

Genomic Surveillance in a Low- or Middle-Income Country: Convergent Colistin Resistance in Epidemic *Klebsiella pneumoniae* (ST11, ST147) in Peshawar, Pakistan

Author: *Maria Khan¹

1. Pathology Department, Peshawar Institute of Cardiology-MTI, Pakistan

*Correspondence to kmaria22@hotmail.com

Disclosure: The author has declared no conflicts of interest.

Keywords: Colistin resistance, convergent resistance, genomic surveillance, *Klebsiella pneumoniae*, *mcr-8*, *mgrB* inactivation, Pakistan, sequence type 147 (ST147).

Citation: EMJ Microbiol Infect Dis. 2026;7[1]:42-43. <https://doi.org/10.33590/emjmicrobiolinfect-dis/IFQG8076>

BACKGROUND AND AIMS

The escalating crisis of antimicrobial resistance has positioned colistin as a 'last-resort' therapy for carbapenem-resistant *Klebsiella pneumoniae*.¹⁻⁵ However, in low- and middle-income countries like Pakistan, unregulated antibiotic use and high infection burdens have accelerated the emergence of colistin resistance. This study provides a critical genomic snapshot of the molecular mechanisms and clonal distribution of colistin-resistant isolates in a tertiary care setting in Peshawar, Pakistan.

MATERIALS AND METHODS

Between January 2024–December 2025, 250 clinical *K. pneumoniae* isolates were collected. Following species identification via matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry, colistin susceptibility was assessed using broth microdilution. Whole-genome sequencing was performed on 35 resistant isolates (14.0%) to characterise sequence types (ST), resistomes, and specific colistin resistance determinants, including chromosomal mutations (e.g., *mgrB*) and plasmid-mediated genes (e.g., *mcr-8*).

RESULTS

Genomic surveillance revealed a high-pressure resistance environment dominated by two international high-risk clones: ST11 (51.4%) and ST147 (20.0%). These lineages were predominantly associated with the carbapenemase gene *bla*_{NDM-1}, highlighting an extensively drug-resistant profile (Table 1).

Resistance was primarily driven by chromosomal alterations in 85.7% of isolates, with *mgrB* inactivation via insertion sequences (ISKpn26 and IS5-like) being the most prevalent mechanism. Plasmid-mediated resistance was identified in 14.3% of isolates, specifically the *mcr-8* gene within the ST147 lineage. Notably, the study documented a critical evolutionary milestone: convergent resistance. Three ST147 isolates simultaneously harboured both plasmid-borne *mcr-8* and chromosomal *mgrB* disruptions. This dual-mechanism profile resulted in significantly higher minimum inhibitory concentration values (90–128 mg/L) compared to isolates with single resistance determinants.

CONCLUSION

The findings underscore a shift toward pan-drug resistance in Pakistan's clinical settings. The convergence of independent resistance pathways within globally disseminated clones like ST147 poses a severe public health threat, as these strains are both highly fit and difficult to treat. The study advocates for an urgent expansion of regional genomic surveillance, stringent antimicrobial stewardship to preserve remaining polymyxins, and enhanced infection control protocols in high-risk units like the ICU to mitigate the spread of these 'super-clones'.

Table 1: Genomic epidemiology and resistance profiles of colistin-resistant *K. pneumoniae* isolates.

Category	Key findings	Data/mechanisms
Prevalence	Overall colistin resistance	14.0% (35/250 isolates)
Primary clones	Dominant sequence types	ST11 (51.4%) and ST147 (20.0%)
Chromosomal	Most frequent mechanism	<i>mgrB</i> inactivation (85.7% of resistant isolates)
Plasmid-mediated	Key resistance gene	<i>mcr-8</i> (found exclusively in ST147)
Convergent resistance	Combined mechanisms	<i>mgrB+mcr-8</i> (MIC 32–128 mg/L)
Associated AMR	Co-carried resistance	<i>bla_{NDM-1}</i> (carbapenemase), <i>bla_{CTX-M-15}</i>

AMR: antimicrobial resistance; MIC: minimum inhibitory concentration; ST: sequence type.

References

1. Khan M. Genomic surveillance in an LMIC: convergent colistin resistance in epidemic *Klebsiella pneumoniae* (ST11, ST147) in Peshawar, Pakistan. Abstract E0846. ESCMID Global, 17-21 April, 2026.
2. Li P et al. Convergence of carbapenem resistance and hypervirulence in a highly-transmissible ST11 clone of *K. pneumoniae*: an epidemiological, genomic and functional study. *Virulence*. 2021;12(1):377-88.
3. Farzana R. A genomic approach to understanding the molecular epidemiology and clinical burden of multi-drug resistant Enterobacterale Infections in Bangladesh. 2020. Available at: https://orca.cardiff.ac.uk/id/eprint/140464/5/Thesis_Farzana_R_200421.pdf. Last accessed: 9 April 2026.
4. Wang X et al. Emergence of colistin resistance gene *mcr-8* and its variant in *Raoultella ornithinolytica*. *Front Microbiol*. 2019;10:228.
5. Földes A et al. Characterization of carbapenemase-producing *Klebsiella pneumoniae* isolates from two Romanian hospitals co-presenting resistance and heteroresistance to colistin. *Antibiotics (Basel)*. 2022;11(9):1171.