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A systematic review and meta-analysis on antibiotic resistance genes in Ghana

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Abstract

Background Addressing antimicrobial resistance (AMR) poses a complex challenge, primarily because of the limited understanding of bacterial antibiotic resistance genes (ARGs) and the spread of these genes across different domains. To bridge this knowledge gap in Ghana, we undertook a comprehensive systematic review and meta-analysis to quantify and estimate the prevalence of circulating ARGs in bacteria isolated from human, animal, and environmental sources.

Methods A thorough literature search was conducted across three major databases—Web of Science, PubMed, and Scopus—to retrieve all relevant articles related to ARGs in Ghana from the inception of the databases to February 25, 2024. A risk-of-bias evaluation was performed using the Newcastle-Ottawa Scale (NOS), and the data analysis involved descriptive statistics and proportional meta-analysis.

Results Of the 371 articles initially obtained, 38 met the inclusion criteria. These studies adequately covered Ghana geographically. The most prevalent ESBL gene identified was $bla_{CTX\text{-}M}$, with a prevalence of 31.6% (95% CI: 17.6–45.7), followed by bla_{TEM} (19.5% [95% CI: 9.7–29.3]), and bla_{SHV} (3.5% [95% CI: 0.3–6.6]). The pooled prevalence of carbapenemase genes ranged from 17.2% (95% CI: 6.9–27.6) for bla_{NDM} to 10.3% (95% CI: 1.9–18.7) for bla_{OXA}. Additionally, other ARGs, including *sul1*, *qnrS*, *gyrA*, *erm(B)*, and *mecA*, were detected, with prevalence ranging from 3.9% (95% CI: 0.0–8.5) to 16.4% (95% CI: 3.1–29.8). Several ARGs were shared across human, animal, and environmental sources.

Conclusion This review revealed that bacteria obtained from human, animal, and environmental samples in Ghana shared genes associated with AMR. This finding provides evidence on the interconnection of AMR across these three domains. Horizontal gene transfer, which enables the dissemination of ARGs between genetically diverse bacteria, can occur, necessitating a multidisciplinary approach to addressing antimicrobial resistance in Ghana.

Keywords Antimicrobial resistance (AMR), Prevalence, Antibiotic resistance genes (ARGs), Ghana, One Health, Multidrug resistance (MDR), Systematic review

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Introduction

Antibiotic resistance genes (ARGs) are DNA segments that enable bacteria to withstand the effects of antibiotics. These genes can be naturally present or acquired through mutation or horizontal gene transfer, during which bacteria exchange genetic material [1, 2]. ARGs complicate the treatment of bacterial infections by allowing bacteria to survive antibiotic treatments that typically eliminate them, resulting in persistent infections [3]. Furthermore, ARGs can spread between different bacteria, including those not previously exposed to antibiotics, accelerating the spread of resistance and potentially leading to outbreaks of infections with antibiotic-resistant bacteria [4].

The World Health Organization (WHO) has identified antimicrobial resistance (AMR) as a critical and urgent global public health issue [5]. Infections caused by antibiotic-resistant bacteria lead to increased mortality rates and prolonged illnesses. For example, in 2019, AMR was associated with an estimated 4.95 million deaths worldwide [6]. This alarming figure exceeds the combined annual global mortality rates of tuberculosis (1.5 million), HIV/AIDS (864,000), and malaria (643,000) [7]. Projections suggest that, without intervention, AMR could result in 10 million deaths annually by 2050 [8]. Low- and middle-income regions bear a disproportionate AMR burden [9]. In sub-Saharan Africa, overburdened health systems struggle to combat resistant infections, compounding crisis-level tuberculosis, HIV/AIDS, and malaria mortality [10, 11].

Ghana faces notable AMR challenges. A recent systematic review by Donkor et al. [12] demonstrated a significant presence of multidrug-resistant bacteria in the country, including *Escherichia coli*, *Klebsiella pneumoniae*, and methicillin-resistant *Staphylococcus aureus* (MRSA). The review underscored the widespread resistance among these key pathogens and highlighted the interconnection of human, animal, and environmental health in the spread of AMR in Ghana. It also pointed out the critical concern of environmental bacteria that are potentially transmitting ARGs to human pathogens. While detailed molecular studies have identified specific resistance genes and their mechanisms, there remains a significant gap in comprehensive data on the molecular determinants of AMR and spread of ARGs across different sectors in Ghana, hindering the ability to track trends over time. Consequently, this review aimed to quantify and estimate the prevalence of circulating ARGs in bacteria isolated from human, animal, and environmental sources in Ghana.

Methodology

This systematic review used the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) methodology [13]. A comprehensive search was conducted across three databases: Web of Science, PubMed, and Scopus. The search terms used were predetermined and focused on gathering research articles related to ARGs in Ghana published from the inception of the databases until February 25, 2024. The search was limited to studies published in English. To ensure a comprehensive search encompassing all relevant studies in the chosen area, a combination of keywords (including terms such as "antibiotic resistance genes", OR "ESBL genes", OR "beta-lactamase genes", OR "carbapenemase genes" AND "Ghana") was employed.

Inclusion and exclusion criteria

This comprehensive review encompassed all studies examining bacterial resistance genes in three distinct settings: humans (clinical contexts), animals (farms), and the environment (hospital surroundings, wastewater, and drinking water). No restrictions related to bacterial species, sample source (human, animal, environment), or study design, were placed on the search. Both observational and interventional study designs were included. To ensure relevance, studies conducted outside of Ghana and review articles were excluded from the analysis. Furthermore, studies that reported on only AMR without the use of molecular tests to characterise ARGs were also excluded, as accurate identification of ARGs requires confirmation at the DNA level. Additionally, studies focusing only on virulence genes or reporting on resistance genes in viruses and parasites were not included in the review, since ARG transmission dynamics differ.

Data extraction

Once ineligible studies were excluded and duplicates were removed, a meticulous analysis of each selected article was undertaken. Two researchers, A.O. and E.S.D., extracted the data using Microsoft Excel. To circumvent the potential for bias, an essential database was created during this process, and this included information such as the study setting and period, sample source, adopted definition of multidrug resistance (MDR), microorganism isolated, number of isolates, MDR occurrence, antimicrobial susceptibility testing (AST) method, minimum inhibitory concentration (MIC) breakpoint used, method for identifying resistance genes, specific genes involved, number of each gene, and author references. Any discrepancies in data extraction between the two reviewers were identified and resolved through discussion and consensus building. In instances when an agreement could not be reached, a third reviewer was consulted to arrive at a final decision.

Evaluation of bias

Risk of bias in individual studies was evaluated using the Newcastle-Ottawa Scale (NOS) for assessing non-randomised studies [14]. The NOS evaluates selection, comparability, and outcome for cross-sectional studies. Each

study received a star rating for the selection of study populations (four stars maximum), comparability of groups (two stars maximum), and ascertainment of outcome of interest (three stars maximum). Studies that achieved a rating of six stars or more were considered to be at a low risk of bias; those that achieved four to five stars were deemed to have a moderate risk, and those that had less than four stars were adjudged to have a high risk of bias. Two reviewers independently applied the NOS, resolving disagreements through consensus building. Results of the quality assessment are presented in Supplementary Table S2.

