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Research paper

THE PREVALENCE AND VIRULENCE DETERMINANTS OF *Proteus mirabilis* IN PREGNANT WOMEN ATTENDING SELECTED PRIMARY HEALTH CARE CENTRES IN NASARAWA SOUTH, NIGERIA

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ABSTRACT

Proteus mirabilis is an important clinically uropathogenic bacterium responsible for urinary tract infections (UTIs) in pregnant women, which can lead to poor maternal and neonatal outcomes. UTIs represent a recurring clinical challenge due to escalating pathogen resistance; *Proteus* exhibits high resistance when present in UTIs. The prevalence, antimicrobial resistance profile and virulence factors of P. *mirabilis* isolates from pregnant women in selected primary healthcare centres in Nasarawa South, Nigeria were studied. A total of 180 midstream urine samples were obtained and examined by standard microbiological and biochemical methods, molecular confirmation and antibiotic resistance profiling. The results demonstrated that the infection is high at PHC Lafia East, with a prevalence of 18.33%, identifying the centre as an area of high prevalence of *Proteus*-associated UTI in pregnancy, compared to MPHC Kadarko, where the prevalence was 6.66%, and MCWC1 Obi, where the prevalence was 3.33% in the study. P. *mirabilis* exhibited high resistance to nearly all drug classes, including penicillin, aminoglycosides, quinolones, and cephalosporins, with quinolones (ciprofloxacin and levofloxacin) effective against a few isolates. Molecular analysis revealed that various resistance genes were found, of which the most common ones were *qnrD, qnrS and aac(6')-1b*, suggesting a high pathogenic potential. The high prevalence of multidrug resistance in patients, which significantly contributes to treatment failure, highlights the need for ongoing monitoring, antibiotic stewardship initiatives and public health measures focused on pregnant people. These findings contribute to the epidemiology of P. *mirabilis* in pregnancy and provide a basis for targeted treatment and prevention strategies.

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Introduction

Urinary Tract Infections (UTIs) are caused by various microbes that are common in the urinary tract [1]. This occurs when pathogens invade, colonise, and multiply within the urinary tract [2]. UTIs are frequent worldwide, with approximately 150 million cases reported annually [1]. Pregnancy and sexual intercourse are the primary factors contributing to the increased vulnerability of women to bacteriuria [3].

UTIs are more common in women than in men [4,5]. This disparity is largely attributed to female anatomical features, specifically a broad, short urethra and the urethra's closeness to the anal opening, which facilitates the migration of bacteria into the bladder [6,7]. Furthermore, the incidence of UTIs among pregnant women rises with gestational duration; the rate begins to climb in the 6th week of the first trimester and reaches its peak between the 22nd and 24th weeks of the second trimester [8].

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During pregnancy, about 90% of women will have dilated ureters that remain so until the birth of the child. This physiological change leads to increased bladder capacity, decreased bladder and ureteral tone, urinary stasis, and vesicoureteral reflux [2].

Sexual activity makes it more possible for bacteria to enter the female urethra, leading to an increased risk for urinary tract infections [9]. In non-pregnant women, sexual activity can lead to the transfer of bacteria up the urethra and cause infection. Some people (specifically pregnant women) may have a UTI without knowing it, which is known as asymptomatic bacteriuria, and it is a risk factor for UTIs. In addition, females consistently have a higher rate of asymptomatic bacteriuria than males, except during the immediate postpartum period. [10,11].

However, *Proteus mirabilis* has emerged as an increasingly significant uropathogen, particularly for complicated urinary tract infections (UTIs), and many gaps remain in our knowledge of its prevalence, genetic diversity, antimicrobial resistance, and clinical implications among pregnant women [12]. The emergence of infections caused by *Escherichia coli (E. coli)* and *Klebsiella pneumoniae (K. pneumoniae)* among pregnant women is well established. Still, few studies have focused on *Proteus mirabilis* (P. mirabilis) as a cause of postnatal urinary tract infections (UTIs) [13].

Most available studies classify *P. mirabilis* as a general Gram-negative group and do not describe its specific epidemiology. Previous studies on bacteriuria in pregnancy in Nigeria have mostly focused on tertiary hospitals, and there is a significant knowledge gap regarding the burden of *P. mirabilis* infections among women attending primary health care centres, particularly in rural and semi-urban areas [14].

