

**TO STUDY THE PREVALENCE OF URINARY TRACT INFECTION
AND THE MOLECULAR CHARACTERIZATION WITH SPECIAL
REFERENCE TO *FIM H* GENE IN UROPATHOGENIC *E. COLI*
ISOLATED FROM URINE SAMPLES AT A TERTIARY CARE
HOSPITAL**

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ABSTRACT

BACKGROUND

UTIs are common infections that happen when bacteria, often from the skin or rectum, enter the urethra, and infect the urinary tract. Most hospital visits globally are caused by urinary tract infections, which are also a major cause of morbidity and comorbidity in patients with underlying medical conditions. UPEC strains are the most common pathogens, accounting for 85% and 50% of community and hospital-acquired UTIs. UPEC strains have unique virulence characteristics, including type 1 fimbriae, which can result in worsening of UTIs.

AIM AND OBJECTIVE

To Study the Prevalence of Urinary Tract Infection of Uropathogenic *E.coli* and the Molecular Characterization with Special Reference to *Fim H* gene from Urine Samples at a Tertiary Care Hospital

MATERIAL & METHODS

This was a cross-sectional study carried out in the Department of Microbiology at a tertiary care hospital for a period of 12 months i.e, 2023 to 2024. A total of 450 Patients were screened from 1000 clinical isolates where 450 were positive of all the age groups and both sex with indwelling urinary catheters for at least 2 days, who were suffering from the symptoms of UTIs (fever > 38°C, urgency, frequency dysuria or suprapubic tenderness) were included in this study. The Antibiotic Susceptibility testing was performed according to the CLSI guidelines 2023. If delayed, samples were refrigerated and processed within 4 - 6 hrs. The identification, biochemicals and the AST pattern was

done according to the CLSI guidelines 2023. The DNA was extracted using the Qiagen DNA Extraction kit and the FIM H gene was detected by the conventional PCR assay.

RESULTS

In the present study the maximum number of cases were found in the age group of 31-40 (44.8%) years, followed by 21-30 (26.2%). the age group of 0-10 (0.6%) years and more than 71 years (2.8%) was least affected with urinary tract infection. It was observed that the Females 284 (63.1%) were more affected with the infection as compared to the Males 166 (36.8%). In the current study *E.coli* (40%) was the most common followed by *Klebsiella spp.* (26.6%), *Pseudomonas aeruginosa* (12.2%), *Staphylococcus aureus* (6.6%), *Acinetobacter baumannii* (5.6%), *Proteus* (5.1%), *Enterococcus* (3.5%). The bacterial isolates were observed to be more sensitive with 89.2% to Imipenem and Nitrofurantoin. The bacterial resistant rate for Ampicillin was observed to be 88.8% followed by Co-trimoxazole (91.1%) and cefotaxime with 89.1%.

The Molecular characterization reveals that in the current study there was FIM H gene studied. In the fim H gene there were 135 (91%) positive cases and negative were 15 (10%). It was observed that from the 5 (35.7%) negative cases that were negative for the association of biofilm formation there were 126 (92.6%) which were positive for the virulence gene Fim H gene.

CONCLUSION

In this study we concluded that UTI was most common in females than males. Symptoms like Dysuria, abdominal pain and chills were found most common in patients having urinary tract infections. Therefore, Regular check-ups and strict adherence to antibiotic stewardship protocols can lower the cost of UTI prophylaxis. By performing these regular examinations, the expense of UTI prevention can be decreased.

KEYWORDS: UTI, Dysuria, Chills, CLSI, Molecular characterization, fimH , DNA, PCR

INTRODUCTION

Urinary tract infections (UTIs) are one of the most common bacterial infections in humans, both in the community as well as in the hospital settings involves one or more structures in the urinary system. The Urinary tract infections are inflammations caused by abnormal growth of the pathogens [1,2]. It is caused by the invasion of the genitourinary tract, which extends

from the renal cortex of the kidney to the urethral meatus [3]. The Enterobacterales order is the most common etiological agent of urinary tract infections because they have several factors associated with their attachment to the uroepithelium such as possession of adhesins [4]. *Escherichia coli* has been documented to be the most common pathogen associated with urinary tract infections in community as well as

hospital settings in many countries [5,6]. Other pathogenic species such as *Klebsiella*, *Enterococcus*, *Staphylococcus aureus*, *Coagulase negative staphylococcus*, *Enterobacter*, *Citrobacter*, *candida*, *Proteus*, *Morganella*, *Providencia*, etc may also accountable for UTI [7].

Uropathogenic *E. coli* (UPEC) strains are the most commonly isolated organisms in community-acquired UTIs (70 to 90%) and among the most commonly isolated in nosocomially acquired UTIs (50%) including CAUTIs [8].

Escherichia coli is a gram-negative, facultatively anaerobic, rod-shaped, coliform bacterium of the genus *Escherichia* and family Enterobacteriaceae that is commonly found in the lower intestine of warm-blooded organisms (endotherms) [9,10].

Uropathogenic *E. coli* (UPEC) is a bacterium that can colonize the bladder and cause cystitis, and in some cases, it can also travel up the ureters to the kidneys and cause pyelonephritis. This organism is a common cause of UTIs, and it is important for healthcare providers to be aware of the potential for recurrent infections in women who have previously experienced UTIs [11].

In recent years, research has suggested that the formation of biofilm on the urinary catheter may play a critical role in the development and resistance to treatment of CAUTIs.

