



## Unveiling the landscape of resistance against high priority critically important antimicrobials in food-producing animals across Africa: A scoping review

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### ARTICLE INFO

#### Keywords:

Antimicrobial resistance

Africa

chicken

*Escherichia coli*

*Salmonella*

Review

### ABSTRACT

The rapid population growth in Africa is associated with an increasing demand for livestock products which in turn can lead to antimicrobial use. Antimicrobial usage in animals contributes to the emergence and selection of resistant bacteria which constitutes a serious public health threat. This study aims to review and summarize the available information on highest priority critically important antimicrobials (HPCIA) resistance in livestock production in Africa. This work will help to inform future policies for controlling antimicrobial resistance (AMR) in the food production chain. A scoping review was conducted according to the Cochrane handbook and following PRISMA 2020 guidelines for reporting. Primary research studies published after 1999 and reporting resistance of *Escherichia coli*, *Enterococcus* spp, *Staphylococcus aureus*, *Salmonella* spp, and *Campylobacter* spp to HPCIA in poultry, cattle, pigs, goats, and sheep in Africa were searched in four databases. A total of 312 articles were included in the review. The majority of the studies (40.7) were conducted in North African countries. More than 49.0% of included studies involved poultry and 26.2% cattle. Cephalosporins and quinolones were the most studied antimicrobial classes. Of the bacteria investigated in the current review, *E. coli* (41.7%) and *Salmonella* spp (24.9%) represented the most commonly studied. High levels of resistance against erythromycin in *E. coli* were found in poultry (MR 96.1%, IQR 83.3–100.0%), cattle (MR 85.7%, IQR 69.2–100.0%), and pigs (MR 94.0%, IQR 86.2–94.0%). In sheep, a high level of resistance was observed in *E. coli* against nalidixic acid (MR 87.5%, IQR 81.3–93.8%). In goats, the low level of sensibility was noted in *S. aureus* against streptomycin (MR 86.8%, IQR 19.4–99.0%). The study provides valuable information on HPCIA resistance in livestock production in Africa and highlights the need for further research and policies to address the public health risk of AMR. This will likely require an investment in diagnostic infrastructure across the continent. Awareness on the harmful impact of AMR in African countries is a requirement to produce more effective and sustainable measures to curb AMR.

### 1. Introduction

An increase of the African population of around 90% has been projected for 2050 (Abramova, 2022). This rapid population growth is correlated with an increasing demand for livestock products and antimicrobial use (AMU) in livestock sector (Schar et al., 2018; OECD/FAO, 2023). An estimated 73% of all antimicrobials sold worldwide are used

in livestock production (Van Boeckel et al., 2017). Between 2010 and 2030, the global consumption of antimicrobials will increase by 67%. A third of the increase in livestock will be imputable to shifting production practices in middle-income countries from subsistence farming to commercial production (Tiseo et al., 2020).

One Health has been defined as “an integrated, unifying approach that aims to sustainably balance and optimize the health of people,

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<https://doi.org/10.1016/j.prevetmed.2024.106173>

Received 3 October 2023; Received in revised form 10 February 2024; Accepted 6 March 2024

Available online 13 March 2024

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animals and ecosystems" (WHO, 2023). Antimicrobial resistance is an intricate problem compounded by various factors. Its complex epidemiology embraces human, animals and the environment. Therefore, it has been claimed that antimicrobial resistance is a good illustration of a health problem that must be tackled using a One Health approach in order to be adequately addressed (Velazquez-Meza et al., 2022).

Antimicrobial usage in animals contributes to the emergence and selection of resistant strains of bacteria in animals and humans. Such resistant bacteria may lead to a negative impact on population health and the economy (Liu et al., 2018; De Oliveira et al., 2020; Dutra et al., 2021). Antimicrobial resistance (AMR) is a serious public health concern and one of the most important health challenges in the 21st century (FDA, 2020; Tarakdjian et al., 2020). Murray et al. (2022). It was estimated that the death rate attributable to AMR in 2019 was highest in western sub-Saharan Africa, reaching a burden of 27.3–114.8 deaths per 100 000 population. According to the same authors, the deaths attributable to and associated with bacterial antimicrobial resistance in Africa are higher than that observed in other regions such as East Asia, western Europe and Central Latin America. The AMR panorama in Africa is compounded by several factors, including, but not limited by, lack of knowledge of stakeholders about AMU and AMR, limited or lack of surveillance systems and options to control the use of antimicrobials in human and veterinary medicine, lack of and/or inadequate border controls, lack of rules and regulation enforcement, inadequate use of antimicrobials or lack of treatment guidelines (Vougat Ngom et al., 2017; Mouiche et al., 2018; Elton et al., 2020).

AMR has a complex epidemiology and resistant bacteria can be transmitted across species and ecosystems. Evidence indicates that a reduction in AMU in animal husbandry would lead to a decrease in AMR levels in food animals (WHO, 2017a; Bennani et al., 2020). The spread in animals of MDR bacteria of clinical relevance in human medicine has raised public health concerns about the use of certain antimicrobials in the veterinary sector (Collignon et al., 2013). This has contributed to lead international organizations to develop policies aimed at preserving the efficacy of medically important antimicrobials. It is with this in mind that the WHO has classified five classes of antibiotics (third and fourth generation cephalosporins, quinolones, glycopeptides, macrolides, and polymyxin mainly represented by colistin and polymyxin B in food-producing animals) as highest priority critically important antimicrobials (HPClAs) based on their clinical importance in human medicine and the risk of resistance transfer from animals (WHO, 2018a). Measures to reduce AMU in animal production are particularly stringent with the use of HPClAs (Diana et al., 2021). Several countries (e.g. Switzerland, Austria) have tried to reduce HPClAs usage in production animals (Diana et al., 2021; Ngom et al., 2022). However, little is known about African countries. Previous studies on AMU and resistance in food producing animals in Africa (i.e. in central Africa) indicated a large deficit of data on antimicrobial usage and resistance (Cuong et al., 2018; Kimera et al., 2020).

Even though various original studies (Coulidiaty et al., 2021; Kagambèga et al., 2021) and reviews (Kimera et al., 2020; Paintsil et al., 2022) have been published on AMR in animals in Africa, to the best of our knowledge none focused on HPClAs. Summarizing available information on HPClAs resistance in Africa is of great importance for designing policies and mitigation strategies to reduce the public health risk of AMR.

The aim of this study is to review and summarize the available information on HPClAs resistance in livestock production in Africa to better inform future policies aiming to control HPClAs in the animal sourced food systems. Poultry, cattle, pigs, goats and sheep were the animal species considered in this review due to their relevance in the African context in terms of livestock production and antimicrobials consumption (FAOSTAT, 2021; Mulchandani et al., 2023). This study focused on resistance of *Escherichia coli*, *Enterococcus* spp, *Staphylococcus aureus*, *Salmonella* spp, and *Campylobacter* spp because of their role as indicator bacteria for AMR surveillance in One health approach or their

foodborne implications and impact on human health (Murray et al., 2022; Paintsil et al., 2022). Most of them are also included in the WHO priority pathogens list to guide research and development of new antibiotics for drug-resistant bacterial infections (WHO, 2017c).

## 2. Methods

This review was performed as described in the Cochrane handbook (Higgins et al., 2021) and reported according to the Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for scoping reviews (PRISMA-ScR) (Tricco et al., 2018). A scoping review protocol was first created according to the Preferred Reporting Items for Systematic Review and Meta-analysis Protocols (PRISMA-P) guidelines (Moher et al., 2015).

### 2.1. Eligibility criteria

Primary research studies reporting *E. coli*, *S. aureus*, *Salmonella* spp, *Campylobacter* spp and *Enterococcus* spp resistance to HPClAs were eligible for inclusion in the scoping review. In addition, these studies must have been conducted in poultry (limited to chicken, duck, turkey and geese), cattle, pigs, goats or sheep, in Africa, and published between 2000 and 2021. Indeed, previous reviews on AMR in Africa (Mouiche et al., 2019; Kimera et al., 2020; Kivumbi and Standley, 2021) showed that most of the studies were carried out after 2010. Considering the languages spoken by the researchers involved in this review, research studies available in English and French were selected.

### 2.2. Information sources

Searches were conducted in March 2022 in CAB abstracts (in Ovid), Pubmed (in MEDLINE) and Web of Sciences (WOS) via access of the University of Bern (Switzerland). In addition, African Journals Online was also consulted. Most WOS databases were used (Web of Science Core Collection, BIOSIS Citation Index, KCI-Korean Journal Database, Medline, Russian Science Citation Index and ScELO Citation Index). Arts & Humanities Citation Index (A&HCI), Conference Proceedings Citation Index-Science (CPCI-S), Conference Proceedings Citation Index-Social Science & Humanities (CPCI-SSH) and Social Sciences Citation Index (SSCI) were excluded because the focus of our study is on microbiological rather than social science data on antimicrobial resistance.

### 2.3. Search strategy

The search strategy included a multi-stranded approach that uses a series of searches, with different combinations of concepts to gather all possibly related research and thus achieve high sensitivity (Higgins et al., 2021). The search string was adapted to each database as needed to reflect differences in database interfaces. As the aim of this study is to review the available information on HPClAs resistance in livestock production in Africa, search strategy included the formatting of the following terms according to different architectures of the databases and their search engines: [HPClAs] AND [Resistance or resistant or susceptibility] AND [poultry or cattle or sheep or goat or pig] AND [African countries]. The search strings used in CAB Abstracts are presented in Table 1. Supplement 1 shows the general search strategy applied.

### 2.4. Selection process

After deduplication in Zotero, citations were uploaded to the Rayyan software for screening. Three pairs of independent reviewers (NR and AT, MJ and ML and WM and GA) carried out the screening at each phase. Each pair screened one third of the total number of uploaded citations.

Firstly, the selection process consisted of title and abstract screening. To increase consistency among reviewers, a calibration exercise was

**Table 1**  
Bibliographic search strategy used to search papers in Cab Abstract database.

Major terms	Key words
#1 highest priority critically important antimicrobial	1 ("highest priority critically important antimicrobial" or HPCIA or HP-CIA or ketolide\$1 or cephalosporin\$1 or cefcapene\$1 or cefdaloxime\$1 or cefdinir\$1 or cefetamet\$1 or cefixime\$1 or cefmenoxime\$1 or cefodizine\$1 or cefotaxime\$1 or cefovecin\$1 or cefpimizole\$1 or cefpodoxime\$1 or cefteraam\$1 or ceftibuten\$1 or ceftiofur\$1 or ceftioleone\$1 or ceftizoxime\$1 or ceftriaxone\$1 or cefoperazone\$1 or ceftazidime \$1 or oxacephem\$1 or quinolone* or Levofloxacin\$1 or ciprofloxacin\$1 or norfloxacin \$1 or danofloxacin\$1 or eurofloxacin\$1 or moxifloxacin\$1 or ofloxacin\$1 or norfloxacin\$1 or marbofloxacin\$1 or gemifloxacin\$1 or enoxacin\$1 or lomefloxacin\$1 or sparfloxacin\$1 or gatifloxacin\$1 or polymyxin\$1 or macrolide\$1 or tilmicosin\$1 or erythromycin\$1 or spiramycin \$1 or tulathromycin\$1 or glycopeptide\$1 or colistin\$1 or tylosin\$1 or vancomycine\$1 or teicoplanine\$1).ti,ab.
#2 resistance	2 (resistance or resistant or susceptibility or susceptible).ti,ab.
#4 poultry or cattle or sheep or goat or pig	3 exp pigs/ 4 exp cattle/ 5 exp poultry/ 6 exp goats/ 7 exp sheep/ 8 3 or 4 or 5 or 6 or 7 9 (pigs or pig or swine* or pork or piglet* or boar* or weaner or sow or fatterer or "Sus domesticus" or chick* or poultry* or broiler* or layer* or turkey* or duck* or geese or goose or fowl* or avian* or egg or eggs or bird* or hen or hens or "Gallus gallus" or flock* or cattle or beef or cow* or calf or calves or "Bos taurus" or "Bos indicus" or heifer* or bull* or bovine or dairy or zebu or sheep* or caprine or goat* or ovine or ewe or "small ruminant" or "food-producing animal*" or "food animal*" or "animal husbandry" or "animal farming" or "domestic animal*" or livestock).ti, ab.1625461
#3 African countries	10 8 or 9 11 (Africa or African or Comoros or Djibouti or Madagascar or Malawi or Seychelles or Cameroon or "Central African Republic" or Chad or Congo or "Equatorial Guinea" or "Atlantic Islands" or Gabon or Morocco or Sudan or Botswana or Lesotho or Swaziland or Benin or "Burkina Faso" or "Cape Verde" or Ghana or Guinea or Mauritania or Niger or Senegal or "Sierra Leone" or Togo or Burundi or Eritrea or Ethiopia or Kenya or Mozambique or Rwanda or Somalia or Tanzania or Uganda or Zambia or Zimbabwe or Angola or Algeria or Egypt or Tunisia or Namibia or "South Africa" or Gambia or Liberia or Mali or Nigeria or "Ivory Cost").ti,ab.
#1 AND #2 AND #3 AND #4	12 1 and 2 and 10 and 11 13 limit 12 to yr="2000–2021"

performed. All the reviewers have first screened 100 randomly selected studies. This calibration exercise enabled online discussion and solved disagreements before carrying out the full selection process (Sanguinetti et al., 2021). Eligibility of studies were assessed with the following questions:

1. Is the abstract of the study available? Yes [Include], No [Exclude]
2. Does the study concern bacterial resistance to antibiotics? Yes [Include], No [Exclude], Unclear [Include]
3. Does the study concern at least one of the following species: poultry, cattle, pig, sheep, goat? Yes [Include], No [Exclude], Unclear [Include]

4. Is the study primary research? Yes [Include], No [Exclude], Unclear [Include]
5. Does the study take place in at least one African country? Yes [Include], No [Exclude] Unclear [Include]

Studies were excluded if both reviewers responded 'no' to any of the screening questions. When consensus between two reviewers was not reached, a third reviewer (MF) was asked to resolve the conflict. The remaining studies passed to the next selection process stage.

The second stage involved the full-text screening. A calibration exercise was also conducted during this stage. For this phase, 30 random papers were screened by all the reviewers. Eligibility of studies was assessed with the following questions:

1. Is a full text available? Yes [Include], No [Exclude]
2. Is the full text available in English or French? Yes [Include], No [Exclude]
3. Does the study concern at least one of these bacteria *E. coli*, *Salmonella* spp, *Campylobacter* spp, *S. aureus* and *Enterococcus* spp Yes [Include], No [Exclude]
4. Does the study concern bacterial resistance to at least one HPCIA? Yes [Include], No [Exclude]

Farm to fork studies were not considered. Studies where bacteria were isolated in meat, milk, or environment (litter, waste, etc.) were also excluded, except when milk from animals with mastitis was analyzed.

