Distribution of clbA Gene and Its Correlation with Antimicrobial Resistance Patterns in MDR *E. coli* From Diverse Host Groups

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Abstract

Introduction: Multidrug-resistant *(MDR) Escherichia coli* poses a significant threat to public health, particularly when harboring virulence genes such as *clbA,* which encodes the genotoxin colibactin. This study aimed to investigate the distribution of the *clbA* gene among MDR *E. coli* isolates from different host groups (normal individuals, cancer patients, and clinical patients) and to evaluate its association with antimicrobial resistance patterns.

Methods: A cross-sectional study was conducted over a twelve-month period (January 2024–December 2024) at Manmohan Memorial Institute of Health Sciences and its Teaching Hospital in Kathmandu, as well as at Capital Reference Laboratory in Bharatpur, Chitwan, Nepal. Samples were collected from diverse host groups and processed using standard microbiological techniques to isolate *E. coli.* The *clbA* gene was detected via PCR, and antimicrobial susceptibility was assessed using standard Kirby-Bauer disk diffusion method. Statistical analyses were performed to determine associations between *clbA* status, host group, and resistance profiles.

Results: The *clbA* gene was detected in 15 of 115 MDR *E. coli* isolates (13.0%), with a significantly higher prevalence in clinical patients (25.0%) compared to cancer patients (8.6%) and normal individuals (5.0%) ($p = 0.0105$). *clbA* positive isolates exhibited significantly higher resistance rates to key antibiotics, including imipenem (100% vs. 15.0%, $p = 0.003$), meropenem (100% vs. 12.5%, $p = 0.001$) and amikacin (100% vs. 10.0%, $p = 0.050$) compared to *clbA* negative isolates.

Conclusions: The presence of the *clbA* gene in MDR *E. coli* is significantly associated with enhanced resistance to multiple critical antibiotics, particularly among clinical patient isolates. These findings suggest a potential link between colibactin-producing *E. coli* and elevated antimicrobial resistance, highlighting the need for integrated surveillance and molecular monitoring strategies to better manage and contain these high-risk strains.

Keywords

Antimicrobial resistance, *clbA* gene, MDR *E. coli, v*irulence.