

INPLASY

A systematic review and meta-analysis of bacterial prevalence, virulence and antibiotic resistance along the poultry production chain in Africa

INPLASY202680083

doi: 10.37766/inplasy2026.8.0083

Received: 21 August 2026

Published: 21 August 2026

Chaves, C; Chave, A; Manecas, M; Salamandane, C; Chambel, L; Salamandane, A; Brito, L.

Corresponding author:

Celso Raul Silambo Chaves

cerassicha@gmail.com

Author Affiliation:

Linking Landscape, Environment, Agriculture and Food (LEAF) Research Centre, Associate Laboratory TERRA, Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, 1349-017 Lisbon, Portugal; BioISI—Biosystems and Integrative Sciences Institute, Faculdade de Ciências, Universidade de Lisboa, 1749-016 Lisbon, Portugal.

ADMINISTRATIVE INFORMATION

Support - This work was supported by FCT - Fundação para a Ciência e Tecnologia, I.P. by project reference 2025.17471.PRT and DOI identifier (DOI: <https://doi.org/10.54499/2025.17471.PRT>), and by institutional funding provided through of LEAF—Linking Landscape, Environment, Agriculture and Food, Research Unit and . BioISI—Biosystems and Integrative Sciences Institute.

Review Stage at time of this submission - Completed but not published.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202680083

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 21 August 2026 and was last updated on 21 August 2026.

INTRODUCTION

Review question / Objective A systematic review and meta-analysis will thus be conducted to map the bacterial, virulence and resistance profiles throughout the poultry production chain. Through the analysis of global data, we will seek to answer fundamental questions such as which links in the chain will represent the greatest risk of dissemination; what genetic determinants will be shaping the current scenario of AR; where these studies will be most concentrated; and the consequent impact of the answers to these questions on human and animal health.

Rationale Livestock farming plays a vital role in global agriculture through its contributions to food security, employment, and income generation (3,4).

It accounts for approximately 40% of the world's agricultural gross domestic product (GDP), rising to as much as 50% in high-income countries (3,5). The expansion of the livestock sector has far-reaching implications for economic growth, rural development, livelihoods, and food security, while also posing important environmental and public health challenges (4,6–8), including greenhouse gas emissions, biodiversity loss, intensive use of water and land, and the spread of antibiotic-resistant bacteria and antibiotic resistance genes (ARGs) (4,6–8). In intensive production systems, the widespread use of antibiotics for growth promotion, disease prevention, and treatment exerts strong selective pressure, facilitating the emergence, persistence, and spread of resistant microorganisms in animal populations, the environment, and the food chain (7,9–11). In recent decades, the livestock sector has increasingly

shifted toward industrialized, vertically integrated, and highly intensive production systems, as in poultry production in Asia and Latin America, further amplifying the risks associated with antibiotic resistance (AR) and environmental degradation (12–14). Although numerous studies have investigated bacterial contamination, carriage, virulence, and antimicrobial resistance (AMR) in African poultry systems, the available evidence remains geographically and methodologically fragmented. This represents an important evidence gap, particularly regarding the distribution and patterns of bacterial species, antimicrobial resistance phenotypes, resistance genes, and virulence-associated genes across different stages of the poultry production chain in African countries. A systematic synthesis is therefore needed to characterize the available evidence and identify patterns and gaps in the current knowledge. This review will synthesize available evidence from African countries and will examine differences according to production-chain stage, bacterial species, sample source, geographic region, antimicrobial agent, resistance phenotype, resistance gene, virulence-associated gene, and other relevant study characteristics.

Condition being studied Antimicrobial resistance (AMR) and bacterial contamination in poultry production systems in Africa, including the prevalence of bacterial species, antimicrobial resistance phenotypes, antimicrobial resistance genes (ARGs), and virulence-associated genes across different stages of the poultry production chain.

METHODS

Search strategy We will search the following three databases: Scopus, PubMed, and Web of Science. Search terms will include "Prevalence" AND "Incidence" AND "Bacterial" AND "Enterobacteriaceae in chickens" AND "Antibiotic resistance" AND "Multidrug resistance" AND "Gene resistance" AND "Virulence gene" AND "Poultry" AND "Poultry farm" AND "Broiler" AND "Broiler chickens" AND "Animal farms" AND "Intensive farming" AND "Integrated farming systems" AND "No-antibiotic-ever" AND "Conventional farming" AND "Chicken waste" AND "Environmental reservoirs" AND "Wastewater" or "Drinking water" AND "One Health" AND "Chickens". Only articles published in English will be considered for inclusion. In addition, articles published in Portuguese will also be eligible, provided they will include an abstract in English since from February 2026 to May 2026.