The presence of biofilm formed by *E. coli* on catheters makes CAUTI one of the most prevalent nosocomial infections [12]. The Gram-positive bacteria as well as the Gram-negative bacteria have the capability in forming biofilms. Bacteria commonly involved include *Enterococcus faecalis*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus viridans*, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus mirabilis*, and *Pseudomonas aeruginosa* [13].

The severity of UTI depends on the virulence of the bacterium and host sensitivity [14]. A number of virulence factors are involved in biofilm formation in *E. coli*, including hemolysin, fimbriae, lipopolysaccharides (LPS), secreted proteins, capsules, and iron-acquisition systems, allowing attachment and bacterial colonization in mucosal epithelial cells lining the urinary tract.

Several virulence factors of UPEC strains are encoded on different PAIs including PAI I536, PAI II536, PAI III536, PAI

IV536, PAI ICFT073, PAI IICFT073, PAI IJ96 and PAI IJ96.

These virulence factors are required to overcome host immunity and include - hemolysin, which aids host invasion, and adhesins, which bind UPEC to the urinary tract epithelium as P-fimbrial adhesions and S-fimbrial adhesins, the cytotoxic necrotizing factor which assists dissemination and persistence of infection in the urinary tract and the iron acquisition systems (aerobactin and yersiniabactin) [15].

Uropathogenic *E. coli* strains are pathogenic due to virulence factors such as adhesion fimbriae (fim-H, iha), toxins (cnf1, hlyA), iron-forming systems (iroN, aer), macrophage degradation agents (ompTprotease), and serum resistance factors (traT), which are commonly encoded in Pathogenicity Islands (PAI). Besides, serum resistance factors (traT) contribute to the pathogenesis of *E. coli* strains in UTIs [16].

Two main virulence determinants of UPEC isolates are involved in biofilm formation: type 1 fimbriae (*fim*), coded by the *fim* gene cluster and Siderophores's Aerobactin coded by aer gene cluster.

The Bacteria adhere to the surfaces and then through irreversible attachment, and eventually develop into an adherent biofilm.

The rapid assessment of virulence determinants detected by polymerase chain reaction (PCR) may be useful for diagnosis and therapeutic strategies. The genetic determinants were those coding for type 1 fimbriae (fimH), pili associated with pyelonephritis (pap), S and F1C fimbriae (sfa and foc), afimbrial adhesins (afa), hemolysin (hly), cytotoxic necrotizing factor (cnf), and aerobactin (aer). FimH protein is the precursor of 300 amino acids.

Due to the increasing infections associated with *E. coli* and different factors involved in bacterial pathogenesis in different parts of the world, as well as the emergence of drug-resistant strains, its virulence gene and correlation of the biofilm formation in uropathogenic *E. coli* it seems necessary to study pathogenic factors in drug-resistant bacteria [17]

Drug-resistant bacterial strains and the high incidence of UTIs should highlight the need for greater understanding of microorganisms that UTIs and their antibiotic susceptibility pattern [18]. Among UPEC adhesions, the sticky subunit

of type 1 fimbriae, FimH, is a crucial factor, with high tropism for urinary tract receptors; consequently, FimH adhesion is important in colonising diverse niches of *E. coli*.

Therefore, the present study was undertaken to study the prevalence of Urinary Tract Infection and the Molecular Characterization with special reference to *Fim H* gene in uropathogenic *E. coli* isolated from urine samples at a Tertiary care Hospital.

MATERIAL AND METHODS

This was a cross-sectional study carried out in the Department of Microbiology at a tertiary care centre. A total of 450 Patients were screened from 1000 clinical isolates where 450 were positive of all the age groups and both sex with indwelling urinary catheters for at least 2 days, who were suffering from the symptoms of UTIs (fever > 38°C, urgency, frequency dysuria or suprapubic tenderness) were included in this study . The Antibiotic Susceptibility testing was performed according to the CLSI guidelines 2023. If delayed, samples were refrigerated and processed within 4 - 6 hrs. The identification , biochemicals and the AST pattern was done according to the CLSI guidelines 2023. The DNA was extracted using the Qiagen DNA Extraction

kit and the FIM H gene was detected by the conventional PCR assay.

Antibiotic susceptibility testing:

Antibiotic susceptibility testing was performed by using standard Kirby–Bauer disk diffusion method by applying a set of antibiotics on pre seeded Muller Hinton Agar plate with *E. coli* isolates. The antibiotic disks (HiMedia) used were ampicillin (10 µg), piperacillin/tazobactam (100/10 µg), ceftriaxone (30 µg), cefotaxime (30 µg), ciprofloxacin (5 µg), norfloxacin (10 µg), amikacin (30 µg), gentamicin (10 µg), cotrimoxazole (1.25/23.75 µg), ceftazidime + sulbactam (75/30 µg), imipenem (10 µg), meropenem (MRP; 10 µg) and Nitrofurantoin(30 µg). Antibiotic susceptibility/resistance was recorded in accordance with Clinical and Laboratory Standards Institute guidelines 2023 [19].

