BACTERIOLOGICAL PROFILE AND ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF URINE CULTURE ISOLATES FROM PATIENTS IN A TERTIARY CARE CENTRE IN LALITPUR

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ABSTRACT

Introduction

Urinary tract infection (UTI) is a microbial infection of the urinary system involving the urinary tract anywhere from kidney to urethra. It is one of the most common bacterial infections affecting men and women in developing countries with a high rate of morbidity and financial cost.

Objectives

The objective of our study is to study the prevalence of UTI in patients attending KIST Medical College & Teaching Hospital (KISTMCTH) and determine the antimicrobial susceptibility pattern of bacteria thus isolated.

Methodology

A total of 3742 urine samples from patients suspected of urinary tract infections presenting with the history and symptoms suggestive of urinary tract infection, attending various departments of KISTMCTH from April 2017 to April 2018 were studied. Isolates were identified by standard microbiological methods and tested for *in vitro* antibiotic susceptibility by modified Kirby-Bauer disc diffusion method.

Results

Pathogenic bacteria were isolated from 646 out of 3742 urine samples (17.26%). *Escherichia coli* was the most common bacteria isolated (67.02%) followed by *Klebsiella pneumoniae* (14.5%). Other bacteria isolated were Enterococcus spp, *Pseudomonas aeurigenosa, Klebsiella oxytoca, Proteus mirabilis, Satphylococcus aureus,* Coagulase negative staphylococcus spp, *Proteus vulgaris,* Acinetobacter spp, *Citrobacter freundii, Citrobacter diversus* and Enterobacter spp. The isolated pathogenic bacterias were most resistant to Ampicillin (46.43%) and least resistant to Imipenem (6.03%). However, the first line antibiotic the bacterias were least resistant to was cefotaxime (7.12%).

Conclusions

Marked resistance has been observed with commonly prescribed antibiotics like Ciprofloxacin and Norfloxacin. Therefore, studies should be conducted routinely to identify the common bacteria causing urinary tract infection and formulate appropriate antibiotic policy.

KEYWORDS

Antimicrobial resistance, escherichia coli, prevalence, urinary tract infection.

INTRODUCTION

Urinary tract infection (UTI) is a microbial infection of the urinary system involving the urinary tract anywhere from kidney to urethra commonly presenting with dysuria, increased urinary frequency, urgency, suprapubic pain and fever.[1,2,3] The clinical presentation of UTIs however depends on the area of the urinary tract involved, the causative agent, infection severity, age of the patient and the their ability to mount an immune response to it [2,3] It is one of the most common bacterial infection seen in clinical practice particularly in developing countries with a high rate of morbidity and financial cost.[1] It affects all age groups and gender in both the community and hospital settings with a marked predilection in females.[2]

Urinary tract infections may be symptomatic or asymptomatic, acute or chronic, and complicated or uncomplicated.

Urinary tract infections are predominantly caused by bacteria and sometimes by viruses and fungi. The most common pathogenic organisms of UTI are *Escherichia coli, Staphylococcus saprophyticus, S. aureus, Proteus sp., Klebsiella pneumoniae, Pseudomonas aeruginosa, and enterococci*.[3] A significant number of urinary tract infections are caused by *Escherichia coli*.[1-4] Urinary tract infection is considered significant and requires treatment when more than 10^5colony forming units per ml (cfu/ml) of bacteria is present in a clean catch mid stream urine sample. Bacterial count of 10^4 cfu/ml is considered significant in specific groups like in children, pregnant women, patients with preexisting kidney diseases or anatomical abnormalities.[5]

Treatment of UTI is often started empirically and therapy is based on information determined from the antimicrobial resistance pattern of the urinary pathogens.[6] The etiological agents and their susceptibility patterns vary in regions and geographical location that tend to change through time.[7] Knowledge of the local bacterial etiology and susceptibility patterns not only helps in empirical therapy but also prevents the threat of emerging antimicrobial resistance.

The deadly combination of emerging uropathogens with wide range of virulence factors and widespread antimicrobial resistance threaten the existence of antibiotics as the only effective treatment option available.[3]

The study intends to determine the prevalence of UTI in patients attending KIST Medical College & Teaching Hospital, find out the antimicrobial susceptibility pattern of bacteria thus isolated.

METHODOLOGY

This hospital based retrospective study was conducted in Department of Microbiology, KIST Medical College and Teaching hospital, Lalitpur, Nepal. Clearance from the Institutional Research Committee (IRC) KISTMCTH was obtained before conducting the study.

All urine samples from patients suspected of urinary tract infections presenting with the history and symptoms suggestive of urinary tract infection, attending various departments of KIST Medical College and Hospital from April 2017 to April 2018 were studied. Unlabeled or mislabeled urine samples, Urinary catheter tips, Urine samples collected till the rim of the container, Urine samples received beyond 2 hours of collection at room temperature or beyond 24 hours of storage at 4 degrees Celsius were excluded from the study.

