

Commentary

Commentary on: Molecular epidemiological exploration of carbapenem-resistant *Enterobacteriaceae* in Africa from a One Health perspectiveKabiru O. Akinyemi^{1*} and Shaimaa W. Abdelmegid²¹Department of Microbiology, Faculty of Science, Lagos State University, Lagos, Nigeria²Department of Biomedical Sciences, Ontario Veterinary College, University of Guelph, Guelph, Canada*Corresponding author: Kabiru O. Akinyemi, kabiru.akinyemi@lasu.edu.ng

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Not applicable

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Carbapenems are potent, broad-spectrum β -lactam antibiotics mainly used to treat severe infections caused by multidrug-resistant (MDR) bacteria, especially those that produce β -lactamase enzymes. These antibiotics are often considered last-resort options for serious infections involving Gram-positive, Gram-negative, and anaerobic bacteria. They work by inhibiting bacterial cell wall synthesis, which is essential for bacterial growth and survival [1]. Common carbapenems used in clinical practice include imipenem, meropenem, ertapenem, and doripenem, each with unique pharmacokinetic properties. These drugs are generally more expensive in Africa compared to other antibiotics and local incomes. The high cost limits their availability and use in many settings. Although clinically necessary, many patients and health systems struggle to afford these antibiotics, and they are not routinely used across healthcare facilities in Africa. Nevertheless, infections caused by carbapenem-resistant or carbapenemase-producing bacteria are increasing, with their prevalence rising over time in hospital settings across nearly all African countries [2, 3, 4, 5]. The market for carbapenem-based antibiotics in the Middle East and Africa is projected to grow from US\$237.42 million in 2021 to US\$297.20 million by 2028, with a compound annual growth rate (CAGR) of 3.3% during 2021–2028. This growth is mainly driven by the rising incidence of bacterial infections and the expansion of public–private partnerships among pharmaceutical companies [6].

We read with great interest the systematic analysis published by Alhaji and colleagues [7]. In their study, the authors identified only eight articles addressing carbapenem-resistant *Enterobacteriaceae* (CRE) across at least two sectors of the One Health. The authors used the PRISMA checklist to ensure that all eligible studies were included in their review, and conducted a literature search through August 2025 using Web of Science, Google Scholar, Scopus, ResearchGate, and PubMed. However,

the period covered by the literature search was not specified in the study design. The study timeframe was between 2019 and 2024, inferred only from the results in Tables 1 and 2. Additionally, the research articles did not seem to have been retrieved properly using appropriate keywords, resulting in a very small number of articles used in the analysis of this important topic in Africa.

Firstly, Alhaji et al. [7] should note that *Enterobacteriaceae* are a large family of Gram-negative bacteria that are part of the commensal flora of human and animal guts. The family includes many pathogens such as *Klebsiella* spp., *Enterobacter* spp., *Citrobacter* spp., *Salmonella* spp., *Escherichia coli*, *Shigella* spp., *Proteus* spp., *Serratia marcescens* and other species. *Enterobacteriaceae*, like all bacteria, can develop resistance to antibiotics, including the carbapenem group, and are referred to as carbapenem-resistant *Enterobacteriaceae* (CRE) and carbapenemase-producing *Enterobacteriaceae* (CPE) [8]. Secondly, the most critical CRE include carbapenem-resistant *Klebsiella pneumoniae*, *Escherichia coli*, *Enterobacter* spp., *Serratia* spp., and *Proteus* spp. These organisms are of particular concern due to their high mortality during infections and their ability to disseminate carbapenem resistance via mobile genetic elements [9, 10]. Unfortunately, Alhaji et al. [7] did not expand the literature search to include keywords for the species of these most important CRE family members. For example, carbapenem-resistant *Klebsiella pneumoniae*, *Escherichia coli*, *Enterobacter* spp., *Serratia* spp., and *Proteus* spp. etc. are supposed to be part of the keywords, thus excluding most articles that reported carbapenem resistance in these pathogens in Africa.

The overall pooled prevalence of CRE across the diverse studies was 18.58%. Although carbapenems are not used in animals, the animal sector exhibited the highest reported prevalence of CRE (9.89%), followed by the

human sector (6.06%) and the environmental sector (2.63%). It is important to note that eight studies are not enough to provide a comprehensive overview of the current situation in Africa. Nonetheless, the findings highlight the circulation of CRE across all One Health sectors and suggest the potential transmission of resistant bacteria or resistance genes among human, animal, and environmental domains. These results emphasize the importance of adopting a One Health approach to controlling antimicrobial resistance (AMR) and zoonotic diseases. However, Alhaji et al. [7] should be aware that CPEs are found in many *Enterobacteriaceae* species. In a five-year, single-center investigation of a CPE outbreak, the spread of *blaKPC*-associated infections was primarily attributed to horizontal gene transfer. A total of 66 strains were identified within the *Enterobacteriaceae*, comprising 13 species, including *Klebsiella*, *Enterobacter*, and *Citrobacter*, as previously reported [11], indicating that the results of Alhaji et al. [7] may not accurately reflect the prevalence of CPE in Africa.

The analysis identified *Escherichia coli* (58.35%) and *Klebsiella pneumoniae* (28.28%) as the most commonly reported CRE isolates. Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) has become one of the most serious issues in modern healthcare, especially in intensive care units. The spread of successful bacterial lineages, the exchange of resistance genes, and gradual genetic adaptation all contribute to the rapid dissemination and long-term persistence of AMR in *Klebsiella*. Several carbapenemase genes, including *blaKPC*, *blaNDM*, and *blaOXA-48*-like, responsible for CRE, are located on mobile genetic elements (MGEs) such as plasmids, transposons, and insertion sequences. These genes are also among the most commonly reported resistance genes in Africa [7]. These elements enable the transfer of resistance genes between bacteria and across different environments. The human gut is central to this process, serving as a reservoir for resistant bacteria. These pathogens can be excreted into the environment and may contaminate water, soil, and crops, spreading resistance further [12].

