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ORIGINAL ARTICLE

Molecular characterization of multidrug-resistant *Proteus mirabilis* isolates from pregnant women with recurrent urinary tract infection in Erbil city, Iraq

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ABSTRACT

Background and Objectives: Urinary tract infections (UTIs) are common in pregnancy and can cause maternal and fetal complications. *Proteus mirabilis* is a significant pathogen in recurrent UTIs due to its virulence factors. This study investigated the virulence genes and antibiotic resistance patterns of *P. mirabilis* isolates from pregnant women with UTIs in Erbil, Iraq.

Materials and Methods: This cross-sectional study (September 2024–January 2025) included 120 urine specimens from pregnant women (15-44 years) with UTI symptoms. Bacterial identification was performed using culture, biochemical tests, as well as the Vitek 2 system. Virulence genes were detected by PCR, and antimicrobial susceptibility was assessed by standard methods.

Results: Of the 120 samples, 103 (85.8%) showed bacterial growth; 8 (6.7%) were positive for *P. mirabilis*, while 95 (79.1%) yielded other bacteria. The most affected age group was 25-34 years (52.5%), predominantly in the second trimester (42.5%) and urban residents (60.8%). Antimicrobial resistance was significant to ampicillin, trimethoprim-sulfamethoxazole, amoxicillin/clavulanic acid, and cephalosporins, although susceptibility was observed with several antibiotics. All *P. mirabilis* isolates harbored the *UreC* gene, and 75% possessed the *MrpA* virulence gene.

Conclusion: Multidrug-resistant *P. mirabilis* with key virulence genes was detected in pregnant women with UTIs. Regular screening and resistance monitoring are essential for effective management.

Keywords: Urinary tract infections; *Proteus mirabilis*; Pregnant people; Virulence factors; Multiple drug resistance

INTRODUCTION

Urinary tract infections (UTIs) are among the most common infectious diseases worldwide, affecting approximately 10% of the population (1). Bacteria are the leading causative agents, accounting for over 95% of cases, with other microorganisms such as fungi and viruses playing lesser roles (2). In particular, UTIs are prevalent in women, with risk factors including sexual activity, pregnancy, menopause, urinary tract abnormalities, catheterization, and immunosuppressive conditions (3). Urinary tract infections (UTIs) are particularly alarming in pregnant women, which affect around twenty percent of this group and contribute to an elevated morbidity rate as a result of physiological and hormonal abnormalities (4, 5).

The primary bacterial pathogens responsible for

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UTIs belong to the *Enterobacteriaceae* family, notably *Proteus mirabilis*, which is recognized as a significant opportunistic pathogen following *E. coli* (6-9). *P. mirabilis* has been shown to potentially cause complicated UTIs, especially in patients with urinary catheters or abnormal anatomy (10). It is thought that some virulence factors play a role in the pathogenicity of *P. mirabilis* including urease production, fimbriae, proteases, hemolysins and endotoxins which assist in colonization, biofilm production and tissue damage (11, 12).

The urease enzyme, encoded by the *UreC* gene, is an important virulence factor, contributing to stone formation and preventing a microenvironment that prevents antibiotic activity and allows the bacteria to remain viable (13). In a similar way, *MrpA* is part of the mannose-resistant *Proteus*-like fimbriae (MR/P) operon that contributes to adherence and biofilm formation, which is important for colonization of the urinary tract and recurrent infections (14, 15). While virulence factors like urease as well as *MrpA* have been identified, knowledge of the prevalence and genetic diversity in clinical isolates from Iraq and neighboring countries is still limited.

Molecular studies in neighboring areas have examined the genetic basis of *P. mirabilis* virulence and antibiotic resistance. For example, in Iran, Turkey, and Jordan, high rates of virulence genes, such as *UreC* and *MrpA*, have been reported, along with strains with multidrug-resistant phenotypes (16-18). However, very little data are yet available regarding Iraq, and there are geographical differences in patterns of antimicrobial resistance, which are problematic for management.