It is important to understand the genetic diversity of *P. mirabilis* to identify sources of infection, monitor the dissemination of virulent or resistant strains, and design specific interventions. But molecular characterisation studies of *P. mirabilis* isolates from pregnant populations in Nigeria remain very limited [15]. In the absence of such information, it is hard to determine whether infections are due to highly virulent clones, locally circulating strains, or imported lineages.

Antimicrobial resistance (AMR) in *P. mirabilis* has been reported elsewhere, but little is known about its prevalence in Nigeria, particularly in primary health care centres. Resistance can vary widely from one region to another and over time, depending on doctors' prescribing habits, the availability of antibiotics, and public health policies. Healthcare providers lack up-to-date information on resistance for *P. mirabilis* isolates. They are forced to rely on outdated empirical guidelines for treatment, which may result in treatment failures, prolonged infections, and risks to the mother and foetus [16,14].

Many primary health centres in Nigeria use routine urine cultures that predominantly look for *E. coli* and less for "less common" pathogens such as *P. mirabilis* [13]. This can result in underdiagnosis or misdiagnosis of infections, leading to inadequate management. This diagnostic bias may lead to underreporting and misrepresentation of the actual clinical burden of *P. mirabilis* in pregnancy.

P. mirabilis infection in pregnancy, if untreated or poorly managed, can result in serious complications such as ascending infection (pyelonephritis), urolithiasis, septicemia, low birth weight, increased perinatal mortality and preterm labour. Nevertheless, few studies in Nigeria have examined direct associations between *P. mirabilis* infections and adverse pregnancy outcomes [17].

Materials and methods

Study Area

This study was conducted in Nasarawa State, Nigeria. In all, 180 participants were drawn from Primary Health Care (PHC) centres in three different Local Government Areas (LGAs) namely: Primary Health Care Lafia East in Lafia LGA, Primary Health Care Maternal and Child Welfare Centre in Obi LGA and Model Primary Health Care Centre Kadarko in Keana LGA in the southern Area of the state. These facilities were selected to ensure representation of the pregnant population within the study area. All pregnant women in the first, second and third trimesters who sought Antenatal Care services at the selected PHCs within the study period were included.

Ethical clearance

For the study to succeed, ethical approval was obtained from the Ethical and Research Committee of the State Ministry of Health, Lafia, Nasarawa State (NIREC protocol No. 18/06/201711/2024).

Sample collection

This study involved administering a questionnaire at the time urine samples were obtained from pregnant women, who carefully responded to the questions. A total of 180 urine samples were collected from pregnant women who volunteered to participate in the study. They were of varying gestational ages and attended

antenatal care at Primary Health Care Lafia East, MCWC1 Obi, and MPHC Kadarko in Nasarawa State, Nigeria. After obtaining written consent and engaging them with interview questionnaires while documenting on the form, sterile early morning samples were collected daily for four weeks, making sure only midstream urine was collected as described by [10] from the various selected Local Governments of Nasarawa State with the assistance of a well-trained Medical Laboratory Technician from each study location. The samples were transferred to the laboratory for analysis.

Isolation and Identification of *Proteus mirabilis*

The isolation medium was Cystine Lactose Electrolyte Deficient (CLED) agar. Plates were inoculated and then incubated at 37°C for 24 hours. Upon completion of incubation, the cultures were inspected macroscopically to evaluate colony morphology, specifically size, colour, appearance, and shape. The bacterial isolates were identified using standard bacteriological procedures and biochemical tests as described by [18]. All isolates were stored on nutrient agar slants in a refrigerator at 2 °C for further analysis.

Antimicrobial Susceptibility Testing

The antimicrobial susceptibility test was performed using the disk diffusion technique on Mueller-Hinton agar, as described in the Clinical and Laboratory Standards Institute (CLSI) guidelines. Per the 2022 CLSI guidelines [19], the commonly used antibiotics for urinary tract infections were selected and included penicillins, aminoglycosides, quinolones, and cephalosporins, represented by ciprofloxacin, levofloxacine, amikacin, cefixime amoxicillin, gentamicin, ampicillin, and ceftriaxone. Growth of the Proteus isolate was suspended in a standard suspension from a 0.5 McFarland standard (1.5×10^8 CFU/mL) and applied to the agar surface with a sterile wire loop, then evenly distributed on the plate. Later, the antimicrobial discs were systematically placed on the inoculated medium with sterile forceps, and the plates were incubated for 18 hours at 37°C. A ruler was used to measure the Zones of Inhibition in millimetres to assess the isolates' sensitivity and resistance to antibiotics [20].

