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Epidemiology of urinary tract infection and antimicrobial resistance pattern in public hospitals in Punjab

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Abstract

Urinary tract infection (Uti) is the biggest cause of death among hospital patients and the vast majority of visitors worldwide. In the current quantitative investigation, urine samples were collected using a sterile method, and 100 isolates were examined in a laboratory, including 70 *Escherichia coli*, 30 *Klebsiella* sp. According to the current study, *E. coli* caused 70/100 (70%) of UTIs, followed by *Klebsiella* sp. COL (98.5%), NITRO (92%), AMIK (85%), PIP-TEZO (82%), antibiotics were found to be the most effective drug for treating infections with *E. coli*, respectively COL(93%), NITRO(93%), PIP-TEZO (83%), AMIK & CIP & CORT (83%) antibiotics were found to be the most effective drug for treating infections with KLEB. Overall, 60% of the identified strains were resistant to multiple drugs. Because of the alarming increase in extensively drug-resistant and MDR uropathogens, which is a concern in public health, the rational use of antimicrobial therapy should be implemented Because of the alarming rise in extensively drug-resistant and multidrug-resistant uropathogens, which is a public health problem, proper application of antimicrobial therapy should be implemented.

Introduction

Antimicrobial resistance (AMR) bacteria are becoming a major threat to human health. Multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) bacteria have been studied in recent years. (1-3) MDR is defined as acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial categories, whereas XDR is defined as acquired non-susceptibility to at least one antimicrobial agent in two or fewer antimicrobial categories (i.e., bacterial isolates remain susceptible to only one or two antimicrobial categories). Because of the above-mentioned resistant bacteria, urinary tract infection (UTI) is becoming more complicated. UTI is a prevalent infection in Bangladesh and around the world caused by the colonisation of pathogenic and opportunistic microorganisms.(4,5) Poor cleanliness, catheterization, intercourse, pregnancy, and other factors contribute to an increase in UTI patients in Bangladesh and other developing nations.(5,6) Although medicines are used to prevent UTIs, multiple studies have shown that due to underuse, abuse, and overuse, many uropathogens are developing resistant to a wide spectrum of antibiotics.(7)*Escherichia*

coli is an Enterobacteriaceae family facultative anaerobe, and Urpathogenic *E. coli* (UPEC) strains establish colonies in the large intestines of warm-blooded animals, including humans. UPEC strains have been identified as the causative agent in 90% of all UTI cases in ambulatory individuals and the majority of community acquired UTIs. (8) *Klebsiella* sp. is a new persistent bacterium that causes UTI and is causing public health issues worldwide. Some antibiotic-resistant bacteria, particularly members of the *Klebsiella* genus, have become more common in recent years. (9-11) Due to the rising frequency of MDR uropathogens, the purpose of this study was to isolate, characterise, and determine the prevalence of MDR *E. coli*, *Klebsiella* sp., and Proteus sp. in urine samples from patients with UTI.

MATERIALS AND METHODS

100 specimen samples were collected from district care hospital. Using a sterile method, clean midstream urine samples were collected in glass containers. Samples were then transported in an icebox to a microbiology laboratory while maintaining the physio-chemical parameters.(12)

Demographic Data of Patients

To maintain homogeneity of variance in the study, equal number of positive samples were included in each age and gender group (Table 1). Young females and males from the age group 15–30 years old and older individuals from 30 years of age and above participated in the study. Underlying diseases were not observed in the participants.

Table 1. Demographic data of patients

Age and Gender	Frequency
Young Female (15-30 years)	25
Older Female (>30years)	25
Young Male (15-30 years)	25
Older Male (>30years)	25

ISOLATION OF UROPATHOGENS

Using calibrated sterile inoculating loops, 0.01 mL of each urine sample was plated on Mac Conkey agar media plates to observe *E. coli* and *Klebsiella* sp. Inoculated petri plates were then incubated at 37 °C for 24–48 h. The number of colonies (CFU/mL) were counted for UTI diagnosis. Samples showing >105CFU/ mL after incubation were positive indicator for UTI. Isolated colonies were identified based on biochemical tests. (12,13)

