Original Article

Prevalence of MDR, XDR and PAN Drug-Resistant Organisms Isolated from Various Clinical Specimens from the Medicine Intensive Care Unit

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Abstract

Background: Antimicrobial resistance (AMR) is a critical global health threat, with multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) organisms increasingly reported from healthcare settings. Local epidemiological data are essential to guide empirical therapy and antimicrobial stewardship. The objective is to determine the prevalence and distribution of MDR, XDR, and PDR organisms isolated from various clinical specimens in a tertiary care hospital. **Material and Methods:** This cross-sectional study was conducted in the Department of Microbiology, Konaseema Institute of Medical Sciences, Amalapuram. Significant bacterial isolates from blood, urine, pus/wound swabs, respiratory secretions, and body fluids were included. Kirby performed antimicrobial susceptibility testing–Bauer disc diffusion and/or automated systems, interpreted according to CLSI guidelines. MDR, XDR, and PDR were defined per standard criteria that Magiorakos et al. proposed. Data were analysed using descriptive statistics. **Results:** A total of 1,250 clinically significant isolates were obtained. Gram-negative bacteria accounted for 68% and Gram-positive bacteria for 32%. The most frequent isolates were Escherichia coli (28%), Klebsiella pneumoniae (21%), and Staphylococcus aureus (15%). 58% were MDR, 16% XDR, and 1.2% PDR. MDR prevalence was highest in K. pneumoniae (68%) and Acinetobacter baumannii (65%), while XDR and PDR isolates were predominantly recovered from respiratory and bloodstream specimens. Among Gram-positive organisms, 47% of S. aureus isolates were MDR, primarily methicillin-resistant S. aureus (MRSA). **Conclusion:** A high prevalence of MDR and XDR organisms was observed, particularly among Gram-negative pathogens from critical specimens. Though infrequent, the emergence of PDR isolates is a cause for concern. These findings underscore the urgent need for continuous surveillance, robust antimicrobial stewardship, and strict infection-control measures to combat the threat of drug-resistant infections.

Keywords: Antimicrobial resistance, multidrug-resistant, extensively drug-resistant, pandrug-resistant, clinical isolates, prevalence.

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Introduction

Antimicrobial resistance (AMR) is increasingly recognised as one of the most urgent global health threats of the 21st century. The World Health Organisation (WHO) has identified AMR as a critical challenge due to its association with prolonged illness, escalating healthcare costs, and rising mortality worldwide.[1] A systematic global burden analysis further highlighted the magnitude of this problem, estimating that bacterial AMR was directly responsible for 1.27 million deaths and played a contributory role in nearly 5 million deaths in 2019.[2]

To ensure consistency in surveillance and reporting, international experts have proposed standardised definitions: multidrug-resistant (MDR) bacteria are resistant to at least one agent in three or more antimicrobial classes, extensively drug-resistant (XDR) strains are resistant to all but two or fewer categories, and pandrug-resistant (PDR) organisms exhibit resistance to all available agents.[3] These categories provide a uniform framework for assessing resistance trends and guiding treatment strategies.

Clinically, MDR and XDR organisms such as Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii, and methicillin-resistant Staphylococcus aureus (MRSA) are frequently recovered from blood, urine, respiratory secretions, and wound swabs.[4–6] Recent hospital-based investigations have reported alarmingly high prevalence rates of MDR and XDR isolates, with sporadic detection of PDR strains, particularly among Gram-negative pathogens.[7] These findings underscore AMR's escalating clinical and epidemiological burden in healthcare settings.

Given the regional variability in resistance patterns, continuous

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surveillance at the institutional level is vital to guide empirical therapy, antibiotic stewardship programs, and infection-prevention strategies.[8-12] This study was therefore undertaken to determine the prevalence of MDR, XDR, and PDR organisms isolated from various clinical specimens in our institution and to assess their distribution across bacterial species and specimen types.

Materials and Methods

Study design and setting: This cross-sectional study was conducted in the Department of Microbiology, Pharmacology and General Medicine, Konaseema Institute of Medical Sciences, Amalapuram. Andhra Pradesh, India, from December 2023 to August 2025. All clinically significant bacterial isolates obtained from various clinical specimens during the study were included. Duplicate isolates from the same patient and commensal contaminants were excluded.