Molecular Analysis

DNA Extraction

Genomic DNA was prepared from the bacterial cultures using the previously described DNA extraction protocol [21, 22], with minor modifications. In brief, a single bacterial isolate was cultured in 1 mL Luria–Bertani (LB) broth overnight. The culture was centrifuged at 14,000 rpm for 3 min, and the supernatant was discarded. The cell pellet was resuspended in 1 mL of sterile distilled water, transferred to a 1.5 mL microcentrifuge tube, and centrifuged again at 14,000 rpm for 10 min. After removal of the supernatant, the pellet was resuspended in 100 µL of sterile distilled water and vortexed vigorously. It was further centrifuged at 14,000 rpm for 10 min. After centrifugation, the supernatant was discarded, and the resulting pellet was resuspended in 500 µL of normal saline. The suspension was incubated at 95°C for 20 min, then placed on ice for 10 min. The lysed cell solution was centrifuged at 14,000 rpm for 3 min. The upper layer containing DNA was carefully pipetted into a fresh 1.5 mL microcentrifuge tube and maintained at –20°C for further analysis.

DNA Quantification

The quantity and quality of the extracted genomic DNA were determined using a NanoDrop 1000 spectrophotometer (Biochrom Ltd., Cambridge, UK). The machine was blanked using 2 µL of sterile distilled water and calibrated with normal saline. After calibration, 2 µL of each DNA sample was loaded onto the lower pedestal, the upper pedestal was lowered, and the DNA was measured according to the user's manual [22].

Amplification of the 16S rRNA Gene of *Proteus mirabilis*

The 16S rRNA gene was PCR-amplified to detect the presence of *Proteus mirabilis* in the isolates. The reaction was performed with 523 bp fragments of the 16S rRNA gene using the following forward and reverse primer sequences: Forward: 5′-CCTGGACAAAGACTGACGCT-3′ and Reverse: 5′-CGCTTCTCTTTGTATGCGCC-3′.

The 16S rRNA gene PCR was performed in a 15 µL reaction volume containing 2.5 µL template DNA (10 ng/µL) (Zymo Research, USA), 7.5 µL of 2× Taq Master Mix (Zymo Research, USA), 1 µL each of 10 µM forward and reverse primer (Zymo Research, USA), and 3.5 µL of deionised water. The thermal cycling protocol in the Applied Biosystems 9700 thermocycler was initial denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 95°C for 1 min, annealing at 55°C for 30 s, extension at 72°C for 1 min, and a final extension at 72°C for 5 min.

PCR Amplification of Quinolone Resistance Genes

PCR for target quinolone resistance genes was performed on *Proteus* isolates using gene-specific primers purchased from Zymo Research (USA). PCR reactions (40 µL total volume) were prepared by mixing 2× DreamTaq Master Mix (Zymo Research, USA), 0.4 µM each of forward and reverse primers (Table 3.2) and DNA template. PCR mix contained Taq DNA polymerase, 5× DreamTaq buffer, dNTPs (at 0.2 mM each) and MgCl2. Amplification was performed using an Applied Biosystems ABI-9700 thermal cycler under the following conditions: initial denaturation at 95°C for 3 min, followed by 40 cycles of denaturation at 95°C for 30 s, primer-specific annealing at the melting temperature (Tm) as shown in Table 3.2 for each primer, extension at 72°C for 30 s, and final extension at 72°C for 7 min. The resulting PCR products were subjected to electrophoresis on a 1% (w/v) agarose gel in 1× Tris-acetate-EDTA (TAE) buffer and visualised by UV transillumination.