ISOLATION AND IDENTIFICATION OF *E.COLI*:

Culture and identification: The urine samples were inoculated onto Cystine Lactose Electrolyte Deficient (CLED) medium with calibrated loops to determine the Colony Forming Units (CFU). The identification of the isolates was done on

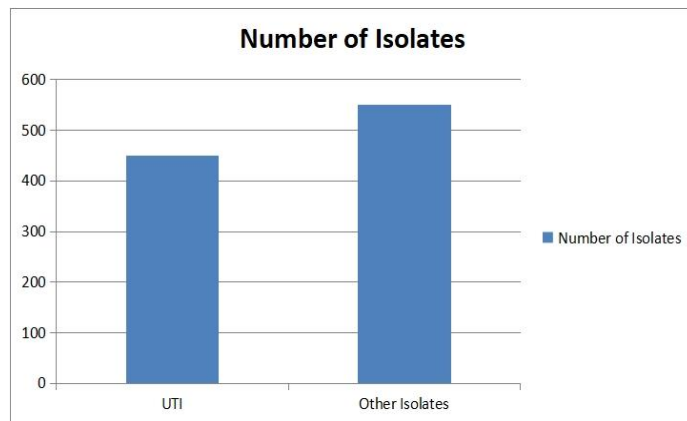
the basis of the colony morphology, gram staining and the standard biochemical tests (catalase test, Indole, Methyl red, Voges-Proskauer test, nitrate reduction, urease production, simmons citrate agar) with the following preliminary and biochemical tests done by standard recommended laboratory methods according to the CLSI guidelines [19].

RESULTS

In the present study a total of 1000 clinically suspected cases were screened out of which total 450 isolates was found positive for UTI infection . Therefore, the prevalence rate of *UTI* was found to be 45%.

S.No.	Type of Isolates	Total No. of samples (n=1000)	Percentage
1.	UTI	450	45%
2.	Other Isolates	550	55%

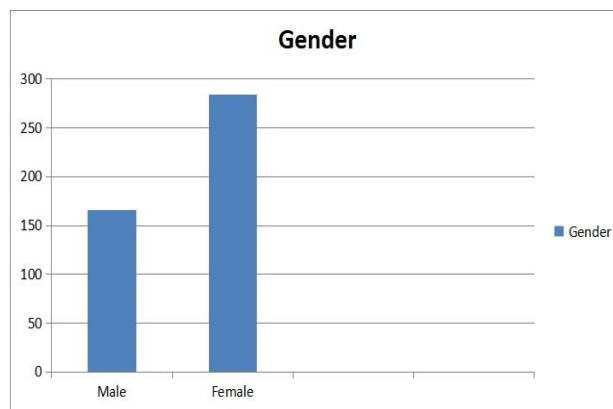
Table No. 1: Total Number of Cases



Graph 1: Total Number of Cases

S.N O.	GENDER	TOTAL NO. OF ISOLATES (N=450)	PERCENT AGE
1.	Male	166	36.8%
2.	Female	284	63.1%

Table No. 2: Gender wise distribution of the Isolates



Graph No. 2: Graphical Representation of the Genderwise distribution

S.NO.	Age	No. of Isolates (n=450)	Percentage
1.	0-10	3	0.6%
2.	11-20	12	2.6%
3.	21-30	118	26.2%
4.	31-40	202	44.8%
5.	41-50	61	13.5%
6.	51-60	25	5.5%
7.	61-70	16	3.5%
8.	≤ 71	13	2.8%

Table No. 3: Agewise distribution of the Isolates

From the present study it was observed that the Females 284 (63.1%) were more affected with the infection as compared to

the Males 166 (36.8%). It was also noted that the age group of 21-30 years of age followed by 31-40 was affected the most. In the age group of 0-10 years and above 71 years was the least affected with the infection.

To study the different Phenotypic Tests For the detection and Identification of:

identified by studying colony characteristics, production of pyocyanin pigments, grapelike odour, growth at 42°C, motility test, Gram staining, and biochemicals was performed according to the CLSI guidelines [66].

Biochemical Test For The Phenotypic Detection

S.No.	Type of the Test
1.	Catalase Test
2.	Oxidase Test
3.	OF Test
4.	Urea Hydrolysis Test
5.	Citrate Utilization Test
6.	Mannitol Motility Test
7.	Triple Sugar Iron Test

Table No. 4: Biochemical Test

Table No. 5 : Types and Number of isolation isolated

Type	No. of Isolates	
<i>E.coli</i>	180	40%
<i>Klebsiella spp.</i>	120	26.6%
<i>Pseudomonas aeruginosa</i>	55	12.2%
<i>Acinetobacter baumannii</i>	26	5.6%
<i>Staphylococcus aureus</i>	30	6.6%
<i>Proteus</i>	23	5.1%
<i>Enterococcus</i>	16	3.5%
Total	450	100%

Graph 3: Types and Number of isolation isolated

In the current study *E.coli* (40%) was the most common followed by *Klebsiella spp.*(26.6%), *Pseudomonas aeruginosa* (12.2%), *Staphylococcus aureus* (6.6%), *Acinetobacter baumannii* (5.6%), *Proteus* (5.1%), *Enterococcus* (3.5%).

