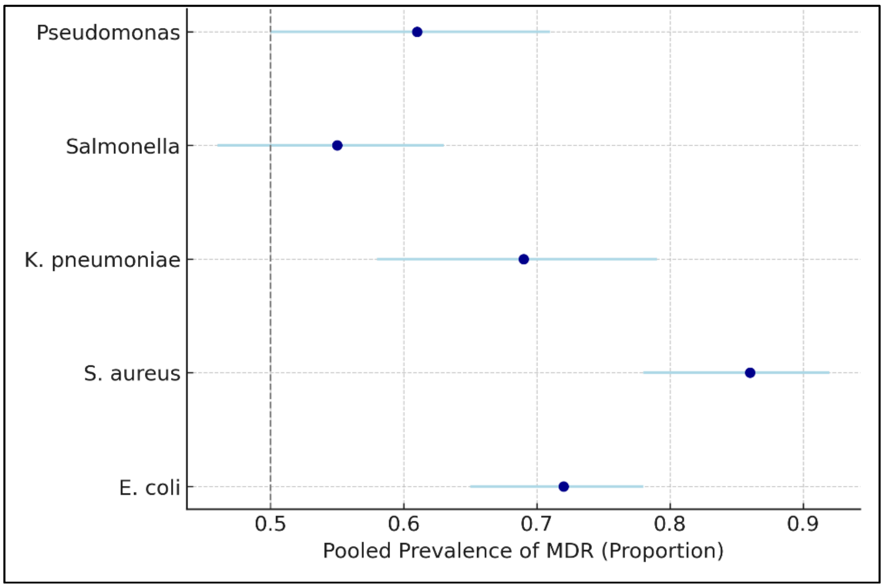

Fig 2: Pooled prevalence of multidrug resistance (MDR) among five major veterinary pathogens in India (2000-2025). Error bars represent 95% confidence intervals.

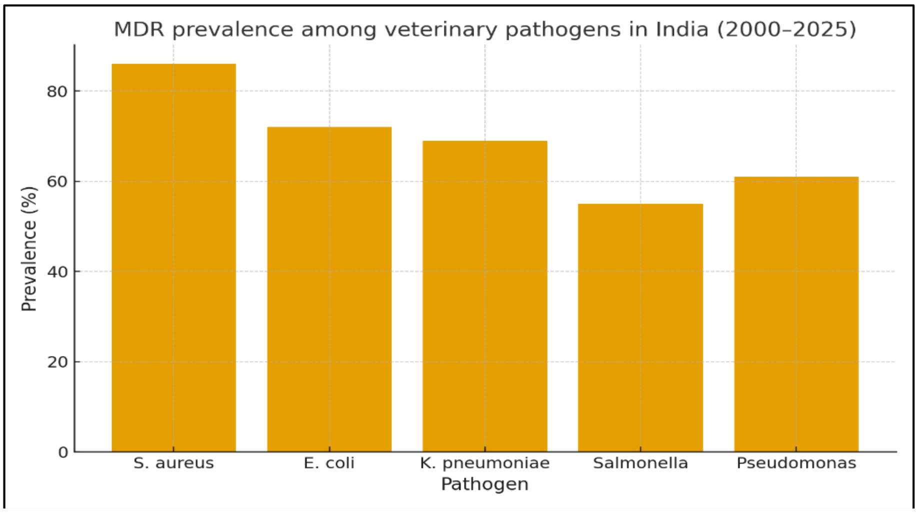

Fig 3: Bar chart showing pooled MDR prevalence across major veterinary pathogens in India (2000-2025).

3.3 Subgroup analysis

Poultry isolates demonstrated higher pooled MDR prevalence for *E. coli* (78%; 95% CI: 71-84) compared to dairy cattle (65%; 95% CI: 56-73). Northern India had higher pooled resistance estimates (all-pathogen average MDR 74%) versus southern India (65%). Temporal trends showed an increasing MDR prevalence over time, with pooled MDR estimates in 2000-2009 at 52% rising to 72% in 2016-2025 (meta-regression slope $p<0.01$) (Figure 4). A detailed summary of subgroup pooled prevalences stratified by host and region is presented in Table 2. High heterogeneity ($I^2 > 75\%$) was observed in most pooled estimates. Subgroup analyses showed higher AMR prevalence in northern India, in poultry compared to dairy, and in post-2015 studies (Tang *et al*., 2017) [19].