Detection of Amplified Genes by Agarose Gel Electrophoresis

A 1% agarose gel was prepared by dissolving 1 g of agarose in a solution containing 10 mL of 10× Tris-borate-EDTA (TBE) and 90 mL of sterile distilled water, then microwaving until fully dissolved. The solution was cooled for 5 min, and 0.7 µL of ethidium bromide (EtBr) was added to the gel solution and mixed thoroughly. The molten gel was transferred into the gel tray, the well former was inserted into the gel solution, and the gel was allowed to solidify on the bench for about 30 min. Then the well former was removed, and the tray was placed in the electrophoresis apparatus containing 1× TBE buffer. After that, the PCR products and the marker DNA were loaded into the wells. The electrophoresis was performed at optimal voltage and time. The DNA bands of the PCR products were visualised under a UV transilluminator and recorded.

DNA samples were diluted in 8 µL of bromophenol blue loading dye for use in sample preparation. 10 µL of the prepared mixture was loaded into each well. This was then sealed, and electrodes were inserted in the electrophoresis chamber. The process of separation was performed at 100-200 mA for 1 hour. The gel was removed from the buffer after electrophoresis and documented under ultraviolet light.

Results and Discussion

Prevalence of *Proteus spp* in Urine Samples of Pregnant Women

Table1 assessed the prevalence and clinical importance of *Proteus* among pregnant women attending three primary healthcare facilities, using 180 midstream urine samples (60 per facility) processed by standard culture, biochemical, and confirmatory molecular and resistance testing, providing a robust estimate of prevalence

The results show that *Proteus* was most prevalent at PHC Lafia East, where the cumulative weekly prevalence reached up to 18.33%, compared with MCWC Obi (3.33%) and MPHC Kadarko (6.66%). The result from PHC Lafia East observed that most women who tested positive were residents of Lafia, a metropolitan commercial centre in northern Nigeria with high population density, where women share various facilities such as pit toilets, open wells, and poor personal hygiene, which may lead to the prevalence of *Proteus* associated urinary tract infection in pregnancy.

This is similar to previous studies that *Proteus mirabilis* is less common than *E. Coli* but can be a clinically important uropathogen in the antenatal population, especially in low-resource settings [15,16,2].

This rate is not particularly high, but clinically significant as a result of the possible complications it may produce during pregnancy. This high prevalence may be due to several factors, including poor sanitation facilities, low literacy about personal hygiene, poor urogenital hygiene, wearing damp underwear, infrequent underwear changes, and limited access to clean water. These factors, coupled with the difficulties for a pregnant woman to ensure adequate personal hygiene due to anatomic and physiologic changes occurring during pregnancy, could make her more susceptible to urinary tract infections caused by *Proteus mirabilis* [16].

Furthermore, *Proteus mirabilis* was detected more in pregnant women from rural areas than in those from urban areas in Osun State, as revealed by a study in Osun State [15], which indicated possible geographic and socio-economic differences.

The higher prevalence observed in this study could also be attributed to other physiological changes that occur during pregnancy, such as urinary stasis secondary to ureteral dilatation and a major decrease in immunity, which increase susceptibility to infection [2].

Table 1: Prevalence of *Proteus spp* in urine samples of pregnant women attending the three selected facilities.

Location	Week	No of samples (N=180)	Positive samples	Percentage (%)
PHC Lafia East	**1**	**12**	**2**	
	2	**12**	**0**	
	3	**12**	**5**	**18.33%**
	4	**12**	**4**	
	5	**12**	**0**	
Mcwc Obi	**1**	**12**	**0**	
	2	**12**	**0**	
	3	**12**	**2**	**3.33%**
	4	**12**	**0**	
	5	**12**	**0**	
MPHC Kadarko	**1**	**12**	**2**	
	2	**12**	**0**	
	3	**12**	**2**	**6.66%**
	4	**12**	**0**	
	5	**12**	**0**	

Biochemical and Molecular Characterisation of Isolate

Biochemical characteristics of the isolates were consistent with classic *Proteus mirabilis* as seen in table 2, which include Gram negative bacilli morphology, positive catalase, urease, indole test, acid production from lactose, glucose and sucrose fermentation and hydrogen sulfide production. These results were consistent with the results of [23,24].

These identifications were confirmed by molecular identification using 16S rRNA gene amplification as illustrated in plate 1. These results were in line with those performed by [25].