## 2.5. Data charting process

Data charting was conducted in Excel 2020 A standardized data-charting form was used for the data extraction. A pre-test was run where all reviewers screened 20 studies The extraction form was developed by the main author and validated by all the authors. Like in the screening phase, each pair of independent reviewers performed the data extraction of one third of the included papers. Discussion sessions were held to solve disagreements (by a third reviewer) for which a consensus was not found.

## 2.6. Data items

Data extracted included publishing year, country where the sample collection was conducted, study design, animal species studied, type of sample collected, bacteria of interest, HPCIA to which bacteria of interest are resistant, method of susceptibility testing, susceptibility testing standards, resistant genes analyzed. All the variables extracted are shown in Supplement 2. Quantitative data on HPCIA (e.g. number of strains tested for HPCIA, number of resistant strains, etc.) were also collected. For the susceptibility testing, intermediate-resistant samples were recorded as resistant in this study (Ahmed et al., 2019). The use of molecular studies has been increasing and they provide an important contribution to better understand the AMR dynamics. In line with this, we collected data on the HPCIA genes identified in these studies.

## 2.7. Data analysis

Characteristics of the included studies were narratively summarized after tabulation. First, the proportion of resistant isolates was calculated for each study based on number of isolates tested and number of isolates resistant to HPCIA. The median and interquartile range (IQR) of the proportion of resistant isolates for each bacterium-HPCIA class/country/species was then assessed to calculate a standardized measure from the collected data. This was done when at least three studies were carried out for the same bacteria-HPCIA combination. Descriptive statistics were performed, and a map was created using Microsoft Excel 2020 and Qgis 3.30. respectively.

### 3. Results

#### 3.1. Study selection

The result of the selection process, based on the inclusion criteria is shown in Fig. 1. Of the 2596 publications initially identified in the search, 1474 records were screened using the title and abstract and 548 were subjected to the full-text screening. Finally, there were 312 articles that evaluated HPClAs resistance of selected bacteria in cattle, poultry, pigs, goats or sheep in Africa.

#### 3.2. Study characteristics

Of the 312 studied included, 46.8% (146/321) were published between 2016 and 2020 and 26.9% (84/321) between 2011 and 2015 (Supplement 1 Table S1). One hundred (32.1%) studies were longitudinal and 46 (14.7%) were cross sectional. Data about antimicrobial resistance in selected animals and targeted bacteria were not available for 61.1% (33/54) of the countries in the African continent. One hundred and twenty-seven out of 312 (40.7%) studies were carried out in the North African region. Only one article was from Central Africa (i.e. Cameroon). Most of the studies were from Egypt (23.7%;74/312), Nigeria (23.4%; 73/312), Ethiopia (9.9%; 31/312) and South Africa (9.9%; 31/312). Almost half (193/312) of included studies involved poultry and 26.4% (103/312) cattle. Most studies focused on *E. coli* (49.4%; 154/312) and *Salmonella* spp (29.5%; 92/312). Disc diffusion was the most commonly used drug susceptibility method (83.6%; 261/312) with Clinical and Laboratory Standards Institute (CLSI) as the main data interpretation guideline (62.4%, 209/331), followed by National Committee for Clinical Laboratory Standards (NCCLS) (9.9%, 33/331), and European Committee on Antimicrobial Susceptibility Testing (EUCAST) (8.9%, 30/344). In total, 45 different HPClAs agents were studied (Supplement 1 Table S2). Most studies focused on gentamycin (74.4%, 232/312), ciprofloxacin (72.8%, 227/312), streptomycin

(51.9%, 162/312), nalidixic acid (44.6%, 139/312), erythromycin (39.1%, 122/312), and cefotaxime (31.7%, 99/312).

Studies about *E. coli* (26.6%, 41/154), *S. aureus* (27.8%, 20/72) and *Enterococcus* spp (25.0%, 5/20) were undertaken mostly in Egypt (Fig. 2). Nigeria had the highest number of studies on *Salmonella* spp (25.0%, 23/92), while South Africa hosted the largest number of studies about *Campylobacter* spp (29.0%, 9/31).

#### 3.3. Antimicrobial resistance in selected studies

*Escherichia coli* was the most common organism studied. It showed high level of resistance to commonly used HPClAs such as erythromycin in poultry (MR 96.1%, IQR 83.3–100.0%) and pigs (MR 94.0%, IQR 86.2–94.0%), nalidixic acid in sheep (MR 87.5%, IQR 81.3–93.8%), flumequine in poultry (MR 86.1%, IQR 82.1–91.7%), neomycin (MR 85.2%, IQR 8.3–86.1%) and erythromycin (MR 85.7%, IQR 69.2–100.0%) in cattle. *E. coli* was found to be less resistant towards cefotaxime in cattle (MR 0%, IQR 0–27.9%), and pigs (MR 0%, IQR 0–17.8%). In poultry, *E. coli* was highly sensitive to ofloxacin (MR 0%, IQR 0–62.1%), cefepime (MR 0%, IQR 0–0.4%) and cefotaxime (MR 0%, IQR 0–11.9%). The majority of *E. coli* isolates from goats were susceptible to HPClAs (Table 2).

As shown in Table 3, for *S. aureus*, most of the included studies conducted in selected animals aimed at testing the susceptibility to erythromycin, gentamycin and streptomycin. Only gentamycin was tested against *S. aureus* isolated from pigs. The highest level of resistance of this bacteria were found against streptomycin in goats (MR 86.8%, IQR 19.4–99.0%) and sheep (MR 83.9%, IQR 41.9–91.9%).

Data on *Salmonella* spp resistance in goats and sheep were not found (Table 4). The highest proportion of resistant isolated against erythromycin were found in poultry (MR 96.9%, IQR 68.4–99.6%) and cattle (MR 80.0%, IQR 55.7–100.0%). Against flumequine the highest level of resistance were found in poultry (MR 83.3% IQR 66.4–100.0%).

As for *Salmonella* spp, the data of resistance of *Campylobacter* spp and

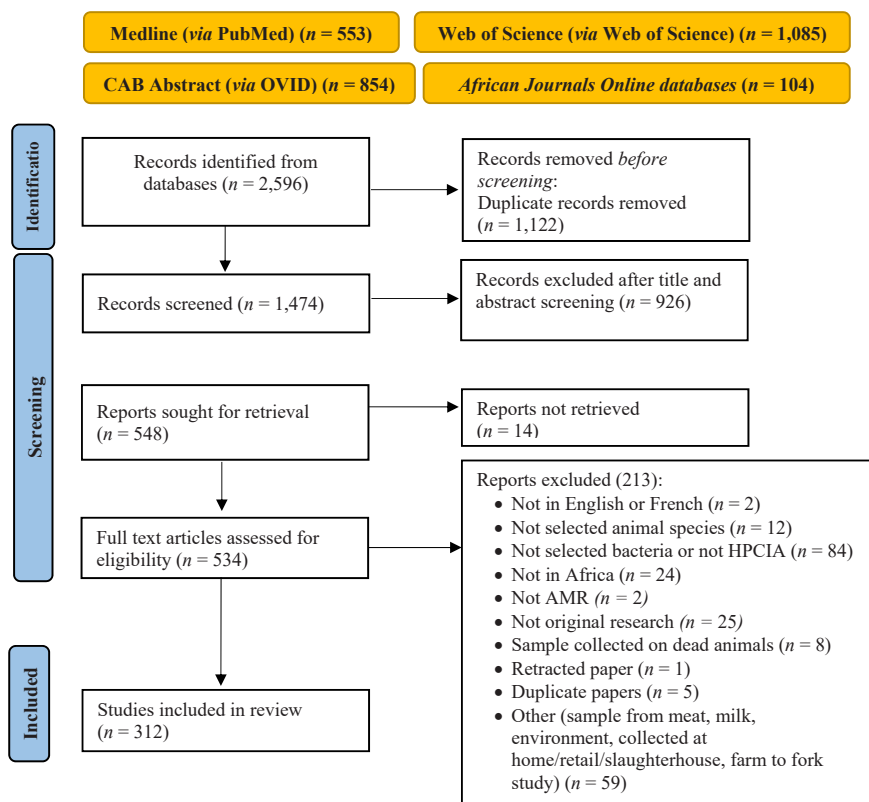


Fig. 1. Flow diagram illustrating the selection of eligible studies.



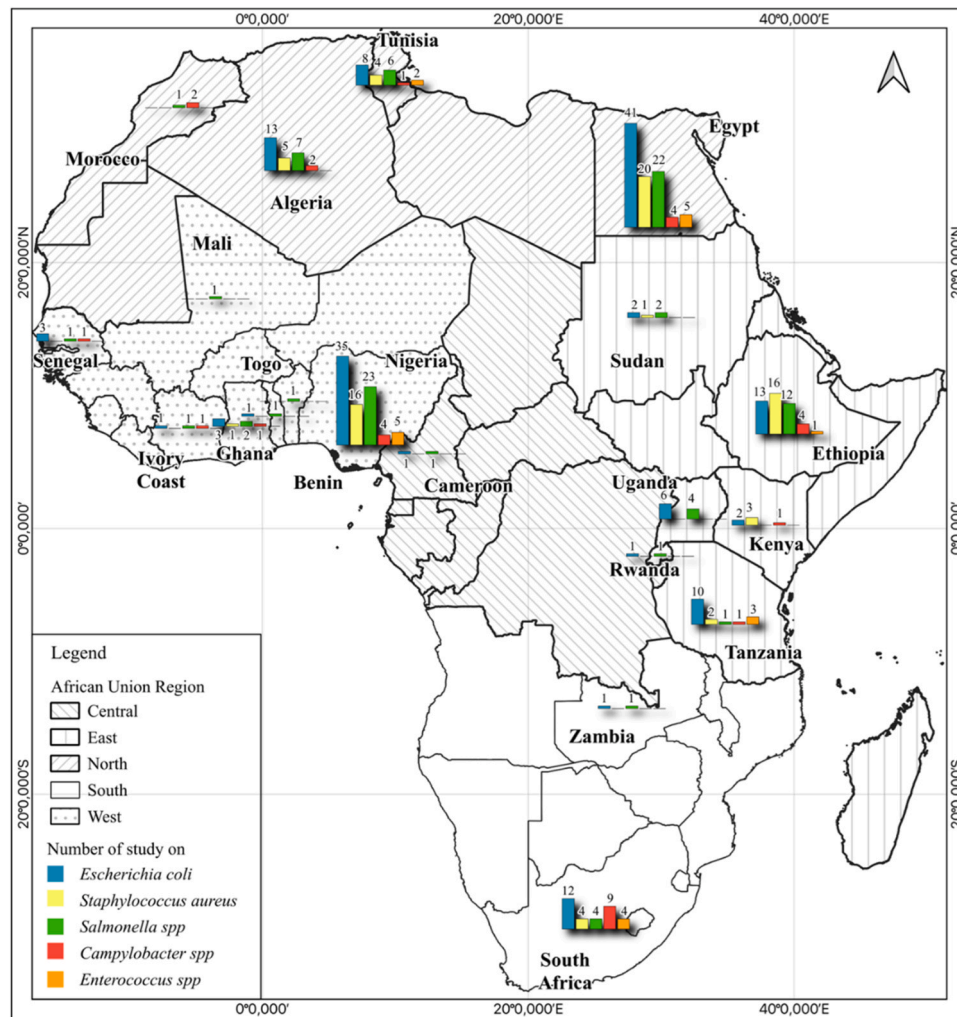


Fig. 2. Map of the Africa showing country and the number of articles included in the review.

*Enterococcus* spp in goats and sheep were not found (Tables 5 and 6). For *Campylobacter* spp, the lowest levels of susceptibility were noted against gentamycin in pigs 60.6 (60.6%). In contrast, the highest resistance of *Enterococcus* spp was found against norfloxacin (MR 94.3%, IQR 85.6–97.1%) and erythromycin (MR 85.8%, IQR 40.6–97.9%) in poultry.

A summary of AMR resistance genes identified in included studies can be found in Table 7. Only 97 (30.2%) articles studied resistant genes. All of them used Polymerase Chain Reaction (PCR) for genes identification. Most genes such as *bla<sub>CTX-M</sub>*, *bla<sub>TEM</sub>*, *bla<sub>Z</sub>*, *ermB*, *ermC*, *qnr*, *vanA*, *vanB*, *str*, *gyr*, *aac(6)-Ib-cr*, and *mrc* were detected in all the animal species. The methods used for the detection of the resistance genes were mainly PCR and Whole genome Sequencing Typing (WGS).

#### 4. Discussion

This study aimed to review and summarize the available information on resistance of *Escherichia coli*, *Enterococcus* spp, *Staphylococcus aureus*, *Salmonella* spp, and *Campylobacter* spp to HPClAs in poultry, cattle, pigs, goats, and sheep in Africa.

Most of the selected studies were conducted after 2010 (>70%) and took place in the North region of Africa (41.1%). This is in accordance with previous reviews performed in Africa on AMR (Kimeru et al., 2020; Ahmed et al., 2017) and can be explained by the increase in importance of AMR due to its impact on public health. However, this review showed that 61.1% of African countries have no published studies that met our

inclusion criteria. The focus of studies was predominantly on poultry and cattle. This is likely due to their higher contribution to meat production in Africa (FAOSTAT, 2021). We also hypothesize that it might be linked to the fact that poultry displays higher resistance rates than other livestock species (Alonso et al., 2017). Geographically, most of the studies were carried out in Egypt (24.6%) and Nigeria (23.7%). This might be associated with their capacity to better afford well-equipped health and research facilities needed to conduct such research (Schroeder et al., 2014).

Of the studied bacteria in the current review, *E. coli* represented the most commonly studied organism among the selected animal species. *E. coli* could be regarded as one of the common food contaminating organisms in animal sourced food, especially in the LMICs. It has also been extensively used in monitoring of AMR (Gruel et al., 2021; Inthavong et al., 2022). One reason for this is that *E. coli* represents a major reservoir of resistance genes, which may be responsible for treatment failures in both human and veterinary medicine (Poirel et al., 2018). In addition, the prevalence and AMR levels in *E. coli* represent a good indicator of the 'selective pressure' among antimicrobials commonly used in food-producing animals either as growth promoters, prophylaxis or treatment (Van Den Bogaard et al., 2000). In general, antimicrobial resistance in *E. coli* is considered one of the major worldwide challenges in both animals and humans (Poirel et al., 2018).

