UMYU Scientifica, Vol. 5 NO. 1, March 2026, Pp 516 – 527
https://doi.org/10.56919/usci.2651.044
ISSN: 2955 – 1145 (print); 2955 – 1153 (online)
A periodical of the Faculty of Natural and Applied Sciences, UMYU, Katsina

ORIGINAL RESEARCH ARTICLE

Spatial and Predictive Modelling for Antimicrobial Resistance in Livestock: A Systematic Review

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ABSTRACT
Antimicrobial resistance (AMR) in livestock has emerged as a major global threat, with direct implications for public health, food security, and sustainable development under the One Health framework. Livestock production systems significantly contribute to global antimicrobial use, exerting selective pressures that drive the establishment and rapid spread of resistant infections across the animal, human, and environmental interfaces. This review examines existing studies on the spatial distribution of AMR in livestock, with emphasis on surveillance databases, spatial statistical techniques, and modeling methods. This underscores the importance of global AMR surveillance resources, such as the ResistanceBank, an open-access livestock AMR database. This systematic review, conducted using the PRISMA guidelines, searched three databases (PubMed, Scopus, and Google Scholar) for studies published between 2016 and 2025. After duplicates were removed and the remaining articles were screened by two independent reviewers based on predefined inclusion and exclusion criteria, 13 studies were included. Study quality was appraised using the McMaster critical evaluation framework, and data on study characteristics, together with the key findings, were extracted. Some studies employed hybrid modeling techniques; most applied spatial modeling (84.62%); over half used Machine Learning (ML) techniques; and some included statistical modeling approaches (53.85%). Spatial analyses revealed clustering, hotspots, and spillover patterns of AMR. ML models exhibited strong predictive performance for AMR features. Hybrid modeling approaches enhanced robustness and interpretability by capturing epidemiological processes and integrating heterogeneous datasets. In conclusion, this review showed that integrating spatial analysis with predictive modeling provides a robust framework for advancing livestock antimicrobial resistance surveillance, improving risk identification, and supporting targeted antimicrobial stewardship and policy interventions.

ARTICLE HISTORY
Received December 04, 2025
Accepted March 20, 2026
Published March 30, 2026

KEYWORDS
Antimicrobial resistance, spatial analysis, predictive modeling, beta regression, machine learning

INTRODUCTION

Antimicrobial resistance (AMR) emerged as a major threat to global health, food security, and sustainable development in the twenty-first century. AMR occurs when microorganisms form resistance that renders antimicrobial agents ineffective, causing persistent infections, elevating morbidity and mortality, and increasing healthcare costs (Prestinaci *et al.*, 2015; Tang *et al.*, 2023; Andrew et al., 2024; Hamisu & Salisu, 2025; Rabiu et al., 2022; Saheed et al., 2025; Salisu et al., 2019, 2017; Usman et al., 2025). AMR is a substantial global burden, with 4.95 million deaths associated with resistant infections alone in 2019 (Murray *et al.*, 2022; Naghavi *et al.*, 2024). Recently, AMR continued to be associated with approximately 5 million deaths every year, making it one of the leading causes of mortality globally (WHO 2024). Projections estimated AMR-related mortality could substantially progress to a cumulative total of more than 39 million deaths between 2025 and 2050 if effective intervention is not provided globally.

Historically, AMR has been examined within clinical and human contexts; however, there is increasing recognition of its complexity and interconnectedness across human, animal, and environmental systems. The interconnected nature of AMR underpins the One Health framework, which highlights the role of livestock production systems in the progress, amplification, and dissemination of AMR pathogens (Chokshi *et al.*, 2019; Abbas *et al.*, 2024; Mohammed et al., 2017). In livestock production systems, especially in intensive farming, antimicrobials are widely used for disease treatment, prevention, and growth promotion, exerting selective pressure that enhances the

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How to cite: Omotoso, R. O., Odetokun, I. A., Abubakar, T. O., & Adejumo, A. O. (2026). Spatial and Predictive Modelling for Antimicrobial Resistance in Livestock: A Systematic Review. *UMYU Scientifica*, 5(1), 516 – 527. https://doi.org/10.56919/usci.2651.044

development of resistant pathogens (Hosain *et al*., 2021; Matheou *et al*., 2025).

AMR in livestock has profound implications for public health. Resistant pathogens can be transmitted to humans through multiple channels, including the food chain, direct animal contact, and environmental pathways such as water and soil contamination (Panicker *et al*., 2025; Meyer *et al*., 2024). AMR in livestock is associated with a substantial economic burden, affecting animal productivity, trade, and livelihoods, particularly in resource-limited regions (Babo Martins *et al*., 2024). Livestock constitute a significant source of human protein, and the inappropriate use of antimicrobials in animals can also facilitate the transfer of AMR pathogens (Babo Martins *et al*., 2024; Trinchera *et al*., 2025). AMU in livestock is estimated to have surpassed human consumption, intensified AMR, and explained the central role of food-producing animal systems in shaping the increased AMR burden (Van Boeckel *et al*., 2015; Salisu et al., 2017; Hosain *et al*., 2021; Babo Martins *et al*., 2024). Factors contributing to inappropriate antimicrobial use (AMU) and poor monitoring of resistance patterns include weak regulatory enforcement, limited access to veterinary services, informal drug markets, and inadequate surveillance systems (Grace, 2015; Iskandar *et al*., 2021; Davis *et al*., 2025). These factors pose AMR challenges in livestock.

