Original Research Article

Spectrum of Bacterial Pathogen and its Antimicrobial Resistance Pattern in Urinary Tract Infection in Western Gujarat

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ABSTRACT

Background

Urinary Tract Infection (UTI) is the most common bacterial infection in human and is one of the most frequently occurring hospital acquired infections. UTIs refer to the presence of microbial pathogens within the urinary tract and it is usually classified by the site of infection as bladder (cystitis), kidney (pyelonephritis) or urine (bacteriuria). Aim of this study was to determine the spectrum of bacteriological pathogens responsible for UTI and to assess the antibiotic resistance pattern of the causative uropathogens.

Material & Methods

A cross sectional study was performed on 393 urine samples from July 2021 to July 2022 to investigate symptomatic patients of UTI among patients attending Gujarat Adani Institute of Medical Sciences medical college (GAIMS), Bhuj-Kutch, Gujarat, India. All urine samples were processed by standard semi-quantitative culture method and sensitivity by Kirby Bauer disk diffusion method. Results of sensitivity testing were interpreted as per CLSI guidelines.

Results

Out of 118 positive culture samples, Escherichia coli is the most prevalent organism with 47.45%, followed by Klebsiella pneumoniae (18.64%), Enterococcus spp.(15.25%), Pseudomonas aeruginosa (5.08%), Staphylococcus aureus (3.38%), Proteus mirabilis (5.08%), Acinetobacter spp.(5.08%). Study shows higher resistance towards beta lactam group of drugs however less resistant to aminoglycoside group of drugs.

Conclusion

Most common organism in this study was E.coli. Current study we observed a generalized drug resistance to commonly used antibiotics. To prevent further drug resistance, strict implementation of antibiotic policy, awareness regarding judicial use of antimicrobial in medical, para medical and general population is a need of the time.

Keywords: UTI- Urinary tract infection, Semi quantitative culture for UTI, Spectrum of pathogen in UTI, Antibiogram of pathogens isolated from UTI

INTRODUCTION

Urinary Tract Infection (UTI) is the most common bacterial infection in human and is one of the most frequently occurring hospital acquired infections. UTIs refer to the presence of microbial pathogens within the urinary tract and it is usually classified by the site of infection as bladder (cystitis), kidney (pyelonephritis) or urine (bacteriuria). UTIs that occur in a normal genitourinary tract with no prior instrumentation are considered as "uncomplicated", whereas "complicated" infections are diagnosed in genitourinary tracts that have abnormalities structural or functional including instrumentation such as indwelling urethral catheters, and are frequently asymptomatic. ^[1,2] UTI more commonly ascending infection than descending.

Many different microorganisms can cause UTIs though the most common pathogens causing the simple ones in the community are Escherichia coli and other Enterobacteriacae, which accounts for approximately 75% of the isolates. ^[3]

Detection of UTI causing pathogens and analysing resistance pattern of these pathogens to commonly prescribed antibiotics in the clinical practice is essential and helpful in improving the efficacy of empirical treatment^[2]

UTI caused by multidrug-resistant (MDR) E. coli increases the cost of treatment, morbidity, and mortality, especially in developing countries like India.^[4,5]

Common pathogen responsible for UTI and their antimicrobial resistant pattern also vary in different hospital and in different geographical area. There is no systemic study done in this geographical area pertaining to UTI and resistance pattern of uropathogen. Hence this study was conducted with aim to study the spectrum of bacteriological pathogen in UTI and their antibiotic resistance pattern. Objectives were to determine the spectrum of bacteriological pathogens responsible for UTI and to assess the antibiotic resistance pattern of the causative uropathogens.

METHODOLOGY

Cross sectional study was performed from July 2021 to July 2022 to investigate symptomatic patients of UTI among patients attending Gujarat Adani Institute of Medical sciences medical college (GAIMS), Bhuj-Kutch, Gujarat, India.

Total 393 urine samples were collected from patients having signs and symptoms of urinary tract infection as per standard collection methods of mid-stream clean catch urine or from catheter clamping. Patient's demographic 25 details and brief clinical history noted. Samples were immediately transported to Microbiology department, GAIMS. Measured amount of urine inoculated on blood agar and MacConkey agar plate each and incubated at 37[°]c aerobically.^[6]

After incubation, plates were observed for any growth, identification of organisms were done by gram staining, motility testing and different biochemical reactions. Colonies are counted and results are interpreted as per standard "Kass theory". Samples were declared sterile only after 48 hours of incubation.^[6]

Antibiotic sensitivity is performed by disk diffusion method and results are interpreted as per CLSI standards ^[7]

RESULTS

Out of total 393 samples of urine samples collected, 118 samples showed growth of bacterial pathogens.