[26] stressed the importance of urease activity as a virulence factor that promotes survival in the urinary tract by alkalinising the urine to allow stone formation. The biochemical characteristics of their isolates were similar to those reported by [26,16] and thus confirmed the validity of the identification techniques employed. Biochemical and molecular methods of identification have good concordance which shows that combined phenotypic and genotypic methods are good for the identification of *Proteus mirabilis*. The presence of the typical biochemical signatures is indicative of the pathogenic potential of the isolates as the enzyme activities are highly associated with virulence and survival mechanisms in *vivo* [35].

Table 2: Biochemical characteristics of *Proteus mirabilis* isolated from urine sample of pregnant women in the study Area.

S/N	Isolate	Gram stain	Shape	Catalase test	Oxidase test	Indole test	Urease test	Lactose test	Glucose test	Sucrose test	H_2S	Suspected organism
1	P1	-	Bacilli	+	-	-	+	A	A	A	+	*Proteus* spp.
2	P2	-	Bacilli	+	-	-	+	A	A	A	+	*Proteus* spp.
3	P4	-	Bacilli	+	-	-	+	A	A	A	+	*Proteus* spp.
4	P5	-	Bacilli	+	-	-	+	A	A	A	+	*Proteus* spp.
5	P7	-	Bacilli	+	-	-	+	A	A	A	+	*Proteus* spp.

KEY: A= Acid production, + = Positive, - =Negative

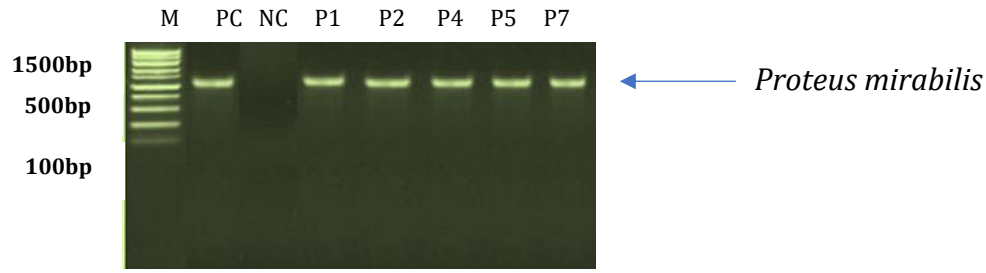


Plate 1: Gel image confirming the presence of *Proteus mirabilis* in urine sample of pregnant women attending selected Primary Health Care Centres in Nasarawa South, Nigeria.

The Antimicrobial Susceptibility Profiles of *Proteus mirabilis*

For *Proteus* isolates, antimicrobial susceptibility testing was performed with four classes of antimicrobial drugs: penicillins, aminoglycosides, quinolones, and cephalosporins. Five isolates (Table 3) were resistant to almost all the antibiotics tested such as ampicillin, amikacin, gentamicin, cefixime, ceftriaxone and amoxicillin. This is similar to the previous findings [28, 29, 30,16] where Proteus mirabilis was found resistant to several classes of antibiotics. However, all of the isolates were susceptible to quinolones except for four isolates that were resistant to quinolone antibiotics, which is consistent with what has been reported by [31]. Multidrug resistance was also found to be high among the isolates, with three isolates (P2, P4, and P7) being resistant to all the antibiotics tested. This growing resistance phenomenon is a major problem in the management of UTI, especially in situations where empirical therapy is often administered without a laboratory diagnosis of the organism and susceptibility.

This resistance profile corresponds with findings reported by [28,29,32,30] where P. mirabilis isolates showed significant resistance to almost all the classes of drugs used ranging from penicillin, aminoglycoside, quinolones and cephalosporin, while quinolones (ciprofloxacine and levofloxacine) remained effective against few isolates. The observed antimicrobial resistance may be attributed to mechanisms such as efflux pump activity, beta-lactamase production, aminoglycoside-modifying enzymes, and plasmid-mediated genetic transfer [16,27,26,33].

Table 3: Antimicrobial susceptibility patterns of *Proteus mirabilis* against commonly used antibiotics.