The global emergence of antibiotic-resistant *P. mirabilis* strains, additionally related to the dissemination of ESBLs (extended-spectrum β-lactamases), adds to treatment complications (19-21). In Iraq, while some surveillance has been completed, comprehensive molecular epidemiological data, including virulence genes as well as resistance profiles, of *P. mirabilis* isolates in pregnant women with recurrent UTIs is nonexistent.

Although *P. mirabilis* virulence factors and resistance mechanisms are recognized as important, there is a distinct lack of data from Iraq and other neighboring countries regarding the molecular characteristics of clinical isolates, particularly in pregnant women. This deficit hampers the potential to develop specific diagnostic and therapeutic guidelines for allowing the treatment of patients with recurrent UTIs caused by this pathogen.

This research aims to bridge this gap by looking at the prevalence of important virulence genes, namely *UreC* and *MrpA*, and their possible connections to antimicrobial resistance patterns in isolates of *P. mirabilis* acquired from pregnant women via recurrent UTIs in Iraq. Through this molecular analysis, we seek to offer beneficial perspectives on the pathogenic potential and resistance profiles of local strains, thereby informing better clinical management and infection control practices.

MATERIALS AND METHODS

Study design and participants. This cross-sectional study was conducted between September 2024 and January 2025, involving 120 pregnant women aged 15-44 years who visited various hospitals in Erbil City with clinical symptoms of urinary tract infection (UTI). Ethical approval was obtained from the General Directorate of Health Erbil/Research Ethics Committee. Participants provided informed consent, and confidentiality was maintained. A pretested structured questionnaire collected demographic and clinical data from all participants.

Sample collection and general examination. Midstream urine samples were aseptically collected from each participant in sterile containers. Women who had taken antibiotics within the previous week were excluded. Samples were transported promptly to the laboratory for analysis. Routine urine examination included assessment for bacteria, pus cells, erythrocytes, epithelial cells, crystals, and yeast.

Bacterial isolation and identification. Urine samples were cultured promptly under sterile conditions on blood agar, MacConkey agar, and Xylose Lysine Deoxycholate (XLD) agar, using a calibrated loop for quantitative streaking. Plates were incubated aerobically at 37°C for 24-48 hours. Growth significance was determined based on colony counts per standard criteria.

Colonies exhibiting morphological features suggestive of *P. mirabilis* (swarming motility, distinctive colony morphology) underwent further identification through conventional biochemical tests, including oxidase, catalase, citrate utilization, urease activity,

and Triple Sugar Iron (TSI) tests. Confirmed isolates were then subjected to identification via the automated Vitek 2 Compact system.

Antibiotic susceptibility test. Identified *P. mirabilis* isolates were tested for antibiotic susceptibility; the test was determined using the disc diffusion method on Mueller-Hinton agar. The bacterial suspensions were adjusted to 0.5 Mac Farland. In order to prepare the Mueller Hinton agar medium, dilution was poured and spread out. After that, the chosen antibiotic disks were positioned on the plates utilizing sterile forceps, and the plates were then incubated for 24 hours at 37°C.

Molecular methods. The study used a commercial genomic DNA extraction kit (Intron Biotechnology/ Korea) to extract genomic DNA from all *P. mirabilis* isolates, which was then used as a PCR template for amplification. The concentration as well as purity of the extracted DNA was determined utilizing a Nanodrop device and confirmed through gel electrophoresis. The existence of significant virulence genes in *P. mirabilis* bacteria was identified through the utilization of conventional polymerase chain reaction (PCR).

Primer pairs preparation. The primers as well as DNA sequence initiator were designed using GenBank's genetic sequence and the primer design program as shown in Table 1. The Canadian company (IDT) prepared the primers, which were used according to manufacturing instructions. Specific virulence genes, including *UreC* (urease production) and *MrpA* (fimbriae production), were amplified using conventional polymerase chain reaction (PCR). The primers were mixed with deionized distilled water, mixed with a vortex device, as well as stored at -20°C until use. The primers were prepared according to the National Biological Information website's sources.

PCR amplification. The detection of virulence genes was achieved through PCR amplification. The amplification reaction mixture was carried out in a 25 µL volume according to the manufacturer's instructions (Promega, USA) using 12.5 µL master mix, 5 ml DNA template, 2.5 µL of 10 pmol/l upstream primers, and 2.5 µL of 10 pmol/l downstream.

