

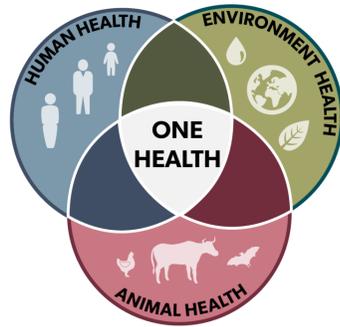
The Emergence of Carbapenem-Resistant Enterobacteriaceae from *Camelus dromedarius* in the UAE: the first report of blaNDM-positive *Escherichia coli*.

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INTRODUCTION

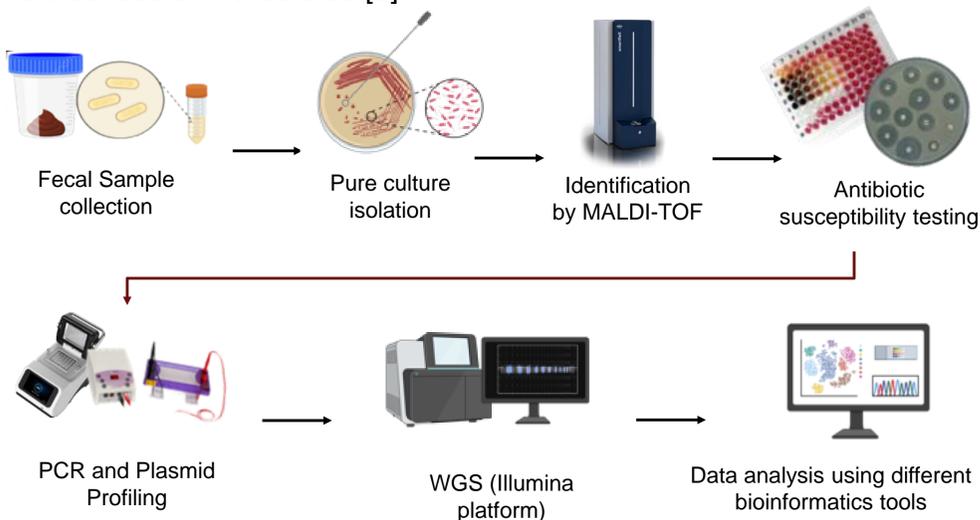
The rising prevalence of carbapenem-resistant Enterobacteriaceae across hospitals, communities, agriculture, animals, and the environment is a major concern, threatening the efficacy of last-resort antibiotics [1]. The primary mechanism behind carbapenem resistance is the production of carbapenemases, with *Klebsiella pneumoniae* carbapenemase (KPC) and New Delhi metallo-beta-lactamase (NDM) being the most encountered types [2].



The potential for CRE transmission from animals to humans represents a significant public health risk. In the UAE, camels play an essential cultural and economic role and may act as reservoirs for CRE. However, the extent of CRE carriage among farm animals in the UAE and neighboring Gulf Cooperation Council (GCC) countries remains largely unexplored.

METHODOLOGY

Fecal samples from 125 camels across different farms in Dubai were analyzed for the presence of carbapenem- and ESBL-producing Gram-negative bacilli using selective culture techniques. Antimicrobial susceptibility testing followed CLSI guidelines, and a multiplex PCR assay was employed to detect carbapenemase and ESBL genes. WGS provided detailed genetic profiles, including sequence types and global relatedness of the isolates [3].



CONCLUSION

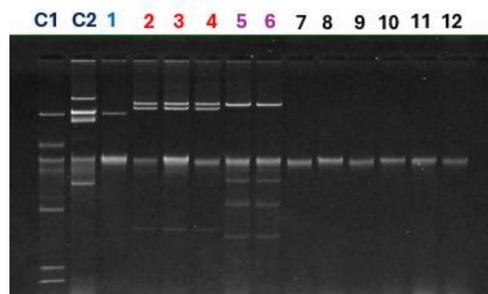
To the best of our knowledge, this is the first report of blaNDM-positive *E. coli* in camels in the UAE, indicating their potential role as reservoirs of antimicrobial-resistant bacteria, including CRE. The presence of blaNDM-harboring strains raises concerns about zoonotic transmission through direct contact or the food chain. These findings highlight the need for targeted surveillance and control measures to curb the spread of carbapenem- and multidrug-resistant bacteria in livestock.

REFERENCES

- [1] Patel G, Bonomo RA. "Stormy waters ahead": global emergence of carbapenemases. *Front Microbiol* 2013;4:48. doi: 10.3389/fmicb.2013.00048.
- [2] Suay-Garcia B, Perez-Gracia MT. Present and Future of Carbapenem-resistant Enterobacteriaceae (CRE) Infections. *Antibiotics* 2019;8(3):122. doi: 10.3390/antibiotics8030122
- [3] Ghazawi A, Strepis N, Anes F, Yaaqeib D, Ahmed A, AlHosani A, AlShehhi M, Manzoor A, Habib I, Wani NA, Hays JP. First Report of Colistin-Resistant *Escherichia coli* Carrying *mcr-1* IncI2 (delta) and *IncX4* Plasmids from Camels (*Camelus dromedarius*) in the Gulf Region. *Antibiotics*. 2024 Feb 28;13(3):227.