Among the HPClAs used in animals studied in this review, highest resistance of *E. coli* was manifested against erythromycin in *E. coli* isolates from poultry, pigs and cattle. Interestingly, according to reports,

**Table 2**  
Median resistance (MR) with interquartile range (IQR) of *E. coli* in different animal species.

HPClAs	Cattle		Poultry		Pigs		Goats		Sheep	
	Included studies/ Total isolates	Median (IQR) in %	Included studies/ Total isolates	Median (IQR) in %	Included studies/ Total isolates	Median (IQR) in %	Included studies/ Total isolates	Median (IQR) in %	Included studies/ Total isolates	Median (IQR)
Cefepime	13/538	31.6 (1.7–41.7)	13/916	0 (0–0.2)	/	/	/	/	/	/
Cefotaxime	57/988	0 (0–27.9)	105/6315	0 (0–6.2)	21/739	0 (0–17.75)	/	/	/	/
Cefpodoxime	5/165	0.8 (0–10.4)	4/218	21.9 (14.1–44.8)	4/67	51.8 (27.7–75.9)	/	/	/	/
Ceftazidime	20/1264	21.1 (0–50.0)	33/15575	5.6 (0–37.5)	7/373	2.0 (0–24.9)	4/177	0 (0–0.8)	/	/
Ceftiofur	/	/	13/597	4.0 (1.25–4.75)	/	/	/	/	/	/
Ceftriaxone	14/989	24.8 (5.5–33.4)	31/1394	43.6 (6.3–75)	6/252	3.6 (0–4.2)	5/181	1.5 (0.4–50.7)	/	/
Ciprofloxacin	38/14633	4.4 (0.4–21.2)	69/18098	39.2 (10.1–63.7)	14/888	2.8 (0.4–9.3)	12/1058	0 (0–0.7)	10317	12.5 (6.3–31.3)
Colistin	9/520	1.5 (0–7.8)	26/5538	6.1 (0–42.9)	3/181	1.5 (0.7–50.7)	/	/	/	/
Erythromycin	12/621	85.7 (69.2–100.0)	16/630	96.1 (83.3–100.0)	4/395	94.0 (86.2–94.0)	5/90	0 (0–30.0)	/	/
Enrofloxacin	9/487	10.7 (8.0–21.6)	17/4257	73.7 (57.7–91.5)	/	/	/	/	/	/
Flumequine	/	/	5/4279	86.1 (82.1–91.7)	/	/	/	/	/	/
Gentamicin	41/2063	13.3 (1.2–32.7)	71/8480	20.4 (4.6–69.7)	18/1090	5.33 (0.4–7.7)	14/275	0 (0–1.5)	100	25.0 (0–51.1)
Levofloxacin	3/627	2.38 (1.2–3.5)	9/384	54.2 (43.8–77.9)	/	/	/	/	/	/
Nalidixic acid	19/1324	32.5 (10.4–78.6)	56/3051	67.1 (23.0–94.0)	10/697	12.5 (4.9–30.3)	9/314	2.2 (0–3.0)	75	87.5 (81.3–93.8)
Neomycin	10/292	85.2 (8.3–86.1)	6/4429	72.8 (33.5–92.2)	/	/	/	/	/	/
Norfloxacin	12/1178	4.6 (0–10.4)	21/4567	75.0 (27.7–84.6)	6/352	8.9 (3.3–10.8)	/	/	/	/
Ofloxacin	5/729	2.6 (0–7.7)	19/1408	0 (0–62.1)	/	/	/	/	/	/
Polymyxin B	4/83	25.0 (22.1–31.3)	/	/	/	/	/	/	/	/
Spectinomycin	3/28	60.0 (30.0–80.0)	4/3773	72.5 (52.1–88.4)	/	/	/	/	/	/
Streptomycin	30/13850	53.3 (20.0–84.6)	51/17163	63.6 (35.0–87.7)	12/601	48.0 (33.5–60.0)	11/10613	22.0 (4.4–50.8)	/	/
Vancomycin	4/104	1.7 (0.9–50.9)	/	/	/	/	/	/	/	/

IQR: interquartile range; /: data not available; MR and IQR were calculated only when at least 3 values were available.

the majority of antimicrobials are used to enhance growth performance, notably of pigs and chickens (Xiong et al., 2018; Van et al., 2020). This high level of resistance against erythromycin has also been reported in some African countries previously (Byarugaba et al., 2011; Katushabe et al., 2022). This finding is not surprising, as erythromycin has been widely used as a growth promoter in food-producing animals across African countries. For instance, in 2016, a survey published by the World Organization for Animal Health on antimicrobial use by region documented that AMU as growth promoters was authorised in 15% of African countries that participated in the survey (WOAH, 2017). It was also reported that the most used antimicrobial classes at the time of the survey in Africa were tetracyclines and macrolides (e.g erythromycin). Antibiotics used as growth promoters are often administered to animals in smaller quantities than for therapeutic purposes. However, this practice is more likely to apply substantial pressure with regard to AMR emergence as it involves exposing bacteria to sublethal amounts of the antibiotic repeatedly (Van et al., 2020).

Similarly, highest resistance levels of *E. coli* isolated from sheep, poultry and cattle were reported against nalidixic acid, flumequine and neomycin, respectively. This could reflect the extensive use of these antimicrobials among these food-producing animals across African countries. In a 3-year retrospective study (2010 – 2012) of antimicrobial usage in livestock production system in Southwestern Nigeria, fluoroquinolones (e.g flumequine), tetracyclines, and  $\beta$ -lactams/

aminoglycosides (e.g neomycin) represented the majority of antimicrobials used, with an increased consumption of 40.4% within the study period (Adesokan et al., 2015). On top of that, the antimicrobials most frequently used in food-producing animals by Ghanaian livestock keepers, either for preventing or treating bacterial infections, were fluoroquinolones, aminoglycosides, tetracyclines and penicillins (Donkor et al., 2012; Boamah and Agyare, 2016). Similarly, a survey in Rwanda indicated that about 97% of livestock farmers use antibiotics in animals mainly for prophylactic purposes either for disease prevention or as growth promoters (Manishimwe et al., 2017). It is important to note that, while the USA and Europe have banned the use of critically important antimicrobials as growth promoters in food-producing animals, other countries or regions such as the African continent do not have any strict regulation over their use and thus, livestock farmers still use these antimicrobial classes as growth promoters. In south-east Asian countries, surveillance for AMR and AMU in the animal production is limited (WHO, 2018b). Many of the critically important drugs of highest priority are used in animals in large quantities (Malik et al., 2023). In this region, 85% of the antibiotics used in layer production were attributed to prophylaxis including growth promotion (Ferdous et al., 2019; Imam et al., 2020).

*E. coli* isolated from cattle, pigs and poultry were highly susceptible to cefotaxime and ofloxacin. One possible reason for this finding may be that these antimicrobials are not used frequently among these food-

**Table 3**  
Median resistance (MR) with interquartile range (IQR) of *S. aureus* in different animal species in Africa.

HPClAs	Cattle		Poultry		Pigs		Goats		Sheep	
	Included studies /Total isolates	Median (IQR) in %	Included studies /Total isolates	Median (IQR) in %	Included studies /Total isolates	Median (IQR) in %	Included studies /Total isolates	Median (IQR) in %	Included studies /Total isolates	Median (IQR) in %
Cefotaxime	4/56	61.1 (41.7–80.6)	/	/	/	/	/	/	/	/
Ceftriaxone	/	/	3/84	78.3 (67.8–89.1)	/	/	4/82	0 (0–35.9)	/	/
Ciprofloxacin	17/318	0 (0–22.3)	/	/	/	/	9/161	0 (0–2.3)	10/203	30.2 (1.7–53.0)
Erythromycin	26/1157	26.1 (4.6–52.0)	15/857	74.7 (72.2–100)	/	/	10/199	69.4 (10.2–99.5)	10/178	50.0 (0–100.0)
Enrofloxacin	9/225	10 (9.4–23.3)	/	/	/	/	/	/	/	/
Gentamycin	31/1182	5.7 (0–20.8)	16/851	21.5 (6.7–33.4)	4/57	45.2 (22.6–67.9)	12/234	0.0 (0–44.4)	/	/
Neomycin	10/409	0 (0–16.2)	/	/	/	/	/	/	/	/
Norfloxacin	6/51	11.2 (0–14.8)	3/368	27.1 (13.5–33.1)	/	/	/	/	/	/
Polymyxin B	6/169	43.3 (11.4–89.9)	/	/	/	/	/	/	/	/
Streptomycin	22/1066	48.2 (21.0–68.6)	14/631	24.6 (9.3–52.1)	/	/	7/184	86.8 (19.4–99.0)	5/59	83.9 (41.9–91.9)
Tylosin	/	/	3/49	0 (0–50.0)	/	/	/	/	/	/
Vancomycin	15/473	20 (0–25.3)	/	/	/	/	6/51	31.25 (15.6–32.3)	/	/

IQR: interquartile range; /: data not available; MR and IQR were calculated only when at least 3 values were available.

**Table 4**  
Median resistance (MR) with interquartile range (IQR) of *Salmonella* spp. in different animal species in Africa.

HPClAs	Cattle		Poultry		Pigs	
	Included studies/ Total isolates	Median (IQR) in %	Included studies/Total isolates	Median (IQR) in %	Included studies/Total isolates	Median (IQR) in %
Azithromycin	/	/	3/26	15.4 (15.4)	/	/
Cefepime	/	/	7/286	47.1 (6.3–82.7)	/	/
Cefotaxime	9/122	0 (0–21.0)	32/865	0 (0–32.1)	5/48	0 (0–6.3)
Ceftazidime	6/37	0 (0–16.7)	12/739	0 (0–50.0)	4/253	3.1 (0–29.7)
Ceftiofur	/	/	8/276	0 (0–12.5)	/	/
Ceftriaxone	9/57	0 (0–10.0)	25/934	25.0 (0–58.3)	7/388	42.1 (1.6–94.5)
Ciprofloxacin	19/201	0 (0–25.0)	65/2359	27.3 (4.6–63.4)	6/394	25 (0.9–31.3)
Colistin	/	/	13/1040	7.8 (0–59.4)	/	/
Erythromycin	6/95	80.0 (55.7–100.0)	14/610	96.9 (68.8–99.6)	/	/
Enrofloxacin	/	/	20/895	31.1 (8.8–49.6)	/	/
Flumequin	/	/	8/640	83.3 (66.4–100.0)	/	/
Gentamycin	14/187	1.2 (0–21.7)	2/2434	19.0 (0–41.8)	65/252	5.0 (0.7–9.9)
Levofloxacin	/	/	5/135	25.6 (12.8–38.546)	/	/
Nalidixic acid	12/163	0 (0–16.7)	51/1535	57.1 (19.3–82.8)	5/384	15.2 (0–25.0)
Neomycin	/	/	22/9077	27.0 (4.6–100.0)	/	/
Norfloxacin	/	/	25/1057	20.6 (11.3–51.4)	/	/
Ofloxacin	4/93	8.5 (4.3–37.6)	13/387	41.4 (1.2–72.2)	/	/
Pefloxacin	/	/	3/615	44.8 (22.4–67.2)	/	/
Spectinomycin	/	/	8/282	7.0 (0.4–53.1)	/	/
Streptomycin	16/191	20 (0–51.8)	48/1830	51.4 (26.2–75.39)	6/63956	12.3 (1.6–25.0)
Vancomycin	/	/	3/20	50.0 (25.0–75.0)	/	/

IQR: interquartile range; /: data not available; MR and IQR were calculated only when at least 3 values were available.

producing animals across the African countries. Non availability/ accessibility of these HPClAs in the market of some countries can also be another reason (Vougat Ngom et al., 2017). In Tunisia, for instance, similar findings were reported among *E. coli* isolates collected from cattle (Tayh et al., 2022). This finding is of public health significance because third-generation cephalosporins, such as cefotaxime, and fluoroquinolones have been widely and extensively used in the management of Gram-negative bacterial infections in humans (Collignon et al., 2009). Drug resistant Gram-negative bacteria are among the most concerning around the world. For example, the Centers for Disease Control reported that carbapenem-resistant Enterobacteriaceae spp. are estimated to have

caused, in 2017, a total of 130 million dollars in U.S. healthcare costs (Morris and Cerceo, 2020). The majority of *E. coli* isolated from sheep were sensitive to HPClAs. This could reflect the minimal usage of these critically important antimicrobials in sheep production across the African countries or that sheep production is mainly managed in an extensive management production systems resulting in low usage of antimicrobials either as growth promoters or for therapeutic purposes.

In this review, the majority of the studies which screened for HPClAs against *S. aureus* isolated from selected food-producing animals across African countries tested against gentamycin, streptomycin and erythromycin. The higher resistance of this bacteria was observed against

**Table 5**Median resistance (MR) with interquartile range (IQR) of *Campylobacter* spp. in different animal species in Africa.

HPClAs	Cattle		Poultry		Pigs	
	Included studies/ Total isolates	Median (IQR) in %	Included studies/Total isolates	Median (IQR) in %	Included studies/Total isolates	Median (IQR) in %
Ceftriaxone	/	/	5/26	57.1 (10.7–100.0)	/	/
Ciprofloxacin	4/170	29.6 (17.7–41.5)	19/1752	45.8 (35–09–71.7)	3/330	28.8 (28.8)
Erythromycin	5/228	29.3 (23.4–57.8)	19/1717	45.7 (14.3–90.0)	3/330	40.9 (40.9)
Gentamycin	4/170	33.4 (19.0–47.7)	16/1334	11.2 (2.3–38.3)	3/330	60.6 (60.6)
Nalidixic acid	5/228	19.8 (9.9–32.3)	18/1331	50.6 (28.1–84.0)	/	/
Ofloxacin	/	/	3/62	2.0 (1.0–2.9)	/	/
Streptomycin	/	/	10681	44.7 (34.3–76.8)	/	/

IQR: interquartile range; /: data not available; MR and IQR were calculated only when at least 3 values were available.

**Table 6**Median resistance (MR) with interquartile range (IQR) of *Enterococcus* spp. in different animal species in Africa.