All patients were instructed on collection of clean catch mid stream urine sample in order to reduce contamination. The urine samples were properly labeled. Each sample was inoculated into Cystiene Lactose Electrolyte deficient media and incubated at 37° C for 24 hours. There is no added benefit to incubating routine urine cultures for 48 hours or beyond as most of the uropathogens grow within 24 hours except for the yeasts.[8, 9] Semi quantitative analysis of the urine sample was done following Kass Criterawhich defined significant bacteriuria as the presence of 100000 or more colonies (CFU) per ml of urine.[10] Bacterial identification was based on standard microbiological methods. Antimicrobial susceptibility was determined by modified Kirby Bauer disk diffusion method following the criteria designed by the Clinical and Laboratory Standards Institute (CLSI 2011).

The obtained data was entered and analysed in WHONET 5.6 program.

Results

A total of 3742 urine samples from patients suspected of urinary tract infections attending various departments of KIST Medical College and Hospital were studied. Significant bacteriuria was found and pathogenic bacteria were isolated from 646 out of 3742 urine samples (17.26%). Fungal growth was obtained in 14 urine samples. There was no growth in 2760 samples. Insignificant growth was found in 26 samples which were not further processed. Majority of urine samples where growth was observed revealed growth of only one type of bacteria. Multiple organisms grew in 296 urine samples (7.91%) which were not processed further and considered as contamination during sample collection. Repeat sample was then advised.

Out of 646 samples that revealed significant bacteriuria, 470 samples (71%) belonged to females and 190 samples (29%) belonged to males.(Figure.1)

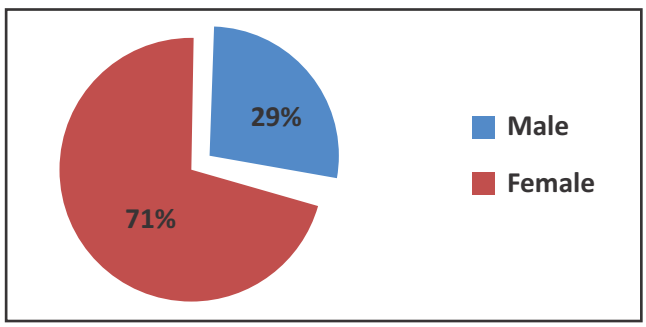


Figure 1: Gender distribution of culture positive isolates

Urine samples from age group ranging 16 years to 30 years revealed maximum culture positivity. (Table.1)

Table 1: Age distribution of patients with culture positive isolates

Age distribution in years	Number of culture positive patients
0- 15	94
16 -30	231
31-45	129
46-60	82
61-75	66
76-90	40
Above 90	4
TOTAL	**646**

Maximum number of growth was found in samples from Department of medicine (28%). Twelve percentage of samples where significant growth was observed belonged to samples from Pediatric group.

The bacteria that were isolated were *Escherichia coli, Klebsiella pneumoniae,* Enterococcus spp, *Pseudomonas aeurigenosa, Klebsiella oxytoca, Proteus mirabilis, Satphylococcus aureus,* Coagulase negative staphylococcus spp, *Proteus vulgaris,* Acinetobacter spp, *Citrobacter freundii, Citrobacter diversus,* Enterobacter spp. *Escherichia coli* was the most common bacteria isolated (67.02%) followed by *Klebsiella pneumoniae* (14.5%) . (Table.2)

Table 2: Bacteria Isolated

S.No	Bacteria isolated	Number	Percentage
1.	Escherichia coli	433	67.02%
2.	Klebsiella pneumoniae	94	14.5%
3.	Enterococcus spp	26	4.02%
4.	Pseudomonas aeurigenosa	15	2.32%
5.	Klebsiella oxytoca	13	2.01%
6.	Proteus mirabilis	12	1.8%
7	Staphylococcus aureus	11	1.7%
8.	Coagulase negative staphylocoocus spp (CoNS)	10	1.5%
9.	Proteus vulgaris	8	1.2%
10.	Acinetobacter spp	7	1.08%
11.	Citrobacter freundii	8	1.23%
12.	Citrobacter diversus	4	0.61%
13.	Enterobacter spp	5	0.77%
	TOTAL	**646**	**100%**

Candida spp was isolated from 14 samples. Antibiotic sensitivity test was performed on all bacterial isolates.

Specimens were not processed for presence of anaerobic bacteria, viruses or parasites.

