Research Article

Prevalence and Antibiotic Susceptibility Profile of *Proteus mirabilis* from Poultry Faeces in Gwagwalada Area Council, F.C.T, Nigeria

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Abstract | *Proteus mirabilis*, a Gram-negative opportunistic pathogen within the family *Enterobacteriaceae,* is increasingly recognized in poultry environments as a reservoir of multidrug resistance genes. This study investigated the prevalence and antibiotic susceptibility of *P. mirabilis* isolated from poultry faeces in Gwagwalada Area Council, Federal Capital Territory (FCT), Nigeria. A total of 50 faecal samples were aseptically collected from randomly selected poultry vendors and subjected to bacteriological culture and biochemical identification. Antimicrobial susceptibility testing was performed on confirmed isolates using the Kirby–Bauer disk diffusion method in accordance with CLSI guidelines. Out of the 50 samples examined, 14 (28%) were positive for *P. mirabilis*. Antibiotic susceptibility profiles revealed complete resistance (100%) to all -lactam antibiotics tested, including amoxicillin, cefuroxime, ceftriaxone, and ceftazidime, suggesting widespread β-lactamase production. High resistance was also observed against gentamicin (71.4%) while streptomycin demonstrated the highest susceptibility rate (71.4%), followed by moderate susceptibility to ofloxacin (50%), cotrimoxazole (42.9%), and levofloxacin (35.7%), while ciprofloxacin exhibited limited activity. The antibiogram clearly indicates the presence of multidrug-resistant *P. mirabilis* in poultry faeces from the study area. These findings underscore the role of poultry farms as reservoirs for resistant *Enterobacteriaceae* with potential zoonotic implications. The observed resistance trends reflect possible indiscriminate antibiotic usage in poultry production and highlight the urgent need for farmer education, biosecurity practices, and regular AMR surveillance.

Keywords | *P. mirabilis*, Culture, Antimicrobial resistance (AMR), Biochemical identification, Prevalence, Zoonotic

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INTRODUCTION

Proteus mirabilis is a facultative anaerobic Gram-negative bacillus of the family *Enterobacteriaceae*, known for its motility by a peritrichous flagella, urease production, and hydrogen sulfide production (Armbruster *et al.*, 2018). *Proteus* species. are considered commensals in the human and animal gastrointestinal tracts, and they are commonly found in various environments, including soil, sewage, as well as water source they are saprophytes, contributing to organic matter decomposition (Drzewiecka, 2016). *Proteus mirabilis* can be an inhabitant of the intestinal tract of poultry birds and could consequently potentially be present on poultry products due to faecal contamination at

the slaughter house (Barbour *et al*., 2012).

Proteus species are opportunistic pathogens, primarily causing infections in immunocompromised individuals and animals who have structural abnormalities, or in hospital settings (nosocomial infections) (Jacobsen *et al*., 2008). *P. mirabilis* is the most clinically significant specie causing approximately 90% of Proteus infections, with catheter-associated urinary tract infections (CAUTIs) being the most clinically significant disease/infection (Shaffer *et al*., 2015). These infections may be accompanied by urolithiasis, which refers to the development of bladder or kidney stones due to alkalinization of urine from urease-catalyzed urea hydrolysis (Armbruster *et al*., 2018).

Clinical signs and manifestations of *Proteus mirabilis* infection in man includes; dysuria, cloudy or foul-smelling urine, sometimes with hematuria, suprapubic pain or lower back pain in complicated cases. Formation of struvite stones (due to urease production, which alkalinizes urine) (Armbruster *et al*., 2018). Redness, swelling, pain, and purulent discharge at wound infection site. *P. mirabilis* can also cause bacteremia, pneumonia, or meningitis, presenting with systemic symptoms like fever, chills, and organ-specific signs. Diagnosis could be done by clinical evaluation, patient history and symptoms (e.g., UTI symptoms, wound infection signs) (Armbruster *et al*., 2018).

Samples required for laboratory tests include; urine culture, wound swabs or tissue cultures, blood cultures in cases of suspected bacteremia or sepsis (Chakkour *et al*., 2024). Biochemical tests like, urease-positive, indole-negative, and motility (flagella-driven swarming) are also required for presumptive diagnosis. Antibiotic sensitivity testing is required to guide treatment, as *P. mirabilis* may exhibit multidrug resistance (e.g., to beta-lactams via extended-spectrum beta-lactamases).

