



THE UNIVERSITY *of* EDINBURGH

**The Royal (Dick) School of Veterinary Studies
College of Medicine and Veterinary Medicine**

Master of Science in One Health Thesis

**A Systemic Review of Phenotypic Antimicrobial Resistance in
Non-Typhoidal *Salmonella* (NTS) Isolated from Food Animals in
Africa**

by

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Word count: 8, 506 words (Excluding the reference list and supplementary materials)

A dissertation submitted in partial fulfilment of the requirements for the degree of Master of Science in One Health at the University of Edinburgh

Acknowledgements

To begin with, I would like to express my sincere gratitude to my MSc supervisors, Dr. Deborah Hoyle and Dr. Jessica Hite. The invaluable support, guidance, and constructive feedback I have received from you both have been instrumental in my success. I extend my heartfelt appreciation to the entire One Health Programme team at the University of Edinburgh, with special thanks to Dr. Neil Anderson and Dr. Glen Cousquer, whose assistance has been pivotal in helping me reach this milestone in my academic pursuits. I would also like to thank Gilbert Eshun and Irene Wainaina, for helping with the screening of the abstracts of the articles. Undoubtedly, my family deserves a special mention for their steadfast support and patience throughout this journey. Last but not least, I am forever grateful to my dear mother for her constant prayers and encouragement, which has been a driving force behind my accomplishments.

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LIST OF ABBREVIATIONS

AMR: Antimicrobial Resistance

MDR: Multi-Drug Resistance

MGE: Mobile Genetic Element

OH: One Health

OHHEP: One Health High-Level Expert Panel

ARG: Antimicrobial Resistant Gene

ARB: Antimicrobial Resistant Bacteria

NTS: Non-Typhoidal *Salmonella*

HGT: Horizontal Gene Transfer

WHO: World Health Organization

WOAH: World Organization for Animal Health

FAO: Food and Agriculture Organisation

WHOCIA: World Health Organization Critically Important Antimicrobials

GLASS: Global Antimicrobial System Surveillance System

AMU: Antimicrobial Use

GDP: Gross Domestic Product

UNEP: United Nations Environmental Programme

PRISMA: Preferred Reporting Items for Systematic Reviews and Meta-Analysis

EMBASE: Excerpta Media Database

NARMS: National Antimicrobial Resistance System

ECDC: European Center for Disease Prevention and Control

EFSA: European Food Safety Authority

EMA: European Medicine Agency

ASLM: African Society for Laboratory Medicine

MAAP: Mapping Antimicrobial Resistance and Antimicrobial Use Partnership

CDC: Center for Diseases Control and Prevention

AIC: Akaike Information Criterion

QAIC: Quasi Akaike Information Criterion

Q-Q: Quantile-Quantile

GLM: Generalized Linear Model

MeSH: Medical Subheadings

TW: Text Word

ERY: Erythromycin

STR: Streptomycin
TET: Tetracycline
AMP: Ampicillin
NIT: Nitrofurantoin
KAN: Kanamycin
NAL: Nalidixic acid
SOX: Sulfisoxazole
AMC: Amoxicillin-clavulanic acid
AMX: Amoxicillin
COT: Co-trimoxazole
CTX: Cefotaxime
SMX: Sulfamethoxazole
TMP: Trimethoprim
CFX: Cefuroxime
ETH: Ethiopia
NGA: Nigeria
ZAF: South Africa
KEN: Kenya
UGA: Uganda
RWA: Rwanda
SEN: Senegal
GHA: Ghana
BEN: Benin
TGO: Togo
EGY: Egypt
DZA: Algeria
MAR: Morocco
TUN: Tunisia
LBY: Libya
ZMB: Zambia
ZWE: Zimbabwe
CMR: Cameroon

Introduction

This study focuses on the antimicrobial resistance (AMR) of non-typhoidal (NTS) *Salmonella* isolated from cattle, sheep, pigs, chickens, goats, turkeys, and farm environments across Africa using point prevalence surveys reporting phenotypic AMR from the year 2000 to 2023. The project's main objective was to understand how the patterns of AMR in NTS vary across the African continent. The study aims to use a systematic literature review approach to identify trends in AMR in the NTS in food animals. This study's findings will contribute to AMR surveillance efforts in Africa, additionally aiming to inform policymakers about areas necessitating urgent attention regarding data gaps about AMR on the African continent.

Antimicrobial Resistance and One Health

One Health is an integrated and collaborative approach that aims to achieve the optimal health of humans, animals, and ecosystems in a sustainable manner. This approach recognises the interconnectedness of human health, the health of domestic and wild animals, plant life, and the broader environment, including ecosystems. Therefore, it brings together different sectors, disciplines, and communities across different societal levels to collaborate in promoting health and addressing challenges to both human and environmental well-being (One Health High-Level Expert Panel (OHHLEP) *et al.*, 2022). For example, veterinarians, physicians, environmental scientists, ecologists, data scientists, modellers, and policymakers collaborate and address global challenges like antimicrobial resistance. The One Health approach enhances our understanding of antimicrobial resistance by integrating expertise from human medicine, veterinary science, and environmental studies, fostering a comprehensive and interconnected perspective on this complex issue.

Antimicrobial resistance can indeed be best addressed using a One Health approach. This is because the anthropogenic hypothesis of AMR involves the three One Health sectors (animal, human, and environment) meaning AMR genes can be transmitted locally, nationally, and internationally between animals, humans, insects, rodents, wild animals, and various environments (Figure 1). For example, the use/misuse of antimicrobials in humans or animals can exert selective pressure on bacteria, thus leading to the development of antimicrobial resistance genes (ARGs) and mobile genetic elements (MGEs) like plasmids which can be transmitted to other bacteria and consequently lead to multidrug resistance (MDR) across different animals and environment locally and internationally (Byrne *et al.*, 2019; Iskandar *et*

al., 2020; Allel *et al.*, 2023). These factors have led to increasing AMR trends across years in low and middle-income economies (Van Boeckel *et al.*, 2019; Tiseo *et al.*, 2020; Schar *et al.*, 2021; Ager *et al.*, 2023). Therefore, AMR is a One Health challenge and complex problem posing a threat to low and middle-income economies.

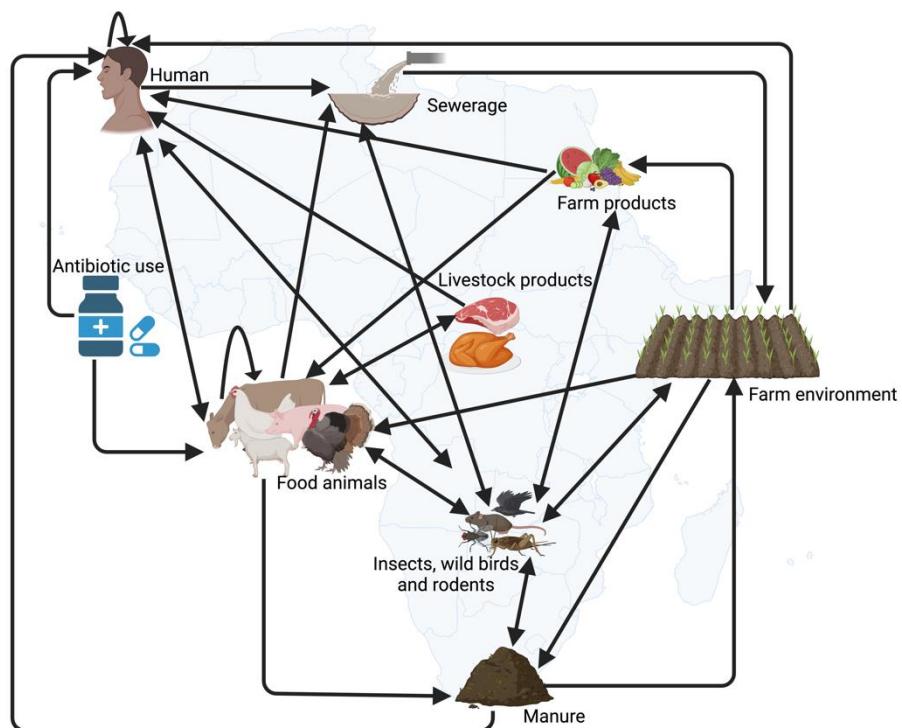


Figure 1: Potential AMR transmission between food animals, humans, environment, farm products, livestock products and insects, wild birds, and rodents.

Impact of Antibiotic Use on Agriculture

Antibiotics remain one of the most powerful biomedical tools used in treatment and prophylaxis in animal agriculture. However, their effectiveness has been threatened by their misuse/overuse in animal agriculture (Tiseo *et al.*, 2020). Furthermore, approximately 75% of antibiotics are used in food animals (Van Boeckel *et al.*, 2015). This over-reliance on antibiotics in raising livestock creates a significant public health risk through the development of resistance genes over time (Iskandar *et al.*, 2020). The transmission of resistance genes across species barriers, particularly from animals to humans, complicates the treatment of both veterinary and human infections, underscoring the interconnected nature of antimicrobial resistance in different ecological niches. In addition, the exposure of animals to antibiotics can disrupt the natural balance of bacterial communities in their gut (Zhou *et al.*, 2021). This disruption can lead to a cascade of unforeseen health problems for the animals. For instance,

the number of commensal gut bacteria can be reduced by antibiotics thus decreasing host-produced antimicrobial molecules in the gut, hence enabling the susceptibility of the bacteria (Brandl *et al.*, 2008; Hill *et al.*, 2010). Consequently, the misuse and overuse of antibiotics in animal agriculture pose significant risks to public health, animal welfare, and the continued effectiveness of these vital antimicrobial drugs, highlighting the need for more sustainable and responsible practices in livestock production.

Impacts of AMR on Farmers

Previous research has found that AMR can have negative effects on farmers and farmworkers who are routinely exposed to antibiotics (Addis *et al.*, 2011; Fagbamila *et al.*, 2023). Exposure to zoonotic bacteria including *Salmonella*, *Staphylococcus aureus*, and *Enterococcus faecium* may reduce farm productivity and pose significant safety risks due to potential human-to-human transmission at the farm level (Chang *et al.*, 2015; Manyi-Loh, Okoh and Lues, 2023). To fully understand these transmission risk dynamics, further research is essential. Of particular concern is the transmission of antimicrobial resistance genes to humans through various pathways, including the consumption of livestock products like eggs and meat (Addis *et al.*, 2011; Afema *et al.*, 2016; Uche, MacLennan and Saul, 2017; Akinyemi *et al.*, 2023). This transmission can occur at multiple stages, from the farm level during the slaughtering process through contamination, to subsequent points along the food chain (Asheg *et al.*, 2023). Given the complexity of these issues, future investigations should prioritise elucidating the intricate pathways of antimicrobial resistance transmission within the agri-food system. Particular emphasis should be placed on quantifying risks associated with livestock husbandry practices and food production processes, as these are critical points of intervention in mitigating the spread of AMR.

Mechanisms of AMR in *Salmonella*

Salmonella like many bacteria, has evolved sophisticated mechanisms to resist the effects of antibiotics (Tack *et al.*, 2020). These defence strategies are diverse and highly effective, allowing the bacteria to survive in the presence of various antimicrobial agents. The primary mechanisms include the active expulsion of antibiotics from bacterial cells through efflux pumps, the production of enzymes that neutralise antibiotics, the alteration of protein structures to prevent antibiotic binding, and the synthesis of alternative biomolecules to bypass affected metabolic pathways (Egorov, Ulyashova and Rubtsova, 2018; Liu *et al.*, 2018; Dawan *et al.*, 2022; Silva, Sundar and Khare, 2023). These adaptive mechanisms have contributed

significantly to *Salmonella*'s prominence as one of the most prevalent antimicrobial-resistant bacteria in food animals across Africa (Zishiri, Mkhize and Mukaratirwa, 2016). The widespread presence of resistant *Salmonella* strains in livestock poses a substantial risk to both animal health and food safety, with potential implications for human health as well.

AMR mitigation Strategies at the Farm level

In the veterinary sector, strategies for managing AMR primarily focus on implementing high animal welfare standards and robust biosecurity measures at the farm level. However, these approaches face significant challenges in low and middle-income regions of Africa, where maintaining farm hygiene is often difficult due to limited resources (Kamara *et al.*, 2017).

The full implementation of biosecurity procedures and efforts to promote animal welfare by reducing stock density are frequently hindered by economic constraints. This stark contrast with developed nations, which have implemented comprehensive strategies to mitigate AMR, highlights the need for tailored approaches in resource-limited settings.

Many developed countries have adopted multi-faceted approaches to mitigate AMR, encompassing policy changes, surveillance programmes, and targeted interventions across healthcare and agricultural sectors. A key component of these strategies is the implementation of computerised systems for tracking antimicrobial usage. For instance, the introduction of the yellow card initiative in Danish pig farms led to a remarkable 20% reduction in AMR prevalence since its introduction in 2010 (Dupont *et al.*, 2017; Lopes Antunes and Jensen, 2020). Similarly, countries like Italy and Spain have reported significant reductions in antimicrobial usage since 2014 following the introduction of electronic veterinary recipes (Foglia Manzillo *et al.*, 2023).

To address the high prevalence of AMR in African countries, where over-the-counter sale of antibiotics without prescription remains common, a multi-faceted approach is necessary. This should include targeted training programs for veterinarians, pharmacists, farm workers, and animal drug store employees on responsible antibiotic administration. Additionally, efforts to improve regulatory frameworks, enhance surveillance systems, and promote public awareness about the risks of AMR are crucial. By adapting successful strategies from high-income countries to the African context and addressing local challenges, significant progress can be made in reducing AMR prevalence and safeguarding both animal and human health across the continent.

Role of International Organizations in Mitigating AMR

International organizations have played an important role in the mitigation of AMR through the development of various strategies. For instance, the World Health Organization (WHO), the World Organisation for Animal Health (WOAH), and the Food and Agriculture Organization (FAO), formerly known as the Tripartite, established the Critically Important Antimicrobials for Human Medicine List (WHO CIA List) which classified antibiotics used in human and veterinary medicine into critically important, highly important and important (World Health Organization, 2019). This list helps manage AMR by ensuring the prudent use of critically important antimicrobials in both human and veterinary medicine (World Health Organization, 2019). At the continent level, the WHO has come up with initiatives like the WHO Global Antimicrobial Resistance Surveillance System (GLASS), which has made efforts to gather AMR data from participating countries (Kariuki *et al.*, 2022). While many African countries do not have surveillance systems, a few countries that do have these systems face challenges like a lack of data in animal agriculture, including data on antibiotic consumption, prevalence, and diversity in food animals.