Spatial heterogeneity is a key feature of AMR, driven by differences in AMU practices, livestock production systems, environmental conditions, and socio-economic factors. Spatial analysis employs powerful tools to quantify geographical dependence, identify resistance clusters, and detect high-risk areas that may require targeted interventions (Spets *et al*., 2023; Legenza *et al*., 2023). Studies on infectious disease and AMR have applied measures of spatial autocorrelation, such as Global and Local Moran's I, to reveal non-random spatial patterns (Kou *et al*., 2025). However, their application to livestock AMR at a global scale remains limited.

Beyond spatial description, predictive models (statistical and machine learning) provide significant insight into the factors contributing to AMR. Regression methods, such as beta regression, are suitable for modeling resistance proportions bounded between 0 and 1, while machine learning (ML) approaches can capture complex, non-linear relationships and feature interactions (Mulchandani *et al*., 2024). Integration of spatial analysis with predictive modeling provides a comprehensive framework for understanding the distribution and determinants of AMR in livestock. This review examines existing studies on the spatial distribution of AMR in livestock, with emphasis on surveillance databases, spatial statistical techniques, and modeling methods.

AMR rapidly increases disease progression, co-infection with pathogens such as salmonellosis, and other transmissible diseases, with the potential to accelerate the spread of the resistant pathogen across the nation or globe. Furthermore, systematic analysis shows that mortality due to six pathogens (*Escherichia coli, Staphylococcus aureus, Klebsiella pneumoniae, Streptococcus pneumoniae, Acinetobacter baumannii*, and *Pseudomonas aeruginosa*) has an estimation of 929000 (660000-1270000 95% UI), with each pathogen accounting for over 250000 deaths due to AMR (Naghavi *et al*., 2024). The analysis provided insight into the global burden of AMR and confirmed that it is a major global challenge. Studies on resistome show that livestock gastrointestinal systems are substantial hosts of diverse AMR pathogens transmissible to environmental or zoonotic pathogens (Ma et al., 2021).

AMR burden is disproportionate in LMICs due to structural vulnerabilities, including limited veterinary facilities, ineffective regulation, high-density farming, lack of biosecurity, and unrestricted access to antimicrobials (Iskandar *et al*., 2021; Odey *et al*., 2024). Additionally, ecological pollution resulting from improper waste management, unmanaged wastewater flow, and livestock effluent runoff accelerates the dissemination of resistance genes in LIMCs (Azabo *et al*., 2022; Meyer *et al*., 2024). The close proximity of livestock, humans, and water systems in these nations further exacerbates One Health transmission mechanisms (Davis *et al*., 2025). However, the lack of spatially focused AMR data limits the identification of hotspots and the effective allocation of resources by policymakers, underscoring a major gap.

SURVEILLANCE AND DATA SOURCES FOR AMR

An adequate surveillance system is important for understanding AMR patterns, identifying threats, and implementing targeted interventions. Several databases exist, but they have different coverage, resolution, and quality.

ResistanceBank

ResistanceBank.org is an open-access database of AMR in livestock and one of the most comprehensive data sources for livestock AMR surveillance (Criscuolo, Pires, & Van Boeckel, 2021). This database compiles study-based AMR data from several countries, pathogens, and livestock species, providing a large-scale dataset on resistance proportions across antimicrobial classes.

The database collated AMR data obtained mainly from prevalence surveys published between 2000 and 2021, compiling over 1200 surveys and 33186 resistance estimates across livestock species, including poultry, cattle, pigs, sheep, ducks, horses, and buffalo. The reports include key public health pathogens: *Escherichia coli, Salmonella, Staphylococcus aureus,* and *Campylobacter* spp. Countries represented in the Resistance Bank database span across Africa, Asia, Latin America, and parts of Europe and North America.

STRENGTHS AND LIMITATIONS OF LIVESTOCK AMR DATA FOR STATISTICAL ANALYSIS

Livestock AMR surveillance encounters structural challenges. Strengths of existing databases include organized laboratory testing protocols, improved global coordination of AMR data reporting, and inclusive datasets covering multiple livestock species, pathogens, and antimicrobial classes.

A major strength that underpins the credibility of AMR data for statistical analysis is its reliance on organized laboratory testing protocols. ResistantBank.org collates AMR data obtained through standard antimicrobial susceptibility testing (AST) procedures carried out in accredited laboratories, with most contributing studies following internationally recognized guidelines such as those of the Clinical and Laboratory Standards Institute (CLSI) and the European Committee on Antimicrobial Susceptibility Testing (EUCAST). This harmonized testing methodology ensured consistency in pathogen isolation, antimicrobial panels, and the interpretation of AMR across diverse data sources.

Improvements in global coordination on AMR data reporting enhance comparability and provide high-quality evidence for informed decision-making, surveillance, and efficient intervention strategies. Particularly in livestock, where AMR patterns are influenced by diverse animal species, production systems, and AMU, ResistanceBank significantly contributes to the coordination of AMR data reporting by serving as a centralized, standardized repository, thereby reducing fragmentation across individual studies.

Furthermore, the availability of multidimensional data enables comparisons across species, pathogens, and antimicrobial classifications, thereby enhancing the identification of shared AMR patterns and transmission pathways within animal populations. Moreover, inclusivity in data collation reduces bias associated with single-species and single-pathogen surveillance approaches and supports robust epidemiological and spatial analyses.

However, its limitations remain significant. This includes sparse geographic coverage in low-income countries (Criscuolo *et al*., 2021; Iskandar *et al*., 2021), a lack of continuous AMR reporting, sampling biases toward outbreaks or commercial farms, limited ability to model predictors or spatial dependencies, and despite the awareness of transmission pathways, there is low environmental and One Health integration. (Bengtsson-Palme *et al*., 2023; Venkateswaran *et al*., 2024).

