African Journal of Rural Development, Vol. 10 (3):2025: pp.340- 359 ISSN 2415-2838
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One Health Review of Carbapenem-Resistant Enterobacterales in the Tropical East Africa to West Asia Belt

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ABSTRACT

Carbapenem-resistant Enterobacterales (CRE) have emerged and spread globally throughout human, animal, and environmental contexts. They are of urgent concern in healthcare settings and are associated with significant morbidity and mortality. Ecological dissemination of CRE occurs globally, and one contributing factor is environmental contamination with residues from human, veterinary, and agricultural use of antimicrobials. High rates of antimicrobial resistance have been documented in the tropical belt of East Africa and West Asia, yet this region remains understudied in terms of coordinated One Health surveillance and response to CRE. This review synthesized data from peer-reviewed articles published between 2013 and 2025 to assess the occurrence, transmission, and control of CRE across the tropical belt from East Africa to West Asia. The most prevalent CRE species were *Klebsiella pneumoniae* and *Escherichia coli* among drug-resistant bacteria sourced from humans, animals, and the environment. The reported prevalence of CRE varied greatly but in some contexts was nearly 70%, with many isolates carrying carbapenemase genes such as blaIMP and blaVIM in this tropical belt. Rising ESBL and carbapenem-resistant bacteria in East Africa and West Asia underscore the urgency for international collaboration, regulation, and data sharing to inform effective strategies and interventions against antimicrobial resistance.

Keywords: Carbapenem-Resistant Enterobacterales, East Africa, One Health, West Asia

RÉSUMÉ

Les Entérobactéries résistantes aux carbapénèmes (ERC) ont émergé et se sont propagées mondialement dans les contextes humains, animaux et environnementaux. Elles suscitent une inquiétude urgente dans les établissements de santé et sont associées à une morbidité et une mortalité importantes. La dissémination écologique des ERC se produit à l'échelle mondiale, l'un des facteurs contributifs étant la contamination environnementale par les résidus issus de l'usage des antimicrobiens en médecine humaine, vétérinaire et en agriculture. Des taux élevés de résistance aux antimicrobiens ont été documentés dans la ceinture tropicale de l'Afrique de l'Est

Cite as: Ferdous, K., Khaitsa, M.L., Park, J.Y., Seo, K.S. and Brookshire, C. 2025. One Health Review of Carbapenem-Resistant Enterobacterales in the Tropical East Africa to West Asia Belt. *African Journal of Rural Development* 10 (3):340-359.

et de l'Asie de l'Ouest, bien que cette région reste peu étudiée en matière de surveillance coordonnée « Une Seule Santé » et de réponse face aux ERC. Cette revue a synthétisé les données issues d'articles évalués par des pairs publiés entre 2013 et 2025 afin d'évaluer l'occurrence, la transmission et le contrôle des ERC dans la ceinture tropicale allant de l'Afrique de l'Est à l'Asie de l'Ouest. Les espèces ERC les plus courantes étaient Klebsiella pneumoniae et Escherichia coli, issues de bactéries résistantes isolées chez les humains, les animaux et dans l'environnement. La prévalence rapportée des ERC variait fortement, atteignant dans certains contextes près de 70 %, de nombreux isolats portant les gènes carbapénémases tels que blaIMP et blaVIM. L'augmentation des bactéries résistantes aux BLSE et aux carbapénèmes en Afrique de l'Est et en Asie de l'Ouest souligne l'urgence d'une collaboration internationale, d'une réglementation adéquate et d'un partage des données pour concevoir des stratégies et interventions efficaces contre la résistance aux antimicrobiens.

Mots clés : Entérobactéries résistantes aux carbapénèmes, Afrique de l'Est, Une Seule Santé, Asie de l'Ouest