Proteus mirabilis can be diagnosed using several laboratory methods. Conventional techniques include microscopy, where Gram staining shows Gram-negative rods and motility tests reveal characteristic swarming, and culture on selective media such as MacConkey or Xylose Lysine Deoxycholate (XLD) agar, which produce non-lactose fermenting or hydrogen sulfide-positive colonies (Liu *et al*., 2025). Biochemical reactions further aid identification, with *P. mirabilis* typically testing indole negative, urease positive, and producing hydrogen sulfide on TSI agar, alongside positive citrate and phenylalanine deaminase tests (Chakkour *et al*., 2024). More advanced approaches include molecular methods such as PCR for detecting virulence genes and whole genome sequencing for epidemiological studies, while automated systems like VITEK 2 and MALDI-TOF MS provide rapid and highly accurate species identification (Armbruster *et al*., 2018).

Prevention is mainly by proper hygiene and control is by the use of antibiotics and disinfection of surfaces and equipment (Murray *et al*., 2021).

Studies across Nigeria have consistently reported *P. mirabilis* among the dominant enteric isolates recovered from poultry droppings and farm environments, with prevalence figures varying by location and sample type (Owoseni *et al*., 2021); for instance, isolates from poultry farms in Lafia, Nasarawa State, showed *P. mirabilis* prevalence ranging from roughly 16% to about 22% across different farms (Owoseni *et al*., 2021), while a study of poultry droppings in poultry farms at Gondar City, Northwest Ethiopia recorded a prevalence of about 12.6% (Tigabie *et al*., 2023). Of greater public health concern is the antibiotic resistance profile of these isolates: poultry-derived *P. mirabilis* has repeatedly shown high resistance to commonly used agents such as tetracycline and ampicillin, while remaining largely susceptible to aminoglycosides such as gentamicin and amikacin (Alqurashi *et al*., 2022) which have consistently emerged as the drugs of choice against Proteus infections in these studies. This pattern reflects the wider problem of antimicrobial misuse in poultry production across Nigeria, where the indiscriminate and unregulated use of antibiotics for growth promotion and disease prevention has been linked to the emergence and spread of multidrug-resistant enteric bacteria in poultry droppings and litter. Given this trend, and the paucity of location-specific data from the Federal Capital Territory, a study of the prevalence and antibiotic susceptibility profile of *P. mirabilis* in poultry faeces from Gwagwalada Area Council is necessary to generate baseline local data that can inform antimicrobial stewardship and food safety practices in the area.

In Nigeria, studies have been conducted on the prevalence and antibiotic susceptibilities of *P. mirabilis* in fishes, but very limited studies in poultry, although it has been reported that *P. mirabilis* can be transmitted to poultry via contaminated environments, with potential zoonotic risks to humans (Ogunleye, 2020). The intensive use of antibiotics and inadequate biosecurity practices in poultry farms may promote its transmission and the emergence of antimicrobial-resistant strains. Despite the importance of poultry farming in Gwagwalada Area Council, there is limited information on the occurrence and antibiotic susceptibility of *P. mirabilis* in the area. Therefore, this study will provide baseline epidemiological data on the prevalence and antimicrobial resistance patterns of *P. mirabilis*, supporting evidence-based disease control, rational antibiotic use, and One Health strategies to improve poultry health, food safety, and public health. This study therefore, aims to determine the occurrence, prevalence and characterization of *P. mirabilis* in poultry

farms at Gwagwalada Area Council FCT, Nigeria, to generate data essential for developing effective control measures and antibiotic stewardship programs, and also to determine their susceptibility to certain antibiotics, as Antimicrobial resistance (AMR) has been a critical global public health issue (Alabi *et al*., 2025).

MATERIALS AND METHODS

Study location

Gwagwalada Market, located in Gwagwalada Area Council of the Federal Capital Territory (FCT), Nigeria is one of the major agricultural and commercial markets in the region (Idowu *et al*., 2022). The market serves as an important center for the sale and distribution of various agricultural commodities, including poultry and poultry products. It attracts poultry farmers, traders, wholesalers, retailers, and consumers from Gwagwalada and neighboring communities. Poultry production is widely practiced in the area, with numerous small- and medium-scale farms supplying live birds, eggs, and poultry meat to the market. These activities make Gwagwalada Market a suitable location for poultry-related studies (Idowu *et al*., 2022).