Statistical analysis

The data analysis involved descriptive statistics and proportional meta-analysis. For the meta-analysis, studies that reported the number of isolates and the number that harboured a resistance gene were included. Using R software, Version 4.3.3 (2024-02-29), and the "metaprop" package, a random-effects meta-analysis was performed to determine the pooled prevalence of resistance genes. The pooled prevalence was estimated in this analysis using a 95% confidence interval. A random-effects meta-analysis was also used to calculate the pooled prevalence ratios (PRs). The random-effects model was chosen for the meta-analysis given the expected heterogeneity between included studies with regard to factors such as geographic locations, time periods, sample types, and bacterial species. Compared to a fixed-effects model, the random-effects approach provides a more conservative estimate by incorporating between-study variability in the pooled prevalence calculation. Using a funnel plot and the "metabias" command, publication bias was examined, and heterogeneity in the data was measured using the $\chi 2$ test.

Publication bias was assessed visually using funnel plots to detect asymmetry that could arise from non-publication of small or non-significant studies. The funnel plots revealed a slight asymmetry (Supplementary Figures S13-S25). However, the Egger linear regression test did not yield statistically significant results, suggesting that small study effects were unlikely to be present. In contrast, the regression-based Egger test indicated potential reporting bias, as evidenced by a p value less than 0.05.

Results

Search result

The search yielded 371 articles from PubMed ($n = 113$), Scopus ($n = 170$), and Web of Science ($n = 88$), with 78 duplicates removed. After the abstracts of the remaining articles were reviewed ($n = 293$), 243 articles were excluded for not meeting the eligibility criteria. These exclusions included studies conducted outside Ghana, review articles, studies lacking molecular or genetic detection of resistance genes, and reports focusing on resistance genes in viruses and parasites. Of the 50 remaining articles, 12 were excluded because they were from unspecified locations and reported only on virulence genes. The remaining 38 articles [15–52] were included in this systematic review and underwent a thorough review to extract data on ARGs (Fig. 1).

Study characteristics

The reviewed studies geographically covered seven of the then ten administrative regions of Ghana (the existing regional demarcation at the time most of the included studies were conducted). However, no study describing the detection and characterisation of ARGs in antibiotic-resistant bacteria (ARB) has been reported for the Upper East, Upper West, and Brong-Ahafo Regions. Among the included studies, 13 involved the Ashanti Region, followed by nine involving the Greater Accra Region. The Northern and Volta Regions had four studies each, whereas the Central and Western Regions had three and two studies, respectively. Three studies provided data on ARGs for two or more regions, indicating the use of a multicentre approach (Table S1).

The studies collected samples from various sources, including humans (urine, blood, stool, sputum, wounds, high vaginal swabs, nasal swabs, ear swabs, endocervical swabs, cerebrospinal fluid oropharynx), animals (poultry meat, poultry litter, cockroaches, sheep, goats, pigs, fresh milk, and fish farms), and the environment (water sources, surroundings of patient beds, latrines, tables, soil, sewage, and latrines). Of the 38 included studies, 25 were conducted in humans only, whereas three focused on environmental sources only. Seven identified ARGs in animals only. Two studies detected ARGs in both human and animal sources, and one identified ARGs across human, animal, and environmental sources (Table S1).

Antimicrobial susceptibility testing (AST)

A total of 27 studies conducted antimicrobial susceptibility testing. Among these, 19 utilised the Kirby-Bauer disk diffusion method, whereas eight employed the VITEK-2 system. Twelve studies followed the recommendations of the European Committee on Antimicrobial Susceptibility Testing (EUCAST), fifteen adhered to the guidelines of the Clinical and Laboratory Standards Institute (CLSI), and three combined the two recommendations for antimicrobial susceptibility testing (Table S1).

Methods for the detection and characterisation of antibiotic resistance genes (ARGs)

The genetic detection and characterisation of ARGs in various sample matrices were primarily performed using three main methods. In 21 studies, PCR coupled with DNA sequencing was employed. Twelve studies utilised

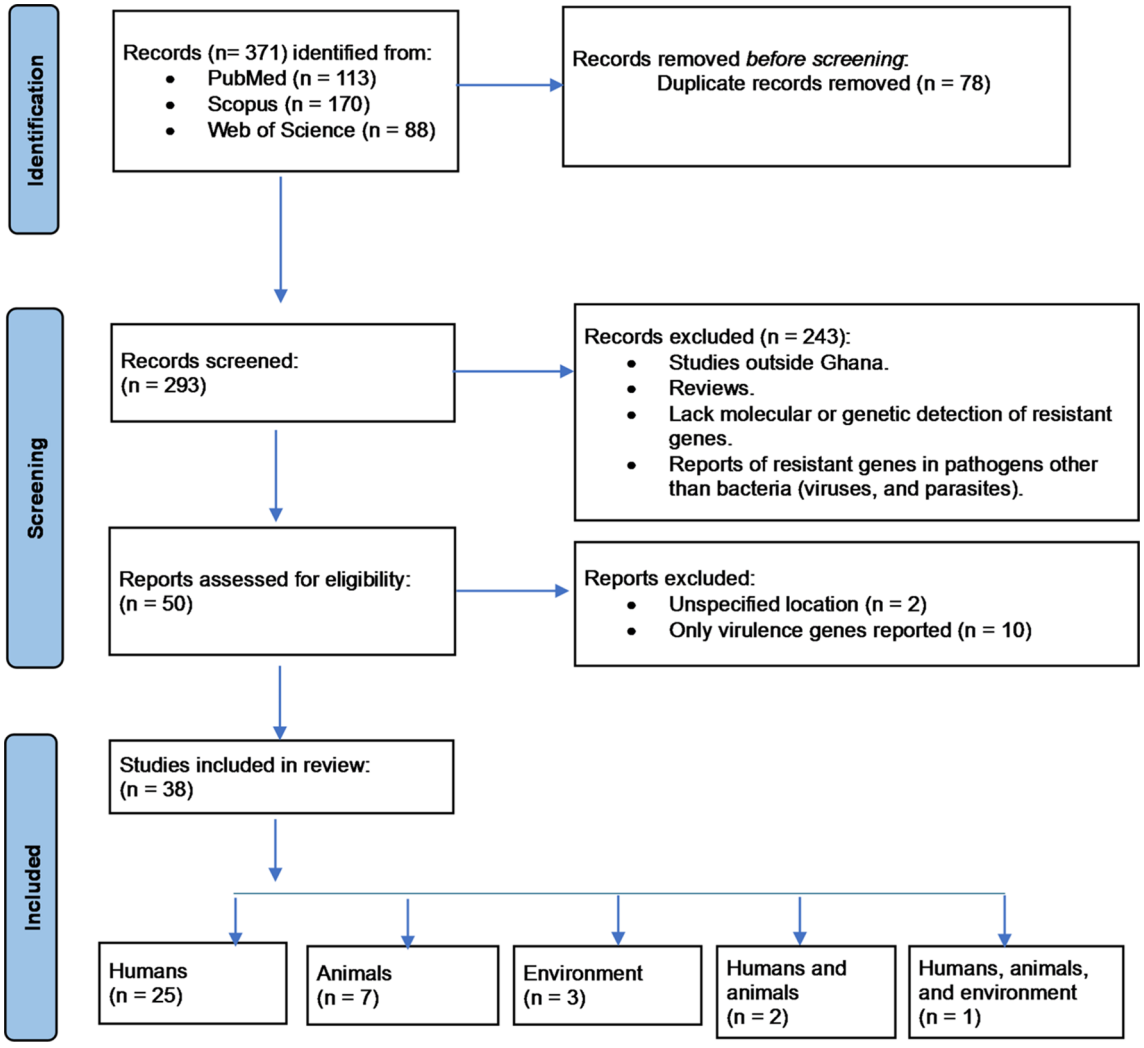

Fig. 1 PRISMA flowchart for article evaluation, screening, and record identification.

a combination of PCR, DNA, and genome sequencing techniques (such as whole-genome sequencing [WGS], multilocus sequence typing [MLST], and Sanger sequencing). Three studies relied solely on DNA and genome sequencing, whereas two studies exclusively employed genome sequencing (Table S1).