For the PCR amplification process, the initial denaturation phase was performed at 94°C for three minutes for *UreC* and for five minutes for *MrpA.* This was followed by 40 cycles of denaturation at 94°C for 1 minute and annealing at 63°C for 30 seconds, as well as extension at 72°C for 1 minute for *UreC.* For the *MrpA* gene, the thirty cycles included denaturation at 94°C for thirty seconds, annealing at 40°C for thirty seconds, as well as extension at 72°C for 7 seconds. For both genes, a last extension was carried out at a temperature of 72°C for seven minutes.

Agarose gel electrophoresis. A total of 1.5 grams of agarose gel was dissolved in 100 milliliters of sodium borate (SB) buffer at a concentration of 1×. This process was carried out on a hot plate for a duration of 15 minutes. At a temperature of 50°C, 3 µL of Red Safe dye was applied and then swirled. After being placed in the electrophoresis tray, the gel was permitted to solidify at room temperature for a period of 15 minutes. A gentle removal of the comb from the gel was then performed in order to create wells for the injection of samples.

Statistical analysis. It was IBM SPSS version 27 that we used for our statistical evaluation. In order to ascertain the statistical differences among the different groups, the chi-square test was employed. By determining statistical significance, a probability of $P < 0.05$ was considered to be significant.

Ethical approval. An ethical approval was acquired by the General Directorate of Health Erbil/Research Ethics Committee, No. (26835), on September 17, 2024, and the study was carried out utilizing that approval. All of the patients were given information regarding the objectives of the study, and they were re-

Table 1. Primer sequences and sizes used to detect certain virulence genes.

Genes	Primer Sequences (5→3)	Size (bp)	Reference
UreC	F: CCG GAA CAG AAG TTG TCG CTG GA R: GGG CTC TCC TAC CGA CTT GAT C	533	AL-Obaidi et al. (22)
MrpA	F: TTC TTA CTG ATA AGA CAT TG R: ATT TCA GGA AAC AAA AGA TG	565	AL-Obaidi et al. (22)

quested to sign a consent form in order to provide their informed consent. They were given the assurance that any and all information that they disclosed would be managed in a manner that was absolutely confidential.

RESULTS

Isolation and identification *Proteus mirabilis*. Out of 120 samples from pregnant women who had UTIs, only 8 isolates of *P. mirabilis* were found, representing a 6.7% isolation rate. Using biochemical testing, microscopical and cultural traits, and the Vitek-2 system criteria, the isolates were identified. Fig. 1 illustrates the bacterial development, showing swarming or rippling movement on blood agar, colorless colonies on MacConkey agar, and yellow cultures on XLD agar with a black core and yellow zones surrounding them. The oxidase test was negative for all *Proteus* isolates, while the catalase, citrate, and urease assays were positive. According to the TSI test, CO_2 and H_2S were produced.

Prevalence of *P. mirabilis* in pregnant women patients. The study revealed that out of 120 urine samples from pregnant women, only 8 (6.7%) were positive for *P. mirabilis*, while 95 (79.1%) were positive for other types of bacteria, and 17 (14.2%) of samples had no growth of bacteria.

Prevalence of UTIs and bacterial culture in patients according to age groups. The results of the current study indicated that the age group of 25 to 34 years old had the greatest infection rate (52.5%), followed by the age group 15-24 years old, which was 34.2%. Therefore, Table 2 indicates that the age group of 25-34 years had the highest positive bacterial culture (87.3%), while the age group of 35-44 years had the lowest (81.3%). The findings also showed that, with a p-value of 0.978, there was no significant difference in the distribution of patients by age group.

Prevalence of UTIs and bacterial culture in patients according to age of gestation. Table 3 revealed that the high occurrences of urinary tract infection were in the second trimester of pregnancy with 42.5%, followed in the third trimester of pregnancy by 35%, while the lowest occurrence of the infection was in the first trimester of pregnancy with 22.5%. The study observed that the most positive bacterial culture was in the second trimester of pregnancy, 88.2%, followed in the third trimester of pregnancy, 85.7%, while the lowest positive bacterial culture was in the first trimester of pregnancy, 81.5%. A statistically non-significant difference (p-value of 0.884) was found between the difference groups.