Out of 118 positive samples, 48 were male and 70 were female. (Table -1)

Table 1:	Gender	wise	distribution	of	positive	urine
culture						

Sex	Number of samples	Percentage
Male	48	40.68 %
Female	70	59.32%

All positive samples are categorized in three groups, paediatric age group, adult group and elderly group. This study suggests 60% of the infections are in adult age group, 23% in paediatric age group and only 17% in elderly group. (Table -2)

Table 2: Age wise distribution of positive urine culture

Age (Years)	Number	Prevalence (%)
≤ 18	27	22.88%
19 - 65	71	60.16%
>65	20	16.94%

Out of 118 positive culture samples, *Escherichia coli* was the most prevalent organism with total 56 occurrences accounting for 47.45%, followed by *Klebsiella pneumoniae* with 22 isolates (18.64%), *Enterococcus spp.* with 18 isolates (15.25%), *Pseudomonas aeruginosa* with 6 isolates (5.08%), *Staphylococcus aureus* with 4 isolates (3.38%), *Proteus mirabilis* with 6 isolates (5.08%), *Acinetobacter spp.* with 6 isolates (5.08%). (Figure – 1) *Kothari K et al. GAIMS J Med Sci 2022;2(2) (Jul-Dec):24-29 Online ISSN: 2583-1763*



Table 3: Antibiotic resistance perce	ntage in Gran	n negative o	organism	causing UI	Γl
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Antibiotics	Conc.	E.coli	Klebsiella pneumoniae	Pseudomonas aeruginosa	Acinetobacter spp.	Proteus mirabilis
Ampicillin	10 µg	89.29%	IR	IR	IR	100%
Cefoperazone	75 μg	71.43%	63.64%	100 %	100 %	100%
Cefotaxime	30 µg	67.56%	63.64%	-	100 %	66.67%
Ceftriaxone	30 µg	71.43%	63.64%	-	100 %	100%
Cefepime	30 µg	71.43%	63.64%	100 %	100 %	100%
Amoxyclav	30 µg	57.14%	72.73%	IR	IR	100%
Piperacillin/ Tazobactam	100/ 10 μg	42.86%	45.46%	33.33%	100 %	33.33%
Cefotaxime/ clavulanic acid	30/10 μg	57.15%	45.46%	-	100 %	33.33%
Amikacin	30 µg	10.71%	36.37%	0 %	100 %	33.33%
Gentamicin	10 µg	10.71%	36.37%	66.66%	100 %	0%
Tobramycin	10 µg	10.71%	36.37%	33.33%	100 %	0%
Levofloxacin	5 µg	60.72%	45.46%	66.66%	66.67%	33.33%
Ofloxacin	1 µg	60.72%	45.46%	-	66.67%	33.33%
Ciprofloxacin	5 µg	60.72%	45.46%	66.66%	66.67%	33.33%
Imipenem	10 µg	32.15%	36.37%	100%	100%	66.67%
Meropenem	10 µg	42.85%	36.37%	66.66%	33.33%	66.67%
Tetracycline	30 µg	35.71%	45.46%	IR	100%	-
Co-trimoxazole	25 µg	42.85%	36.37%	IR	100%	100%
Aztreonam	30 µg	60.72%	45.46%	66.66%	IR	33.33%
Nitrofurantoin	300µg	14.28%	27.27%	-	66.67%	66.67%

Antibiotic	Conc.	Staphylococcus aureus	Enterococcus spp.
Penicillin	10 µg	100%	77.78%
Doxycycline	30 µg	0%	-
Azithromycin	15 µg	100%	-
Erythromycin	15µg	100%	-
Clindamycin	2 µg	0%	IR
Tetracyclin	30 µg	0%	-
Co-Trimoxazole	25 µg	0%	IR
Cefoxitin	30 µg	50%	IR
Linezolid	30 µg	0%	22.22%
Minocycline	30 µg	0%	-
Vancomycin	30 µg	0%	33.33%
Chloramphenicol	30 µg	0%	-
Ciprofloxacin	5 µg	100%	66.67%
Levofloxacin	5 µg	100%	66.67%
Gentamicin	10 µg	0%	IR
Teicoplanin	30 µg	-	44.44%
Nitrofurantoin	300 µg	-	44.44%
High level gentamycin	120 µg	-	55.56%

Table 4: Antibiotic resistance percentage in Gram positive organism causing UTI

DISCUSSION

UTI are the most frequent infection in women often caused by bacteria. *E.coli* is the most common organism causing UTI.