Risk of bias

Based on the risk of bias assessment, the quality of included studies [15–52] was generally good. Of the 38 studies, 33 (87%) were adjudged to have a low risk of bias, and five (13%), a moderate risk. No "high-risk" study was found. For selection of study populations, most scores were high (3 or 4), as the studies included were representative of bacterial isolates from defined populations or included all eligible specimens within the study period. However, one study scored lower (2), as its eligibility criteria were not clearly defined. Comparability of groups was commonly moderate risk due to a lack of consistent control for location and year of sample collection, which may influence outcomes. Outcome ascertainment was typically low-risk as ARGs were detected using validated molecular techniques such PCR in certified laboratories.

Prevalence of Multidrug-resistant bacteria

Multidrug-resistant bacteria, including *Staphylococcus aureus*, *Escherichia coli*, *Campylobacter* spp., *Salmonella* spp., *Arcobacter butzleri*, *Staphylococus sciuri*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter* spp., and *Pseudomonas putida*, were identified in 12 studies across human, animal, and environmental sources, with a pooled prevalence of 40.8% (95% CI: 21.5–60.2) (Fig. 2).

Prevalence of circulating ARGs

ARGs that were identified in three or more studies were included in the meta-analysis. Twelve genes met this requirement, including *ermB*, bla_{SHV}, *mecA*,

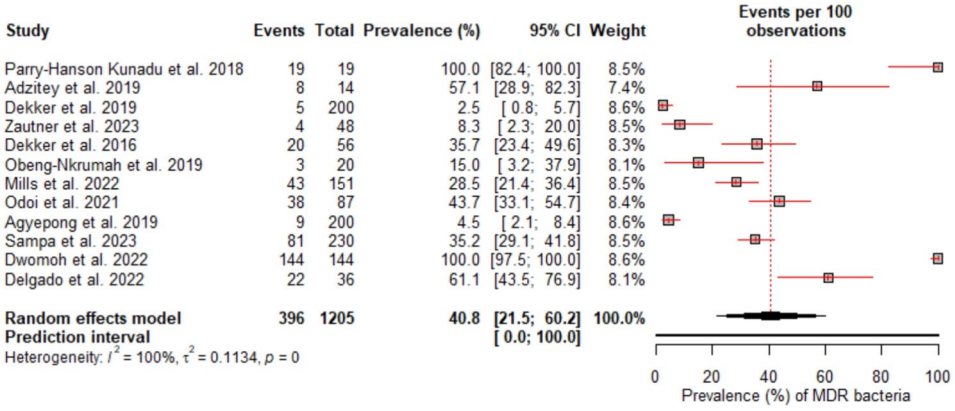

Fig. 2 Pooled prevalence of multidrug-resistant bacteria

bla$_{OXA}$ (including *bla*$_{OXA-48}$, *bla*$_{OXA-61}$, and *bla*$_{OXA-1}$), *bla*$_{NDM}$ (including *bla*$_{NDM-1}$), *qnr* (including *qnrS, qnrS1, qnrB, qnrS1, qnrB2, qnrB19, qnrB1, qnrA, qnrC,* and qnrD), *gyrA, qepA, sul* (including *sul1, sul2,* and *sul3*), *bla*$_{TEM}$ (including *bla*$_{TEM-1b}$ and *bla*$_{TEM-24}$), *tet* (including *tet(W), tet (K), tet (L), tet (G), tet (A), tet (O), tet (M)* and t*et (B)*), and *bla*$_{CTX-M}$ (including *bla*$_{CTX-M-15}$, *bla*$_{CTX-M-914}$, *bla*$_{CTX-M-825}$, *bla*$_{CTX-M-28}$, *bla*$_{CTX-M-1}$, *bla*$_{CTX-M-9}$, *bla*$_{CTX-M-3}$, *bla*$_{CTX-M-27}$ and *bla*$_{CTX-M-14}$). In contrast, genes identified in fewer than three studies were excluded from the meta-analysis. These genes included *cat1, cat 4, bla*$_{EBC}$, *cmIA, fosA, mcr-1, mcr-2, TOHO-1, oqxA, oqxB, fosB, bla*$_{CMY}$, *bla*$_{VIM}$, *bla*$_{DIM-1}$, *bla*$_{CARB}$, *aac(6'')-Iy, mdtK, mdsA, mdsB, mdsC, golS, rssB+, sdiA, dfrA14, ant(9), mdf(A), aph(3'')-Ib, aph(6)-Id, aadA5, fosA7, catA1, catA2, strA, strB, str, aac(3)-II, aadD, aadB, mexB, bla*$_{VIM-1}$, *bla*$_{FOX-M}$, *bla*$_{EBC-M}$, *bla*$_{DHA-M}$, *aac(6')-Ib-cr, parC, mefA, sal(A), cat(pC221), dfrG, dfrK, aac(6')-aph(2''), cmeB, aadE, oprD,* and *aacA4*.

The most predominant ESBL gene identified was *bla*$_{CTX-M}$, with a prevalence of 31.6% (95% CI: 17.6–45.7), followed by *bla*$_{TEM}$ (19.5% [95% CI: 9.7–29.3]), and *bla*$_{SHV}$ (3.5% [95% CI: 0.3–6.6]). The pooled prevalence of carbapenemase genes ranged from 17.2% (95% CI: 6.9–27.6) for *bla*$_{NDM}$ (including *bla*$_{NDM-1}$) to 10.3% (95% CI: 1.9-18.7) for *bla*$_{OXA}$ (including *bla*$_{OXA-48}$, *bla*$_{OXA-61}$, and *bla*$_{OXA-1}$). In addition to resistance genes for beta-lactam and carbapenem resistance, other ARGs were detected. These included genes conferring resistance to sulfonamides (including *sul1, sul2,* and *sul3*), fluoroquinolones and quinolones (including *qnrS, qnrS1, qnrB, qnrS1, qnrB2, qnrB19, qnrB1, qnrA, qnrC, qnrD, qepA* and *gyrA*), tetracycline (including *tet(W), tet (K), tet (L), tet (G), tet (A), tet (O), tet (M),* and *tet (B)*), macrolides (*ermB*), and methicillin (*mecA*). The pooled prevalence of these genes ranged from 3.9% (95% CI: 0.0–8.5) to 16.4% (95% CI: 3.1–29.8) (Table 1).

Genes shared across human, animal, and environmental sources

Several ARGs were shared across human, animal, and environmental sources (Fig. 3). These genes were *bla*$_{CTX-M-15}$, *bla*$_{CTX-M}$, *bla*$_{TEM-1b}$, *bla*$_{SHV}$, *bla*$_{NDM}$ (including *bla*$_{NDM-1}$), *bla*$_{OXA-48}$, *sul1, gyrA, ermB, qnrS,* and *gyrA*. The *bla*$_{CTX-M-15}$, *bla*$_{NDM-1}$, *bla*$_{OXA-48}$, and *sul1* genes were detected in human, animal, and environmental sources. Shared genes between humans and animals included *gyrA, ermB, mecA, bla*$_{SHV}$, *bla*$_{CTX-M}$ and *bla*$_{TEM-1b}$. Animals and the environment shared the *bla*$_{OXA-48}$ gene. Additionally, the *bla*$_{NDM}$ gene was found to be shared between humans and environmental sources.