This systematic review synthesises available literature on antimicrobial resistance in Africa, compiling and analysing data on AMR trends and resistance patterns. This study addresses critical knowledge gaps and provides a foundation for evidence-based policy decisions. The study's integrated approach, examining AMR across human, animal, and environmental contexts, aligns with the One Health paradigm. Consequently, it offers valuable insights for the readership of the *One Health* journal, contributing to the broader understanding of AMR's complex, interconnected nature across different health domains in the African continent.

Objectives

To identify the broad-scale patterns of antimicrobial resistance in *Salmonella* isolates from food animals across diverse African regions and countries across various species like chicken, cattle, pigs, sheep, goats and environmental samples

Aims

1. To identify and characterise antimicrobial resistance hotspots and areas of high prevalence across Africa.

2. To compare antimicrobial resistance profiles in *Salmonella* isolates across various food animal species, including poultry, cattle, swine, small ruminants (sheep and goats), and associated environmental samples.
3. To assess temporal trends and spatial variations in antimicrobial resistance patterns, providing insights into the evolution and spread of resistance across the continent.

A Systemic Review of Phenotypic Antimicrobial Resistance in Non-Typhoidal *Salmonella* (NTS) Isolated from Food Animals in Africa

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Abstract

Antimicrobial resistance (AMR) poses a significant threat to global public and animal health, with low- and middle-income countries (LMICs) disproportionately affected due to limited healthcare and veterinary resources. This systematic review investigates AMR trends in non-typhoidal *Salmonella* isolates from food animals and farm environments across Africa. Our analysis reveals an increase in overall AMR prevalence, from 26% in 2002 to 54% in 2022. Furthermore, our results reveal high resistance prevalence to erythromycin, especially in West Africa, with 84% resistance in chicken, 88% in pigs, and 95% in environmental isolates. These findings indicate the potential for widespread transmission of resistant bacteria through the food chain and environment, posing risks to both animal and human health. Our study underscores the urgent need for comprehensive antimicrobial stewardship programs, targeted farmer education initiatives, and the implementation of a One Health approach integrating human, animal, and environmental health sectors. We emphasise the critical importance of pan-African collaboration to address the escalating AMR threat, calling for substantial investments in robust surveillance systems and evidence-based interventions.

Introduction

Antimicrobial resistance (AMR) poses a significant threat to both animal and human sectors, particularly in low and middle-income countries (LMICs) (Van Boeckel *et al.*, 2019; Walsh *et al.*, 2023). In 2019 alone, bacterial AMR contributed to approximately 1.27 million deaths, emerging as one of the major causes of human deaths worldwide (Antimicrobial Resistance Collaborators, 2022). The impact of AMR extends beyond human health, significantly affecting animal health and global economics. In the livestock sector, AMR is projected to reduce production by up to 7.5% (Jonas *et al.*, 2017). Beyond the direct impact on livestock production, and animal and human health AMR also poses a significant economic burden. For instance, projections suggest that AMR could lead to a global gross domestic product (GDP) reduction of about 3.8% by 2050 (Rupasinghe *et al.*, 2024). These multifaceted consequences underscore the urgent need for comprehensive strategies to mitigate AMR across various sectors.

While the impacts of AMR are widespread, its drivers can be linked to specific practices, particularly in the agricultural sector. The intensification of livestock farming, driven by the growing global demand for animal-source protein, has played a crucial role in the development and spread of AMR (Henchion *et al.*, 2017). In these intensive livestock production systems, the widespread prophylactic and therapeutic use of antibiotics has become common practice, significantly contributing to the development of resistant bacteria (Akinyemi *et al.*, 2023). This connection between agricultural practices and AMR is particularly evident in certain regions and production systems. For instance, antimicrobial usage in livestock production is hypothesised to be one of the major drivers of AMR in agriculture, with cattle and poultry production systems in Africa accounting for the largest consumption of antibiotics (Van Boeckel *et al.*, 2015; Tiseo *et al.*, 2020).

The emergence of antimicrobial-resistant pathogens in these agricultural settings has far-reaching consequences for human health, with *Salmonella* serving as an example of this interconnection. *Salmonella*, especially non-typhoidal *Salmonella* (NTS), has emerged as a significant public health concern, particularly in LMICs. Africa bears 79% of global *Salmonella* infections, with approximately 77,500 deaths annually and a case-fatality ratio of 15.8% (Tack *et al.*, 2020). Conversely, developed countries have a lower disease burden in both human and animal populations, compared to LMICs like Africa (Antimicrobial Resistance Collaborators, 2022). This disparity in disease burden between developed countries and LMICs

can be attributed to the implementation of robust control strategies in more developed nations, including vaccine development and stringent biosecurity measures (Akegbe *et al.*, 2023). Non-typhoidal *Salmonella*, which comprises all *Salmonella* serotypes other than *Salmonella typhi* and *Salmonella paratyphi*, primarily causes gastroenteritis in humans and animals (Sodagari *et al.*, 2020). These bacteria spread through contaminated food or water, especially undercooked poultry, eggs, and unpasteurized dairy products (Ahmed *et al.*, 2019). Notably, farm workers face increased exposure to antibiotic-resistant *Salmonella* strains due to their close contact with livestock and animal waste (Soliani *et al.*, 2023).

The prevalence of antibiotic-resistant *Salmonella* in LMICs is exacerbated by multiple interconnected factors. Limited access to quality diagnostics leads to antibiotic over-prescription, while poor hygiene, poverty, and inadequate housing contribute to adverse health outcomes and widespread antibiotic use (Byrne *et al.*, 2019). In addition, natural disasters and conflicts further amplify AMR spread. In low-income countries, flooding can mix with groundwater, spreading antibiotic resistance genes, while wars exacerbate AMR through the migration of displaced populations who are already exposed (Asaduzzaman, 2022) and exposure to heavy metals in ammunition (Jerving, 2022). Inadequate investment in research, development, and surveillance poses significant barriers to tackling AMR in Sub-Saharan Africa (Allel *et al.*, 2023). This lack of funding is compounded by fragmented policy frameworks, with inconsistent and poorly executed national and regional policies governing antibiotic use, accessibility, and surveillance (Antimicrobial Resistance Collaborators, 2022; Gulumbe *et al.*, 2022). For instance, some countries allow over-the-counter antibiotic sales, while others have strict but poorly enforced regulations (Okolie *et al.*, 2023). These multifaceted challenges underscore the need for a One Health approach to effectively mitigate AMR across different sectors and levels of governance.

The One Health approach involves the integration of efforts across the human, veterinary, and environmental sectors. Recognising this necessity, in 2022, a quadripartite alliance including the World Health Organization (WHO), the Food and Agriculture Organisation (FAO), the UN Environmental Programme (UNEP), and the World Organisation for Animal Health (WOAH) developed a joint plan of action to address AMR (World Health Organization, 2023). This plan focuses on building One Health capacities for health systems, addressing food safety risks, and combating antimicrobial resistance (WHO, 2022). Moreover, the WHO has implemented

antimicrobial stewardship programs in Africa to reduce AMR by promoting the prudent use of antibiotics and changing prescription practices (WHO, 2019).

The global recognition of AMR as a critical threat has led to broader international initiatives. In 2015, the WHO urged countries to develop national action plans to counter rising AMR trends by promoting awareness and strengthening surveillance and research (Charani *et al.*, 2023). However, the implementation of these plans has been limited, particularly in Africa. By 2018, only seven Sub-Saharan African countries had established action plans meeting global standards for AMR prevention (Dakorah M.P. *et al.*, 2022). Furthermore, antimicrobial stewardship activities were reported in just three countries: Tanzania, Kenya, and South Africa. As of 2022, only six African nations had reported implementing their national AMR action plans (Shrestha, Zahra and Cannady, 2022). This slow progress highlights the urgent need for more widespread and coordinated efforts to effectively address AMR across the continent, emphasizing the gap between policy creation and practical implementation in many African countries. The disparity between global initiatives and local implementation underscores the complex challenges facing African nations in their fight against AMR, calling for tailored strategies that account for regional constraints and capabilities.

One of the key regional constraints hindering AMR mitigation efforts in Africa is the limited availability. Data availability plays a crucial role in understanding and addressing AMR. For example, data enables monitoring the spread of resistant bacteria, identifying trends, and assessing the impact of interventions on AMR (Fuhrmeister and Jones, 2019). However, Africa faces challenges in AMR data availability. Limited available AMR data are often kept as paper records and not available electronically, which may lead to loss or inaccessibility of the AMR data (Fleming Fund, 2022; Gulumbe *et al.*, 2022). In addition, lack of data on antimicrobial usage, AMR in the environment, limited surveillance, and scarcity of accurate and reliable data in many African countries highlight some of the data gaps in the region (Sartorius *et al.*, 2024). These data gaps hinder the development and implementation of evidence-based interventions that are crucial for mitigating AMR.

Recognizing these critical data challenges and their impact on AMR mitigation efforts, this study aims to address the gap in *Salmonella* AMR data across Africa through a comprehensive analysis of point prevalence surveys. Our research has three aims: (1) Identify and characterise antimicrobial resistance high-prevalence areas across Africa. (2) Compare and contrast AMR

profiles in *Salmonella* isolates across various food animal species (poultry, cattle, swine, sheep and goats) and associated environmental samples. (3) Assess temporal trends in AMR patterns to provide insights into the evolution and spread of resistance across the continent. This study seeks to provide valuable insights that can inform targeted surveillance efforts and guide the development of interventions and policies to mitigate AMR in Africa.

Methods

Search strategy

We searched three electronic databases, PubMed, Web of Science, and EMBASE, following PRISMA guidelines (Rethlefsen *et al.*, 2021). The literature search was limited to studies published between 2000-2023 which focused on antimicrobial resistance in *Salmonella*. In addition, grey literature including the National Antimicrobial Resistance Monitoring System (NARMS), FAO Antimicrobial Resistance, WHO GLASS, the European Centre for Disease Prevention and Control (ECDC), the European Food Safety Authority (EFSA), and the European Medicines Agency (EMA), Mapping Antimicrobial Resistance and Antimicrobial Use Partnership (MAAP), African Society for Laboratory Medicine (ASLM) and Africa CDC websites were searched. The literature was limited to studies written in English only.

The reference lists of included studies and other systematic literature reviews and metanalysis on antimicrobial resistance of foodborne pathogens were thoroughly searched to source additional articles. To ensure better literature search outcomes, search terms were divided into different concepts such as “livestock”, “antimicrobial resistance”, “host”, “pathogen” and “Africa”. We did not include each country's name in the search term because it does not always produce good results. We used Boolean logic terms (“AND” and “OR”) to conduct our literature searches. The search terms were used to develop the text words (TW) and medical subject headings (MeSH). Each search term was modified to match the three database search requirements (Supplementary materials, S1). Three authors participated in the abstract screening process. Two authors independently reviewed each abstract, with any disagreements resolved through discussion or consultation with a third reviewer. This approach ensured a thorough and unbiased selection of relevant studies for our analysis.

Study inclusion and exclusion criteria

We included studies on antimicrobial resistance in *Salmonella* in food animals and products from cattle, sheep, goats, pigs, and poultry. Additionally, we considered environmental

samples, including farm environments, animal housing, soil, and manure at the farm level. Eligible studies were those conducted in Africa, written in English only, and involving the phenotypic detection of AMR. We excluded studies that focused on AMR in aquaculture, wild animals, insects, or animals other than food animals. Studies conducted outside Africa, those focused on imported food products from outside Africa, reviews, meta-analyses, book chapters, unrelated topics, and those involving genotypic detection of AMR were also excluded.

Data extraction and abstract screening

Records were exported from electronic databases to the Zotero reference manager for deduplication. Afterwards, the records were exported to a Microsoft Excel sheet for screening. The abstract screening was conducted by three independent screeners. Following the abstract screening, records were assessed for eligibility using the inclusion and exclusion criteria. A dataset was created in an Excel file with the following columns: doi, author, publication year, antimicrobial class, antimicrobial compound, species, number of isolates tested, number of isolates resistant, number of isolates susceptible, country, and region. In addition, to extract data from published graphs, the Web Plot Digitizer software was employed (Rohatgi, 2021).

Statistical Analysis

All the data analyses and maps generated in this study were conducted using R version 4.3.2 (R core Team, 2023). The data was pooled into (number of resistant isolates, number of susceptible isolates), country and year. The generalized linear models (GLMs) with quasibinomial distributions were utilised to determine the temporal antimicrobial resistance trends as previously described by Ager *et al.*, 2023 . The model was specified as follows including (number of resistant isolates, number of susceptible isolates), Year, country, region, species and antimicrobial and study id.

In this model, the response variable was the (number of resistant isolates and, the number of susceptible isolates). Fixed effects included year, country, region, species, and antimicrobial. To account for potential publication bias, we included a random effect for each study id. The model was weighted by the total number of isolates to account for variations in sample sizes across studies. We inputted raw isolate numbers for each antibiotic tested, pooled by country and year. This approach allows for appropriate weighting of studies based on their sample sizes, preventing large studies from dominating the analysis. To determine temporal

antimicrobial resistance trends, we employed `glm` with a quasibinomial distribution (Crawley, 2013).

Model Diagnostics

The quasi-Akaike Information Criterion (QAIC) was employed to address the overdispersion in our data (Burnham & Anderson, 2004). This approach is more appropriate for over-dispersed data compared to the standard AIC (Burnham and Anderson, 2004). We selected the model with the lowest QAIC value, balancing model fit and complexity. We calculated the QAIC using the formula below:

$$\text{QAIC} = (-2\log\text{Lik} / \hat{\epsilon}) + 2K$$

Where:

$\log\text{Lik}$ is the log-likelihood of the model

$\hat{\epsilon}$ is the estimated dispersion parameter

K is the number of parameters in the model

To validate our generalized linear model and ensure its assumptions were met, we conducted an assessment using standard diagnostic plots (Weisberg and Fox, 2011; Schweinberger, 2022). Our evaluation included (1) residuals vs. linear predictor plot (Figure 2a): This plot shows a relatively even scatter of residuals around zero across the range of linear predictors. While there is some vertical striping, which is not uncommon in binomial data, the overall pattern suggests that the assumptions of linearity and homoscedasticity are reasonably met. (2) The normal Q-Q plot (Figure 2b): The most of points closely follow the reference line, indicating that the residuals largely conform to a normal distribution. Minor deviations at the extremes are observed, which is not unusual for large datasets and binomial outcomes (Gelman and Hill, 2006). (3) Cook's distance plots (Figures 2c and 2d): These plots reveal that most observations have low Cook's distance values, suggesting limited individual influence on the model estimates. While a few points show higher Cook's distance values, this is expected in large datasets and does not necessarily indicate problematic observations given the robustness of generalized linear models to minor departures from assumptions (Hardin and Hilbe, 2012).