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INTRODUCTION

In recent years, the rapid emergence and spread of Carbapenem-Resistant *Enterobacterales* (CRE) has occurred alongside carbapenem antibiotic use, and potentially misuse. Genetic determinants of resistance occur on both chromosomes and transmissible mobile elements, such as plasmids (Partridge *et al.*, 2018). These plasmids can easily spread between different bacteria, including interspecies transmission, while pathogenic CRE bacterial strains can also spread between patients (El-Defrawy *et al.*, 2022). CREs are capable of spreading rapidly through healthcare systems (Giannella *et al.*, 2014), communities, animals, and the environment (Sivalingam *et al.*, 2019), and infections due to these organisms are associated with significant morbidity and mortality (Logan *et al.*, 2017). The recent discovery of plasmid-borne colistin resistance in humans has raised concerns that these additional sources of CRE could fuel the spread of resistance in communities, as these organisms are no longer limited to healthcare settings (McGann *et al.*, 2016). Improper use of antimicrobials can occur in human healthcare, veterinary healthcare (both companion animal and food producing animals), as well as other forms of agriculture (e.g., citrus farming). There are limited classes of antimicrobials, and some classes are used very broadly across many applications (e.g., tetracycline antibiotics). In several countries, agricultural veterinary use accounts for a large percentage of total antibiotic consumption on a kilogram basis, sometimes up to 80% (Manyi-Loh *et al.*, 2018; Todman *et al*, 2023). It is estimated that between 100,000 and 200,000 tonnes of antibiotics from both medical and veterinary use are released into the global environment each year (Danner *et al.*, 2019). Antibiotics are also widely used in aquaculture for disease prevention and to promote growth, which contributes to environmental contamination and can affect the fish and shellfish that people eat (Shen *et al.*, 2020). Many countries in Europe and North America have moved to systems of animal care that no longer use antibiotics for growth promotion (WHO, 2017), but global standards do not exist for protecting the use of antimicrobials for medically necessary contexts only. There is an urgent need for coordinated monitoring and control efforts through a One Health approach, particularly in regions with high rates of antimicrobial resistance combined with high rates of potentially unnecessary use of antimicrobials across all sectors utilizing these compounds.

In East Africa, antibiotic resistance has been documented in humans (Moses *et al.*, 2014; Mushi *et al.*, 2014), livestock (Madoshi *et al.*, 2016; Seni *et al.*, 2016), wildlife (Katakweba *et al.*, 2015), and the environment (Erb *et al.*, 2018; Kateete *et al.*, 2019). Carbapenem resistance has been identified in *Enterobacterales* and other gram-negative bacteria (Mushi *et al.*, 2014; Ampaire *et al*, 2015; Okoche *et al.*, 2015; Kateete *et al.*, 2016; Henson *et al.*, 2017). The high rates of carbapenem-resistant *Klebsiella pneumoniae* and *Escherichia coli* pose a serious challenge to the effective treatment of infections caused by carbapenemase-producing *Enterobacteriaceae* (Ssekatawa *et al.*, 2018).

Similarly, in West Asia, highly resistant *Klebsiella pneumoniae* clones started dominating the United Arab Emirates (UAE) since 2009, where their dissemination is facilitated by international travel, trade, and tourism, severely impacting the overall antibiotic resistance patterns, including those of colistin and tigecycline (Thomsen *et al.*, 2023). The appearance of Enterobacterales with both AmpC/ESBL enzymes and reduced susceptibility to carbapenems, along with *Klebsiella pneumoniae* strains showing resistance to both colistin and carbapenemases, underscores significant treatment challenges in the Asia-Pacific region (Chen *et a.l*, 2022).

The tropical belt stretching from East Africa to West Asia is characterized by high population mobility, diverse ecosystems, intensive agriculture, and variable healthcare infrastructure, all of which contribute to the emergence and spread of antimicrobial resistance (AMR). Yet, this region remains understudied in terms of coordinated One Health surveillance and response to CRE. Due to the interconnected nature of humans, animals, and the environment, antibiotic use, the presence of antibiotic residues, and the spread of antibiotic-resistant bacteria are all closely tied to the One Health framework (Ahmad *et al.*, 2023). To effectively combat and control antibiotic resistance (ABR), strong surveillance across all sectors, both individually and collectively, must be established at national and international levels. This effort should include addressing laboratory capacity challenges and ensuring the implementation of coordinated plans and actions under the One Health approach.

In this review, we synthesize current knowledge on the occurrence, transmission, and control of CRE across human, animal, and environmental domains from published articles in the tropical East Africa to the West Asia corridor. We aim to identify gaps, highlight emerging patterns, and propose integrated strategies for surveillance and mitigation grounded in the One Health framework. By focusing on this geostrategic and ecologically dynamic region, this review contributes to a more nuanced understanding of CRE's transboundary risks and the need for coordinated regional and global responses.

MATERIALS and METHODS

Study Area. The tropical belt stretching from East Africa to West Asia including countries such as Kenya, Uganda, Tanzania, Rwanda, Ethiopia, the Democratic Republic of the Congo (DRC), Malawi, Egypt, and Sudan Kuwait, Iran, Iraq, United Arab Emirates (UAE) and Turkey.

Search Criteria. Searchengines such as PubMed, Scopus, ScienceDirect, and Google Scholar were used to conduct the literature review. The websites and repositories of pertinent sector ministries were searched further, but no additional information was found there. The search keywords used were "carbapenem resistance in tropical East Africa", "antimicrobial resistance in human-animal-environment", "carbapenem resistance genes in East Africa", "risk factors for Carbapenem-

Resistant Enterobacterales (CRE) in East Africa and West Asia", "prevalence and genotypic characterization of antimicrobial resistance in Africa". The inclusion criteria included full-text research articles published between 2013 and 2025 that described the prevalence of carbapenemase-producing (CP) bacteria isolated from patients and environments. Non-English language articles from African countries were excluded.