HPClAs	Cattle		Poultry		Pigs	
	Included studies/ Total isolates	Median (IQR) in %	Included studies/ Total isolates	Median (IQR) in %	Included studies/ Total isolates	Median (IQR) in %
Cefotaxime	3/152	16.88 (9.7–24.1)	/	/	/	/
Ciprofloxacin	11/704	0.8 (0–12.3)	7/360	31.5 (11.25–100)	3/525	70.3 (35.2–73.9)
Erythromycin	10/840	31.3 (17.5–72.0)	9/713	85.8 (40.6–97.9)	4/720	76.55 (57.21–86.1)
Enrofloxacin	3/355	42.2 (38.4–46.1)	/	/	/	/
Gentamycin	9/355	50.0 (32.0–78.8)	8/479	81.3 (27.9–98.6)	3/400	79.5 (40.7–89.7)
Neomycin	3/394	72.73 (36.4–81.7)	/	/	/	/
Norfloxacin	/	/	230	94.3 (85.6–97.1)	/	/
Streptomycin	7/536	36.3 (0–45.5)	4/449	33.3 (21.2–48.5)	/	/
Vancomycin	10/840	4.1 (0–18.6)	7/489	44.4 (3.1–78.2)	/	/

IQR: interquartile range; /: data not available; MR and IQR were calculated only when at least 3 values were available.

streptomycin in goat and sheep. This may be indicative of high usage of this antimicrobial in small ruminants mainly for therapeutic purposes against mastitis in sheep and goats. Indeed *S. aureus* is a significant public health bacterial pathogen, causing mastitis in cattle, sheep and goats (Ajose et al., 2022; El-Deeb et al., 2022). It has been shown that aminoglycosides (e.g streptomycin) is one of the frequently utilized antimicrobials in mastitis therapy (Vakanjac et al., 2013; Vidović et al., 2022). This is a serious issue as sheep and goats represent an important category of small ruminants commonly raised by poor-resource communities in African nations as a source of meat, milk and immediate cash (El-Deeb et al., 2022). *Staphylococcus aureus* causes great economic losses in dairy farms (Martins et al., 2019). Resistance of *S. aureus* can complicate the treatment of mastitis, which is considered an increasing challenge (Gordon and Lowy, 2008). It has also been documented as a common cause of hospital- and community-acquired infections (Guo et al., 2020).

*Salmonella* spp and *Campylobacter* spp are major worldwide public health concerns. *Salmonella* spp accounts for 93.8 million foodborne illnesses and 155,000 deaths per year (Marchello et al., 2020). Animals are the primary source of this pathogen, and animal-based foods are the main transmission route to humans (Ferrari et al., 2019). Meanwhile, acquisition of resistance to various antimicrobials, which might help decrease the effectiveness of treatment of foodborne illnesses, represent an additional risk for public health. In this review, *Salmonella* spp isolated from poultry and cattle were found to show the highest resistance to erythromycin, nalidixic acid, pefloxacin and ciprofloxacin. The high antimicrobial-resistant median observed is in line with the previous studies reported in low-and-middle income countries (Asuming-Bediako et al., 2019; Gahamanyi et al., 2020; Paintsil et al., 2022) showing an increasing trend of antimicrobial resistance in *Salmonella* spp and *Campylobacter* spp. This could be due to the fact that quinolones (ciprofloxacin) and macrolides are amongst the first line antimicrobials used to counteract the impact of *Salmonella* spp (Marchello et al., 2020) and *Campylobacter* spp (Gahamanyi et al., 2020) infections in food animal production and hence contributing to an increase of the selection and

emergence of resistance to this class of antimicrobials. In addition, lack of knowledge of farmers towards biosecurity measures in livestock production in Africa represents another major issue for antimicrobial use and emergence of resistant bacteria (Moffo et al., 2021), which might have consequences for public health. Misuse of antibiotics, failure to consult veterinarians before the antibiotherapy, absence of a clear regulation on the use of antibiotics in animals in Africa and the widespread use of standard drugs (Vougat Ngom et al., 2017; Jaime et al., 2022) are among the potential factors that justified the emergence and selection of multi-drug resistant foodborne pathogens.

The high median proportion of resistant *Campylobacter* spp from poultry against ciprofloxacin and erythromycin is an indicator of their overuse for prevention and cure diseases, which affected poultry production in many African countries (Caudell et al., 2020; Kiambi et al., 2021). In poultry farms, antimicrobials are mostly administered through drinking water for a specific indication and might also affect non target bacteria present in the gastro-intestinal tract. Interference of non-target bacteria with non-specific antimicrobials increases their chance to acquire resistance. This is also a serious issue for animal and human health because campylobacteriosis is a serious bacterial infection, which is a common foodborne disease epidemiologically linked to the consumption of poultry products (Asmai et al., 2020). In 2019 in the European Union, 220,682 human cases of campylobacteriosis were confirmed with an average notification rate of 59.7 per 100,000 people (EFSA, 2021). In many parts of Africa, campylobacteriosis is considered a significant public health problem (Hlashwayo et al., 2021).

*Enterococcus* spp are considered in various antimicrobial resistance surveillance programmes as an indicator of AMR (WHO, 2017b) for Gram positive bacteria. In this review, it was found that *Enterococcus* spp showed the highest resistance against norfloxacin and erythromycin in poultry production. This result is in line with that reported by De Jong et al. (2018) in European Union countries where, among the HPClAs studied, *Enterococcus* spp had higher resistance only to erythromycin in animals. Resistance of pathogens responsible for foodborne illnesses to highly critically antimicrobials agents present the higher risk for public



**Table 7**  
HPCIA resistance genes detected in food animals in Africa.

Animal species	HPCIA resistance genes identified	References
Cattle	<i>mecA</i> , <i>bla<sub>CTX-M-15</sub></i> , <i>bla<sub>Z</sub></i> , <i>bla<sub>TEM</sub></i> , <i>ermB</i> , <i>ermC</i> , <i>norA</i> , <i>qnrS</i> , <i>qnr</i> , <i>mfI</i> , <i>vatA</i> , <i>arnA</i> , <i>bla<sub>CTX</sub></i> , <i>mcr-1</i> , <i>mcr-2</i> , <i>mcr-3</i> , <i>qnrB</i> , <i>strA</i> , <i>ermA</i> , <i>mec</i> , <i>aph(30)-III</i> , <i>spc</i> , <i>qnrqfm</i> , <i>mecA1</i> , <i>mecA2</i> , <i>mecC</i> , <i>ermF</i> , <i>ermQ</i> , <i>bla<sub>CTX-M-1</sub></i> , <i>mphA</i> , <i>aadA2</i> , <i>sak</i> , <i>scn</i> , <i>sea</i> , <i>hly</i> , <i>mermB</i> , <i>bla<sub>ACC</sub></i> , <i>bla<sub>CIT</sub></i> , <i>vanB</i> , <i>vanC2/3</i> , <i>strB</i> ,	Saidi et al. (2015); Sghaier et al. (2019); Youssif et al. (2021); Zaatout et al. (2019); Raheel et al. (2020); Okubo et al. (2019); Elmonir et al. (2021); Tartor et al. (2021); Badi et al. (2018); Emeru et al. (2019); Awad et al. (2017); Freitas et al. (2020); Elsayed et al., 2019; Braun et al. (2016); Algammal et al., 2020; Ahmed et al. (2020); Ahmed et al. (2019); Sahar et al., 2018; Abdeen et al. (2021); Monistero et al. (2020); Matloko et al. (2021); Madoshi et al. (2018); Iweriebor et al. (2016); Gwida et al. (2020); Iweriebor et al. (2015); Montso et al. (2019)
Poultry	<i>gyrA</i> , <i>bla<sub>CTX-M</sub></i> , <i>bla<sub>OXA</sub></i> , <i>bla<sub>SHV</sub></i> , <i>ermC</i> , <i>qnrS</i> , <i>aacC</i> , <i>bla<sub>TEM</sub></i> , <i>bla<sub>CMY</sub></i> , <i>mrc-1.1</i> , <i>bla<sub>CTX-M-15</sub></i> , <i>bla<sub>TEM-1B</sub></i> , <i>bla<sub>TEM-1</sub></i> , <i>bla<sub>OXA-1</sub></i> , <i>aac(3)-IIa</i> , <i>aadA2</i> , <i>strA</i> , <i>strB</i> , <i>parC</i> , <i>aadA</i> , <i>Asp87-Asn</i> , <i>bla<sub>OXA-61</sub></i> , <i>bla<sub>CTM-1</sub></i> , <i>qnrB69</i> , <i>bla<sub>CMY-98</sub></i> , <i>qnrB</i> , <i>aadA1</i> , <i>qnrA</i> , <i>qepA</i> , <i>mfI</i> , <i>qnr</i> , <i>ermB</i> , <i>vanA</i> , <i>vanB</i> , <i>vatA</i> , <i>arnA</i> , <i>aadA</i> , <i>vanC</i> , <i>qnrS1</i> , <i>CITM</i> , <i>ere</i> , <i>aac(3)-(IV)</i> , <i>dfr(A1)</i> , <i>ASTeSuTnp</i> , <i>aac(6')-Ib-cr</i> , <i>bla<sub>Z</sub></i> , <i>aac(6') aph(2'')</i> , <i>bla<sub>SHV-12</sub></i> , <i>cmeB</i> , <i>bla<sub>OXA-61</sub></i> , <i>sul1</i> , <i>dfrA</i> , <i>qnrD</i> , <i>pyrC</i> , <i>aadA2b</i> , <i>aadA5</i> , <i>arnA</i> , <i>aac(3)-IIa</i> , <i>aac(3)-Ib</i> , <i>aph(3)-Ia</i> , <i>aph(3)-Ib</i> , <i>aph(3)-Id</i> , <i>ant(2)-Ia</i> , <i>qnrB1</i> , <i>qnrB19</i> , <i>qnrB52</i> , <i>qnrS1</i> , <i>qnrS2</i> , <i>qnrS3</i> , <i>qnrS7</i> , <i>qnrS11</i> , <i>qnrS13</i> , <i>pare</i> , (PMRC)- <i>mrc-1.1</i> , <i>aac2</i> , <i>gyrB</i> , <i>aac3-1</i> , <i>mphA</i> , <i>aadA14</i> , <i>acrA</i> , <i>qnrB2</i> , <i>qnrA1</i> , <i>aadA2</i> , <i>mrx</i> , <i>qnrB5</i> , <i>bla<sub>CMY-2</sub></i>	Tuan et al.; 2016; Yhiler et al., 2019; Younis et al., (2017); Pillay et al., (2020); Shabana et al., (2019); Ramadan et al., (2018); Soliman et al., (2021); Ojo et al., (2016); Salem et al. (2016); Reddy and Zishiri, (2017); Sghaier et al., (2019); Raufu et al. (2021); Vounba et al., (2018); Roshdy et al., (2016); Okubo et al., (2019); Osman et al., (2019); Vounba et al. (2019); Raufu et al., (2013); Badi et al., (2018); Amer et al., (2018); Barka et al., (2021); Benameur et al., (2018); El-Aziz and Gharib, (2015); Amen et al., (2019); Gharbi et al. (2021); Elkenany et al., (2018); Awad et al., (2016); Aworh et al., (2021); Ezzeldeen et al. (2013); Ayandiran et al., (2018); Ammar et al., (2015); Anyanwu et al., (2021); Barbieri et al., (2017); Ammar et al., (2019); Djeflal et al. (2017); Farghaly et al., (2013); Benameur et al., (2021); Abdelgader et al., (2018); Ahmed et al., (2013); Sahar et al. (2018); Hassan et al., (2021); Moawad et al., (2018); Larbi et al., (2021); Yhiler et al. (2019); Mnif et al., (2012); Jouini et al., (2021); Ibrahim et al., (2019); Mthembu et al., (2019); Lebdah et al., (2017); Kimera et al., (2021); Kilani et al., (2015); Messaïli et al., (2019); Abdeen et al., (2018); Agabou et al., (2016)
Pigs	<i>gyrA</i> , <i>parC</i> , <i>bla<sub>TEM-1B</sub></i> , <i>aac(3)-IIa</i> , <i>aac(3)-Id</i> , <i>aadA7</i> , <i>cmeB</i> , <i>mfI</i> , <i>qnr</i> , <i>ermB</i> , <i>vanB</i> , <i>vanA</i> , <i>vatA</i> , <i>arnA</i> , <i>bla<sub>CTX-M</sub></i> , <i>bla<sub>TEM</sub></i> , <i>strA</i> , <i>aac(6)-Ib-cr</i> , <i>qnrB</i> , <i>vanC1</i> , <i>vanC2/3</i>	Raufu et al. (2021); Sithole et al. (2021); Okubo et al. (2019); Olowe et al. (2015); Fashae and Hendriksen (2014); Iwu et al. (2017); Kimera et al. (2021); Iweriebor et al. (2015)
Goats	<i>bla<sub>CTX-M-15</sub></i> , <i>mfI</i> , <i>qnr</i> , <i>ermB</i> , <i>vanA</i> , <i>vanB</i> , <i>vatA</i> , <i>arnA</i>	Sghaier et al. (2019); Okubo et al. (2019); El-Zamkan and Mohamed (2021); Gharsa et al. (2015)
Sheep	<i>bla<sub>CTX-M-1</sub></i> , <i>bla<sub>CTX-15</sub></i> , <i>bla<sub>TEM-1</sub></i> , <i>ermB</i> , <i>erm(C)</i> , <i>vanA</i> , <i>qnrA</i> , <i>qnrB</i> , <i>qepA</i> , <i>aac(6')-Ib-cr</i>	Sghaier et al. (2019); El-Zamkan and Mohamed (2021); El-Aziz and Gharib (2015); Gharsa et al. (2012)

health in Africa and worldwide. Better policies concerning antimicrobial usage associated with capacity building, awareness campaigns of stakeholders should be increased to prevent misuse of critically antimicrobials agents for human medicine in food animals in order to preserve public health.

The resistance of bacteria observed against HPCIA in this review might also be the result of cross and co resistance patterns and not only a result of the use of these antimicrobials in livestock production.

This review revealed that only 30.2% articles studied resistance genes and all of them used PCR. The most frequently reported genes were *bla<sub>CTX-M</sub>*, *bla<sub>TEM</sub>*, *bla<sub>Z</sub>*, *ermB*, *ermC*, *qnr*, *vanA*, *vanB*, *str*, *gyr*, *aac(6')-Ib-cr*, and *mrc*. This finding is similar with those of Kimera et al. (2020). This can be explained by the lack of equipment in Africa. Indeed, performing molecular analysis requires technology which is very expensive and not always accessible in most laboratories facilities in countries with limited resources and where the diagnostic capacities are suboptimal. African countries should improve their policies because enhancing the diagnostic capacity of laboratories is an essential step for generating reliable and accurate data, particularly in settings where fundamental gaps and capacity constraints may prevent the early and rapid detection of many animal diseases (FAO, 2023).

