



Detection of *afa* and *yqi* in Ciprofloxacin Resistant Uropathogenic *Echerichia coli*

Suaad Ali Ahmed^{1*}  and May Talib Flayyih² 

^{1,2}Department of Biology, College of Science, University of Baghdad, Baghdad, Iraq.

*Corresponding Author.

Received: 10 September 2023

Accepted: 21 November 2023

Published: 20 April 2025

doi.org/10.30526/38.2.3670

Abstract

Antibiotic resistance has dramatically increased among UTI patients with UPEC infections. They are crucial to the pathophysiology of UTIs because UPEC invades the bladder through a variety of virulence factors. Afa adhesins are produced by human-derived *Echerichia coli* and have been shown to bind to the (DAF, CD55) as a receptor, while Yqi adhesin recreates a denotative role in colonization, the initial stage of pathogenesis, during infection with *E.coli*. *E.coli* isolates from 200 urine samples of credible UTI patients were detected. By employing different media, VITEK, and the biochemical identification. Susceptibility to the Ciprofloxacin antibiotic was established by using the disc diffusion approach, while the susceptibility to Ciprofloxacin and other 15 antibiotics was achieved by the VITEK 2 compact system. A tissue culture plate was used in order to analyze the adherence ability of bacteria. Genomic DNA was pulled from cells according to the protocol of ABIO pure extraction. (Quantus Fluorometer) was used to get the concentration of DNA. *afa* and *yqi* genes were detected in 22 *E.coli* isolates amplified by PCR using certain primers. To ascertain whether the evaluated genes were present in the bacterial isolates, PCR products were checked on a gel. Twenty-one bacterial isolates from 40,52.5% were resistant to ciprofloxacin. The highest resistance of UPEC isolates was to ampicillin (34/40, 85%) and cefazolin (33/40, 82.5%), while the lowest resistance was to amikacin and tagicycline (0/40, 0%). The results appeared to indicate that (11/25,44%) of tested UPEC were strong biofilm-forming, while the rest of the isolates (14/25,56%) were moderate biofilm-forming. The analysis of PCR products on an agarose gel revealed that out of 22 UPEC isolates, 17/22,77.27%) had the *afa* gene and 7/22,31.81%) had the *yqi* gene. The aim of this research was screening of *afa* and *yqi* genes in UPEC isolated from different UTI patients.

Keywords: *Afa* gene, *yqi* gene, Urinary tract infection, Uropathogenic *E.coli*, Antibiotic resistance.

1. Introduction

Although antibiotics are currently the go-to therapy for bacterial illnesses, misuse of them may hasten the resistant strains from appearing and allow microorganisms to change their own



pathogenicity (1, 2). A common bacterial infection is urinary tract infection (UTI), and the organism that creates sharp infections most frequently is *E. coli* (3,4,5), especially among women (6). Wide-spectrum antibiotics like fluoroquinolones and quinolones are frequently used to treat UTIs caused by *E.coli* (7, 8). Ciprofloxacin is the most frequently given fluoroquinolone for UTIs due to its availability in both oral and intravenous formulations. Following oral administration, the digestive tract effectively absorbs it (9). Unfortunately, among UTI patients with UPEC infections, antibiotic resistance has significantly increased (10). Because UPEC applies a range of virulence managers to colonize the bladder, they are essential to the pathophysiology of UTIs (11, 12). Type 1 and 2 fimbriae, also known as P, Dr adhesin, S, and F1C fimbriae, are the two primary virulence agents that interact with the host cell adhesin (13, 14). *E. coli* that expresses Dr/Afa adhesins may predispose to the development of chronic or recurring infections; UPEC penetrated the epithelial cells through AfaD and AfaE, evading host immune surveillance and antibiotic therapy (3, 15). *Afa* determinants are ingredients of the (Afa/Dr family) of gene bunches, located on chromosomes that also encompass the (*dra* and *daa*) genes, which encode the (Dr and F1845) adhesins discretely (16, 17). An extremely conserved DNA section including the (*afaB*, *afaC*, and *afaD*) genes was found in *afa* gene clusters, whereas the *afaE* sequences showed variability, resulting in the development of adhesins that are antigenically unique (18, 19). The *Afa* operons reported in uropathogenic and diarrheal *E. coli* belong to the *Afa* family of gene clusters. The gene subtypes (*afaE1*, *afaE2*, *afaE3*, *afaE5*, *dra*, *dra2*, *daa*, and *nfa*) encode the Afa/Dr adhesins. Human-derived *E. coli* produces these adhesin, which bind to the DAF (CD55) as a receptor (20). a large number of new genes, including those that encode presumed adhesin like (*yad*, *yqi*, and *yeh*) (21). Now, it has been discovered that the adhesin, Yqi, recreates a denotative role in colonization, the initial stage of pathogenesis, during infection with *E.coli* (18). More than 50% of *E.coli*, including APEC and UPEC were discovered to carry the adhesin-encoding gene *yqi*, but none of the examined intestine pathogenic *E. coli* strains did (20). Multiple pilus systems are likely advantageous for niche adaptation, and the mixture of tissue-specific receptor synthesis and receptor specificity will eventually dictate the position of action for a particular pilus during attack (21).

