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Research Article

The Prevalence of Swarming Genes in *Escherichia coli* Isolated from UTI and Catheter-Associated UTI

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Abstract:

Background: Urinary tract infections (UTIs) are one of the most common bacterial illnesses among the public and in hospital settings. A prevalent nosocomial disease is catheter-associated urinary tract infection (CAUTI). The risk of infection increases with urinary catheterization, making it easier for Escherichia coli to colonize the urinary system. Uropathogenic *E. coli* (UPEC) specifically adapts to survive in challenging urinary tract conditions. Treating CAUTI accurately and effectively can be difficult. An important health concern nowadays is drug-resistant bacteria.

Objectives: To assess the prevalence of swarming genes in *E. coli* responsible for UTIs and catheter-associated UTIs, and determine their antibiotic resistance.

Methods: A total of 143 clinical specimens of urine and catheter samples were collected from two teaching hospitals in Baghdad city between October and December 2023. The bacteria were identified, and their antimicrobial susceptibility was tested. Conventional PCR methods were used to determine the bacteria and detect swarming genes (*flhC*, *flhD*, and *recA*).

Results: Out of 143 samples, 44 isolates were identified as *E. coli* (35 isolates from UTIs and 9 isolates from catheters). These isolates exhibited varying sensitivities to antibiotics, most being multi-drug resistant (MDR). They were highly resistant to tetracycline (72.7%) and highly susceptible to imipenem (93.2%). Among these isolates, 16 were identified (12 from UTIs and 4 from catheters). All the highly swarming and multidrug-resistant *E. coli* isolates were found to possess the three tested swarming genes (*flhC*, *flhD*, and *recA*), as determined by conventional PCR.

Conclusion: *Escherichia coli* is more prevalent in UTIs than in catheters. The number of isolates demonstrating the ability to swarm was found to be higher in UTIs, and these isolates also exhibited the capability to swim. Most *E. coli* isolates are multidrug-resistant and can swarm.

Key Words: *Escherichia coli*; *flhC; flhD*; Swarming motility; *recA*.

Introduction:

Urinary tract infection (UTI) is one of the most common bacterial diseases in humans. While E. coli is often associated with UTIs, it has also been found in the bladders of individuals who do not show any symptoms of lower urinary tract infection. This condition is known as asymptomatic bacteriuria (1). *E. coli* is also related to several extra-intestinal illnesses (2). Most *E. coli* strains found in the colon are harmless. However, certain pathogenic strains can cause contamination inside or outside the colon, depending on their virulence-associated traits (3). *E. coli* is the main and most common cause of UTI, cholangitis, cholecystitis, traveler's diarrhea**,** bacteremia, septicemia, neonatal meningitis, and others (4). One of the most common hospital-acquired infections is catheter-associated urinary tract infection (CAUTI). Urinary catheterization increases the risk of infection and promotes *E. coli* colonization of the urinary tract (5). *Escherichia coli* and other bacteria with peritrichous flagella can swim in a liquid environment by using a random walk pattern. This smooth movement, known as a run, happens when all flagella rotate counterclockwise to form a helical bundle. *E.coli* displays two types of flagella-driven motility: Swimming and swarming. Single-cell motility takes place when cells move in a liquid medium or soft semisolid agar while swarming happens when cells collectively move over semisolid surfaces (6). Flagellar-driven motility enables bacteria to colonize favorable sites in response to environmental cues, potentially increasing the risk of some species. Flagellated bacteria can move freely in bulk liquid or swarm on a semi-solid surface (7).

Escherichia coli uses several genes to control swarming, including *flhD*, *flhC*, and *recA*. The *flhD* operon, found at the beginning of the flagellar regulon, is the primary focus of control. It consists of two genes, *flhD*, and *flhC*, whose products combine to form the FlhD/FlhC heterotetrameric transcriptional regulatory

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complex (8)**.** *E. coli recA* has been discovered to have a new physiological function in promoting *E.coli*'s movement during swarming, but not during swimming. The exact molecular mechanism through which *recA* controls *E. coli*'s swarming movement is still unknown, however, it appears that *recA* does not affect swarming movement through the formation of large classical *recA* nucleofilaments (9)**.**

The first and crucial step in a UTI is when UPEC invades and colonizes the periurethral and vaginal areas. Bacterial motility is often associated with the severity of bacterial infections. In UPEC UTIs, the flagella enable motility and contribute to the bacterial virulence. A transcriptional regulator called PapX was found at the 3′ end of the P fimbrial operon in UPEC. When PapX is overexpressed, it reduces the synthesis of flagella, the flagellin protein (FlaA), and bacterial motility. On the other hand, the downregulation of PapX stimulates the transcription of the *flhDC* gene which is a transcriptional repressor that acts as a master regulator of flagellar motility. It plays crucial roles in adhesion, maturation, and proliferation. This is supported by the regulation of flagella-related gene expression during the growth phase of *E. coli* (10).