Specimen collection and processing: Clinical specimens included blood, urine, pus/wound swabs, respiratory secretions (sputum, tracheal aspirates, bronchoalveolar lavage), body fluids (ascitic, pleural, cerebrospinal), and catheter tips submitted to the microbiology laboratory as part of routine diagnostic workup. Specimens were processed using standard microbiological procedures.[13,14] As per availability, bacterial isolates were identified by conventional biochemical methods and/or automated identification systems (e.g., VITEK 2, bioMérieux, France).

Antimicrobial susceptibility testing: Antimicrobial susceptibility was determined by the Kirby–Bauer disc diffusion method on Mueller–Hinton agar and/or automated systems, and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines, latest edition available at the time of the study (15), for specific agents (e.g., colistin, tigecycline), broth microdilution or automated minimum inhibitory concentration (MIC) testing was used, following CLSI recommendations. Escherichia coli ATCC 25922, Staphylococcus aureus ATCC 25923, and Pseudomonas aeruginosa ATCC 27853 were quality control strains.

Definitions of resistance categories

Standard definitions proposed by Magiorakos et al,[3] were used:

Multidrug-resistant (MDR): Non-susceptibility to at least one agent in three or more antimicrobial categories.

Extensively drug-resistant (XDR): Non-susceptibility to at least one agent in all but two or fewer categories (i.e., bacterial isolates remain susceptible to only one or two categories).

Pandrug-resistant (PDR): Non-susceptibility to all agents in all antimicrobial categories tested.

Data collection and analysis: Data on patient demographics, specimen type, bacterial species, and antimicrobial susceptibility were recorded. The prevalence of MDR, XDR, and PDR isolates was calculated overall and stratified by specimen type and organism. Statistical analysis was performed using [SPSS version 13]. Categorical data were expressed as percentages, and differences between groups were analysed using chi-square or Fisher's exact test, with $p < 0.05$ considered statistically significant.

Results

One thousand two hundred fifty clinical specimens yielded significant bacterial growth during the study period. The majority of isolates were recovered from urine (32%), pus/wound swabs (26%), respiratory samples (20%), blood (15%), and other body fluids (7%).

Distribution of bacterial isolates: Among the 1,250 isolates, Gram-negative bacteria constituted 68% and Gram-positive bacteria 32%. The most frequently isolated organisms were Escherichia coli (28%), Klebsiella pneumoniae (21%), Pseudomonas aeruginosa (12%), Acinetobacter baumannii (7%), Staphylococcus aureus (15%), and Enterococcus spp. (7%), and others (10%).

Table 1: Distribution of bacterial isolates by specimen type

Specimen type	Total isolates (n=1250)	Commonest isolates identified
Urine (n=400)	32%	E. coli, Enterococcus spp.
Pus/Wound swab (n=325)	26%	S. aureus, P. aeruginosa
Respiratory (n=250)	20%	K. pneumoniae, A. baumannii
Blood (n=190)	15%	K. pneumoniae, S. aureus
Body fluids (n=85)	7%	E. coli, K. pneumoniae
Total	1250	—

Prevalence of MDR, XDR and PDR organisms: Out of 1,250 isolates, 725 (58%) were classified as MDR, 195 (16%) as XDR, and 15 (1.2%) as PDR. Gram-negative organisms showed significantly higher XDR and PDR rates than Gram-positive organisms ($p < 0.05$).

Among Gram-negative bacilli, MDR prevalence was highest in K. pneumoniae (68%), followed by A. baumannii (65%), and P. aeruginosa (60%).

Among Gram-positive cocci, MDR was most frequent in MRSA (62%) and Enterococcus spp. (50%).

Table 2: Prevalence of MDR, XDR, and PDR among major bacterial species

Organism	Total isolates (n)	MDR n (%)	XDR n (%)	PDR n (%)
Escherichia coli	350	180 (51%)	30 (9%)	0 (0%)
Klebsiella pneumoniae	260	178 (68%)	52 (20%)	6 (2.3%)
Pseudomonas aeruginosa	150	90 (60%)	28 (19%)	3 (2.0%)
Acinetobacter baumannii	85	55 (65%)	20 (24%)	4 (4.7%)
Staphylococcus aureus	190	90 (47%)	15 (8%)	1 (0.5%)
Enterococcus spp.	90	45 (50%)	10 (11%)	1 (1.1%)

Others (n=125)	87 (69%)	40 (32%)	0 (0%)	
Total (n=1250)	725 (58%)	195 (16%)	15 (1.2%)	

Specimen-wise resistance pattern: MDR organisms were most frequently isolated from pus/wound swabs (64%) and respiratory samples (61%), while XDR and PDR isolates were predominantly recovered from respiratory and blood specimens.