S/N	Ciprofloxacin	Levofloxacine	ceftriaxone	Cefixime	Amoxicillin	Ampicillin	Gentamicin	Amikacin
				Zone of inhibition (mm)				
P1	21	23	17	14	9	8	10	12
P2	6	12	18	15	10	9	9	13
P3	28	22	29	25	21	20	23	25
P4	11	9	15	12	7	6	8	10
P5	24	19	19	15	11	10	12	14
P6	26	20	27	23	19	18	21	23
P7	12	10	16	13	8	7	11	11
P45	18	15	21	17	12	11	14	16
P67	23	18	24	20	17	16	19	20
P76	22	17	23	19	18	17	18	19
P92	27	21	28	24	20	19	22	24
P105	21	17	23	19	18	17	17	18
P115	25	19	26	22	6	6	20	21
P127	22	18	24	20	17	16	18	19
P132	19	14	20	16	14	12	13	15
P147	23	18	25	21	11	10	19	20
P150	24	19	25	21	6	6	6	22

KEY P= *Proteus mirabilis,* S=sensitivity, I= intermediate, R= resistance (CLSI 2022) Ciprofloxacine:S>= 21, I=16, R<=15, Levofloxacin: S>= 17, I=14, R<=13, Ampicillin: S>= 17, R<= 13, Amoxicillin:S>= 17, R<= 13, Ceftraixone:S>= 23, I=16, R<= 19, Cefixime: S>= 19, I=18, R<= 15, Gentamicin: S>= 15, I=13, R<= 12, Amikacin: S>= 18, R<= 14

Resistant Genes Present in *Proteus mirabilis* from Urine Sample of Pregnant Women

The isolates were genetically analyzed and showed intra-species diversity with some strains showing identical 16S rRNA gene sequence and others showing differences in gene sequence, yet all grouped within *Proteus mirabilis*. Importantly, all isolates harbored the resistance genes qnrD, qnrS, and aac(6')-Ib. As demonstrated in Table 4, Plates 2-4 indicated plasmid-mediated resistance to quinolones and aminoglycosides. The three *Proteus mirabilis* isolated from PHC Lafia East (P2, P4, and P7) had quinolones and aminoglycoside genes.

P2 had both Quinolone and aminoglycoside resistant genes (QnrS & aac(6')-1b), P4 had only aminoglycoside aac(6')-1b, and P7 had quinolone resistant gene QnrS &QnrD. In MPHC Kadarko two *Proteus mirabilis*, P1 had only quinolone resistant gene QnrD whereas P5 had all the resistant gene present (QnrS, QnrD, and Aac (6')-1b).

The qnr genes encode proteins which protect DNA gyrase and topoisomerase IV from the effects of quinolone antibiotics, including ciprofloxacin and levofloxacin, while the aac(6')-Ib gene encodes an enzyme, acetyltransferase, which inactivates aminoglycosides [32, 34, 30]. The co-occurrence of these resistance determinants indicates worrying levels of multidrug resistance. This growing antimicrobial resistance also makes the management of UTI more challenging, especially in situations where treatment is often empirical, without laboratory identification of the pathogen or susceptibility testing.

This practice potentially fuels resistance development due to the use of suboptimal antibiotics. These results reflect the selective pressure exerted by antibiotic misuse and are consistent with global trends reported by [35,28]. Similar findings have been reported by [29,30] who described widespread resistance in *Proteus mirabilis* clinical isolates associated with quinolones and aminoglycoside-modifying resistance genes.

Table 5: Resistance Genes in *Proteus mirabilis* from pregnant women in selected Primary Health Care Centres in Nasarawa South, Nigeria

LOCATION	ISOLATES	QnrS	QnrD	Aac(6')-1b
PHC Lafia East	**P2**	**+**	**-**	**+**
	P4	**-**	**-**	**+**
	P7	**+**	**+**	**-**
MPHC Kadarko	**P1**	**-**	**+**	**-**
	P5	**+**	**+**	**+**

KEY: + =Positive - =Negative, P=*Proteus mirabilis*

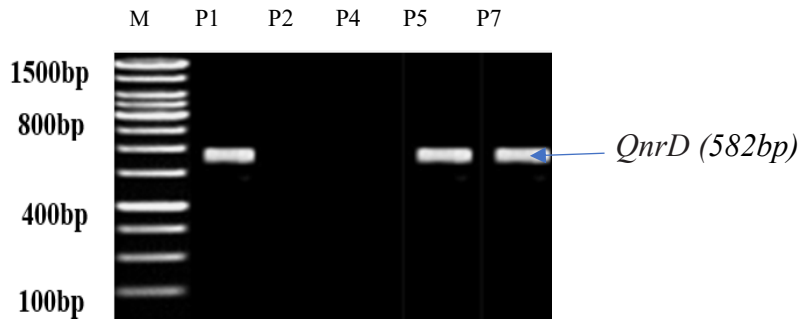


Plate 2: *Proteus mirabilis* showing the presence of QnrD (582bp) gene in urine sample of pregnant women.