2. Materials and Methods

2.1. Isolation and identification of organism

By employing (MacConkey, EMB, Blood) agar and (Hichrome *E.coli*, Hichrome UTI) agar (Himedia, India), Gram stain, VITEK, and the biochemical identification, a total of *E.coli* isolates from 200 urine samples of probable UTI patients were detected (22, 23).

2.2. Susceptibility of bacteria to ciprofloxacin and other antibiotics

Susceptibility to Ciprofloxacin antibiotic discs (Cipropharm, Pharma International) was established by using the Disc Diffusion approach (24, 25). Overnight, the isolated colony was cultivated in nutritional broth. It was diluted to 1×10^8 (cell/ml) before being cultured on Muller-Hinton agar. After adhering the antibiotic discs, we stored the plates at 37°C overnight (26). The outcomes were then linked with CLSI data from 2020 (27). The VITEK 2 compact achieved susceptibility to Ciprofloxacin and other 15 antibiotics (Ampicillin, Piperacillin/Tazobactam, Cefazolin, Cefoxitin, Ceftazidime, Ceftriaxone, Cefepime, Ertapenem, Imipenem, Amikacin, Gentamicin, Levofloxacin, Tigecycline, Nitrofurantoin, and Trimethoprim/Sulfamethoxazole).

2.3. Biofilm formation

Bacterial isolates were cultured in nutrient broth containing 91% glucose on a tissue culture plate in order to analyze the adherence ability. After incubation, we used DDW to thoroughly clean the wells three times. then left overnight to dry. 200 µl of 0.1% crystal violet was used to color the affixed cells for 15 min; any extra stain was washed away with distilled water and then allowed to dry. 200 µl of 96% ethanol were used to dissolve the crystal violate, and a spectrophotometer was used to assess the absorbance at 490 nm. (28). Three triplicates of the experiment are run. As the negative control, the absorbance of wells bearing sterile N.B. was used. We used the optical density cutoff (ODc) to differentiate the isolates based on adhesion quantities (ODc = average OD of negative control + 3 standard deviation (SD) of negative control) (29). Optical density $OD \leq 2 \times ODc$ represents weak adherence, while $4 \times ODc \leq OD$ refers to strong biofilm and moderate adherence between them (30).

2.4. DNA Extraction

Genomic DNA was extracted from cells according to the protocol of ABIO Pure Extraction (ABIO Pure, USA). (Quantus Fluorometer) (Promega, USA) was employed to gauge the quality of samples for use in subsequent applications by measuring the concentration of DNA that had been extracted. For 1 µl of DNA, add 200 µl of diluted Quantifluor dye. Incubated at room temperature (5 min); thereafter, DNA concentration values were found.

2.5. Amplification of *afa* and *yqi* genes of uropathogenic *E.coli*

The *afa* and *yqi* genes were detected in 22 *E.coli* isolates amplified by PCR using certain primers (Macrogen, Korea) (Table 1). The following were the PCR scenarios: early denaturing at 95 °C (5 min), then 30 cycles, each for 30 sec; denaturation at 95°C, annealing, and extension steps. Finally, one extension cycle at 72 °C (7 min) and hold at 10 °C (10 sec). After amplification, PCR yields were determined (31, 32).

Table 1. Primers

Genes	{5' → 3'}	Annealing Tm	Product size	Reference
<i>afa</i>	F : CGGCTTTTCTGCTGAACTGGCAGGC R : CCGTCAGCCCCACGGCAGACC	65	672	22
<i>yqi</i>	F : ATGCAATGGCAGTACCCCTTC R : CTGGTGGCAACATCAAATTG	60	375	21

2.6. Statistical analysis

Program: IBM SPSS version 27.0 was used to calculate the biofilm control mean and Standard Deviation (SD) to determine the adhesion quantities for bacterial isolates.

3. Results and Discussion

3.1. Isolation and identification of organism

According to the results of cell growth on different media, Gram stain and biochemical tests (40 *E.coli* isolates) from 200 urine samples of probable UTI patients were detected, and the results were confirmed with the VITEK Compact 2 system (33, 34).

3.2. Susceptibility of bacteria to ciprofloxacin and other antibiotics

The results obtained by using the Kerby pour method for the susceptibility of UPEC isolates to Ciprofloxacin discs were identical with the results of the VITEK 2 Compact system: 21 bacterial

isolates from 40 (52.5%) were resistant to ciprofloxacin (**Figures 1 , 2**). The results of the susceptibility of UPEC isolates to different antibiotics by using the VITEK 2 Compact system revealed that the most resistant of UPEC isolates was to ampicillin (34/40) (85%) and Cefazolin (33/40) (82.5%), while the least resistant were to Amikacin and Tagicycline (0/40) (0%). The results also showed that 31/40) (77.5%) of UPEC isolates were MDR, and 20/31) (64.5%) of these MDR isolates were resistant to Ciprofloxacin (**Table 2**).

