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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
Urinary tract infections, or UTIs, are common diseases caused by bacteria that enter the urethra from the skin or rectum. Urinary tract infections account for the majority of hospital visits worldwide and are a significant contributor to morbidity and comorbidity in individuals with underlying medical disorders. Uropathogenic Escherichia coli (UPEC) express a multitude of virulence factors (VFs) to break the inertia of the mucosal barrier of the urinary tract 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
A study on prevalence of urinary tract infection of uropathogenic E.coli and the molecular characterization with special reference to fim H gene from urine samples.

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, 2024 to 2025. A total of 200 Patients were screened from 600 clinical isolates where 200 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 > 38ºC, urgency, frequency dysuria or suprapubic tenderness) were included in this study. The Antibiotic Susceptibility testing was performed according to the CLSI guidelines 2024. 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 2024. 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 a total of 600 clinically suspected cases were screened out of which total 200 isolates was found positive for UTI infection . Therefore, the prevalence rate of UTI was found to be 33%. From the present study it was observed that the Females 114 (57%) were more affected with the infection as compared to the Males 86 (43%). It was also noted that the age group of 31-40 years of age followed by 41-50 years was affected the most. In the age group of 0-10 years, 11-20 years and above 71 years was the least affected with the infection. In the current study E.coli (31%) was the most common followed by Klebsiella spp.(24%), Pseudomonas aeruginosa (18%), Staphylococcus aureus (7.5%), Acinetobacter baumanii (9%), Proteus (5.5%), Enterococcus (5.5%).
In the present study the resistant rate for Ampicillin was observed to be 75% followed by Co-trimoxazole (92.5%) . Imipenem and Nitrofurantoin were sensitive with 89%. There were other research investigators whose finding were

parallel to the current study where Enterobacteriaceae showed high resistant to commonly used antimicrobials. In the current study there was fim H gene studied. In the fim H gene there were 165 (82.5%) positive cases and negative were 35 (17.5%).

CONCLUSION

This study found that UTIs were more common in women than in men. The most common symptoms, such as chills, dysuria, and abdominal pain, were reported in patients with urinary tract infections. Therefore, regular exams and strict adherence to antibiotic stewardship recommendations can lower the cost of UTI prophylaxis. By performing these routine tests, the expense of avoiding UTIs can be decreased.

Keywords: UTI, CLSI, Molecular characterization, fimH , DNA, PCR

1. INTRODUCTION

One of the inflammatory conditions caused by the high proliferation of several pathogens in the urinary apparatus is urinary tract infections (UTIs), which affect the kidneys' and urinary tract's normal function. Nearly 50–80% of women experience UTIs at least once in their lives, and 20–50% of them will experience recurrent episodes, making UTIs a significant issue for women in particular [1,2].

The genitourinary tract, which runs from the kidney's renal cortex to the urethral meatus, is the source of the invasion [3]. Due to a number of characteristics, including the presence of adhesins, that are linked to their attachment to the uroepithelium, the Enterobacterales group is the most frequent cause of UTIs [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].

In addition to colonising the bladder and causing cystitis, the bacteria Uropathogenic E. coli (UPEC) can occasionally induce pyelonephritis by moving up the ureters to the kidneys. Given that this organism frequently causes UTIs, healthcare professionals should be mindful of the possibility of repeat infections in women who have already had 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 bacterium's virulence and the host's susceptibility determine how severe a UTI is [14]. Haemolysin, fimbriae, lipopolysaccharides (LPS), secreted proteins, capsules, and iron-acquisition systems are among the virulence factors that contribute to the production of biofilms in E. coli. These factors enable the bacteria to attach to and colonise the mucosal epithelial cells that line the urinary tract.

Different PAIs, such as PAI I536, PAI II536, PAI III536, PAI IV536, PAI ICFT073, PAI IICFT073, PAI IJ96, and PAI IIJ96, encode a number of UPEC strain virulence factors.

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

The virulence factors that are commonly encoded in Pathogenicity Islands (PAI) and make uropathogenic E. coli strains pathogenic include adhesion fimbriae (fim-H, iha), toxins (cnf1, hlyA), iron-forming systems (iroN, aer), macrophage degradation agents (ompTprotease), and serum resistance factors (traT). Additionally, the pathophysiology of E. coli strains in UTIs is influenced by serum resistance factors (traT) [16]. Type 1 fimbriae (fim), encoded by the fim gene cluster, and Siderophores's Aerobactin, encoded by the aer gene cluster, are the two primary virulence factors of UPEC isolates that contribute to biofilm formation.