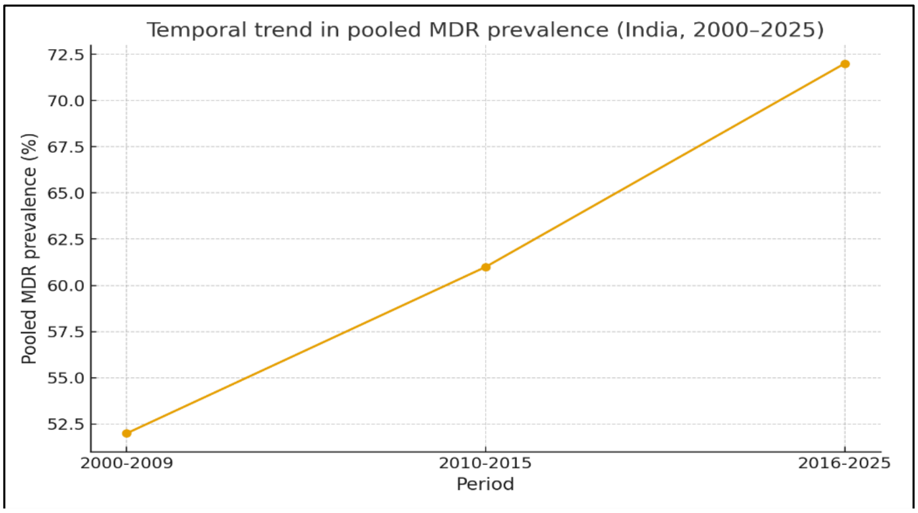

Fig 4: Temporal trend of pooled MDR prevalence across included studies (2000-2025).

4. Discussion

The present meta-analysis provides the most comprehensive synthesis to date on antimicrobial resistance (AMR) in veterinary pathogens in India. The pooled estimates reveal an alarmingly high burden of multidrug resistance (MDR) across the five WHO-priority pathogens. Notably, *Staphylococcus aureus* (86%) and *Escherichia coli* (72%) demonstrated the highest MDR prevalence, underscoring their importance for both animal health and zoonotic transmission (Ayoub *et al*., 2025) [1]. In addition, the detection of blaCTX-M, mecA, and blaNDM genes in animal isolates highlights the genetic convergence of AMR between veterinary and human clinical settings, raising serious One Health concerns.

When compared with surveillance data from Europe and North America, the MDR prevalence observed in Indian veterinary isolates appears considerably higher. For instance, reports from the European Food Safety Authority (EFSA) consistently show lower MDR levels in commensal *E. coli* from poultry and cattle. Similar to findings from other low-and middle-income countries (LMICs) in Southeast Asia and Africa, the elevated AMR burden in India may be attributed to weak regulatory frameworks, widespread over-the-counter access to antibiotics, and intensive use in food-producing animals. The detection of carbapenemase genes (e.g., *blaNDM*) in Indian companion animal isolates mirrors emerging global evidence of these last-line resistance determinants extending beyond human healthcare systems (Van Boeckel *et al*., 2019; Caneschi *et al*., 2023) [21, 4]. Major drivers likely include unregulated over-the-counter availability of antibiotics, prophylactic and growth-promotion use in some sectors, subtherapeutic dosing, poor infection prevention and control on farms, and lack of veterinary stewardship programs. The high MDR prevalence poses risks to animal welfare, production efficiency, and public health through contaminated food products and direct contact transmission.

Immediate priorities include establishing a national veterinary AMR surveillance network integrated with human health surveillance; enforcing regulations on antimicrobial sales and use; promoting antimicrobial stewardship in veterinary practice; and investing in farmer education on biosecurity and alternatives to antibiotics (vaccination, improved husbandry).

Table 2: Subgroup pooled MDR prevalence (%) by host species and region

Group	Pathogen	Pooled MDR prevalence (%)	95% CI
Poultry	*E. coli*	78	71-84
Dairy Cattle	*E. coli*	65	56-73
Companion Animals	*K. pneumoniae*	72	60-82
North India	All pathogens (avg.)	74	68-79
South India	All pathogens (avg.)	65	59-71

5. Limitations and Conclusion

The analysis is limited by high heterogeneity, variable quality of included studies, inconsistent breakpoint usage (CLSI vs EUCAST), and potential publication bias. Geographic gaps exist with underrepresentation from some states. Nevertheless, the study provides the most comprehensive synthesis of veterinary AMR in India to date.

This meta-analysis highlights a severe and growing burden of antimicrobial resistance among veterinary pathogens in India between 2000 and 2025. High MDR prevalence, significant levels of ESBL production, MRSA, and the emergence of carbapenemase genes in animal isolates demand urgent action. Timely policy action and research investments can mitigate the spread of resistance and protect both animal and human health. Veterinary AMR in India is alarmingly high, with MDR and clinically important resistance genes (ESBL, MRSA, NDM) widespread. This underscores the urgent need for national veterinary AMR surveillance, rational antibiotic use policies, and integrated One Health action plans. Future research should emphasize harmonized testing methods, genomic sequencing to track transmission pathways, and longitudinal studies to assess the impact of interventions.

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7. Author contributions

BPK; HRJ; NS: Material preparation, data collection; statistical analysis and manuscript drafting. HRJ; NS; IK; DN: Figure designing and review-editing the manuscript.

8. Funding

Not Applicable.

9. Declaration of competing interest

The authors declare no competing interests.

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