Data Analysis. The data were extracted using a template set of characteristics, including study period, study location, publication year, country, source of sample, bacterial species isolates, number of CRE isolates, methods of carbapenemase genes detection, and prevalence of carbapenem-resistant isolates.

RESULTS and DISCUSSION

CRE in Humans. Carbapenem-resistant Enterobacterales present a major public health threat in the tropical East Africa to West Asia corridor, with rising prevalence documented across healthcare settings. In East Africa, studies from Uganda, Tanzania, and Kenya report frequent detection of carbapenem-resistant *Klebsiella pneumoniae* and *Escherichia coli* in clinical samples (Mushi *et al.*, 2014; Okoche *et al.*, 2015; Henson *et al.*, 2017). At Mulago National Referral Hospital in Uganda, over 20% of *Enterobacterales* isolates exhibited carbapenem resistance, primarily associated with bla$_{\text{VIM}}$ genes (Okoche *et al.*, 2015). In Tanzania, bla$_{\text{IMP}}$ and bla$_{\text{VIM}}$ genes were also prevalent among multidrug-resistant isolates (Mushi *et al.*, 2014). In Egypt, high levels of CRE colonization and infection have been attributed to antibiotic overuse, with bla$_{\text{OXA-48}}$ emerging as the dominant carbapenemase gene (El-Defrawy et al., 2022). In West Asia, the United Arab Emirates (UAE) has experienced an increase in CRE prevalence, with a 12-year surveillance study reporting an overall rate of 3.8% and a concerning rise in ertapenem resistance (Thomsen *et al.*, 2023). The authors attribute dissemination in part to international travel, trade, and tourism. Similarly, CRE strains co-harboring bla$_{\text{NDM}}$ and bla$_{\text{OXA-48}}$ have been documented in Iran and Iraq, underscoring the transboundary nature of resistance (Solgi *et al.*, 2017; Hosseinzadeh *et al.*, 2018; Ali Albadery *et al.*, 2022). These findings reflect a growing public health burden and highlight the urgent need for strengthened antimicrobial stewardship and infection control infrastructure across the region.

CRE in Animals. Although carbapenem use is largely restricted in veterinary medicine, CRE and similar types of resistance have been reported in animals across East Africa and West Asia, raising concerns about environmental and food-chain transmission. In East Africa, studies in Tanzania have identified ESBL-producing *Enterobacterales* in a broad range of species, including livestock, companion animals, and wildlife such as buffalo, wildebeest, and zebra (Katakweba *et al.*, 2015; Madoshi *et al.*, 2016; Seni *et al.*, 2016). While direct reports of CRE in animals remain limited, the detection of resistance in wildlife and domestic animals living in close proximity to human settlements suggests a potential for bidirectional transmission. In Egypt, CRE genes such as bla$_{\text{OXA-48}}$, bla$_{\text{NDM}}$, and bla$_{\text{VIM}}$ have been identified in *E. coli* isolated from farmed Nile tilapia (*Oreochromis niloticus*), with a positive correlation between resistance gene detection and elevated water temperature (Hamza *et al.*, 2020). This indicates that resistance genes may have originated in healthcare settings and subsequently reached farms, potentially via infected human carriers or through contaminated sewage discharge (Hamza *et al.*, 2016). Colistin-resistant strains have also been isolated from aquaculture systems in Egypt, indicating co-selection and environmental spread of resistance genes (Shen *et al.*, 2020). In West Asia, Lebanon has reported CRE in poultry, pigs, and cattle, as part of broader surveillance highlighting the role of food-producing animals in AMR epidemiology (Osman *et al.*, 2019). These findings support growing evidence that antimicrobial resistance including to last-resort antibiotics is not confined to clinical settings but extends to the animal sector through complex ecological and anthropogenic pathways.

Environmental CRE. The environment serves as a critical reservoir and conduit for the dissemination of CRE, particularly in settings where antibiotic use and waste disposal are poorly regulated. In East Africa, high rates of ESBL-producing *E. coli* have been detected in shared and private latrines in informal urban settlements in Tanzania, suggesting significant fecal contamination and potential environmental exposure to resistant organisms (Erb *et al.*, 2018). Environmental isolates have also been shown to contribute to the local spread of pathogenic *E. coli* strains in Egypt, reinforcing the role of environmental reservoirs in AMR dissemination (El-Sher *et al.*, 2021).