Despite the strengths, livestock AMR surveillance, such as ResistanceBank, is disproportionately populated with data from countries where laboratory infrastructure, routine surveillance systems, and reporting capacity are more established. Figure 1 shows the disproportionate representation of low-income and low-middle-income countries in Resistance Bank data, resulting in substantial data gaps across many countries, where AMU in food processing animals is often less regulated, and surveillance systems are absent.

Another notable setback of existing livestock AMR databases, particularly ResistanceBank, is the lack of continuous, longitudinal AMR data collection. Much of the collated data in the ResistanceBank was obtained from cross-sectional studies, periodic surveys, or short-term surveillance rather than sustained, routine monitoring systems. This results in the absence of continuous reporting, with substantial gaps between reporting periods for many countries and livestock species. This limited the ability to accurately assess temporal trends, seasonal variations, and the long-term impact of antimicrobial stewardship interventions in the livestock production system. Discontinuity in AMR data reduces statistical power and may introduce bias in spatial and temporal epidemiological analyses, thereby limiting the utility of ResistanceBank for trend modeling and predictive risk assessment, and delaying early detection of emerging resistance patterns and timely public health and veterinary intervention.

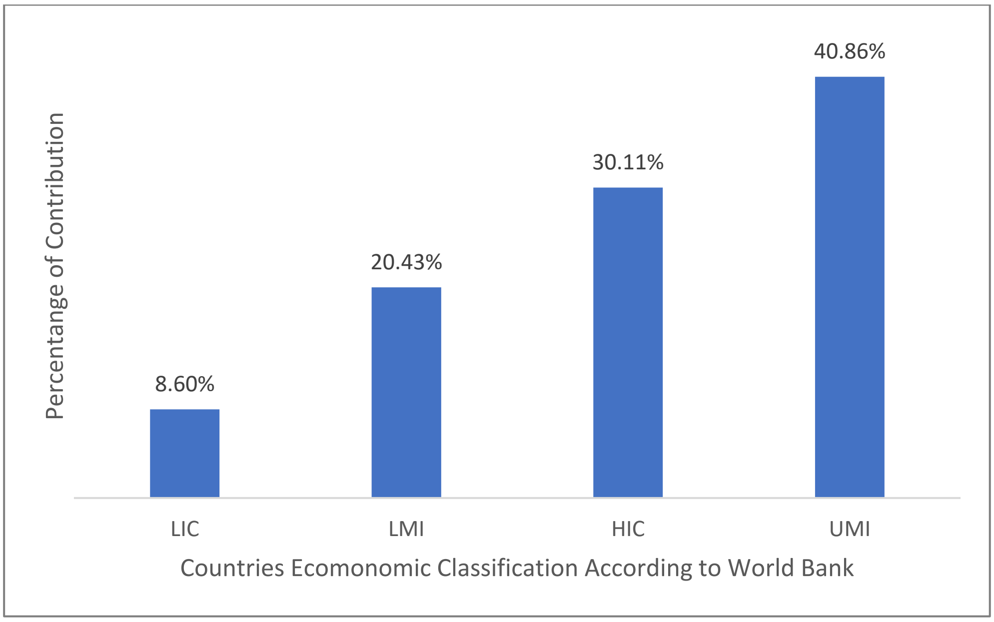

Figure 1: Contribution of Countries' Economic Classification in the ResistanceBank Database According to the World Bank

LIC – Low Income Country, LMI – Low Middle Income, HIC – High Income country, UMI – Upper Middle Income