Sample size determination

Sample size was determined using the method as described by Thrusfield (2007).

$$n = Z^2Pq/d^2$$

Where; n= Sample size, Z= Appropriate value from the normal for the desired confidence (1.96), P= Expected prevalence rate, q= 1-P, d = Desired precision (12.5%).

The calculated prevalence from previous study = 78.4% (Eze *et al*. 2020).

therefore, 1.962 × 0.784 × (1-0.784) / 0.1252 = 41.62 samples. The sample size was increased to 50 for precision.

Study design

This is a cross-sectional descriptive study with an objective to determine the prevalence of *P. mirabilis* and its antibiotic susceptibility at a specific point in time. The sample collection was conducted from various poultry vendors situated within Gwagwalada market and a total of 50 fecal droppings were collected via convenience sampling of freshly voided fecal droppings from poultry in the Gwagwalada Area Council. A convenience sampling technique was used to select five (5) poultry vendors within Gwagwalada market based on accessibility and farmer`s consent. 10 samples were collected from each vendor to make a total of fifty (50) fresh fecal samples collected for this study.

Sample collection and transportation

The study involved a one-time sampling of poultry faecal samples from selected number of poultry vendors within the Gwagwalada market. A total of 50 fresh faecal droppings were aseptically collected from the litter or dropping trays of apparently healthy birds into sterile sample bottles, ensuring samples were freshly voided to minimize environmental contamination and all samples were labelled, stored in a cool box at 4 °C and transported immediately, to the Veterinary Microbiology Laboratory of the Faculty of Veterinary Medicine, University of Abuja for processing.

Laboratory analysis

Media preparation: The media used in this study (MacConkey Agar, Oxoid) were prepared following the instructions of the manufacturer.

Identification of Proteus mirabilis

Upon arrival at the laboratory, each faecal sample was homogenized in 5ml of already prepared Peptone water. They were incubated at 37°C for 24 hours to resuscitate and enrich potential bacterial pathogens (Enrichment). After 24 hours, an inoculating loop was used to streak the samples onto a MacConkey agar Figure, which was then incubated again at 37°C for another 24 hours. After incubation, the Figures were examined for colonies characteristic of Proteus species, that is, non-lactose fermenting pale or colourless colonies.

Microscopic identification of the isolates

A single colony from the MacConkey agar was smeared on a clean glass slide, heat-fixed, and stained using the Gram staining technique. The slides were viewed under a binocular microscope, with 100× magnification, and isolates exhibiting Gram-negative, rod-shaped morphology were stored for biochemical testing.

Biochemical identification of P. mirabilis

Presumptive *P. mirabilis* isolates underwent a series of biochemical tests for confirmation, as per standard protocols. All tests were conducted under aseptic conditions (O'Hara *et al*., 2000), and isolates that were urease-positive, indole-negative, citrate-positive, and produced H_2S on TSI were confirmed as *Proteus mirabilis*.

Antibiotic susceptibility of P. mirabilis

The antibiotic susceptibility of the*P. mirabilis* isolates were determined using the Kirby-Bauer disk diffusion method Bauer *et al.* (1959) on Mueller-Hinton Agar (MHA) as per the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2020). Panels of ten antibiotics from different classes, selected based on their common use in veterinary and human medicine in Nigeria, were used:

Amoxicillin (AMX), Ceftazidime (CTZ), Ceftriaxone (CTX), Cefuroxime (CEF), Gentamicin (CN), Streptomycin (S), Ciprofloxacin (CPX), Levofloxacin (LEV), Ofloxacin (OFX), and Cotrimoxazole (SXT). The diameter of the zones of inhibition were carefully measured using a ruler, then the results were recorded, and interpreted as Susceptible (S), Intermediate (I), or Resistant (R) according to CLSI (2020) guidelines. Multidrug resistance (MDR) was defined as resistance to at least three or more different antimicrobial classes.