Antibiotics and resistance genes frequently enter the environment through human and animal waste, agricultural runoff, and aquaculture effluent. An estimated 100,000 – 200,000 tonnes of antibiotics are released into the global environment each year from both human and veterinary use (Danner *et al.*, 2019). In aquaculture systems, the use of antimicrobials likely contributes to the development of resistance in aquatic organisms and environmental compartments. Notably, colistin resistance genes have been detected in aquaculture samples from Egypt, indicating environmental transmission pathways relevant to CRE (Shen *et al.*, 2020).

Environmental **c**onditions in tropical regions, including high temperatures and humidity, may further accelerate resistance gene transfer and persistence. A recent study from Egypt linked elevated water temperatures to increased detection of carbapenemase genes in aquaculture-derived *E. coli* (El Badawy *et al.*, 2025). Furthermore, environmental stressors and suboptimal antimicrobial storage under such conditions can lead to degradation and exposure to sub-lethal concentrations of antibiotics, promoting selective pressure for resistance (Beceiro *et al.*, 2013; Fagunwa *et al.*, 2024). Collectively, these findings emphasize the importance of environmental surveillance as a core pillar of One Health efforts to monitor and control the spread of CRE in the tropical East Africa to West Asia region.

The risk factors for emergence and transmission dynamics. The factors that contribute to the development and spread of carbapenem resistance among animals, humans, and in the environment vary within and between the countries (Table 1). The spread of antimicrobial resistance (AMR) has been linked to various food production and livestock management practices (Allcock *et al*, 2017). Pigs and chickens represent the most investigated species, in which carbapenem resistance in Enterobacteralese has been most frequently observed (Bonardi *et a.*, 2019). Food-producing animals and food products are recognized sources of ESBL-producing *E. coli* in Lebanon (Osman *et al.*, 2019). Over the past decade, there has been widespread reporting of resistance to third-generation cephalosporins, often accompanied by resistance to carbapenems, colistin, and various other antimicrobial agents among animal populations (Al-Mir *et al*, 2021). The first study from Egypt in 2013 reported high rates of ESBLs and carbapenemases (65.09% and 11.32%, respectively) in Enterobacteriaceae isolated from retail chicken meat (Abdallah *et al*, 2015). The overall frequency of carbapenem-resistant Enterobacterales in the region ranges from 0%-68% (Table 2). Unregulated and illegal use of extended-spectrum cephalosporins (ESC) in the poultry sector has long been identified as a major cause of massive spread of ESC-resistant *Escherichia coli* (Al-Mir *et al.*, 2021).

To overcome the resistance against extended-spectrum cephalosporins (ESC) and cephamycins in *Enterobacteriaceae*, carbapenems have been introduced in human medicines (Taggar *et al.*, 2020). The burden of bacterial AMR would be correspondingly higher with higher antibiotic consumption in high-resource settings, and the study found that the highest rates of death were in sub-Saharan Africa and South Asia (Murray *et al.*, 2022).

Older age was identified as a factor associated with a higher likelihood of carrying ESBL-producing Enterobacteriaceae (ESBL-PE) in community settings in Mwanza City, Tanzania (Mshana *et al.*, 2016). Higher carriage rates of these bacteria have also been observed in individuals over 65 years old, likely due to repeated hospitalizations (Sonda *et al.*, 2018). In several studies the history of antibiotic use is reported as the main driver in the Colonization of intestinal microbiota with carbapenemase-producing Enterobacteriaceae in pediatric patients (Eshetie *et al.*, 2015; Knöppel *et al.*, 2017; Nour *et a.l*, 2017; Ghaith *et al.*, 2019). Nour *et al.*, 2017 also found that the duration of the central venous device is a significant risk factor for transmission and emergence of carbapenem resistance in Egypt. In Tanzania, neonatal colonization with ESBL-producing Enterobacteriaceae (ESBL-PE) in a tertiary hospital was linked to maternal colonization and prior antibiotic use (Marando *et al*, 2018). Another study on the genetics of carbapenemase-producing *Escherichia coli* responsible for sepsis in Egyptian children found that colonization with ESBL-producing *E. coli* constitutes a significant risk factor (Zaki *et al.*, 2019). In addition to microbial colonization, underlying patient-related factors such as a history of disease and chronic health conditions like chronic obstructive pulmonary disease (COPD) have also been identified as important contributors to susceptibility (Al Fadhli *et al.*, 2020; Dong *et al.*, 2025). Several studies on Carbapenem-Resistant Isolates from the Tertiary Care Hospitals stated that mechanical ventilation and urinary catheterization in Egypt (Al-Baz *et al.*, 2022), the hospital environment, such as patients' beds in ICUs and the premature unit in Tanzania (Silago *et al*, 2022), previous antibiotic exposure in Ethiopia, Egypt (Eshetie *et al.*, 2015; Nour *et al.*, 2017; Ghaith *et al.*, 2019) facilitated the coexistence of chromosomal and plasmid mediated carbapenem genes in children and adult humans and also their companion animals both in East Africa and West Asia. Risk factors associated with CRKP (carbapenem-resistant *Klebsiella pneumoniae*) infection include immunosuppression, admission to the ICU, prior exposure to antibiotics such as carbapenems, quinolones, glycopeptides, and β-lactam/β-lactamase inhibitors, surgical procedures, use of mechanical ventilation, central venous catheterization, indwelling urinary catheters, and nasogastric intubation (Li *et al.*, 2020). The other most contributory factors include the political and socioeconomic issues, regional Environment/Climate conditions. In low- and middle-income countries, there is limited laboratory infrastructure, which often prevents access to microbiological testing needed to guide and optimize antibiotic use (WHO Sepsis Technical Expert meeting, 2018). The other most contributory factors include the political and socioeconomic issues, regional Environment/Climate conditions. In low- and middle-income countries, there is limited laboratory infrastructure, which often prevents access to microbiological testing needed to guide and optimize antibiotic use (WHO Sepsis Technical Expert meeting, 2018). The high burden of bacterial antimicrobial resistance (AMR) results from both the widespread presence of resistant strains and the high incidence of serious infections, such as lower respiratory tract infections, bloodstream infections, and intra-abdominal infections, which are more common in these regions **(**Vos *et al.*, 2020**).**

