Genotypic to Phenotypic Resistance Discrepancies Identified Involving beta-Lactamase Genes, blaKPC, blaIMP, blaNDM-1, and blaVIM in Uropathogenic Klebsiella pneumoniae

By: Urmi, UL (Urmi, Umme Laila)[1]; Nahar, S (Nahar, Shamsun)[1]; Rana, M (Rana, Masud)[1]; Sultana, F (Sultana, Fahmida)[1]; Jahan, N (Jahan, Nusrat)[1]; Hossain, B (Hossain, Billal)[1]; Alam, M (Alam, Mohammed)[2]; Mosaddek, AM (Mosaddek, Abu Syed Md)[3]; McKimm, J (McKimm, Judy)[4]; Rahman, NAA (Rahman, Nor Azlina A.)[5] ...More

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Abstract

Introduction: Klebsiella pneumoniae carbapenemase (KPC) belongs to the Group-A beta-lactamases that incorporate serine at their active site and hydrolyze various penicillins, cephalosporins, and carbapenems. Metallo-beta-lactamases (MBLs) are group-B enzymes that contain one or two essential zinc ions in the active sites and hydrolyze almost all clinically available beta-lactam antibiotics. Klebsiella pneumoniae remains the pathogen with the most antimicrobial resistance to KPC and MBLs.

Methods: This research investigated the blaKPC, and MBL genes, namely, blaIMP, blaVIM, and blaNDM-1 and their phenotypic resistance to K. pneumoniae isolated from urinary tract infections (UTI) in Bangladesh. Isolated UTI K. pneumoniae were identified by API-20E and 16s rDNA gene analysis. Their phenotypic antimicrobial resistance was examined by the Kirby-Bauer disc diffusion method, followed by minimal inhibitory concentration (MIC) determination. blaKPC, blaIMP, blaNDM-1, and blaVIM genes were evaluated by polymerase chain reactions (PCR) and confirmed by sequencing.

Results: Fifty-eight K. pneumoniae were identified from 142 acute UTI cases. Their phenotypic resistance to amoxycillin-clavulanic acid, cephalexin, cefuroxime, ceftriaxone, and imipenem were 98.3%, 100%, 96.5%, 91.4%, 75.1%, respectively. Over half (31/58) of the isolates contained either blaKPC or one of the MBL genes. Individual prevalence of blaKPC, blaIMP, blaNDM-1, and blaVIM were 15.5% (9), 10.3% (6), 22.4% (13), and 19% (11), respectively. Of these, eight isolates (25.8%, 8/31) were found to have two genes in four different combinations. The co-existence of the ESBL genes generated more resistance than each one individually. Some isolates appeared phenotypically susceptible to imipenem in the presence of blaKPC, blaIMP, blaVIM, and blaNDM-1 genes, singly or in combination.

Conclusion: The discrepancy of genotype and phenotype resistance has significant consequences for clinical bacteriology, precision in diagnosis, the prudent selection of antimicrobials, and rational prescribing. Heterogeneous phenotypes of antimicrobial susceptibility testing should be taken seriously to avoid inappropriate diagnostic and therapeutic decisions.

Keywords

Author Keywords: Klebsiella pneumoniae; bla KPC; bla IMP; bla NDM-1; bla VIM; co-resistance; heteroresistance; urinary tract infections; Bangladesh

KeyWords Plus: URINARY-TRACT-INFECTIONS; FUNCTIONAL-ASPECTS; ESCHERICHIA-COLI; ENTEROBACTERIACEAE; EPIDEMIOLOGY; CARBAPENEMS; EMERGENCE; EVOLUTION; DIAGNOSIS; BACTERIA

Author Information

Reprint Address:

Jahangirnagar University Jahangirnagar Univ, Dept Microbiol, Dhaka 1342, Bangladesh.
Universiti Pertahanan Nasional Malaysia Natl Def Univ Malaysia, Fac Med & Def Hlth, Kuala Lumpur 57000, Malaysia.

Corresponding Address: Islam, S (corresponding author)

+ Jahangirnagar Univ, Dept Microbiol, Dhaka 1342, Bangladesh.

Corresponding Address: Haque, M (corresponding author)

+ Natl Def Univ Malaysia, Fac Med & Def Hlth, Kuala Lumpur 57000, Malaysia.