This study was subject to certain limitations. This review focused on peer-reviewed publications and had limited scope for inclusion of "grey" literature or governmental and non-governmental reports. In addition, since for certain region like central Africa, we only found data from less than half of the countries, the findings may not be generalizable to the entire region. Furthermore, most of the AMR studies were based on phenotypic rather than molecular techniques, thus limiting understanding of transmission dynamics. Risk of bias assessment of the selected studies was not performed as it is not a mandatory step for a scoping review. However, it must be stressed that the quality of individuals studies has an impact on the results presented in this review. For example, lack of standardized laboratory protocol may account for variations in the level of AMR reported in the included studies. In addition, the proportion of resistance presented in this review was calculated when at least three studies were carried out for the same bacteria-HPCIA combination even if only one isolate was studied. It would have been preferable to include studies reporting high number of isolates to ensure a high degree of precision of the data. Our search string did not specifically target resistance genes. Therefore, a more detailed review of molecular analysis conducted in African research should be conducted.

## 5. Conclusion

Research articles on HPCIA resistance of selected bacteria and animal species in Africa were not available from 61.1% of countries and only 30.2% articles studied resistant genes. This highlights that there is a knowledge gap regarding the current levels of HPCIA resistance in bacteria isolated from livestock. Such gap might have implications in the public health management and policies that are implemented in African countries. It is therefore relevant to have a clearer picture of the resistance patterns to HPCIA, as well as to develop a better understanding of the emergence and selection of AMR in the African continent with a focus on those countries which are not or underrepresented in this review. This will likely require a financial and technical investment in diagnostic infrastructure at basic level across Africa. Awareness of different stakeholders on the harmful impact of AMR in Africa countries and improvement of farm biosecurity are important alternatives that can also contribute to address AMR.

## Funding

This research did not receive any financial support

## Registration and protocol

The protocol of this review was archived at the Veterinary Public Health Institute of the University of Bern in Switzerland website ([http://www.vphi.ch/unibe/portal/fak\\_vetmedizin/c\\_dept\\_dcr-vph/f\\_inst\\_vphi/content/e21055/e76940/e1046889/e1206018/310322-ScopingReviewProtocol-HPCIASresistanceinAfrica\\_Final\\_eng.pdf](http://www.vphi.ch/unibe/portal/fak_vetmedizin/c_dept_dcr-vph/f_inst_vphi/content/e21055/e76940/e1046889/e1206018/310322-ScopingReviewProtocol-HPCIASresistanceinAfrica_Final_eng.pdf)) and registered in the Systematic Reviews for Animals and Food (SYREAF) website (<https://syreaf.org>).

## CRedit authorship contribution statement

**Leina M. Mimboe:** Data curation, Formal analysis. **Mohamed MM Mouiche:** Data curation, Formal analysis. **Gertraud Schuepbach-Regula:** Conceptualization, Methodology, Supervision, Writing – original draft, Writing – review & editing. **Luís Pedro Carmo:** Conceptualization, Data curation, Methodology, Supervision, Writing – original draft, Writing – review & editing. **Akenghe Tanyienow:** Data curation, Formal analysis. **Frédéric Moffo:** Data curation, Formal analysis, Methodology, Project administration. **Hippolyte M. Watsop:** Data curation, Formal analysis. **Ronald Vougat Ngom:** Conceptualization, Methodology, Project administration, Writing – original draft, Writing – review & editing. **Saleh M. Jajere:** Data curation, Formal analysis. **Gaspard JA Ayissi:** Data curation, Formal analysis.

## Declaration of Competing Interest

The authors declare no conflict of interest

## Acknowledgments

The authors would like to acknowledge CHOUTO Steven who made the map.

## Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.prevetmed.2024.106173](https://doi.org/10.1016/j.prevetmed.2024.106173).

## References

- Abdeen, E., Elmonir, W., Suelam, I.I.A., Mousa, W.S., 2018. AntibioGram and genetic diversity of *Salmonella enterica* with zoonotic potential isolated from morbid native chickens and pigeons in Egypt. *J. Appl. Microbiol.* 124, 1265–1273.
- Abdeen, E.E., Mousa, W.S., Abdel-Tawab, A.A., El-Faramawy, R., Abo-Shama, U.H., 2021. Phenotypic, genotypic and antibiogram among *Staphylococcus aureus* isolated from bovine subclinical mastitis. *Pak. Vet. J.* 41, 289–293.
- Abdelgader, S.A., Shi, D., Chen, M., Hassan, L.Z., Hejair, M.A., Muhammad, U., Yao, H., Zhang, W., 2018. Antibiotics resistance genes screening and comparative genomics analysis of commensal *Escherichia coli* isolated from poultry farms between China and Sudan. Article ID 5327450 *Biomed. Res. Int.* 2018, 9. <https://doi.org/10.1155/2018/5327450>.
- Abramova, I.O., 2022. The population of Africa under the conditions of transformation of the World Order. *Her. Russ. Acad. Sci.* 92, S1306–S131.
- Adesokan, H.K., Akanbi, I.O., Akanbi, I.M., Obaweda, R.A., 2015. Pattern of antimicrobial usage in livestock animals in South-Western Nigeria: the need for alternative plans. *Onderstepoort J. Vet. Res.* 82, 1–6. <https://doi.org/10.4102/ojvr.v82i1.816>.
- Agabou, N., Lezzar, Z., Ouchenane, S., Khemissi, D., Satta, Sotto, J., Lavigne, P., Pantel, A., 2016. Clonal relationship between human and avian ciprofloxacin-resistant *Escherichia coli* isolates in North-Eastern Algeria. *Eur. J. Clin. Microbiol. Infect. Dis.* 35, 227–234.
- Ahmed, A.M., Shimamoto, T., Shimamoto, T.A., 2013. Molecular characterization of multidrug-resistant avian pathogenic *Escherichia coli* isolated from septicemic broilers. *Int. J. Med. Microbiol.* 303, 475–483.
- Ahmed, I., Rabbi, M.B., Sultana, S., 2019. Antibiotic resistance in Bangladesh: a systematic review. *Int. J. Infect. Dis.* 80, 54–61.
- Ahmed, W., Neubauer, H., Tomaso, H., El Hofy, F.I., Monecke, S., Abdeltawab, A.A., Hotzel, H., 2020. Characterization of *Staphylococci* and *Streptococci* isolated from Milk of Bovides with Mastitis in Egypt. *Pathogens* 9, 381. <https://doi.org/10.3390/pathogens9050381>.
- Ajose, D.J., Oluwarinde, B.O., Abolarinwa, T.O., Fri, J., Montso, K.P., Fayemi, O.E., Aremu, A.O., Ateba, C.N., 2022. Combating Bovine Mastitis in the Dairy Sector in an Era of Antimicrobial Resistance: ethno-veterinary medicinal option as a viable alternative approach. *Front. Vet. Sci.* 9, 800322. <https://doi.org/10.3389/fvets.2022.800322>.
- Alonso, C.A., Zarazaga, M., Ben Sallem, R., Jouini, A., Ben Slama, K., Torres, C., 2017. Antibiotic resistance in *Escherichia coli* in husbandry animals: the African perspective. *Let. Appl. Microbiol.* 64 (5), 318–334.
- Amen, O., Hussein, A.G., Sayed, A.M., Ibrahim, R.S., 2019. Detection of antibiotic resistance genes in *Staphylococcus aureus* isolated from poultry farms. *Assiut Vet. Med. J.* 65, 1–9.
- Amer, M.M., Mekky, H.M., Amer, A.M., Fedawy, H.S., 2018. Antimicrobial resistance genes in pathogenic *Escherichia coli* isolated from diseased broiler Chicken in Egypt and their relationship with the phenotypic resistance characteristics. *Vet. World* 11, 1082–1088.
- Ammar, A.M., El-Hamid, M.I.A., Eid, S.E.A., El-Oksh, A.S., 2015. Insights into antimicrobial resistance and virulence genes of emergent multidrug resistant avian pathogenic *Escherichia coli* in Egypt: how closely related are they? *Rev. Med. Vet.* 166, 304–314.
- Ammar, A.M., Abdeen, E.E., Abo-Shama, U.H., Fekry, E., Kotb Elmahallawy, E., 2019. Molecular characterization of virulence and antibiotic resistance genes among *Salmonella* serovars isolated from broilers in Egypt. *Let. Appl. Microbiol.* 68, 188–195. <https://doi.org/10.1111/lam.13106>.
- Anyanwu, M.U., Marrolo, R., Paolucci, M., Brovarone, F., Nardini, P., Chah, K.F., Shoyinka, S.V.O., Carretto, E., 2021. Isolation and characterisation of colistin-resistant Enterobacteriales from Chicken in Southeast Nigeria. *J. Glob. Antimicrob. Resist.* 26, 93–100. <https://doi.org/10.1016/j.jgar.2021.04.030>.
- Asmai, R., Karrouan, B., Es-Soucrati, K., En-Nassiri, H., Bouchrif, B., Karib, H., Triqui, R., 2020. Prevalence and antibiotic resistance of *Campylobacter coli* isolated from broiler farms in the Marrakesh Safi region, Morocco. *Vet. World* 13, 1892–1897. <https://doi.org/10.14202/vetworld.2020.1892-1897>.
- Asuming-Bediako, N., Parry-Hanson Kunadu, A., Abraham, S., Habib, I., 2019. *Campylobacter* at the Human-Food Interface: the African Perspective. *Pathogens* 8, 87.
- Awad, A., Arafat, N., Elhadidy, M., 2016. Genetic elements associated with antimicrobial resistance among avian pathogenic *Escherichia coli*. *Ann. Clin. Microbiol. Antimicrob.* 15 (1), 8.
- Awad, A., Ramadan, H., Nasr, S., Ateya, A., Atwa, S., 2017. Genetic characterization, antimicrobial resistance patterns and virulence determinants of *Staphylococcus aureus* isolated from bovine mastitis. *Pak. J. Biol. Sci.* 20, 298–305. <https://doi.org/10.3923/pjbs.2017.298.305>.
- Aworh, M.K., Kwaga, J.K.P., Hendriksen, R.S., Okolocha, E.C., Thakur, S., 2021. Genetic relatedness of multidrug resistant *Escherichia coli* isolated from humans, Chicken and poultry environments. *Antimicrob. Resist. Infect. Control.* 10 (1), 13. <https://doi.org/10.1186/s13756-021-00930-x>.
- Ayandiran, T.O., Falgenhauer, L., Schmiede, J., Chakraborty, T., Ayeni, F.A., 2018. High resistance to tetracycline and ciprofloxacin in bacteria isolated from poultry farms in Ibadan, Nigeria. *J. Infect. Dev. Ctries* 12, 462–470. <https://doi.org/10.3855/jidc.9862>.
- Badi, S., Cremonesi, P., Abbassi, M.S., Ibrahim, C., Snoussi, M., Bignoli, G., Castiglioni, M.L.B., Hassen, A., 2018. Antibiotic resistance phenotypes and virulence-associated genes in *Escherichia coli* isolated from animals and animal food products in Tunisia. *FEMS Microbiol. Lett.* 365, fny088. <https://doi.org/10.1093/femsle/fny088>.
- Barbieri, N.L., Nielsen, D.W., Wannemuehler, Y., Cavender, T., Hussein, A., Yan, ShiGan, Nolan, L.K., Logue, C.M., 2017. Mcr-1 identified in Avian Pathogenic *Escherichia coli* (APEC). *PLoS ONE* 12, e0172997. <https://doi.org/10.1371/journal.pone.0172997>.
- Barka, M.S., Cherif-Anantar, A., Benamar, I., 2021. Antimicrobial resistance patterns and transferable traits in Enterobacteriaceae isolates from poultry in Tlemcen, Algeria. *Afr. J. Clin. Exp. Microbiol.* 22, 196–203. <https://doi.org/10.4314/ajcm.v22i2.12>.
- Benamer, Q., Tali-Maamar, H., Assaous, F., Guettou, B., Boutaiba Benklouou, M., Rahal, K., Ben-Mahdi, M.H., 2018. Characterization of quinolone-resistant Enterobacteriaceae strains isolated from poultry in Western Algeria: first report of *qnrS* in an Enterobacter cloacae. *Vet. World* 11, 469–473.
- Benamer, Q., Gervasi, T., Giarratana, F., Vitale, M., Anzà, D., La Camera, E., Nostro, A., Cicero, N., Marino, A., 2021. Virulence, Antimicrobial Resistance and Biofilm Production of *Escherichia coli* Isolates from Healthy Broiler Chicken in Western Algeria. *Antibiotics* 10, 1157. <https://doi.org/10.3390/antibiotics10101157>.
- Bennani, H., Mateus, A., Mays, N., Eastmure, E., Stärk, K.D.C., Häslar, B., 2020. Overview of evidence of antimicrobial use and antimicrobial resistance in the food chain. *Antibiot. (Basel)* 9, 49. <https://doi.org/10.3390/antibiotics9020049>.
- Boamah, V.E., Agyare, C., Odoi, H., Dalsgaard, A., 2016. Antibiotic practices and factors influencing the use of antibiotics in selected poultry farms in Ghana. *J. Antimicrob. Agents* 2, 120. <https://doi.org/10.4172/2472-1212.1000120>.
- Braun, S.D., Ahmed, M.F.E., El-Adawy, H., Hotzel, H., Engelmann, I., Weiss, D., Monecke, S., Ehrlich, R., 2016. Surveillance of extended-spectrum beta-lactamase-producing *Escherichia coli* in dairy Cattle farms in the Nile Delta, Egypt. *Front. Microbiol.* 7, 1020.
- Byarugaba, D.K., Kisame, R., Olet, S., 2011. Multi-drug resistance in commensal bacteria of food of animal origin in Uganda. *Afr. J. Microbiol. Res* 5, 1539–1548. (<http://www.academicjournals.org/ajmr>).
- Caudell, M.A., Dorado-Garcia, A., Eckford, S., Creese, C., Byarugaba, D.K., Afakey, K., Chansa-Kabali, T., Fasina, F.O., Kabali, E., Kiambi, S., Kimani, T., Mainda, G., Mangesho, P.E., Chimpangu, F., Dube, K., Kikimoto, B.B., Koka, E., Mugara, T., Rubegwa, B., Swiswa, S., 2020. Towards a bottom-up understanding of antimicrobial use and resistance on the farm: a knowledge, attitudes, and practices survey across livestock systems in five African countries. *PLoS One* 15, e0220274. <https://doi.org/10.1371/journal.pone.0220274>.