The study aimed to explore the most prevalent bacteria in UTIs and catheters, to determine which antibiotics are most resisted by the isolated bacteria, and identify the most prevalent genes associated with the swarming phenomena.

Materials and method:

Isolation and identification of bacteria: One hundred and forty-three samples were taken from urine (91 samples) and catheter surgery (52 samples) by transport swabs, from Al-Karama and Al-Yarmouk Teaching Hospitals between October and December 2023. The samples were taken and streaked onto MacConkey, EMB, and blood agar in a laboratory setting under aseptic conditions. The samples were then incubated at 37°C (11). The isolates underwent traditional biochemical testing to verify their identity, all tests were conducted following the standard procedures (12) (13).

Antibiotic susceptibility assay: The selection of antibiotics followed the Clinical & Laboratory Standards Institute (CLSI) 2023 recommendations, with disks for imipenem, amikacin, gentamicin, ciprofloxacin, azithromycin, tetracycline, cefotaxime, and ceftriaxone. By following the Kirby-Bauer protocol, the antibiotic sensitivity test was prepared (14). One or two colonies from an overnight nutrient agar plate culture were transferred into 3 mL of normal saline. A turbidity adjustment of 0.5 McFarland was made. Muller Hinton agar plates were inoculated using a sterile cotton swab dipped in the bacterial solution. The disks of various antibiotics were placed on the plate′s medium, for 18 to 24 hours. The plates were incubated at 37°C. The inhibition zones that resulted were quantified and contrasted with CLSI 2023 breakpoints. The isolate was categorized as susceptible, intermediate or resistant to a particular antibiotic by comparing it to the standard inhibition zones (15)**.**

Swarming and swimming assay: 1g% tryptone, 0.5g% glucose, 0.5g% NaCl, 0.5g% yeast extract, 0.5g% agar and 1.5g% Eiken agar was autoclaved at 121°C for 15 minutes, then cooled to 50°C and poured into Petri dishes (16). In this study, the media were modified by changing the agar percentage to 0.4 g% and the peptone percentage to 1 g%. Single colonies of *E.coli* were cultured in 5 ml of Brain-Heart infusion broth overnight. A 0.5 McFarland turbidity correction was used. On the two swarming agar plates, 5 µl of bacterial cultures was spotted. The plates were incubated at 37°C for 18 to 24 hours (17).

Swimming test media was prepared according to Kinoshita et al. (18), with modification, which include 1 g% peptone water, 0.5 g% NaCl, and 0.3 g% agar. Single colonies of *E.coli* were cultured in 5 ml of Brain-Heart infusion broth overnight. A 0.5 McFarland turbidity correction was used. 5 µl of bacterial cultures was spotted on a modified swimming medium.

Genotypic identification and detection of swarming genes: All steps are done according to Promega manufacturers (Part 9PIM712).

DNA extraction of bacteria: Nine *E.coli* isolates, six from urine and three from catheter surgery, were selected to detect the housekeeping gene (GAPDH) and swarming genes (flhC, flhD, and recA). Using a commercial Wizard genomic DNA purification kit (Promega, USA), genomic DNA was extracted from these isolates. The Quantus Fluorometer was then used to measure the concentration and purity of DNA.

PCR Amplification: The sequence of the particular pair of primers was used in Table (1). The PCR reaction was used to detect bacteria that possess GAPHD and swarming genes. A 25 µl volume was used for the PCR reactions, which included 12.5 µl of green master mix (Promega, USA), 1 µl of each primer (10 Pmol), and 2 µl of DNA template. The reaction volume was adjusted to 25 µl by using deionized distilled water. For the housekeeping gene (GAPDH), the annealing temperature was 53°C, while for the other gene, it was 56°C. Usually the annealing process takes between 30 and 60 seconds.

