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Original Article

STUDY OF MULTIDRUG-RESISTANT GRAM-NEGATIVE BACILLI IN URINARY TRACT INFECTIONS AND THEIR ANTIBIOGRAM AT A TERTIARY CARE HOSPITAL

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ABSTRACT

Objective: To study the frequency of multidrug-resistant Gram-negative bacilli in urinary tract infections and antibiotic susceptibility pattern of multidrug-resistant Gram-negative bacilli in urinary tract infections.

Methods: This study was conducted on urine samples received at the Department of Microbiology, Andhra Medical College, for a period of six months from August 2022 to January 2023. During the study period, a total of 3361 urine samples were processed and conventional microbiological techniques were used to isolate uropathogens. Antibiotic susceptibility was tested by the Kirby-Bauer Disc diffusion method and interpreted according to Central Laboratory Standard Institute (CLSI) guidelines 2022. Multidrug-resistant bacilli in this study were defined as Gram-negative bacilli that were resistant to at least one agent in three or more antibiotic classes.

Results: Out of 3361 urine samples received from outpatient and inpatient departments of our hospital, 858 samples were culture positive-839 were Gram-negative isolates and 19 were Gram-positive isolates. Mean age was 40-60 y. Urinary tract infections were more common in females than males. Among Gram-negative bacilli isolated, *Escherichia coli* was the most common organism isolated-435(50.69%), followed by *Klebsiella species*-232(27.03%), *Acinetobacter species*-105(12.25%), *Pseudomonas species*-55(6.41%), *Proteus species*-10(1.16%), *Citrobacter species*-2(0.23%). Among Gram-positive cocci, *Staphylococci*-17(1.98%) and *Enterococci*-2(0.23%) were isolated. Out of 858 isolates, 177 (20.62%) were identified as multidrug-resistant bacilli and all were resistant to the drug groups Cephalosporins, Carbapenems and Quinolones. Most of the Multidrug-resistant gram-negative bacilli were sensitive to Fosfomycin and Nitrofurantoin.

Conclusion: Multidrug-resistant Gram-negative bacilli in urinary tract infections have become a major health problem. Assessment of Risk factors, Surveillance of Resistance patterns and policies for proper use of antibiotics are urgently needed.

Keywords: Urine, Infections, Isolates, Antibiotics, Multidrug resistance

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INTRODUCTION

Urinary tract infection (UTI) refers to microbial invasion of the urinary tract by one or more uropathogenic bacteria species, leading to significant bacteriuria and the presence of symptoms such as dysuria. Two main types of UTIs are known based on how the infection is acquired: hospital-acquired UTI (Nosocomial UTI) and community-acquired UTI [1]. *Escherichia coli* is the commonest cause of both community and hospital acquired UTI. Other common uropathogens encountered in community acquired UTI include *Klebsiella species, Acinetobacter species, Pseudomonas species* and *Citrobacter species.* Incidence of UTIs in adult females is more likely than in men [2].

Urinary tract infections are one of the most frequently occurring infections, the majority of which are caused by multidrug-resistant uropathogens [3].

Urinary tract infection is defined as the invasion of pathogens to the urinary tract tissues extending from the normal cortex to the urethra, which includes the prostate, urinary bladder, kidney can occur in both the lower part (cystitis) and the upper part (pyelonephritis)of the urinary tract and also varies according to age and sex [4, 5].

The increase in multidrug resistance among uropathogens is a global health problem. For the empirical treatment of urinary tract infections, it is highly important to have knowledge about the etiological agents of urinary tract infections and also about the susceptibility to commonly prescribed antibiotics. The present study is aimed to find out the bacterial uropathogens responsible for urinary tract infections and determine the antibiotic susceptibility pattern of the selected urinary cultures, which may help the clinician to choose the right empirical treatment [6].

Urinary tract infections are an important cause of illness in humans. While all portions of urinary tract may be affected, most common urinary tract infections are those of bladder(cystitis) and renal pelvis or kidneys (pyelonephritis). Urinary tract infection is the most common cause of both community-acquired and nosocomial infections. The isolates which are resistant to atleast one drug in three or more classes of antibiotics are classified as multidrug-resistant [7]. This study determines the frequency of multidrug-resistant Gram-negative bacilli in urinary tract infections and antibiotic susceptibility patterns of multidrug-resistant Gram-negative bacilli.

MATERIALS AND METHODS

This study was conducted on urine samples received in the Department of Microbiology, Andhra Medical College, for a period of six months from August 2022 to January 2023. During the study period, a total of 3361 urine samples were processed and conventional microbiological techniques were used to isolate uropathogens. Antibiotic susceptibility was tested by the Kirby-Bauer Disc diffusion method and interpreted according to Central Laboratory Standard Institute (CLSI) guidelines 2022. Multidrug-resistant bacilli in this study were defined as Gram-negative bacilli that were resistant to at least one agent in three or more antibiotic classes.

RESULTS

Out of 3361 urine samples received from outpatient and inpatient departments of our hospital, 858 samples (25%) were culture positive-839 were Gram-negative isolates and 19 were Gram-positive isolates and 2503 samples (75%) were culture-negative. Mean age was 40-60 y. Urinary tract infections were more common in females (60%) than males (40%). Among Gram-negative bacilli isolated, *Escherichia coli* was the most common organism isolated, followed by *klebsiella species*, *Acinetobacter species, Pseudomonas* *species, Proteus species and Citrobacter species* were isolated. In this study, *Escherichia coli* was the most common organism isolated-435(50.69%), followed by *Klebsiella species*-232(27.03%), *Acinetobacter species*-105(12.25%), *Pseudomonas species*-55(6.41%), *Proteus species*-10(1.16%), *Citrobacter species*-2(0.23%) (table 1).