- Collignon, P., Aarestrup, F.M., Irwin, R., et al., 2013. Human deaths and third-generation cephalosporin use in poultry, Europe. *Emerg. Infect. Dis.* 19, 1339–1340.
- Collignon, P., Powers, J.H., Chiller, T.M., Aidara-Kane, A., Aarestrup, F.M., 2009. World Health Organization ranking of antimicrobials according to their importance in human medicine: a critical step for developing risk management strategies for the use of antimicrobials in food production animals. *Clin. Infect. Dis.* 49, 132–141. <https://doi.org/10.1086/599374>.
- Couliadiaty, A.G.V., Sanou, A., Hounbedji, C.A., Djibougou, D.A., Dicko, A., Kobo, G., Bonfoh, B., 2021. Prevalence and sensitivity to antibiotics of campylobacter spp. in chicken, farmers and soil in bobo-dioulasso, Burkina Faso. *PAMJ-One Health* 4, 8.
- Cuong, N.V., Padungtod, P., Thwaites, G., Carrique-Mas, J.J., 2018. Antimicrobial usage in animal production: a review of the literature with a focus on low-and middle-income countries. *Antibiotics* 7, 75.
- De Jong, A., Simjee, S., Garch, F.E., Moyaert, H., Rose, M., Youala, M., et al., 2018. Antimicrobial susceptibility of enterococci recovered from healthy cattle, pigs and chickens in nine EU countries (EASSA study) to critically important antibiotics. *Vet. Microbiol.* 216, 168–175. <https://doi.org/10.1016/j.vetmic.2018.02.010>.
- De Oliveira, D.M., Forde, B.M., Kidd, T.J., Harris, P.N., Schembri, M.A., Beatson, S.A., Paterson, D.L., Walker, M.J., 2020. Antimicrobial resistance in ESKAPE pathogens. *Clin. Microbiol. Rev.* 33, e00181-19 <https://doi.org/10.1128/cmr.00181-19>.
- Diana, A., Penasa, M., Santinello, M., Scali, F., Magni, E., Alborali, G.L., Bertocchi, L., De Marchi, M., 2021. Exploring potential risk factors of antimicrobial use in beef cattle. *Animal* 15, 100091. <https://doi.org/10.1016/j.animal.2020.100091>.
- Djeflal, S., Mamache, B., Elgroud, R., Bouaziz, O., 2017b. Emergence of multi drug resistant Salmonella isolated from broiler chicken farms and slaughterhouses in the province of Skikda (Algeria) [Conference poster]. 12e Journ. De. la Rech. Avic. Et. Palmipedes a Foie Gras (JRA-JRPF 2017), 5–6 avril 2017, Tours, Fr. 819–824.
- Djeflal, S., Bakour, S., Mamache, B., Elgroud, R., Agabou, A., Chabou, S., Hireche, S., Bouaziz, O., Rahal, K., Rolain, J.M., 2017a. Prevalence and clonal relationship of ESBL-producing Salmonella strains from humans and poultry in northeastern Algeria. *BMC Vet. Res.* 13 (1), 9. <https://doi.org/10.1186/s12917-017-1050-3>.
- Donkor, E.S., Newman, M.J., Yeboah-Manu, D., 2012. Epidemiological aspects of non-human antibiotic usage and resistance: implications for the control of antibiotic resistance in Ghana. *Trop. Med. Int. Health* 17, 462–468. <https://doi.org/10.1111/j.1365-3156.2012.02955.x>.
- Dutra, M.C., Moreno, L.Z., Dias, R.A., Moreno, A.M., 2021. Antimicrobial Use in Brazilian Swine Herds: assessment of use and reduction examples. *Microorganisms* 9, 881.
- EFSA, European food safety authority, 2021. European centre for disease prevention and control. The European union one health 2020 zoonoses report. EFSA J. 19 (12), e06971. (<https://www.efsa.europa.eu/en/efsajournal/pub/6971>) (Available at).
- El-Aziz, N.K.A., Gharib, A.A., 2015. Coexistence of plasmid-mediated quinolone resistance determinants and AmpC-Beta-lactamases in *Escherichia coli* strains in Egypt. *Cell. Mol. Biol.* 61, 29–35.
- El-Deeb, W., Cave, R., Fayez, M., Alhumam, N., Quadri, S., Mkrtychyan, H.V., 2022. Methicillin Resistant Staphylococci Isolated from Goats and Their Farm Environments in Saudi Arabia Genotypically Linked to Known Human Clinical Isolates: a Pilot Study. *Microbiol Spectr.* 10, e00387-22 <https://doi.org/10.1128/spectrum.00387-22>.
- Elkenany, R.M., Eladl, A.H., El-Shafei, R.A., 2018. Genetic characterisation of class 1 integrons among multidrug-resistant Salmonella serotypes in broiler chicken farms. *J. Glob. Antimicrob. Resist.* 14 202–208. <https://doi.org/10.1016/j.jgar.2018.04.009>.
- Elmonir, W., Shalaa, S., Tahoun, A., Mahmoud, S.F., Remela, E.M.A., Eissa, R., El-Sharkawy, H., Shukry, M., Zahran, R.N., 2021. Prevalence, antimicrobial resistance, and genotyping of Shiga toxin-producing *Escherichia coli* in foods of cattle origin, diarrhetic cattle, and diarrhetic humans in Egypt. *Gut Pathog.* 13, 1–11. <https://doi.org/10.1186/s13099-021-00402-y>.
- Elton, L., Thomason, M.J., Tembo, J., Velavan, T.P., Pallerla, S.R., Arruda, L.B., Vairo, F., Montaldo, C., Ntoumi, F., Hamid, A.M.M., Haider, N., Ippolito, R.K., Zumla, A., McHugh, T.D., the PANDORA-ID-NET consortium, 2020. Antimicrobial resistance preparedness in sub-Saharan African countries. *Antimicrob. Resist. Infect. Control* 9, 1–11.
- El-Zamkan, M.A., Mohamed, H.M.A., 2021. Antimicrobial resistance, virulence genes and biofilm formation in *Enterococcus* species isolated from milk of Sheep and Goat with subclinical mastitis. *PLoS ONE* 16, e0259584. <https://doi.org/10.1371/journal.pone.0259584>.
- Emeru, B.A., Messele, Y.E., Tegegne, D.T., Yalaw, S.T., Bora, S.K., Babura, M.D., Beyene, M.T., Werid, G.M., 2019. Characterization of antimicrobial resistance in *Staphylococcus aureus* isolated from bovine mastitis in Central Ethiopia. *J. Vet. Med. Anim. Health* 11, 81–87. <https://doi.org/10.5897/JVMAH2019.076>.
- FAO, Food and Agriculture Organization of the United Nations, 2023. Veterinary laboratory testing protocols for priority zoonotic diseases in Africa. FAO Animal Production and Health Guidelines No. 34. Rome. <https://doi.org/10.4060/cc3956en>.
- Farghaly, E.M., Erfan, A.M., Badr, H., Ibrahim, A.A., Al-Atfeehy, N.M., Nasef, S.A., 2013. Studies on some quinolone resistance of salmonella strains of avian origin. In *Proceedings of the 6th Scientific Conference of Animal Wealth Research in the Middle East and North Africa, Hurgada, Egypt, 27-30 September 2013* (pp. 92–110). Massive Conferences and Trade Fairs. ([https://www.researchgate.net/profile/Soad-Nasef/publication/279196250\\_Studies\\_on\\_some\\_quinolone\\_resistance\\_of\\_salmonella\\_s\\_strains\\_of\\_avian\\_origin/links/558e6bf208ae15962d896273/Studies-on-some-quinolone-resistance-of-salmonella-strains-of-avian-origin.pdf](https://www.researchgate.net/profile/Soad-Nasef/publication/279196250_Studies_on_some_quinolone_resistance_of_salmonella_s_strains_of_avian_origin/links/558e6bf208ae15962d896273/Studies-on-some-quinolone-resistance-of-salmonella-strains-of-avian-origin.pdf)).
- Fashae, K., Hendriksen, R.S., 2014. Diversity and antimicrobial susceptibility of *Salmonella enterica* serovars isolated from Pig farms in Ibadan, Nigeria. *Folia Microbiol* 59, 69–77. <https://doi.org/10.1007/s12223-013-0270-6>.
- FDA Task Force on Antimicrobial Resistance: Key Recommendations and Report. Available online:<http://fda.gov/downloads/ForConsumers/ConsumerUpdates/UCM143458.pdf> (accessed on 30 November 2020).
- Ferdous, J., Sachi, S., Al Noman, Z., Hussani, S.A.K., Sarker, Y.A., Sikder, M.H., 2019. Assessing farmers' perspective on antibiotic usage and management practices in small-scale layer farms of Mymensingh district, Bangladesh. *Vet. World* 12 (9), 1441. <https://doi.org/10.14202/vetworld.2019.1441-1447>.
- Ferrari, R.G., Rosario, D.K., Cunha-Neto, A., Mano, S.B., Figueiredo, E.E., Conte-Junior, C.A., 2019. Worldwide epidemiology of Salmonella serovars in animal-based foods: a meta-analysis. *Appl. Environ. Microbiol.* 85 (14), e00591–19.
- Freitas, A.R., Tedim, A.P., Duarte, B., Elghaieb, H., Abbassi, M.S., Hassen, A., Read, A., Alves, V., Novais, Peixe, L.L., 2020. *Enterococcus faecium* strains colonizing humans and bovines on different continents: Similarity without epidemiological link. *J. Antimicrob. Chemother.* 75, 2416–2423. <https://doi.org/10.1093/jac/dkaa227>.
- Gahamanyi, N., Mboera, L.E.G., Matee, M.I., Mutangana, D., Komba, E.V.G., 2020. Prevalence, risk factors, and antimicrobial resistance profiles of thermophilic campylobacter species in humans and animals in sub-saharan africa: a systematic review. Article ID 2092478 *Int. J. Microbiol.* 2020, 12. <https://doi.org/10.1155/2020/2092478>.
- Gharsa, H., Slama, K.B., Gomez-Sanz, E., Lozano, C., Zarazaga, M., Messadi, L., Boudabous, A., Torres, C., 2015. Molecular characterization of *Staphylococcus aureus* from nasal samples of healthy farm animals and pets in Tunisia. *Vector Borne Zoonotic Dis.* 15, 109–115. <https://doi.org/10.1089/vbz.2014.1655>.
- Gharsa, H., Ben Slama, K., Lozano, C., Gómez-Sanz, E., Klibi, N., Ben Sallem, R., Gómez, P., Zarazaga, M., Boudabous, A., Torres, C., 2012. Prevalence, antibiotic resistance, virulence traits and genetic lineages of *Staphylococcus aureus* in healthy Sheep in Tunisia. *Vet. Microbiol.* 156, 367–373. <https://doi.org/10.1016/j.vetmic.2011.11.009>.
- Gordon, R.J., Lowy, F.D., 2008. Pathogenesis of methicillin-resistant staphylococcus aureus infection. *Clin. Infect. Dis.* 46, S350–S359.
- Gruel, G., Sellin, A., Riveiro, H., Pot, M., Breurec, S., Guyomard-Rabenirina, S., Talarmin, A., Ferdinand, S., 2021. Antimicrobial use and resistance in *Escherichia coli* from healthy food-producing animals in Guadeloupe. *BMC Vet. Res.* 17 (1), 10. <https://doi.org/10.1186/s12917-021-02810-3>.
- Guo, Y., Song, G., Sun, M., Wang, J., Wang, Y., 2020. Prevalence and therapies of antibiotic-resistance in staphylococcus aureus. *Front. Cell. Infect. Microbiol.* 10, 107. <https://doi.org/10.3389/fcimb.2020.00107>.
- Gwida, M., Awad, A., El-Ashker, M., Hotzeld, H., Monecke, S., Ehrlich, R., Müller, E., Reig, A., Barth, S.A., Berens, C., Braun, S.D., 2020. Microarray-based detection of resistance and virulence factors in commensal *Escherichia coli* from livestock and farmers in Egypt. *Vet. Microbiol.* 240, 108539 <https://doi.org/10.1016/j.vetmic.2019.108539>.
- Hassan, I.Z., Wandrag, B., Gouws, J.J., Qekwana, D.N., Naidoo, V., 2021. Antimicrobial resistance and mcr-1 gene in *Escherichia coli* isolated from poultry samples submitted to a bacteriology laboratory in South Africa. *Vet. World* 14, 2662–2669.
- Higgins, J.P.T., Thomas, J., Chandler, J., Cumpston, M., Li, T., Page, M.J., Welch, V.A., 2021. Cochrane Handbook for Systematic Reviews of Interventions version 6.2 (updated February 2021). Cochrane. Available from ([www.training.cochrane.org/handbook](http://www.training.cochrane.org/handbook)).
- Hlshwayo, D.F., Sigauque, B., Noormahomed, E.V., Afonso, S.M., Mandomando, I.M., Bila, C.G., 2021. A systematic review and meta-analysis reveal that Campylobacter spp. and antibiotic resistance are widespread in humans in sub-Saharan Africa. *PLoS One* 16 (1), e0245951.
- Ibrahim, M.S., Hussein, A.H., Eid, A.A.M., Lebda, M.A., 2019. Molecular characterization of *Escherichia coli* strains causing respiratory signs in broiler chicken in Egypt. *Zag. Vet. J.* 47, 168–182.
- Imam, T., Gibson, J.S., Foysal, M., Das, S.B., Gupta, S.D., Fournié, G., Henning, J., 2020. A cross-sectional study of antimicrobial usage on commercial broiler and layer chicken farms in Bangladesh. *Front. Vet. Sci.* 7, 576113.
- Inthavong, P., Chanthavong, S., Nammanininh, P., Phommachanh, P., Theppangna, W., Agunos, A., Wagenaar, J.A., Douangneun, B., Loth, L., 2022. Antimicrobial resistance surveillance of pigs and chickens in the Lao People's Democratic Republic, 2018–2021. *Antibiotics* 11, 117. <https://doi.org/10.3390/antibiotics11020177>.
- Iweriebor, B.C., Obi, L.C., Okoh, A.I., 2015b. Virulence and antimicrobial resistance factors of *Enterococcus* spp. isolated from fecal samples from Piggery farms in Eastern Cape, South Africa. *BMC Microbiol* 15, 1–11.
- Iweriebor, B.C., Obi, L.C., Okoh, A.I., 2016. Macrolide, glycopeptide resistance and virulence genes in *Enterococcus* species isolates from dairy Cattle. *J. Med. Microbiol.* 65, 641–648.
- Iweriebor, B.C., Iwu, C.J., Obi, L.C., Nwodo, U.U., Okoh, A.I., 2015a. Multiple antibiotic resistances among Shiga toxin producing *Escherichia coli* O157 in feces of dairy Cattle farms in Eastern Cape of South Africa. *BMC Microbiol* 15, 1–9.
- Iwu, C.J., Jaja, I.F., Iweriebor, B.C., Obi, L.C., Okoh, A.I., 2017. Antibiotic resistance profiles of *Escherichia coli* O26, O145, and O157:H7 isolated from swine in the Eastern Cape Province, South Africa. *Asian Pac. J. Trop. Dis.* 7, 553–559.
- Jaime, G., Hobeika, A., Figuié, M., 2022. Access to veterinary drugs in Sub-Saharan Africa: roadblocks and current solutions. *Front. Vet. Sci.* 8, 558973 <https://doi.org/10.3389/fvets.2021.558973>.
- Jouini, A., Klibi, A., Elarbi, I., Chaabene, M.B., Hamrouni, S., Souiai, O., Hanachi, M., Ghran, A., Maaroufi, A., 2021. First Detection of Human ST131-CTX-M-15-O25-B2 Clone and High-Risk Clonal Lineages of ESBL/pAmpC-Producing *E. coli* Isolates from Diarrhetic Poultry in Tunisia. *Antibiotics* 10, 670. <https://doi.org/10.3390/antibiotics10060670>.
- Kagambea, A., Thibodeau, A., Soro, D.K., Barro, N., Fravallo, P., 2021. Detection of *Campylobacter* Sp. from Poultry Feces in Ouagadougou, Burkina Faso. *Food Nutr. Sci.* 12, 107–114.



