



Research Article

BACTERIAL PATHOGENS AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERN ISOLATED FROM URINARY TRACT INFECTION IN A TERTIARY CARE CENTRE

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ABSTRACT

Urinary Tract Infection (UTI) remains the most common bacterial infection in human population. The sequelae of complicated UTIs are substantial. It is well established that in the presence of obstruction, calculus, Diabetes mellitus, and other risk factors, UTIs can lead to progressive renal damage. The aim of this study was to determine bacterial agents responsible for urinary tract infection and to evaluate their susceptibility pattern. Urine sample was cultured on Cystine Lactose Electrolyte Deficient (CLED) media by calibrated loop technique. Antimicrobial susceptibility testing was performed by Kirby bauer disc diffusion method. Out of 320 samples, 155 samples revealed growth of one type of bacteria, and 15 showed growth of 2 types of bacteria. E. Coli was most common bacteria (115/185=62.16%) followed by other enterobacteriaceae, Pseudomonas and a few gram positive cocci. Many bacteria were found to be multidrug resistant while most of gram negative bacteria were susceptible to Imipenem, and most of gram positive bacteria were susceptible to linezolid.

KEYWORDS: Uropathogens, significant bacteriuria

INTRODUCTION

Urinary Tract Infection (UTI) remains the most common bacterial infection in human population affecting men and women of ages and varies dramatically in their presentation and sequelae). [1]. Annual global incidence is almost 250 million [2][3].

Most of these infections are caused by facultative anaerobes originating from intestinal flora. UTI is more common in females than in males as female urethra structurally found less effective for preventing the bacterial entry, proximity of the genital tract and urethra, and

adherence of urothelial mucosa to the mucopolysaccharide lining [4][5][6].

The sequelae of complicated UTIs are substantial. It is well established that in the presence of obstruction, calculus, Diabetes mellitus, and other risk factors, UTIs can lead to progressive renal damage [7].

Emerging drug resistance among urinary pathogens further complicate the situation, and therefore it becomes necessary to have knowledge of distribution of these pathogens and their susceptibility to antibiotics in a particular setting [8][9].

The aim of this study was to determine bacterial etiologic agents responsible for urinary tract infection and to evaluate their in vitro susceptibility pattern to commonly used antimicrobial agents.

MATERIAL AND METHODS

This study was conducted in the department of Microbiology, and department of Surgery, Gandhi Medical College & Hamidia hospital Bhopal. A hospital based study was conducted for 12 months duration where in all the patients attending OPD or hospitalised and having urinary symptoms were included in the study. A mid-stream urine sample was obtained after proper instructions in a sterile universal container. Catheterised samples were not included in the study. All the samples were processed within 30 min of collection.

Urine sample was cultured on Cystine Lactose Electrolyte Deficient (CLED) media by calibrated loop technique. Bacterial growth $\geq 10^4$ cfu/ml was considered significant. More than 2 types of bacterial colonies were regarded as collection contamination and a repeat sample was taken. Bacteria were identified by standard laboratory techniques.

Antimicrobial susceptibility testing was performed by Kirby bauer disc diffusion method for various antimicrobial agents as per CLSI guidelines.

OBSERVATIONS

A total of 320 samples were processed during the study period. Out of these, 150 were OPD patients and 170 were hospitalized patients. Among the 150 OPD patients, 71 were male and 79 were females, and among 170 hospitalized patients, 98 were male, and 79 were female. The age and gender wise distribution is shown in Chart 1.

Out of 320 samples, 106 were sterile, 19 had insignificant bacteriuria, 19 revealed growth of candida, and 9 showed growth of 3 or more type of bacterial colonies suggestive of collection contamination. A total of 170 samples showed significant bacterial growth. A total of 155 samples revealed growth of one type of bacteria, and 15 showed growth of 2 types of bacteria. E. Coli was most common bacteria (115/185=62.16%) followed by other enterobacteriaceae, Pseudomonas and a few gram positive cocci also.

The distribution of bacteria identified is shown in Chart 2.