Table (1): Primers used in this study.

Id	Primer Name	Sequence	Product size (bp)	Reference
1	*GAPDH*-F	5'ACTTACGAGCAGATCAAAGC3'	190	(17)
2	*GAPDH*-R	5'AGTTTCACGAAGTTGTCGTT3		
3	*FlhC*-F	5'CCGGTTTGTGTAATGGCGTC3'	122	Designed in this study
4	*FlhC*-R	5'CAAACCGCACCAATGTCCAG3'		
5	*FlhD*-F	5'TTAGCGGCACTGACTCTTCC3'	87	
6	*FlhD*-R	5'TCGTCTGGTGGCTGTCAAAA3'		
7	*RecA*-F	5'GGGCCGTATCGTCGAAATCT3'		
8	*RecA*-R	5'GCGTCACAGATTTCCAGTGC3'	218	

Extension: The extension reaction is usually carried out between 72°C and 74°C, which is the ideal temperature for Taq DNA polymerase. The amplified DNA is given 1 minute per kilobyte. It is advised to extend for a final 5 minutes at 72°C–74°C. The amplified DNA is given 1 minute per kilobyte. It is recommended to continue at 72°C–74°C for the last five minutes. The PCR reaction products were stored at -20°C or immediately separated on 2% agarose gels.

Agarose gel electrophoresis of the PCR product: Agarose gel was prepared in 1% concentration as described by Lee *et al.,* (19). through dissolving 0.75 g of agarose powder in 75 ml 1X TBE buffer. Five microliters of a 100 base pair DNA ladder were aliquoted and put in the first well, on the left side of the agarose gel. After that, the DNA amplicons were cautiously put into the appropriate wells. The electrophoresis tank was then sealed with its unique lid. After that, the electrodes were positioned as directed, and 150 volts of electric current (corresponding to 5 V/cm) was applied for 40 minutes.

The loading buffer's bromophenol blue movement served as a monitor for the migration. Lastly, the gel documentation system was used to quickly take photos of the anticipated DNA bands once they had been inspected using an ultraviolet transilluminator.

Statistical analysis:

To determine the impact of different elements on research parameters, the IBM SPSS statistics program (29.0.2.0) was utilized. The chi-square test was used to determine the association between the studied variables.

Results:

Isolation and identification of bacteria: Out of the 143 samples (91 from urinary tract infections, 52 from catheters), 44 (30.8%) isolates were identified as *E.coli*, 35 (24.5%) in UTI, and 9 (6.3%) in catheters, by using MacConkey agar, EMB agar, and blood agar for characterization of colonies. The identification was conferred by biochemical test, Table (2).

Table (2): Biochemical Identification Results of *E.coli*

No.	Biochemicals test	Results
1	Catalase production	+ve
2	Oxidase test	-ve
3	Indole production	+ve
4	Urease production	-ve
5	Citrate	-ve
6	MR (Methyl red)	+ve
7	TSIA (Triple Sugar Iron Agar)	Acid/Acid, Gas +ve

The highest percentage of *E.coli* isolates was in urine samples 35/91 (38.5%) compared to catheters 9/52 (17.3%). In urine sample the predominant species was *E.coli* isolates 35 (38.5%), followed by 24 (26.4%) *Klebsiella* spp, 5 (5.5%) *Pseudomonas* spp, 2 (2.2%) *Proteus* spp. Out of the 52 samples of catheter, 22 (42.3%) isolates showed growth with 9 *E.coli* (17.3%) of catheter isolates, followed by *Klebsiella* spp 6 (11.5%), *Serratia* spp 4 (7.6%) and *Staphylococcus* spp 3 (5.8%), table (3). There was no significant association between the source of the sample and the number of *E,coli* isolates (P> 0.05). This was true for the other types of bacteria isolated (P> 0.05).