- Katushabe, P., Byamukama, B., Byaruhanga, J., 2022. Burden of Multidrug-Resistant *Escherichia coli* in Pigs Slaughtered in Uganda and Its Implication on Veterinary Public Health. *Open J. Vet. Med.* 12, 187–200. <https://doi.org/10.4236/ojvm.2022.1212015>.
- Kiambi, S., Mwanza, R., Sirma, A., Czerniak, C., Kimani, T., Kabali, E., Dorado-Garcia, A., Eckford, S., Price, C., Gikonyo, S., Byarugaba, D.K., Caudell, M.A., 2021. Understanding Antimicrobial Use Contexts in the Poultry Sector: challenges for Small-Scale Layer Farms in Kenya. *Antibiotics* 10, 106. <https://doi.org/10.3390/antibiotics10020106>.
- Kilani, H., Abbassi, M.S., Ferjani, S., Mansouri, R., Sghaier, S.B., Salem, R., Jaouani, I., Douja, G., Brahim, S., Hammami, S.B., Chehida, N., Boubaker, I.B., 2015. Occurrence of blaCTX-M-1, qnrB1 and virulence genes in avian ESBL-producing *Escherichia coli* isolates from Tunisia. *Front. Cell. Infect. Microbiol.* 5, 38. <https://doi.org/10.3389/fcimb.2015.00038>.
- Kimera, Z.I., Mshana, S.E., Rweyemamu, M.M., Mboera, L.E., Matee, M.I., 2020. Antimicrobial use and resistance in food-producing animals and the environment: an African perspective. *Antimicrob. Resist. Infect. Control.* 9, 1–12.
- Kimera, Z.I., Mgaya, F.X., Misinzo, G., Mshana, S.E., Moremi, N., Matee, M.I.N., 2021. Multidrug-Resistant, Including Extended-Spectrum Beta Lactamase-Producing and Quinolone-Resistant, *Escherichia coli* Isolated from Poultry and Domestic Pigs in Dar es Salaam, Tanzania. *Antibiotics* 10, 406. <https://doi.org/10.3390/antibiotics10040406>.
- Kivumbi, M.T., Standley, C.J., 2021. Efforts to Identify and Combat Antimicrobial Resistance in Uganda: a systematic review. *Trop. Med. Infect. Dis.* 6, 86. <https://doi.org/10.3390/tropicalmed6020086>.
- Larbi, R.O., Ofori, L.A., Sylverken, A.A., Ayim-Akonor, M., Obiri-Danso, K., 2021. Antimicrobial Resistance of *Escherichia coli* from Broilers, Pigs, and Cattle in the Greater Kumasi Metropolis, Ghana. Article ID 5158185 *Int. J. Microbiol.* 2021, 7. <https://doi.org/10.1155/2021/5158185>.
- Lebdah, M.A., Mohammed, W.M., Eid, S., Hamed, R.I., 2017. Molecular detection of some antimicrobial resistance genes in salmonella species isolated from commercial layers in Egypt. *Zagazig Vet. J.* 45, 29–38.
- Liu, C.M., Stegger, M., Aziz, M., Johnson, T.J., Waits, K., Nordstrom, L., Gauld, L., Weaver, B., Rolland, D., Statham, S., Horwinski, J., Sariya, S., Davis, S.G., Sokurenko, E., Keim, P., Johnson, J.R., Price, L.B., 2018. *Escherichia coli* ST131-H 22 as a foodborne uropathogen. *MBio* 9, 10–1128. <https://doi.org/10.1128/mBio.00470-18>. PMID: 30154256.
- Madoshi, B.P., Mtambo, M.M.A., Muhairwa, A.P., Lupindu, A.M., Olsen, J.E., 2018. Isolation of vancomycin-resistant *Enterococcus* from apparently healthy human animal attendants, Cattle and Cattle wastes in Tanzania. *J. Appl. Microbiol.* 124, 1303–1310.
- Malik, H., Singh, R., Kaur, S., Dhaka, P., Bedi, J.S., Gill, J.P.S., Gongal, G., 2023. Review of antibiotic use and resistance in food animal production in WHO South-East Asia Region. *J. Infect. Public Health* 16, 172–182.
- Manishimwe, R., Nishimwe, K., Ojok, L., 2017. Assessment of antibiotic use in farm animals in Rwanda. *Trop. Anim. Health Prod.* 49, 1101–1106. <https://doi.org/10.1007/s11250-017-1290-z>.
- Marchello, S.C., Carr, D.S., Crump, A.J., 2020. Systematic review on antimicrobial resistance among *Salmonella* Typhi. *Worldw. Am. J. Trop. Med. Hyg.* 103 (6), 2518–2527. <https://doi.org/10.4269/ajtmh.20-0258>.
- Martins, S., Martins, V.C., Cardoso, F.A., Germano, J., Rodrigues, M., Duarte, C., Bexiga, R., Cardoso, S., Freitas, P.P., 2019. Biosensors for On-Farm Diagnosis of Mastitis. *Front. Bioeng. Biotechnol.* 7, 186.
- Matloko, K., Fri, J., Ateba, T.P., Molale-Tom, L.G., Ateba, C.N., 2021. Evidence of potentially unrelated AmpC beta-lactamase producing Enterobacteriaceae from Cattle, Cattle products and hospital environments commonly harboring the blaACC resistance determinant. *PLoS One* 16, e0253647. <https://doi.org/10.1371/journal.pone.0253647>.
- Messaili, C., Messai, Y., Bakour, R., 2019. Virulence gene profiles, antimicrobial resistance and phylogenetic groups of fecal *Escherichia coli* strains isolated from broiler Chicken in Algeria. *Vet. Ital.* 55, 35–46.
- Mnif, Ktari, Rhimi, S., Hammami, A.F.M., 2012. Extensive dissemination of CTX-M-1 and CMY-2-producing *Escherichia coli* in poultry farms in Tunisia. *Lett. Appl. Microbiol.* 55, 407–413.
- Moawad, A.A., Hotzel, H., Neubauer, H., Ehrlich, R., Monecke, S., Tomaso, H., Hafez, H.M., Roessler, U., El-Adawy, H., 2018. Antimicrobial resistance in Enterobacteriaceae from healthy  $\beta$ -lactamase-producing *Escherichia coli* broilers in Egypt: emergence of colistin-resistant and extended-spectrum. *Gut Pathog.* 10, 1–12.
- Moffo, F., Mouiche, M.M.M., Djomgang, H.K., Tombe, P., Wade, A., Kochivi, F.L., Dongmo, J.B., Mbah, C.K., Mapieyou, N.P., Ngogang, M.P., Awah-Ndukum, J., 2021. Poultry Litter Contamination by *Escherichia coli* Resistant to Critically Important Antimicrobials for Human and Animal Use and Risk for Public Health in Cameroon. *Antibiotics* 10, 402. <https://doi.org/10.3390/antibiotics10040402>.
- Moher, D., Shamseer, L., Clarke, M., Ghersi, D., Liberati, A., Petticrew, M., Shekelle, P., Stewart, L.A., 2015. Preferred reporting items for systematic review and meta-analysis protocols (PRISMA-P) 2015 statement. *Syst. Rev.* 4, 1–9. <https://doi.org/10.1186/2046-4053-4-1>.
- Monistero, V., Barberio, A., Biscarini, F., Cremonesi, P., Castiglioni, B., Graber, H.U., Bottini, E., Ceballos-Marquez, A., Kroemker, V., Petzer, I.M., Pollera, C., Santisteban, C., Veiga Dos Santos, M., Bronzo, V., Piccinini, R., Re, G., Cocchi, M., Moroni, P., 2020. Different distribution of antimicrobial resistance genes and virulence profiles of *Staphylococcus aureus* strains isolated from clinical mastitis in six countries. *J. Dairy Sci.* 103, 3431–3446.
- Montso, K.P., Dlamini, S.B., Kumar, A., Ateba, C.N., 2019a. Antimicrobial Resistance Factors of Extended-Spectrum Beta-Lactamases pneumoniae Isolated from Cattle Farms and Raw Beef Producing *Escherichia coli* and *Klebsiella* in North-West Province, South Africa. Article ID 4318306 *Biomed. Res. Int.* 2019, 13. <https://doi.org/10.1155/2019/4318306>.
- Montso, P.K., Mlambo, V., Ateba, C.N., 2019b. The First Isolation and Molecular Characterization of Shiga Toxin-Producing Virulent Multi-Drug Resistant Atypical Enteropathogenic *Escherichia coli* O177 Serogroup From South African Cattle. *Front. Cell. Infect. Microbiol.* 9, 333. <https://doi.org/10.3389/fcimb.2019.00333>.
- Morris, S., Cerceo, E., 2020. Trends, epidemiology, and management of multi-drug resistant gram-negative bacterial infections in the hospitalized setting. *Antibiotics* 9 (4), 196.
- Mouiche, M.M.M., Mazra, M., Moffo, F., Mpouam, S.E., Ngoujigne, A.I., Feussom, K.J.M., Akoda, G.K., Awah-Ndukum, J., 2018. Veterinary drugs market in Cameroon: regulations, organization and distribution channels. *Bull. Anim. Health Prod. Afr.* 66, 591–605.
- Mouiche, M.M.M., Moffo, F., Akoachere, J.F.T.K., Okah-Nnane, N.H., Mapieyou, N.P., Ndeze, V.N., Wade, A., Djukwo-Teukeng, F.F., Toghona, D.G.T., Zambou, H.R., Feussom, J.M.K., 2019. Antimicrobial resistance from a one health perspective in Cameroon: a systematic review and meta-analysis. *BMC Public Health* 19 (1), 20.
- Mthembu, T.P., Zishiri, O.T., Zowalaty, M.E.E., 2019. Molecular detection of multidrug-resistant salmonella isolated from livestock production systems in South Africa. *Infect. Drug Resist* 12, 3537–3548.
- Mulchandani, R., Wang, Y., Gilbert, M., Van Boeckel, T.P., 2023. Global trends in antimicrobial use in food-producing animals: 2020 to 2030. *PLOS Glob. Public Health* 3, e0001305. <https://doi.org/10.1371/journal.pgph.0001305>.
- Murray, C.J., Ikuta, K.S., Sharara, F., Swetschinski, L., Aguilar, G.R., Gray, A., Tasak, N., 2022. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet* 399, 629–655. [https://doi.org/10.1016/S0140-6736\(21\)02724-0](https://doi.org/10.1016/S0140-6736(21)02724-0).
- Ngom, R.V., Silva, L.C., Carmo, L.P., Schüpbach, G., Sidler, X., Kümmerlin, D., 2022. Antimicrobial usage in Swiss fattening pig farms: is there still potential for improvement? *Tier. ärztliche Prax. Ausg. G: GroßTiere/Nutztier* 50, 7–13.
- OECD/FAO, Organisation for Economic Co-operation and Development/Food and Agriculture Organization, 2023. OECD-FAO Agricultural Outlook 2023-2032. OECD Publishing, Paris. <https://doi.org/10.1787/08801ab7-en>.
- Ojo, O.E., Schwarz, S., Michael, G.B., 2016. Detection and characterization of extended-spectrum  $\beta$ -lactamase-producing *Escherichia coli* from chicken production chains in Nigeria. *Vet. Microbiol.* 15, 62–68. <https://doi.org/10.1016/j.vetmic.2016.04.022>.
- Okubo, T., Yossapol, M., Maruyama, F., Wampande, E.M., Kakooza, S., Ohya, K., Tsuchida, S., Asai, T., Kabasa, J.D., Ushida, K., 2019. Phenotypic and genotypic analyses of antimicrobial resistant bacteria in livestock in Uganda. *Transbound. Emerg. Dis.* 66, 317–326. <https://doi.org/10.1111/tbed.13024>.
- Olowe, O.A., Adewumi, O., Odewale, G., Ojuronbe, O., Adefioye, O.J., 2015. Phenotypic and Molecular Characterisation of Extended-Spectrum Beta-Lactamase Producing *Escherichia coli* Obtained from Animal Fecal Samples in Ado Ekiti, Nigeria. Article ID 497980 *J. Environ. Public Health* 2015, 7. <https://doi.org/10.1155/2015/497980>.
- Osman, K.M., Badr, J., Orabi, A., Elbehiry, A., Saad, A., Ibrahim, M.D., Hanafy, M.H., 2019. Poultry as a vector for emerging multidrug resistant *Enterococcus* spp. First report of vancomycin (van) and the chloramphenicol-florfenicol (cat-fex-cfr) resistance genes from Pigeon and duck faeces. *Micro Pathog.* 128, 195–205. <https://doi.org/10.1016/j.micpath.2019.01.006>.
- Paintsil, E.K., Ofori, L.A., Adobea, S., Akenten, C.W., Phillips, R.O., Maiga-Ascofare, O., Lamshöft, M., May, J., Obiri Danso, K., Krumkamp, R., Dekker, D., 2022. Prevalence and Antibiotic Resistance in *Campylobacter* spp. Isolated from Humans and Food-Producing Animals in West Africa: a Systematic Review and Meta-Analysis. *Pathogens* 11, 140. <https://doi.org/10.3390/pathogens11020140>.
- Pillay, S., Amoako, D.G., Abia, A.L., Somboro, A.M., Shobo, C.O., Perrett, K., Bester, L.A., Essack, S.Y., 2020. Characterisation of *Campylobacter* SPP. isolated from poultry in KwaZulu-Natal, South Africa. *Antibiotics* 9, 42. <https://doi.org/10.3390/antibiotics9020042>.
- Poirel, L., Madec, J.Y., Lupo, A., Schink, A.K., Kieffer, N., Nordmann, P., Schwarz, S., 2018. Antimicrobial resistance in *Escherichia coli*. *Microbiol. Spectr.* 6 (4), 6–4.
- Raheel, I.A.E.R., Hassan, W.H., Salem, S.S.R., Salam, H.S.H., 2020. Biofilm forming potentiality of *Escherichia coli* isolated from bovine endometritis and their antibiotic resistance profiles. *J. Adv. Vet. Anim. Res* 7, 442–451.
- Ramadan, H.H., Jackson, C.R., Taha, S.A., Moawad, A.A., Barrett, J.B., Woodley, T.A., 2018. Contribution of healthy Chicken to antimicrobial-resistant *Escherichia coli* associated with human extraintestinal infections in Egypt. *Vector Borne Zoonotic Dis.* 18, 408–416. <https://doi.org/10.1089/vbz.2017.2237>.
- Raufu, I., Bortolaia, V., Svendsen, C.A., Ameh, J.A., Ambali, A., Aarestrup, F.M., Hendriksen, R.S., 2013. The first attempt of an active integrated laboratory-based *Salmonella* surveillance programme in the north-eastern region of Nigeria. *J. Appl. Microbiol.* 115, 1059–1067. <https://doi.org/10.1111/jam.12304>.
- Raufu, I.A., Ahmed, O.A., Aremu, A., Ameh, J.A., Ambali, A., 2021a. Isolation and genomic characterization of “unassigned” *Salmonella enterica* serovars from poultry in Ilorin, north-central Nigeria. *Sokoto J. Vet. Sci.* 19, 188–196. <https://doi.org/10.4314/sokjvs.v19i3.4>.
- Raufu, I.A., Ahmed, O.A., Aremu, A., Ameh, J.A., Timme, R.E., Hendriksen, R.S., Ambali, A.G., 2021b. Occurrence, antimicrobial resistance and whole genome sequence analysis of *Salmonella* serovars from Pig farms in Ilorin, North-central Nigeria. *Int. J. Food Microbiol.* 350, 109245. <https://doi.org/10.1016/j.ijfoodmicro.2021.109245>.
- Reddy, S., Zishiri, O.T., 2017. Detection and prevalence of antimicrobial resistance genes in *Campylobacter* spp. isolated from Chicken and humans. *Onderstepoort J. Vet. Res.* 84, 1–6.
- Roshdy, H., Farghaly, E.M., Nasef, S.A., Shalaby, A.G., 2016. Molecular characterization, spread and evolution of quinolones resistance in *E. coli* of avian origin. *Alex. J. Vet. Sci.* 49, 60–67. <https://doi.org/10.5455/ajvs.220124>.