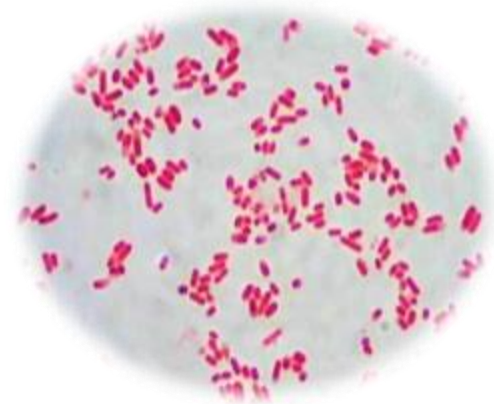
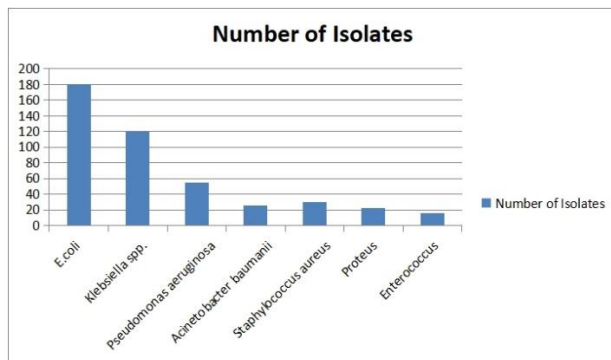


Figure 1: Microscopic examination of *E.coli*



Days of catheterization	Gender		Total
	Female	Male	
1-3	15 (5.2%)	5 (3.0%)	20 (4.4%)
4-7	170 (59.8%)	82 (49.3%)	252 (56%)

8-12	96(33.8%)	75 (45.1%)	171 (38)
13-14	3 (1%)	4 (2.4%)	7(1.5%)
Total	284(100%)	166(100%)	450(100%)

P= 0.02; Significant;

Table No. 6 : Days of catheterization-Frequency distribution of patients studied

Table No. 7:COMORBID CONDITIONS- Frequency distribution of patients studied

Variables	Gender		Total	P Value
	Female	Male		
DIABETICS				
• No	240 (84.5%)	136 (81.9%)	376(83.5%)	0.563
• Yes	44 (15.4%)	30 (18%)	74 (16.4%)	
HYPERTENSION				

• No	215(75.7%)	100 (60.2%)	315(70%)	0.052
• Yes	69(24.2%)	66 (39.7%)	135(30%)	
KIDNEY DISEASE				
• No	220 (77.4%)	128 (77.1%)	348(77.3%)	0.04
• Yes	64 (22.5%)	38(32.7%)	102(22.6%)	
Total	284(100%)	166(100%)	450 (100%)	

Chi-Square Test/Fisher Exact Test

P= 0.052 and P= 0.04 Significant; P= 0.563; Not Significant,

Table No. 8: COMORBID CONDITIONS- Frequency distribution of patients studied

Days since Fever	Gender		Total
	Female	Male	

1-3	114(40%)	69 (41.5%)	183(40.6%)
4-7	160(56.3 %)	91(54.8%)	251(55.7 %)
8-12	10(3.5%)	6(3.6%)	16 (3.5%)
Total	284 (100%)	166(100 %)	450(100%)

P=0.0766, Not Significant,

Chi-Square Test

Table No. 9: SIGNS AND SYMPTOMS

Variable s	Gender		Total	P val ue
	Femal e	Male		
DYSURI A				
• N o	54(19 %)	29 (17.4 %)	83 (18.4 %)	0.0 10
• Y es	230 (80.9 %)	137 (82.5 %)	367 (81.5 %)	
ABDOM INAL PAINS				
• N o	76 (26.7 %)	45 (27.1 %)	121 (26.8 %)	0.3 10
• Y es	208 (73.2 %)	121 (26.8 %)	329 (73.1 %)	

CHILLS				
• N o	84 (29.5 %)	32 (19.2 %)	116 (25.7 %)	0.0 27
• Y es	200 (70.4 %)	134 (80.7 %)	334 (74.2 %)	
Total	284(10 0%)	166(10 0%)	450(10 0%)	

P=0.010 and P=0.027

Significant, P= 0.310 Not Significant

In the current study among 284 females, symptoms like Dysuria present in 230 cases (80.9%), Abdominal pains present in 208 cases (73.2%) and Chills present in 200 cases (70.4%).

Among 166 males, symptoms like Dysuria, abdominal pain and chills present in 82.5%, 26.8% and 80.7% respectively.

Out of 284 females, maximum number of UTI cases were occurred in those where days of catheterization were between 4 -7 days.

The Identification of Drug Resistance Pattern : Antibiotic susceptibility testing was performed by Kirby bauer Disk



diffusion method as per the CLSI guidelines .

Fig 2: ZONE OF INHIBITION OF 18MM OBSERVED

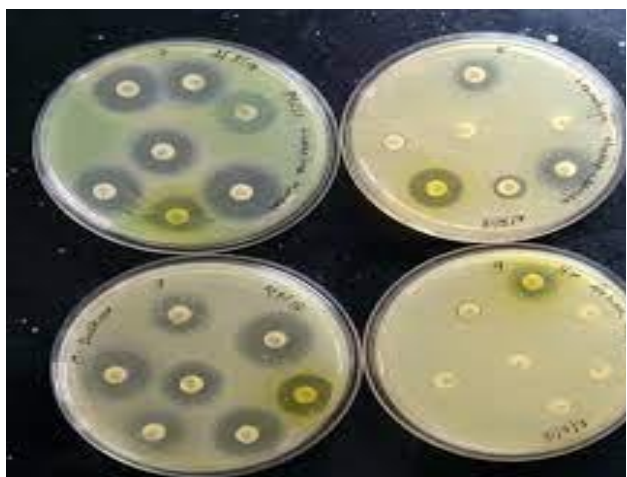


Figure 3: AST plate for *E.coli* against Antibiotics ; zones of growth inhibition for Meropenem referred > or = 14 (susceptible), 12-13 (intermediate) and < or = 11 (resistant) mm.