In our study, females(59.32%) are more commonly affected by UTI than males(40.68%), which is correlating well with studies of Mulugata K et al, Malik N at al and other studies. ^[8,9,10,11,12] This may be because of short female urethra and hormonal factors.

In our study adult age group(60.16%) is more commonly affected then elderly(16.94%) and children age group(22.88%). In Ali M at al they also found adult age group commonly get affected by UTI than other groups. ^[10] This could be described by active sexual life.

In our study Escherichia coli is the most prevalent organism 47.45%. In Mulugata et al study E.coli was isolated in 63.6%, in Malik at al it was isolated in 62.5%, in Raive et al study it was isolated in 50 % of the cases and in Shah et al it was 42.8%, in all the above studies E.coli was the most common pathogen in UTI. ^[11,12,13,14]

Klebsiella pneumoniae was the second most common isolate with 18.64%, correlated with other studies except in Shah et al study, surprisingly they isolated CoNS as second most common pathogen.

Other common pathogens in the present studies were Enterococcus spp. 15.25%, Pseudomonas aeruginosa 5.08%, Staphylococcus aureus with 3.38%, Proteus mirabilis 5.08%, Acinetobacter spp. 5.08%. Variation in different studies may be due to geographical differences.

In our study we found Penicillin group of drugs shows almost resistance to all gram negative as well as Gram positive pathogens. In Mulugatta et al study penicillin group is restistant in 83.9%, in Saha et al penicillin group was resistant in 83% of isolates, in present study resistance was detected in 60 to 70 %. In the Saha et al, Amox-clave shows resistance in 71%, in our study it was resistant in 57.14%. Piperacillin tazobactam was resistant in 15% but in present study this drug is 42% resistance. ^[13] *Kothari K et al. GAIMS J Med Sci 2022;2(2) (Jul-Dec):24-29 Online ISSN: 2583-1763*

Cephalosporin showed resistance in 70 % of isolates which correlates with Saha R et al study(74%). Aminoglycosides is showing only 10% resistance in this study, as

gentamycine is available in only injectable form it is not suitable for empirical therapy in UTI. This may be the cause of increasing gentamycin sensitivity. E.coli is showing resistance to fluroquinolones in 60% isolates, while in Saha R et al study it showed 46 % resistance. ^[13] Carbapenems, Tetracyclines, Cotrimoxazole are resistant in 40% isolates of E.coli and Klebsiella. Aztreonam is resistant in 60 % however nitrofurantoin can be preferred drug as it shows resistance only in 14% isolates and it is having higher urinary concentration.

In present study, we found all the isolates of staphylococcus aureus were resistant to Penicillin,

Macrolides and Fluroquinolones, thats why empirical use of these drugs is questionable if staphylococcus infection is suspected.

Limitations of present study are we could not confirm the nosocomial and community acquired UTI. Species of all bacteria could not be identified because of conventional culture method used.

There are significant geographic differences in the susceptibility of commonly used antimicrobials against uropathogens. In the current study we observed a generalized drug resistance to commonly used antibiotics. So, accurate knowledge on local epidemiology and antimicrobial resistance pattern of organisms causing UTI is essential to design effective therapy.

	In present study	Mulugata et al ^[11]	Malik et al ^[12]	Rai V et al ^[14]	Saha et al ^[13]
E.coli	47.45	63.6	62.5	50	42.8
Klebsiella pneumoniae	18.64	8.5	6.61	34.31	3.7
Proteus mirabilis	5.08	8.2	0	3.5	1.9
Pseudomonas aeruginosa	5.08	6.9	0	0	0
Acinetobacter spp	5.08	0	0	0	7.5
Stahylococcus aureus	3.38	3.8	0	0	0
Enterococcus spp	15.25	0	2.94	0	1.9
CoNS	-	0	2.94	0	35.4
Enterobacter spp	-	2.2	5.88	0	4.3
Citrobacter spp		1.6	8.08	3.84	

Table 5: Comparison of different study with present study

CONCLUSION

Most common organism in this study was E.coli. In current study we observed a generalized drug resistance to commonly used antibiotics. To prevent further drug resistance, strict implementation of effective antibiotic policy, awareness regarding judicial use of antimicrobial in medical, para medical and general population is the need of time.

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