Participant or population The population of interest comprises poultry, including chickens and other domestic poultry species, and poultry-derived samples collected at different stages of the poultry production chain in African countries. Eligible populations may include live birds, poultry farms, slaughterhouses and processing facilities, poultry carcasses, meat and other poultry-derived food products, as well as environmental samples associated with poultry production and processing, depending on the study setting.

Intervention Not applicable. This systematic review does not evaluate a specific intervention. It synthesizes observational evidence on bacterial prevalence, virulence, and antimicrobial resistance across the poultry production chain in African countries.

Comparator Not applicable. This review does not require a specific comparator or control group, as it synthesizes observational studies reporting bacterial prevalence, virulence, and antimicrobial resistance across different stages of the poultry production chain in African countries.

Study designs to be included Cross-sectional studies, prevalence surveys, surveillance studies, and other observational studies reporting primary data on bacterial prevalence, antimicrobial resistance, antimicrobial resistance genes (ARGs), and/or virulence-associated genes in poultry or poultry-derived samples from African countries will be included. Both prospective and retrospective observational studies will be eligible.

Eligibility criteria Observational studies reporting primary data on bacterial prevalence, bacterial carriage or contamination, virulence, antimicrobial resistance phenotypes, antimicrobial resistance genes (ARGs), and/or virulence-associated genes in poultry or poultry-derived samples from African countries will be included. Eligible study designs will include cross-sectional studies, prevalence surveys, surveillance studies, and other observational studies providing relevant quantitative data. Both prospective and retrospective observational studies will be considered eligible where applicable. see table 1

Eligibility criteria and excluded

Item Checklist item Example

Inclusion criteria

Population and context Studies conducted in African countries, focusing on the poultry production chain Farms, slaughterhouses, processing plants, retail) and/or workers involved in poultry farming or processing

Study type Original research articles providing primary data -

Microbiological scope Studies reporting microbiological data related to poultry Detection, prevalence, or characterization of bacterial pathogens or indicators, resistance and Virulence Factor

Outcome measures Studies presenting quantitative microbiological outcomes Prevalence, counts, or proportions

Data availability Sufficient methodological and results information to allow data extraction
Description of population, sample source, number of samples/isolates, methods used

Study design Observational or experimental designs Cross-sectional, cohort, case-control, or intervention trials conducted in the poultry chain

Language and publication status Full-text articles published in peer reviewed journals in English. Articles written in Portuguese were also included, provided that they contained an abstract in English -

Exclusion criteria

Publication type Reviews (narrative or systematic), conference proceedings, theses/dissertations, editorials, letters, short communications without sufficient data, or other non-primary research formats -

Irrelevant sector studies not related to the poultry production chain Focusing exclusively on other animal species or food chains

Lack of quantitative data Studies without quantitative microbiological data Purely descriptive or qualitative reports without numerical outcomes

Study design limitations Case reports or studies with designs that did not allow extraction or comparison of microbiological outcomes -

Population or context outside scope Studies conducted outside African countries or not involving poultry, poultry products, or poultry-chain workers -

Outcome not aligned with objectives Studies focusing solely on clinical outcomes without microbiological investigation, or on topics unrelated to microbial contamination, carriage, or transmission in the poultry chain. -

Insufficient data for analysis Articles with incomplete or unclear information, preventing reliable data extraction missing details on sample source, number of samples/isolates, or methods used

Microbiological scope limitations Studies addressing only non-microbiological aspects without any microbiological component economic, social, or management issues

Accessibility constraints Articles for which the full text was not available despite reasonable efforts to obtain it.

Information sources We will search the following three databases: Scopus, PubMed, and Web of Science.

Main outcome(s) The primary outcomes will be the prevalence of bacterial species identified in poultry and poultry-derived samples across different stages of the poultry production chain in African countries, and the prevalence of antimicrobial resistance among the identified bacterial isolates. Antimicrobial resistance outcomes will include resistance phenotypes to individual antimicrobial agents or antimicrobial classes and the prevalence of antimicrobial resistance genes (ARGs). Where data are available, the prevalence of virulence-associated genes and virulence characteristics will also be assessed.

Additional outcome(s) Additional outcomes will include variations in bacterial prevalence, antimicrobial resistance phenotypes, antimicrobial resistance genes (ARGs), and virulence-associated genes according to production-chain stage, sample source, geographic region, bacterial species, poultry type, antimicrobial agent or antimicrobial class, and other relevant study characteristics. Where sufficient data are available, subgroup analyses will be conducted to explore potential sources of heterogeneity across these categories.