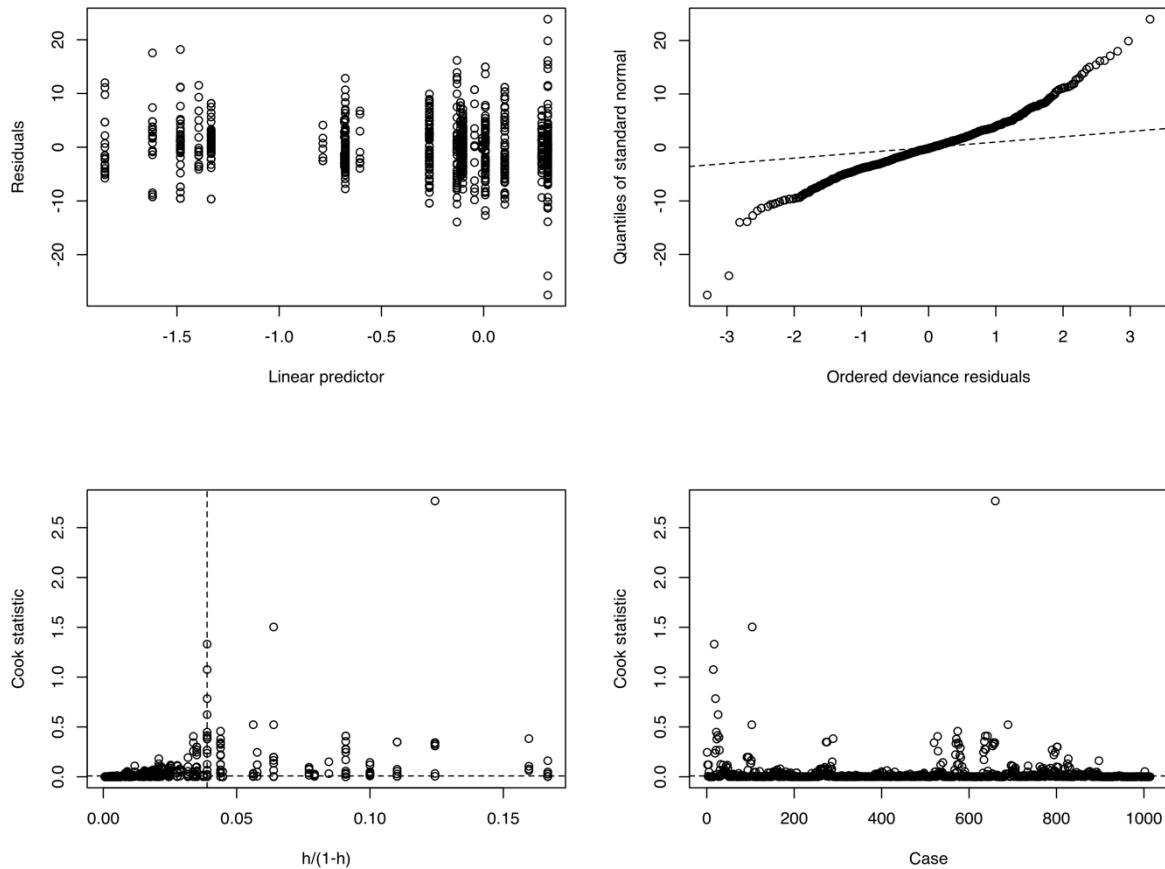


Figure 2: Diagnostic plots for the generalized linear model. (a) residuals vs. linear predictor: Shows the distribution of residuals across the range of predicted values, indicating homoscedasticity and linearity of the model. (b) Q-Q plot of ordered deviance residuals: Assesses the normality of residuals by comparing their distribution to theoretical quantiles of a normal distribution. (c) cook's statistic vs. leverage: Identifies potentially influential observations based on their impact on model coefficients and leverage. (d) Cook's statistic vs. Case number: Displays the influence of individual cases on the model fit across the dataset.

Results

Search results

Our initial search yielded articles published between 2000-2023 from the three databases. No relevant data/records were found in the grey literature sources. After deduplication, 136 records were excluded, and an additional 600 records on unrelated topics were removed. During the screening process, we excluded 22 reviews, 42 studies from regions other than Africa, 41 studies with missing prevalence data, 30 studies on other bacterial strains and hosts (e.g., insects and rats), and one duplicate record. This screening process resulted in 80 eligible records. To ensure a comprehensive review, we searched the reference lists of

included records and literature reviews on AMR in Africa, identifying an additional 15 relevant records. In total, 95 records were included in this review (Figure 3a).

The included studies covered data from 18 African countries. Most studies originated from three countries: Ethiopia (ETH) ($n = 23$; 24.5%), Nigeria (NGA) ($n = 19$; 20.2%), and South Africa (ZAF) ($n = 14$; 13.8%). To provide a regional perspective, we aggregated the results into different African regions: East Africa ($n = 30$): Ethiopia (ETH) ($n = 23$), Kenya (KEN) ($n = 3$), Uganda (UGA) ($n = 3$), and Rwanda (RWA) ($n = 1$). West Africa ($n = 28$): Nigeria (NGA) ($n = 19$), Senegal (SEN) ($n = 4$), Ghana (GHA) ($n = 3$), Benin (BEN) ($n = 1$), and Togo (TGO) ($n = 1$). North Africa ($n = 18$): Egypt (EGY) ($n = 8$), Algeria (DZA) ($n = 4$), Morocco (MAR) ($n = 3$), Tunisia (TUN) ($n = 2$), and Libya (LBY) ($n = 1$). Southern Africa ($n = 17$): South Africa (ZAF) ($n = 14$), Zambia (ZMB) ($n = 2$), and Zimbabwe (ZWE) ($n = 1$) and Central Africa: Cameroon (CMR) ($n = 2$) (Figure 3b).

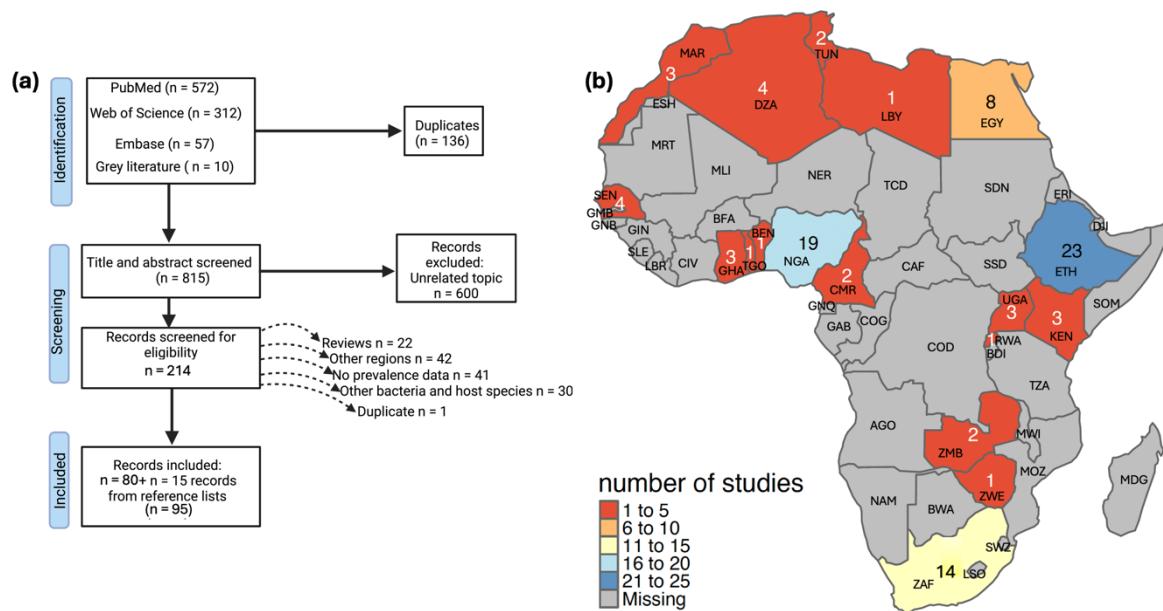


Figure 3: (a) PRISMA flow diagram showing the number of records included. (b) Map showing 18 countries included in the review and the number of studies per country. The grey-shaded countries represent countries with missing data.

Antimicrobial resistance temporal trends

Our results showed an overall increasing trend in the median AMR prevalence between 2002 and 2022, rising from 26% (95% CI: 18%-35%) to 54% (95% CI: 45%-63%), with a statistically significant difference ($p < 0.005$) (Figure 4). Further analysis at the regional level showed varying trends in AMR prevalence across different African regions.

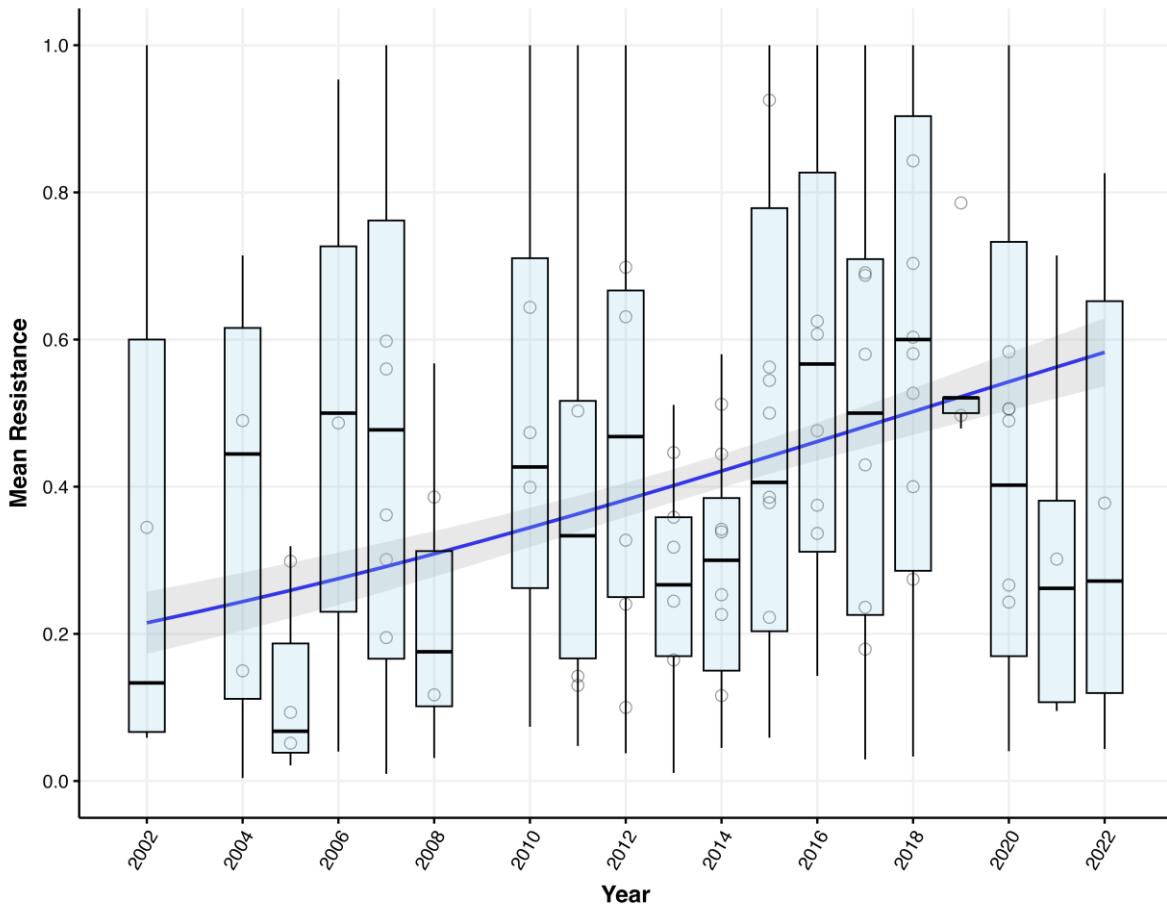
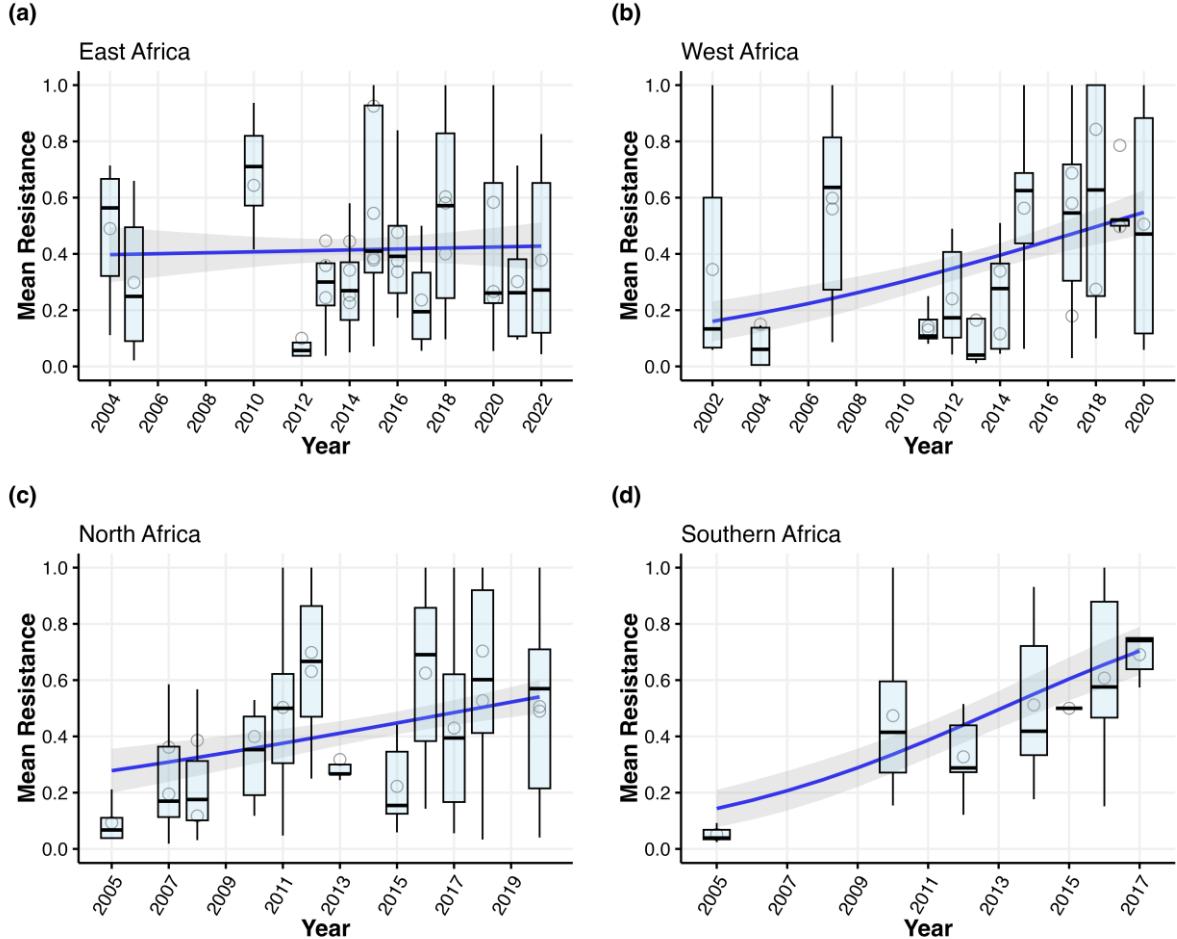


Figure 4: Temporal Trends in median AMR prevalence for Salmonella in Africa, 2002-2022. The median resistance prevalence is calculated from reported antibiotic compound prevalence data per study per year, irrespective of host or source. Each grey dot represents an individual survey ($n = 71$ surveys) included in the analysis. The horizontal box lines represent the first quartile, median, and third quartile. The blue line shows a weighted generalized linear model (GLM) regression fit, with the grey-shaded area indicating 95% confidence intervals. The model accounts for study ID as a random effect and is weighted by the number of isolates per study.

