



Microbiological Profile of Urinary Tract infections among Patients attending a Tertiary care Hospital

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Abstract

Background: UTI is a common infection among all age groups. Timely detection and management of urinary tract infection is important as it leads to varied morbidity and mortality. Causative agents of UTI are *E.coli*, *Klebsiella* spp, *Proteus* spp, *Pseudomonas* spp, *Staphylococcus* spp, *Enterococcus* spp. In recent years resistance has been seen to various antibiotics used to treat urinary tract infection. Therefore, it is important to know the antibiotic profile of various organism involved in causing urinary tract infection. Thus, this study aimed to determine the bacteriologic agents causing UTI and to evaluate their in vitro susceptibility pattern

Material and Methods: Urine sample from 2100 patients with clinical symptoms of UTI were collected. Pure isolated bacteria were identified using biochemical tests and subjected to antimicrobial susceptibility testing using disc diffusion method as per CLSI guidelines.

Results: *Escherichia coli* 114(57.3%) was the predominant organism followed by *Klebsiella pneumoniae* 22(11.1%) and *enterococcus fecalis* 19(9.5 %). *E. coli* resistance to various antibiotics were as follows, cotrimoxazole (67.5%) , norfloxacin (66.6%), cefoperazone/sulbactam (57%), piperacillin/tazobactam (50.8%), nitrofurantoin (35%), ertapenem(33.3%), gentamicin and meropenem (32.4%), ciprofloxacin (23.6%) imipenem (14%) and amikacin (13.1%) . *K. pneumoniae* showed resistance to cotrimoxazole (77.2%) , nitrofurantoin (72.7%), cefoperazone/sulbactam (68.1%), gentamicin (54.5%), piperacillin/tazobactam and ciprofloxacin (50%), norfloxacin (45.4 %), imipenem (40.9%) , ertapenem(31.8%), meropenem and amikacin (9.09%). *E.fecalis* showed 57.8% resistance to levofloxacin, ampicillin, ampicillin/sulbactam, amoxicillin/clavulanic acid and piperacillin/tazobactam (26.3%), nitrofurantoin(10.5%). All isolates of *E.fecalis* were sensitive to vancomycin and linezolid.

Conclusion: Findings from this study revealed that *E.coli* remains the most predominant etiology of UTIs followed by *Klebsiella*. Resistance of *E.coli* was high towards cotrimoxazole, flouroquinolones and cephalosporins. *Klebsiella* showed high resistance to cotrimoxazole, nitrofurantoin, gentamicin, cephalosporins, flouroquinolones. *E.fecalis* showed 57.8% resistance to levofloxacin, penicillins. The results show that the antimicrobial resistance patterns of the causes of UTI are highly variable and continuous surveillance of trends in resistance patterns of uropathogens is important. The presence of multi-drug resistance bacteria was high. Hence, It's necessary to treat UTIS patients based on microbiology test results in order to prevent or minimize emergence and spread of multidrug resistant bugs.

Keywords: Urinary tract infection, Antibiogram, Culture, Invitro susceptibility.

Introduction

Urinary tract infections are amongst the most common infections encountered in clinical practice with an estimated annual global incidence of at least 150 to 250 million ^[1,2,3]. Anatomically UTI is divided into upper portion composed of kidney, renal pelvis, ureters and lower portion made up of urinary bladder and urethra. UTI are also the most common hospital acquired infection, accounting for as many as 35% of nosocomial infections.⁽⁴⁾ The most common pathogenic organisms of UTI are *Escherichia coli*, *Staphylococcus saprophyticus*, *Staphylococcus aureus*, *Proteus spp.*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *enterococci* ^(5,6,7)

Most often these infections are treated by physicians empirically with broad spectrum antibiotics rather than specific antibiotics. This along with poor patient compliance leads to development of resistance to many antibiotics. The resistance of common pathogens varies with different regions. The estimation of local etiology and susceptibility profile could support the most effective empirical treatment. Thus, the aim of this study was to determine bacterial etiologic agent of uropathogen and evaluate their *in vitro* susceptibility pattern to commonly used antimicrobial agents.

Material and Methods

The study was carried out at the Department of Microbiology Sher-i-Kashmir Institute of Medical sciences Srinagar, India for a period of 6 months from January to June, 2017. The study included all the patients who were admitted or visited the outpatient department in the hospital with symptoms of urinary tract infection during the study period and had positive cultures. Only one sample from each subject was considered. A clean catch midstream urine sample was collected in a wide mouthed sterile container. In patients where midstream sample could not be obtained a suprapubic aspirate was taken.

Urine was inoculated on Hicrome agar using a calibrated loop designed to deliver a volume of

0.01ml. Once inoculated, the plates were streaked to obtain isolated colonies. After this, the cultures were incubated at 35°C for 24 hours. Next day, the plates were examined for colony morphology, significant colony count, and their characteristics. Those colonies that could not be identified on chromogenic media were subjected to conventional methods like biochemical tests and further confirmed by VITEK 2. The antibiotic susceptibility pattern of the isolates was determined by the Kirby-Bauer disk diffusion method ⁽⁸⁾. The antibiotics used in the discs were ampicillin, amoxicillin-clavulanic acid, piperacillin/tazobactam, norfloxacin, imipenem, cefoperazone/sulbactam, amikacin, ceftazidime, clindamycin, ciprofloxacin, nitrofurantoin, gentamicin, cotrimoxazole, linezolid, vancomycin that were routinely used in hospital. Resistance data were interpreted according to CLSI (Clinical Laboratory Standard Institute).

