e- ISSN - 2348-2184 Print ISSN - 2348-2176



AMERICAN JOURNAL OF BIOLOGICAL AND PHARMACEUTICAL RESEARCH



Journal homepage: www.mcmed.us/journal/ajbpr

GEOGRAPHICAL DISPARITIES IN ANTIBIOTIC SUSCEPTIBILITY PATTERNS OF UROPATHOGENS: A CROSS-SECTIONAL STUDY ON URINARY TRACT INFECTIONS

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Article Info	ABSTRACT
Received 29/05/2020	This research delves into the diverse microbial infections affecting the urinary tract,
Revised 16/06/2020	encompassing urethral, kidney, and bladder infections. UTIs, prevalent across all age
Accepted 25/06/2020	groups, pose significant mortality risks. While bacteria predominantly cause UTIs, the role
	of viruses, fungi, and parasites cannot be overlooked. The use of different antibiotics in
Key words: -	community and hospital settings influences uropathogen prevalence. This study
Urinary tract infections,	investigates potential disparities in antibiotic susceptibility patterns among uropathogens in
Uropathogens,	rural and urban areas. Conducted as observational cross-sectional research, 690 clean-catch
Antibiotic	midstream urine samples from clinically suspected UTI cases were examined. A
susceptibility,	KirbyBauer disc diffusion method assessed antibiotic susceptibility, guided by CLSI
Microbial prevalence,	protocols. UTIs exhibited a wide array of isolates, including Escherichia coli, Klebsiella
Empirical antibiotic	spp., Enterococcus faecalis, Staphylococcus aureus, and Enterococcus niger. Given the
therapy.	variation in bacterial uropathogen prevalence and antibiotic sensitivity across locations and
	over time, accurate UTI diagnosis relies on clinical signs, symptoms, positive urine culture,
	and uropathogen-specific antibiotic susceptibility. Initiation of empirical antibiotic therapy
	without such knowledge may prolong disease, lead to complications, and contribute to
	multidrug resistance development.

INTRODUCTION

It affects all age groups, including neonates, geriatrics, all races, ethnicities, and both sexes. Urinary tract infections (UTIs) have become one of the most prevalent microbial disorders in human history. There are nearly 150 million people around the world who are affected by these conditions each year, resulting in more than 7 million medical visits and more than 100,000 hospitalizations annually, which may involve part of the urinary tract from the urethra to the kidneys [1-3].

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A UTI is classified as complicated if there is anatomical or functional abnormality in the urinary tract, or if catheterization is involved, and uncomplicated if there is no abnormality in the urinary tract [4].

A UTI can either be communityacquired or hospitalacquired, depending on the settings in which it originates. Communityacquired UTI occurs within the first 48 hours of hospitalization [5].

UTIs are caused by a wide range of microorganisms, including viruses, fungi, and parasites, however, 90% of these infections are caused by Gramnegative bacteria such as Escherichia coli, Klebsiella spp, Proteus spp, Pseudomonas aeruginosa, and Acinetobacter spp., and 10% by Grampositive bacteria such as



Enterococcus spp., Staphylococcus aureus, and coagulasenegative Staphylococcus aureus [6,7]. Clinical symptoms such as burning micturition, dysuria,

Clinical symptoms such as burning micturition, dysuria, suprapubic pain, pyuria, etc., can be analyzed to diagnose UTIs, as can laboratory tests [8].

A variety of factors contribute to differences in the prevalence of uropathogens associated with UTIs, including demographic features, hospitalization and communitybased settings, and antibiotic use [9].

To know the prevalence of uropathogens in UTI cases and antibiotic susceptibility patterns, this study was conducted at our institution to create a database of reference for rural areas with a population of 1.5 lakh to control and manage UTI cases. As there is little knowledge of uropathogens and their antibiotic susceptibility pattern in our area, empirical therapy with broadspectrum antibiotics may lead to the emergence of antimicrobial resistance (AMR), leading to a negative outcome and serious clinical complications in such patients after antibiotic therapy.

Materials and Method

In the Department of Microbiology, the present study was conducted in the Bacteriology Laboratory. There were 690 cleancatch midstream urine samples from clinically suspected cases of UTI collected from various clinical departments in the attached tertiary care hospital, which were received in sterile universal containers from the outpatient and inpatient facilities. As soon as they were collected, they were processed within 2 hours and stored for up to 6 hours in a refrigerator at 28°C.