Table 3. Specimen-wise distribution of MDR, XDR, and PDR isolates

Specimen type	Total isolates	MDR n (%)	XDR n (%)	PDR n (%)
Urine (n=400)	210 (53%)	25 (6%)	0 (0%)	
Pus/Wound (n=325)	210 (64%)	32 (10%)	2 (0.6%)	
Respiratory (n=250)	152 (61%)	60 (24%)	7 (2.8%)	
Blood (n=190)	115 (61%)	40 (21%)	4 (2.1%)	
Body fluids (n=85)	38 (45%)	12 (14%)	2 (2.3%)	
Total (n=1250)	725 (58%)	195 (16%)	15 (1.2%)	

Discussion

In this study, we observed a high prevalence of multidrug-resistant (MDR) organisms (58%), with a significant proportion of isolates categorised as extensively drug-resistant (XDR, 16%) and a small but concerning percentage as pandrug-resistant (PDR, 1.2%). These findings underscore the escalating global challenge of antimicrobial resistance and emphasise the urgent need for robust antimicrobial stewardship and stringent infection-control practices.[8,9]

Comparison with other studies: The MDR prevalence identified in our cohort is consistent with previous hospital-based reports from South Asia and beyond. Abbas et al,[8] documented an XDR prevalence of 12% in a Pakistani tertiary care centre, while Cosgrove,[9] highlighted the substantial impact of AMR on mortality, hospital stay, and healthcare costs. Kumarasamy et al,[10] described the emergence of New Delhi metallo-β-lactamase (NDM-1), reinforcing concerns about transferable carbapenem resistance across India, Pakistan, and the UK. Laxminarayan et al,[11] emphasised the need for global solutions to curb AMR, while early WHO surveillance data from Africa by Tornimbene et al,[12] confirmed the widespread and growing nature of resistance.

Our observed XDR prevalence (16%) aligns with multicentric European surveillance studies, where Klebsiella pneumoniae and Acinetobacter baumannii showed MDR rates above 50%.[14,16] Humphries et al,[15] stressed the importance of evolving CLSI standards for resistance detection, and Peñalva et al,[16] demonstrated the feasibility of quarterly AMR surveillance across multiple European nations.

Though limited (1.2%), the detection of PDR isolates is worrisome. Prior reports from India (Gandra et al,[17]) and Egypt (Ramadan et al,[18]) have described sporadic PDR emergence in Acinetobacter baumannii and Pseudomonas aeruginosa, mirroring our results.

Species-wise resistance: Species-specific analysis revealed that K. pneumoniae and A. baumannii carried the highest MDR/XDR burden, consistent with previous studies.[18,19] Pseudomonas aeruginosa showed significant resistance, particularly in respiratory isolates, likely due to selective pressure from prolonged antibiotic exposure and invasive ventilation.[8,20,21] Among Gram-positive organisms, methicillin-resistant Staphylococcus aureus (MRSA) remained an important contributor, with nearly half of isolates resistant, consistent with the 40–60% prevalence reported across Asia,[22] Although less frequent, vancomycin-resistant Enterococcus (VRE) remained clinically important, with 11% showing XDR profiles.

Specimen-wise trends: Resistance patterns varied by specimen type, with respiratory samples and blood cultures harbouring the highest proportions of XDR and PDR isolates. This aligns with global evidence linking invasive infections such as pneumonia and bloodstream infections with greater resistance, largely due to heavy broad-spectrum antimicrobial use in critical care.[11,21]

Clinical implications: The high burden of MDR and XDR organisms complicates empirical therapy, often necessitating the use of last-resort agents such as colistin, tigecycline, or combination therapy. This not only escalates treatment costs but also increases toxicity risks.[22] The emergence of PDR isolates underscores the urgent need for novel antimicrobials, rapid diagnostic tools, and stringent antimicrobial stewardship interventions.

Limitations: Our study was single-centred and may not reflect community-level resistance patterns. Automated susceptibility testing was not uniformly available for all agents, which may have limited exact categorisation in some cases. Nevertheless, the study provides valuable local data for guiding empirical therapy and stewardship efforts.

Conclusion

The prevalence of MDR, XDR, and PDR organisms in our institution is high, particularly among Gram-negative pathogens isolated from respiratory and bloodstream specimens. These findings emphasise the urgent need for hospital-based surveillance, rational antibiotic use, and effective infection-control strategies to curb the spread of resistant pathogens.

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Conflicts of interest

There are no conflicts of interest.

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