RESULTS

Cultural isolation

Out of the 50 poultry samples that were collected and cultured on MacConkey agar, 22 were identified as non-lactose fermenters (Figure 1) due to their characteristic pale and colourless appearance. In contrast, the other 28 samples were lactose fermenters (Figure 2), which were identified by their pink to reddish colonies on the MacConkey agar Figures. To obtain pure isolates for further analysis, the 22 non-lactose fermenters were subcultured onto fresh MacConkey agar Figures. This process yielded 20 pure non-lactose fermenting isolates, which were then subjected to subsequent biochemical tests and microscopic identification to confirm the presence of *Proteus mirabilis*.

Table 1: The biochemical characteristics of 14 Proteus mirabilis isolates.

Biochemical test	*P. mirabilis* expected result	Observed result
Urease	Positive	14/14 Positive (Pink)
Indole	Negative	14/14 Negative (No red ring)
Citrate	Positive	14/14 Positive (Blue)
H_2S production (TSI Agar)	Positive	14/14 Positive (Black precipitate)

Table 2: Prevalence of *Proteus mirabilis* isolates from collected samples.

Sample	Number of samples	No. of positive samples	Prevalence %
Fecal sample	50	14	28

Microscopic identification

Following the initial isolation of non-lactose fermenting colonies on culture media, all twenty (20) pure isolates were subjected to Gram staining and examined microscopically. Microscopic examination revealed that all isolates were Gram-negative, rod-shaped (bacilli) bacteria, appearing as short to moderately elongated rods that stained pink-red following the Gram-staining procedure (Figure 3). This morphology is characteristic of members of the family Enterobacteriaceae, including *Proteus mirabilis*. The uniform Gram-negative bacillary appearance observed among the isolates provided important preliminary evidence supporting their identification as *P. mirabilis*. These findings are consistent with previous reports that describe *Proteus mirabilis* as a motile, Gram-negative, rod-shaped bacterium commonly associated with enteric and urinary tract infections (Chakkour *et al*., 2024).

Figure 1: Non-lactose fermenting colonies on MacConkey Agar.

The microscopic characteristics observed in this study, when considered alongside the non-lactose fermenting colonial morphology and subsequent biochemical identification, further confirmed that the isolates belonged to the genus Proteus (Mohammed, 2025). Gram staining therefore served as an essential preliminary identification technique, allowing differentiation of the isolates from Gram-positive organisms and supporting their classification as *Proteus mirabilis* (Chakkour *et al*., 2024).

Biochemical identification

Following microscopic identification, all twenty (20) pure non-lactose fermenting isolates were subjected to a series of standard biochemical tests for definitive species identification. The biochemical characteristics evaluated included Urease production (Figure 4), indole H_2S production (Figure 6), and Citrate utilization (Figur 5), which are commonly employed in the identification of *Proteus mirabilis*. The biochemical profiles obtained were compared with the established characteristics of *P. mirabilis*, namely urease-positive, indole-negative, and citrate-positive reactions as shown in Table 4.

The results showed that fourteen (14) of the twenty isolates consistently exhibited the characteristic biochemical profile of *Proteus mirabilis*. These isolates produced positive urease and citrate utilization reactions while remaining negative for indole production. The

remaining six (6) isolates displayed biochemical patterns that differed from the expected profile and were therefore excluded from further analysis. The observed biochemical reactions are in agreement with previous studies that describe *P. mirabilis* as a strongly urease-producing organism that is typically indole-negative and capable of utilizing citrate as a sole carbon source (Sastry, 2017). Consequently, only the fourteen isolates that conformed to the established biochemical criteria were considered confirmed *Proteus mirabilis* isolates and were retained for subsequent analyses.