Results

A total of 2100 urine samples were subjected to culture and sensitivity out of which 199 (0.09%) were culture positive. Various bacterial isolates and their frequency is given in Table 1. The antibiogram of different isolates is given in Table 2 and 3.

Table 1 Frequency of bacterial isolates.(N=199)

Bacterial isolates	Frequency (%)
<i>Escherichia coli</i>	114(57.3%)
<i>Klebsiella pneumoniae</i>	22(11.1%)
<i>Enterococcus faecalis</i>	19(9.5%)
<i>Enterococcus spp.</i>	15(7.5%)
<i>Pseudomonas</i>	11(5.5%)
<i>Enterococcus faecium</i>	07(3.5%)
MSSA	03(1.5%)
<i>Acinetobacter baumannii</i>	02 (1.0%)
<i>Acinetobacter spp</i>	02(1.0%)
<i>Proteus vulgaris</i>	02(1.0%)
<i>Proteus mirabilis</i>	02(1.0%)
Total bacterial isolates	199(100%)

Table 2. Antibiotic resistance among Gram negative isolates

Organism	AMK	GEN	CIP	NORF.	NITR	COT	PIP/T AZ	CEFO/SULB	IMI	MERP	ERTA
<i>E.coli</i> (N=114)	15/114 (13.1%)	37/114 (32.4%)	27/114 (23.6%)	76/114 (66.6%)	40/114 (35%)	77/114 (67.5%)	58/114 (50.8%)	65/114 (57%)	16/114 (14%)	37/114 (32.4%)	38/114 (33.3%)
<i>K.pneumoniae</i> (N=22)	2/22 (9.09%)	12/22 (54.5%)	11/22 (50%)	10/22 (45.4%)	16/22 (72.7%)	17/22 (77.2%)	11/22 (50%)	15/22 (68.1%)	9/22 (40.9%)	02/22 (9.09%)	07/22 (31.8%)
<i>Pseudomonas</i> (N=11)	05/11 (45.4%)	07/11 (63.6%)	07/11 (63.6%)	07/11 (63.6%)	5/11 (45.4%)	6/11 (54.5%)	09/11 (81.8%)	08/11 (72.7%)	03/11 (27.2%)	4/11 (36.36%)	01/11 (9.09%)
<i>P.vulgaris</i> (N=02)	0/2 (0%)	01/02 (50%)	1/2 (50%)	1/2 (50%)	0/0 (0%)	0/2 (0%)	1/2 (50%)	0/2 (0%)	0/2 (0%)	-	-
<i>P.mirabilis</i> (N=02)	1/2 (50%)	1/2 (50%)	1/2 (50%)	1/2 (50%)	0/2 (0%)	1/2 (50%)	0/2 (0%)	0 (0%)	1/2 (50%)	-	0/2 (0%)
<i>A.baumannii</i> (N=02)	2/2 (100%)	2/2 (100%)	1/2 (50%)	2/2 (100%)	1/2 (50%)	1/2 (50%)	2/2 (100%)	1/2 (50%)	2/2 (100%)	1/2 (50%)	-
<i>A.spp</i> (N=02)	1/2 (50%)	2/2 (100%)	2/2 (100%)	2/2 (100%)	2/2 (100%)	0/2 (0%)	2/2 (100%)	2/2 (100%)	0/1 (0%)	0/1 (0%)	-

AMK=Amikacin, GEN= Gentamycin, CIP= Ciprofloxacin, NORF= Norfloxacin, COT= Cotrimoxazole, PIP/TAZ= Pipracillin+Tazobactam, CEFO/SULB=Cefperazone+Salbactam, IMI=Imipenam, MERA=Meropenam, ERTA=Ertapenam

Table 3. Antibiotic resistance among Gram positive isolates

Organism	No. of bacterial species (%) resistant to antibiotics								
	AMP	VAN	LINZ	AMX/CLAV	NITROF	TICA/CLAV	LEVOF	PIP/TAZ	AMP /SULB
<i>Enterococcus fecalis</i> (N=19)	5/19 (26.3%)	0/19 (0%)	0/19 (0%)	5/19 (26.3%)	2/19 (10.5%)	3/19 (15.7%)	11/19 (57.8%)	5/19 (26.3%)	5/19 (26.3%)
<i>Enterococcus spp</i> (N=15)	6/15 (40%)	1/15 (6.6%)	0/15 (0%)	5/10 (50%)	1/15 (6.6%)	4/15 (26.6%)	6/15 (40%)	6/15 (40%)	2/15 (13.3%)
<i>Enterococcus fecium</i> (N=07)	3/7 (42.8%)	1/7 (14.2%)	0/7 (0%)	3/7 (42.8%)	2/7 (28.5%)	2/7 (28.5%)	4/7 (57.1%)	3/7 (42.8%)	3/7 (42.8%)
<i>MSSA</i> (N=03)	0/3 (0%)	0/3 (0%)	0/3 (0%)	0/3 (0%)	0/1 (0%)	1/3 (33.3%)	1/1 (100%)	0/3 (0%)	0/3 (0%)