Antimicrobial susceptibility test revealed that the isolated bacterias were most resistant to ampicillin (46.43%). The isolated bacterias were least resistant to Imipenem and Amoxicillin clavulinic acid showing resistance of 6.03% and 6.81% respectively. However, the first line antibiotic the bacterias were least resistant to was cefotaxime (7.12%). Among the Gram positive organism, Nitrofurantoin was found to be the most sensitive drug (85.11%). Among the Gram negative bacteria, Imipenem was found to be the most sensitive drug (93.9%) followed by cefotaxime (93%). *Escherichia coli* was found to be most sensitive to Imipenem (96.07%) and amoxicillin clavulinic acid (93.31%). (Table.3 and Table.4)

Table.3: Antibiogram of Gram positive isolates

S. No.	Name of the isolates	No. of isolates	Antibiotic resistance pattern											
			Amp (10µg)	Cip (5µg)	Na (30µg)	Nx (10µg)	Nit (300µg)	Cot (25µg)	Gen (10µg)	C (30µg)	E 15µg)	P (2µg)	Va (30µg)	Cx (30µg)
1.	Enterococcus spp	26	6 (37.5)	16 (61.53)	11 (42.30)	16 (61.53)	5 (19.23)	10 (38.46)	11 (42.30)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
2.	*Staphylococcus aureus*	11	4 (36.36)	6 (54.54)	5 (45.45)	7 (63.63)	2 (18.18)	7 (63.63)	2 (18.18)	-	0 (0)	0 (0)	0 (0)	0 (0)
3.	Coagulase egative Staphylococcus spp	10	3 (30)	2 (20)	0 (0)	3 (30)	0 (0)	3 (30)	0 (0)	-	0(0(0)	0 (0)	0 (0)	0 (0)
	TOTAL	47	13 (27.65)	24 (51.06)	16 (34.04)	26 (55.31)	7 (14.89)	20 (42.55)	13 (27.65)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)

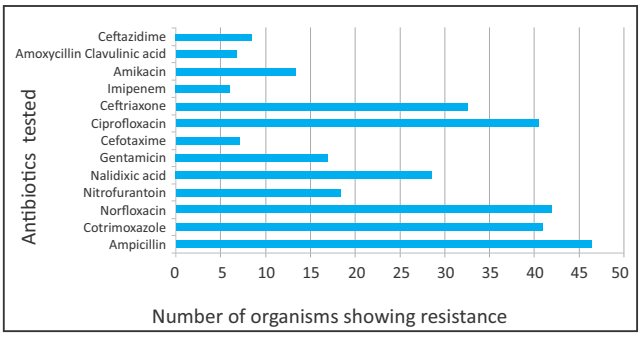
Numbers in parenthesis indicate percentage

TABLE 4 : Antibiogram of Gram negative isolates

S. No.	Name of the isolates	Number of isolates	Antibiotic resistance pattern												
			AMP (10µg)	COT (25µg)	NX (10µg)	NIT (300µg)	NA (30µg)	GEN (10µg)	CTX (30µg)	CIP (5µg)	CTR (30µg)	IPM (10µg)	AK (10µg)	AMC (30µg)	OF (5µg)
1.	*E.coli*	433	208 (48.03)	181 (41.80)	181 (41.80)	36 (8.31)	128 (29.5)	50 (11.54)	30 (6.92)	183 (42.26)	143 (33.02)	17 (3.9)	34 (7.85)	29 (6.69)	31 (7.15)
2.	*Kleb. pneumoniae*	94	52 (55.3)	36 (38.2)	38 (40.4)	47 (50)	21 (22.3)	30 (31.9)	7 (7.44)	33 (35.1)	36 (38.2)	14 (14.8)	23 (24.4)	6 (6.3)	9 (9.5)
3.	*Pseudomonas aeurigenosa*	15	5 (33.3)	8 (53.3)	9 (60)	10 (66.6)	4 (26.6)	9 (60)	1 (6.6)	8 (53.3)	6 (40)	3 (20)	8 (53.3)	0 (0)	5 (33.3)
4.	*Klebsiella oxytoca*	13	3 (23)	17 (7.6)	2 15.3	1 (7.6)	3 (23)	0 (0)	1 (7.6)	2 (15.3)	2 (15.3)	1 (7.6)	0 (0)	1 (7.6)	0 (0)
5.	*Proteus mirabilis*	12	3 (25)	7 58.3	4 33.3	9 (75)	6 (50)	3 (25)	1 (8.3)	4 (33.3)	4 (33.3)	0 (0)	2 (16.6)	2 (16.6)	0 (0)
6.	*Proteus vulgaris*	8	6 (75)	5 (62.5)	3 (37.5)	3 (37.5)	2 (25)	1 (12.5)	0 (0)	2 (25)	0 (0)	0 (0)	2 (25)	0 (0)	0 (0)
7.	*Citrobacter freundii*	8	3 (37.5)	3 (37.5)	2 (25)	4 (50)	0 (0)	0 (0)	0 (0)	2 (25)	2 (25)	1 (12.5)	1 (12.5)	2 (25)	1 (12.5)
8.	*Citrobacter diversus*	4	2 (50)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (25)	0 (0)	1 (25)	0 (0)	0 (0)	0 (0)	0 (0)
9.	Acinetobacter spp	7	2 (28)	3 (42.8)	5 (71.4)	5 (71.4)	2 (28.5)	3 (42.85)	1 (14.28)	4 (57.14)	2 (28.57)	0 (0)	4 (57.14)	1 (14.2)	0 (0)
10.	Enterobacter spp	5	3 (66)	1 (20)	1 (20)	0 (0)	3 (60)	0 (0)	0 (0)	0 (0)	0 (0)	1 (20)	0 (0)	1 (20)	1 (20)
	TOTAL	**599**	**287 (47.9)**	**261 (43.5)**	**245 (40.9)**	**115 (19.1)**	**169 (28.2)**	**96 (16.02)**	**42 (7)**	**236 (39.3)**	**196 (32.7)**	**37 (6.1)**	**74 (12.3)**	**42 (7.01)**	**47 (7.8)**