Table 1. Risk factors for the emergence and transmission of CRE in East Africa and West Asia

Carbapenem Resistance Study	Risk Factors Investigated	Significant Risk Factor(s)	Hosts	Country	Reference
Colonization of intestinal microbiota with carbapenemase-producing *Enterobacteriaceae* in paediatric	Age, gender, ward class; specific co-morbid conditions (cardiovascular, renal, pulmonary, etc.); exposure (≥1 day(s)) to antimicrobials (imipenem, meropenem, ertapenem, doripenem, ciprofloxacin, vancomycin, cephalosporins, piperacillin-tazobactam, metronidazole)	Antibiotic exposure	children	Egypt	Ghaith *et al*, 2019
Carbapenemase-producing Enterobacteriaceae among patients with urinary tract infection	History of hospitalization, ICU admission, prior antibiotic use, prior UTI, and chronic diseases, pregnancy status, presence of urinary catheter, and mechanical ventilation	Antibiotic exposure	Human	Ethiopia	Eshetie *et al*, 2015
Risk factors and clinical outcomes for carbapenem-resistant Gram-negative late-onset sepsis in a neonatal intensive care unit	Birth weight, gestational age, inborn or outborn, time to start enteral feeding, type of feeding, previous antibiotics therapy and their types, previous use of total parenteral nutrition (TPN), presence and duration of use of central line devices, previous corticosteroid therapy, previous surgery, mechanical ventilation and its duration, and underlying chronic conditions	Previous antibiotic use, Previous antibiotic duration, and Duration of central venous device	Children	Egypt	Nour *et al*, 2017
Genetic study of carbapenemase-producing Escherichia coli causing sepsis among Egyptian children	Age, primary bloodstream infection, duration of hospital stays, and the presence of devices such as mechanical ventilator, Central Venous Catheter (CVC) or urinary catheter, positive ESBL-producing *E. coli* colonization, and positive CPE colonization	Positive colonization with ESBL-producing *E. coli*	Infants and children	Egypt	Zaki *et al*, 2019
Prevalence and Antibiotic Resistance Profiles of Carbapenem-Resistant Klebsiella Pneumoniae Isolated from Tertiary Care Hospital	Hypertension, Diabetes mellitus, Renal insufficiency, Congenital anomaly, Mechanical ventilation, Urinary catheterization, Central venous catheterization, Period of ICU admission	Mechanical ventilation and urinary catheterization	Human	Egypt	Al-Baz *et al*, 2022
Prevalence of Carbapenemase-Encoding Genes and Antimicrobial Resistance Pattern of Enterobacteriaceae Isolated from Hospitalized Patients	Age group, gender, and teaching hospitals and hospital wards	CPE prevalence across the three Khartoum State Teaching Hospitals was significant	Human	Sudan	M. Hamid *et al*, 2021