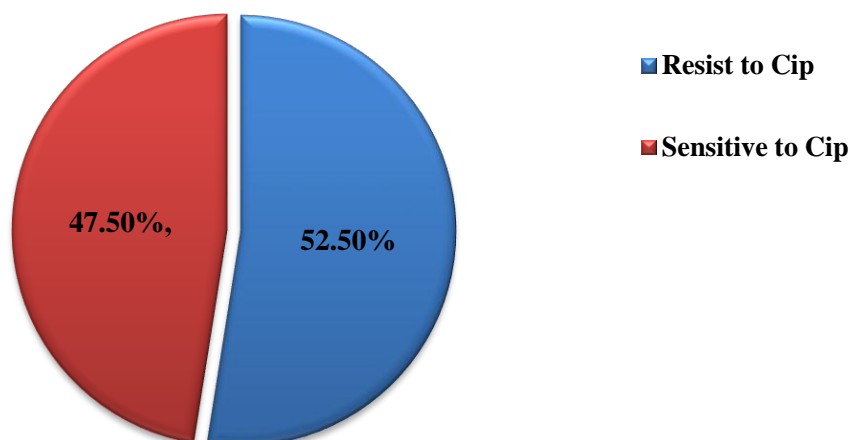


Figure 1. Percentage of Ciprofloxacin resistant UPEC.

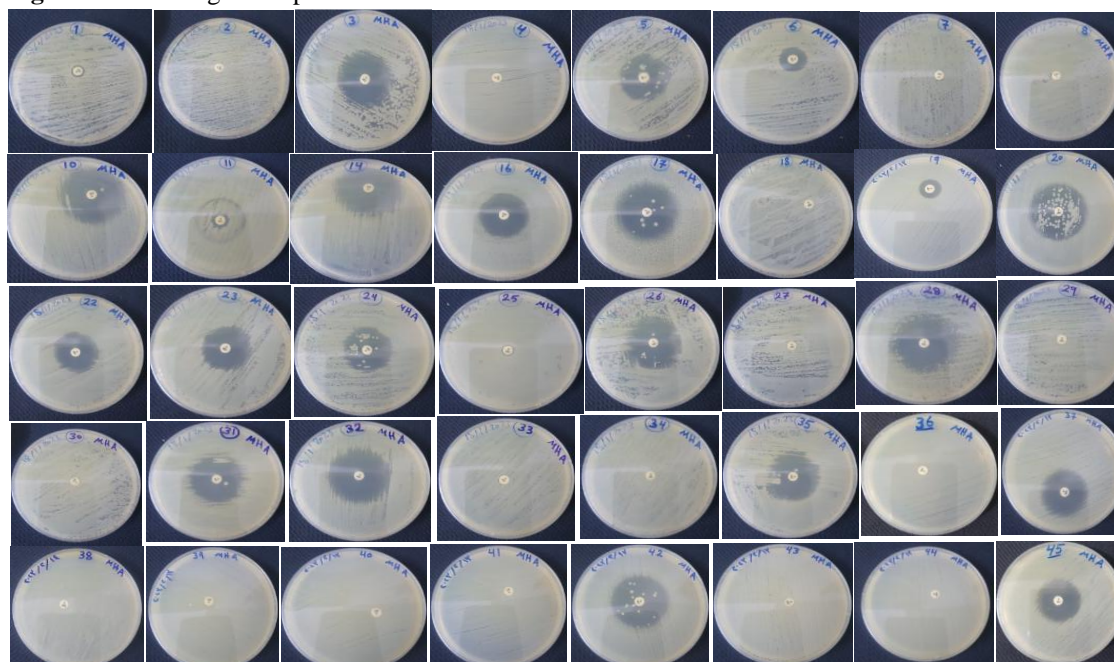


Figure 2. Susceptibility of UPEC to Ciprofloxacin discs on MHA by sing Kerby pour method.

Resistance transfer genes are simple for *E. coli* to obtain and can be carried on plasmids. (35,36). A wide-scale antibiotic named ciprofloxacin acts by averting DNA gyrase (topoisomerase II and IV) from performing on its target (37). Bacterial resistance to ciprofloxacin has been revealed to be on the rise (22.4%)) and male UTI patients were more likely to undergo this resistance (38). (39) reported that out of 324 UPECs analyzed, 61 (18.8%) were resistant to Ciprofloxacin (39). High resistance (76%) to Ciprofloxacin was obtained from testing 50 UPEC isolates (40). These findings showed that multidrug resistance was linked to ciprofloxacin resistance disseminated by UPEC that led to communicable UTIs. (38, 41).

Table 2. Percentage of resistant UPEC to different antibiotics.

Antibiotic	No. of resistant UPEC	%
Ampicillin	34	85
Piperacillin/Tazobactam	4	10
Cefazolin	33	82.5
Cefaxitin	7	17.5
Ceftazidime	20	50
Ceftriaxone	30	75
Cefepime	7	17.5
Ertapenem	1	2.5
Imipenem	2	5
Amikacin	0	0
Gentamicin	14	35
Ciprofloxacin	21	52.5
Levofloxacin	21	52.5
Tagecycline	0	0
Nitrofurantoin	3	7.5
Trimethoprim/Sulfamethoxazole	28	70

(40) demonstrated that Ampicillin had the highest level of resistance (94%), whereas imipenem, Amikacin, and Nitrofurantoin had the lowest amount of resistance to UPEC (0%) (40, 42). (43) reported that the highest resistance rate (95.23%) among UPEC was to cefepime (43). Other findings revealed resistance to Ampicillin was the highest (85%), while Amikacin displayed a decreased frequency (38). Our study was able to identify all of these findings; thus, we can suggest Amikacin and Tagicycline as the best medicines to treat UTIs.