Table (3): The percentage of *E.coli* isolates and other bacteria from different sources

Sample source	No. of samples	No. and (%) of E.coli isolates	Other bacteria		
Urine	91	35 (38.5)	*Klebsiella* spp	*Pseudomonas* spp	*Proteus* spp
			24 (26.4%)	5 (5.5%)	2 (2.2%)
Catheter	52	9 (17.3)	*Serratia* spp	*Klebsiella* spp	*Staphylococcus* spp
			4 (7.6%)	6 (11.5%)	3 (5.8%)
P value	P>0.05		P>0.05		

Antibiotic susceptibility assays: The antibiotic susceptibility test results for *E. coli* are presented in Table (4), showing variations in susceptibility to the antibiotics. This test involved 44 isolates tested against eight antibiotics. Out of these, 41 isolates (93.2%) were sensitive to imipenem, 35 isolates (79.5%) to amikacin followed by 34 isolates (77.3%), which were sensitive to Azithromycin and 29 isolates (65.9%) to gentamicin, whereas, 32 isolates (72.7%) were resistant to Tetracycline and 30 isolates (68.2%) to cefotaxime and ceftriaxone. There is a statistically significant association between the type of antibiotic used and the bacterial sensitivity / resistance detected, ($P < 0.05$).

Table (4): Antibiotic susceptibility result of *E.coli*

Antibiotic	Number of isolates		
	Sensitive	Intermediate	Resistant
imipenem	41 (93.2%)	1 (2.3%)	2 (4.5%)
amikacin	35 (79.5%)	4 (9.1%)	5 (11.4%)
gentamicin	29 (65.9%)	5 (11.4%)	10 (22.7%)
ciprofloxacin	14 (31.8%)	2 (4.5%)	28 (63.63%)
Azithromycin	34 (77.3%)	0	10 (22.7%)
Tetracycline	11 (25.0%)	1 (2.3%)	32 (72.7%)
cefotaxime	14 (31.8%)	0	30 (68.2%)
ceftriaxone	14 (31.8%)	0	30 (68.2%)
P value	$P < 0.05$		

Swarming and swimming assay

Out of 44 isolates, 16 (36.4%) showed the ability to swarm on the two types of swarming media, as shown in Figure (1). Among these, 12 (27.3%) were UTI isolates and 4 (9.1%) were catheter isolates. Two isolates demonstrating swarming ability were sensitive to all antibiotics, while 14 were Multi-Drug Resistant (MDR). Additionally, 8 out of the 16 isolates that exhibited swarming ability also showed swimming ability on the modified medium. Not all isolates exhibited the same swarming strength. Each isolate swarming differed from the others in both dispersal strength and shape.

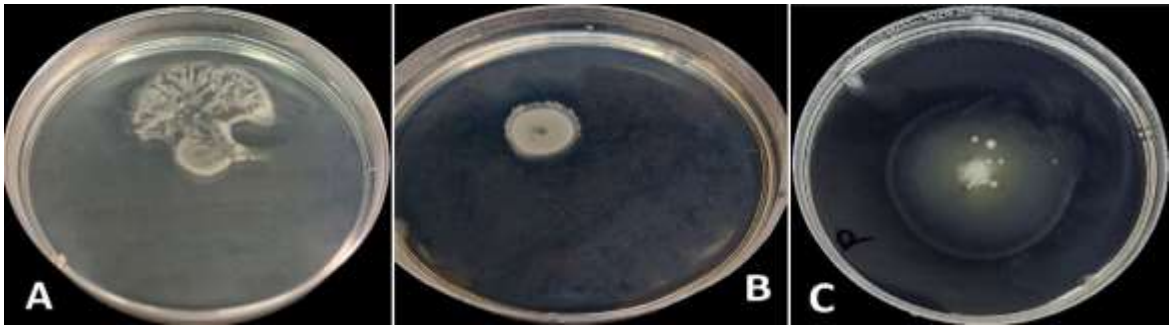

Figure (1): swarming of *E.coli*. A) Swarming on modified medium (0.4g% agar). B) Swarming on original medium (0.5g% agar). C) Swimming on a modified medium.

Genotypic identification and detection of swarming genes of *E. coli* isolates:Nine isolates of *E. coli* were selected because of the strong swarming and multi-resistance. The identification of these isolates was confirmed by using the housekeeping gene *GAPDH,* by conventional PCR. The result showed that all isolates were positive for the *GAPDH* gene, with an amplified size of 190 bp, using agarose gel electrophoresis, Figure 2. Swarming genes (flhC, flhD, and recA) were detected in 9 *E.coli* isolates by using conventional PCR. The results indicated that all isolates possessed the three tested swarming genes, with band sizes of 122 bp for flhC, 87 bp for flhD, and 218 bp for recA, Figure 2.