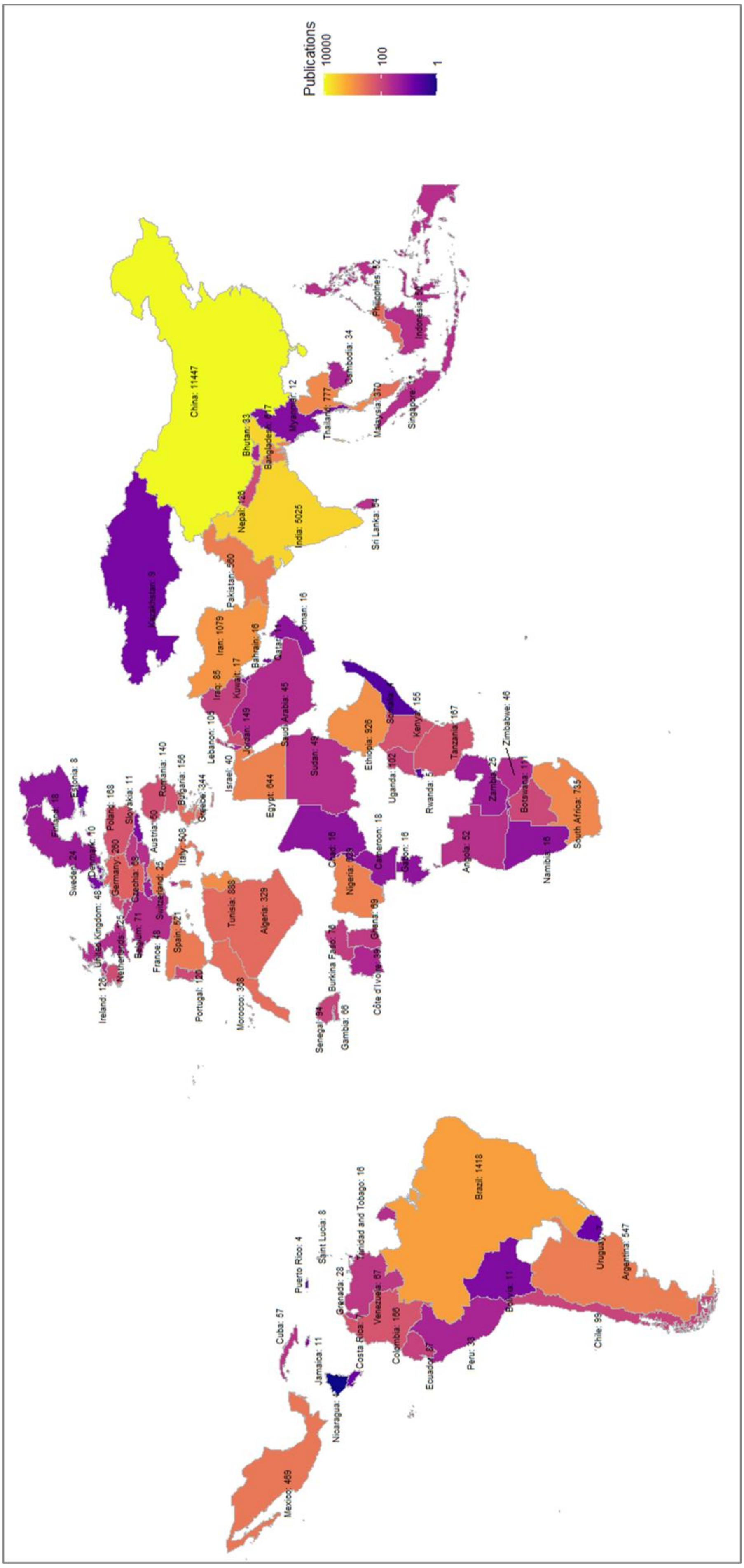

Figure 2: Spatial distribution of countries' publications reported in ResistanceBank

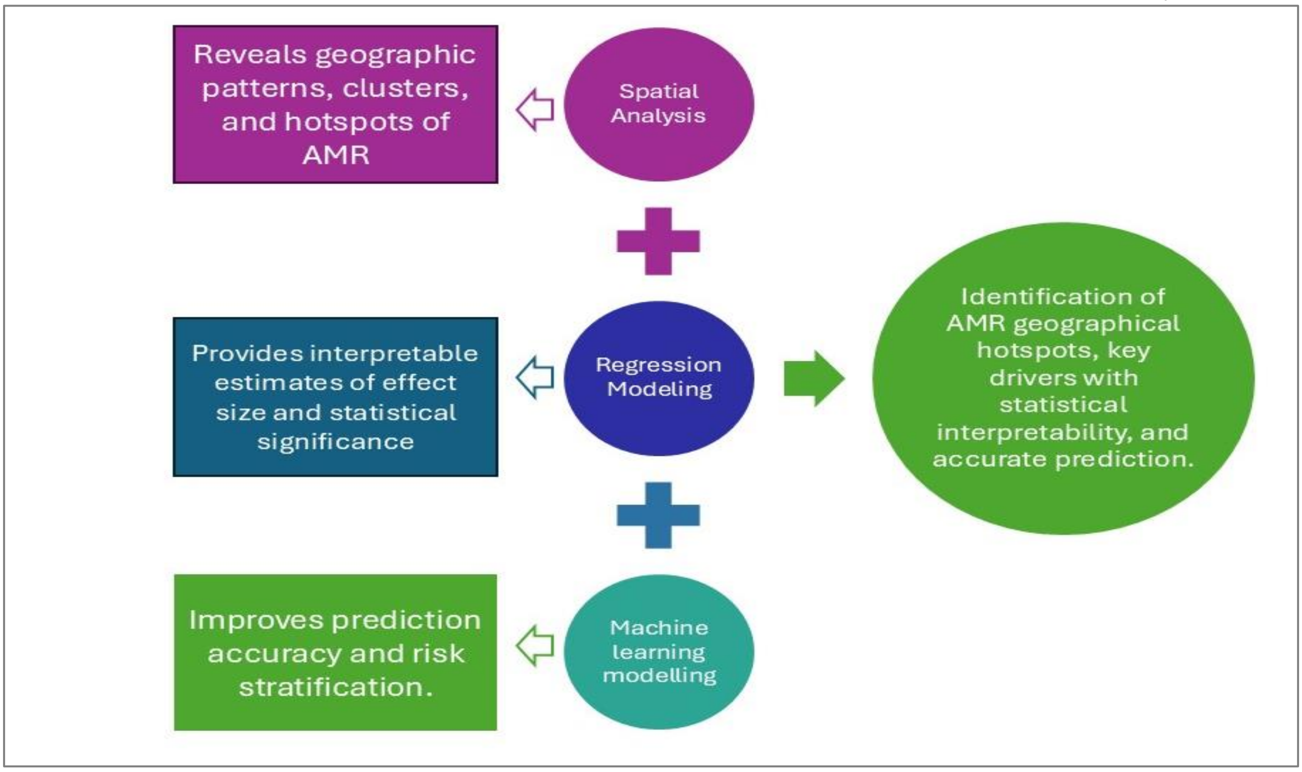

Figure 3: Contribution of spatial analysis, regression modeling, and machine learning modeling in understanding AMR patterns

Additionally, Figure 2 shows that livestock AMR data, such as those from ResistanceBank, are often subject to sampling biases, with disproportionate contributions from China, India, and Brazil, and with data often obtained from research-driven studies rather than routine sampling across subsistence production systems. The disproportionate sampling may overestimate resistance prevalence and limit the comparability and generalisability of findings to broader livestock populations. Moreover, despite growing awareness of AMR transmission pathways at the human-animal-environment interface, One Health integration remains constrained within existing livestock datasets, such as ResistanceBank, which primarily focus on isolates from animals with little linkage to environmental reservoirs, such as water, soil, and farm waste, or to human clinical data.