Discussion

This systematic review adopted a comprehensive "One Health" approach to investigate the available literature on the prevalence of ARGs in bacteria isolated from human, animal, and environmental sources in Ghana. The findings carry significance for public health policies and programmes, as well as future research efforts. Notably, the high prevalence of ESBL genes observed, particularly *bla*$_{CTX-M-15}$, underscores the need for strengthened containment measures. Though the prevalence of carbapenem resistance genes currently appears relatively low, ongoing vigilance is prudent given its potential negative implications for treatment outcomes. The extensive gene sharing revealed reinforces interconnected reservoirs facilitating resistance spread. Coordinated multi-sectoral stewardship is imperative to curtail further development and dissemination. By establishing an evidence base integrating human, animal, and environmental data, this review facilitates strategic planning. The One Health nature of resistance underscores the importance of collaborative surveillance and containment support across sectors.

A total of 38 studies that adequately covered Ghana identified several prevalent ARGs. Although data for the Upper East, Upper West, and Brong-Ahafo Regions were

Table 1 Summary of the pooled prevalence of ARGs included in the meta-analysis

Gene	Frequency (n)	Proportion (%)	Bacteria harbouring the gene(s)	Total number of bacterial isolates	Pooled prevalence of gene among bacterial isolates	I^2 (%)	*p*-value	Sources
bla_{OXA} (including bla_{OXA-48}, bla_{OXA-61}, and bla_{OXA-1})	75	3.6	*Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter baumannii*, and *Proteus mirabilis*	965	10.3% (95% CI: 1.9–18.7)	89	< 0.01	Human, animal and environment
bla_{NDM} (including bla_{NDM-1})	137	6.5	*P. mirabilis*, *Acinetobacter* spp., *Pseudomonas aeruginosa*, *E. coli*, *Cronobacter sakazakii*, and *Providencia stuartii*	873	17.2% (95% CI: 6.9–27.6)	96	< 0.01	Human, animal and environment
bla_{SHV} (including bla_{SHV-3} and bla_{SHV-73})	36	1.7	*K. pneumoniae*, *E. coli*, *Enterobacter* spp., *P. mirabilis*, *P. aeruginosa*, and *Salmonella* spp.	1051	3.5% (95% CI: 0.3–6.6)	78	< 0.01	Human and animal
bla_{TEM} (bla_{TEM-1b}, bla_{TEM-14}, and bla_{TEM-24})	311	14.8	*Staphylococcus aureus*, *Streptococcus* spp., *Micrococcus* spp., *Cellobiococcus* spp., *Athrobacter* spp., *E. coli*, *Klebsiella* spp., *Citrobacter* spp., *Enterobacter* spp., *Proteus* spp., and *Acinetobacter* spp.	1613	19.5% (95% CI: 9.7–29.3)	97	< 0.01	Human and animal
bla_{CTX-M} (including $bla_{CTX-M-15}$, $bla_{CTX-M-914}$, $bla_{CTX-M-825}$, $bla_{CTX-M-28}$, $bla_{CTX-M-1}$, $bla_{CTX-M-9}$, $bla_{CTX-M-3}$, $bla_{CTX-M-27}$, and $bla_{CTX-M-14}$)	969	46.2	*E. coli*, *K. pneumoniae*, *Enterobacter* spp., *Salmonella* spp., *Citrobacter* spp., *P. mirabilis*, *Acinetobacter* spp., *Citrobacter* spp., and *Providentia* spp.	3379	31.6% (95% CI: 17.6–45.7)	100	< 0.001	Human, animal and environment
tet (including *tet(W)*, *tetK*, *tetL*, *tetG*, *tetA*, *tetO*, *tetM*, and *tetB*)	89	4.2	*S. aureus*, *A. butzleri*, *Campylobacter* spp., *E. coli*, *P. aeruginosa*, *K. pneumoniae*, and *S. pneumoniae*	1621	6.4% (95% CI: 1.9–11.0)	86	< 0.01	Human, animal and environment
qepA	20	1.0	*E. coli*, *Klebsiella spp.*, *Citrobacter* spp., and *Enterobacter* spp.	700	4.7% (95% CI: 0.0–11.1)	83	< 0.01	Human
qnr (including *qnrS*, *qnrS1*, *qnrB*, *qnrS1*, *qnrB2*, *qnrB19*, *qnrB1*, *qnrA*, *qnrC*, and *qnrD*)	173	8.2	*Campylobacter* spp., *Arcobacter butzleri*, *Salmonella* spp., *E. coli*, *S. aureus*, *K. pneumoniae*, *Citrobacter* spp., and *Enterobacter* spp.	3049	6.3% (95% CI: 3.4–9.1)	89	< 0.01	Human
gyrA	66	3.1	*C. freundii*, *Campylobacter* spp., *A. butzleri*, and *Salmonella* spp.	638	10.0% (95% CI: 1.1–19.0)	96	< 0.01	Human and animal
ermB	13	0.6	*A. butzleri*, *Campylobacter* spp., *Staphylococcus* spp., and *Streptococcus pneumoniae*	351	3.9% (95% CI: 0.0–8.5)	78	0.01	Human and animal
sul (including *sul1*, *sul2*, and *sul3*)	144	6.9	*C. freundii*, *Klebsiella* spp., *Enterobacter* spp., *Salmonella* spp., *E. coli*, and *P. aeruginosa*	1066	16.4% (95% CI: 3.1–29.8)	96	< 0.01	Human, animal and environment
mecA	65	3.1	*S. aureus* and *Staphylococcus hominis*	320	17.2% (95% CI: 0.0–34.8)	96	< 0.01	Human and animal

unavailable, ARGs were found to be widespread across the country. The majority of these studies focused on human populations. The $bla_{CTX-M-15}$ gene was found to be the most prevalent β-lactamase gene in humans, animals, and the environment in Ghana. This observation aligns with similar studies conducted in other countries. For example, a study in the Philippines examined the prevalence of the $bla_{CTX-M-15}$, bla_{TEM} and bla_{SHV} genes in *E. coli* isolates from broiler farms and revealed $bla_{CTX-M-15}$ as the predominant β-lactamase gene [53]. Similarly, another study conducted in Bangladesh reported that the $bla_{CTX-M-15}$ gene was highly prevalent in *E. coli* isolates that cause extraintestinal infections [54]. Furthermore, a study in India revealed a significant prevalence of the $bla_{CTX-M-15}$ gene in *E. coli* strains obtained from an urban aquatic environment [55]. These data demonstrate the global dissemination of $bla_{CTX-M-15}$. Given its high regional circulation, vigorous monitoring of this ESBL gene is important for Ghana to prevent local spread and limit its prevalence from increasing within high-risk settings such as hospitals and farms.