Many bacteria were found to be multidrug resistant while most of gram negative bacteria were susceptible to Imipenem, and most of gram positive bacteria were susceptible to linezolid. Their susceptibility pattern is shown in Table 1 and Table 2.

Chart 1: Showing Age and gender wise distribution of patients

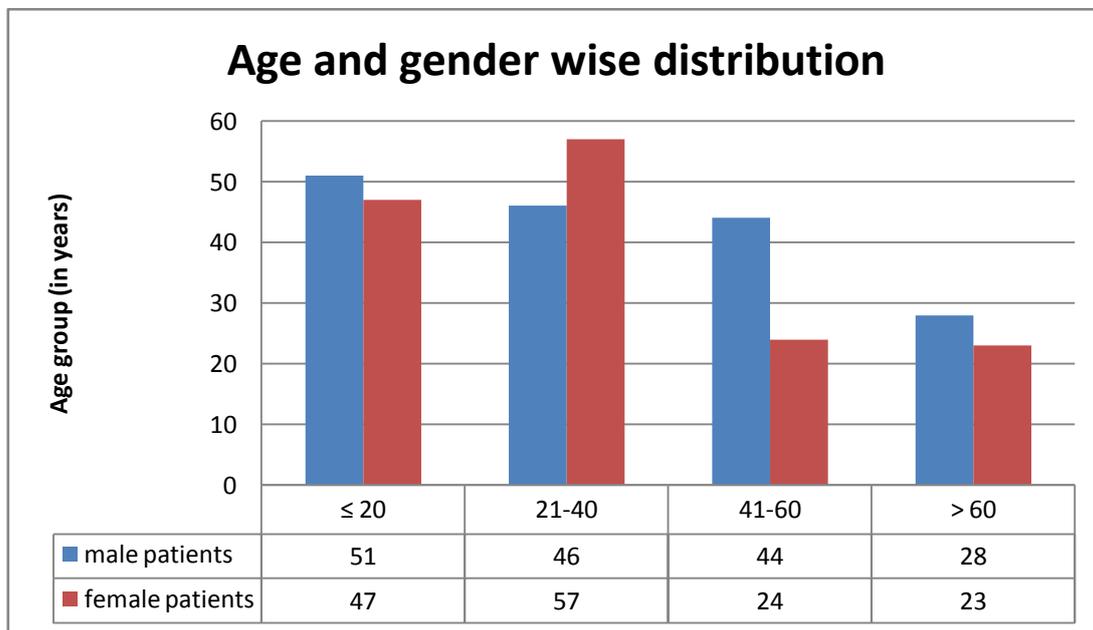


Chart 2: Showing distribution of bacterial isolates

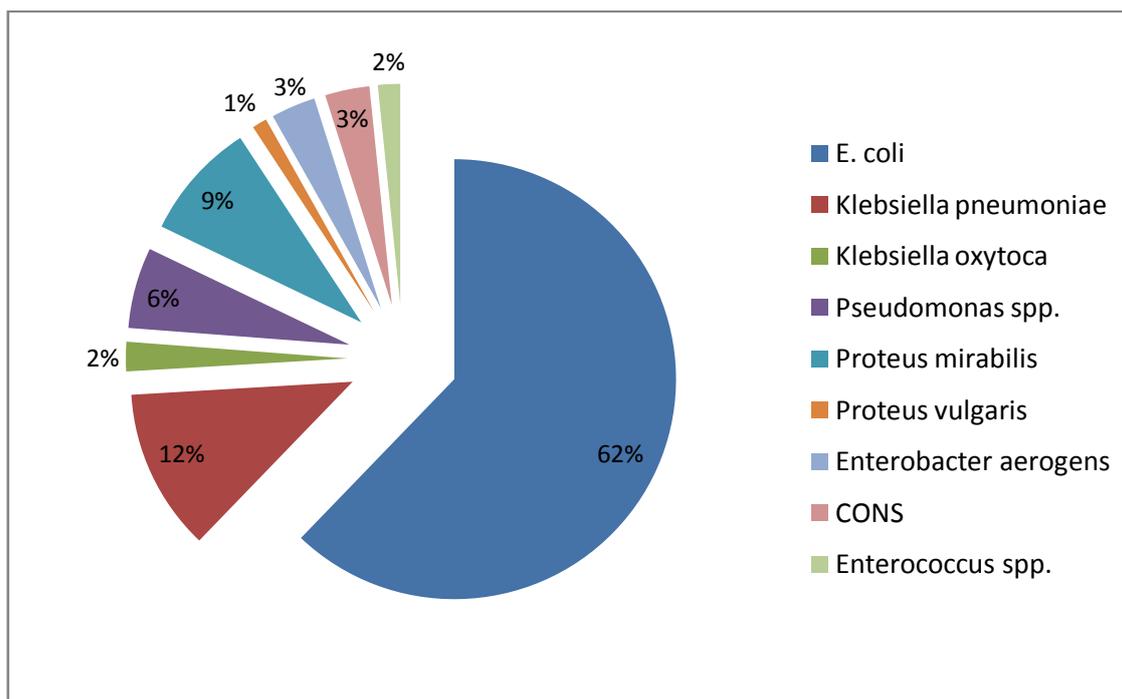


Table 1: Showing antimicrobial susceptibility pattern of gram negative bacteria

Antimicrobial agent	E. coli (n=115)	Klebsiella spp. (n=26)	Pseudomonas spp. (n=11)	Proteus spp. (n=18)	Enterobacter aerogens (n=6)
Amoxicillin	10.43	15.38	0	11.1	16.67
Cotrimoxazole	13.04	23.07	0	16.67	16.67
Gentamicin	43.47	34.6	36.36	44.44	33.33
Amikacin	64.34	50	54.54	55.56	33.33
Ciprofloxacin	14.78	19.2	9.9	22.22	33.33
Norfloxacin	39.13	34.6	45.45	38.89	50
Nitrofurantoin	46.95	50	0	55.56	50
Cephoperazone	9.56	11.5	9.9	16.67	16.67
Piperacillin	16.52	19.2	36.36	22.22	33.33
Imipenem	84.34	76.9	81.81	83.33	83.3

Table 2: Showing antimicrobial susceptibility pattern of gram positive bacteria

Antimicrobial agent	CONS (n=6)	Enterococcus spp. (n=3)
Penicillin	33.33	0
Cotrimoxazole	50	0
Ciprofloxacin	66.67	33.33
Gentamicin	66.67	33.33
Clindamicin	66.67	33.33
Linezolid	100	100
Norfloxacin	50	33.33
Nitrofurantoin	50	66.67



DISCUSSION

In our study, most common uropathogen was E. Coli (62%) followed by Klebsiella and other enterobacteriaceae, Pseudomonas, and a few gram positive bacteria like Enterococci and CONS.