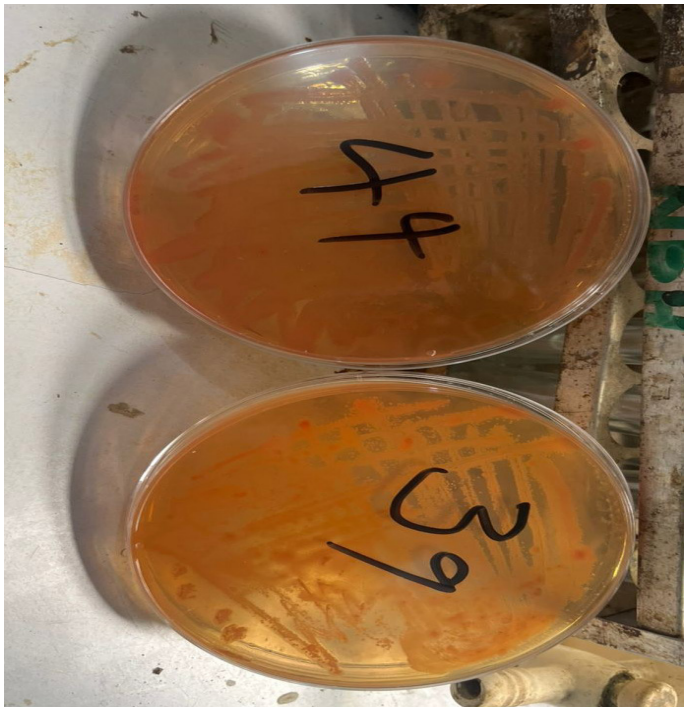

Figure 2: Lactose fermenting colonies on MacConkey Agar.

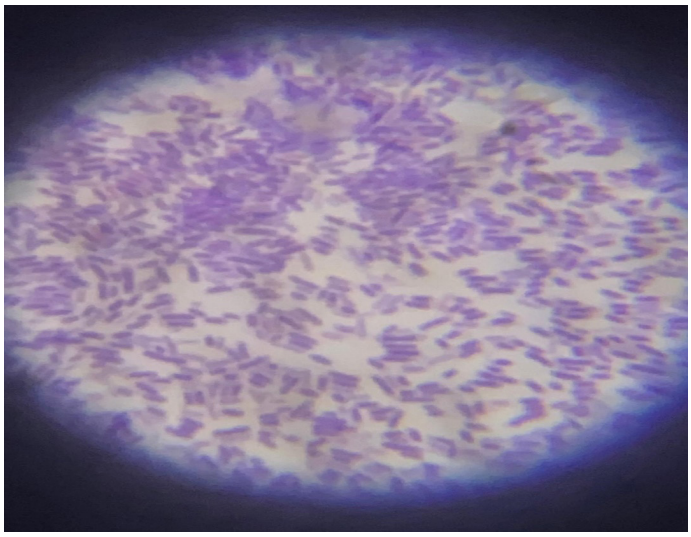

Figure 3: Microscopic appearance of Gram`s Stained non-lactose fermenting colonies of *P. mirabilis* viewed at X 100.

Prevalence of proteus mirabilis

Following the definitive biochemical identification, the overall prevalence of *Proteus mirabilis* in poultry faecal samples collected from Gwagwalada Area Council was determined. Out of a total of 50 poultry faecal samples processed, 14 isolates were biochemically confirmed as *Proteus mirabilis*.

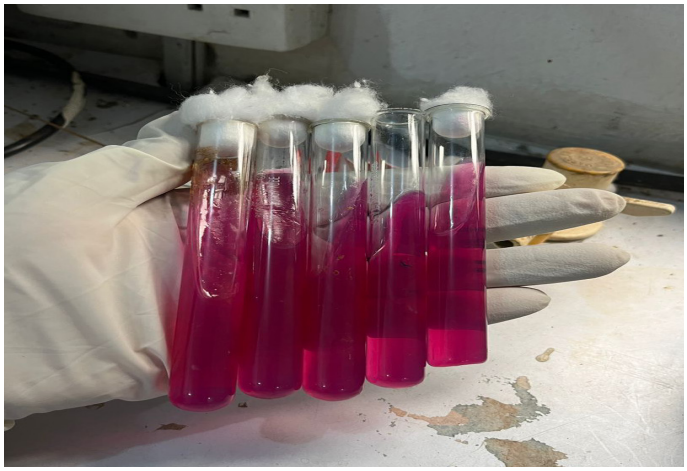

Figure 4: Conventional Biochemical reaction of the isolates showing Pink colouration indicating a positive Urease test.

Antibiotic susceptibility pattern

The 14 confirmed *Proteus mirabilis* isolates were subjected to antibiotic susceptibility testing using the Kirby-Bauer disk diffusion method, following CLSI guidelines (CLSI, 2020). The antibiotic agents used includes; Ceftazidime (30 µg), Streptomycin (30 µg), Amoxilcilin (20 µg), Ciprofloxacin (10 µg), Levofloxacin (20 µg), Ceftriaxone (30 µg), Gentamycin (10 µg), Ofloxacin (10 µg), Cefuroxime (30 µg), and Cotrimoxazole (25 µg).