Numbers in parenthesis indicate percentage

Order for resistance pattern was Ampicillin > Norfloxacin > Cotrimoxazole > Ciprofloxacin> Ceftriaxone > Nalidixic acid > Nitrofurantoin > Gentamicin > Amikacin> Ceftazidime > Cefotaxime > Amoxycillin clavulinic acid > Imipenem. (Figure.2)



DISCUSSION

In developing countries urinary tract infection (UTI) is one of the most commonly diagnosed disease among the patients seeking medical treatment with frequency of 180 per 10,000.[11] Our study shows the prevalence rate of 17.26% which was similar to studies conducted in Kathmandu medical college & hospital and B&B hospital, Lalitpur which reported a prevalence rate of 13.8% and 25.24% respectively.[11,12] A study conducted in Western Nepal shows a higher prevalence rate of 43.25%.[13] However, prevalence was found to be 39.69% in a rural community of Nigeria.[14] This variations in the prevalence of UTIs may result from different environmental conditions, host factors, socioeconomic status, hygiene practices and execution of healthcare and education programmes within communities of different geographical areas.

As shown in Figure.1 ,prevalence rate was found to be higher in females (71%) than in males (29%) were similar to studies conducted in Nepal and other countries. [1-3, 11-14] This might be because of the short urethra and close proximity of the urethra to the perianal region and the lack of secretion produced from prostate present in males which has bactericidal property.[1]

The organism isolated from this study as depicited in Table.2 is similar to the studies conducted in different parts of the world. [1-3,5-7,11-14] In our study, *Escherichia coli* was the most common bacteria isolated (67.02%) followed by *Klebsiella pneumoniae* (14.5%) which was similar to the study conducted in Kathmandu Medical College & Hospital and Nepal medical college & Hospital in Kathmandu and in a multicenter study conducted in India.[11,15,16] The organisms were most resistant to Ampicillin(46.43%) as shown in Figure.2 which was similar to studies conducted by Russel Kabir et al, Rijal et al and Thapa et al in Nepal.(3,5,6) In contrast to our study, organisms were most sensitive to ciprofloxacin (63%) in a study conducted in Kathmandu Medical College. However, in our study ciprofloxacin was sensitive in only 59.45%. *Escherichia coli* was found to be most sensitive to Imipenem (96.07%) which was similar to a study conducted in Punjab. In a study conducted by Kibret *et al*, Nitrofurantoin, Gentamicin and ciprofloxacin were considered as appropriate antimicrobials for empirical treatment of UTI in the area of Ethiopia which was in contrast to our study.[17]

CONCLUSION

Urinary tract infection is the most common bacterial infection seen in clinical practice. *Escherichia coli* remains the most common pathogen causing UTI. Female patients in reproductive age groups are more prone to develop UTI. The bacteria isolated were most sensitive to Imipenem & amoxicillin clavulinic acid. However, the first line antibiotic that the bacteria were most sensitive remains cefotaxime. Marked resistance has been observed with commonly prescribed antibiotics like Ciprofloxacin and Norfloxacin. Therefore, studies should be conducted routinely to identify the common bacteria causing UTI and formulate appropriate antibiotic policy.

RECOMMENDATIONS

Surveillance programs should be conducted regularly to identify the prevalent organisms and their antibiotic sensitivity pattern to formulate antibiotic policy that can be implemented for making proper guidelines regarding empirical therapy.

LIMITATIONS OF THE STUDY

- Only aerobic bacteriological assessment was carried out. Routine urine examination was not included to justify urine culture as it can be a prospective study in itself.
- Extended Spectrum Beta Lactamase(ESBL) producing bacteria were not identified.
- Molecular identification of the isolates was not included in the study to substantiate epidemiological relationship.

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CONFLICT OF INTEREST

None

FINANCIAL DISCLOSURE

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