3.3. Biofilm producing UPEC

Twenty-five UPEC were explored for their talent to prompt biofilm by using Microtiter plates (21 isolates were resistant to Ciprofloxacin, and four isolates were sensitive to all 16 antibiotics tested by the VITEK 2 Compact). The cutoff value (0.083) was calculated according to (29), and the results appeared to indicate that (11/25) were strong biofilm-forming (44%), while the rest of the isolates (14/25) were moderate biofilm-forming (56%) (**Table 3**).

Table 3. Biofilm producing UPEC.

Biofilm producer	Resistant UPEC	Sensitive UPEC	Total NO.	%
Strong	9	2	11	44
Moderate	12	2	14	56
Weak	0	0	0	0

More than 60% of human illnesses have documented biofilm formation in the environment (39). *E. coli* has the ability to aggregate and adhere to solid surfaces, creating intricate formations known as biofilms (44,45). Additionally, quorum sensing processes frequently regulate transcriptional alterations that correlate with these bacteria's creation of biofilms. This may result in the differential expression of distinct virulence factors and antibiotic resistance determinants (39). Biofilm-producing isolates displayed higher levels of antibiotic resistance than non-biofilm producers (46). Prostatitis, biliary tract infections, and urinary catheter cystitis are only a few of the major health issues that can result from biofilms comprised by clinical *E. coli* strains (47).

About 46% of UPEC isolates exhibited curli production. The strong collaboration between biofilm formation and the MDR phenotype leads to the recurrence of infections (48).

3.4.Detection of *afa* and *yqi* in uropathogenic *E.coli* isolates

After analyzing PCR products on an agarose gel, the appearance of the (*afa* and *yqi* genes) in (22) UPEC isolates, including 21 isolates that were resistant to ciprofloxacin and one isolate that produced the strongest biofilm among the four isolates that were sensitive to ciprofloxacin and other antibiotics, was discovered. Out of 22 UPEC isolates, the results showed that 17 (77.27%) had the *afa* gene **Figure 3** and 7(31.81%) had the *yqi* gene **Figure 4**.

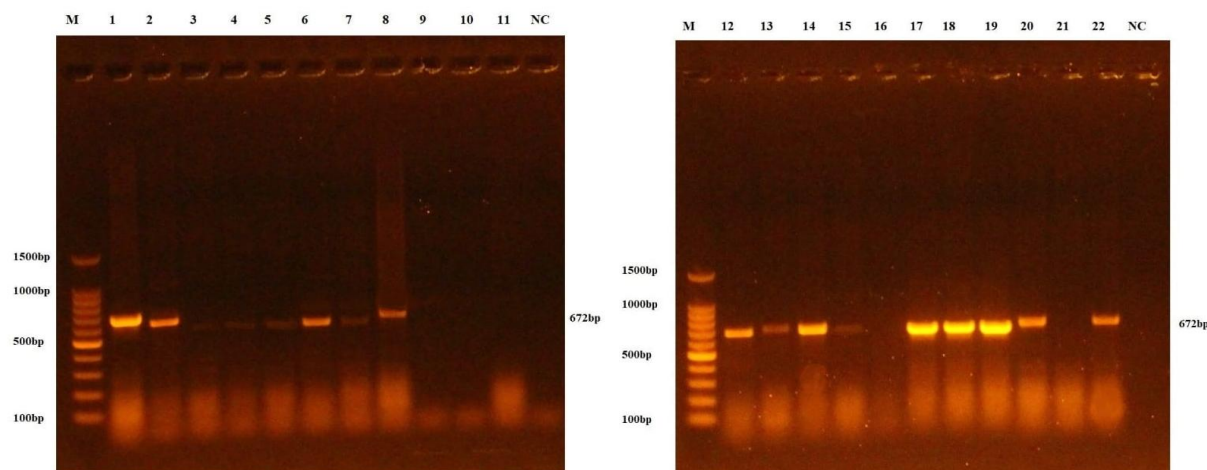


Figure 3. Results of *afa* gene (672 bp) of *E. coli* samples were fractionated on gel electrophoresis.