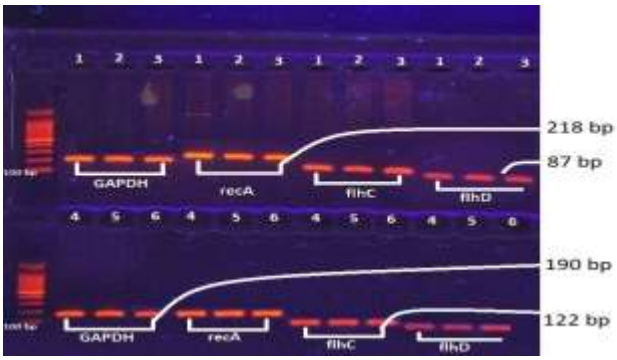

Figure (2): PCR detection of swarming genes of *E.coli* isolates were fractionated on 1.5% agarose gel electrophoresis stained with ethidium bromide, 40 minutes. Lane M: 100bp DNA ladder marker

Discussions:

Escherichia coli was the most prevalent in urine samples, followed by *Klebsiella* spp, *Pseudomonas* spp, and *Proteus* spp. The distribution of the types of bacterial isolates in the present study was consistent with those reported by other studies on UTIs. Khalaf and Flayyih (20) found that the urine samples revealed a majority of *E. coli* (70%) and that 75% of uncomplicated UTI cases were caused by UPEC. However, opportunistic UTIs are caused by other less prevalent pathogens such as group *B. streptococcus*, *K. pneumoniae*, *S. saprophyticus*, *E. faecalis*, *P. mirabilis*, *P. aeruginosa*, *S. aureus,* and other pathogenic bacteria. Over half of the cases of complex UTIs are caused by UPECs (10)**.** A study on 85 UTI cases reported a female preponderance (60%), and that 56.7% of the cases were under 40 years of age. All of the bacterial isolates demonstrated complete sensitivity to meropenem (13). In another study, *E. coli* was identified as the most common bacteria causing lower UTIs (46%), followed by *K. pneumoniae* (23%), *P. aeruginosa* (13%), *P. mirabilis* (10%), and *S. epidermidis* (8%). Female preponderance was also reported (62%), with males experiencing infections most frequently between the ages of 35 and 60 (21).

In a study conducted by Hameed *et al.* (22), it was found that out of 50 newborns, 6 (12%) had UTIs confirmed through urine culture and *E. coli* was the most commonly isolated microorganism. Notably, UTIs were more prevalent in female patients, with 66% of cases occurring in the first two months of life. Among the symptoms associated with UTIs, irritability was the most prevalent, observed in 83% of affected newborns. Interestingly, among jaundiced newborns with UTIs, a higher elevation in conjugated bilirubin was observed. However, it was found that jaundice resolved after appropriate antibiotics were administered.

The diagnosis of CAUTI requires more than just bacteriuria, and additional signs and symptoms like fever, flank discomfort, or suprapubic tenderness are necessary. Antibiotics are not recommended for patients with catheter-associated asymptomatic bacteriuria (CAASB) who are not at high risk of serious illness (4). The current study found that catheter isolates exhibited high resistance to cefotaxime, ceftriaxone, and ciprofloxacin (88.8%) followed by Tetracycline (66.6%), and showed high sensitivity to amikacin (88.8%) and imipenem (77.7%) El-Mahdy *et al*. reported that UPEC strains isolated from CAUTIs were found to be highly resistant to ampicillin (100%), amoxicillin-clavulanate and cefuroxime (86.7%), tetracycline (75.6%), ciprofloxacin, norfloxacin (71.1%), trimethoprim-sulfamethoxazole (66.7%), ceftazidime (55.6%), and aztreonam (53.3%). Likewise, the strains isolated from community UTIs showed an increased resistance to ampicillin (100%), cefuroxime (84.4%), tetracycline (75.6%), amoxicillin-clavulanate (73.3%), ciprofloxacin (66.7%), trimethoprim-sulfamethoxazole (62.2%), norfloxacin (60%), aztreonam, and ceftazidime (46.7%). Low resistance to amikacin, meropenem, and gentamicin was demonstrated by the isolates recovered from CAUTIs and community UTIs, which were 4.4%, 6.7%, and 26.7% in CAUTI and 2.2%, 4.4%, and 20% in community UTIs respectively. The resistance pattern of UPEC isolated from CAUTI and community UTIs did not significantly differ from one another (23).