Although the prevalence of the carbapenem resistance genes in Ghana seemed generally lower than those observed for the ESBL genes, their prevalence, which ranged from 10.3% (95% CI: 1.9–18.7) for bla_{OXA-48} to 17.2% (95% CI: 6.9–27.6) for bla_{NDM-1}, are arguably high, given their superior public health significance. In other African settings as well, carbapenem resistance has been

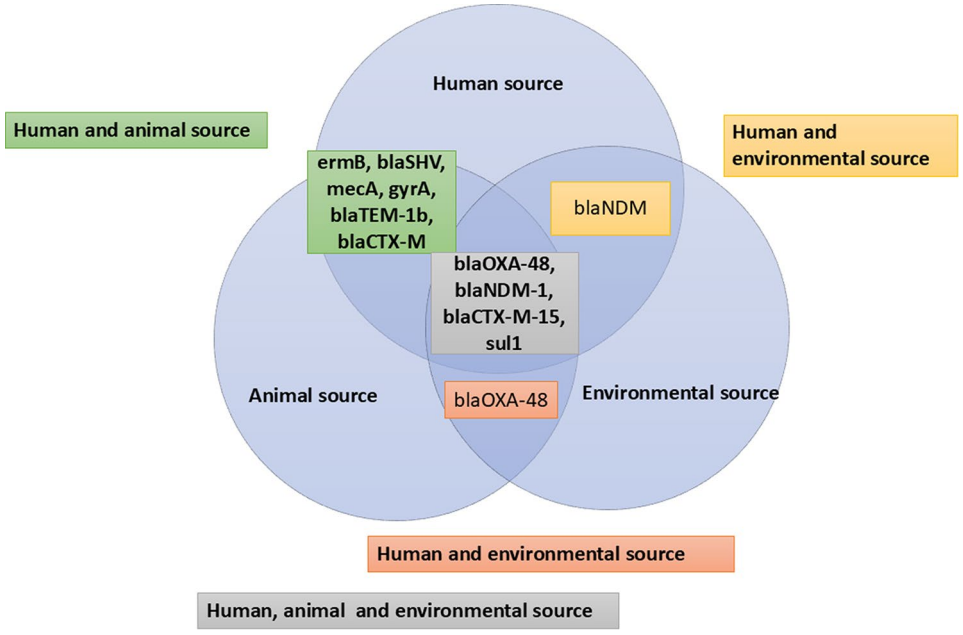

Fig. 3 Shared ARGs from human, animal and environmental sources

demonstrated as a rising threat to public health. To illustrate, in Egypt [56] and Cameroon [57] where bla_{NDM} and bla_{OXA} (or related genes thereof) have been detected, carbapenem-resistant pathogen prevalence of 28% and 25% have been respectively reported. Besides, especially in Asia, dissemination of the bla_{NDM} gene has been observed in animals, particularly livestock. For example, He et al. [58] demonstrated the persistence of bla_{NDM}-positive bacteria in chickens and farm environments in China. This study revealed the transmission of bla_{NDM}-positive bacteria and bla_{NDM}-bearing plasmids between different farms and locations, indicating that poultry could act as reservoirs for the spread of bla_{NDM}. The bla_{NDM} gene is known to confer resistance to carbapenem antibiotics, which are crucial last-resort treatments for various bacterial infections [59–61].

In addition to carbapenemase and β-lactamase genes, other ARGs that confer resistance to a wide range of antibiotics, such as trimethoprim, fosfomycin, chloramphenicol, rifampicin, aminoglycosides, fluoroquinolones, quinolones, tetracycline, streptomycin, lincosamide, sulfonamides, and colistin, were identified. A major concern is the potential transfer of these resistance genes from environmental bacteria to human pathogens. The *sul1* gene, which confers sulfonamide resistance, was found in isolates from animal, human, and environmental sources, implying that horizontal gene transfer is taking place. Notably, the availability of molecular surveillance data on ARGs in various environmental reservoirs in Ghana is scarce. The limited use of longitudinal investigations introduces uncertainties regarding the seasonal and temporal dynamics of resistance gene abundance and identities as they move through environmental reservoirs such as soil, waterways, and air. To address this issue, incorporating environmental monitoring into disease treatment and advocacy efforts is essential for public health.

We identified *E. coli* and *S. aureus* as the predominant multidrug-resistant bacterial species in Ghana, with an overall prevalence of 40.8% (95% CI: 21.5–60.2). This is lower than the prevalence reported in Bangladesh, where *S. aureus* and *E. coli* exhibited high MDR rates in chickens [62]. The mechanisms of β-lactam resistance in *S. aureus* include target modification, drug inactivation, biofilm formation, and efflux pump expression [63]. Coagulase-negative staphylococci (CoNS) serve as reservoirs for transferable resistance genes that support the survival of specific *S. aureus* strains [64]. The widespread use of last-resort antibiotics in agriculture, such as tetracyclines, sulfonamides, and streptomycin-penicillin combinations, has contributed to the emergence and spread of MRSA strains with increased resistance to non-β-lactam antibiotics [65, 66]. Similarly, *E. coli*, a common gut bacterium in humans and animals, has developed resistance to cephalosporins due to the production of ESBLs [67, 68]. This MDR phenotype in *E. coli* poses a significant therapeutic challenge, as it limits the available treatment options. The declining efficacy of multiple antibiotic classes highlights the urgent need for continued monitoring of resistance gene profiles and the implementation of antimicrobial stewardship measures to address the growing threat of AMR in Ghana.

Strength and limitation

Our systematic review is the first to comprehensively examine the prevalence of ARGs in Ghana. It adopted a One Health approach, considering ARGs across human, animal, and environmental settings to provide a holistic understanding of the country's AMR landscape. However, the findings are limited by some deficiencies in the available data. Some of the studies had incomplete or missing information on the number of resistance genes detected, precluding their inclusion in the final analysis. Methodological heterogeneity, such as the use of varying resistance gene detection methods (culture-based vs. molecular techniques), may have affected the reliability of the quantitative estimates. Furthermore, the reliance on convenience sampling from single hospitals or regions limits the generalisability of the resistance profiles, especially to underrepresented rural areas. The scarcity of data from animal agriculture and environmental settings also hinders the understanding of potential transmission dynamics between these sectors.

Conclusion

According to this review, bacteria isolated from human, animal, and environmental sources in Ghana harbour genes linked to antibiotic resistance. AMR is interconnected, as evidenced by the detection of multiple resistance genes in diverse sectors. The high prevalence of carbapenemase genes such as bla_{NDM-1} and bla_{OXA-48}, as well as ESBL genes such as $bla_{CTX-M-15}$, highlights the urgent need for focused public health interventions. Since horizontal gene transfer allows ARGs to spread resistance between bacteria in different domains, it is clear that the problem of AMR cannot be solved in isolation. Fostering interdisciplinary collaborations between public health, veterinary, and environmental agencies will be important to designing integrated surveillance systems, conducting joint field studies, and coordinating response initiatives attuned to AMR's complex drivers.

Recommendations

It is important to strengthen integrated AMR surveillance systems and conduct longitudinal, multi-sector studies to better understand AMR transmission dynamics across human, animal, and environmental domains in Ghana.

Abbreviations

AMR	Antimicrobial resistance
ARGs	Antibiotic resistance genes
AST	Antimicrobial susceptibility testing
CLSI	Clinical and Laboratory Standards Institute
DNA	Deoxyribonucleic Acid
ESBL	Extended-spectrum beta-lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
LMICs	Low- and middle-income countries
MDR	Multidrug resistance
MIC	Minimum inhibitory concentration
MLST	Multilocus sequence typing
MRSA	Methicillin-resistant *Staphylococcus aureus*
PCR	Polymerase chain reaction
PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analyses
WGS	Whole-Genome Sequencing

Supplementary Information

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Supplementary Material 1

Supplementary Material 2

Supplementary Material 3

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Author contributions

E.S.D. and A. O wrote the main manuscript. A.O., E.S.D., A.-H.O., S.D. and F.C.N.K. revised the manuscript. E.S.D. supervised the work. All authors read and approved the final version.