Northern Africa, Western Africa, and Southern Africa exhibited significantly increasing median AMR prevalence over the study period. In Western Africa, the median AMR prevalence increased from 19% (95% CI: 7%-43%) in 2002 to 54% (95% CI: 37%-70%) in 2020 ($p < 0.05$) (Figure 5b). Similarly, Northern Africa reported an increase from 22% (95% CI: 13%-34%) in 2005 to 60% (95% CI: 48%-72%) in 2019 ($p < 0.05$), while Southern Africa showed an increase from 13% (95% CI: 5%-28%) in 2005 to 65% (95% CI: 51%-75%) in 2017 ($p < 0.05$) (Figure 5c and 5d).

In contrast, the AMR prevalence in the Eastern African region remained constant, with a median prevalence of 39% (95% CI: 22%-58%) in 2004 and 39% (95% CI: 27%-52%) in 2022

(Figure 5a). Due to the limited number of records ($n = 2$), the Central African region was excluded from the temporal analysis.



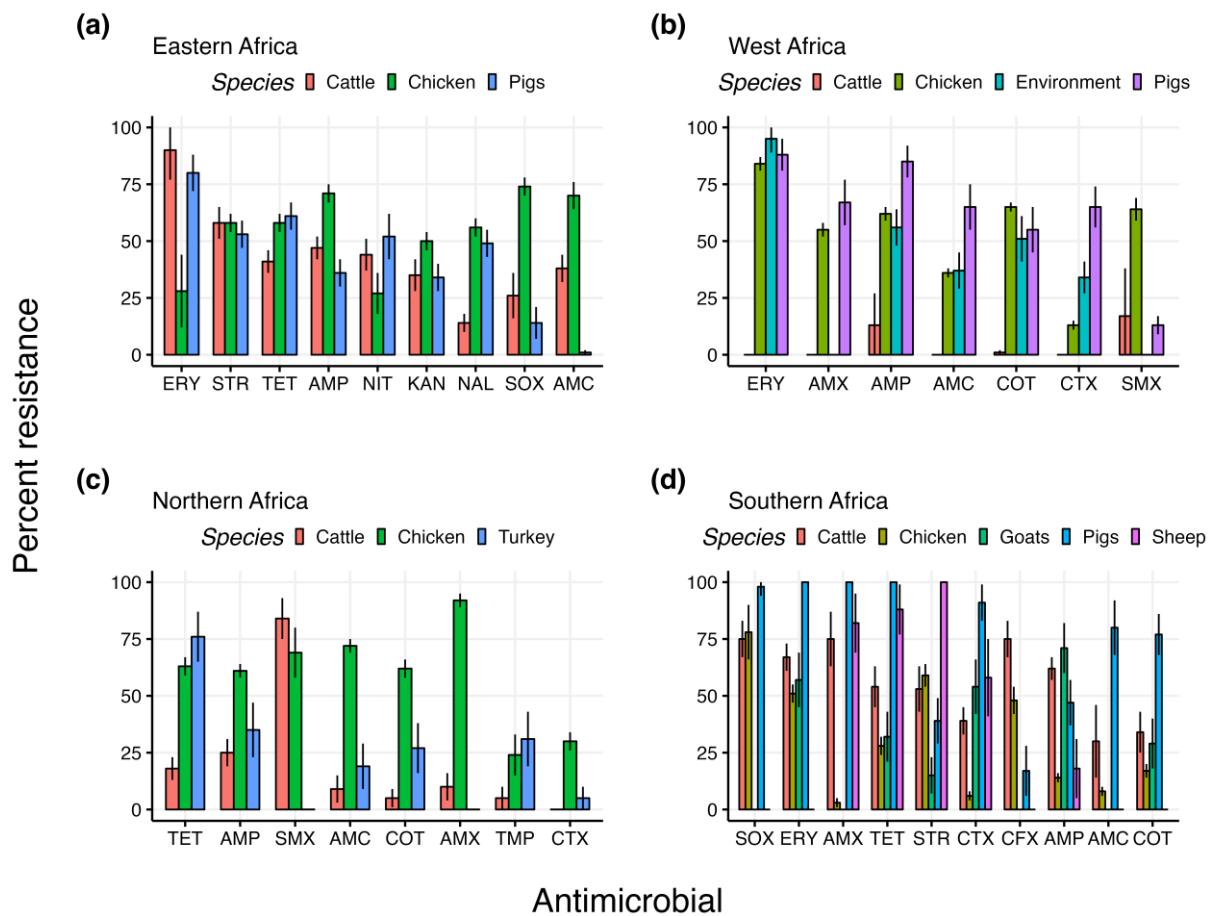
*Figure 5: Regional temporal trends in AMR prevalence for *Salmonella* across Africa. The Median resistance prevalence trends of AMR in *Salmonella* in 4 African regions (a) East Africa $n = 28$, (b) West Africa $n = 19$, (c) North Africa $n = 17$, and (d) Southern Africa $n = 7$). n represents the number of studies. Each grey dot represents an individual survey. The horizontal box lines indicate the first quartile, median, and third quartile of the prevalence data for each year. The red line shows a generalized linear model regression fit, with the grey-shaded areas representing 95% confidence intervals. The model accounts for study ID as a random effect and is weighted by the number of isolates per study. Prevalence was calculated from reported antibiotic compound prevalence data per study per year, irrespective of host or source by region.*

Antimicrobial prevalence across regions

We analysed antimicrobial resistance patterns across four African regions, considering various livestock species and antimicrobials. The number of isolates (n) is reported for key percentages to provide context. In Eastern Africa, erythromycin resistance was highest in cattle (90%, 95%

CI: 77%-100%, n = 21) and pigs (80%, 95% CI: 72%-88%, n = 95). Streptomycin resistance was notable in both cattle and chicken (58%, 95% CI: 51%-65%, n = 208 and 58%, 95% CI: 54%-62%, n = 534, respectively). Pigs showed low resistance to amoxicillin-clavulanic acid (1%, 95% CI: 0%-2%, n = 208) (Figure 6a). West Africa exhibited high erythromycin resistance across species, particularly in farm environment isolates (95% CI: 89%-100%, n = 55), pigs (88%, 95% CI: 81%-95%, n = 88), and chicken (84%, 95% CI: 81%-87%, n = 520). Ampicillin resistance was high in pigs (95% CI: 78%-92%, n = 101). Notably, cattle showed very low resistance to co-trimoxazole (1%, 95% CI: 0%-2%, n = 258), while chicken demonstrated low resistance to cefotaxime (13%, 95% CI: 11%-15%, n = 1106) (Figure 6b).

In Northern Africa, amoxicillin resistance was high in chicken (92%, 95% CI: 89%-95%, n = 256), and sulfamethoxazole resistance was high in cattle (84%, 95% CI: 75%-93%, n = 64). Turkey isolates showed high tetracycline resistance (76%, 95% CI: 65%-87%, n = 62). Lower resistance levels were observed for co-trimoxazole in cattle (5%, 95% CI: 1%-9%, n = 98) and cefotaxime in turkey (5%, 95% CI: 1%-10%, n = 64) (Figure 6c). Southern Africa reported 100% resistance to erythromycin in pigs (n=93) and streptomycin in sheep (n=33), albeit with relatively small sample sizes. In contrast, chicken isolates demonstrated low resistance to several antibiotics, including amoxicillin (3%, 95% CI: 1%-5%, n = 463), cefotaxime (6%, 95% CI: 4%-8%, n = 423), and amoxicillin-clavulanic acid (8%, 95% CI: 6%-10%, n = 571) (Figure 6d).



*Figure 6: Antimicrobial resistance patterns in *Salmonella* across different hosts (cattle, chicken, pigs, sheep, goats, turkey, and farm environment) and African regions (a) Eastern, (b) Western, (c) Northern, and (d) Southern Africa). The error bars represent $\pm 95\%$ confidence intervals. The drugs have been classified according to the WHO guidelines classification of importance. ERY-Erythromycin, STR-Streptomycin, TET-Tetracycline, AMP-Ampicillin, NIT-Nitrofurantoin, KAN-Kanamycin, NAL-Nalidixic acid, SOX-Sulfisoxazole, AMC-Amoxicillin-clavulanic acid, AMX-Amoxicillin, AMP-Ampicillin, COT-Co-trimoxazole, CTX-Cefotaxime, SMX-Sulfamethoxazole, TET-Tetracycline, TMP-Trimethoprim, CFX-Cefuroxime. n = number of isolates. Prevalence was calculated from reported antibiotic compound prevalence data, irrespective of host, year or source by region. (Supplementary Table 1)*

Resistance Prevalence by antibiotic class and host species

To determine patterns across different livestock species and antimicrobial classes. We assessed AMR prevalence by drug class at the host species level. Our analysis of AMR prevalence across host species and drug classes revealed varying patterns. Tetracycline resistance was highest in turkeys (76%) and cattle (68%), while sheep showed lower resistance (30%). For penicillin, pigs and environmental isolates demonstrated high resistance (73% and 66% respectively), contrasting with lower levels in cattle (18%). Sulfonamide resistance was most prevalent in sheep (91%) and environmental isolates (65%), compared to 27% in cattle. Cephalosporin

resistance varied widely, with sheep and goats showing higher prevalence (58% and 46%) than pigs and turkeys (8% and 5%). These patterns are illustrated in (Figure 7a,7b,7c and 7d). The data are aggregated at the antibiotic class level.

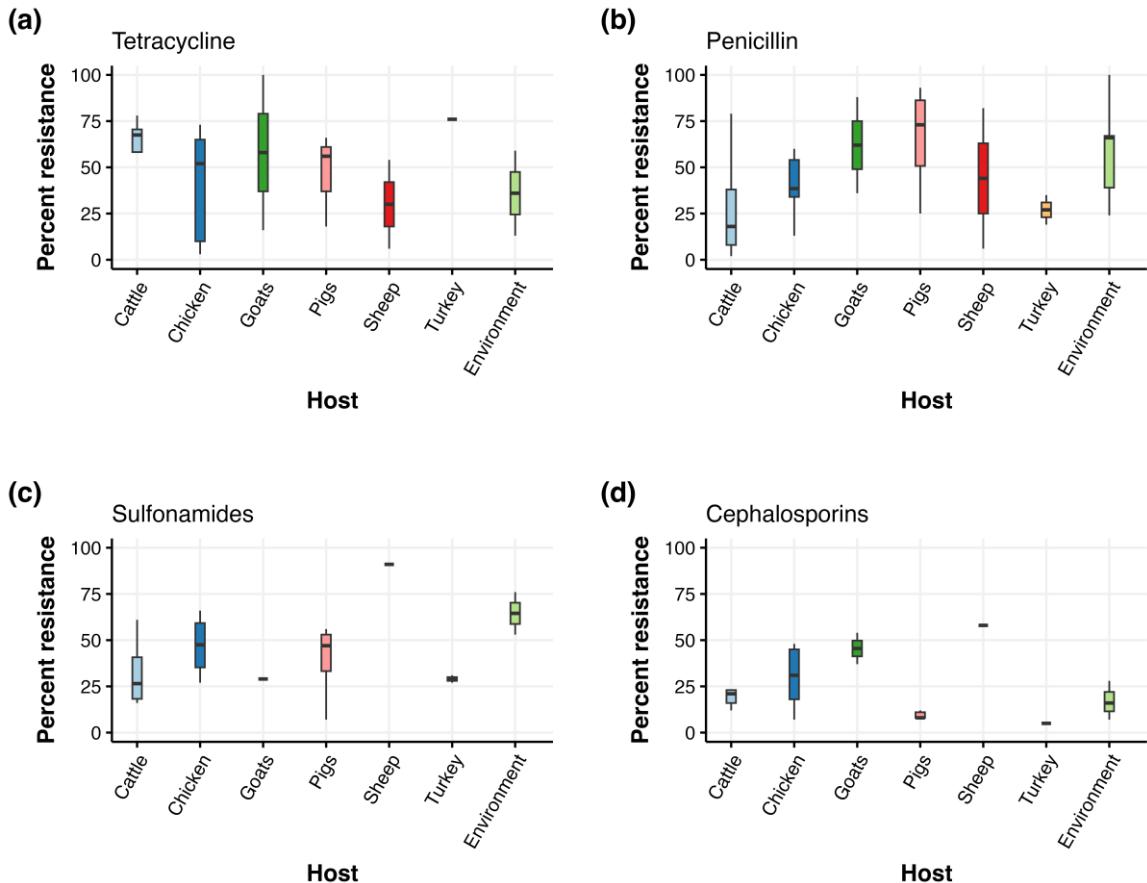


Figure 7: Showing the overall Median AMR prevalence of tetracycline (a), penicillin (b), cephalosporin (c) and sulfonamides (d) cephalosporins drug classes. The horizontal box lines represent the first quartile, median, and third quartile. The data was generated by aggregating Mean resistance prevalence by antibiotic class and host.

Discussion

Our results reveal an increasing trend of AMR prevalence in Africa, from 26% in 2002 to 54% in 2022. Our findings are consistent with previous research that has reported rising AMR levels in various livestock species, including pigs, chickens, and cattle, across low- and middle-income countries (Van Boekel *et al.*, 2019; Schar *et al.*, 2021; Pires *et al.*, 2022; Zhao *et al.*, 2024). The primary driver behind this increasing AMR trend might be the increasing use of antibiotics in livestock production systems to meet the increasing demand for animal protein sources (Paintsil *et al.*, 2021). This demand is fuelled by the rising gross domestic product

(GDP) in most developing countries, including African nations, thus improving the purchasing power for animal products (Mendelsohn *et al.*, 2023).