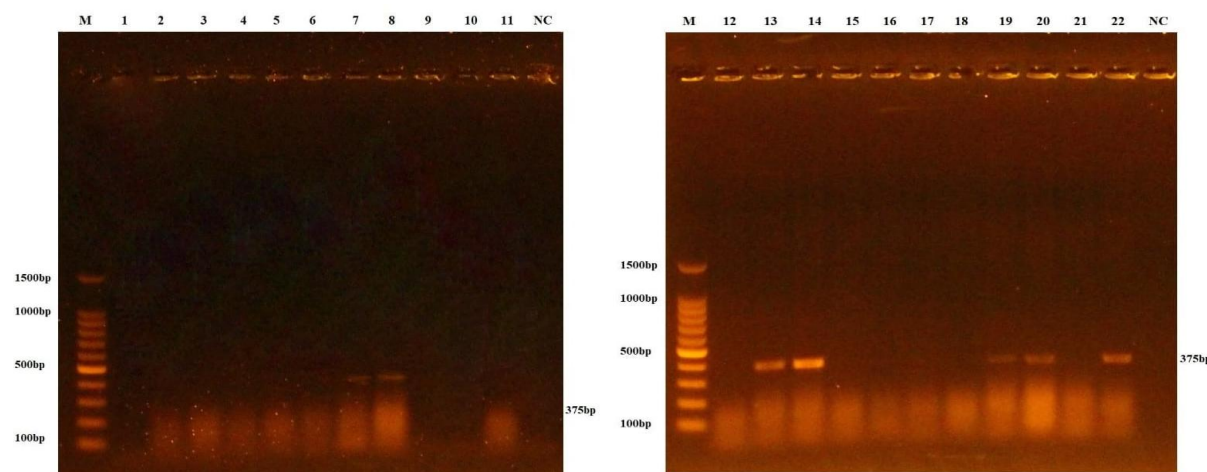


Figure 4. Results of *Yqi* gene (375 bp) of *E. coli* samples were fractionated on gel electrophoresis.

Dr. wFamily afimbrial adhesins have a particular renal tissue tropism associated with UTI. This characteristic may encourage the development of persistent and recurrent UTI (49). Many UPEC strains include the Dr Family afimbrial adhesins Afa-I and Afa-III, which attach to the receptor on the blood group A_{gs} are formed on (DAF), preventing complement activity from lysing cells (22). *afaA*, *afaB*, *afaC*, *afaD*, and *afaE* represent transcriptional regulator, Periplasmic chaperone, Outer membrane usher protein, Afimbrial adhesion, and Adhesin protein, respectively (50). Out of the 212 UPEC isolates that were studied for the appearance of the (*afa* gene, 49 (23.1%) did (22). (51) reported that two of the 56 UPEC isolates had the *afa* gene (3.57%). Also, (52) reported that 12% of the *E. coli* isolates from 100 urine samples carried the

afa gene. Other findings indicated that none of the 10 UPEC isolates carrying the *afa* gene were from other UTIs or intestinal demeanors, and all were placed in the recurrent lower UTI group (3). The highly pathogenic Extraintestinal pathogenic *E. coli* (ExPEC) strains Avain pathogenic *E. coli* (APEC), Uropathogenic *E. coli* (UPEC), and Newborn meningitic *E. coli* (NMEC) are known to be associated with *Yqi*, also known as ExPEC adhesin I (21). *Yqi* may have a very certain role in the pathogenesis of ExPEC. Recently, it has been discovered that *Yqi* is crucial to colonization (18). The prevalence of the *yqi* gene was (65.9%), (54.4%), and (60.0%) in 138 UPEC, 406 APEC, and 25 NMEC, respectively, while none of the 153 intestine pathogenic *E. coli* isolates were discovered to have the *yqi* gene (21). In another study, it was found that the *yqi* gene was found in 7% of intestinal commensal isolates; however, the occurrence was much lower (27%) than in UPEC strains (3).

4. Conclusion

The highly pathogenic Extraintestinal pathogenic *E. coli* (ExPEC) strains Avain pathogenic *E. coli* (APEC), Uropathogenic *E. coli* (UPEC), and Newborn meningitis *E. coli* (NMEC) are known to be associated with *Yqi*, also known as ExPEC adhesin I. *Yqi* may have a very certain role in the pathogenesis of ExPEC. Recently, it has been discovered that *Yqi* is crucial to colonization. The prevalence of the *yqi* gene was detected in UPEC, APEC, and NMEC, while none of the intestine pathogenic *E. coli* isolates were discovered to have the *yqi* gene.

Acknowledgment

Many thanks to the Department of Biology at the College of Science, University of Baghdad, for their invaluable support in assisting the practical sections of this article.

Conflict of Interest

The authors declare that they have no conflicts of interest.

Funding

No funding.

Ethical Clearance

The study advanced after receiving institutional ethical committee (IEC) approval. The College of Science Ethics committee approves the research proposal to be conducted in the presented form. None of the investigators and co-investigators participating in this study took part in the decision-making and voting procedure for this study.

References

1. Derakhshan S, Ahmadi S, Ahmadi E, Nasser S, Aghae A. Characterization of *Escherichia coli* isolated from urinary tract infection and association between virulence expression and antimicrobial susceptibility. BMC Microbiol. 2022;22. <https://doi.org/10.1186/s12866-022-02506-0>.
2. Adamus-Białek W, Wawszczak M, Arabski M, Majchrzak M, Gulba M, Jarych D, Parniewski P, Głuszek S. Ciprofloxacin, amoxicillin, and aminoglycosides stimulate genetic and phenotypic changes in uropathogenic *Escherichia coli* strains. Virulence. 2019;10:260–76. <https://doi.org/10.1080/21505594.2019.1596507>.
3. Qin X, Hu F, Wu S, Ye X, Zhu D. Comparison of adhesin genes and antimicrobial susceptibilities