Distribution of antibiotic susceptibility test of *P. mirabilis*

The distribution of zones of inhibition among the fourteen (14) *Proteus mirabilis* isolates demonstrated considerable variation in their response to the antibiotics tested as shown in Table 3. Overall, the largest inhibition zones were observed with Ofloxacin (OFX), Levofloxacin (LEV), Ciprofloxacin (CPX), and Streptomycin (S), indicating greater antibacterial activity against the isolates. In contrast, Amoxicillin (AMX), Cefuroxime (CEF), and Ceftriaxone (CTX) produced little or no inhibition in most isolates, reflecting poor antimicrobial effectiveness.

Ofloxacin (OFX) exhibited the highest antibacterial activity, with inhibition zones ranging from 12 mm to 30 mm, and several isolates showing zones of 28–30 mm. Levofloxacin (LEV) also demonstrated strong activity, producing inhibition zones between 14 mm and 30 mm. Similarly, Ciprofloxacin (CPX) showed appreciable activity, with zones ranging from 17 mm to 28 mm among susceptible isolates.

Table 3: Distribution of antibiotic susceptibility profile of *P. mirabilis* showing zones of inhibition to the nearest millimeters.

S. N	Isolates	CTZ 30 µg	S 30 µg	AMX 20 µg	CPX 10 µg	LEV 20 µg	CTX 30 µg	CN 10 µg	OFX 10 µg	CEF 30 µg	SXT 25 µg
1	SN 3	0	18	0	20	20	0	12	28	0	18
2	SN 5	13	18	12	0	0	0	0	18	0	10
3	SN 8	0	20	12	24	22	0	20	16	0	0
4	SN 20	12	18	0	21	18	12	12	30	0	0
5	SN 29	0	16	0	20	20	0	0	12	0	14
6	SN 30	0	16	0	28	22	0	17	12	0	15
7	SN 33	0	16	0	26	14	0	0	20	0	10
8	SN 37	0	20	0	26	20	0	0	24	0	15
9	SN 39	0	26	0	22	22	0	15	29	0	20
10	SN 42	0	14	0	17	17	0	0	28	0	18
11	SN 44	0	0	0	18	18	12	0	23	0	22
12	SN 45	0	26	0	22	22	0	22	30	0	17
13	SN 47	0	12	0	24	22	0	0	28	0	18
14	SN 50	0	14	0	0	30	12	0	30	0	13

Key: CTZ = Ceftazidime, S = Streptomycin, AMX = Amoxicillin, CPX = Ciprofloxacin, LEV = Levofloxacin, CTX = Ceftriaxone, CN = Gentamycin, OFX = Ofloxacin, CEF = Cefuroxime, SXT = Cotrimoxazole.

Table 4: Antibiotic susceptibility pattern of *P. mirabilis* tested.

S. N	Isolates	CTZ 30 µg	S 30 µg	AMX 20 µg	CPX 10 µg	LEV 20 µg	CTX 30 µg	CN 10 µg	OFX 10 µg	CEF 30 µg	SXT 25 µg
1	SN 3	R	S	R	R	I	R	R	S	R	S
2	SN 5	R	S	R	R	R	R	R	I	R	R
3	SN 8	R	S	R	I	S	R	R	I	R	R
4	SN 20	R	S	R	R	I	R	S	S	R	S
5	SN 29	S	S	R	R	I	R	R	R	R	I
6	SN 30	R	S	R	S	S	R	I	I	R	I
7	SN 33	R	S	R	S	R	R	R	I	R	I
8	SN 37	R	S	R	S	I	R	R	I	R	R
9	SN 39	R	S	R	R	I	R	I	S	R	I
10	SN 42	R	I	R	R	I	R	R	S	R	S
11	SN 44	R	R	R	R	I	R	R	I	R	S
12	SN 45	R	S	R	I	S	R	S	S	R	S
13	SN 47	R	I	R	I	S	R	R	S	R	S
14	SN 50	R	I	R	R	S	R	R	S	R	I

Key: CTZ = Ceftazidime, S = Streptomycin, AMX = Amoxicillin, CPX = Ciprofloxacin, LEV = Levofloxacin, CTX = Ceftriaxone, CN = Gentamycin, OFX = Ofloxacin, CEF = Cefuroxime, SXT = Cotrimoxazole.