Data management The full texts of the selected publications will be analyzed in Rayyan by two researchers. In case of disagreement, a third researcher will be consulted to reach a consensus. The extracted data will include study period, year of publication, country, sample type (specific chicken chain production, human, or environmental source), reservoirs studied (human, chicken chain production, and environment), different bacteria, detection methods, number of isolates from each source (production chain, human, environment), prevalence of isolates, multidrug resistance pattern and virulence genes. The information found in the different articles will then be exported to Microsoft Excel (Microsoft 365 Apps for enterprise) and compiled using the above search criteria.

Quality assessment / Risk of bias analysis

Quality assessment will be performed using the Joanna Briggs Institute (JBI) checklist for prevalence studies (15). This checklist will consist of nine questions; each will be scored with "1" for a "Yes" answer and "0" for a "No" answer (16).. The assessment will be performed independently by two reviewers.

Each study will be assessed as “low risk,” “unclear risk,” or “high risk” in selection bias, performance bias, detection bias, attrition bias, reporting bias, and other bias. Disagreements will be resolved by the third reviewer.

Strategy of data synthesis The data extracted and exported to Excel based on the inclusion and exclusion criteria will be used for descriptive statistics. Further analyses will be performed in several stages. The data will be organized in Excel and subsequently exported to R (version 2026.1.2.418), where the metafor and meta packages (version 4.8.0) will be loaded and analyzed using RStudio (version 4.5.0).

All generated data will be analyzed using a binary random-effects model based on the Der Simonian–Laird method (17), with a 95% confidence interval. The random-effects model will be applied to calculate the pooled prevalence for each sample type. Heterogeneity between studies will be assessed using the inverse variance index (I^2), which will also be used to estimate the random-effects model. An I^2 value greater than 75% will be considered indicative of substantial heterogeneity. Statistical significance will be defined as a p-value < 0.05.

Subgroup analysis Subgroup analyses will also be performed according to bacterial prevalence, sample type, country, antibiotic, resistance genes, and virulence genes, grouping the data according to these criteria. A meta-regression analysis will be conducted to determine statistically significant differences between each subgroup and the overall pooled prevalence, with $p < 0.05$ as statistically significant.

Sensitivity analysis Sensitivity analyses will assess the robustness of the findings by: excluding studies judged to have high risk of bias; excluding studies with very small sample sizes; excluding studies with unclear denominators; excluding studies using nonstandard antimicrobial susceptibility criteria; comparing GLMM and transformed-proportion approaches; comparing different estimators of between-study variance; conducting leave-one-out analyses; assessing the influence of individual studies.

Language restriction Studies published in English will be considered eligible. Studies published in other languages will be excluded due to language restrictions.

Country(ies) involved Portugal.

Other relevant information This systematic review and meta-analysis focuses on bacterial prevalence, virulence, and antimicrobial resistance along the poultry production chain in African countries from a One Health perspective. The review considers evidence from different stages of the poultry production chain and from different sample sources, with particular emphasis on bacterial species, antimicrobial resistance phenotypes, antimicrobial resistance genes (ARGs), and virulence-associated genes. Where sufficient and comparable data are available, quantitative synthesis and subgroup analyses will be conducted to explore differences according to geographic region, production-chain stage, bacterial species, sample source, antimicrobial agent, and other relevant study characteristics.

Keywords Poultry; Livestock chain; Antibiotic resistance; One health surveillance; Africa.

Dissemination plans The findings of this systematic review and meta-analysis will be disseminated through publication in a peer-reviewed scientific journal. The results may also be presented at relevant scientific conferences, workshops, and other academic or professional forums related to antimicrobial resistance, poultry production, veterinary public health, food safety, and One Health. The findings will be made available to researchers, public health and veterinary professionals, policymakers, and other stakeholders interested in antimicrobial resistance and bacterial health risks within poultry production systems in Africa.

Contributions of each author

Author 1 - Celso Chaves - Conceptualization, formal analysis and investigation, data curation, writing—original draft preparation, review and editing.

Email: cerassicha@gmail.com

Author 2 - Albertino Chave - Conceptualization, formal analysis and investigation and data curation.

Email: albertinoraul4@gmail.com

Author 3 - Maniza Quinto Manecas - Conceptualization and formal analysis and investigation, data curation and review and editing.

Email: manizaquinto@gmail.com

Author 4 - Cátia Salamandane - Conceptualization, formal analysis and investigation, data curation.

Email: csalamandane@unilurio.ac.mz

Author 5 - Lélia Chambel - formal analysis and investigation, data curation, writing—original draft preparation, review and editing.

Email: lmchambel@ciencias.ulisboa.pt

Author 6 - Acácio Salamandane -
Conceptualization, formal analysis and
investigation, data curation, writing—original draft
preparation, review and editing.

Email: salamandane@gmail.com

Author 7 - Luísa Brito - formal analysis and
investigation, data curation, writing—original draft
preparation, review and editing.

Email: lbrito@isa.ulisboa.pt