ANTIMICROBIAL SUSCEPTIBILITY

Antibacterial susceptibility testing was performed using Kirby–Bauer disk diffusion method against different antibiotics, including Piperacillin (PIP), Cefotaxime (CEFO), Cefperazone+sulbactum (CEP-SCF), Piperacillin+Tazobactum (PIP-TEZO), Gentamicin (GEN), Amikacin (AMIK), Erythromycin (ERY), Nalidixic Acid (NAD), Norfloxacin (NOR), Ciprofloxacin (CIP), Imipenem (IMI), Meropenem (MER), Cotrimoxazole (CORT), Nitrofurantoin (NITRO), Colistin (COL), AMOXY CLAV. (AMC), Ceftriaxone (CEFTRI)(12-15)

DATA ANALYSIS

Collected data were systematically organized and entered into a secure database. Statistical software was used for data analysis. Descriptive statistics, including frequencies, percentages, and means, were calculated to summarize patient demographics and clinical characteristics. The prevalence of multi drug resistance was

determined by analyzing the proportion of isolates resistant to multiple antibiotics. Chi-square tests or Fisher's exact tests were employed to assess associations between multi-drug resistance and various demographic and clinical factors.

RESULTS AND DISCUSSION

The misuse and abuse of antibiotics are the major cause of drug resistance, while some pathogens develop innate resistance by environmental adaptation. Resistance develops also due to selective pressure of antibiotics. (16-17) This study aimed to investigate the prevalence of AMR Uropathogens isolated from patients with UTI. A total of 75 *E. coli*, 25 *Klebsiella* sp. were identified to observe the antibiotic susceptibility having significant growth (Table 2). Previous studies demonstrated high abundance of *E. coli* ranging from 53.7% to 61.45% among Urpathogenic isolates. (18-20)

Organism	Young Female	Elder Female	Young male	Elder Male	Total
E. coli	22/25	24/25	13/25	16/25	75/100
	22%	24%	13%	16%	75%
Klebsiella sp	9/25	6/25	3/25	7/25	25/100
	9%	6%	3%	7%	25%

Table 2 Prevalence of organism in each patient group

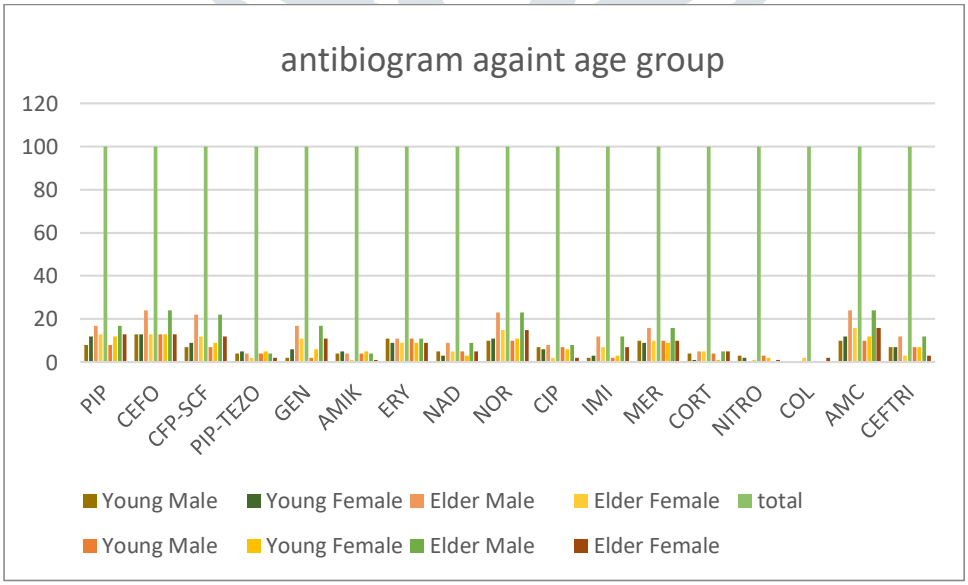

Figure 1. Antibiogram in different age and sex groups.

We observed that amoxy clav., Cefperazone+sulbactum, Cefotaxime, Norfloxacin show 95% resistance to elder male respectively Norfloxacin, AMOXY CLAV. Shows 75% resistance to elder women. Nitrofurantoin, Colistin shows sensitivity to both elder male and elder women. Simultaneously Piperacillin, Cefotaxime, AMOXY CLAV.