Streptomycin (S) produced moderate to large zones of inhibition ranging from 12 mm to 26 mm, suggesting good activity against most isolates. Cotrimoxazole (SXT) showed moderate effectiveness, with inhibition zones ranging from 10 mm to 22 mm.

In contrast, Amoxicillin (AMX) and Cefuroxime (CEF) failed to inhibit the growth of any isolate, as evidenced by the absence of inhibition zones (0 mm) across all isolates. Ceftriaxone (CTX) also demonstrated very poor activity, with most isolates showing no inhibition and only a few isolates exhibiting small zones of 12 mm. Ceftazidime (CTZ) displayed limited activity, with only a few isolates showing inhibition zones of 12–13 mm, while most isolates recorded no inhibition. Likewise, Gentamicin (CN) exhibited variable activity, producing inhibition zones ranging from 12 mm to 22 mm, although several isolates showed complete resistance. As shown in Table 3 and where Interpreted using the CLSI, 2020 standard to identify resistant (R), sensitive (S) and intermediate (I).

Table 5: Antibiotic susceptibility testing of the isolates showing the percentage of sensitive, intermediate and resistance to the ten antibiotics tested.

	CTZ 30 µg	S 30 µg	AMX 20 µg	CPX 10 µg	LEV 20 µg	CTX 30 µg	CN 10 µg	OFX 10 µg	CEF 30 µg	SXT 25 µg
Resistant (%)	100.0	7.1	100.0	57.1	14.3	100.0	71.4	7.1	100.0	21.4
Intermediate (%)	0.0	21.4	0.0	21.4	50.0	0.0	14.3	42.9	0.0	35.7
Susceptible (%)	0.0	71.4	0.0	21.4	35.7	0.0	14.3	50.0	0.0	42.9

χ^2 = 97.23; Key: CTZ = Ceftazidime, S = Streptomycin, AMX = Amoxicillin, CPX = Ciprofloxacin, LEV = Levofloxacin, CTX = Ceftriaxone, CN = Gentamycin, OFX = Ofloxacin, CEF = Cefuroxime, SXT = Cotrimoxazole.

The zone diameter (Figure 8) distribution suggests that the fluoroquinolones (Ofloxacin, Levofloxacin, and Ciprofloxacin) and Streptomycin were the most active antibiotics against the *P. mirabilis* isolates, whereas the β-lactam antibiotics (Amoxicillin, Ceftriaxone, Cefuroxime, and Ceftazidime) exhibited poor activity. These findings support the susceptibility results and indicate a high prevalence of resistance to β-lactam antibiotics among the isolates.

Figure 5: Conventional Biochemical reaction of the isolates showing Blue colouration indicating a positive Citrate test.

Antibiotic susceptibility pattern of *P. mirabilis* tested

The antibiotic susceptibility pattern of the fourteen (14) confirmed *Proteus mirabilis* isolates revealed varying responses to the antimicrobial agents tested as shown in Table 4. The results showed that the isolates exhibited high levels of resistance to several antibiotics, particularly the β-lactam antibiotics.

All fourteen isolates (100%) were resistant to Amoxicillin (AMX), Ceftriaxone (CTX), and Cefuroxime (CEF), indicating complete resistance to these antibiotics. Similarly, thirteen (92.9%) isolates were resistant to Ceftazidime (CTZ), with only one isolate (7.1%) showing susceptibility. These findings suggest widespread resistance of the isolates to cephalosporins and penicillin derivatives.

Streptomycin (S) demonstrated the highest level of effectiveness among the antibiotics tested, with eleven isolates (78.6%) being susceptible, two isolates (14.3%) showing intermediate susceptibility, and only one isolate (7.1%) exhibiting resistance. Likewise, Ofloxacin (OFX) showed considerable activity against the isolates, with seven isolates (50.0%) susceptible, six isolates (42.9%) intermediate, and one isolate (7.1%) resistant.

The response to Levofloxacin (LEV) was moderate, with six isolates (42.9%) susceptible, six isolates (42.9%) intermediate, and two isolates (14.3%) resistant. Cotrimoxazole (SXT) also demonstrated moderate activity, with six isolates (42.9%) susceptible, five isolates (35.7%) intermediate, and three isolates (21.4%) resistant.