IMPORTANCE OF SPATIAL TECHNIQUES IN MAPPING AMR IN LIVESTOCK

International travel and trade make the transmission of resistant pathogens across nations inevitable, creating the need for intensified global interventions to address AMR (Prestinaci *et al.* 2015; Chhokshi *et al.* 2019). With the availability of environmental data, the use of spatial techniques helps in understanding the spread of AMR across countries (Legenza *et al.*, 2023).

The robust framework offered by spatial epidemiology techniques for analyzing the geographic spread of diseases and resistance patterns enables researchers to identify clusters and hotspots and to investigate the influence of environmental and socioeconomic factors (Spets *et al.*, 2023). With regards to AMR in livestock, spatial techniques are important because resistance does not occur at random; it reflects connections between AMU practices, livestock production systems, environmental contamination, and regional health and policies (Kou *et al.*, 2025).

Spatial autocorrelation estimates the degree of similarity in observations at nearby locations. Positive spatial autocorrelation underscores clustering of similar values (e.g., high AMR in neighboring nations), while negative autocorrelation underlines spatial heterogeneity (Spet *et al.*, 2023). Global Moran's I is a measure of spatial autocorrelation that examines the overall spatial pattern across regions (Moran, 1950; Anselin, 1995). It is useful for identifying AMR clusters, dispersion, or randomness. Local Moran's I (LISA) is also useful for identifying specific clusters (hotspots and coldspots), enabling regionalized policymaking and interventions. These spatial techniques have been widely applied in disease mapping but remain underused in livestock AMR research, particularly in Low-income countries.

REGRESSION FOR MODELLING AMR IN LIVESTOCK

Resistance is often measured in proportion (percentage of resistant isolates). Values bounded between 0 and 1 violate the assumptions of ordinary least squares (OLS) regression. Beta regression is therefore preferred because it accommodates boundness, heteroscedasticity, and non-normality (Matheou *et al.*, 2025).

Beta regression is commonly employed in ecological and environmental health studies but is rarely used in livestock AMR modeling, despite its suitability for modeling resistance proportions across species, pathogens, and antimicrobial classes. It also permits flexible link functions and precision parameters, enhancing improved model fit compared with linear models, and produces accurate and interpretable estimates of resistance levels across livestock species, pathogens, and regions. Beta regression enhances the ability to capture spatial dependency, and when integrated with spatial analysis, it supports more reliable identification of AMR hotspots linked to animal trade, strengthening spatial epidemiological insight. The use of explanatory modeling techniques enables the clear identification of the driver of AMR emergence in livestock populations.