Prevalence and Characterization of Carbapenem-Resistant Enterobacteriaceae Isolated from Referral Hospital	Age, gender, and resistance to cephalosporins	-	Human	Uganda	Okoche *et al*, 2015
Klebsiella pneumoniae carbapenamases in Escherichia coli isolated from humans and livestock		-	Humans and their corresponding livestock	Uganda	Tuhamize *et al*, 2023
Co-existence of two *bla*$_{\text{NDM-5}}$ and *bla*$_{\text{OXA-181}}$ on distinct plasmids in a carbapenem-resistant *Klebsiella pneumoniae* from a tertiary hospital	Age, antibiotic exposure	-	Paediatric and adult human patients	Tanzania	Mapunda *et al*, 2025
First Identification and genomic characterization of multidrug-resistant carbapenemase-producing Enterobacteriaceae clinical isolates	Hospitals wards	Intra-hospital spread	Human	Malawi	Kumwenda *et al*, 2019
Predominance of Acinetobacter spp., Harboring the blaIMP Gene, Contaminating the Hospital Environment in a Tertiary Hospital	Hospital's ICUs surfaces, and highly dependent units (HDUs) surfaces, antibiotic exposure	Patients' beds in ICUs and the premature unit-	Infant, Human, and Hospital Environment	Tanzania	Silago *et al*, 2022
Molecular epidemiology of *Klebsiella pneumoniae* invasive infections over a decade		-	Children and adult humans	Kenya	Henson *et al*, 2017
Prevalence, aetiology and antibiotic sensitivity profile of asymptomatic bacteriuria isolates from pregnant women in selected antenatal clinics	Age, parity, education, and gestational age	-	Human	Kenya	Ayoyi *et al*, 2017
High Prevalence of Antimicrobial Resistance	Age, medical condition predisposing to infection- elderly, HIV, indwelling urinary catheter, diabetes mellitus,	-	Human	Rwanda	Ntirenganya *et al*, 2015

Among Common Bacterial Isolates in a Tertiary Healthcare Facility	severe malnutrition, malignancy, comorbidity- at least one comorbidity, two or more comorbidities				
Antimicrobial resistance in urinary isolates from inpatients and outpatients at a tertiary care hospital		-	Human	Democratic Republic of Congo)	Irenge *et al*, 2014
High Prevalence of New Delhi Metallo-β-Lactamase-1 (NDM-1) Producers among Carbapenem-Resistant *Enterobacteriaceae*	Age, gender, patients with UTI, BSI, wound or tissue infection, history of travelling	UTI	Human	Kuwait	Jamal *et al*,2015
Molecular characterization of intestinal carriage of carbapenem-resistant Enterobacteriaceae among inpatients at two Iranian university hospitals: first report of co-production of blaNDM-7 and blaOXA-48	Age, gender, unit of hospitalization, invasive medical device utilization, history of surgery, presence of wounds, transfer from another hospital, transfer between hospital units, and exposure to antibiotics	Exposure to the antibiotics, ICU, mechanical ventilation, urinary catheter, recent surgery, patients transferred from another hospital, transfer between hospital units, male patients	Human	Iran	Solgi *et al*, 2017
Emergence of blaNDM-1 and blaOXA-48-like harboring carbapenem-resistant ***Klebsiella pneumoniae*** isolates from hospitalized patients	Sex, hospital wards,	No statistically significant risk factor found	Human	Iran	Hosseinzadeh *et al*, 2018
Prevalence of carbapenem-resistant Enterobacteriaceae and emergence of high rectal colonization rates of blaOXA-181-positive isolates in patients admitted to intensive care units	Age, gender, sample type, nationality, travel history, previous hospitalization within one year of current admission, diagnosis, co-morbidity, and prior antibiotic use	Chronic obstructive pulmonary disease (COPD) comorbidity, previous hospitalization, and nationality	Human	Kuwait	Al Fadhli *et al*, 2020

Phenotyping and Genotyping Evaluation of E. coli Produces Carbapenemase Isolated from Cancer Patients	Age, gender, UTI, antimicrobial exposures	Antimicrobial exposures	Human	Iraq	Ali Albadery *et al*, 2022