Despite the overall increasing trend, our study revealed significant regional variations. Notably, AMR levels in the Eastern African region remained relatively steady from 2004 to 2022, maintaining an average of 39%. This regional stability contrasts with the overall increasing trend observed across the continent, highlighting the complexity of AMR dynamics and the importance of considering local and regional factors. However, these findings should be interpreted with caution, as point prevalence surveys provide only periodic snapshots of antimicrobial resistance, in the absence of systematic surveillance (Ngoma *et al.*, 2023).

Our study reveals a concerning trend in AMR across Africa, particularly in livestock and the environment. A notable finding is the high prevalence of resistance to critically important antibiotics, especially erythromycin, in pigs, chickens, and environmental isolates. This corroborates previous research that found >80% median resistance prevalence of erythromycin in cattle and chickens infected with *Salmonella* (Ngoma *et al.*, 2023). The widespread resistance can be attributed to several interconnected factors, including the long-term use of erythromycin since the 1950s, its affordability, and broad-spectrum activity (Kiambi *et al.*, 2021). The ongoing use of erythromycin for prophylaxis, growth promotion, and disease treatment in African livestock further exacerbates the problem (Kiambi *et al.*, 2021; Bedekelabou *et al.*, 2022; Mankhomwa *et al.*, 2022). Additionally, the high AMR prevalence of erythromycin in the environment could be attributed to the widespread circulation of resistance genes such as *erm(B)* on mobile genetic elements in LMICs (Van Boeckel *et al.*, 2019; Liu *et al.*, 2023). This dissemination is likely facilitated by horizontal gene transfer (HGT), enabling the rapid spread of resistance between diverse bacterial species, even in the absence of direct antibiotic pressure (Thomas and Nielsen, 2005).

The high AMR prevalence extends beyond erythromycin to other antibiotic classes, particularly first-generation and broad-spectrum antibiotics. Penicillin and tetracycline exhibited significantly higher AMR prevalence compared to newer generations of antibiotics like cephalosporins. This trend is likely due to their historical use as growth promoters since the early 1950s and their continued preference in Africa for their affordability and broad-spectrum activity (Nelson and Levy, 2011; Manyi-Loh *et al.*, 2018). The inappropriate use of antibiotics is driven by various socioeconomic factors, including expensive veterinary services

that lead farmers to seek cheaper alternatives from unqualified individuals (Arvidsson *et al.*, 2022). This is particularly prevalent in rural or remote regions with limited access to licensed veterinarians. The lack of awareness among farmers about the importance of qualified veterinary care and proper antibiotic use, coupled with limited access to information regarding animal health, further contributes to the problem (Odey *et al.*, 2023). Consequently, farmers may unknowingly contribute to the development and spread of AMR by relying on untrained practitioners who may inappropriately prescribe or administer antibiotics.

Our analysis also revealed significant gaps in AMR research across different livestock species. While we found a high prevalence of sulfonamide resistance in sheep, this finding should be interpreted cautiously due to the underrepresentation of sheep-focused studies in our analysis ($n = 2$). AMR research predominantly focuses on cattle, poultry, and pigs, likely due to their economic importance and role in human health, particularly as sources of *Salmonella* infections (Soliani *et al.*, 2023). This skewed focus creates knowledge gaps in AMR patterns across diverse livestock species. To address this issue, Arnold and colleagues propose pan-national investments in scientific capacity building and comprehensive AMR surveillance systems involving various stakeholders, including national governments (Arnold *et al.*, 2024). This approach aims to ensure more balanced data collection across diverse African countries, habitats, and species, thereby providing a more comprehensive understanding of AMR dynamics in the region's livestock sector.

The complex interactions between the environment, animals, and humans in AMR spread highlight the need for a One Health approach. Our results on high erythromycin resistance in chickens, pigs, and the environment underscore the interconnected nature of AMR transmission across these domains. The use of animal manure and sewage sludge as fertilizers introduces antimicrobial residues, ARB, and ARGs into the soil, illustrating how agricultural and human activities contribute to environmental AMR. This introduction of AMR elements into soil creates potential pathways for their entry into various production systems, highlighting the risk of cross-sector transmission (Larsson and Flach, 2022). To effectively combat this multifaceted issue, a holistic strategy is essential. The One Health approach recognises that addressing AMR requires simultaneous efforts in human medicine, veterinary care, agriculture, and environmental protection. Implementing this approach can lead to more effective AMR mitigation strategies, including the development of integrated surveillance systems, improved waste management practices, farm-to-fork antibiotic stewardship programs, and

comprehensive environmental risk assessments. Implementing cross-sector collaboration in research and policy-making, can ensure coordinated interventions that address the complexities of AMR spread (Aslam *et al.*, 2021; Velazquez-Meza *et al.*, 2022).

Like many reviews, our study has limitations that should be considered when interpreting the results. Our search results cover AMR prevalence data from only 18 countries, which could be due to our focus on a single pathogen (*Salmonella*). While this approach allowed us to draw more reliable conclusions about AMR prevalence for *Salmonella*, it may have led to an underrepresentation of data. Expanding the scope of future studies to include multiple clinically relevant pathogens could provide a more comprehensive understanding of the AMR landscape across the African continent. Additionally, we only included studies published in English, potentially omitting relevant records published in other major languages like French, which is widely used in the West African region. To address this limitation, future reviews should aim for collaborations among researchers proficient in diverse languages spoken across the African continent. Lastly, due to inadequate data and missing sampling dates from multiple studies, we could not conduct spatio-temporal modelling of AMR prevalence using maps. This challenge highlights the need for more comprehensive and consistently reported data in AMR studies. Increased investment in quality research on antimicrobial resistance in bacteria in the African region could help address these issues and enable more sophisticated analyses of AMR trends over time and space.

Despite these limitations, our study provides valuable insights into the AMR prevalence of *Salmonella* across the African continent and underscores the importance of continued surveillance, research, and collaboration to mitigate the growing threat of antimicrobial resistance. By addressing the identified limitations and gaps in future studies, we can work towards a more comprehensive understanding of AMR in Africa and develop targeted interventions to mitigate its impact on public health. The adoption of a One Health approach, combined with increased investment in research and surveillance, offers a promising pathway to develop more nuanced, interconnected strategies that can effectively address the multifaceted challenges posed by AMR in our increasingly interconnected world.

Conflict of interest

The Authors declare no known conflict of interest.

Authors contribution

All the authors contributed to this study. E.A.O designed the study. E.A.O, GE, and IW did the literature search and records screening. EA conducted the data analysis. JLH assisted with developing R codes. EA prepared the manuscript. Supervision from study design, data collection, analysis, manuscript preparation, and proofreading of the final manuscript was done by DH and JLH.

Funding

This research received no specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Data availability

All data generated from this study are available on the Zenodo public repository:

<https://doi.org/10.5281/zenodo.12668662> (Ager *et al.*, 2024).

Code availability

R code used to analyse the data are available on the Zenodo public repository:

<https://doi.org/10.5281/zenodo.12668662> (Ager *et al.*, 2024).

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Discussion

Our study aimed to investigate the broad patterns of AMR in *Salmonella* isolated from food animals across Africa. Here, we focus on the issues and challenges faced during the study, incorporating insights from the One Health approach to enhance our understanding and provide recommendations.

This review aimed to identify trends in antimicrobial resistance (AMR) among *Salmonella* species across Africa, a critical endeavour for developing effective interventions to combat this growing public health threat (Zhou *et al.*, 2021). However, our efforts to conduct comprehensive spatiotemporal analyses and identify AMR hotspots and cold spots through spatial autocorrelation were hindered by data limitations. The primary obstacle in performing robust spatiotemporal and spatial autocorrelation analyses was incomplete data. Many countries lacked data on AMR across space and time, creating substantial temporal gaps. Despite these challenges, our study lays a foundation for future research and surveillance efforts. While our study highlights challenges and limitations affecting AMR surveillance in Africa, addressing these challenges is important for improving future research and interventions. Therefore, we make the following recommendations:

1. Enhancing surveillance is crucial for mitigating antimicrobial resistance (AMR) in Africa. Widespread adoption of the WHO Global Antimicrobial Resistance and Use Surveillance System would markedly improve data quality, consistency, and comparability across the continent (Okolie *et al.*, 2023). This standardized approach would enable more precise tracking of AMR trends, forming a robust basis for evidence-driven interventions. To successfully implement GLASS, countries must prioritize investments in laboratory infrastructure, workforce training, and stringent quality control measures.
2. The One Health approach to AMR surveillance recognizes the interconnectedness of human, animal, and environmental health. By integrating data from these three domains, we can gain a more comprehensive understanding of AMR transmission dynamics. This holistic perspective is particularly relevant in Africa, where close interactions between humans, livestock, and wildlife are common (Hassell *et al.*, 2019). Implementing this approach will require breaking down silos between different sectors and fostering collaboration among diverse experts including veterinarians, medical practitioners, environmental scientists, ecologists and data scientists.

3. Developing context-appropriate antimicrobial use policies is crucial given the diverse healthcare landscapes across Africa. The challenge lies in balancing AMR mitigation efforts with ensuring access to essential medications, especially in underserved areas (Loosli *et al.*, 2021). This requires nuanced, flexible regulatory frameworks that can be adapted to local contexts. Engaging community leaders and healthcare providers in policy development can ensure that strategies are both culturally sensitive and practically implementable.
4. Education and training programs are essential for mitigating AMR. By targeting key stakeholders such as healthcare providers, pharmacists, farmers, and the general public, we can promote responsible antimicrobial use practices (Fuller *et al.*, 2023). However, these initiatives must be tailored to local contexts and cultural norms to be effective. This may involve leveraging existing community structures and communication channels.
5. Strengthening research and innovation is vital for addressing knowledge gaps in AMR in the African context. Prioritizing longitudinal studies, increasing focus on AMR in environment research, developing cost-effective diagnostic tools, and exploring alternative therapies could yield valuable insights and solutions (Arnold *et al.*, 2024). However, this will require sustained funding and support for African researchers and institutions.
6. Fostering regional and international collaboration can leverage shared resources and expertise to tackle AMR more effectively. A pan-African AMR network could facilitate knowledge sharing and collaborative research, while engagement with global initiatives could accelerate the development of new treatments and diagnostic tools (Wernli *et al.*, 2022; Arnold *et al.*, 2024). However, ensuring equitable partnerships and building local capacity should be key considerations in these collaborations.

Implementing these recommendations will require sustained commitment, resources, and coordination among various stakeholders. While challenging, this comprehensive approach offers the best chance of effectively mitigating AMR in *Salmonella* and other pathogens

across Africa, ultimately protecting public health and preserving the efficacy of antimicrobial treatments for future generations.

Conclusion

Antimicrobial resistance poses a significant threat to both animal and public health, particularly in the African continent. This review has highlighted the broad-scale patterns of AMR prevalence in non-typhoidal *Salmonella* within livestock in Africa which appear to be increasing over the years despite mitigation efforts. The rise in AMR has been linked to various anthropogenic activities, underscoring the need for immediate action. Mitigation strategies including educational programs, strict legislation on antibiotic usage, improved hygiene and biosecurity practices, research and development, and increased surveillance are essential in mitigating the AMR phenomenon. However, these efforts are faced with challenges like limited data availability, data quality, lack of standardization of laboratory methods and guidelines, and underrepresentation of countries and animal species. Therefore, to effectively mitigate AMR, a comprehensive One Health approach is necessary. This multidisciplinary collaboration brings together various fields, including animal health, human health, environmental science, ecology, modelling, GIS, and policymaking. These collaborations can lead to data-driven decision-making and international cooperation, thus leading to the sharing of knowledge and the development of different strategies to mitigate the spread of antimicrobial resistance.

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Supplementary Information

Supplementary Material 1: (S1)

Database search terms

Databases

1. PubMed
2. Web of Science
3. EMBASE

1. PubMed Search terms

Antibiotic Resistance:

("drug resistance, microbial" [MeSH terms] OR ("antimicrobial" [TW] AND "resistan*" [TW]) OR ("antibacterial" [TW] AND "resistan*" [TW]) OR ("antibiotic" [TW] AND "resistan*" [TW]) OR (("drug" [TW] AND "resistan*" [TW]) AND (antibiotic [tw] OR antibiotics[tw])) OR "antimicrobial susceptibility" [TW] OR "antibacterial susceptibility" [TW] OR "antibiotic susceptibility testing" [TW] OR "antimicrobial susceptibility patterns" [TW] OR "antimicrobial stewardship" [MeSH Terms] OR "antimicrobial stewardship" [TW] OR "microbiological profile" [TW] OR "microbiological profiles" [TW] OR "microbiological profiling" [TW] OR "phylogenetic profile" [TW] OR "phylogenetic profiles" [TW] OR "phylogenetic profiling" [TW] OR "phenotypic" [TW])

Livestock:

("goats" [MeSH Terms] OR "goat" [TW] OR "goats" [TW] OR "capra" [TW] OR "caprine" [TW] OR "caprines" [TW] OR "cattle" [MeSH Terms] OR "cow" [TW] OR "cows" [TW] OR "cattle" [TW] OR "bovine" [TW] OR "bos" [TW] OR "sheep, domestic" [MeSH terms] OR "sheep" [TW] OR "lamb" [TW] OR "poultry" [MeSH Terms] OR "poultry" [TW] OR "turkey" [TW] OR "chicken" [TW] OR "duck" [TW] OR "swine" [TW] OR "sow" [TW] OR "pig" [TW] OR "pigs" [TW] OR "livestock" [MeSH Terms] OR ("livestock" [TW] AND "meat" [TW]) OR ("livestock" [TW] AND ("dairy" [TW] OR "milk" [TW])) OR "beef" [TW] OR "meat production" [TW] OR "dairy production" [TW] OR "dairy farm*" [TW] OR pork [TW] OR ("broiler" [TW] AND ("chick" [TW] OR "flock" [TW])) OR ("layer" [TW] AND ("chick" [TW] OR "flock" [TW])) OR "egg" [TW] OR "eggs" [TW] OR "cheese" [TW] OR

"milk" [TW] OR "cheese" [MeSH Terms] OR "Milk" [MeSH Terms] OR "cultured milk products" [MeSH Terms])

Bacteria:

("campylobacter*"[MeSH Terms] OR "campylobacter*"[TW] OR "campylobacters"[TW] OR "escherichia coli"[MeSH Terms] OR "e coli"[TW] OR "escherichia coli"[TW] OR "salmonella"[MeSH Terms] OR "salmonella"[TW] OR "salmonellas"[TW] OR "salmonellae"[TW] OR (Escherichia OR E. coli OR coliform OR STEC OR salmonella* OR salmonella spp. OR salmonella serovar* OR salmonella serotype* OR Nontyphoidal Salmonella NOT (typhoidal Salmonella) OR campylobacter spp. OR C. jejuni OR C. coli)

2. Web of Science

Livestock:

livestock OR cattle OR cow* OR bovine* OR beef OR herd OR milk OR cheese OR sheep* OR lamb* OR goat* OR pig* OR swine OR Sow OR meat OR pork OR chick* OR flock OR poultry OR egg* OR broiler OR turkey*

Bacteria:

bacteri* OR “Escherichia coli” OR “E. Coli” OR Salmonella* OR Campylobacter OR “enteric bacteria”

Antibiotic Resistance:

(antimicrob* NEAR/2 resistan*) OR (antibiotic* NEAR/2 resistan*) OR (drug NEAR/2 resistan*) OR (antibacter* NEAR/2 resistan*) OR (antimicrob* NEAR/2 susceptib*) OR (antibacter* NEAR/2 susceptib*) OR (antibiotic NEAR/2 susceptib*)

3. EMBASE

((antimicrobial OR antibiotic OR drug) AND (resistance OR resistant OR susceptibility)) AND ((conventional OR organic) AND (agriculture OR farming OR dairy OR livestock OR poultry OR “Escherichia coli” OR “E. Coli” OR Salmonella* OR Campylobacter))

Grey literature search terms:

(Antimicrobial resistance OR antibiotic resistance OR drug resistance) AND (bacteria species)

The grey literature to be searched.