After adhering to the surfaces in an irreversible manner, the bacteria finally form an adherent biofilm. For diagnosis and treatment plans, the quick evaluation of virulence factors found by polymerase chain reaction (PCR) may be helpful. Type 1 fimbriae (fimH), pyelonephritis-associated pili (pap), S and F1C fimbriae (sfa and foc), afimbrial adhesins (afa), haemolysin (hly), cytotoxic necrotising factor (cnf), and aerobactin (aer) were the genetic determinants. The precursor of 300 amino acids is the protein FimH.

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]
The need for a better knowledge of the microorganisms that cause UTIs and their pattern of antibiotic susceptibility should be highlighted by drug-resistant bacterial strains and the increased frequency of UTIs [18]. With a high affinity for urinary tract receptors, the sticky subunit of type 1 fimbriae, FimH, is a critical component of UPEC adhesions. As a result, FimH adhesion plays a significant role in colonising various E. coli habitats. In order to determine the frequency of urinary tract infections and the molecular characteristics of uropathogenic *E. coli* isolated from urine samples at a tertiary care hospital, with particular reference to the Fim H gene, the current study was conducted.

2. MATERIAL AND METHODS

This cross-sectional investigation was conducted in a tertiary care centre, Department of Microbiology. After screening 600 clinical isolates, 200 patients of both sexes and all age groups who had indwelling urinary catheters for at least two days and who had UTI symptoms (fever > 38ºC, urgency, frequency, dysuria, or suprapubic tenderness) were included in the study. The Antibiotic Susceptibility testing was performed according to the CLSI guidelines 2024. 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 2024. 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), cefoperazone + sulbactam (75/30 µg), imipenem (10 µg), meropenem (MRP; 10 µg) and Nitrofuratoin(30 µg). Antibiotic susceptibility/resistance was recorded in accordance with Clinical and Laboratory Standards Institute guidelines 2024 [19].

3. ISOLATION AND IDENTIFICATION OF *E.COLI:*

Culture and identification: To measure the Colony Forming Units (CFU), the urine samples were inoculated onto Cystine Lactose Electrolyte Deficient (CLED) medium using calibrated loops. The following preliminary and biochemical tests were carried out using standard recommended laboratory methods in accordance with the CLSI guidelines [19]. The isolates were identified based on colony morphology, gramme staining, and the standard biochemical tests (catalase test, Indole, Methyl red, Voges-Proskauer test, nitrate reduction, urease production, and Simons citrate agar).

Figure No.1: The Reagents used for the DNA Extraction

The Molecular Characterization of the Gene by Genotypic method
The DNA was isolated using the Qiamp DNA Blood Mini Kit (QIAGEN, Germany) as per the manufactures guidelines. The extracted DNA and the gene was confirmed by the PCR to detect the presence of the Fim H gene.
The DNA was eluted in 60 µl elution buffer and preserve at -20 °C till PCR analysis. For amplification of the target gene, PCR was carried out in a 50 µL reaction mixture with 30 no. of cycles. The primers were purchased from "**Saha gene'** and was reconstituted with sterile double distilled water based on the manufacturer's instruction.

Figure No. 2: The Fim H gene primer

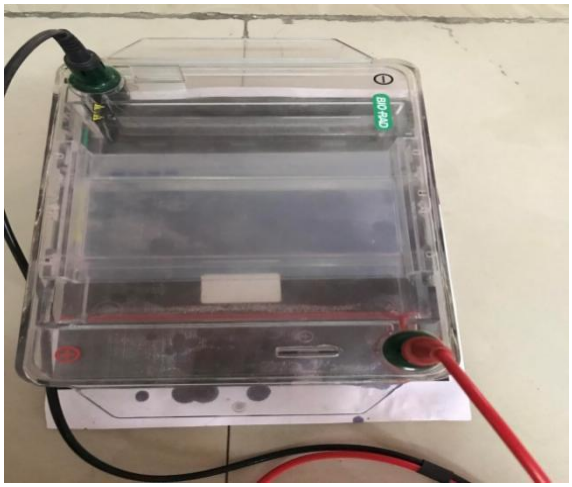


Figure No.3 : Gel Electrophoresis for the DNA Extraction

The Primers

Gene	Primer sequence	Length (bp)	Reference
fimH	Forward- 5- GAGAAGAGGTTTGATTTAACTTATTG-3	559bp	[20]
	Reverse 5-AGAGCCGCTGTAGAACTGAGG- -3		

Table No. A : Primers for fimH Gene Polymorphism

- The primers for aer and FimH for the detection of gene of interest was designed and confirmed by NCBI.