Prevalence of infections and bacterial culture in patients according to habitation. According to Table 4, the highest rate of urinary tract infection among pregnant women from urban regions was 73 (60.8%), whereas the lowest prevalence was 47 (39.2%) in rural areas. The current study found the patients who were from the city had the highest positive bacterial culture (86.3%), while those in the village had the lowest (85.1%). According to habitation, the findings likewise showed a significant difference (p-value < 0.020).

Antimicrobial susceptibility testing of *P. mirabilis*. Table 5 displays the results of antibiotic sensitivity tests, which reveal the different levels of resistance

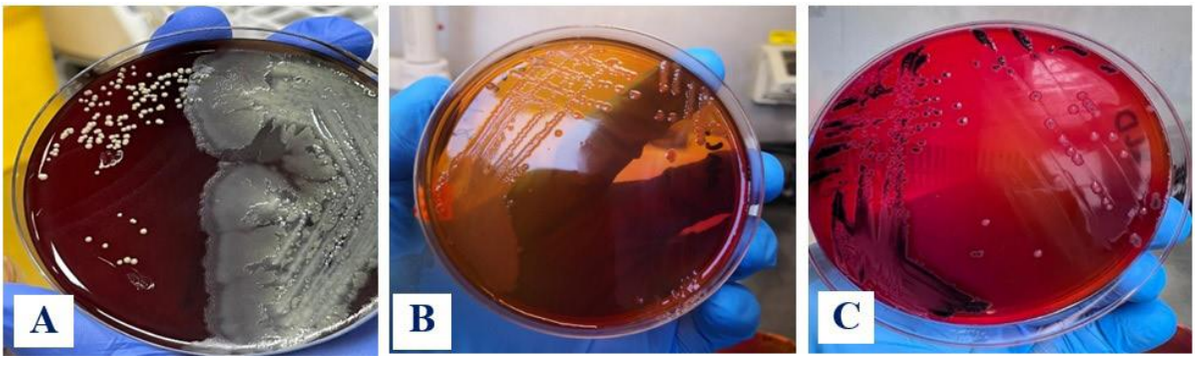

Fig. 1. Morphology characteristics of *P. mirabilis* on A. Blood agar, B. MacConkey agar, C. XLD agar

Table 2. Prevalence of UTIs and bacterial culture in patients according to age groups.

Age group (years)	Bacterial growth		No bacterial growth		Total sample		Chi- Square test
	No.	%	No.	%	No.	%	(P value)
15-24	35	85.4	6	14.6	41	34.2	0.045
25-34	55	87.3	8	12.7	63	52.5	(0.978) NS
35-44	13	81.2	3	18.8	16	13.3	
Total	103	85.8	17	14.2	120	100	

NS: Nonsignificant difference between groups (P > 0.05).

Table 3. Prevalence of UTIs and bacterial culture in patients according to month of pregnancy

Gestational Age	Bacterial growth		No bacterial growth		Total sample		Chi- Square test
(months)	No.	%	No.	%	No.	%	(P value)
0-3	22	81.5	5	18.5	27	22.5	0.246
4-6	45	88.2	6	11.8	51	42.5	(0.884) NS
7-9	36	85.7	6	14.3	42	35	
Total	103	85.8	17	14.2	120	100	

NS: Nonsignificant difference between groups (P > 0.05).

Table 4. Prevalence of infection and bacterial culture in patients according to residence

Residence	Bacterial growth		No bacterial growth		Total sample		Chi- Square test
	No.	%	No.	%	No.	%	(P value)
Urban	63	86.3	10	13.7	73	60.8	5.422
Rural	40	85.1	7	14.9	47	39.2	(0.020) S
Total	103	85.8	17	14.2	120	100	

S: Significant difference between groups (p value < 0.05)

and susceptibility of *P. mirabilis* strains isolated from pregnant patients with UTIs to 12 medications. High resistance rates were observed, with 87.5% of strains showing resistance to ampicillin and trimethoprim-sulfamethoxazole, 75% to amoxicillin/clavulanic acid, cephalexin, and nitrofurantoin, and 62.5% to ceftriaxone, cefotaxime, and cefixime. However, the strains showed better susceptibility: 87.5% with gentamicin and 75% with amikacin, ciprofloxacin, and ertapenem. The chi-squared test showed a significant difference in susceptibility patterns among the tested antibiotics.