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Data availability

Data is provided within the manuscript or supplementary information files.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

All the authors have given their consent for the publication of this manuscript.

Competing interests

The authors declare no competing interests.

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References

1. Domingues S, Nielsen KM, da Silva GJ. Various pathways leading to the acquisition of antibiotic resistance by natural transformation. Mob Genet Elem. 2012;2(6):257–60.
2. Tao S, Chen H, Li N, Wang T, Liang W. The spread of antibiotic resistance genes in vivo model. Can J Infect Dis Med Microbiol. 2022;2022:1–11.
3. Windels EM, Van den Bergh B, Michiels J. Bacteria under antibiotic attack: different strategies for evolutionary adaptation. PLoS Pathog. 2020;16(5):e1008431.
4. Endale H, Mathewos M, Abdeta D. Potential causes of spread of Antimicrobial Resistance and Preventive measures in One Health Perspective-A Review. Infect Drug Resist. 2023;16:7515–45.
5. Antimicrobial resistance [Internet]. [cited 2024 Aug 26]. https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance

6. Murray CJL, Ikuta KS, Sharara F, Swetschinski L, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Lancet. 2022;399(10325):629–55.
7. Walsh TR, Gales AC, Laxminarayan R, Dodd PC. Antimicrobial Resistance: addressing a global threat to humanity. PLoS Med. 2023;20(7):e1004264.
8. de Kraker MEA, Stewardson AJ, Harbarth S. Will 10 million people die a year due to Antimicrobial Resistance by 2050? PLoS Med. 2016;13(11):e1002184.
9. Sulis G, Sayood S, Gandra S. Antimicrobial resistance in low- and middle-income countries: current status and future directions. Expert Rev Anti Infect Ther. 2022;20(2):147–60.
10. Kariuki S, Kering K, Wairimu C, Onsare R, Mbae C. Antimicrobial Resistance Rates and Surveillance in Sub-saharan Africa: where are we now? Infect Drug Resist. 2022;15:3589–609.
11. Godman B, Egwuenu A, Wesangula E, Schellack N, Kalungia AC, Tiroyakgosi C, et al. Tackling antimicrobial resistance across sub-saharan Africa: current challenges and implications for the future. Expert Opin Drug Saf. 2022;21(8):1089–111.
12. Donkor ES, Odoom A, Osman AH, Darkwah S, Kotey FCN. A systematic review on Antimicrobial Resistance in Ghana from a one health perspective. Antibiotics. 2024;13(7):662.
13. Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ. 2021;372.
14. Wells G, Wells G, Shea B, Shea B, O'Connell D, Peterson J et al. The Newcastle-Ottawa Scale (NOS) for Assessing the Quality of Nonrandomised Studies in Meta-Analyses. 2014.
15. Akenten CW, Ofori LA, Khan NA, Mbwana J, Sarpong N, May J, et al. Prevalence, characterization, and Antimicrobial Resistance of extended-spectrum beta-lactamase-producing *Escherichia coli* from Domestic Free-Range Poultry in Agogo, Ghana. Foodborne Pathog Dis. 2023;20(2):59–66.
16. Agbeko R, Aheto DW, Asante DKA, Asare NK, Boateng AA, Adinortey CA. Identification of molecular determinants of antibiotic resistance in some fish farms of Ghana. Heliyon [Internet]. 2022;8(9):e10431–e10431. https://pubmed.ncbi.nlm.nih.gov/36097488
17. Parry-Hanson Kunadu A, Holmes M, Miller EL, Grant AJ. Microbiological quality and antimicrobial resistance characterization of Salmonella spp. in fresh milk value chains in Ghana. Int J Food Microbiol [Internet]. 2018;277:41–9. https://doi.org/10.1016/j.ijfoodmicro.2018.04.025
18. Adzitey F, Assoah-Peprah P, Teye GA. Whole-genome sequencing of Escherichia coli isolated from contaminated meat samples collected from the Northern Region of Ghana reveals the presence of multiple antimicrobial resistance genes. J Glob Antimicrob Resist [Internet]. 2019;18:179–82. https://doi.org/10.1016/j.jgar.2019.03.014
19. Dekker D, Eibach D, Boahen KG, Akenten CW, Pfeifer Y, Zautner AE et al. Fluoroquinolone-Resistant Salmonella enterica, Campylobacter spp., and Arcobacter butzleri from Local and Imported Poultry Meat in Kumasi, Ghana. Foodborne Pathog Dis [Internet]. 2019/03/23. 2019;16(5):352–8. https://pubmed.ncbi.nlm.nih.gov/30907631
20. Zautner AE, Riedel T, Bunk B, Spröer C, Boahen KG, Akenten CW et al. Molecular characterization of Arcobacter butzleri isolates from poultry in rural Ghana. Front Cell Infect Microbiol [Internet]. 2023;13:1094067. https://pubmed.ncbi.nlm.nih.gov/36761899
21. Eibach D, Dekker D, Gyau Boahen K, Wiafe Akenten C, Sarpong N, Belmar Campos C et al. Extended-spectrum beta-lactamase-producing Escherichia coli and Klebsiella pneumoniae in local and imported poultry meat in Ghana. Vet Microbiol [Internet]. 2018;217:7–12. https://doi.org/10.1016/j.vetmic.2018.02.023
22. Agyekum A, Fajardo-Lubián A, Ansong D, Partridge SR, Agbenyega T, Iredell JR. blaCTX-M-15 carried by IncF-type plasmids is the dominant ESBL gene in Escherichia coli and Klebsiella pneumoniae at a hospital in Ghana. Diagn Microbiol Infect Dis [Internet]. 2016;84(4):328–33. https://doi.org/10.1016/j.diagmicrobio.2015.12.010
23. Eibach D, Campos CB, Krumkamp R, Al-Emran HM, Dekker D, Boahen KG et al. Extended spectrum beta-lactamase producing Enterobacteriaceae causing bloodstream infections in rural Ghana, 2007–2012. International Journal of Medical Microbiology [Internet]. 2016;306(4):249–54. https://doi.org/10.1016/j.ijmm.2016.05.006