Escherichia coli isolated from UTIs is becoming increasingly resistant to antibiotics and posing a serious public health concern. It is crucial to identify antibiotic resistance patterns in *E. coli* isolates for accurate prescriptions (24). The prevalence of bacterial pathogens producing extended-spectrum beta-lactamases (ESBLs) has led to a rise in UTI complications, presenting numerous management and epidemiological challenges, accounting for the majority of ESBL-producing organisms, most of which are nosocomial. However, the problem has recently become more severe due to the increased prevalence of MDR*, E. coli,* and ESBL. The majority of ESBL and *E. coli* are resistant to fluoroquinolones, trimethoprim, and gentamycin, as well as a variety of non-beta lactams, such as cephalosporins, penicillins, and piperacillin/tazobactam (25). According to Wang *et al*., sputum isolates exhibited higher resistance to 12 antibiotics compared to blood or urine isolates. Levofloxacin resistance was found to be higher in urine isolates. Additionally, urine isolates from young people displayed more resistance to certain antibiotics than those from older people. Furthermore, isolates from the elderly demonstrated greater resistance to most of the antibiotics tested compared to sputum strains isolated from children. (26).

The bacterial swarming on the modified media was generally stronger and better than on other media. The results indicated a wider spread of swarming on the modified medium, with a higher number of isolates demonstrating the ability to swarm. This suggests that the quantity of agar has a significant impact on the movement and spread of bacteria. This was further confirmed in swimming assays, where a lower agar concentration (0.3%) resulted in a wider spread for most isolates, considering an incubation temperature of 37°C for 24 hours. In a nutrient-rich plate with less than 0.3% agar (swimming assay), the bacteria exhibited chemotaxis, moving toward the nutrients through the agar pores and utilizing the nutrients. For the swarming assay, it is crucial to use an agar concentration higher than 0.3% to avoid swimming and accurately identify swarming motility (27)**.**

The ability of *E. coli* to move in urine isolates was found to be greater than in catheters, indicating that the environment plays a significant role in facilitating motility. Motility is a crucial factor for UPEC to travel

to the upper urinary tract, and it is one of UPEC's pathogenic traits. This ability allows the bacteria to ascend the ureters to the kidneys more quickly and efficiently (28). Many processes that occur on surfaces, such as adhesion, and interactions between bacteria and hosts, are influenced by the movement of bacteria's flagella. Thus, surface contact can control the expression of genes related to flagellar function and pathogenicity. Certain bacterial species have been shown to use their flagella as mechano-sensors (29).

In the current study, the identification of the *E. coli* isolates was confirmed using the housekeeping gene *GAPDH* with conventional PCR. Al-Imam and Flayyih used the *16SrRNA* gene to confirm the identification of *E. coli* O157:H7 isolates, which were positive for it, with 213bp (30).

In the current study, the presence of swarming genes (*flhC, flhD,* and *recA*) was confirmed in all tested *E. coli* isolates using conventional PCR. All isolates were found to have these three swarming genes, indicating that they are essential for swarming. The flagellar regulon is controlled by two master regulators, *flhD* and *flhC*. Mutant cells lacking these regulators are unable to move and do not have flagella. FlhDC activates specific promoters in response to environmental and metabolic signals (8). The flagellum is produced as a response to environmental stress, and the expression of *flhDC* is essential for its development. Catabolite suppression through cAMP affects the expression of *flhDC*. Acetyl phosphate inhibits flagellum development at high temperatures, likely due to OmpR phosphorylation, which suppresses *flhDC* production (31).

Escherichia coli recA has been found to play a new physiological role in promoting the bacterium's movement during swarming. In *E. coli* cells lacking the *recA* gene, swarming over a semi-solid surface is affected, while their swimming ability remains unchanged. These cells show reduced motility at the individual cell level when grown on a semi-solid surface and completely lose their collective swarming motion (9). Lane *et al*.'s research showed that a gene called *fliC* is important for this movement. Bacteria without this gene had reduced presence in the kidneys and disappeared from the spleen, indicating that wild-type UPEC use flagella to move and spread during UTI (32).

Conclusion:

Escherichia coli is more prevalent in UTIs than in catheters. The number of isolates demonstrating the ability to swarm was found to be higher in UTIs, and these isolates also exhibited the capability to swim. Most *E. coli* isolates are multidrug-resistant and can swarm.