Table No. 10: Antibiotic resistance/Sensitivity pattern of patients studied

Antibiotic	Strength In µg	RESISTANCE N=450	SENSITIVITY N=450
AMP	100 µg	400 (88.8%)	50(11.1%)
PTZ	20 µg	190 (42.2%)	260 (57.7%)
CTR	30 µg	401 (89.1%)	49 (10.8%)
CTX	30 µg	401 (89.1%)	49 (10.8%)
CIP	5 µg	401(89.1%)	49 (10.8%)
NOR	30 µg	395(87.7%)	55(12.2%)
AMK	10 µg	110(24.4%)	340 (75.5%)
GEN	10 µg	390 (86.6%)	60 (13.3%)
COT	10 µg	410(91.1%)	40 (8.8%)
CFS	50 µg	85 (18.8%)	365 (81.1%)
IMP	10 µg	47 (10.4%)	403 (89.5%)

MERO	10 µg	98(21.7%)	352(78.2%)
NIT	30 µg	47 (10.4%)	403 (89.5%)
Total		450(100%)	450 (100%)

Variables	No. of Patients	%
FIM H		
• Negative	25	13.8
• Positive	155	86.1
Total	180	100.0

Table No. 11: Detection of fim H Gene

In the current study there was fim H gene studied. In the fim H gene there were 155 (86.1%) positive cases and negative were 25 (13.8%).

Variables	Biofilm Result		Total
	Negative	Positive	
fim H			
• Negative	10 (40%)	15 (9.6%)	25 (13.8%)

• Positive	15 (60%)	140 (90.3%)	155 (86.1%)
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Table No. 12: FIM H GENE-Frequency distribution in relation to Biofilm results

In the current study it was clear that from the 10 (40%) negative cases that were negative for the association of biofilm formation there were 140 (90.3%) which were positive for the virulence gene Fim H gene



Figure No.4: The Gene Extraction FIMH gene:

L corresponds to the DNA Ladder; L1 corresponds to the sample positive for FIMH gene; L2 is the Negative Control for FIMH gene; L3-L6 are the sample positive for FIMH gene

DNA Ladder

269BP

DISCUSSION

In clinical practice, urinary tract infections (UTIs) are among the most prevalent infections. Around the world, empirical treatment for both severe and uncomplicated UTIs has been used because delaying treatment could increase morbidity and death. Over 15% of all outpatient antibiotic prescriptions are for UTIs, which is a public health concern [20]. Biofilm-forming infections are linked to AMR and recurrent UTIs, both of which are on the rise worldwide at the moment.

[21]. However, there is a dearth of information on biofilm-forming UTI characterisation in connection to AMR rates in sub-Saharan Africa. We show a high rate of antibiotic resistance to routinely used antibiotics, a significant number of outpatient clinic patients with UTI symptoms developed UTIs, and 50% of UPEC isolates formed.

In the present study, the prevalence rate of UTI in Female was more than Male (Female 63.1% and Male 36.8%) which was in accordance with other studies the incidence of UTIs in women also was higher. The results of these studies are consistent with the results of our study, due

to anatomical differences between men and women, including a short urethra and its external opening adjacent to the vagina and anus in women.

Study	Year	Result
Ghimire A et al., [22]	2018	M-43.16% F-56.83%
Mohapatra A et al., [23]	2022	M-27.5% F-72.5%
Mlugu, E.M. et al., [24]	2023	M-23.6% F-76.4%
Hawra AL Lawati et al., [25]	2024	M- 40% F- 60%
Present Study	2023	M-36.8% F-63.1%

Table No. 14 : Comparison of gender wise distribution with other study

In our study, most commonly affected age group was 31-40 yrs (44.8%) followed by 21-30 yrs (26.2%) which was in accordance to study [23] 2022 most commonly affected age group was 19-35yrs (56.9%).

In our study the most common risk factor was Hypertension (30%), diabetes mellitus (16.4%) follow by Kidney disease (22.6%)

.The other study of risk factors are as depicted in Table

Study	Year	Result
Akhtar A et al., [26]	2021	Diabetics-43.1 Hypertension-33.9 Kidney Disease-10.4
Karishetti M et al., [27]	2019	Diabetics-9.71 Kidney Disease-7.94
Present Study	2023	Diabetics-16.4 Hypertension-30 Kidney Disease-22.6

Table No. 15: Distribution of Comorbidity of UTI with other study.

In the present study , Most of the patients had Dysuria (81.5%), followed by pain abdomen (73.1%), and chills (74.2%). This finding was in accordance [28] were the most common presenting symptoms were urinary complaints (63%) such as burning micturition (dysuria), increased frequency of micturition followed by fever (23%), pain abdomen (11%), and other nonspecific complaints (3%).and similar study [27]

were most of the patients had fever with chills (65.60%), followed by pain abdomen (47.00%), and dysuria (2.60%) .