Table 2. Prevalence of CRE in East Africa and West Asia

Source	**Most Prevalent CRE Species Identified**	**Overall CRE Prevalence**	**Most Prevalent CRE Gene**	**Country**	**Reference**
Urine	*E. coli, K. pneumoniae, and E. aerogenes*	2.73%	-	Ethiopia	Eshetie *et al*, 2015
Blood	*K. pneumoniae*	37.9%	-	Egypt	Nour *et al*, 2017
Poultry liver, lungs and trachea, droppings drinking water, and human faecal sample working in poultry farms	*K. pneumoniae*	43%	*bla*$_{KPC}$, *bla*$_{OXA-48}$, *and bla*$_{NDM}$	Egypt	Hamza *et al*, 2016
Tilapia fish (liver, spleen, and kidney), fishpond water inlets, tap water, outlet water	*E. coli*	68.2%	*bla*$_{KPC}$, *bla*$_{OXA-48}$, *and bla*$_{NDM}$	Egypt	Hamza *et al*, 2020
Blood	*E. coli,*	63.33%	*bla*$_{IMP}$	Egypt	Zaki *et al*, 2019
Wound swab, urine samples, sputum, urine catheter, other body fluid	*E. coli*	31.8%	*bla*$_{IMP}$	Sudan	M. Hamid *et al*, 2021
Pus swabs	*K. pneumoniae*	28.6%	*bla*$_{VIM}$	Uganda	Okoche *et al*, 2015
Stool	*E. coli*	41.7%	*bla*$_{KPC}$	Uganda	Tuhamize *et al*, 2023
Blood and wound swabs	*K. pneumoniae*	9.9%	*bla*$_{NDM-5}$ and *bla*$_{OXA-181}$	Tanzania	Mapunda *et al*, 2025
Blood, urine	*K. pneumoniae*	8%	*bla* $_{KPC-2}$	Malawi	Kumwenda *et al*,2019
Urine, blood, rectal swabs, and patients' bed swabs	*Acinetobacter spp*	68.8%	*bla*$_{IMP}$	Tanzania	Silago *et al*, 2022
Blood, Cerebrospinal fluid, and other sterile site samples	*No isolates were found to be phenotypically resistant to carbapenems*	0%	*bla*$_{OXA}$*-89 and bla*$_{OXA}$*-58 with weak carbapenemase activity*	Kenya	Henson *et al*, 2017
Urine	*K. pneumoniae*	5.9%	-	Kenya	Ayoyi *et al*, 2017

Urine, blood, sputum, and pus swab	*E. coli*	8%	-	Rwanda	Ntirenganya *et al*, 2015
Urine	*Enterobacter spp.*	0.16%	-	Democratic Republic of Congo)	Irenge *et al*, 2014
Urine, wound and tissue, blood, respiratory secretion, abscess, central venous pressure line tip, peritoneal dialysis fluid, cerebrospinal fluid, pericardial fluid, and screening rectal and throat swabs	*K. pneumoniae*	8%	$bla_{\text{NDM-1}}$	Kuwait	Jamal *et al*,2015
rectal swab	*K. pneumoniae*	37.9%	bla_{OXA}*-48*	Iran	Solgi *et al*, 2017
Blood, urine, sputum, Central venous catheter, pleural swab, wound swab, throat swab	*K. pneumoniae*	-	$bla_{\text{NDM-1}}$	Iran	Hosseinzadeh *et al*, 2018
Rectal swabs	*K. pneumoniae*	9.8%	$bla_{\text{OXA-181}}$	Kuwait	A-Fadhli *et al*, 2020
Urine	*E. coli*	53.65%	bla_{VIM}	Iraq	Ali Albadery *et al*, 2022
Blood, urine, sputum, tracheal aspirate, CSF, tissue, catheter swab	*K. pneumoniae*	67%	-	Turkey	Unlu *et al*, 2021

In the absence of fast, reliable, and cost-effective point-of-care diagnostics to determine whether an infection is bacterial or viral, both adults and children presenting with fever or respiratory symptoms, often due to viral causes are frequently prescribed antibiotics, which are commonly seen as a convenient treatment option (*CIDRAP*, April 19, 2023). Studies revealed that, in Uganda, most drugs are available over the counter without a prescription from a clinician (Jackson *et al.*, 2013). These observations present a worrying trend of antimicrobial resistance in the East African region (Okoche *et al.*, 2015).

Contributing factors to antimicrobial resistance include the misuse of antibiotics due to weak regulatory enforcement and their widespread availability, limited access to second- and third-line treatment options, the presence of counterfeit or poor-quality antibiotics that promote resistance (Holmes *et al.*, 2016; Laxminarayan *et al.*, 2013; Kelesidis *et al.*, 2015), and inadequate sanitation and hygiene (Collignon *et al.*, 2018; Hendriksen *et al.*, 2019).

Environmental conditions and tropical climate significantly contribute to the proliferation of antibiotic resistance in ecosystems by increasing selective pressure on bacteria and facilitating horizontal gene transfer of resistance genes (Fernández Salgueiro *et al.*, 2024). The wide range of resistance gene combinations detected, especially in warmer months, highlights the role of environmental factors like temperature and pH in shaping the emergence and development of antibiotic resistance (El Badawy *et al.*, 2025). The hot humid tropical conditions of East Africa and West Asia might play a crucial role in rising antibiotic resistance. Besides this, it might affect antimicrobials as they are transported and stored until the point of use and, subsequently, may impact the development of resistant microbial strains (Fagunwa *et al.*, 2024). This suboptimal eradication of pathogens can facilitate the survival of bacteria, which, having been exposed to sub-lethal doses of the drug, consequently, evolve resistance mechanisms (Beceiro *et al.*, 2013). A study on *Escherichia coli* isolated from Egyptian hospitals and environments gives findings to support the fact that environmental isolates contribute to the local spread of *E. coli* pathogenicity in Egypt, and these isolates may serve as reservoirs for transmission of resistance (El-Sher *et al.*, 2021).