The figure above shows Agarose gel electrophoresis of the amplified quinolone gene. Lane P1, P5 and P7 represent the expression of the QnrD (582bp) gene. Lane M represents 100bp - 1500bp DNA molecular ladder as shown above.

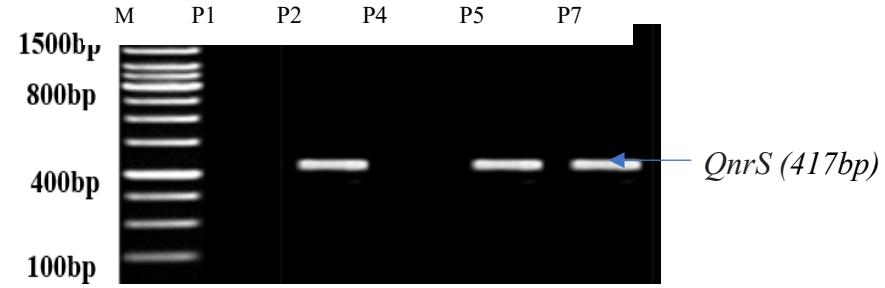
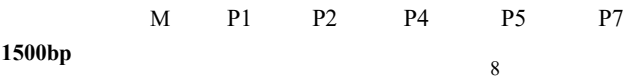


Plate 3: *Proteus mirabilis* showing the presence of QnrS(417bp) gene in urine sample of pregnant women.

Agarose gel electrophoresis of amplified quinolone gene shows Lane P2, P5 and Lane P7 represents the expression of the QnrS(417bp) gene. Lane M represents 100bp - 1500bp DNA molecular ladder as shown above.



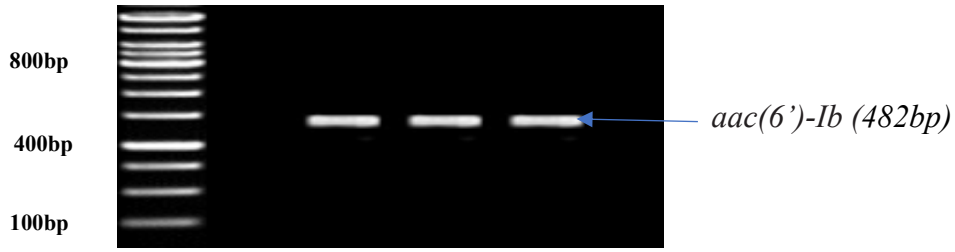


Plate 4: *Proteus mirabilis* showing the presence of aac(6')-Ib(482bp) gene in urine sample of pregnant women.

The figure above shows agrose gel electrophoresis of amplified quinolone gene which shows Lane P2, P4 and Lane P5 represents the expression of the aac(6')-1b(482bp) gene. Lane M represents 100bp - 1500bp DNA molecular ladder as shown above.

Conclusion

This study confirms *Proteus mirabilis* as a clinically relevant uropathogen in pregnant women, which shows that infection is high at PHC Lafia East, where prevalence reached up to 18.33% identifying the centre as an area of high prevalence of *Proteus* associated UTI in pregnancy compared to MPHC kadarko which the prevalence was 6.66% and MCWC1 Obi was 3.33% in the study. The isolates exhibited typical biochemical and molecular characteristics consistent with *Proteus mirabilis*, including strong virulence-associated enzyme activities that support their pathogenic potential. The genetic characterization showed some variability between the strains, but all of them shared the presence of the major resistance determinants qnrD, qnrS, and aac(6')-Ib, suggesting a concerning multidrug resistance profile. Concurrently, antibiotic susceptibility testing showed high resistance to common antibiotic drugs, highlighting the challenge of successful therapy, especially when empirical therapy is used without laboratory based diagnostic and susceptibility information. The results highlight the need for strengthened education about hygiene, better diagnostic screening, including molecular techniques, and antimicrobial stewardship, to improve the management of Proteus mirabilis infections, and to protect maternal health

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