In our study, the most common organisms were *Escherichia coli* (40%), *Klebsiella spp* (26.6%), *Pseudomonas aeruginosa* (12.2%), *Acinetobacter baumannii* (5.6%), *Staphylococcus aureus* (6.6%), *Proteus* (5.1%) and *Enterococcus faecalis* (3.5%). This spectrum is similar to the other studies. (Table no.3) Most authors have reported *Escherichia coli* and *Klebsiella pneumoniae* among the top causative organisms for UTI , which is similar to our study. The causative spectrum is very much similar, with the top six organisms having more or less the same prevalence in both the periods of our study.

Study	Year	Result
Ghimire A et al., [22]	2018	<i>E.coli</i> -62.24%
		<i>Klebsiella spp.</i> -19.38%
		<i>Pseudomonas aeruginosa</i> -9.18%
		<i>Proteus spp</i> -9.18%
		<i>Staphylococcus aureus</i> - 24.74%
Akhtar A et al.,	2021	<i>E.coli</i> - 56.6%

[26]		<i>Klebsiella spp.</i> - 14.7%
		<i>Enterococcus</i> - 11.6%
Mohapatra A et al., [23]	2022	<i>E.coli</i> -68.3%
		<i>Klebsiella spp.</i> -17.6%
		<i>Acinetobacter baumannii</i> -1.2%
		<i>Enterococcus</i> -5.6%
		<i>Others</i> -4%
Present Study	2023	<i>E.coli</i> -40%
		<i>Klebsiella spp.</i> -26.6%
		<i>Pseudomonas aeruginosa</i> -12.2%
		<i>Acinetobacter baumannii</i> -5.6%
		<i>Staphylococcus aureus</i> -6.6%
		<i>Proteus</i> -5.1%
		<i>Enterococcus</i> -3.5%

Table No. 16: Distribution of organism with other study.

In the present study the resistant rate for Ampicillin was observed to be 88.8% followed by Co-trimoxazole (91.1%) and cefotaxime with 89.1%. Imipenem and Nitrofurantoin were sensitive with (89.5%). There were other research investigators whose finding were parallel to the current study where Enterobacteriaceae showed high resistant to commonly used antimicrobials

Study	Ampicillin	Co-trimoxazole	Cefotaxime	Gentamicin	Nitrofurantoin
Shah L et al., [29]	96	83	-	72	71
Tuehm KB et al., [30]	80	54	38	38	-
Gajamer VR et al., [31]	85	75	-	15	30
Akhtar A et al., [26]	81.1	60.7	70.6	47.2	62.8

Pre sent Study	88.8	91.1	89.1	86.6	87.7
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Table No. 17: Prevalence of antimicrobial resistance reported across various studies.

In the present study the prevalence of UTI was found to be 45%. This finding was similar to the study performed by the other authors Ahmad S et al and Suhail A. et al, where the prevalence was found to be 20.54% and 32% respectively [32, 33].

In the present study it was observed that between the resistance gene the percentage Resistance by fim H-gene was with 90.3% . This study was in accordance to the study performed by the other author where fimH gene was observed to be more prevalent [34,35].

According to the results of the PCR test for the identification of surveyed virulence genes, the highest frequency belonged to the FimHgene, which was detected in 93.8% (135 isolates) of the isolates [34]. Similar study was performed by Adnan

Malboh Jaber et al., [36] stated that 57 out of 60 isolates(95%) have fimH gene.

A similar study was conducted in Ethiopia by Dadi BR et al, 2020 [37] in which genetic determinants were studied including those coding for type 1 fimbriae [fimH], pili associated with pyelonephritis[pap], S and F1C fimbriae [sfa and foc], afimbrialadhesins [afa], hemolysin [hly], cytotoxic necrotizingfactor [cnf], and aerobactin [aer]. Virulence genes in E. coli isolates. The most frequent *E.coli* virulence gene was *fimH* 164 (82%), followed by *aer* 109 (54.5%), *hly* 103 (51.5%), *pap* 59 (29.5%), *cnf* 58(29%), *sfa* 50 (25%) and *afa* 24 (12%). This finding was also in accordance with our findings. This is also in agreement with studies conducted in Romania, 86%;Mongolia, 89.9%, Iran, 86.17% and China, 87.4%.

Study	Year	Results
Salih <i>et al.</i> ,[38]	2015	91%
Hojati <i>et al</i> [39]	2015	92.2%

Merza et al., [40]	2017	94.5%
Al-Taalet al., [41]	2018	100%
Adnan Malooh Jaber et al. [36]	2020	95%
Dadi BR et al [37]	2020	82%
H Hyun M et al., [34]	2021	93.8%

Table No. 18: Prevalence of Fim H gene

The current study observed that beta-lactam antibiotics had limited efficacy in treating UTI in patients, perhaps due to the high prevalence of antibiotic resistance among *E. coli* in this region. The right measures may help to lower the risk of UTI infection because of these related factors, such as resistance, which may lead to an inaccurate antibiotic prescription, which may then select for new resistance genes. It is noteworthy that multidrug resistance (MDR) is increasingly spreading globally. This is alarming, since it indicates that we are quickly running out of options for treating simple bacterial infections.

Educating practitioners on the high probability of multidrug resistance should be a priority.

Declarations:

Conflicts of interest: There is no any conflict of interest associated with this study

Consent to participate: There is consent to participate.

Consent for publication: There is consent for the publication of this paper.