The wet film preparations were prepared with 50 ml of wellmixed uncentrifuged urine for all samples, and after placing a coverslip, it was examined with a high-power microscope to observe the presence of microorganisms, pus cells, epithelial cells, etc [10].

On Cysteine Lactose Electrolyte Deficient Agar (CLED agar), samples were plated, and isolation was performed using surface streaks and calibrated loop techniques for semiquantitative methods. Incubated aerobically at 35-37°C for 24 hours, negative cultures were incubated for another 24 hours [11]. The presence of more than 105 cfu/ml of urine (significant bacteriuria) was considered significant for pure growth of an isolate in culture media.

Gram stain and conventional biochemical tests were used to identify the isolates from cases of significant bacteriuria [12]. The antibiotic sensitivity of all isolates was tested by the KirbyBauer disk diffusion method using broth culture inoculums with turbidity equivalent to Mc Farland 0.5 standard and lawn culture on Müller Hintonagar and allowed to dry for 24 hours. By using sterile forceps, the antibiotic discs were placed on top of the surface and incubated overnight, and the results were interpreted according to CLSI guidelines [13].

RESULTS

A total of 690 nonduplicate cleancatch midstream urine samples from OPDs and IPDs of different clinical departments from the attached tertiary care hospital at our institute have been submitted to the bacteriology laboratory in the department of microbiology from suspected UTI cases. A semiquantitative standard loop test was used to assess 204 samples (29.63%) with significant bacteriuria (105 cfu/ml), and the remaining samples were either sterile or did not show significant bacteriuria.

Table 1: The number of urina	ry samples analysed o	luring the study
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No. of samples	No. of culture positive isolates
690	204 (23.65%)

Table 2: Graph illustrating the gender-based distribution of culture positivity

Gender	No. of isolates	Percentage (%)
Female	130	64
Male	74	36
Total	204	100

Table 3: Isolation Frequency for Bacteria

Isolates	No. of isolates	Percentage (%)
Gram negative	176	86.48
Gram positive	28	13.52
Total	204	100

Table 4: A study showing bacterial isolates in cases of UTI

Organism	Isolates (%)
Escherichia coli	114 (56.02)
Klebsiella spp	34 (16.95)

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Enterococcus faecalis	22 (10.81)
Pseudomonas aeruginosa	17 (8.35)
Enterobacter spp	9 (4.42)
Staphylococcus aureus	5 (2.7)
Proteus mirabilis	1 (0.25)
Citrobacter freundii	1 (0.25)
Acinetobacter baumannii	1 (0.25)

Table 5: Indicating the antibiotic susceptibility pattern of gram-negative bacteria (%)

Organism (total isolates)	AMC	AMP	AK	GEN	NX	СОТ	NIT
E. coli	94 (41.66)	32 (13.59)	180 (83.33)	165 (72.80)	74 (32.01)	116 (50.43)	193 (84.21)
Klebsiella spp	21 (28.98)	-	62 (92.75)	62 (86.95)	33 (46.37)	33 (46.37)	44 (62.31)
Pseudomonas aeruginosa	-	-	21 (58.82)	19 (52.94)	18 (50)	-	7 (17.64)
Enterobacter spp.	-	-	17 (88.88)	16 (83.33)	9 (44.44)	9 (44.44)	-
Acinetobacter baumannii	-	-	1 (100)	1 (100)	1 (100)	0 (0)	0 (0)
Proteus mirabilis	0 (0)	0 (0)	0 (0)	1 (100)	1 (100)	0 (0)	-
Citrobacter freundii	-	-	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)

Table 6: The pattern of antibiotic susceptibility of gram-negative bacteria (%) was shown to continue