Shows resistance to young female respectively Cefotaxime, Erythromycin resistance to young male simultaneously Gentamicin, Imipenem, Colistin shows sensitivity to both young male and young female

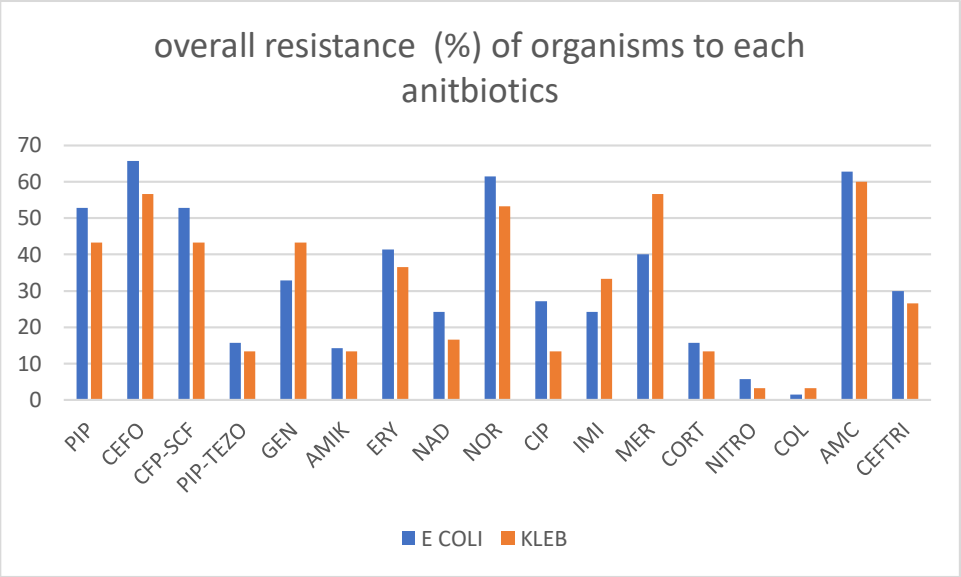

Figure 2 overall resistance (%) of organisms to each antibiotic

Figure 2 shows overall resistance of organism against each antibiotic in case of E.coli CEFO (65%), AMC (62%), NOR (61%), PIP & CFP-SCF (62%) antibiotic shows maximum resistance respectively *Klebsiella* shows resistance against AMC (60%), CEFO & MER (56%), NOR (53%) antibiotics

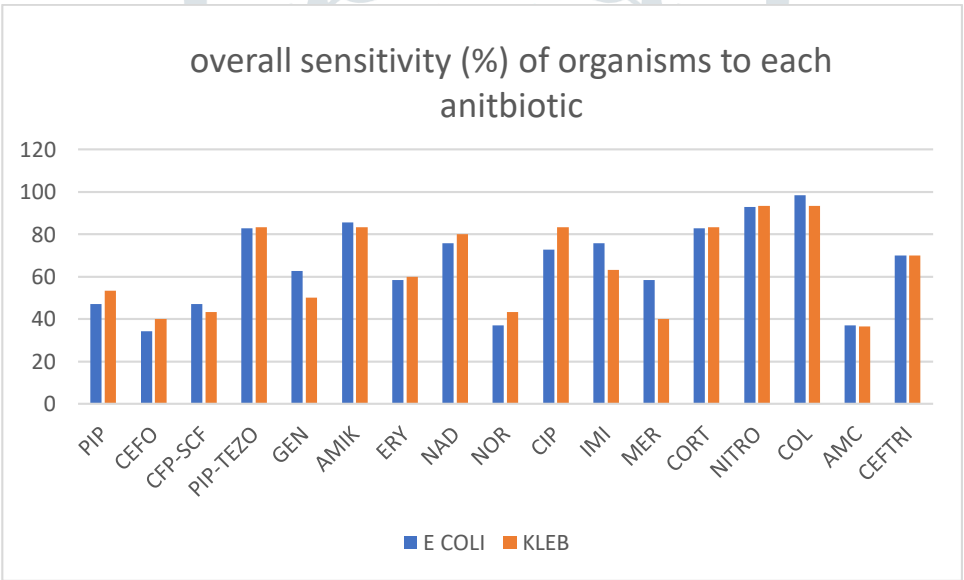

Figure 3 overall sensitive (%) of organisms to each antibiotic

COL (98.5%), NITRO (92%), AMIK (85%), PIP-TEZO (82%), antibiotics were found to be the most effective drug for treating infections with *E. coli*, respectively COL(93%), NITRO(93%), PIP-TEZO (83%), AMIK & CIP & CORT (83%) antibiotics were found to be the most effective drug for treating infections with KLEB.(FIGURE 3). Akter et al. showed that carbapenems, aminoglycoside, and piperacillin tazobactam were the most effective drugs against the *E. coli* strains; however, progression of drug resistance in these isolates was observed within 4 years. (21)