Authors' declaration

We confirm that all the Figures and Tables in the manuscript are ours. Besides, the figures and images, which are not ours, have been given permission for re-publication attached to the manuscript.

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Authors' Contributions:

Study conception & design: (May Talib Flayyih. Literature search: (Hamza Ibrahim Kaittan). Data acquisition: (Hamza Ibrahim Kaittan. Data analysis & interpretation: (May Talib Flayyih). Manuscript preparation: (Hamza Ibrahim Kaittan). Manuscript editing & review: (May Talib Flayyih & Hamza Ibrahim Kaittan).

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انتشار جينات العج في الإشريكية القولونية المعزولة من التهاب المسالك البولية والتهاب المسالك البولية المرتبط بالقسطرة

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الخلاصة:
خلفية البحث: تعد إلتهابات المسالك البولية من بين الأمراض البكتيرية الأكثر شيوعا في كل من الأماكن العامة والمستشفيات. أحد أكثر أمراض المستشفيات إنتشارا هو عدوى المسالك البولية المرتبطة بالقسطرة. تزيد القسطرة البولية من خطر العدوى وتسهل على الإشريكية القولونية إستعمار الجهاز البولي. تم تكيف الإشريكية القولونية المسببة للأمراض البولية خصيصا للبقاء على قيد الحياة في الظروف الصعبة للمسالك البولية، حيث يمكن لهذه البكتيريا أن تلتصق بالمسالك البولية وتستعمرها، وتشكل مجتمعات بكتيرية داخل الخلايا باستخدام الشعيرات اللاصقة وتنشر عوامل الفوعة لتسبب العدوى. قد يكون علاج عدوى المسالك البولية المرتبطة بالقسطرة بفعالية ودقة أمرا صعبا. البكتيريا المقاومة للأدوية هي واحدة من أهم المخاوف الصحية في الوقت الحاضر.
الأهداف: تقييم مدى انتشار جينات العج (swarming genes) في الإشريكية القولونية التي تسبب التهاب المسالك البولية والتهاب المسالك البولية المرتبط بالقسطرة، وكذلك تحديد مدى مقاومتها للمضادات الحيوية.
المرضى والمنهجية: تم جمع 143 عينة سريرية من عينات الإدرار والقسطرة من مستشفيين تعليميين في مدينة بغداد خلال الفترة الممتدة من تشرين الأول - كانون الأول 2023. تم تشخيص البكتيريا بعد سلسلة من خطوات الزراعة والتنقية. تم إستخدام طرق تفاعل البوليميريز المتسلسل التقليدية للتعرف على البكتيريا والتحري عن وجود جينات العج (*recA*، *flhD*، و*flhC*). تم إتباع بروتوكول كيربي باورفي إعداد اختبار الحساسية المضادة للميكروبات.
النتائج: من 143 عينة، تم التعرف على 44 عزلة على أنها بكتيريا الإشريكية القولونية (35 من التهابات المسالك البولية، 9 من القسطرة). أظهرت هذه العزلات حساسية مختلفة للمضادات الحيوية، معظمها كانت متعددة المقاومة للأدوية، وأظهرت العزلات مقاومة عالية للتتراسيكلين (72.7%) وحساسية عالية للإيميبينيم (93.2%). كانت هناك 16 عزلة، 12 منها من التهابات المسالك البولية وأربع من القسطرة. تمتلك جميع عزلات الإشريكية القولونية القوية ومتعددة المقاومة للأدوية جينات العج الثلاثة التي تم اختبارها (*recA*، *flhD*، و *flhC*) بواسطة تفاعل البوليميريز المتسلسل التقليدي .
الإستنتاجات: تنتشر البكتيريا الإشريكية القولونية بشكل أكبر في حالات التهاب المسالك البولية مقارنة بالقسطرة. وقد وجد أن عدد العزلات التي أظهرت القدرة على التحشد أعلى في حالات التهاب المسالك البولية، كما أظهرت هذه العزلات أيضا القدرة على السباحة. معظم عزلات البكتيريا الإشريكية القولونية مقاومة للأدوية المتعددة ويمكنها التحشد.
مفتاح الكلمات: الاشريكية القولونية، حركة العج، حركة السباحة، recA، flhC، flhD