- between uropathogenic and intestinal commensal *Escherichia coli* strains. PLoS One. 2013;8. <https://doi.org/10.1371/journal.pone.0061169>.
4. Boroumand M, Naghmachi M, Ghatee MA. Detection of phylogenetic groups and drug resistance genes of *Escherichia coli* causing urinary tract infection in Southwest Iran. Jundishapur J Microbiol. 2021;14. <https://doi.org/10.5812/jjm.112547>.
 5. Barber AE, Norton JP, Wiles TJ, Mulvey MA. Strengths and limitations of model systems for the study of urinary tract infections and related pathologies. Microbiol Mol Biol Rev. 2016;80:351–67. <https://doi.org/10.1128/MMBR.00067-15>.
 6. Al-Fatlawi BG, Jasim AL. Determining the prevalence of upper and lower urinary tract infections' pathogens and their antibiotic susceptibility profile for adult patients in Al-Diwaniya, Iraq. Iraqi J Pharm Sci. 2022;31:86–91. <https://doi.org/10.31351/vol31>.
 7. Drago L, Vecchi ED, Momeblli B, Nicola L, Valli M, Gismondo MR. Activity of levofloxacin and ciprofloxacin against urinary pathogens. J Antimicrob Chemother. 2001;48:37–45. <https://doi.org/10.1093/jac/48.1.37>.
 8. Rashki A, Rahdar M, Ghalehnoo ZR. Characterization of uropathogenic *Escherichia coli*: Distribution of adhesin-encoding genes and O-serotypes among ciprofloxacin susceptible and resistant isolates. Jundishapur J Microbiol. 2019;12. <https://doi.org/10.5812/jjm.89179>.
 9. Fasugba O, Gardner A, Mitchell BG, Mnatzaganian G. Ciprofloxacin resistance in community- and hospital-acquired *Escherichia coli* urinary tract infections: A systematic review and meta-analysis of observational studies. BMC Infect Dis. 2015;15. <https://doi.org/10.1186/s12879-015-1055-5>.
 10. Assafi MSF, Ali F, Polis RF, Sabaly NJ, Qarani SM. An epidemiological and multidrug resistance study for *E. coli* isolated from urinary tract infection. Baghdad Sci J. 2022;19:7–15. <https://doi.org/10.21123/bsj.2022.19.1.0007>.
 11. Terlizzi ME, Gribaudo G, Maffei ME. Uropathogenic *Escherichia coli* (UPEC) infections: Virulence factors, bladder responses, antibiotic, and non-antibiotic antimicrobial strategies. Front Microbiol. 2017;8. <https://doi.org/10.3389/fmicb.2017.01566>.
 12. Ebraheem AA, Alwendawi SA. Screening for in vitro biofilm formation ability of locally isolated uropathogenic *Escherichia coli* (UPEC). Iraqi J Sci. 2015;56:1310–4.
 13. Govindarajan DK, Kandaswamy K. Virulence factors of uropathogens and their role in host-pathogen interactions. Cell Surf. 2022;8. <https://doi.org/10.1016/j.tcs.2022.100075>.
 14. Bodelón G, Palomino C, Fernández LA. Immunoglobulin domains in *Escherichia coli* and other enterobacteria: From pathogenesis to applications in antibody technologies. FEMS Microbiol Rev. 2013;37:204–50. <https://doi.org/10.1111/j.1574-6976.2012.00347.x>.
 15. Rojas-Lopez M, Monterio R, Pizza M, Desvaux M, Rosini R. Intestinal pathogenic *Escherichia coli*: Insights for vaccine development. Front Microbiol. 2018;9. <https://doi.org/10.3389/fmicb.2018.00440>.
 16. Keller R, Ordoñez JG, Oliveira RR, Trabulsi LRT, Baldwin J, Knutton S. Afa, a diffuse adherence fibrillar adhesin associated with enteropathogenic *Escherichia coli*. Infect Immun. 2002;70:2681–9. <https://doi.org/10.1128/iai.70.5.2681-2689.2002>.
 17. Olesen B. Characterization of four *Escherichia coli* clonal groups. APMIS. 2017. <https://doi.org/10.1111/apm.12737>.
 18. Antão EM, Wieler LH, Ewers C. Adhesive threads of extraintestinal pathogenic *Escherichia coli*. Gut Pathog. 2009; 1:22. <https://doi.org/10.1186/1757-4749-1-22>.
 19. Servin AL. Pathogenesis of Afa/Dr diffusely adhering *Escherichia coli*. Clin Microbiol Rev. 2005;18:264–92. <https://doi.org/10.1111/j.1574-6968.2006.00144.x>.
 20. Le Bouguénec C, Servin AL. Diffusely adherent *Escherichia coli* strains expressing Afa/Dr adhesins (Afa/Dr DAEC): Hitherto unrecognized pathogens. FEMS Microbiol Lett. 2006;256:185–94.
 21. Antão EM. Identification of avian pathogenic *E. coli* (APEC) genes important for the colonization of