Table 1: No. of isolates and percentage of isolates in the study (n=858)

S. No.	Isolates	No. of Isolates	%
1	*Escherichia coli*	435	50.69
2	*Klebsiella spp*	232	27.03
3	*Acinetobacter spp*	105	12.25
4	*Pseudomonas spp*	55	6.41
5	*Proteus spp*	10	1.16
6	*Citrobacter spp*	2	0.23
7	*Staphylococcus aureus*	17	1.98
8	*Enterococcus*	2	0.23
	Total	858	

Multidrug-resistant isolates in this study, *Escherichia coli*-97(54.8%), followed by *Klebsiella species*-54(30.5), *Acinetobacter species*-13(7.3), *Pseudomonas species*-7(4%), *Proteus species*–5(2.8%), *Citrobacter species*-1(0.56%) *(fig. 1).*

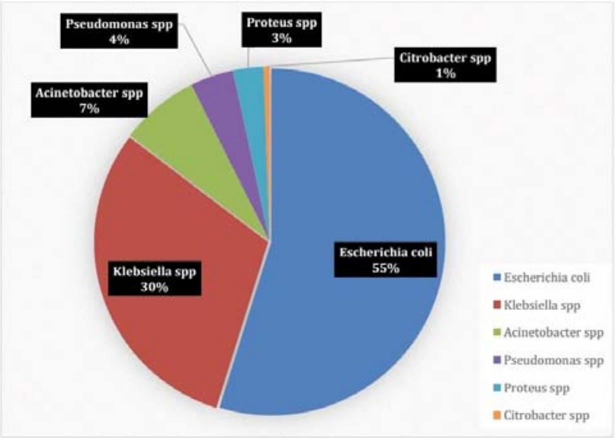

Fig. 1: Showing no. of multidrug-resistant gram-negative bacilli and their percentage (n=839)

Out of 839 Gram-negative isolates,177 (20.62%) were identified as multidrug-resistant bacilli and all were resistant to the drug groups Cephalosporins, Carbapenems and Quinolones. Most of the Multidrug-resistant Gram-negative bacilli were sensitive to Fosfomycin and Nitrofurantoin. Multidrug-resistant strains were highly resistant to Cephalosporins, Quinolones and Carbapenems. Carbapenems-Imipenem and Meropenem, Cephalosporins-Ceftazidime, Cefixime, Ceftriaxone and Ceftazidime+Clavulonicacid. Quinolones-Ciprofloxacin, Norfloxacin, Nalidixic acid, Ofloxacin and Levofloxacin.

DISCUSSION

In this study, 858 samples were culture positive-839 were Gram-negative isolates and 19 were Gram-positive isolates. In this study, *Escherichia coli* was the most common organism isolated-435(50.69%), followed by *Klebsiella species*-232(27.03%), *Acinetobacter species*-105(12.25%), *Pseudomonas species*-55(6.41%), *Proteus species*-10(1.16%), *Citrobacter species*-2(0.23%).

According to Mitesh. H. Patel *et al.* [8], *Escherichia coli*-35.98%, followed by *Klebsiella species*-21.95%, *Acinetobacter species*-9.15%, *Pseudomonas species*-19.51%, *Proteus species*-10.98%, *Citrobacter species*-0.61%. According to A. Dablool *et al.* [9], *Escherichia coli*-44%, *Klebsiella species*-20%, *Pseudomonas species*-6%, *Proteus species*-1%. According to Abha Sharma *et al.* [10], *Escherichia coli*-52%, *Klebsiella species*-17.6, *Pseudomonas species*-12.9% (table 2).

Table 2: Comparative study of the isolates (n=858)

Comparative study	This study (%)	Mites. H. Patel *et al.* (%)	A. Dablool *et al.* (%)	Abha Sharma *et al.* (%)
Escherichia coli spp	50.69	35.98	44	52
Klebsiella spp	27.03	21.95	20	17.6
Acinetobacter spp	12.25	9.15	-	-
Pseudomonas Spp	6.41	19.51	6	12.9
Proteus spp	1.16	10.98	1	-
citrobacter spp	0.23	0.61	-	-
Staphylococcus	1.98	-	5.5	-

CONCLUSION

Multidrug-resistant urinary tract infections have become a major health problem. The current study revealed that multidrug-resistant cases are increasing continuously. Healthcare professionals need to be aware of the current situation of antibiotic resistance and focus on prescribing antibiotics after obtaining culture and sensitivity reports. Assessment of Risk factors, Surveillance of Resistance patterns and policies for proper choice of antibiotics can prevent the emergence of multidrug-resistant uropathogens.

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AUTHORS CONTRIBUTIONS

First author of the study Dr. P. Suneetha, contributed conceptual design, literature search, and collected the data. The second and third authors contributed data analysis statistical analysis and wrote the first draft of the manuscript. The fourth author guided in the literature review. The fifth and sixth authors corrected the final draft of the manuscript.

CONFLICTS OF INTERESTS

The study declared 'no conflicts of interest

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