Table No.B : Primer used for the Fim H gene amplification

The Polymerase Chain Reaction

For the PCR amplification, 2 µl of template DNA was added to 18 µl reaction containing 10 µl of Qiagen master mix, 2 µl of primer mix (1 µl each of the respective forward and reverse primers) and 6 µl of molecular-grade water.
The cyclic conditions for FIM H gene, initial denaturation at 95 °C for 15 min, 30 cycles of 94 °C for 30 s, 59 °C for 1 min 30 s and 72 °C for 1 min 30 s were followed by extension of 72 °C for 10 min.

4. THE PCR CYCLING CONDITIONS

Step	Program Fim H Time Temperature	Cycles
Initial denaturation	15 min 95 ºC	
Denaturation	30 s 94 ºC	
Annealing	1 min30 s 59 ºC	30
Extension	1 min 30 s 72º C	
Final extension	10 min 72º C	

Table No. 2 : The PCR cycling conditions to amplify Fim H gene fragments.

The Agarose gel preparation and visualized by Gel Doc™ EZ Gel Documentation System
The Agarose Gel Electrophoresis was performed in order to identify the Purified PCR Product which was previously identified by its amplified DNA fragments. The resulting PCR product was subjected to 1% agarose gel electrophoresis and visualized by Gel Doc™ EZ Gel Documentation System (Bio-Rad Laboratories Inc., Hercules, CA, USA). A 1 kb DNA Ladder (Thermo Fisher Scientific ™, Waltham, MA, USA) was used as the marker to evaluate the PCR product of the sample .

5. STATISTICAL ANALYSIS

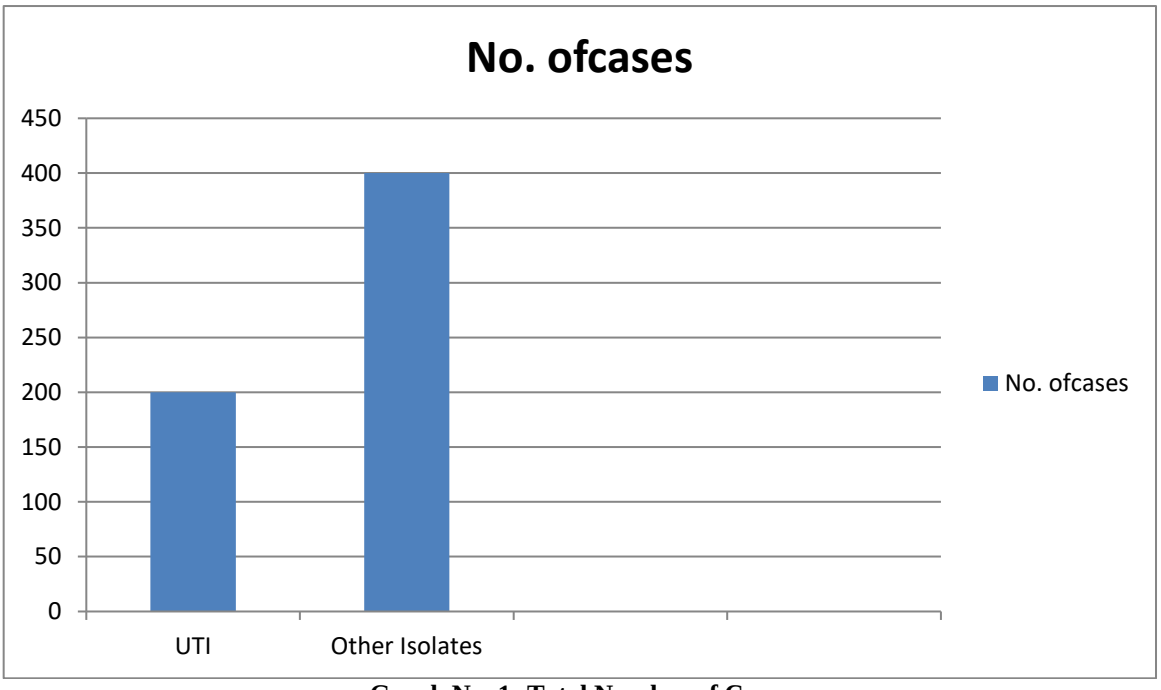
Data recorded on the report form and structured proforma were subsequently entered into a spreadsheet. Data management and analysis were performed using Microsoft Excel.