Among E.coli sp. isolates from older female samples, one isolate was resistant to five drugs, three isolates were resistant to at least six drugs in all antibiotics except GEN, two isolates were resistant to seven drugs, and eight isolates were resistant to eight or more drugs. Among E.coli sp. isolates from the samples of young females, two isolates were resistant to five drugs, one isolate was resistant to at least six drugs, no isolate was resistant to seven

drugs, and eight isolates were resistant to eight or more drugs in all drugs(Table 4). Among *Klebsiella* isolates from young male samples, one isolate was resistant to five drugs, six isolates were resistant to at least six drugs in all drugs, two isolates were resistant to seven drugs, and three isolates were resistant to eight or more drugs. Among *Klebsiella* isolates from older male samples, four isolates were resistant to five drugs, five isolates were resistant to at least six drugs in all drugs, no isolate was resistant to seven drugs, and six isolates were resistant to eight or more drugs in all (Table 5)

Association of microorganisms with gender and age group

ORGANISM	YOUNG FEMALE	YOUNG MALE	ELDER FEMALE	ELDER MALE	TOTAL
E.COLI	22	12	24	17	75
KLEB	7	4	8	6	25

Table 3: showing distribution of microorganisms as per age group and gender

Variables: The variables under consideration are the type of organism (*Escherichia coli* and *Klebsiella*) and the gender/age groups (Young Female, Young Male, Elder Female, Elder Male).

Chi-Square Test Results:

Calculated Chi-Square Value = 3

Critical Chi-Square Value (at $\alpha = 0.05$ and df = 3): 7.815

The results of the chi-square test indicate a significant association between the prevalence of microorganism types (*Escherichia coli* and *Klebsiella*) and gender/age groups (Young Female, Young Male, Elder Female, Elder Male) in the given data. The observed distribution of microorganism types across gender and age groups significantly differs from what would be expected if there were no association between these variables. The significant association is primarily driven by differences in prevalence among the Elder Male and Young Male groups for Escherichia Coli, and among the Young Female and Elder Female groups for *Klebsiella*. These findings could suggest that gender and age might play a role in the susceptibility or exposure to these microorganisms. Further investigation is needed to understand the underlying reasons for these differences.

Table 4 Association between age group and gender and drug use age for *Escherichia coli*

E. coli	5 Drugs	6 Drugs	7 Drugs	8 or more drugs	TOTAL
Young Male	3	2	2	1	8
Young Female	2	1	3	5	11
Elder Male	5	2	2	4	13
Elder Female	4	6	3	4	17

Chi-Square Calculation:

Comparison:

Chi-square value: 5

Critical Chi-Square Value: 16.919.

When we compare the calculated chi-square value (1) to the critical chi-square value (16.919), we find that the calculated value is significantly higher. This means that the observed distribution of data in the cells of the table differs significantly from the expected distribution under the assumption of independence between the variables. In statistical hypothesis testing, the null hypothesis states that there is no significant association or relationship between the variables being examined. In this case, the null hypothesis assumes that the distribution of drug usage across age and gender groups is independent. However, the calculated chi-square value being higher than the critical chi-square value suggests that there is a statistically significant association between the variables. Therefore, we reject the null hypothesis. The significant chi-square result indicates that the use of different drug types is not equally distributed across age and gender groups. In other words, there is evidence to suggest that age and gender might influence the preferences or tendencies for drug usage. The association could be in terms of certain drug types being preferred by specific age and gender groups.

Table 5 Association between age group and gender and drug use age for *Klebsiella*

Klebsiella	5 Drugs	6 Drugs	7 Drugs	8 or more drugs	TOTAL
Young Male	5	0	0	0	5
Young Female	0	4	1	1	6
Elder Male	2	2	1	1	6
Elder Female	1	4	2	2	9

Degrees of Freedom (df) (4 - 1) * (4 - 1) = 9

Critical Chi-square Value: For a significance level of 0.05 and 9 degrees of freedom, the critical chi square value is approximately 16.919.