The lack of data from Central Africa and the low representation of Southern Africa reflect broader surveillance gaps rather than true low prevalence. Variability in sampling and detection methods across the articles evaluated by Alhaji et al. [7] complicates data pooling. The review noted that the presence of CRE across different domains suggests interface zones but does not confirm transmission routes without long-term data. Dossouvi et al. [13] conducted a systematic review on carbapenem-resistant Enterobacterales in African studies across animal, environmental, and food sectors. Although they did not include a single pooled prevalence estimate, they highlighted the presence of CRE in non-human domains and advocated for One Health prevention

strategies [13]. This aligns with Alhaji et al. [7] review on animals, although a lack of integrated data was noted.

Generally, the analyzed studies did not cover all regions of the continent. More research is needed across different parts of Africa, involving patients, their animals, and the surrounding environment. Investigating infection sources and understanding transmission dynamics are crucial. This can be done through plasmid analysis and whole-genome sequencing of isolates collected from all sectors of One Health. The review revealed a high burden of CRE, particularly *Escherichia coli* and *Klebsiella pneumoniae*, along with their resistance genes, at the human-animal-environment interface in at least two areas across the One Health sectors in Africa.

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References

1. Papp-Wallace KM, Endimiani A, Taracila MA, Bonomo RA. Carbapenems: Past, present, and future. *Antimicrob Agents Chemother*. 2011;55(11):4943-60. <https://doi.org/10.1128/aac.00296-11>
2. Yaqub Y, Muhammed Y, Musa B, Daninna ZR, Aliyu MS, Tanko ZL, et al. Risk factors associated with rectal carriage of carbapenem-resistant Enterobacterales in northern Nigeria: A hospital surveillance. *BMC Infect Dis*. 2025;25(1):1454. <https://doi.org/10.1186/s12879-025-11944-w>
3. Abera D, Mihret A, Fentaw S, Beyene E, Negash AA, Abegaz WE. Extended-spectrum β -lactamase and carbapenemase-producing Enterobacterales among adult patients and their family members at Tikur Anbessa Specialized Hospital, Addis Ababa, Ethiopia. *PLoS One*. 2026;21(1):e0341636. <https://doi.org/10.1371/journal.pone.0341636>
4. Sow O, Oueslati S, Ndiaye I, Vanparis O, Gueye AB, Mehidi I, et al. Molecular insights into carbapenemase-producing Enterobacterales from Senegal. *J Antimicrob Chemother*. 2025;80(11):2989-3000. <https://doi.org/10.1093/jac/dkaf328>
5. Moloto K, Newton-Foot M, Dramowski A, Ayala-Montano S, Akintayo I, Whitelaw A, et al. Carbapenem-resistant *Klebsiella pneumoniae* isolates at a tertiary hospital in Cape Town, South

- Africa, are dominated by specific local clones rather than previously described international lineages. PLoS Pathog. 2026;22(1):e1013859. <https://doi.org/10.1371/journal.ppat.1013859>
6. Middle East and Africa Carbapenem-Based Antibiotics Market Forecast to 2028: Available at <https://www.marketresearch.com/TI-P-Knowledge-Services-v4095/Middle-East-Africa-Carbapenem-Based-31470051/> (2022). Accessed 10.02.2026.
7. Alhaji NB, Salihu A, Odetokun IA, Mohammed IG, Mellace M, Hassan MIA. Molecular epidemiological exploration of carbapenem-resistant *Enterobacteriaceae* in Africa from One Health perspective: A systematic review. One Health Microbiology & Infection. 2025;1(1):3-11.
8. van Duin D, Doi Y. The global epidemiology of carbapenemase-producing *Enterobacteriaceae*. Virulence. 2017;8(4):460-9. <https://doi.org/10.1080/21505594.2016.1222343>
9. Gupta N, Limbago BM, Patel JB, Kallen AJ. Carbapenem-resistant *Enterobacteriaceae*: Epidemiology and prevention. Clin Infect Dis. 2011;53(1):60-7. <https://doi.org/10.1093/cid/cir202>
10. Ramírez-Castillo FY, Guerrero-Barrera AL, Avelar-González FJ. An overview of carbapenem-resistant organisms from food-producing animals, seafood, aquaculture, companion animals, and wildlife. Front Vet Sci. 2023;10:1158588. <https://doi.org/10.3389/fvets.2023.1158588>
11. Sheppard AE, Stoesser N, Wilson DJ, Sebra R, Kasarskis A, Anson LW, et al. Nested Russian doll-like genetic mobility drives rapid dissemination of the carbapenem resistance gene *blaKPC*. Antimicrob Agents Chemother. 2016;60(6):3767-78. <https://doi.org/10.1128/aac.00464-16>
12. Elbehiry A, Marzouk E, Abalkhail A. Molecular insights into carbapenem resistance in *Klebsiella pneumoniae*: From mobile genetic elements to precision diagnostics and infection control. Int J Food Microbiol. 2026;27(3). <https://doi.org/10.3390/ijms27031229>
13. Dossouvi KM, Ametepe AS. Carbapenem resistance in animal-environment-food from Africa: A systematic review, recommendations and perspectives. Infect Drug Resist. 2024;17:1699-728. <https://doi.org/10.2147/idr.S458317>