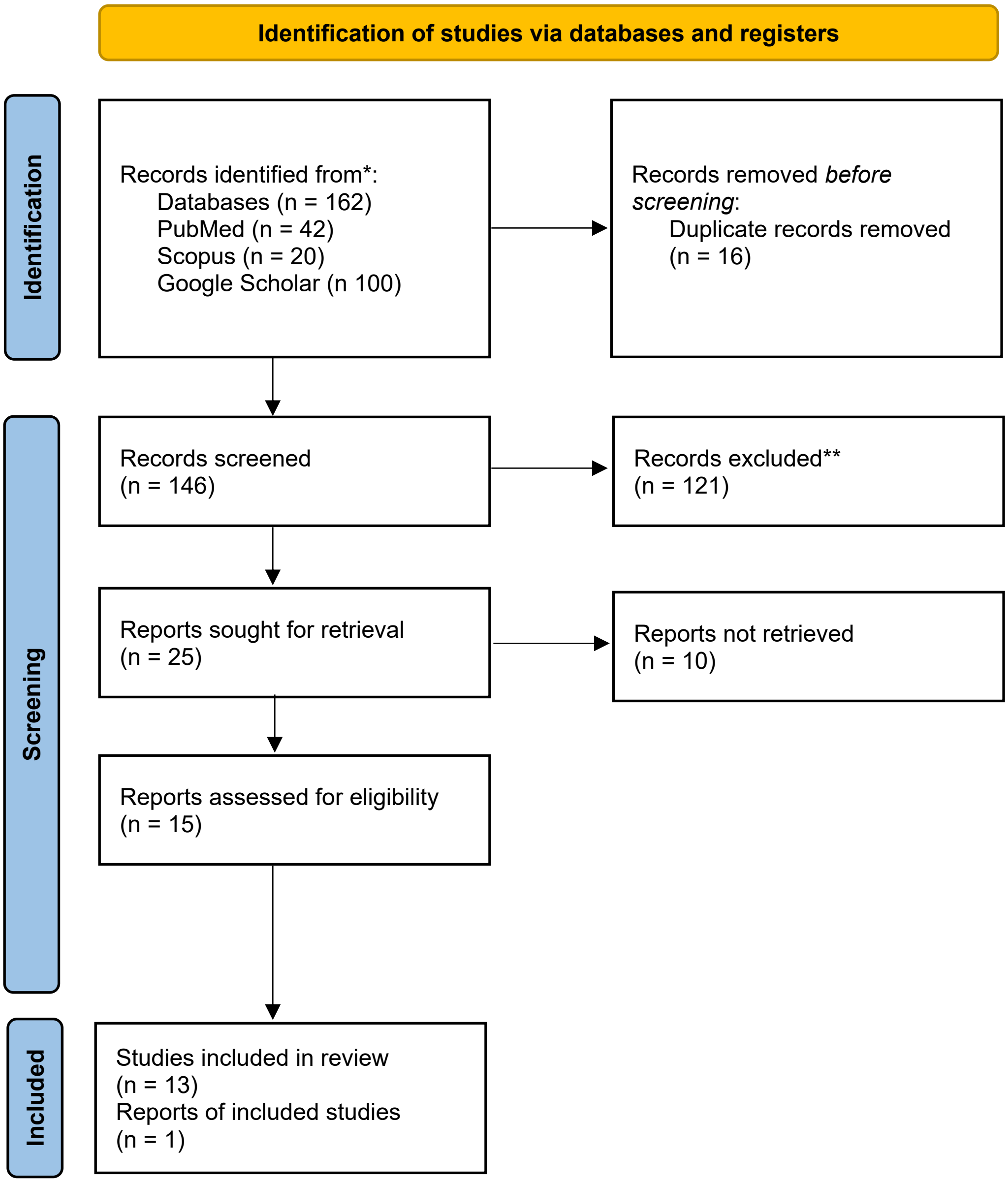

Figure 4: PRISMA flow diagram of study identification, screening, and inclusion for antimicrobial resistance in livestock studies

USE OF MACHINE LEARNING MODELLING IN LIVESTOCK AMR PREDICTION

Machine learning (ML) techniques – such as gradient boosting, random forests, and neural networks – give powerful alternatives for identifying nonlinear relationships among AMR predictors (Lewnard *et al.*, 2024). ML approaches are mainly valuable when independent variables exhibit complex interactions, relationships are not linear, and data possess high-dimensional features such as pathogen, drug class, species, and environmental metadata.

Beyond improved prediction accuracy, the use of ML models in livestock AMR surveillance can enhance risk stratification and decision-making in data-limited settings. When integrated with spatial analysis, ML techniques can provide early warning systems, identify high-risk livestock populations, and inform targeted intervention. Consequently, a combination of ML models with explainable models and domain-informed features represents a major pathway for advancing livestock AMR modeling, because the deployment of ML in this context relies on careful model validation, transparency, and interpretability to ensure AMR predictions are epidemiologically meaningful.

Figure 3 highlights the contributions of spatial techniques, regression modeling, ML modeling techniques, and the integration of three analytical methods in understanding AMR trends in Livestock.

Table 1: Overview of modeling techniques and key findings in antimicrobial resistance studies

Authors	Aim	Modelling Techniques	Modelling Type	Study Region	Pathogen	Key Result
Fang *et al.* 2025	To analyze global temporal trends and predict future antibiotic resistance in GBS	Genomic analysis, geospatial analysis, Random Forest prediction	Machine learning + Spatial analysis	Global	*Streptococcus agalactiae*	4-fold increase in ARG abundance; Asia identified as a hotspot; 187% predicted
Sobkowich *et al.* 2024	To assess the prevalence and trends of CRE in animals	Space-time cluster analysis, temporal trend analysis	Spatial + Statistical modeling	USA	Enterobacter ales	Low prevalence (98.86% susceptibility); identified regional clusters
Adedeji *et al.* 2025	To identify predictors of AMR and develop predictive models using surveillance data	Random Forest, LightGBM, linear regression, chi-square tests	Machine learning + Statistical modeling	Africa	*Multiple bacteria*	RF showed high classification performance; LightGBM achieved ~81% accuracy; and identified key AMR drivers.
Garcia-Vozmediano *et al.* 2025	To develop a data-driven surveillance framework for *Salmonella*	Statistical models + machine learning integration	Hybrid (Statistical + ML)	Italy	*Salmonella enterica*	Improved surveillance through the One Health framework (data-driven integration)
Mulchandani *et al.* 2024	To map AMR prevalence and identify hotspots	Geospatial modeling, predictive mapping	Spatial modelling	Europe	*E. coli, Salmonella, Campylobacter*	Identified AMR hotspots and geographic variation; supports targeted interventions
Zhao *et al.* 2024	To map AMR prevalence globally using survey data	Geospatial modeling using point-prevalence surveys	Spatial modelling	Global	*E. coli, Salmonella*	Identified global AMR hotspots; predicted future resistance thresholds geographically
Smit *et al.* 2025	To analyze small-scale spatial and temporal variation in AMR	Geospatial mapping, temporal trend analysis	Spatial + Statistical modeling	Australia	*E. coli*	Resistance varied by region and time; identified local hotspots
Teng *et al.* 2020	To analyze the spatial distribution and risk factors of Salmonella infection	Bayesian spatial regression (BYM2), Moran's I, spatial scan statistics	Spatial + Statistical modeling	Spain	*Salmonella*	Identified spatial clusters and a west-to-east risk gradient
Ou *et al.* 2025	To study TB transmission using genomic and spatial data	Logistic regression, spatial analysis, genomic clustering	Spatial + Statistical modeling	China	*Mycobacterium tuberculosis*	High recent transmission (~50%); spatial hotspots identified
Zhelyazkova *et al.* 2021	To predict AMR risk and sample origin using spatial modeling	Bayesian spatial convolution model, ML (RF, GBM, NN)	Hybrid (Spatial + ML)	Global	*Multiple bacteria*	RF performed best; spatial modeling improves AMR risk estimation
Shang *et al.* 2022	To analyze TB distribution and forecast trends	Spatial analysis, exponential smoothing model	Spatial + Time-series modeling	China	*Mycobacterium tuberculosis*	Identified clusters and seasonal peaks; the model is effective for forecasting
Warren *et al.* 2018	To investigate spatial spillover of MDR-TB	Hierarchical Bayesian modelling, spatial analysis	Spatial + Statistical modeling	Peru	*Mycobacterium tuberculosis*	Spillover risk extends ~5.47 km; evidence of community transmission

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Table 1 continued

Authors	Aim	Modelling Techniques	Modelling Type	Study Region	Pathogen	Key Result
Kou *et al.* 2025	To assess spatial patterns and drivers of *E. coli* antimicrobial resistance	Spatial panel modelling, spatial econometric analysis	Spatial modelling	China	*Escherichia coli*	Significant spatial clustering; clear interregional spillover effects; AMR drivers identified

GBS – Group B *Streptococcus,* ARG – Antimicrobial Gene, CRE – *Carbapenem-resistant Enterobacterales*, ML – Machine Learning, AMR – Antimicrobial Resistance, TB – Tuberculosis, MDR-TB – Multidrug-Resistant Tuberculosis

METHODS

The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement was used in conducting this systematic review (Moher *et al.*, 2015). A search protocol was designed and registered on Rayyan.