Molecular detection of virulence genes. The results of polymerase chain reaction (PCR) amplification illustrated that all isolates of *P. mirabilis* amplified a species-specific region by producing a single band of the *UreC* gene of 533 base pairs, as shown in Fig. 2.

According to Fig. 3, it was revealed that 6 (75%) of *P. mirabilis* isolates having the *MrpA* gene exhibited a consistent length of 565 base pairs.

Distribution of virulence genes and antibiotic resistance patterns in *Proteus mirabilis* isolates. Table 6 shows that *UreC* was present in all isolates, while *MrpA* appeared in 75%. Most isolates exhibited multidrug resistance, especially to ampicillin, trimethoprim- sulfamethoxazole, amoxycillin /clavulanic acid, and cephalosporins. Isolates 1, 2, 5, and 8 were the most resistant to nearly all tested antibiotics,

Table 5. Antibiotic sensitivity test (disc diffusion test) for *P. mirabilis* isolated from pregnant women patients with UTIs.

No.	Antibiotics	Code	Number of susceptible (S) strains No. (%)	Number of intermediate resistant (I) strains No. (%)	Number of resistant (R) strains No. (%)
1	Amikacin	AK	6 (75%)	1 (12.5%)	1 (12.5%)
2	Amoxycillin /clavulanic acid	AMC	2 (25%)	0	6 (75%)
3	Ampicillin	AMP	0	1 (12.5%)	7 (87.5%)
4	Cefixime	CFM	3 (37.5%)	0	5 (62.5%)
5	Cefotaxime	CTX	1 (12.5%)	2 (25%)	5 (62.5%)
6	Ceftriaxone	CRO	2 (25%)	1 (12.5%)	5 (62.5%)
7	Cephalexin	KF	2 (25%)	0	6 (75%)
8	Ciprofloxacin	CIP	6 (75%)	1 (12.5%)	1 (12.5%)
9	Ertapenem	ETP	6 (75%)	2 (25%)	0
10	Gentamycin	CN	7 (87.5%)	1 (12.5%)	0
11	Nitrofurantoin	F	2 (25%)	0	6 (75%)
12	Trimethoprim- sulfamethoxazole	SXT	0	1 (12.5%)	7 (87.5%)
	Chi-squared test (p-value)			48.637 (< 0.001 S)	

S: Significant difference between groups (p value < 0.05)

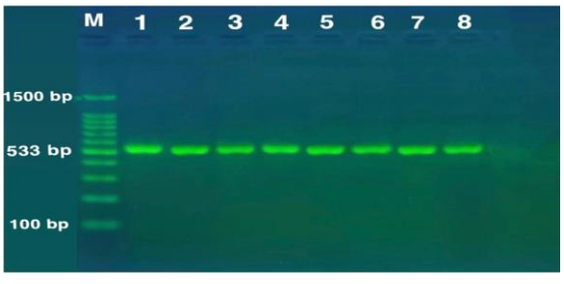

Fig. 2. PCR product generated by utilizing *P. mirabilis* utilizing *UreC*-specific primers and then electrophoresed on an agarose gel. Lane M is the 100 bp DNA ladder, while Lanes 1-8 are the identified *UreC* gene. For the *UreC* gene, the product has a size of 533 bp.