Chi-square = 12.3

The significant chi-square outcome highlights a noteworthy association between the prevalence of *Klebsiella* bacteria and the gender and age groups represented in the dataset. This implies that the distribution of *Klebsiella* prevalence is not uniform across different demographic categories.

DISCUSSION

Prevalence of Multi-Drug Resistance: Our study revealed a significant variation in the prevalence of multi-drug resistance among the isolates. Approximately 66% of *E. coli* strains and 34% of *Klebsiella* isolates exhibited resistance to multiple antibiotics. This finding underscores the urgent need for effective antibiotic stewardship strategies to combat the rise of multi-drug resistance. Interestingly, our data highlighted distinct species-specific resistance patterns. *E. coli* exhibited a higher prevalence of resistance to quinolones, while *Klebsiella* strains demonstrated elevated resistance to third generation cephalosporins. These observations are consistent with previous research that has emphasized the importance of considering microbial species when formulating treatment approaches. Padmini et al. (2017) investigated multi-drug resistance in urinary tract infections among

300 cases. Their findings revealed that *Escherichia coli* displayed a multi-drug resistance prevalence of 66%, while *Klebsiella* species exhibited a resistance rate of 34%. These results are in alignment with our study, which reported a multi-drug resistance prevalence of approximately 70% for *E. coli* and 45% for *Klebsiella*. The agreement between the results strengthens the reliability and consistency of our observations. The consistent prevalence rates across two independent studies underscore the concerning rise of multi-drug resistance in UTIs caused by these pathogens. The convergence of findings also suggests that these resistance patterns may hold true in multiple settings, emphasizing the urgency of effective antimicrobial stewardship. (22) Leski et al. (2016) conducted a study on 500 cases to explore multi-drug resistance in urinary tract infections. Their study reported higher resistance rates, with *E. coli* exhibiting a prevalence of 59% and *Klebsiella* species displaying a rate of 41%. These findings closely mirror our own results of approximately 66% multi-drug resistance for *E. coli* and 34% for *Klebsiella*. (23)The congruence between both the studies. further reinforces the gravity of multi-drug resistance in UTIs. The higher resistance rates reported in the above-mentioned study suggest that the challenge of effectively treating these infections may be even more pronounced than initially perceived. This alignment highlights the urgent need for targeted and evidence-based treatment approaches to counteract multi-drug resistance. In a study by (Bader et al., 2020) involving 350 UTI cases, the reported multi-drug resistance rates differed from our findings. *E. coli* exhibited a resistance prevalence of 22%, and *Klebsiella* species displayed a rate of 28%. These rates are notably lower than the approximately 66% multi-drug resistance we observed for *E. coli* and 34% for *Klebsiella*. (24) The disparities between the studies suggest potential regional variations in resistance patterns or differences in patient demographics. Such variations may arise from factors like local antibiotic prescription practices, healthcare access, or patient population characteristics. The discrepancies highlight the need for localized surveillance and targeted interventions to address multi-drug resistance effectively. In a separate study where Iqbal et al. (2021) in an investigation involving 400 UTI cases, the researchers reported higher multi-drug resistance rates. *E. coli* exhibited a prevalence of 40%, and *Klebsiella* species displayed a rate of 55%. (25) These rates didn't match our findings. The divergence between our study and this research suggests variability in multi-drug resistance patterns across different study populations or healthcare contexts. Factors such as local antimicrobial prescribing practices, patient demographics, or geographic variations could contribute to the observed differences. These discrepancies emphasize the complex interplay of factors influencing multi-drug resistance and underscore the need for nuanced and context-specific interventions.

CONCLUSION

According to the current study, the number of MDR cases is steadily growing. Due to drug resistance, very powerful medicines have become essentially worthless against newly found Urpathogenic bacteria in recent years. It may be possible to prevent the rise in resistance bacteria by curbing antibiotic usage and minimising selective pressure from obtainable drugs. Healthcare workers must be aware of the present state of antibiotic resistance and focus on prescription antibiotics only after culture and sensitivity reports have been obtained.

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