Three databases (PubMed, Scopus, and Google Scholar) were systematically searched to obtain relevant articles published between January 1, 2016, and December 30, 2025. The search strategy combined keywords and related vocabulary for AMR, Spatial Modeling, and ML modeling. The core search string for the database search is ("antimicrobial resistance" OR "antibiotic resistance" OR "drug resistance") AND ("spatial analysis" OR "spatial modeling" OR "geospatial" OR GIS OR "spatial epidemiology") AND ("predictive modeling" OR "machine learning" OR "statistical modelling"). Filters were applied to the publication year range and language. The final search was conducted; a total of 162 articles were identified (Figure 4) and uploaded to Rayyan. Sixteen duplicate articles were deleted, and 146 articles were subjected to primary screening. In addition to this review's comprehensive search strategy, a blind search was conducted across the primary databases, leading to the inclusion of one additional article and further strengthening the review and confirming a detailed assessment of the relevant literature.

To determine the article to included in the review, these inclusion criteria were developed – studies focusing on AMR, studies using spatial analysis or predictive modelling techniques, original research articles, studies published in English, studies that focus on livestock or zoonotic diseases, and studies published between 2016 and 2025 – together with is exclusion criteria – reviews, editorials, opinion papers, studies with modelling components, human focused articles, and non-English publications. Two independent reviewers conducted the primary (title and abstract screening) and secondary (full-text screening), and disputes were resolved through discussion. The reporting quality and bias selection in the included studies were appraised by two independent reviewers using the McMaster critical evaluation methods for both quantitative and qualitative study design, study location, animal type, sample type, and the method of detection (Ducat and Kumar, 2015).

A data extraction form was developed to capture the following information: author names, year, aim, modeling techniques, modeling type, study region, pathogen, and key results, which are considered crucial for this study.

RESULTS

Thirteen articles were found eligible for this study (Figure 4), including publications from 2018 to 2025. These studies covered diverse geographical regions, including global analyses (23.08%), continental level studies (15.38%) (Africa and Europe), and country-specific studies (61.54%), particularly in China, Italy, Spain, Australia, the United States of America (USA), and Peru (Table 1).

MODELLING APPROACHES

Spatial Modelling

The majority of the studies (84.62%) employed spatial modeling approaches to identify geographical patterns, clustering, and hotspots of AMR. The techniques employed include geospatial mapping, spatial econometric models, Bayesian spatial regression, Moran's I and spatial scan statistics. Studies by Zhao *et al.* (2024) and Muchandani *et al.* (2024) identified global and regional AMR hotspots, while Teng et al. (2020) and Kou et al. (2025) demonstrated significant spatial clustering and spillover effects. A key finding from Warren *et al.* (2018) showed that multidrug-resistant tuberculosis spillover extended approximately 5.47km, highlighting the role of localized transmission forces (Table 1).

Machine Learning Modelling

Predictive modeling techniques were applied in many studies (69.23%), focusing on identifying AMR drivers. ML models were widely employed, including Random Forests (RF), Gradient Boosting Machines (GBM), LightGBM, and Neural networks. RF was identified as a top-performing algorithm, and LightGBM estimated high prediction accuracy. Overall, ML approaches demonstrated strong predictive performance and efficiently identified some key determinants of AMR. For example, Feng *et al.* reported a fourfold increase in antimicrobial resistance gene (ARG) abundance using RF alongside genomic and geospatial analyses to predict global trends of *Streptococcus agalactiae,* while Adedeji *et al.* (2025) employed multiple ML algorithms, including Random Forest and Light Gradient Boosting Machine (LightGBM), to analyze surveillance data in Africa. Their findings highlighted the robustness of ML techniques for determining key AMR drivers.

Statistical Modelling

Several studies (53.85%) also employed statistical modeling techniques, including logistic growth models, Bayesian semi-mechanistic models, and regression-based models. These models were used to capture underlying epidemiological processes, account for data heterogeneity across sources, and improve the robustness of AMR trend predictions. For instance, models trained on heterogeneous datasets showed improved predictive accuracy and reliability. Hybrid approaches integrated spatial, statistical, and ML techniques to improve both predictability and interpretability.

Warren *et al.* (2018) demonstrated the strength of hierarchical Bayesian modeling in capturing spatial spillover effects of multidrug-resistant tuberculosis (MDR-TB) in Peru, estimating a spillover risk extending approximately 5.47km and providing evidence of community-level transmission. Likewise, Teng *et al.* (2020) applied Bayesian spatial regression (BYM2), along with Moran's I and spatial scan statistics, to identify significant spatial clusters and a west-to-east gradient in *Salmonella* infection risk in Spain. Ou *et al.* (2025) employed logistic regression in combination with spatial and genomic analyses to investigate transmission patterns of *Mycobacterium tuberculosis* in China, revealing a high level of recent transmission (~50%) and identifying key hotspots.