6. RESULTS

In the present study a total of 600 clinically suspected cases were screened out of which total 200 isolates was found positive for UTI infection . Therefore, the **prevalence rate of *UTI* was found to be 33%**.

S.No.	Type of Isolates	Total No. of samples (n=600)	Percentage
1.	UTI	200	33%
2.	Other Isolates	400	67%

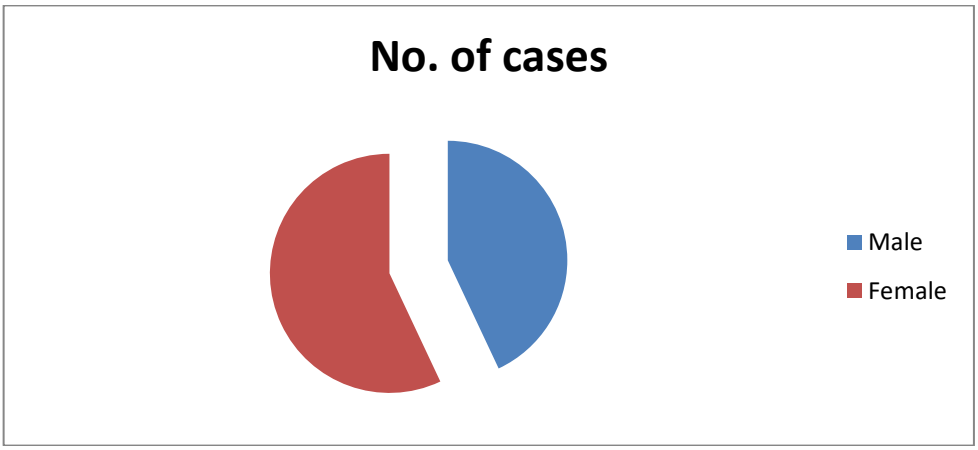
Table No. 1: Total Number of Cases



Graph No. 1: Total Number of Cases

S.NO.	GENDER	TOTAL NO. OF ISOLATES (N=200)	PERCENTAGE
1.	Male	86	43%
2.	Female	114	57%

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=200)	Percentage	
1.	0-10	1	0.5%	
2.	11-20	10	5%	
3.	**21-30**	**35**	**17.5%**	
4.	**31-40**	**72**	**36%**	
5.	**41-50**	**48**	24%	
6.	51-60	12	6%	
7.	61-70	12	6%	
8.	≤ 71	10	5%	

Table No. 3: Agewise distribution of the Isolates

From the present study it was observed that the Females 114 (57%) were more affected with the infection as compared to the Males 86 (43%). It was also noted that the age group of 31-40 years of age followed by 41-50 years was affected the most. In the age group of 0-10 years, 11-20 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 .

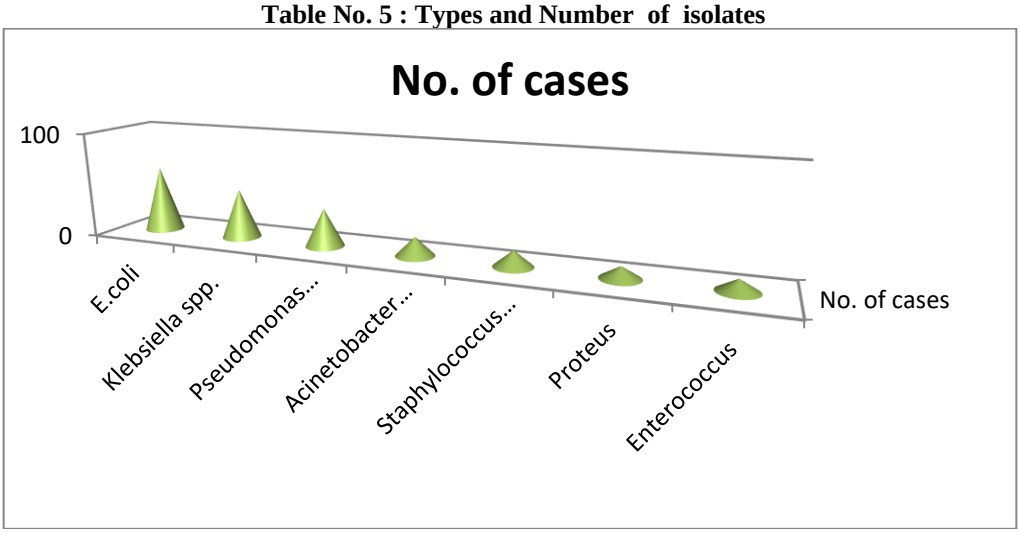
Biochemical Test For The Phenotypic Detection