Most of the studies from India and world have shown similar distribution of bacteria. In a study by Joshi et al 2011, the commonest organisms isolated were E. Coli (64%), Klebsiella (20%), Pseudomonas (9.1%) and Staphylococcus spp (6.3%)[10].

In another study by Gupta et al. 2002, the distribution of bacterial pathogens in UTI was found to be almost similar among OPD and IPD patients and E.coli, Klebsiella were being most common isolates, however some rare isolates like Acinetobacter was also reported in a few patients[11]. Many other studies have also shown similar results [12].

Looking at these studies, one can say that E. Coli and Klebsiella account for over 80% of all bacterial pathogens causing UTI.

Regarding antimicrobial susceptibility pattern, in our study we found that more than 80% gram negative isolates were susceptible to Imipenem, and around 56% to Amikacin. Around 45 to 60% susceptibility was observed for Nitrofurantoin and Norfloxacin.

Among the gram positive isolates, Linezolid was most effective drug as no resistant isolate was seen, followed by other drugs like Nitrofurantoin, ciprofloxacin, and clindamicin.

Other similar studies have revealed varying susceptibility pattern which suggests their local and geographical variation which could be multi factorial.

Thus knowing the organisms causing UTI and their susceptibility pattern is of importance to effectively treat these infections and also to formulate an antibiotic policy that may help at times for empirical treatment.

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