24. Pankok F, Taudien S, Dekker D, Thye T, Oppong K, Wiafe Akenten C et al. Epidemiology of Plasmids in Escherichia coli and Klebsiella pneumoniae with Acquired Extended Spectrum Beta-Lactamase Genes Isolated from Chronic Wounds in Ghana. Antibiotics (Basel) [Internet]. 2022;11(5):689. https://pubmed.ncbi.nlm.nih.gov/35625333
25. Forson AO, Adjei DN, Olu-Taiwo M, Quarchie MN, Asmah HR. Characterization of Campylobacter associated gastric enteritis among patients with Human Immunodeficiency Virus (HIV) in a hospital in Accra, Ghana. PLoS One [Internet]. 2020;15(10):e0240242–e0240242. https://pubmed.ncbi.nlm.nih.gov/33057408
26. Obeng-Nkrumah N, Labi AK, Blankson H, Awuah-Mensah G, Oduro-Mensah D, Anum J et al. Household cockroaches carry CTX-M-15-, OXA-48- and NDM-1-producing enterobacteria, and share beta-lactam resistance determinants with humans. BMC Microbiol [Internet]. 2019;19(1):272. https://pubmed.ncbi.nlm.nih.gov/31801455
27. Egyir B, Dsani E, Owusu-Nyantakyi C, Amuasi GR, Owusu FA, Allegye-Cudjoe E et al. Antimicrobial resistance and genomic analysis of staphylococci isolated from livestock and farm attendants in Northern Ghana. BMC Microbiol [Internet]. 2022;22(1):180. https://pubmed.ncbi.nlm.nih.gov/35864456
28. Mills RO, Abdullah MR, Akwetey SA, Sappor DC, Gámez G, Hammerschmidt S. Molecular epidemiology of multidrug-resistant pneumococci among Ghanaian children under five years post PCV13 using MLST. Microorganisms [Internet]. 2022;10(2):469. https://doi.org/10.3390/microorganisms10020469
29. Oduro-Mensah D, Obeng-Nkrumah N, Bonney EY, Oduro-Mensah E, Twum-Danso K, Osei YD et al. Genetic characterization of TEM-type ESBL-associated antibacterial resistance in Enterobacteriaceae in a tertiary hospital in Ghana. Ann Clin Microbiol Antimicrob [Internet]. 2016;15:29. https://pubmed.ncbi.nlm.nih.gov/27145868
30. Akenten CW, Khan NA, Mbwana J, Krumkamp R, Fosu D, Paintsil EK et al. Carriage of ESBL-producing Klebsiella pneumoniae and Escherichia coli among children in rural Ghana: a cross-sectional study. Antimicrob Resist Infect Control [Internet]. 2023;12(1):60. https://pubmed.ncbi.nlm.nih.gov/37400910
31. Namboodiri SS, Opintan JA, Lijek RS, Newman MJ, Okeke IN. Quinolone resistance in Escherichia coli from Accra, Ghana. BMC Microbiol [Internet]. 2011;11:44. https://pubmed.ncbi.nlm.nih.gov/21352598
32. Dela H, Egyir B, Majekodunmi AO, Behene E, Yeboah C, Ackah D et al. Diarrhoeagenic E. coli occurrence and antimicrobial resistance of Extended Spectrum Beta-Lactamases isolated from diarrhoea patients attending health facilities in Accra, Ghana. PLoS One [Internet]. 2022;17(5):e0268991–e0268991. https://pubmed.ncbi.nlm.nih.gov/35617316
33. Odoi H, Boamah VE, Boakye YD, Agyare C. Prevalence and Phenotypic and Genotypic Resistance Mechanisms of Multidrug-Resistant Pseudomonas aeruginosa Strains Isolated from Clinical, Environmental, and Poultry Litter Samples from the Ashanti Region of Ghana. J Environ Public Health [Internet]. 2021;2021:9976064. https://pubmed.ncbi.nlm.nih.gov/34221030
34. Ayibieke A, Sato W, Mahazu S, Prah I, Addow-Thompson J, Ohashi M et al. Molecular characterisation of the NDM-1-encoding plasmid p2189-NDM in an Escherichia coli ST410 clinical isolate from Ghana. PLoS One [Internet]. 2018;13(12):e0209623–e0209623. https://pubmed.ncbi.nlm.nih.gov/30576382
35. Adedze-Kpodo RK, Feglo PK, Agboli E, Asmah RH, Kwadzokpui PK. Genotypic characterization of extended-spectrum β-lactamase producing urinary isolates among pregnant women in Ho municipality, Ghana. Heliyon [Internet]. 2022;8(12):e12513–e12513. https://pubmed.ncbi.nlm.nih.gov/36593819
36. Sah AK, Feglo PK. Plasmid-mediated quinolone resistance determinants in clinical bacterial pathogens isolated from the Western Region of Ghana: a cross-sectional study. Pan Afr Med J [Internet]. 2022;43:207. https://pubmed.ncbi.nlm.nih.gov/36942137
37. Deku JG, Duedu KO, Kpene GE, Kinanyok S, Feglo PK. Carbapenemase Production and Detection of Colistin-Resistant Genes in Clinical Isolates of Escherichia Coli from the Ho Teaching Hospital, Ghana. Can J Infect Dis Med Microbiol [Internet]. 2022;2022:1544624. https://pubmed.ncbi.nlm.nih.gov/35795863
38. Deku JG, Duedu KO, Ativi E, Kpene GE, Feglo PK. Burden of fluoroquinolone resistance in clinical isolates of Escherichia coli at the Ho Teaching Hospital, Ghana. Ethiop J Health Sci [Internet]. 2022;32(1):93–102. https://doi.org/10.4314/ejhs.v32i1.11
39. Agyepong N, Govinden U, Owusu-Ofori A, Amoako DG, Allam M, Janice J et al. Genomic characterization of multidrug-resistant ESBL-producing Klebsiella pneumoniae isolated from a Ghanaian teaching hospital. International Journal of Infectious Diseases [Internet]. 2019;85:117–23. https://doi.org/10.1016/j.ijid.2019.05.025
40. Deku JG, Duedu KO, Ativi E, Kpene GE, Feglo PK. Occurrence and distribution of extended-spectrum β-lactamase in clinical Escherichia coli isolates at Ho Teaching Hospital in Ghana. Ghana Med J [Internet]. 2021;55(4):298–307. https://pubmed.ncbi.nlm.nih.gov/35957938