- the chicken lung and characterization of the novel ExPEC adhesin I. Tag der mündlichen Prüfung. 2010;1–123. <https://doi.org/10.18452/16132>.
22. Nachammai SM, Jayakumar K, Suresh V, Kousalya M. The DR family – A fimbrial adhesin gene in uropathogenic *Escherichia coli* isolated from patients suspected with urinary tract infection. Int J Adv Res. 2019;7:202–5. <https://dx.doi.org/10.21474/IJAR01/8622>.
 23. O’Sullivan J, Bolton DJ, Duffy G, Baylis C, Tozzoli R, Wasteson Y. Methods for Detection and Molecular Characterisation of Pathogenic *Escherichia coli*. Ashtown Food Res Center, Teagasc; 2007: p.32. ISBN: 1 84170 506 3.
 24. Hasan HM, Jasim HM, Salih GM. Detection of carbapenem-resistant genes and specific biofilm association genes in *Klebsiella pneumoniae* isolated from medical samples. Egypt J Hosp Med. 2022;89:6356–60. <https://dx.doi.org/10.21608/ejhm.2022.269974>.
 25. Qiu J, Jiang Z, Ju Z, Zhao X, Yang J, Guo H, Su S. Molecular and phenotypic characteristics of *Escherichia coli* isolates from farmed minks in Zhucheng, China. Biomed Res Int. 2019; 2019(1):1-12. <https://doi.org/10.1155/2019/3917841>.
 26. Sweedan EG, Shehab ZH, Flayyih MT. Effect of gentamicin and doxycycline on expression of relB and relE genes in *Klebsiella pneumoniae*. J Adv Biotechnol Exp Ther. 2022;5:667–75. <https://doi.org/10.5455/jabet.2022.d145>.
 27. CLSI. Performance Standards for Antimicrobial Susceptibility Testing. 30th ed. Supplement M100. Wayne, PA: Clinical and Laboratory Standards Institute; 2020.
 28. Obaid HH, Khalaf ZZ, Tawfeeq HK, Sabri RT, Abdul-Jabbar ZA. Antimicrobial Effect of Rheum ribes and TiO₂ NPs on Bacterial Biofilm in *Escherichia coli*. IOSR J Pharm Biol Sci. 2017;12:14-20. <http://dx.doi.org/10.9790/3008-1203041420>.
 29. Atshan SS, Shamsudin MN, Sekawi ZL, Lung TT, Hamat RA. Prevalence of Adhesion and Regulation of Biofilm-Related Genes in Different Clones of *Staphylococcus aureus*. J Biomed Biotechnol. 2012; 2012(1):1-10. <https://doi.org/10.1155/2012/976972>.
 30. Muhaimeed AA, Ghareeb AM. Prevalence of Multi-Antibiotic Resistance marA and Quorum Sensing luxS Genes and Evaluation of Biofilm Formation in Uropathogenic *Escherichia coli*. Iraqi J Biotechnol. 2023;22:252-261. <https://jige.uobaghdad.edu.iq/index.php/IJB/article/view/594>.
 31. Naziri Z, Derakhshandeh A, Borchaloei AS, Poormaleknia M, Azimzadeh N. Treatment Failure in Urinary Tract Infections: A Warning Witness for Virulent Multi-Drug Resistant ESBL-Producing *Escherichia coli*. Infect Drug Resist. 2020;13:1839-1850. <https://doi.org/10.2147/idr.s256131>.
 32. DebRoy C, Maddox CW. Identification of virulence attributes of gastrointestinal *Escherichia coli* isolates of veterinary significance. Anim Health Res Rev. 2001;1:129-140. <https://doi.org/10.1079/AHRR200131>.
 33. Alfuraiji N, Al-Hamami A, Ibrahim M, Rajab HK, Hussain BW. Uropathogenic *Escherichia coli* virulence characteristics and antimicrobial resistance amongst pediatric urinary tract infections. J Med Life. 2021. <https://doi.org/10.25122/jml-2021-0148>.
 34. Rahman S. Detection of Bacterial Population in Air Conditioner and Determine the Ability to Produce Biofilm. Iraqi J Sci. 2019;60:432-437. <https://doi.org/10.24996/ijs.2019.60.3.2>.
 35. Madelung M, Kronborg T, Doktor TK, Struve C, Krogfelt KA, Møller-Jensen J. DFI-seq identification of environment-specific gene expression in uropathogenic *Escherichia coli*. BMC Microbiol. 2017;17. <https://doi.org/10.1186/s12866-017-1008-4>.
 36. Hameed A, Zwain A, Maher D, Farag PF. Isolation and Diagnosis of Bacteria in Bacteremia Patients and Study Their Resistance to Antibiotics in Kirkuk Hospitals. IHJPAS. 2023;36. <https://doi.org/10.30526/36.3.3097>.
 37. Shariati A, Arshadi M, Khosrojerdi MA, Abedinzadeh M, Ganjalishahi M, Maleki M, Heidary S, Khoshnood S. The resistance mechanisms of bacteria against ciprofloxacin and new approaches for enhancing the efficacy of this antibiotic. Front Public Health. 2022.

