

Detection of carbapenemase genes in Gram negative bacterial isolates from patients with urinary tract infections

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Introduction and Objective: Carbapenem-resistant organisms (CROs) are of critical concern, complicating the treatment of urinary tract infections (UTIs). Therefore, this study aimed to determine the presence of carbapenemase genes among different bacterial species isolated from urine.

Methods: Urinary isolates confirmed as resistant and/or intermediate to meropenem and/or imipenem were collected from University Hospital, Kotelawala Defense University, Sri Lanka and Apeksha Hospital, Sri Lanka from January to December 2023. Ninety-seven isolates were collected and subjected to species-level identification by BD PhoenixTM automated system. PCR was performed to detect carbapenemase genes using Hi-PCR® carbapenemase (Multiplex) PCR kit (Catalogue no: MBPCR132). We identified eight carbapenemase genes; *bla*_{KPC}, *bla*_{NDM}, *bla*_{VIM}, *bla*_{IMP}, *bla*_{OXA-23}, *bla*_{OXA-48}, *bla*_{OXA-51}, and *bla*_{OXA-58}. Descriptive statistics were analysed by SPSS 25 software.

Results: Of 97 CROs, *Klebsiella pneumoniae* was the commonest species (34.0%). Seventy-two of 97 isolates (74.2%) were positive for at least one carbapenemase gene tested. A single gene was detected in 34 (35.1%) while two or more genes co-occurred in 38 (39.2%) of the isolates.

Table 1. Distribution of CROs and carbapenemase genes detected

CRO (n=97)	%	Single genes		Gene co-occurrences	
		Gene	n (%)	Gene combination	n (%)
<i>K. pneumoniae</i> (n=33)	34.0	<i>bla</i> _{OXA-48}	11 (33.3)	<i>bla</i> _{NDM} + <i>bla</i> _{OXA-48}	3 (9.1)
<i>P. aeruginosa</i> (n=6)	16.5	<i>bla</i> _{VIM}	4 (25.0)	<i>bla</i> _{NDM} + <i>bla</i> _{OXA-51} + <i>bla</i> _{OXA-58}	2 (12.5)
<i>E. coli</i> (n=5)	15.5	<i>bla</i> _{OXA-51} / <i>bla</i> _{OXA-58} (equal %)	8 (53.3)	<i>bla</i> _{OXA-51} + <i>bla</i> _{OXA-58}	2 (13.3)
<i>A. baumannii</i> / <i>calcoaceticus</i> complex (n=8)	8.2	<i>bla</i> _{OXA-51}	5 (62.5)	<i>bla</i> _{OXA-23} + <i>bla</i> _{OXA-51}	3 (37.5)
<i>A. baumannii</i> (n=6)	5.2	<i>bla</i> _{OXA-23} / <i>bla</i> _{OXA-51} (equal %)	3 (60.0)	<i>bla</i> _{OXA-23} + <i>bla</i> _{OXA-51}	3 (60.0)
Other GNB (n=20)	20.6	<i>bla</i> _{OXA-51}	7 (35.0)	<i>bla</i> _{NDM} + <i>bla</i> _{OXA-51} + <i>bla</i> _{OXA-58}	3 (15.0)

GNB – Gram negative bacteria

Overall, the highest gene occurrence was *bla*_{OXA-51} (n=46; 47.4%), followed by *bla*_{OXA-58} (n=40; 41.2%), *bla*_{OXA-23} (n=23; 23.7%), *bla*_{VIM} (n=17; 17.5%), *bla*_{OXA-48} (n=16; 16.5%), *bla*_{NDM} (n=9; 9.3%), *bla*_{IMP} (n=3; 3.1%) and *bla*_{KPC} (n=1; 1.0%). The highest gene diversity was observed in *K. pneumoniae*, including 11 gene combinations with a maximum of four co-existing genes (*bla*_{NDM}+*bla*_{IMP}+*bla*_{OXA-48}+*bla*_{OXA-51}, 3.0%; n=1). Table 1 shows the distribution of CRO species, and carbapenemase genes detected in the study sample.

Conclusions: A noteworthy diversity of carbapenemase genes were observed, with *K. pneumoniae* being the commonest species with a high variety of resistant genes. Continuous surveillance and implementation of targeted infection control and antibiotic stewardship programs are needed to mitigate further spread of carbapenemase genes.

Keywords: Carbapenem resistant organisms, carbapenemase genes, multiplex PCR, urinary tract infections, Sri Lanka

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