Discussion

UTI is one of the important cause infection worldwide affecting all age groups. The etiological agents and their susceptibility pattern of UTI vary in regions and geographical locations. Knowledge of the local bacterial etiology and susceptibility pattern is required to trace any change that might had occurred in time so that updated recommendation for optimal empirical therapy of UTI can be made⁽¹³⁾.

Escherichia coli, 114(57.3%) was the predominant organism followed by *Klebsiella pneumoniae* 22 (11.1%). In a study by Tajbakhsh et al. *E. coli* was identified as the predominant cause of UTIs (51.70%), followed by *Klebsiella pneumoniae* (16.32%)⁽³⁾. Our study was similar to the findings of Mandal et al⁽⁹⁾, Sharma and Paul⁽¹⁰⁾ There were many other

studies which showed that *E coli* is the most common causative organism for UTI.^(12,13-17) Other Gram negatives organism isolated were *Pseudomonas* (5.5%), *Acinetobacter baumannii* (1.0%), *Acinetobacter spp* (1.0 %), *Proteus vulgaris* (1.0 %), *Proteus mirabilis* (1.0 %). In a study by Shanthi and Kayathri, *Citrobacter* spp.were the second most frequently isolated bacterial agents (14%)⁽¹¹⁾. In our study, among gram positive predominant organism isolated was enterococcus fecalis (43%), enterococcus spp (34%), enterococcus fecium (16%) and MSSA (07%) respectively. In a study by Kalpana Devi Venkatesan et al *E. faecalis* (77.7%) was the major species isolated.⁽¹⁸⁾ In another study by Setu et al among the Gram positive bacteria, the main organism identified was *Enterococci* (75.07%) followed by *Staphylococcus aureus* (12.88%).⁽¹⁹⁾

Gram negative contributed to 77.8% and Gram positive 22.2 % . Gram negative bacteria were more responsible for UTI than Gram positive bacteria and this finding is in agreement with findings of previous studies. Gram-negative bacteria including *Enterobacteriaceae* have several factors responsible for their attachment to uroepithelium. They colonize in the urogenital mucosa with adhesins, pili, fimbriae, and P-1 blood group phenotype receptor. ⁽²⁰⁾

In our study *E. coli* showed highest resistance to cotrimoxazole (67.5%), norfloxacin (66.6%), cefoperazone/sulbactam (57%), piperacillin/tazobactam (50.8%), while resistance was low against nitrofurantoin(35%), ertapenem (33.3%), gentamicin (32.4%), meropenem (32.4%), ciprofloxacin (23.6%) and imipenem (14%), amikacin (13.1%).

K.pneumoniae showed high resistance to cotrimoxazole (77.2%), nitrofurantoin (72.7%), cefoperazone/sulbactam (68.1%) , gentamicin (54.5%), piperacillin/tazobactam (50%), ciprofloxacin (50%), norfloxacin (45.4 %), imipenem (40.9%), and low resistance to ertapenem (31.8%), meropenem and amikacin (9.09%).

Other organism like pseudomonas showed high resistance to pip/taz (81.8%), cefoperazone/sulbactam(72.7%), gentamicin, ciprofloxacin, norfloxacin (63.6%) and Fluoroquinolones are one of the most widely used antibiotics for treating UTIs, even in complicated cases, given their broad-spectrum action, bactericidal potency, excellent oral bioavailability, good tolerance, and marked post antibiotic effect ^(21,22). However, various studies have reported high resistance rates to these antibiotics. ⁽²³⁾

E.fecalis showed 57.8% resistance to levofloxacin, ampicillin, ampicillin/sulbactam, amoxicillin/clavulanic acid and piperacillin/tazobactam (26.3%), nitrofurantoin(10.5%). *E.fecalis* showed no resistance against vancomycin and linezolid. *Enterococcus spp* showed resistance to amoxicillin/clavulanic acid (50%), levofloxacin (40%), piperacillin/tazobactam (40%). No

resistance was seen against vancomycin while 6.65 resistance was seen against linezolid. *E.faecium* showed resistance to levofloxacin (57.1%), vancomycin (14.2%) but no resistance against linezolid was seen.

Overall, Gram-negative isolates showed higher resistance in the present study. This high antibiotic resistance is mostly due to widespread use of antimicrobials as well as irrational prescription of antimicrobials which are available over-the-counter.

Conclusion

The results show that the antimicrobial resistance patterns of the causes of UTI are highly variable and continuous surveillance of trends in resistance patterns of uropathogens is important. The presence of multi-drug resistance bacteria was high. Hence, It's necessary to treat UTI patients based on microbiology test results in order to prevent or minimize emergence and spread of multidrug resistant bugs.

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