Integrated strategies for surveillance and mitigation grounded in the One Health framework in East Africa and West Asia. The World Health Organization, along with the Food and Agriculture Organization of the United Nations and the World Organization for Animal Health, has called for a comprehensive, multisectoral strategy to tackle the issue of antimicrobial resistance (AMR) while most low–middle economies have little to no programs to address this issue (Founou *et al.*, 2016) due to limited resources, human capacity, laboratories, drugs, policies, and formal programs (Cox *et al.*, 2017). This has been strengthened by the collaboration of regional consortia involving local and regional academic and research institutions in Africa (Katele *et al.*, 2020) while antimicrobial stewardship education programs are needed to preserve the effectiveness and availability of efficacious antimicrobial drugs and to ensure judicious use of antimicrobials to combat AMR in Uganda (Sente *et al.*, 2025). Regional partnerships, such as the Southern African Centre for Infectious Disease Surveillance (SACIDS), and Middle East Consortium on Infectious Disease Surveillance (MECIDS) Foundation for One Health, have collaborated with institutions like the London School of Hygiene and Tropical Medicine, the London International Development Centre, the Royal Veterinary College, Chatham House (Royal

Institute of International Affairs, UK), and the American Society for Microbiology (USA) to combat antimicrobial resistance (AMR) through coordinated research and capacity-building initiatives. The establishment of effective and sustainable AMR surveillance programs in Africa is challenged by inadequate infrastructure and limited resources necessary for conducting high-quality monitoring (Kariuki *et al.,* 2018).

Asia-Pacific Economic Cooperation (APEC) projects are focusing on AMR control strategies in humans and food-producing animals to evaluate the status of AMR integrated surveillance in various APEC economies at different development levels (Lapierre *et al.,* 2017). The link between antibiotic use and the development of resistance is highly complex and depends heavily on the existing composition and dynamics of bacterial populations and earlier studies have shown that there is no single 'silver bullet' solution to fully explain or address this issue (Ahmad *et al.,* 2023). Rather than relying on a single solution, efforts to prevent and reduce the burden of antibiotic resistance (ABR) within a One Health framework should adopt a comprehensive, collaborative approach (Van Puyvelde *et al.,* 2018). This involves addressing specific patterns of antibiotic use, understanding the types and prevalence of resistance within each sector, and considering the potential interactions both within and across human, animal, and environmental systems (Holmes *et al,* 2016).

CONCLUSIONS

The findings discussed in this review confirm the widespread presence of carbapenemase-producing bacteria and their associated resistance genes across various sources, including food-producing animals, aquaculture, wildlife, human factors and environmental components. This widespread distribution poses a significant threat to both human and animal health. Multiple studies have revealed genetic similarities between carbapenem-resistant isolates from humans and animals, indicating the potential for cross-species transmission of these resistant bacteria. Epidemiological and genotypic analyses are essential to gain a deeper understanding of the transmission dynamics of antimicrobial resistance between humans, animals, and the environment. The One Health approach plays a vital role in implementing global surveillance programs and conducting antimicrobial risk assessments across zoonotic and environmental sectors to effectively respond to carbapenem resistance (CR) emergencies. Identifying and sharing best practices and policies on an international scale is crucial. Moreover, strong collaboration between governments is essential to tackle the cross-border public health threats posed by CR. Therefore, harmonized One Health guidelines for antibiotic use, along with strict regulations on their importation and sale, are essential. The rising and dynamic trends in extended-spectrum beta-lactamase (ESBL) and carbapenem-resistant (CAR) carriage rates present a growing public health concern in East Africa and West Asia. Collaborative antimicrobial resistance (AMR) surveillance conducted in partnership with regional and international institutions through an integrated One Health approach is crucial. Such collaboration enables expert knowledge exchange, technology transfer, and effective information sharing to support evidence-based policymaking and intervention strategies.

FUNDING INFORMATION

This work was supported by the National Institute of General Medical Sciences of the National Institutes of Health (NIH) under Award Number U54GM115428.

ACKNOWLEDGMENTS

The authors thanks the University of Mississippi Medical Center (UMMC) for their continuous support. We also thank the Mississippi State University librarian for assistance with the literature review and search of databases (PubMed, Scopus, ScienceDirect, Google Scholar, and Web of Science).

DECLARATIONS OF CONFLICT OF INTEREST

The authors declare no conflict of interest in this paper

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