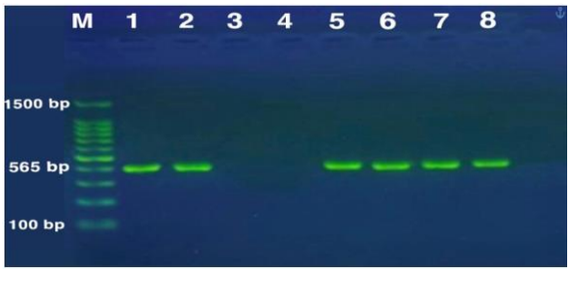

Fig. 3. Gel electrophoresis of the *MrpA* gene shows that isolates 1, 2, 5, 6, 7, and 8 are represented by the positive band. The 100 bp DNA ladder is known as lane M. The *MrpA* gene has a product size of 565 bp.

whereas isolates 3 and 4 were the least resistant and remained susceptible to several cephalosporins and fluoroquinolones. Overall, the results underscore the predominance of MDR strains, with only a few isolates showing partial susceptibility.

DISCUSSION

Urinary tract infections during pregnancy are linked to significant morbidity for both the mother as well as the fetus. Significant changes to the urinary system occur during pregnancy as a result of a combination of mechanical, hormonal, and physiological alterations. These changes have a significant effect on the development of bacteriuria during pregnancy (23). The increased risk of UTI among pregnant women, coupled with the rise in the incidence of various uropathogens globally, may impose a substantial burden on healthcare resources (24). Moreover, the frequent use of antibiotics for UTIs in pregnant women raises concerns about antimicrobial resistance, complicating treatment strategies (25).

Among the 120 pregnant women enrolled in this study, 85.8% showed positive bacterial cultures, while 14.2% tested negative. These findings are consistent with several previous Iraqi studies (26), including those conducted by Nahab HM et al.,

Table 6. Distribution of the 8 isolates of *P. mirabilis* according to the virulence genes, and antibiotic resistance profile.

No. of isolate	Result of gene		Susceptibility to antibiotics							
	UreC	*MrpA*	AMP	SXT	AMC	KF	F	CFM	CTX	CRO
1	P	P	R	R	R	R	R	R	R	R
2	P	P	R	R	R	R	R	R	R	R
3	P	N	S	R	S	R	S	S	S	S
4	P	N	R	S	S	S	R	S	S	R
5	P	P	R	R	R	R	R	R	R	S
6	P	P	R	R	R	R	S	S	R	R
7	P	P	R	R	R	S	R	R	S	R
8	P	P	R	R	R	R	R	R	R	S

P = positive, N = negative, R = resistance, S = susceptible

who documented an infection rate of 86%.

In the present study, out of 120 urine samples collected from pregnant women, *P. mirabilis* was identified in only 8 cases, representing a prevalence of 6.7%. This result aligns closely with previous findings by Al-Sarray HAK (6%) and Mahdi AG (7.28%) (27, 28), further supporting the consistency of *P. mirabilis* occurrence in similar populations.

Regarding the age distribution, the highest proportion of UTI cases (52.5%) occurred among pregnant women aged 25-34 years. This finding agrees with prior studies (26), which identified the same age group as being at greater risk for UTIs. A possible explanation is that individuals within this age range may experience heightened reproductive activity and consequently increased sexual activity. Additionally, immune system fluctuations and a greater likelihood of interacting with the healthcare system could contribute to a higher incidence of infection (26).

In this research, the second trimester of pregnancy appeared to have the most UTI occurrences. The causes of more UTIs in the second trimester may be due to the various effects of hormonal changes, physical changes, immune system changes, and increased urine, therefore allowing more opportunity for bacteria to grow and increased risks of infection (29). These results reiterate the findings in the research by Ejerssa AW et al. (30).

This study revealed a higher prevalence of urinary tract infections (UTIs) among pregnant women from urban areas compared to those from rural regions. These findings are in line with previous research (5, 31). The increased incidence in urban populations may be attributed to various factors, including lifestyle habits, elevated stress levels, poor hygiene practices, higher rates of sexual activity, underlying health conditions, and rising antibiotic resistance. Collectively, these factors significantly contribute to the heightened risk of UTIs in pregnant women living in urban settings (32).

The research showed that *P. mirabilis* isolates exhibit multiple drug resistance profiles and heterogeneity in their antibiotic sensitivities. The study highlights the significance of ongoing monitoring of resistance as well as accountable antibiotic utilization to inform an ongoing threat of antimicrobial resistance and successful treatment outcomes.