- a. National Antibiotic Monitoring Program (USDA)
- b. NARMS Reports/Summaries | NARMS interactive data
- c. FAO Antimicrobial Resistance
- d. WHO GLASS database
- e. ECDC/EFSA/EMA first joint report on the integrated analysis of the consumption of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from humans and food-producing animals
- f. Antimicrobial resistance surveillance in Europe 2022 - 2020 data
- g. Estimating the burden of foodborne diseases (who.int)
- h. <https://africacdc.org/download/mapping-antimicrobial-resistance-and-antimicrobial-use-partnership-maap-country-reports/>
- i. <https://aslm.org/what-we-do/maap/>
- j. <https://africacdc.org/news-item/findings-in-amr-surveillance-data-across-africa-to-shape-health-policy-reform/>

Supplementary Material 2: (S2)

Table 1: Table of Surveys included in the review

doi	author	pub_date	country	region	species	no_isolate
10.1002/mbo3.1067	Dagnew et al.2020	2020	Ethiopia	Eastern Africa	Chicken	372
10.1002/vms3.762	Mohammed et al.2022	2022	Ethiopia	Eastern Africa	Chicken	230
10.1007/s00284-022-02900-x	Oueslati et al.2022	2022	Tunisia	Northern Africa	Chicken	962
10.1007/s10661-014-4218-3	Dahshan et al.2015	2015	Egypt	Northern Africa	Chicken	40
10.1007/s10661-014-4218-3	Dahshan et al.2015	2015	Egypt	Northern Africa	Environment	30
10.1007/s11250-008-9181-y	Zewdu and Cornelius 2009	2009	Ethiopia	Eastern Africa	Chicken	234
10.1007/s11250-008-9181-y	Zewdu and Cornelius 2009	2009	Ethiopia	Eastern Africa	Pigs	91
10.1007/s11250-008-9181-y	Zewdu and Cornelius 2009	2009	Ethiopia	Eastern Africa	Sheep	39
10.1007/s11250-014-0680-8	Igbinosa.2015	2015	South Africa	Southern Africa	Cattle	1312
10.1007/s11250-014-0680-8	Igbinosa.2015	2015	South Africa	Southern Africa	Goats	1088
10.1007/s12223-013-0270-6	Fashae and Hendricksen .2014	2014	Nigeria	West Africa	Pigs	1568
10.1016/j.actatropica.2018.11.003	Jaja et al.2019	2019	South Africa	Southern Africa	Cattle	258
10.1016/j.actatropica.2018.11.003	Jaja et al.2019	2019	South Africa	Southern Africa	Sheep	462
10.1016/j.actatropica.2022.106620	Ramtahal et al.2022	2022	South Africa	Southern Africa	Chicken	517
10.1016/j.foodcont.2020.107440	Kunadu et al.2020	2020	Ghana	West Africa	Environment	770

10.1016/j.heliyon.2018.e01025	Hiko, Adem et al.2018	2018	Ethiopia	Eastern Africa	Cattle	196
10.1016/j.ijfoodmicro.2006.04.018	Stevens et al.2006	2006	Senegal	West Africa	Cattle	4940
10.1016/j.ijfoodmicro.2021.109245	Raufu et al.2021	2021	Nigeria	West Africa	Pigs	208
10.1016/j.jgar.2018.04.009	Elkenany et al.2018	2018	Egypt	Northern Africa	Chicken	484
10.1016/j.lwt.2021.111834	Elshebrawy et al.2021	2021	Egypt	Northern Africa	Chicken	2528
10.1016/j.micpath.2017.02.042	Ed-Dra et al.2017	2017	Morocco	Northern Africa	Cattle	612
10.1016/j.prevetmed.2014.03.009	Ikwap et al.2014	2014	Uganda	Eastern Africa	Pigs	636
10.1017/S0950268814001708	Abd-Elghany et al.2014	2014	Egypt	Northern Africa	Chicken	2324
10.1017/S0950268816001126	Andoh et al.2016	2016	Ghana	West Africa	Chicken	846
10.1080/03079457.2012.667558	Makaya et al.2012	2012	Zimbabwe	Southern Africa	Chicken	1854
10.1089/fpd.2008.0150	Raufu et al.2009	2009	Nigeria	West Africa	Chicken	368
10.1089/fpd.2011.1032	Mezali et al.2012	2012	Algeria	Northern Africa	Cattle	832
10.1089/fpd.2018.2459	Fall-Niang et al.2019	2019	Senegal	West Africa	Chicken	3549
10.1089/fpd.2018.2562	Dekker et al.2019	2019	Ghana	West Africa	Chicken	144
10.1089/mdr.2009.0127	Wouafu et al.2010	2010	Cameroun	Central Africa	Chicken	1133
10.1089/mdr.2019.0357	Igbinosa et al.2021	2021	Nigeria	West Africa	Pigs	1932
10.1089/vbz.2011.0667	Soufie et al.2012	2012	Tunisia	Northern Africa	Chicken	370
10.1111/j.1365-2672.2005.02618.x	Cardinale et al.2005	2005	Senegal	West Africa	Chicken	693
10.1111/j.1439-0450.2006.00900.x	Molla, et al.2006	2006	Ethiopia	Eastern Africa	Pigs	2256
10.1111/j.1863-2378.2008.01164.x	Elgroud et al.2009	2009	Algeria	Northern Africa	Chicken	275

10.1111/jam.12304	Raufu et al.2013	2013	Nigeria	West Africa	Cattle	214
10.1111/jam.12304	Raufu et al.2013	2013	Nigeria	West Africa	Chicken	364
10.1111/jam.13697	Abdeen et al.2018	2018	Egypt	Northern Africa	Chicken	204
10.1111/jam.15477	Shittu et al.2022	2022	Nigeria	West Africa	Chicken	506
10.1111/jfs.12783	Adiseyun et al.2020	2020	South Africa	Southern Africa	Chicken	4
10.1111/lam.13106	Ammar et al.2019	2019	Egypt	Northern Africa	Chicken	450
10.1111/zph.12490	Eguale et al.2018	2018	Ethiopia	Eastern Africa	Cattle	900
10.1111/zph.12490	Eguale et al.2018	2018	Ethiopia	Eastern Africa	Chicken	468
10.1111/zph.12490	Eguale et al.2018	2018	Ethiopia	Eastern Africa	Pigs	144
10.1155/2016/4290506	Ejo et al.2016	2016	Ethiopia	Eastern Africa	Cattle	36
10.1155/2016/4290506	Ejo et al.2016	2016	Ethiopia	Eastern Africa	Chicken	45
10.1155/2017/4317202	Azage and Kibret 2017	2017	Ethiopia	Eastern Africa	Cattle	231
10.1155/2018/9794869	Ketema et al.2018	2018	Ethiopia	Eastern Africa	Cattle	476
10.1155/2020/1910630	Asfaw et al.2020	2020	Ethiopia	Eastern Africa	Chicken	450
10.1155/2022/5121273	Ramtahal et al.2022	2022	South Africa	Southern Africa	Chicken	4410
10.11648/j.ajhr.2015030 2.14	Nchawa et al.2015	2015	Nigeria	West Africa	Chicken	900
10.11648/j.ajhr.2015030 2.14	Nchawa et al.2015	2015	Nigeria	West Africa	Environment	1200
10.1186/s12866-016-0638-2	Eguale et al.2016	2016	Ethiopia	Eastern Africa	Cattle	390
10.1186/s12866-022-02504-2	Gebeyehu et al.2022	2022	Ethiopia	Eastern Africa	Cattle	360
10.1186/s12866-023-02901-1	Akinyemi et al.2023	2023	Nigeria	West Africa	Chicken	1104
10.1186/s12879-017-2437-2	Abdi, Reta, et al.2017	2017	Ethiopia	Eastern Africa	Chicken	450
10.1186/s12917-017-1050-3	Djeffal et al.2017	2017	Algeria	Northern Africa	Chicken	585

10.1186/s12917-017-1291-1	Odoch et al.2017	2017	Uganda	Eastern Africa	Chicken	234
10.1186/s12917-018-1539-4	Eguale Tadesse 2018	2018	Ethiopia	Eastern Africa	Chicken	416
10.1186/s12917-019-1867-z	Elkenany et al.2019	2019	Egypt	Northern Africa	Chicken	2508
10.1186/s12917-021-02938-2	Jibril et al.2021	2021	Nigeria	West Africa	Chicken	130
10.1186/s13104-019-4068-8	Langata, Lydia, et al.2019	2019	Kenya	Eastern Africa	Chicken	144
10.1186/s13104-019-4341-x	Deguenon et al.2019	2019	Benin	West Africa	Chicken	160
10.1186/s13104-019-4516-5	Tadesse et al.2019	2023	Ethiopia	Eastern Africa	Chicken	996
10.1186/s13756-015-0062-7	Garedew et al.2015	2015	Ethiopia	Eastern Africa	Cattle	424
10.1186/s41043-017-0131-z	Wabeto et al.2017	2017	Ethiopia	Eastern Africa	Cattle	672
10.12834/VetIt.2553.167 33.2	Kolapo et al.2022	2022	Nigeria	West Africa	Chicken	168
10.1371/journal.pone.015 2130	Afema et al.2016	2016	Uganda	Eastern Africa	Chicken	1430
10.1371/journal.pone.026 2308	Worku et al.2022	2022	Ethiopia	Eastern Africa	Cattle	138
10.1371/journal.pone.027 3790	Tonjo et al.2022	2022	Ethiopia	Eastern Africa	Cattle	438
10.1371/journal.pone.028 1329	Igbinosa et al.2023	2023	Nigeria	West Africa	Chicken	516
10.1371/journal.pone.028 7043	Tigabie et al.2023	2023	Ethiopia	Eastern Africa	Chicken	276
10.1371/journal.pone.029 0754	Fagbamila et al.2023	2023	Nigeria	West Africa	Chicken	1974
10.14202/vetworld.2020.2528-2533	Kapena et al.2020	2020	Zambia	Eastern Africa	Chicken	46
10.1556/030.66.2019.034	Ajayi et al.2019	2019	Nigeria	West Africa	Cattle	132
10.1556/030.66.2019.034	Ajayi et al.2019	2019	Nigeria	West Africa	Chicken	408
10.1556/030.66.2019.034	Ajayi et al.2019	2019	Nigeria	West Africa	Sheep	192
10.20506/rst.36.3.2726	El Allaoui et al.2017	2017	Morocco	Northern Africa	Turkey	930
10.21161/mjm.211115	Iweriebor et al.2021	2021	South Africa	Southern Africa	Cattle	1296

10.2147/IDR.S217421	Akinola et al.2019	2019	South Africa	Southern Africa	Chicken	605
10.3329/jhpn.v27i5.3637	Akoachare et al.2009	2009	Cameroon	Central Africa	Cattle	900
10.3382/ps.2011-01620	Bounar-Kechih et al.2012	2012	Algeria	Northern Africa	Chicken	424
10.3390/ani11041013	Manishimwe et al.2021	2021	Rwanda	Eastern Africa	Cattle	48
10.3390/ani11041013	Manishimwe et al.2021	2021	Rwanda	Eastern Africa	Chicken	48
10.3390/ani11041013	Manishimwe et al.2021	2021	Rwanda	Eastern Africa	Goats	48
10.3390/ani11041013	Manishimwe et al.2021	2021	Rwanda	Eastern Africa	Pigs	48
10.3390/antibiotics10070773	Agbaje et al.2021	2021	Nigeria	West Africa	Chicken	110
10.3390/antibiotics8020075	Oloso et al.2019	2019	Nigeria	West Africa	Chicken	9072
10.3390/app8112088	Manyi-Loh et al.2018	2018	South Africa	Southern Africa	Cattle	330
10.3390/ijerph20020984	Manyi-Loh et al.2023	2023	South Africa	Southern Africa	Pigs	630
10.3390/pathogens10030273	Mokgophi et al.2021	2021	South Africa	Southern Africa	Chicken	3408
10.36380/scil.2019.wvj20	Tsepo et al.2019	2019	South Africa	Southern Africa	Chicken	552
10.3855/jidc.103	Bouchrif et al.2009	2009	Morocco	Northern Africa	Cattle	728
10.3855/jidc.17553	Abayneh et al.2023	2023	Ethiopia	Eastern Africa	Chicken	168
10.3855/jidc.3861	Onyango et al.2014	2014	Kenya	Eastern Africa	Pigs	1615
10.3855/jidc.7437	Ammar et al.2016	2016	Egypt	Northern Africa	Chicken	170
10.3855/jidc.7885	Kemal et al.2016	2016	Ethiopia	Eastern Africa	Chicken	96
10.3855/jidc.909	Fashae et al.2010	2010	Nigeria	West Africa	Chicken	770
10.4102/ojvr.v83i1.1067	Zishiri et al.2016	2016	South Africa	Southern Africa	Chicken	1020