DISCUSSION

This systematic analysis reviewed literatures on the application of spatial and predictive modeling methods in AMR research. The findings demonstrate growing integration of these techniques in understanding the distribution, drivers, and future trajectories of AMR across diverse settings. The complementary roles of spatial and predictive modeling approaches are a notable finding of this review: spatial models were used to characterize geographic heterogeneity, clustering, and hotspot identification, while predictive models focused on forecasting and identifying determinants of AMR. The increased use of hybrid frameworks suggests a methodological shift toward integrated modeling, aligning with the need for multidimensional modeling in AMR studies.

This review provides strong evidence of significant spatial heterogeneity in AMR distribution, along with the identification of hotspots at both global and local levels. Evidence of spatial spillover effects and short-range transmission underscores the role of geographic proximity and connectivity in the spread of AMR. Machine learning models, including RF, GBM, and neural networks, are able to capture nonlinear relationships and high-dimensional interactions, making them particularly suitable for AMR prediction and consistently showing strong predictive performance across studies. However, despite their predictive strength, many machine learning models lacked interpretability, which is essential for public health decision-making. Conversely, statistical models such as Bayesian and logistic models provide better insight into underlying epidemiological processes, though often at the cost of predictive accuracy.

The existing literature demonstrates the growing potential of spatial AMR analysis, but it remains limited. A systematic review by Spet et al. (2023) found that AMR in environmental hosts exhibited significant spatial clustering driven by anthropogenic contamination. Geospatial modeling conducted by Legenza et al. (2023) examined neighborhood-level antibiotic susceptibility in the United States and demonstrated how spatial heterogeneity can reveal local antibiotic-resistant hotspots. Kou *et al.* (2025) employed spatial panel data analysis to assess AMR trends in *E. coli* across China, exhibiting substantial spatial spillover effects. Bengtsson-Palme *et al.* (2023) stressed that environmental AMR surveillance requires spatially explicit frameworks given the uneven distribution of antimicrobial resistance genes (ARGs) worldwide.

In these examples, most spatial AMR studies focus on environmental or human health data. Very few studies on AMR in low-income livestock countries exist, even though these nations face the most severe AMR challenges (Iskandar *et al.*, 2021). Thus, employing spatial techniques to analyze livestock resistance data bridges a major methodological and geographic gap. The incorporation of spatial analysis enables a clearer understanding of how AMR spreads across nations – whether through livestock trade, shared water sources, or farm management practices. This abides with One Health principles, highlighting the interconnectedness of humans, animals, and the environment (Trinchera *et al.*, 2025; Panicker *et al.*, 2025). The application of ML to livestock AMR in LMICs is underexplored, even though it has been widely adopted in clinical AMR modeling. The few studies that compared livestock AMR models show that ML can outperform classical methods in predictive accuracy.

IDENTIFIED GAPS IN THE UTILIZATION OF SPATIAL ANALYSIS AND PREDICTIVE MODELLING FOR AMR IN LIVESTOCK

Although substantial progress has been made in understanding AMR patterns globally, this literature identifies persistent gaps in the utilization of spatial and predictive analyses for AMR in livestock.

Limited Spatial Studies of AMR in Livestock Across LMICs

Despite improvements in recognition of the spatial determinants of AMR, few studies have employed spatial autocorrelation techniques, such as Global Moran's I or LISA, to analyze livestock datasets in LMICs. Tang *et al.* (2023) note that most AMR studies focus on clinical pathogens in human hospitals, with little emphasis on geospatial epidemiology in animal production systems. Similarly, Venkateswaran et al. (2024) emphasized the scarcity of spatially disaggregated livestock AMR data, due to incomplete laboratory coverage and fragmented reporting structures. As a result, the lack of spatial maps highlighting clusters, hotspots, or emerging threats within livestock systems affects policymaking.

The availability of a global AMR surveillance repository represents a significant advance in consolidating livestock AMR data, yet these data are underused in the scientific literature. Studies show that many researchers rely on small-scale or local datasets, mainly because global AMR repositories are relatively new and require advanced analytical skills. However, this resulted in a lack of comprehensive multi-country LMIC analyses that employed standard comparable livestock AMR data for predictive and spatial modeling. These gaps support the relevance and novelty of this study.

Underutilization of Machine Learning in Spatial AMR Modeling

Researchers (Prestinaci *et al.*, 2015; Chokshi et al., 2019) emphasized the dynamic complexity of AMR, yet most studies rely on classical statistical models, despite ML's capacity to model nonlinear relationships between species, pathogens, antimicrobial classifications, and environmental conditions. Machine learning models such as XGBoost, decision trees, and random forests are underused in AMR surveillance, especially in LMIC livestock settings, where data may be incomplete or imbalanced.

Lack of Integrated Approaches Combining Spatial Statistics with Predictive Models.

Some studies explain AMR patterns, others explore predictive modeling, and very few incorporate spatial statistics with ML. WHO (2021) 's Global strategy highlights the importance of system-level surveillance; however, current research rarely combines autocorrelation detection with regression or ML-based predictors. This limits the ability to understand not only where AMR occurs, but also why it emerges in a specific nation and production system.

CONCLUSION

In conclusion, this review shows that AMR in livestock exhibits pronounced spatial heterogeneity, influenced by AMU, production patterns, environmental contamination, and socio-economic factors. Global databases such as ResistanceBank provide a substantial foundation for robust analyses, but are limited by uneven geographical coverage and weak One Health integration. Beyond descriptive analysis, integrating spatial statistics with predictive modeling offers a robust framework for advancing livestock AMR surveillance towards risk identification. Overall, a shift towards spatially informed predictive modeling approaches will strengthen livestock AMR research, enable the identification of resistance hotspots and elucidation of resistance drivers, and support targeted antimicrobial stewardship and interventions.

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