The study uncovered that the *P. mirabilis* isolates from pregnant women were pan-resistant to ampicillin, amoxicillin/clavulanic acid, trimethoprim-sulfamethoxazole and nitrofurantoin in this study. This aspect, combined with previous studies (1, 33), highlighted our concern regarding antibiotic resistance. Widespread resistance is likely due to the uncontrolled overuse of antibiotics in both human medicine and veterinary practices, which promotes the production of β-lactamase enzymes and contributes to the development of multidrug-resistant strains.

Regarding extended-spectrum cephalosporins, the current study reported about 62.5% resistance to ceftriaxone, cefotaxime and cefixime. These results were higher than that reported by (33, 34). The antimicrobial susceptibility testing in the current study demonstrated high sensitivity among these isolates to gentamicin, amikacin, ciprofloxacin, and ertapenem. These results come in line with prior

studies (1, 30).

The misuse of antimicrobial drugs, particularly by unauthorized individuals like farmers, can lead to the development as well as distribution of multidrug-resistant pathogens like *P. mirabilis.* These pathogens have developed strategies for survival and transmission from animal to human, involving various mechanisms.

Bacteria often override the activity of antimicrobial drugs (AMDs) through genetic changes, leading to resistance. Some plasmids encode for resistance to multiple antibiotics, resulting in a high-resistance gene pool among pathogens causing UTIs (35). Enzymes like β-lactamase may explain absolute resistance to penicillin. Gross misuse of antimicrobial agents, particularly with low doses and short durations, can lead to increased mutations and bacterial resistance. Highly enforced AMDs used as growth promoters and to control infectious diseases may also contribute to the development of multidrug resistance (MDR) due to changes in bacteria's genetic composition. Incorrect administration of antimicrobial agents and lack of good controlling mechanisms can increase the prevalence of multidrug-resistant microorganisms (36).

Molecular detection of *Proteus mirabilis* virulence genes. The molecular detection of virulence genes revealed that *P. mirabilis* strains harbor the *UreC* gene in 100% of isolates, consistent with prior reports (22, 37, 38). *UreC* encodes the urease enzyme, a critical factor in the pathogenesis of *P. mirabilis*-related UTIs. Urease plays a dual role: it increases urine pH, facilitating stone formation leading to urolithiasis, and creates a protective crystalline biofilm matrix that shields bacteria from antibiotics, contributing to persistent infections (39, 40). This biofilm formation complicates treatment, often resulting in chronic or recurrent UTIs, particularly in immunocompromised pregnant women.

In addition, the *MrpA* gene was detected in 75% of isolates, with a size of 565 bp. This study is consistent with a previous study (40, 41) that found detection rates of the *MrpA* gene of 80% and 81.17%, respectively, but disagrees with the findings of (22), which reported a 100% detection rate. The *MrpA* gene encodes a component of the Mannose-Resistant *Proteus*-like (MR/P) fimbriae, which are vital in bacterial adhesion, colonization, and biofilm formation in the urinary tract (39, 42). These fimbriae aid in the localization of bacteria to discrete areas within the urinary tract and hinder the host immune system, as well as the maintenance of infection. The presence of *MrpA* represents a potential increase in virulence, which could affect treatment outcome by promoting resistance of bacteria to both host defenses and antimicrobial agents.

Limitations of the study. Despite its contributions, this study has limitations, including a relatively small sample size and a cross-sectional design, which may restrict the generalizability of the findings. Additionally, the study did not assess the expression levels of the virulence genes, which could vary during different stages of infection and impact pathogenicity.

CONCLUSION

This research demonstrates that urinary tract infections are frequent in pregnancy and that *Proteus mirabilis* is a particularly important organism because of its virulence factors. Most *P. mirabilis* isolates showed multidrug resistance, although gentamicin, amikacin, ciprofloxacin, and ertapenem showed good susceptibility. This emphasizes the importance of early detection of *P. mirabilis* strains and strain characterization for specific management and then potentially complications. Further studies will be important to discover new methods for prevention and treatment, thereby improving maternal and fetal health.

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