10.4102/ojvr.v83i1.1109	Madoroba et al.2016	2016	South Africa	Southern Africa	Cattle	330
10.4102/ojvr.v86i1.1667	Ahmed et al.2019	2019	Nigeria	West Africa	Chicken	462
10.4315/0362-028X.JFP-15-224	Iwu et al.2006	2006	South Africa	Southern Africa	Pigs	864
10.4315/0362-028x-72.11.2423	Dione et al.2009	2009	Senegal	West Africa	Chicken	9064
10.5430/jer.v6n1p35	Mulingisa-Muonga et al.2021	2021	Zambia	Eastern Africa	Chicken	45
10.5455/OVJ.2023.v13.i 5.17	Asheg et al.2023	2023	Libya	Northern Africa	Chicken	435
10.5829/idosi.ajbas.2016.8.3.23546	Tsegaye et al.2006	2006	Ethiopia	Eastern Africa	Chicken	572
10.5897/AJMR11.950	Fasure et al.2012	2012	Nigeria	West Africa	Chicken	576
10.5897/AJMR2020.943 7	Bedecklabou et al.2020	2020	Togo	West Africa	Chicken	28
10.5897/AJMR2020.943 7	Bedecklabou et al.2020	2020	Togo	West Africa	Pigs	13
10.9734/mrji/2019/v28i4 30136	Ibrahim et al.2019	2019	Nigeria	West Africa	Chicken	1001
PMID: 23057283	Wesonga et al.2010	2010	Kenya	Eastern Africa	Chicken	130

Table 2: Table of Regional Resistance Patterns Dataset

Compound	Species	Region	Mean	NIsolates	CILow	CIHigh
AMC	Cattle	Central Africa	91	75	85	97
AMK	Cattle	Central Africa	9	75	3	15
AMP	Cattle	Central Africa	100	75	100	100
CAZ	Cattle	Central Africa	33	75	22	44
CHL	Cattle	Central Africa	49	75	38	60
CIP	Cattle	Central Africa	1	75	0	3

COT	Cattle	Central Africa	61	75	50	72
DOX	Cattle	Central Africa	68	75	57	79
FFC	Cattle	Central Africa	51	75	40	62
GEN	Cattle	Central Africa	16	75	8	24
OFX	Cattle	Central Africa	7	75	1	13
TET	Cattle	Central Africa	100	75	100	100
AMC	Chicken	Central Africa	1	103	0	3
CHL	Chicken	Central Africa	1	103	0	3
COT	Chicken	Central Africa	12	103	6	18
NAL	Chicken	Central Africa	34	103	25	43
STR	Chicken	Central Africa	45	103	35	55
TET	Chicken	Central Africa	84	103	77	91
TMP	Chicken	Central Africa	19	103	11	27
AMC	Cattle	Eastern Africa	38	264	32	44
AMK	Cattle	Eastern Africa	17	78	9	25
AMP	Cattle	Eastern Africa	47	359	42	52
AMX	Cattle	Eastern Africa	49	78	38	60
CAZ	Cattle	Eastern Africa	4	23	0	12
CFL	Cattle	Eastern Africa	31	112	22	40
CHL	Cattle	Eastern Africa	22	300	17	27
CIP	Cattle	Eastern Africa	11	229	7	15
CLI	Cattle	Eastern Africa	38	56	25	51
COT	Cattle	Eastern Africa	12	320	8	16
CRO	Cattle	Eastern Africa	23	56	12	34

CTX	Cattle	Eastern Africa	52	63	40	64
ERY	Cattle	Eastern Africa	90	21	77	100
FOX	Cattle	Eastern Africa	9	103	3	15
GEN	Cattle	Eastern Africa	10	333	7	13
KAN	Cattle	Eastern Africa	35	204	28	42
NAL	Cattle	Eastern Africa	14	286	10	18
NEO	Cattle	Eastern Africa	6	108	2	10
NIT	Cattle	Eastern Africa	44	221	37	51
OXT	Cattle	Eastern Africa	82	28	68	96
PMB	Cattle	Eastern Africa	4	28	0	11
SMX	Cattle	Eastern Africa	43	28	25	61
SOX	Cattle	Eastern Africa	26	80	16	36
STR	Cattle	Eastern Africa	58	208	51	65
TET	Cattle	Eastern Africa	41	342	36	46
TMP	Cattle	Eastern Africa	3	136	0	6
AMC	Chicken	Eastern Africa	70	240	64	76
AMP	Chicken	Eastern Africa	71	568	67	75
AMX	Chicken	Eastern Africa	29	154	22	36
CAZ	Chicken	Eastern Africa	22	23	5	39
CFL	Chicken	Eastern Africa	27	93	18	36
CFX	Chicken	Eastern Africa	5	63	0	10
CHL	Chicken	Eastern Africa	45	570	41	49
CIP	Chicken	Eastern Africa	33	603	29	37
COT	Chicken	Eastern Africa	52	551	48	56

CTX	Chicken	Eastern Africa	18	33	5	31
ERY	Chicken	Eastern Africa	28	29	12	44
FFC	Chicken	Eastern Africa	27	211	21	33
FOX	Chicken	Eastern Africa	33	168	26	40
GEN	Chicken	Eastern Africa	4	365	2	6
KAN	Chicken	Eastern Africa	50	494	46	54
NAL	Chicken	Eastern Africa	56	481	52	60
NEO	Chicken	Eastern Africa	11	160	6	16
NIT	Chicken	Eastern Africa	27	90	18	36
OXT	Chicken	Eastern Africa	53	133	45	61
SOX	Chicken	Eastern Africa	74	399	70	78
SPT	Chicken	Eastern Africa	54	26	35	73
STR	Chicken	Eastern Africa	58	534	54	62
TET	Chicken	Eastern Africa	58	543	54	62
TMP	Chicken	Eastern Africa	7	186	3	11
AMC	Pigs	Eastern Africa	1	208	0	2
AMP	Pigs	Eastern Africa	36	261	30	42
CB	Pigs	Eastern Africa	87	95	80	94
CFL	Pigs	Eastern Africa	4	204	1	7
CHL	Pigs	Eastern Africa	30	254	24	36
CIP	Pigs	Eastern Africa	19	261	14	24
COT	Pigs	Eastern Africa	16	204	11	21
CRB	Pigs	Eastern Africa	2	101	0	5
ERY	Pigs	Eastern Africa	80	95	72	88

GEN	Pigs	Eastern Africa	26	257	21	31
KAN	Pigs	Eastern Africa	34	250	28	40
NAL	Pigs	Eastern Africa	49	261	43	55
NEO	Pigs	Eastern Africa	8	102	3	13
NIT	Pigs	Eastern Africa	52	102	42	62
NOR	Pigs	Eastern Africa	21	95	13	29
OFX	Pigs	Eastern Africa	24	95	15	33
SMX	Pigs	Eastern Africa	80	148	74	86
SOX	Pigs	Eastern Africa	14	109	7	21
SPT	Pigs	Eastern Africa	19	196	14	24
STR	Pigs	Eastern Africa	53	261	47	59
TET	Pigs	Eastern Africa	61	261	55	67
TMP	Pigs	Eastern Africa	5	162	2	8
AMC	Cattle	Northern Africa	9	104	3	15
AMP	Cattle	Northern Africa	25	202	19	31
AMX	Cattle	Northern Africa	10	98	4	16
CFX	Cattle	Northern Africa	9	34	0	19
CHL	Cattle	Northern Africa	4	202	1	7
COT	Cattle	Northern Africa	5	98	1	9
CST	Cattle	Northern Africa	32	34	16	48
FAM	Cattle	Northern Africa	12	34	1	23
FFC	Cattle	Northern Africa	6	34	0	14
KAN	Cattle	Northern Africa	6	34	0	14
NAL	Cattle	Northern Africa	9	202	5	13

NIT	Cattle	Northern Africa	3	64	0	7
OFX	Cattle	Northern Africa	12	34	1	23
PEF	Cattle	Northern Africa	5	64	0	10
PIP	Cattle	Northern Africa	5	64	0	10
SMX	Cattle	Northern Africa	84	64	75	93
SOX	Cattle	Northern Africa	21	34	7	35
STR	Cattle	Northern Africa	21	202	15	27
TET	Cattle	Northern Africa	18	202	13	23
TIC	Cattle	Northern Africa	5	64	0	10
TIM	Cattle	Northern Africa	12	34	1	23
TMP	Cattle	Northern Africa	5	64	0	10
AMC	Chicken	Northern Africa	72	682	69	75
AMK	Chicken	Northern Africa	35	270	29	41
AMP	Chicken	Northern Africa	61	761	58	64
AMX	Chicken	Northern Africa	92	256	89	95
AZI	Chicken	Northern Africa	18	44	7	29
AZT	Chicken	Northern Africa	20	119	13	27
CEC	Chicken	Northern Africa	39	228	33	45
CFL	Chicken	Northern Africa	49	118	40	58
CFX	Chicken	Northern Africa	81	103	73	89
CHL	Chicken	Northern Africa	27	651	24	30
CIP	Chicken	Northern Africa	27	807	24	30
CLI	Chicken	Northern Africa	100	158	100	100
COT	Chicken	Northern Africa	62	657	58	66

CST	Chicken	Northern Africa	24	323	19	29
CTX	Chicken	Northern Africa	30	547	26	34
DOX	Chicken	Northern Africa	44	316	39	49
ENR	Chicken	Northern Africa	20	71	11	29
ERT	Chicken	Northern Africa	9	119	4	14
ERY	Chicken	Northern Africa	99	211	98	100
FEP	Chicken	Northern Africa	19	258	14	24
FFC	Chicken	Northern Africa	4	47	0	10
FOX	Chicken	Northern Africa	3	119	0	6
GEN	Chicken	Northern Africa	20	505	17	23
KAN	Chicken	Northern Africa	20	444	16	24
LCM	Chicken	Northern Africa	100	29	100	100
LVF	Chicken	Northern Africa	5	158	2	8
MEM	Chicken	Northern Africa	8	158	4	12
NAL	Chicken	Northern Africa	74	646	71	77
NEO	Chicken	Northern Africa	52	211	45	59
NIT	Chicken	Northern Africa	41	94	31	51
NOR	Chicken	Northern Africa	29	208	23	35
OFX	Chicken	Northern Africa	25	67	15	35
OXA	Chicken	Northern Africa	100	158	100	100
OXT	Chicken	Northern Africa	89	166	84	94
SMX	Chicken	Northern Africa	69	74	58	80
SOX	Chicken	Northern Africa	61	256	55	67
STR	Chicken	Northern Africa	72	821	69	75

TET	Chicken	Northern Africa	63	454	59	67
TIC	Chicken	Northern Africa	47	45	32	62
TMP	Chicken	Northern Africa	24	82	15	33
AMC	Turkey	Northern Africa	19	62	9	29
AMP	Turkey	Northern Africa	35	62	23	47
CAZ	Turkey	Northern Africa	5	62	0	10
CHL	Turkey	Northern Africa	13	62	5	21
CIP	Turkey	Northern Africa	34	62	22	46
COT	Turkey	Northern Africa	27	62	16	38
CTX	Turkey	Northern Africa	5	62	0	10
FFC	Turkey	Northern Africa	5	62	0	10
GEN	Turkey	Northern Africa	18	62	8	28
KAN	Turkey	Northern Africa	18	62	8	28
NAL	Turkey	Northern Africa	37	62	25	49
SPT	Turkey	Northern Africa	32	62	20	44
STR	Turkey	Northern Africa	69	62	57	81
TET	Turkey	Northern Africa	76	62	65	87
TMP	Turkey	Northern Africa	31	62	19	43
AMC	Cattle	Southern Africa	30	33	14	46
AMP	Cattle	Southern Africa	62	304	57	67
AMX	Cattle	Southern Africa	75	48	63	87
CAZ	Cattle	Southern Africa	69	108	60	78
CFL	Cattle	Southern Africa	47	190	40	54
CFX	Cattle	Southern Africa	75	108	67	83

CHL	Cattle	Southern Africa	33	163	26	40
CIP	Cattle	Southern Africa	7	130	3	11
COT	Cattle	Southern Africa	34	115	25	43
CTX	Cattle	Southern Africa	39	271	33	45
ENR	Cattle	Southern Africa	12	66	4	20
ERY	Cattle	Southern Africa	67	223	61	73
FFC	Cattle	Southern Africa	87	15	70	100
GEN	Cattle	Southern Africa	11	130	6	16
IMP	Cattle	Southern Africa	49	123	40	58
KAN	Cattle	Southern Africa	31	81	21	41
MEM	Cattle	Southern Africa	71	123	63	79
MIN	Cattle	Southern Africa	100	82	100	100
NAL	Cattle	Southern Africa	10	115	5	15
NEO	Cattle	Southern Africa	67	123	59	75
NOR	Cattle	Southern Africa	60	123	51	69
OFX	Cattle	Southern Africa	82	82	74	90
OXA	Cattle	Southern Africa	9	82	3	15
OXT	Cattle	Southern Africa	52	66	40	64
PEN	Cattle	Southern Africa	79	82	70	88
SMX	Cattle	Southern Africa	100	15	100	100
SOX	Cattle	Southern Africa	75	108	67	83
STR	Cattle	Southern Africa	53	97	43	63
TET	Cattle	Southern Africa	54	130	45	63
TMP	Cattle	Southern Africa	73	108	65	81

VAN	Cattle	Southern Africa	100	82	100	100
AMC	Chicken	Southern Africa	8	571	6	10
AMP	Chicken	Southern Africa	14	832	12	16
AMX	Chicken	Southern Africa	3	463	1	5
AZI	Chicken	Southern Africa	15	257	11	19
CAZ	Chicken	Southern Africa	2	423	1	3
CFL	Chicken	Southern Africa	27	101	18	36
CFX	Chicken	Southern Africa	48	257	42	54
CHL	Chicken	Southern Africa	12	673	10	14
CIP	Chicken	Southern Africa	9	571	7	11
COT	Chicken	Southern Africa	17	786	14	20
CTX	Chicken	Southern Africa	6	423	4	8
DOX	Chicken	Southern Africa	58	217	51	65
ENR	Chicken	Southern Africa	3	252	1	5
ERY	Chicken	Southern Africa	51	576	47	55
FOX	Chicken	Southern Africa	2	257	0	4
GEN	Chicken	Southern Africa	9	673	7	11
KAN	Chicken	Southern Africa	17	521	14	20
NAL	Chicken	Southern Africa	11	571	8	14
NIT	Chicken	Southern Africa	1	257	0	2
NOR	Chicken	Southern Africa	11	268	7	15
OXT	Chicken	Southern Africa	76	268	71	81
PEF	Chicken	Southern Africa	15	257	11	19
RMP	Chicken	Southern Africa	100	46	100	100