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

Type	No. of Isolates	Percentage
E.coli	62	31%
Klebsiella spp.	47	24%
Pseudomonas aeruginosa	36	18%
Acinetobacter baumanii	18	9%
Staphylococcus aureus	15	7.5%
Proteus	11	5.5%
Enterococcus	11	5.5%
Total	**200**	**100%**

Table No. 5 : Types and Number of isolates



Graph No. 3: Types and Number of isolation isolated

In the current study *E.coli* (31%) was the most common followed by *Klebsiella spp.*(24%), *Pseudomonas aeruginosa* (18%), *Staphylococcus aureus* (7.5%), *Acinetobacter baumanii* (9%), *Proteus* (5.5%), *Enterococcus* (5.5%).

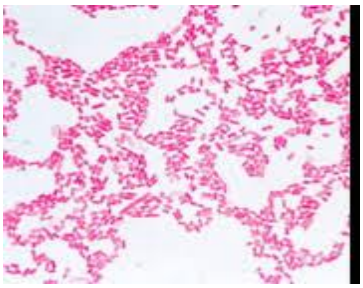


Figure No. 2: Microscopic examination of *E.coli*

Days of catheterization	Gender		Total
	Female	Male	
1-3	11 (9.6%)	10(11.6%)	21(10.5%)
4-7	59 (57.7%)	40 (46.5%)	99 (49.5%)
8-12	41(35.9%)	30 (34.8%)	71 (35.5%)
13-14	3 (2.6%)	6 (6.9%)	9(%)
Total	114 (57%)	86 (43%)	200 (100%)

P= 0.02; Significant;

Table No. 6 : Days of catheterization of cases

The Identification of Drug Resistance Pattern : Antibiotic susceptibility testing was performed by Kirby bauer Disk diffusion method as per the CLSI guidelines .

Antibiotic	Strength In µg	RESISTANCE	SENSITIVITY
AMP	100 µg	150 (75%)	50(25%)
PTZ	20 µg	175 (87.5%)	25 (12.5%)
CTR	30 µg	178 (89%)	22 (11%)
CTX	30 µg	178 (89%)	22 (11%)
CIP	5 µg	178 (89%)	22 (11%)
NOR	30 µg	189 (94.5%)	11 (7.5%)
AMK	10 µg	48 (24%)	152 (76%)
GEN	10 µg	175 (87.5%)	25 (12.5%)
COT	10 µg	185 (92.5%)	15 (7.5%)
CFS	50 µg	35 (17.5%)	165 (82.5%)
IMP	10 µg	22 (11%)	178 (89%)
MERO	10 µg	45 (22.5%)	155 (77.5%)
NIT	30 µg	22 (11%)	178 (89%)
Total		200(100%)	

Table No. 7: Antibiotic resistance/Sensitivity pattern of patients studied

In the present study the resistant rate for Ampicillin was observed to be 75% followed by Co-trimoxazole (92.5%) . Imipenem and Nitrofurantoin were sensitive with 89%. There were other research investigators whose finding were parallel to the current study where Enterobacteriaceae showed high resistant to commonly used antimicrobials

Variables	No. of Patients	%
FIM H		
• Negative	35	17.5
• Positive	165	82.5
Total	200	100.0

Table No. 8: Detection of fim H Gene

In the current study there was fim H gene studied. In the fim H gene there were 165 (82.5%) positive cases and negative were 35 (17.5%).

