



Original Research Article

Antibiotic susceptibility pattern in UTI patients with bacterial pathogens

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A B S T R A C T

Keywords

Antibiotic,
susceptibility,
UTI,
nosocomial,
bacteria.

Urinary tract infection (UTI) accounts for a large part of antibacterial drug consumption. Antibiotic resistance, due to irrational use, is increasing every day, especially in the countries with non-restricted policies against wide consumption of antibiotics and no precise plans, like Iran. This investigation is therefore designed to determine the prevalence and antibiotic susceptibility pattern of microbial agents that cause UTI in patients which are suspected to have UTI. The sensitivity of the strains against various antibiotics was determined by using antibiotic sensitivity discs; namely amikacin, gentamicin, ciprofloxacin and piperacillin. The most common pathogen was *Escherichia coli* (50%) and *K. pneumonia* (17.3%). Our study showed 100%, 30.76% and 92.30% sensitivity rate of *E coli* to Imipenem, ciprofloxacin and piperacillin, etc.

Introduction

Urinary Tract Infection (UTI) remains the most common bacterial infection in human population and is also one of the most frequently occurring nosocomial infections¹.

Its annual global incidence is of almost 250 million^{2,3}. UTI is second only to respiratory tract in acquiring microbial infection especially in female.⁴ About 20% of women experience a single episode of UTI during

their life time and 3% of woman have more than one episode of UTI per year⁵. They are asymptomatic or symptomatic. 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 structural or functional abnormalities including instrumentation such as in dwelling urethral catheters, and are frequently asymptomatic^{6,7}. Many

different microorganisms can cause UTIs though the most common pathogens causing the simple ones in the community are *Escherichia coli* and other Enterobacteriaceae, which accounts for approximately 75% of the isolates⁸. Treatment of UTI is often started empirically and therapy is based on information determined from the antimicrobial resistance pattern of the urinary pathogens⁹. Microbial resistance to nearly all classes of antimicrobials continue to rise despite increasing awareness and concern world wide¹⁰. Isolated pathogen frequency and antimicrobial resistant rates can vary dramatically even within the same nation^{11,12}. To ensure appropriate therapy current knowledge of the organism that cause UTI and their susceptibility pattern is mandatory¹³. Herein we studied antimicrobial susceptibilities of bacteria isolated from the urine of the patients attending lab of Excel Hospital, Kanpur and Ambikashish Pathology and Microbiology Centre, Kanpur.

Materials and Methods

Patients have been drawn from OPD and indoor wards of LLR and associated hospitals in Kanpur and some private hospitals in Kanpur.

These cases have been diagnosed on the basis of clinical symptoms, urine routine microscopy and urine culture at microbiology laboratory.

Collection of samples

Sample collected are midstream clean-catch urine after giving proper instruction to the patient.

- a. Clean the genitalia properly(in case of male, retract the prepuce, clean it with sterile normal saline , in case of females wash perineum periurethral with soap and water)
- b. Collect a “clean catch” mid stream urine sample in a sterile container. Transportation should be immediate. If a delay of more than 1-2 hours then refrigerated at 4° C.

Isolation of Microbial Flora

The microbial flora was isolated from urine samples of UTIs patient by using different technique.

Identification of Microbial Flora

It is based on Gram stain, biochemical reactions such as oxidase, catalase, indole, MR, VP, citrate utilization, urease, triple sugar iron agar (TSI), germ tube test(GTT), coagulase and motility test and subjected to antibiotic sensitivity testing (AST) by Kirby Baur Disc Diffusion method. Control strains of *E. Coli* and *P. aeruginosa* were used.

Results and Discussion

Out of 175 urine samples collected for the study (30.23%) showed the significant bacteriuria. Isolates are shown in Table 1. The mean age in years was 35.6 (0-93 years). Male were 93 and female 79. The antibiogram of the isolated pathogens is shown in Table 2. Among the tested antibiotics the highest susceptibility for the Gram negative bacteria was shown by Amikacin, Ceftriaxone and Ciprofloxacin followed by Gentamicin and Nitrofurantoin.

Table.1 Frequencies of isolates

Isolates	Frequency (%)
<i>Escherichia coli</i>	26 (50%)
<i>K.pneumonia</i>	09 (17.30%)
<i>K.oxytoca</i>	04(7.69%)
<i>P.aeruginosa</i>	05(9.61%)
<i>Acinetobacter. sp</i>	03(5.76%)
<i>Citrobacter koseri</i>	01(1.92%)
<i>P.vulgaris</i>	01 (1.92%)
<i>Candida non albicans</i>	03 (5.76%)

Table.2 Antibiogram Analysis

Total no. of urine samples = 175 ; Total no. of isolates =52 ; Gram negative isolates=49 ; Gram positive isolates=00
Fungal isolates=03

% of Antibiotic Sensitivity

Name of bacteria	Total No. Of isolates	%	Male %	Female %	Flouroquinolones		Aminoglycoside		Cephalosporins		Mono Bactams	Carbapenems		Penecillins		Urinary Antiseptics	
					CI	LV	GM	AK	CS	CZ		AO	IS	MR	PT	TC	NA
E.coli	26	50	42.2	57.6	30.76	30.76	88.46	96.15	88.46	-	46.15	100	96.15	92.30	57.69	23.07	92.30
K.pneumoniae	09	17.3	55.5	44.4	22.22	22.22	66.66	66.66	66.66	-	11.11	77.77	66.66	55.55	33.33	22.22	77.77
K.oxytoca	04	7.69	25	75	00	00	50	50	50	-	00	50	50	50	00	00	50
P.aeruginosa	05	9.61	40	60	20	20	20	60	80	60	100	40	40	60	60	00	20
Acinetobactor	03	5.76	100	00	00	00	33.33	33.33	66.66	-	00	33.33	33.33	33.33	00	00	00
C.koseri	01	1.92	00	100	100	100	100	100	100	-	00	100	100	100	100	100	100
P.vulgaris	01	1.92	100	00	100	100	00	00	100	-	00	100	100	100	100	00	00
Candida non albicans	03	5.76	33.3	66.6													

Where:

CI= ciprofloxacin
LV=levofloxacin
GM= gentamycin
AK=amikacin

CS=cefoperazome
CZ=ceftazidime
AO=aztreonam
IS=imepenem

MR=meropenem
PT=piperacillin-clavulanic acid
TC=ticarillin-tazobactam
NA=nalidixic acid

FU=nitrofurantoin

The main aim of the study was isolation, identification and characterization of microbial flora of UTI patients. It is immense importance to know their exact variations/similarities, if any, between the important organisms at genomic level by using different molecular techniques.

This will also be helpful to know the epidemiology of disease before developing any faster and safer molecular medicine method for their detection and diagnosis for UTIs in India. Assessing whether any similarities/ variations exist at genomic level among various isolates from UTIs patient were attempted for the first time in north Indian patients. This study shows effect of drugs and persistence mutations in UTI isolates and for better understanding the mechanism of unknown mutation during multidrug resistance therapy.

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