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REFERENCES

1. Tenke P, Kovacs B, Bjerklund Johansen TE, Matsumoto T, Tambyah PA, Naber KG. European and Asian guidelines on management and prevention of catheter-associated urinary tract infections. *Int J Antimicrob Agents*. 2008; 31(1): S68-78.
2. Tenke P, Kovacs B, Johansen TE. An update on prevention and treatment of catheter-associated urinary tract

- infections. *Curr Opin Infect Dis.* 2014; 27(1):102-107.
3. Maria E. Terlizzi, Giorgio Gribaudo, and Massimo E. Maffei. UroPathogenic *Escherichia coli* (UPEC) Infections: Virulence Factors, Bladder Responses, Antibiotic, and Non-antibiotic Antimicrobial Strategies. *Frontiers of Microbiology.* 2017; 8:1566.
 4. F. S. Nas, M. Ali, M. S. Abdallah, and A. U. Zage, Prevalence and antibiotic susceptibility pattern of *Escherichia coli* isolated from urine samples of urinary tract infection patients. *ARC Journal of Urology.* 2019; 4(1). 36: 100716
 5. M. Gajdács, M. Ábrók, A. Lázár, and K. Burián, “Comparative epidemiology and resistance trends of common urinary pathogens in a tertiary-care hospital: a 10-year surveillance study,” *Medicina.* 2019; 55(7).
 6. M. Gajdács and E. Urbán, “Resistance trends and epidemiology of citrobacter-enterobacter-serratia in urinary tract infections of inpatients and outpatients (RECESUTI): a 10-year survey,”. *Medicina.* 2019; 55(6):1–13.
 7. Gołębiewska J, Dębska-Ślizień A, Komarnicka J, Samet A, Rutkowski B. Urinary tract infections in renal transplant recipients. *Transplant Proc.* 2011 ;43(8):2985-90.
 8. Jaggi N, Sissodia P. Multimodal supervision programme to reduce catheter associated urinary tract infections and its analysis to enable focus on labour and cost effective infection control measures in a tertiary care hospital in India. *J Clin Diagn Res.* 2012; 6:1372– 6.
 9. Teh AH, Wang Y, Dykes GA. The influence of antibiotic resistance gene carriage on biofilm formation by two *Escherichia coli* strains associated with urinary tract infections. *Can J Microbiol.* 2014; 60:105-11.
 10. Rashki A, Abdi HA, Shookohi M. Prevalence of genes encoding outer membrane virulence factors among fecal *Escherichia coli* isolates. *Int J Basic Sci Med.* 2017; 2(1):52–7.
 11. Neamati F, Firoozeh F, Saffari M, Zibaei M. Virulence genes and antimicrobial resistance pattern in uropathogenic *Escherichia coli* isolated from hospitalized patients in Kashan, Iran. *Jundishapur J Microbiol.* 2015; 8(2). e17514.

12. Momtaz H, Karimian A, Madani M, Safarpour Dehkordi F, Ranjbar R, Sarshar M, et al. Uropathogenic *Escherichia coli* in Iran: serogroup distributions, virulence factors and antimicrobial resistance properties. *Ann Clin Microbiol Antimicrob*. 2013;12:8.
13. Behzadi P, Urban E, Gajdacs M. Association between biofilmproduction and antibiotic resistance in uropathogenic *Escherichia coli* (UPEC): an in vitro study. *Diseases*. 2020; 8(2).
14. Katongole P, Nalubega F, Florence NC, Asimwe B, Andia I. Biofilm formation, antimicrobial susceptibility and virulence genes of Uropathogenic *Escherichia coli* isolated from clinical isolates in Uganda. *BMC Infect Dis*. 2020; 20(1):453.
15. De Alegria Puig, C.R, Pilares, L, Marco, F, Vila, J, Martinez-Martinez, L, NNavas, J. Comparison of the Vitek MS and Bruker Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry Systems for Identification of *Rhodococcus equi* and *Dietzia* spp. *J. Clin. Microbiol*. 2017; 55, 2255–2260.
16. Gabriel Kambale Bunduk, Eva Heinz , Vincent Samuel Phiri , Patrick Noah , Nicholas Feasey, and Janelisa Musaya. Virulence factors and antimicrobial resistance of uropathogenic *Escherichia coli* (UPEC) isolated from urinary tract infections: a systematic review and metaanalysis. *BMC Infectious Diseases* . 2021; 21:753. <https://doi.org/10.1186/s12879-021-06435-7>
17. Chhaya Shah, Ratna Baral, Bijay Bartaula & Lok Bahadur Shrestha .Virulence factors of uropathogenic *Escherichia coli* (UPEC) and correlation with antimicrobial resistance. *BMC. Infectious Diseases*. 2019; 19(204): 1587-3 .
18. Sabir N, Ikram A, Zaman G, Satti L, Gardezi A, Ahmed A, Ahmed P. Bacterial biofilm-based catheter-associated urinary tract infections: Causative pathogens and antibiotic resistance. *Am J Infect Control*. 2017; S0196-6553(17)30693-4.
19. Clinical and Laboratory Standards Institute. Performance Standards for Antimicrobial Susceptibility Testing; Twenty Sixth Informational Supplement, CLSI Document M100S-26. Wayne, PA: Clinical and Laboratory Standards Institute 2023.