- Saidi, R., CantekIn, Z., Khelif, D., Ergun, Y., Solmaz, H., Kaidi, R., 2015. Antibiotic susceptibility and molecular identification of antibiotic resistance genes of staphylococci isolated from bovine mastitis in Algeria. *Kafkas Univ. Vet. Fak. Derg.* 21, 513–520 <https://vetdergikafkas.org/uploads/pdf/KVFD1782.pdf>.
- Sanguinetti, V.M., Ganshorn, H., Agbese, S., Windeyer, M.C., 2021. Protocol for a systematic review of disease control strategies used to prevent infectious mortality and morbidity in pre-weaned beef calves. *PRISM Repos.*
- Schar, D., Sommanustweechai, A., Laxminarayan, R., Tangcharoensathien, V., 2018. Surveillance of antimicrobial consumption in animal production sectors of low- and middle- income countries: optimizing use and addressing antimicrobial resistance. *PLoS One* 15, 1–9.
- Sghaier, S., Abbassi, M.S., Pascual, A., Serrano, L., Díaz-De-Alba, P., Said, M.B., Hassen, B., Ibrahim, C., Hassen, A., López-Cerero, L., 2019. Extended-spectrum  $\beta$ -lactamase-producing Enterobacteriaceae from animal origin and wastewater in Tunisia: first detection of O25b-B23-CTX-M-27-ST131 Escherichia coli and CTX-M-15/OXA-204-producing Citrobacter freundii from wastewater. *J. Glob. Antimicrob. Resist.* 17, 189–194. <https://doi.org/10.1016/j.jgar.2019.01.002>.
- Shabana, S.M., Helmy, S.M., Hegazy, A.E.H.M., 2019. Characterization of Class 1 integrons and some antimicrobial resistance genes in Salmonella species isolated from poultry in Egypt. *Slov. Vet. Res* 56, 725–734.
- Sithole, V., Amoako, D.G., Abia, A.L.K., Perrett, K., Bester, L.A., Essack, S.Y., 2021. Occurrence, Antimicrobial Resistance, and Molecular Characterization of *Campylobacter* spp. in Intensive Pig Production in South Africa. *Pathogens* 10, 439. <https://doi.org/10.3390/pathogens10040439>.
- Soliman, A.M., Ramadan, H., Zarad, H., Sugawara, Y., Yu, L., Sugai, M., Shimamoto, T., Hiott, L.M., Frye, J.G., Jackson, C.R., Shimamoto, T., 2021. Coproduction of Tet (X7) conferring high-level tetracycline resistance, fosfomycin FosA4, and colistin Mcr-1.1 in Escherichia coli strains from chickens in Egypt. *Antimicrob. Agents Chemother.* 65, 10–1128.
- Tarakdjian, J., Capello, K., Pasqualin, D., Santini, A., Cunial, G., Scollo, A., Mannelli, A., Tomao, P., Vonesch, N., Di Martino, G., 2020. Antimicrobial use on Italian pig farms and its relationship with husbandry practices. *Animals* 10, 417. <https://doi.org/10.3390/ani10030417>.
- Tartor, Y.H., Gharieb, R.M., Abd El-Aziz, N.K., El Damaty, H.M., Enany, S., Khalifa, E., Attia, A.S.A., Abdellatif, S.S., Ramadan, H., 2021. Virulence Determinants and Plasmid-Mediated Colistin Resistance mcr Genes in Gram-Negative Bacteria Isolated From Bovine Milk. *Front. Infect. Microbiol.* 11, 761417 <https://doi.org/10.3389/fcimb.2021.761417>.
- Tayh, G., Boubaker, S.M., Khedher, R., Ben, Jbeli, Chehida, M., Ben, F., Mamlouk, A., Daaoul-Jedidi, M., Messadi, L., 2022. Prevalence, virulence genes, and antimicrobial profiles of Escherichia coli O157:H7 isolated from healthy cattle in Tunisia. *J. Infect. Dev. Ctries* 16, 1308–1316. <https://doi.org/10.3855/jidc.15855>.
- Tiseo, K., Huber, L., Gilbert, M., Robinson, T.P., Van Boeckel, T.P., 2020. Global trends in antimicrobial use in food animals from 2017 to 2030. *Antibiotics* 9, 918.
- Tricco, A.C., Lillie, E., Zarin, W., O'Brien, K.K., Colquhoun, H., Levac, D., et al., 2018. PRISMA extension for scoping reviews (PRISMA-ScR): checklist and explanation of the PRISMA-ScR statement. *Ann. Intern Med* 169, 467–473. <https://doi.org/10.7326/M18-0850>.
- Vakanjac, S., Pavlovic, V., Magas, V., Pavlovic, M., Djuric, M., Maletic, M., Nedic, S., Soco, I., 2013. Investigations of efficacy of intramammary applied antimicrobials and glucocorticosteroids in the treatment of subclinical and clinical mastitis in cows. *Vet. Glas.* 67, 15–27. <https://doi.org/10.2298/vetgl1302015v>.
- Van, T.T.H., Yidana, Z., Smooker, P.M., Coloe, P.J., 2020. Antibiotic use in food animals worldwide, with a focus on Africa: Pluses and minuses. *J. Glob. Antimicrob. Resist.* 20, 170–177. <https://doi.org/10.1016/j.jgar.2019.07.031>.
- Van Boeckel, T.P., Glennon, E.E., Chen, D., Gilbert, M., Robinson, T.P., Grenfell, B.T., Levin, S.A., Bonhoeffer, S., Laxminarayan, R., 2017. Reducing antimicrobial use in food animals. *Science* 357, 1350–1352.
- Van Den Bogaard, A.E.J.M., London, N., Stobberingh, E.E., 2000. Antimicrobial resistance in pig faecal samples from The Netherlands (five abattoirs) and Sweden. *J. Antimicrob. Chemother.* 45, 663–671. <https://doi.org/10.1093/jac/45.5.663>.
- Velazquez-Meza, M.E., Galarde-López, M., Carrillo-Quiróz, B., Alpuche-Aranda, C.M., 2022. Antimicrobial resistance: one health approach. *Vet. World* 15 (3), 743.
- Vidović, J., Stojanović, D., Cagnardi, P., Kladar, N., Horvat, O., Ćirković, I., Bijelić, K., Stojanac, N., Kovačević, Z., 2022. Farm Animal Veterinarians' Knowledge and Attitudes toward Antimicrobial Resistance and Antimicrobial Use in the Republic of Serbia. *Antibiotics* 11, 64. <https://doi.org/10.3390/antibiotics11010064>.
- Vougat Ngom, R.R.B., Tomdieu, T., Ziébé, R., Foyet, H.S., Moritz, M., Vondou, L., Schruck, D.E., Imerman, P.M., Rumbelha, W.R., Garabed, R.B., 2017. Quality of veterinary pharmaceuticals and their use by pastoralists in the Far North Region of Cameroon. *Pastoralism* 7, 1–14.
- Vounba, P., Arsenault, J., Bada-Alambédji, R., Fairbrother, J.M., 2019a. Prevalence of antimicrobial resistance and potential pathogenicity, and possible spread of third generation cephalosporin resistance, in Escherichia coli isolated from healthy chicken farms in the region of Dakar, Senegal. *PLoS One* 14, e0214304. <https://doi.org/10.1371/journal.pone.0214304>.
- Vounba, P., Kane, Y., Ndiaye, C., Arsenault, J., Fairbrother, J.M., Bada Alambédji, R., 2018. Molecular characterization of Escherichia coli isolated from Chicken with colibacillosis in Senegal. *Foodborne Pathog. Dis.* 15, 517–525. <https://doi.org/10.1089/fpd.2017.2394>.
- Vounba, P., Rhouma, M., Arsenault, J., Alambédji, R.B., Fravallo, P., Fairbrother, J.M., 2019b. Prevalence of colistin resistance and mcr-1/mcr-2 genes in extended-spectrum  $\beta$ -lactamase/AmpC-producing Escherichia coli isolated from Chicken in Canada, Senegal and Vietnam. *J. Glob. Antimicrob. Resist.* 19, 222–227.
- WHO, (World Health Organization), 2017a. Guidelines on Use of Medically Important Antimicrobials in Food-Producing Animals: Web Annex A: Evidence Base. World Health Organization. (No. WHO/NMH/FOS/EZD/17.2). World Health Organization. (<https://apps.who.int/iris/bitstream/handle/10665/259241/WHO-NMH-FOS-?sequence=1>).
- WHO (World Health Organization), 2017b. Integrated surveillance of antimicrobial resistance in foodborne bacteria: application of a one health approach: guidance from the WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR). (<https://apps.who.int/iris/bitstream/handle/10665/255747/9789241512411-eng.pdf>).
- WHO, (World Health Organization), 2017c. Prioritization of pathogens to guide discovery, research and development of new antibiotics for drug-resistant bacterial infections, including tuberculosis. WHO/EMP/IAU/2017.12, Geneva.
- WHO (World Health Organization), 2018a. Critically important antimicrobials for human medicine, 6th revision Online: <https://apps.who.int/iris/bitstream/handle/10665/312266/9789241515528-eng.pdf?ua=1df> (who.int); last accessed: 19.05.2021.
- WHO (World Health Organization), 2018b. Situational Analysis on Antimicrobial Resistance in the South-East Asia Region. 2018. <https://apps.who.int/iris/bitstream/handle/10665/272873/AMR>.
- WHO (World Health Organization), 2023. The One Health Definition and Principles Developed by One Health High Level Expert Panel. Updated on July 24, 2023. 9P. <https://www.who.int/publications/m/item/one-health-definitions-and-principles>.
- WOAH (World Organisation for Animal Health), 2017. OIE Annual report on the use of antimicrobial agents in animals. Better understanding of the global situation. Online: [https://www.woah.org/fileadmin/Home/fr/Our\\_scientific\\_expertise/docs/pdf/AMR/Survey\\_on\\_monitoring\\_antimicrobial\\_agents\\_Dec2016.pdf](https://www.woah.org/fileadmin/Home/fr/Our_scientific_expertise/docs/pdf/AMR/Survey_on_monitoring_antimicrobial_agents_Dec2016.pdf); last accessed: 12.05.2023.
- Xiong, W., Sun, Y., Zeng, Z., 2018. Antimicrobial use and antimicrobial resistance in food animals. *Environ. Sci. Pollut. Res.* 25, 18377–18384. <https://doi.org/10.1007/s11356-018-1852-2>.
- Yhiler, N.Y., Basse, B.E., Paul, I., Francis, U.M., Anne, A., Okocha-Ejeko, A., 2019a. Antimicrobial Resistance Pattern in Salmonella Enterica from Clinical and Poultry Sources in Calabar, Nigeria. *J. Microbiol. Antimicrob.* 11, 5–10. <https://doi.org/10.5897/jma2019.0413>.
- Yhiler, N.Y., Basse, B.E., Paul, I.E., Francis, U.M., Anne, A., Okocha-Ejeko, A., 2019b. Extended spectrum beta-lactamase production and plasmid mediated quinolone resistance among lactose non-fermenting Enterobacteriaceae isolated from poultry sources in Calabar, Nigeria. *Afr. J. Microbiol. Res.* 13, 400–406.
- Younis, G.A., Elkenany, R.M., Radwan, M.M., Allah, M.M.A., 2017. Antimicrobial Resistant Profiles of Methicillin-Resistant Staphylococcus aureus (MRSA) Recovered from Broiler Chicken Populations in Egypt. *Indian J. Poult. Sci.* 52, 332–337. <https://doi.org/10.5958/0974-8180.2017.00062.9>.
- Youssif, N.H., Hafiz, N.M., Halawa, M.A., Aziz, H.M., 2021. Genes conferring antimicrobial resistance in Cattle with subclinical mastitis. *Bulg. J. Vet. Med.* 24, 67–85. <https://doi.org/10.15547/bjvm.2019-0028>.
- Zaatout, N., Ayachi, A., Kecha, M., Kadlec, K., 2019. Identification of staphylococci causing mastitis in dairy Cattle from Algeria and characterization of Staphylococcus aureus. *J. Appl. Microbiol.* 127, 1305–1314.