41. Sampah J, Owusu-Frimpong I, Aboagye FT, Owusu-Ofori A. Prevalence of carbapenem-resistant and extended-spectrum beta-lactamase-producing Enterobacteriaceae in a teaching hospital in Ghana. PLoS One [Internet]. 2023;18(10):e0274156–e0274156. https://pubmed.ncbi.nlm.nih.gov/37903118
42. Owusu FA, Obeng-Nkrumah N, Gyinae E, Kodom S, Tagoe R, Tabi BKA et al. Occurrence of Carbapenemases, Extended-Spectrum Beta-Lactamases and AmpCs among Beta-Lactamase-Producing Gram-Negative Bacteria from Clinical Sources in Accra, Ghana. Antibiotics (Basel) [Internet]. 2023;12(6):1016. https://pubmed.ncbi.nlm.nih.gov/37370334
43. Codjoe FS, Donkor ES, Smith TJ, Miller K. Phenotypic and Genotypic Characterization of Carbapenem-Resistant Gram-Negative Bacilli Pathogens from Hospitals in Ghana. Microbial Drug Resistance [Internet]. 2019;25(10):1449–57. https://doi.org/10.1089/mdr.2018.0278
44. Kini P, Wireko S, Osei-Poku P, Asiedu SO, Amewu EKA, Asiedu E et al. Antibiotic resistance and mecA characterization of Staphylococcus hominis from filarial lymphedema patients in the Ahanta West District, Ghana: A cross-sectional study. Health Sci Rep [Internet]. 2023;6(2):e1104–e1104. https://pubmed.ncbi.nlm.nih.gov/36778776
45. Olu-Taiwo MA, Opintan JA, Codjoe FS, Obeng Forson A. Metallo-Beta-Lactamase-Producing Acinetobacter spp. from Clinical Isolates at a Tertiary Care Hospital in Ghana. Biomed Res Int [Internet]. 2020;2020:3852419. https://pubmed.ncbi.nlm.nih.gov/33029505
46. Dwomoh FP, Kotey FCN, Dayie N, Osei MM, Amoa-Owusu F, Bannah V et al. Phenotypic and genotypic detection of carbapenemase-producing Escherichia coli and Klebsiella pneumoniae in Accra, Ghana. PLoS ONE. 2022;17(12).
47. Acolatse JEE, Portal EAR, Boostrom I, Akafity G, Dakroah MP, Chalker VJ et al. Environmental surveillance of ESBL and carbapenemase-producing gram-negative bacteria in a Ghanaian Tertiary Hospital. Antimicrob Resist Infect Control [Internet]. 2022;11(1):49. https://pubmed.ncbi.nlm.nih.gov/35296353
48. Delgado-Blas JF, Valenzuela Agüi C, Marin Rodriguez E, Serna C, Montero N, Saba CKS et al. Dissemination Routes of Carbapenem and Pan-Aminoglycoside Resistance Mechanisms in Hospital and Urban Wastewater Canalizations of Ghana. mSystems [Internet]. 2022/02/01. 2022;7(1):e0101921–e0101921. https://pubmed.ncbi.nlm.nih.gov/35103490
49. Odonkor ST, Simpson SV, Morales Medina WR, Fahrenfeld NL. Antibiotic-Resistant Bacteria and Resistance Genes in Isolates from Ghanaian Drinking Water Sources. J Environ Public Health [Internet]. 2022;2022:2850165. https://pubmed.ncbi.nlm.nih.gov/36246472
50. Dekker D, Wolters M, Mertens E, Boahen KG, Krumkamp R, Eibach D et al. Antibiotic resistance and clonal diversity of invasive Staphylococcus aureus in the rural Ashanti Region, Ghana. BMC Infect Dis [Internet]. 2016;16(1):720. https://pubmed.ncbi.nlm.nih.gov/27899074
51. Acheampong G, Owusu M, Owusu-Ofori A, Osei I, Sarpong N, Sylverken A et al. Chromosomal and plasmid-mediated fluoroquinolone resistance in human Salmonella enterica infection in Ghana. BMC Infect Dis [Internet]. 2019;19(1):898. https://pubmed.ncbi.nlm.nih.gov/31660876
52. Dekker D, Pankok F, Thye T, Taudien S, Oppong K, Akenten CW, et al. Clonal clusters, Molecular Resistance mechanisms and virulence factors of Gram-negative Bacteria isolated from chronic wounds in Ghana. Antibiotics. 2021;10(3):339.
53. Gundran RS, Cardenio PA, Villanueva MA, Sison FB, Benigno CC, Kreausukon K et al. Prevalence and distribution of bla(CTX-M), bla(SHV), bla(TEM) genes in extended- spectrum β- lactamase- producing E. coli isolates from broiler farms in the Philippines. BMC Vet Res [Internet]. 2019;15(1):227. https://pubmed.ncbi.nlm.nih.gov/31277658
54. Mazumder R, Abdullah A, Ahmed D, Hussain A. High Prevalence of bla(CTX-M-15) Gene among Extended-Spectrum β-Lactamase-Producing Escherichia coli Isolates Causing Extraintestinal Infections in Bangladesh. Antibiotics (Basel) [Internet]. 2020;9(11):796. https://pubmed.ncbi.nlm.nih.gov/33187055
55. Singh NS, Singhal N, Virdi JS. Genetic Environment of bla(TEM-1), bla(CTX-M-15), bla(CMY-42) and Characterization of Integrons of Escherichia coli Isolated From an Indian Urban Aquatic Environment. Front Microbiol [Internet]. 2018;9:382. https://pubmed.ncbi.nlm.nih.gov/29563901
56. El-Defrawy I, Gamal D, El-Gharbawy R, El-Seidi E, El-Dabaa E, Eissa S. Detection of intestinal colonization by carbapenem-resistant Enterobacteriaceae (CRE) among patients admitted to a tertiary care hospital in Egypt. Egyptian Journal of Medical Human Genetics [Internet]. 2022;23(1). https://doi.org/10.1186/s43042-022-00295-9
57. Djuikoue CI, Djouela Djoulako PD, Same Njanjo HV, Kiyang CP, Djantou Biankeu FL, Guegang C et al. Phenotypic Characterization and Prevalence of Carbapenemase-Producing Pseudomonas aeruginosa Isolates in Six Health Facilities in Cameroon. BioMed [Internet]. 2023;3(1):77–88. https://doi.org/10.3390/biomed3010006
58. He W, Gao M, Lv L, Wang J, Cai Z, Bai Y, et al. Persistence and molecular epidemiology of blaNDM-positive Gram-negative bacteria in three broiler farms: a longitudinal study (2015–2021). J Hazard Mater. 2023;446:130725.
59. Acman M, Wang R, van Dorp L, Shaw LP, Wang Q, Luhmann N, et al. Role of mobile genetic elements in the global dissemination of the carbapenem resistance gene blaNDM. Nat Commun. 2022;13(1):1131.
60. Codjoe FS, Donkor ES, Smith TJ, Miller K. Phenotypic and genotypic characterization of Carbapenem-Resistant Gram-negative Bacilli pathogens from hospitals in Ghana. Microb Drug Resist. 2019;25(10):1449–57.
61. Codjoe FS, Brown CA, Smith TJ, Miller K, Donkor ES. Genetic relatedness in carbapenem-resistant isolates from clinical specimens in Ghana using ERIC-PCR technique. PLoS ONE. 2019;14(9):e0222168.
62. Parvin MS, Ali MY, Mandal AK, Talukder S, Islam MT. Sink survey to investigate multidrug resistance pattern of common foodborne bacteria from wholesale chicken markets in Dhaka city of Bangladesh. Sci Rep [Internet]. 2022;12(1):10818. https://pubmed.ncbi.nlm.nih.gov/35752640
63. Mlynarczyk-Bonikowska B, Kowalewski C, Krolak-Ulinska A, Marusza W. Molecular Mechanisms of Drug Resistance in Staphylococcus aureus. Int J Mol Sci [Internet]. 2022;23(15):8088. https://pubmed.ncbi.nlm.nih.gov/35897667
64. França A, Gaio V, Lopes N, Melo LDR. Virulence Factors in Coagulase-Negative Staphylococci. Pathogens [Internet]. 2021;10(2):170. https://pubmed.ncbi.nlm.nih.gov/33557202
65. Lade H, Joo HS, Kim JS. Molecular Basis of Non-β-Lactam Antibiotics Resistance in Staphylococcus aureus. Antibiotics (Basel) [Internet]. 2022;11(10):1378. https://pubmed.ncbi.nlm.nih.gov/36290036
66. Mehndiratta PL, Bhalla P. Use of antibiotics in animal agriculture & emergence of methicillin-resistant Staphylococcus aureus (MRSA) clones: Need to assess the impact on public health. Indian J Med Res [Internet]. 2014 Sep 1 [cited 2024 Oct 13];140(3):339. http://pmc/articles/PMC4248379/
67. Ramos S, Silva V, Dapkevicius M, de LE, Caniça M, Tejedor-Junco MT, Igrejas G et al. Escherichia coli as Commensal and Pathogenic Bacteria Among Food-Producing Animals: Health Implications of Extended Spectrum β-lactamase (ESBL) Production. Animals (Basel) [Internet]. 2020;10(12):2239. https://pubmed.ncbi.nlm.nih.gov/33260303
68. Shaikh S, Fatima J, Shakil S, Rizvi SMD, Kamal MA. Antibiotic resistance and extended spectrum beta-lactamases: types, epidemiology and treatment. Saudi J Biol Sci. 2015;22(1):90–101.

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