Organism	PB	MRP	IPM	PIT	CFS	CTR	CAZ
(total isolates)							
E. coli	114(100)	106 (92.98)	87 (75.87)	78 (67.98)	64 (56.14)	32 (27.26)	32 (27.26)
Klebsiella spp	35 (100)	26 (73.91)	23 (66.66)	17 (49.27)	17 (49.27	12 (34.78)	13 (36.23)
Pseudomonas aeruginosa	15 (85.29)	12 (67.64)	9 (50)	11 (64.70)	7 (41.17)	-	6 (35.29)
Enterobacter spp	9(100)	7 (72.22)	6 (66.66)	5 (50)	8 (50)	4 (44.44)	4 (44.44)
Acinetobacter baumannii	1 (100)	1 (100)	1 (100)	0 (0)	1 (100)	0 (0)	0 (0)
Proteus mirabilis	-	1 (100)	0 (0)	1 (100)	1 (100)	0 (0)	0 (0)
Citrobacter freundii	1 (100)	0 (0)	0 (0)	0 (0)	-	-	-

Table 7: A comparison of antibiotic susceptibility patterns among gram-positive bacteria (%)

Organism (total isolates)	IPM	PIT	CFS	CTR	AMC	AMP	GEN	NX
Staphylococcus aureus	-	-	2 (37.33)	2 (37.33)	2 (37.33)	-	3 (46.45)	1 (19.18)
Enterococcus faecalis	10 (44.45)	12 (48.72)	-	-	-	10 (46.45)	-	4 (19.18)

Table 8: A pattern of antibiotic susceptibility was observed for gram-positive bacterial isolates (%)

Organism (total	СОТ	NIT	LZ	VA	CX	Р	Е	Т	CD
isolates)									
Staphylococcus	3 (53.42)	3 (53.42)	6 (100)	6 (100)	2 (37.29)	1 (19.26)	2 (28.34)	3 (44.39)	3 (44.39)
aureus									
Enterococcus	2 (8.87)	11 (50)	22 (100)	17	-	9 (37.87)	2 (8.86)	5 (21.81)	-
faecalis				(76.94)					

DISCUSSION

Depending on the location, the demography, the type of infection (community or hospital acquired), and the type of antibiotic used in various hospital settings without a pre-test, urinary tract infections are one of the most common infections in medical practice. Despite advances in treatment, antibiotic policy still affects all age groups of the population, even with adequate preventative measures and adequate precautions. It is a common infection both in hospital and outpatient settings. There are several microorganisms responsible for UTIs, but bacteria cause the majority of infections. At our institution, we conducted the present study to determine the prevalence of uropathogens and the antibiotic susceptibility patterns of these pathogens, which vary from place to place. In order to treat patients with bacterial UTIs properly, the infecting pathogen and their antibiotic susceptibility pattern must be considered.

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In the present study, a total of 690 midstream urinary samples from suspected cases of UTI received from various departments of our attached hospital have been processed according to standard protocol and guidelines wherein these samples 407 (29.53%) were culture positive isolates satisfying the Kass concept which were further processed for their identification and antibiotic susceptibility pattern. [14] In correlation with this finding, 130 of the isolates came from female patients, while 78 came from male patients [15-17]. A total of 208 bacteria were isolated, including 126 Gram-negative bacteria which cause UTIs, and 28 Grampositive bacteria which correlate with UTIs. The majority of Gram-negative isolates were Escherichia coli, followed by Klebsiella, Pseudomonas aeruginosa, Enterobacter, Proteus mirabilis, Citrobacter freundii, Acinetobacter baumannii, and Grampositive isolates. The most prevalent Grampositive isolate was Enterococcus faecalis, followed by Staphylococcus aureus.

Amikacin, meropenem, nitrofurantoin, and amikacin showed the highest antibiotic susceptibility pattern in Escherichia coli isolates, followed by polymyxinB, nitrofurantoin, and meropenem. Among the antibiotics most susceptible to norfloxacin, ceftriaxone, and ceftazidime were amikacin, gentamicin, meropenem, and norfloxacin, co-trimoxazole, ceftazidime and ceftriaxone were the least susceptible.

Grampositive isolates of Enterococcus faecalis were most susceptible to linezolid; other drugs most susceptible were vancomycin, nitrofurantoin, piperacillintazobactam, imipenem, penicillin, tetracycline, norfloxacin, erythromycin and cotrimoxazole. According to our study, Staphylococcus aureus isolates were most sensitive to vancomycin, linezolid, and cotrimoxazole; least sensitive to erythromycin, penicillin, and norfloxacin.

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