SOX	Chicken	Southern Africa	78	46	66	90
SPT	Chicken	Southern Africa	89	213	85	93
STR	Chicken	Southern Africa	59	416	54	64
TET	Chicken	Southern Africa	28	564	24	32
TMP	Chicken	Southern Africa	84	102	77	91
AMP	Goats	Southern Africa	71	68	60	82
CFL	Goats	Southern Africa	37	68	26	48
CHL	Goats	Southern Africa	29	68	18	40
COT	Goats	Southern Africa	29	68	18	40
CTX	Goats	Southern Africa	54	68	42	66
ERY	Goats	Southern Africa	57	68	45	69
GEN	Goats	Southern Africa	24	68	14	34
MIN	Goats	Southern Africa	100	68	100	100
NAL	Goats	Southern Africa	6	68	0	12
OFX	Goats	Southern Africa	25	68	15	35
PEN	Goats	Southern Africa	88	68	80	96
STR	Goats	Southern Africa	15	68	7	23
TET	Goats	Southern Africa	32	68	21	43
VAN	Goats	Southern Africa	100	68	100	100
AMC	Pigs	Southern Africa	80	45	68	92
AMK	Pigs	Southern Africa	17	48	6	28
AMP	Pigs	Southern Africa	47	93	37	57
AMX	Pigs	Southern Africa	100	45	100	100
CAZ	Pigs	Southern Africa	25	48	13	37

CFL	Pigs	Southern Africa	8	48	0	16
CFX	Pigs	Southern Africa	17	48	6	28
CHL	Pigs	Southern Africa	54	93	44	64
CIP	Pigs	Southern Africa	30	93	21	39
COT	Pigs	Southern Africa	77	93	68	86
CTX	Pigs	Southern Africa	91	45	83	99
ERY	Pigs	Southern Africa	100	93	100	100
FOX	Pigs	Southern Africa	42	48	28	56
GEN	Pigs	Southern Africa	6	93	1	11
NAL	Pigs	Southern Africa	43	93	33	53
NIT	Pigs	Southern Africa	71	45	58	84
NOR	Pigs	Southern Africa	8	48	0	16
OXT	Pigs	Southern Africa	75	48	63	87
PMB	Pigs	Southern Africa	92	48	84	100
SOX	Pigs	Southern Africa	98	45	94	100
STR	Pigs	Southern Africa	39	93	29	49
TET	Pigs	Southern Africa	100	93	100	100
AMP	Sheep	Southern Africa	18	33	5	31
AMX	Sheep	Southern Africa	82	33	69	95
CIP	Sheep	Southern Africa	24	33	9	39
CTX	Sheep	Southern Africa	58	33	41	75
FFC	Sheep	Southern Africa	27	33	12	42
GEN	Sheep	Southern Africa	18	33	5	31
IMP	Sheep	Southern Africa	12	33	1	23

KAN	Sheep	Southern Africa	15	33	3	27
MEM	Sheep	Southern Africa	18	33	5	31
NEO	Sheep	Southern Africa	18	33	5	31
NOR	Sheep	Southern Africa	21	33	7	35
SMX	Sheep	Southern Africa	91	33	81	100
STR	Sheep	Southern Africa	100	33	100	100
TET	Sheep	Southern Africa	88	33	77	99
AMP	Cattle	West Africa	13	23	0	27
CHL	Cattle	West Africa	1	270	0	2
CIP	Cattle	West Africa	1	270	0	2
COT	Cattle	West Africa	1	258	0	2
MIN	Cattle	West Africa	55	11	26	84
NAL	Cattle	West Africa	1	270	0	2
NIT	Cattle	West Africa	62	247	56	68
NOR	Cattle	West Africa	1	258	0	2
SMX	Cattle	West Africa	17	12	0	38
SOX	Cattle	West Africa	15	247	11	19
SPT	Cattle	West Africa	1	259	0	2
STR	Cattle	West Africa	21	259	16	26
TET	Cattle	West Africa	3	270	1	5
AMC	Chicken	West Africa	36	1543	34	38
AMK	Chicken	West Africa	5	903	4	6
AMP	Chicken	West Africa	62	1364	59	65
AMX	Chicken	West Africa	55	926	52	58
AZI	Chicken	West Africa	16	206	11	21
AZT	Chicken	West Africa	36	70	25	47
CAZ	Chicken	West Africa	14	1146	12	16
CB	Chicken	West Africa	13	75	5	21
CEX	Chicken	West Africa	48	48	34	62
CFL	Chicken	West Africa	14	1100	12	16
CFM	Chicken	West Africa	100	24	100	100
CFU	Chicken	West Africa	7	45	0	14
CFX	Chicken	West Africa	50	96	40	60
CHL	Chicken	West Africa	11	1371	9	13
CIP	Chicken	West Africa	35	2519	33	37
COT	Chicken	West Africa	65	1592	63	67
CST	Chicken	West Africa	41	804	38	44

CTX	Chicken	West Africa	13	1106	11	15
DOX	Chicken	West Africa	55	506	51	59
ENR	Chicken	West Africa	81	504	78	84
ERT	Chicken	West Africa	52	48	38	66
ERY	Chicken	West Africa	84	520	81	87
FEP	Chicken	West Africa	36	70	25	47
FFC	Chicken	West Africa	40	629	36	44
FLU	Chicken	West Africa	100	504	100	100
FOF	Chicken	West Africa	43	58	30	56
FOX	Chicken	West Africa	3	695	2	4
GEN	Chicken	West Africa	31	2093	29	33
IMP	Chicken	West Africa	5	562	3	7
LVF	Chicken	West Africa	2	86	0	5
MEM	Chicken	West Africa	10	254	6	14
MFX	Chicken	West Africa	17	48	6	28
MIN	Chicken	West Africa	3	34	0	9
NAL	Chicken	West Africa	28	1260	26	30
NEO	Chicken	West Africa	48	661	44	52
NIT	Chicken	West Africa	11	500	8	14
NOR	Chicken	West Africa	46	1225	43	49
PEF	Chicken	West Africa	49	916	46	52
PIP	Chicken	West Africa	60	113	51	69
PIP-TAZ	Chicken	West Africa	36	70	25	47
SMX	Chicken	West Africa	64	335	59	69
SOX	Chicken	West Africa	70	548	66	74
SPT	Chicken	West Africa	65	527	61	69
STR	Chicken	West Africa	19	913	16	22
TET	Chicken	West Africa	48	2027	46	50
TGC	Chicken	West Africa	19	211	14	24
TIC	Chicken	West Africa	5	687	3	7
TMP	Chicken	West Africa	13	846	11	15
TOB	Chicken	West Africa	7	470	5	9
AMC	Environment	West Africa	37	155	29	45
AMK	Environment	West Africa	6	100	1	11
AMP	Environment	West Africa	56	155	48	64
CAZ	Environment	West Africa	16	100	9	23
CB	Environment	West Africa	24	100	16	32
CFX	Environment	West Africa	7	55	0	14

CHL	Environment	West Africa	3	155	0	6
CIP	Environment	West Africa	8	155	4	12
COT	Environment	West Africa	51	100	41	61
CTX	Environment	West Africa	34	155	27	41
DORI	Environment	West Africa	49	55	36	62
ERY	Environment	West Africa	95	55	89	100
GEN	Environment	West Africa	6	155	2	10
OXA	Environment	West Africa	100	55	100	100
PEF	Environment	West Africa	58	55	45	71
TET	Environment	West Africa	38	155	30	46
TGC	Environment	West Africa	13	55	4	22
TMP	Environment	West Africa	53	55	40	66
AMC	Pigs	West Africa	65	85	55	75
AMP	Pigs	West Africa	85	101	78	92
AMX	Pigs	West Africa	67	84	57	77
CAZ	Pigs	West Africa	6	17	0	17
CFL	Pigs	West Africa	18	84	10	26
CHL	Pigs	West Africa	19	324	15	23
CIP	Pigs	West Africa	1	324	0	2
COT	Pigs	West Africa	55	100	45	65
CRO	Pigs	West Africa	6	16	0	18
CST	Pigs	West Africa	31	84	21	41
CTX	Pigs	West Africa	65	101	56	74
DOX	Pigs	West Africa	34	85	24	44
ERY	Pigs	West Africa	88	84	81	95
FOX	Pigs	West Africa	6	16	0	18
GEN	Pigs	West Africa	2	325	0	4
IMP	Pigs	West Africa	75	84	66	84
MEM	Pigs	West Africa	2	84	0	5
NAL	Pigs	West Africa	16	241	11	21
OFX	Pigs	West Africa	67	84	57	77
OXT	Pigs	West Africa	56	84	45	67
PEN-G	Pigs	West Africa	93	84	88	98

PMB	Pigs	West Africa	75	84	66	84
SAM	Pigs	West Africa	62	84	52	72
SMX	Pigs	West Africa	13	224	9	17
STR	Pigs	West Africa	15	325	11	19
TET	Pigs	West Africa	36	325	31	41
TMP	Pigs	West Africa	6	16	0	18
TOB	Pigs	West Africa	15	84	7	23
MIN	Sheep	West Africa	6	16	0	18
TET	Sheep	West Africa	6	16	0	18

Supplementary Material 3: (S3)

An R ReadMe file explaining the analysis. All codes and datasets are presented in

<https://doi.org/10.5281/zenodo.12668662> (Ager *et al.*, 2024).

An R-based analysis of antimicrobial resistance patterns in non-typhoidal *Salmonella* from food animals across Africa.

This R Markdown document implements numerical procedures for analyzing antimicrobial resistance (AMR) data in non-typhoidal *Salmonella* isolated from food animals in Africa. The analysis covers various aspects of AMR patterns and trends.

The analysis allows for four different types of analyses:

- a) Map of studies: A geospatial visualization showing the number of studies covered in each African country.
- b) Temporal trends analysis: Plots showing temporal trends in antimicrobial resistance, both overall and by region. This includes generalized linear model analysis, diagnostic plots and statistical tests.
- c) Regional resistance patterns: Analysis of resistance levels of antibiotic compounds aggregated by species at the regional level.
- d) Antibiotic class resistance: Examination of median resistance of antibiotic classes aggregated by species.

The analysis uses several R packages for data manipulation, visualization, and statistical analysis, including tidyverse, ggplot2, and various mapping libraries.

```
## Getting Started
```

```
## Data
```

All the datasets used are created from the dataset named AMR_clean.csv in the data folder. SalMeandf.csv (S3) is created from AMR_clean.csv for analysis of temporal trends.

Analysis Modules

1. Map of Studies

This section generates a map showing the number of studies covered in each African country. The process involves:

- Loading and preprocessing the AMR data
- Using the `rnatural-earth` package to create a base map of Africa
- Aggregating the number of studies per country
- Visualizing the data using `tmap` to create a choropleth map
- The resulting map uses a color gradient to represent the number of studies in each country, with a legend explaining the color scale

2. Temporal Trends Analysis

This analysis examines how antimicrobial resistance has changed over time. The process includes:

- Aggregating resistance data by year, country, and region
- Fitting generalized linear models (GLMs) to assess trends over time
- Creating plots showing overall and regional trends in resistance over the years
- Using boxplots to show the distribution of resistance levels for each year
- Applying statistical tests (Fisher's exact test) to assess the significance of temporal trends
- The results are visualized using ggplot2, with separate plots for overall trends and regional trends (East, West, North, and South Africa)
- we also generate diagnostic plots to assess the model fit and assumptions using boot package
- we also calculated QAIC using the formula $QAIC = -2 * \log(Likelihood) + 2 * k$, where k is the number of parameters in the model

3. Regional Resistance Patterns

This section analyzes how resistance patterns vary across different regions of Africa:

- Aggregating resistance data by antibiotic compound, species, and region
- Creating bar plots to show resistance levels for different antibiotic compounds in each region
- Using ggplot2 to generate separate plots for East, West, North, and Southern Africa
- Each plot shows resistance levels for various antibiotic compounds, with different colors representing different animal species
- Error bars are included to show the confidence intervals for the resistance estimates

4. Antibiotic Class Resistance

This analysis focuses on resistance patterns across broader antibiotic classes:

- Grouping individual antibiotics into larger classes (e.g., Tetracyclines, Penicillins, Cephalosporins)
- Calculating median resistance levels for each antibiotic class across different animal species
- Creating box plots to visualize the distribution of resistance levels for each antibiotic class
- Separate plots are generated for each major antibiotic class (Tetracyclines, Penicillins, Cephalosporins, Aminoglycosides, Fluoroquinolones, Sulfonamides)
- The plots allow for comparison of resistance levels across different animal species within each antibiotic class

Model 7 summary (the best fitting model)

Call:

```
glm(formula = cbind(no_isolates_resistant/no_isolate) ~ Year +  
(1 | doi), family = quasibinomial, data = data1, weights = no_isolate)
```

Coefficients: (1 not defined because of singularities)

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.60495 0.63289 -0.956 0.3394

Year2004	-1.01473	0.68214	-1.488	0.1372
Year2005	-1.24733	0.67803	-1.840	0.0661
Year2006	0.56050	0.69947	0.801	0.4231
Year2007	0.33943	0.64951	0.523	0.6014
Year2008	-0.78864	0.71045	-1.110	0.2672
Year2010	0.70829	0.64908	1.091	0.2754
Year2011	-0.72792	0.67385	-1.080	0.2803
Year2012	0.47435	0.64876	0.731	0.4649
Year2013	-0.87816	0.65548	-1.340	0.1806
Year2014	-0.07175	0.64684	-0.111	0.9117
Year2015	0.49172	0.67105	0.733	0.4639
Year2016	0.50323	0.65955	0.763	0.4457
Year2017	0.91867	0.63768	1.441	0.1500
Year2018	0.88957	0.67386	1.320	0.1871
Year2019	0.59781	0.68688	0.870	0.3843
Year2020	0.61310	0.64626	0.949	0.3430
Year2021	-0.18152	1.01574	-0.179	0.8582
Year2022	-0.07636	0.86832	-0.088	0.9299
1 doiTRUE	NA	NA	NA	NA

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 19.94866)

Null deviance: 27962 on 1013 degrees of freedom

Residual deviance: 22249 on 995 degrees of freedom

AIC: NA

Number of Fisher Scoring iterations: 5

References

1. Crawley, Michael J. (2013). *The R book*. Chichester, West Sussex, United Kingdom :Wiley,
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3. Schweinberger, Martin. 2022. Fixed- and Mixed-Effects Regression Models in R. Brisbane: The University of Queensland. url: <https://slcladal.github.io/regression.html> (Version 2022.09.14).
4. Ager, E. *et al.* (2024) ‘A Systemic Review of Phenotypic Antimicrobial Resistance in Non-Typhoidal Salmonella (NTS) Isolated from Food Animals in Africa’. Zenodo. Available at: <https://doi.org/10.5281/zenodo.12668662>.