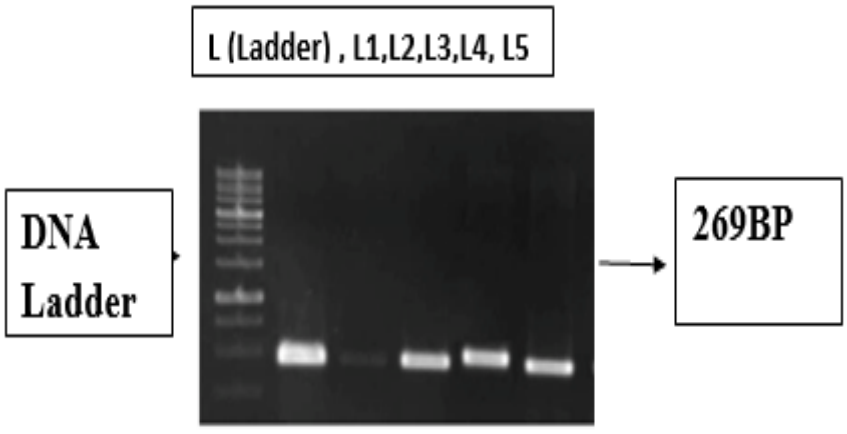


Figure No.2: The FIMH gene:
L corresponds to the DNA Ladder; L1 corresponds to the sample positive for FIMH gene; L2 is the Negative Control for FIMH gene; L3-L5 are the sample positive for FIMH gene

7. DISCUSSION

Escherichia coli is the most frequent pathogen responsible for up to 80% of UTIs . This bacteria is responsible for 85% and 50% of community and hospital acquired UTIs, respectively. Uropathogenic *E. coli* (UPEC) strains have special virulence factors, including pili or fimbriae, which mediate attachment to uroepithelial and vaginal cells, resistance to human serum bactericidal activity, haemolysin production, and increased amounts of K capsular antigen [20]. 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 [21].

In the present study, the prevalence rate of UTI in Female was more than Male (Female 57% and Male 43%) which was in accordance with other studies where the incidence of UTIs in women also was higher. The results of these studies were in 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	2025	M-43% F-57%

Table No. 9: Comparison of gender wise distribution with other study

It was also noted that the age group of 31-40 years of age followed by 41-50 years was affected the most. In the age group of 0-10 years, 11-20 years and above 71 years was the least affected with the infection.

In the current study *E.coli* (31%) was the most common followed by *Klebsiella spp.*(24%), *Pseudomonas aeruginosa* (18%), *Staphylococcus aureus* (7.5%), *Acinetobacter baumanii* (9%), *Proteus* (5.5%), *Enterococcus* (5.5%).

Study	Year	Result
Ghimire A et al., [22]	2018	*E.coli*-62.24% *Klebsiella spp.*- 19.38% *Pseudomonas aeruginosa*- 9.18% *Proteus spp -9.18%* *Staphylococcus aureus*- 24.74%
Akhtar A et al., [26]	2021	*E.coli*- 56.6% *Klebsiella spp.*- 14.7% *Enterococcus* - 11.6%
Mohapatra A et al., [23]	2022	*E.coli -68.3%* *Klebsiella spp.-17.6%* *Acinetobacter baumanii-1.2%* *Enterococcus-5.6%* *Others -4%*
Present Study	2024	

In the current study *E.coli* (31%) was the most common followed by *Klebsiella spp.*(24%), *Pseudomonas aeruginosa* (18%), *Staphylococcus aureus* (7.5%), *Acinetobacter baumanii* (9%), *Proteus* (5.5%), *Enterococcus* (5.5%).

Table No. 10: Distribution of organism with other study.

In the present study the resistant rate for Ampicillin was observed to be 75% followed by Co-trimoxazole (92.5%) . Imipenem and Nitrofurantoin were sensitive with 89%. There were other research investigators whose finding were parallel to the current study where Enterobacteriaceae showed high resistant to commonly used antimicrobials**.**
UTI is particularly a major problem for females; nearly 50–80% of the female population endures from UTI at least once in lifetime and 20-50% of them will have recrudescent events [27,28].

Study	Ampicillin	Co-trimoxazole	Cefotaxime	Gentamicin	Norfloxacin
Shah L et al., [29]	96	83	-	72	71
Tuem 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
Present Study	88.8	91.1	89.1	86.6	87.7

Table No. 11: Prevalence of antimicrobial resistance reported across various studies.

In the present study the prevalence of UTI was found to be 33.3%. 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 82.5% . This study was in accordance to the study performed by the other author where fimH gene was observed to be more prelevant [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 Malooh 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 *et al.*,[38]	2015	91%
Hojati *et al* [39]	2015	92.2%
Merza et al., [40]	2017	94.5%
Al-Taai*et 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. 12: Prevalence of Fim H gene

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 [42,43]. 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.

8. CONCLUSION

FimH may be used to create a vaccine that prevents *E. coli* infections by preventing bacterial attachment and colonisation. This is because FimH's high binding capacity may lead to enhanced bacterial adhesion to target cells and increased pathogenicity of *E. coli*. Furthermore, FimH may be employed as a tool to expand assays based on quick detection.

9. 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.
Authors' contributions: Author equally contributed the work.

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