- <https://doi.org/10.3389/fpubh.2022.1025633>.
38. Reis ACC, Santos SRS, Souza SC, Saldanha MG, Pitanga TN, Oliveira RR. Ciprofloxacin resistance pattern among bacteria isolated from patients with community-acquired urinary tract infection. *Rev Inst Med Trop Sao Paulo*. 2016. <https://doi.org/10.1103/PhysRevB.75.184420>.
 39. Behzadi P, Urbán E, Gajdács M. Association between Biofilm-Production and Antibiotic Resistance in Uropathogenic *Escherichia coli* (UPEC): An In Vitro Study. *Diseases*. 2020;8. <https://doi.org/10.3390/diseases8020017>.
 40. Awadallah G, Amer GA, Emam SM, Ramadan AE. Multidrug Efflux Pump In Relation To Antibiotic Resistance Pattern in *Escherichia coli* Strains Isolated From Benha University Hospital Mohamed. *Egypt J Med Microbiol*. 2020;29:87-94. <https://doi.org/10.21608/ejmm.2020.250025>.
 41. Shah C, Baral R, Bartaula B, Shrestha LB. Virulence factors of uropathogenic *Escherichia coli* (UPEC) and correlation with antimicrobial resistance. *BMC Microbiol*. 2019;19. <https://doi.org/10.1186/s12866-019-1587-3>.
 42. Al-Azzawi SNA, Abdullah RM. Detection of Antibiotic Resistance of the Phylogenetic Group E among *E. coli* Isolated from Diarrheal Cases in Children Under Five Years. *Ibn Al-Haitham J Appl Pure Sci*. 2023;36. <https://doi.org/10.30526/36.3.3107>.
 43. Al-Hasnawy HH, Judi MR, Hamza HJ. The Dissemination of Multidrug Resistance (MDR) and Extensively Drug Resistant (XDR) among Uropathogenic *E. coli* (UPEC) Isolates from Urinary Tract Infection Patients in Babylon Province, Iraq. *Baghdad Sci J*. 2019;16. <https://doi.org/10.21123/bsj.2019.16.4%28suppl.%29.0986>.
 44. Ballén V, Gabasa Y, Ratia C, Sánchez M, Soto S. Correlation Between Antimicrobial Resistance, Virulence Determinants and Biofilm Formation Ability Among Extraintestinal Pathogenic *Escherichia coli* Strains Isolated in Catalonia, Spain. *Front Microbiol*. 2022;12. <https://doi.org/10.3389/fmicb.2021.803862>.
 45. Ahmed NA, Ahmed ST, Almohaidi AM. Investigation of biofilm formation ability and Assessment of cupB and rhlR Gene Expression in Clinical Isolates of *Pseudomonas aeruginosa*. *Iraqi J Biotechnol*. 2022;21:641-650. <https://jige.uobaghdad.edu.iq/index.php/IJB/article/view/540>.
 46. Shah T, Preethishree A, Ashwini P, Pai V. Bacterial Profile of Urinary Tract Infections: Evaluation of Biofilm Formation and Antibiotic Resistance Pattern of Uropathogenic *Escherichia coli*. *J Pure Appl Microbiol*. 2020;14:2577-2584. <https://doi.org/10.22207/JPAM.14.4.33>.
 47. Ren D, Zuo R, Barrios AF, Bedzyk LA, Eldridge GR, Pasmore ME, Wood TK. Differential Gene Expression for Investigation of *Escherichia coli* Biofilm Inhibition by Plant Extract Ursolic Acid. *Appl Environ Microbiol*. 2005;71:4022-4034. <https://doi.org/10.1128/aem.71.7.4022-4034.2005>.
 48. Gawad WE, Helmy OM, Tawakkol WM, Hashem AM. Antimicrobial Resistance, Biofilm Formation, and Phylogenetic Grouping of Uropathogenic *Escherichia coli* Isolates in Egypt: The Role of Efflux Pump-Mediated Resistance. *Jundishapur J Microbiol*. 2018;11. <https://doi.org/10.5812/jjm.14444>.
 49. Blanc-Potard AB, Tinsley C, Scaletsky I, Bouguenec CL, Guignot J, Servin AL, Nassif X, Camard MF. Representational Difference Analysis between Afa/Dr Diffusely Adhering *Escherichia coli* and Nonpathogenic *E. coli* K-12. *Infect Immun*. 2002;70:5503-5511. <https://doi.org/10.1128/iai.70.10.5503-5511.2002>.
 50. Malberg Tetzschner AM, Johnson JR, Johnston BD, Lund O, Scheutz F. In Silico Genotyping of *Escherichia coli* Isolates for Extraintestinal Virulence Genes by Use of Whole-Genome Sequencing Data. *J Clin Microbiol*. 2020;58. <https://doi.org/10.1128/JCM.01269-20>.
 51. AL-Ganimi AKA, AL-Khafaji JKT. Some Virulence Factors Genes and Phylogenetic Groups of Uropathogenic *Escherichia coli* (UPEC) Isolated from Karbala Patients. *Karbala J Med*. 2015;9:2376-2385.
 52. Rahdar M, Rashki A, Miri HR, Ghalehnoo MR. Detection of Adhesin-Encoding Operons in

Uropathogenic *Escherichia coli*. Jundishapur J Microbiol. 2015;8. <https://doi.org/10.5812/jjm.22647>.