RESULTS

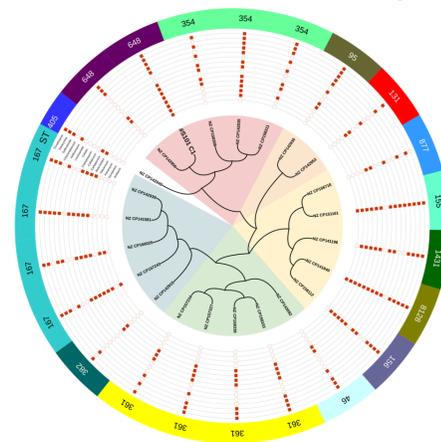
Carbapenem resistance was found in 32.8% (41/125) of the camels. The CR-*Escherichia coli* isolate carried the blaNDM gene, conferring carbapenem resistance, but lacked other tested carbapenemase genes. Antimicrobial susceptibility testing showed multidrug resistance (MDR) to multiple antibiotic classes.



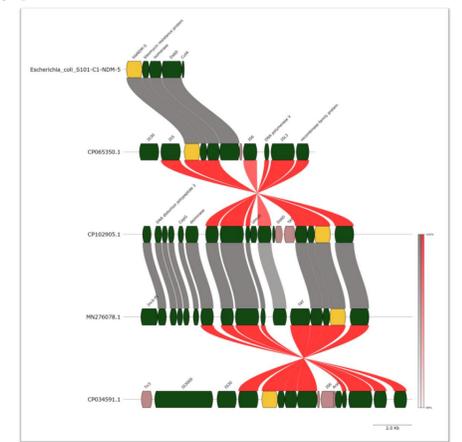
Plasmid profiling determined the number and size of various plasmids, facilitating bacterial typing. WGS was performed on representative isolates exhibiting distinct profiles.

	Ceftazidime	Ceftazidime/Avibactam	Cefotaxime	Aztreonam	Gentamicin	Amikacin	Meropenem	Imipenem	Tigecycline	Ciprofloxacin	Colistin
S101-C1	R	R	R	R	R	S	R	R	S	R	S
S101-E1	R	S	R	R	S	S	S	S	S	I	S
S101-E7	S	S	R	S	S	S	S	S	S	S	S
S101-E11	S	S	R	R	S	S	S	S	S	S	S

Antibiotic susceptibility profile of the strains



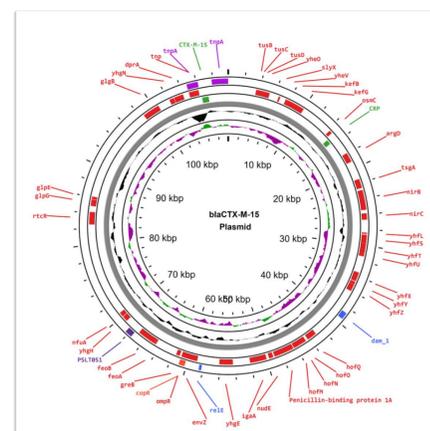
Phylogenetic tree of NDM-5



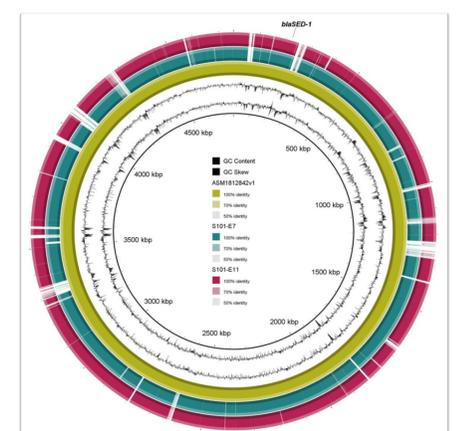
Genetic Context of blaNDM-5

NDM-5 Producing *E. coli* ST648 Complex

S101-C1 (ST648 complex): Displayed an extensive resistance profile, harboring blaNDM-5, blaCTX-M-15, blaOXA-1, blaTEM-1, and resistance genes for aminoglycosides (aac(6')-Ib-cr5, aadA5), sulfonamides (sul1), tetracyclines (tet(B)), and macrolides (mph(A)).



blaCTX-M-15 Plasmid



Citrobacter sedlakii

101-E1 (ST155 complex): Exhibited MDR, with resistance genes blaCTX-M-15, blaTEM-1, tet(A), qnrS1. Efflux-related genes (acrF/mdtM) were also present.

Citrobacter sedlakii - has gained attention due to its emerging role in AMR and its potential to cause opportunistic infections in hospitalized patients.