20. McLellan LK, Hunstad DA. Urinary tract infection: Pathogenesis and Outlook. *Trends Mol Med*. 2016; 22(11):946–57.
21. Brumbaugh AR, Smith SN, Mobley HL. Immunization with the yersiniabactin receptor, FyuA, protects against pyelonephritis in a murine model of urinary tract infection. *Infect Immun*. 2013; 81(9):3309–16.
22. Ghimire A, Pradeep. Pattern of Antibiotic Resistance Bacteria isolated from various Clinical Specimens.. *IOSR Journal of Dental and Medical Sciences*. 2018; 17. 40-42.
23. Mohapatra A, Sarita et al. “Prevalence and resistance pattern of uropathogens from community settings of different regions: an experience from India.” *Access microbiology*. 2022; 4 (2) :000321
24. Mlugu, E.M., Mohamedi, J.A., Sangeda, R.Z. et al. Prevalence of urinary tract infection and antimicrobial resistance patterns of uropathogens with biofilm forming capacity among outpatients in morogoro, Tanzania: a cross-sectional study. *BMC Infect* . 2023; Dis 23, 660
25. .Hawra Al Lawati et al. Urinary Tract Infections: Core Curriculum 2024.
26. Akhtar A, Ali et al. “A Cross-Sectional Assessment of Urinary Tract Infections Among Geriatric Patients: Prevalence, Medication Regimen Complexity, and Factors Associated With Treatment Outcomes.” *Frontiers in public health*. 2021; 9 : 657199.
27. Karishetti M, Mallikarjun S.; Shaik, Hussain Basha. Clinicomicrobial assessment of urinary tract infections in a tertiary care hospital. *Indian Journal of Health Sciences and Biomedical Research (KLEU)* . 2019; 12(1): 69-74.
28. Mythri Set al. “Urinary Tract Infection in Chronic Kidney Disease Population: A Clinical Observational Study.” *Cureus* . 2021; 13 (1) .12486
29. Shah L, Vaghela G, Mahida H Urinary tract infection: bacteriological profile and its antibiotic susceptibility in western India.. http://njmr.in/uploads/5-1_71-74.pdf *Nat J Med Res*. 2015;5:71–74.
30. Tuem KB, Desta R, Bitew H, Ibrahim S, Hishe HZ. Antimicrobial resistance patterns of uropathogens isolated between 2012 and 2017 from a tertiary hospital in Northern Ethiopia. *J Global Antimicrob Resist*. 2019;18:109–114.
31. Gajamer VR, Bhattacharjee A, Paul D, et al. High prevalence of

- carbapenemase, AmpC β -lactamase and aminoglycoside resistance genes in extended-spectrum β -lactamase-positive uropathogens from Northern India. *J Global Antimicrob Resist.* 2020; 20:197–203.
32. Ahmad S, Ahmad F. Urinary tract infection at a specialist hospital in Saudi Arabia. *Bangladesh Med Res Counc Bull.* 1995; 21:95-8.
33. Syed Suhail Ahmed, Ali Shariq, Abdulaziz Ajlan Alsalloom, Ibrahim H. Babikir, Badr N. Alhomoud. Uropathogens and their antimicrobial resistance patterns: Relationship with urinary tract infections. *International Journal of Health Sciences.* 2019; Vol. 13, Issue 2 .
34. H Hyun M, Lee JY, Kim HA. Differences of virulence factors, and antimicrobial susceptibility according to phylogenetic group in uropathogenic *Escherichia coli* strains isolated from Korean patients. *Research Square.* 2021; 10; 20(1):77.
35. Mostafa Boroumand , Asghar Sharifi , Mohammad Amin Ghatei and Mohsen Sadrinasab. Evaluation of Biofilm Formation and Virulence Genes and Association with Antibiotic Resistance Patterns of Uropathogenic *Escherichia coli* Strains in Southwestern Iran. *Jundishapur J Microbiol.* 2021 September; 14(9):e117785.
36. Adnan Malooh Jaber and Hasan A. Aal Owaif. Detection of genes involved in biofilms formation by *Escherichia coli* isolated from patients suffering of urinary tract infections. *plant archives.* 2020; 20 (2) :5987-5992.
37. Belayneh Regasa Dadi, Tamrat Abebe, Lixin Zhang, Adane Mihret, Workeabeba Abebe and Wondwossen Amogne, Distribution of virulence genes and phylogenetics of uropathogenic *Escherichia coli* among urinary tract infection patients in Addis Ababa, Ethiopia; *BMC Infectious Diseases.* 2020; 20:108.
38. Salih, E.G.M., M.I. Nader and M.N. Rasheed. *Rapid Detection of Uropathogenic Escherichia Coli virulence factors in Iraqi patients by multiplex polymerase chain Reaction.* 2015
39. Hojati, Z., B. Zamanzad, M. Hashemzadeh, R. Molaie and A. Gholipour. Detection of fimH gene in uropathogenic *Escherichia coli* strains isolated from patients with urinary tract infection. *Jundishapur Journal of Microbiology.* 2015; 8(2): 12-15.

40. Merza, N.S. Prevalence and Molecular Characterization of *Fim H* Gene in *Escherichia Coli* Isolates Recovered From Patients With Utis. *Medical Journal of Babylon*. 2017; 14(3): 470–477.
41. Taai, H.R.R., Z.A.S. Al-Jebouri, B.H. Khalaf and Y.Q.Mohammed . Antibiotic resistance patterns and adhesion ability of uropathogenic *Escherichia coli* in children. *Iraqi Journal of Biotechnology*. 2018; 17(1): 18-26.