Resistance to Gentamicin (CN) was relatively high, as nine isolates (64.3%) were resistant, three isolates (21.4%) susceptible, and two isolates (14.3%) intermediate. Similarly, Ciprofloxacin (CPX) showed limited effectiveness, with eight isolates (57.1%) resistant, three isolates (21.4%) intermediate, and only three isolates (21.4%) susceptible.

The susceptibility pattern indicates that the *P. mirabilis* isolates were predominantly resistant to β-lactam antibiotics, including amoxicillin and cephalosporins. In contrast, Streptomycin and Ofloxacin demonstrated the greatest antimicrobial activity, while Levofloxacin and Cotrimoxazole showed moderate effectiveness. The observed multidrug resistance pattern highlights the importance of routine antimicrobial susceptibility testing in guiding appropriate treatment and monitoring the emergence of resistant *P. mirabilis* strains.

Antibiotic susceptibility test of P. mirabilis

The antibiotic susceptibility profile of the *Proteus mirabilis* isolates revealed varying levels of resistance, intermediate susceptibility, and sensitivity to the antibiotics tested is diaplayed in Table 5. The results indicate a concerning pattern of multidrug resistance among the isolates. The antibiotic susceptibility test results of the *Proteus mirabilis* isolates revealed varying degrees of resistance, intermediate susceptibility, and sensitivity to the antibiotics tested. The findings indicate that the isolates exhibited high levels of resistance to several commonly used antibiotics, while showing moderate to high susceptibility to others.

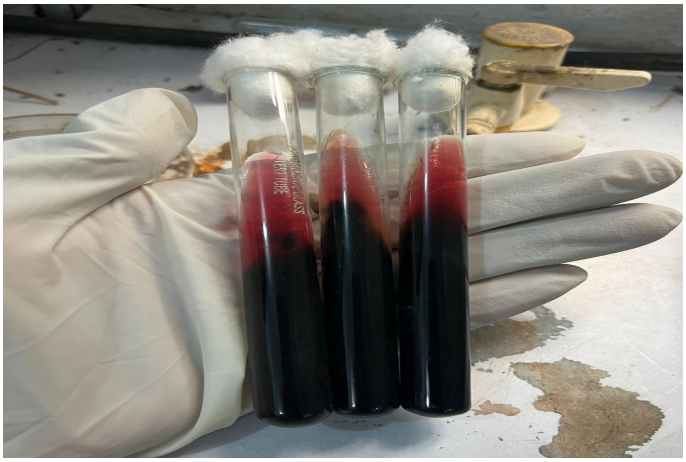

Figure 6: Conventional Biochemical reaction of the isolates showing Black precipitate indicative of positive H_2S.

The isolates demonstrated 100% resistance to Ceftazidime (CTZ), Amoxicillin (AMX), Ceftriaxone (CTX), and Cefuroxime (CEF), indicating that all tested isolates were resistant to these antibiotics. This suggests that these antimicrobial agents may have limited or no therapeutic value against the *P. mirabilis* strains recovered in this study. A high level of resistance was also observed against Gentamicin (CN), with 71.4% of the isolates resistant and only 14.3% susceptible. Similarly, Ciprofloxacin (CPX) showed a resistance rate of 57.1%, with only 21.4% of isolates being susceptible, indicating reduced effectiveness against the isolates.

Figure 7: Red arrows showing zones of inhibition indicating that the Isolates are susceptible to the antibiotics tested.

In contrast, Streptomycin (S) was the most effective antibiotic tested, with 71.4% susceptibility, 21.4% intermediate susceptibility, and only 7.1% resistance. Ofloxacin (OFX) also exhibited good activity against the isolates, with 50.0% susceptibility, 42.9% intermediate susceptibility, and only 7.1% resistance. Cotrimoxazole (SXT) demonstrated moderate effectiveness, with 42.9% susceptibility, 35.7% intermediate susceptibility, and 21.4% resistance. The response to Levofloxacin (LEV) was mixed, with 35.7% susceptible, 50.0% intermediate, and 14.3% resistant isolates. The high percentage of intermediate susceptibility suggests that the effectiveness of levofloxacin may vary depending on the dosage used and the clinical severity of infection.

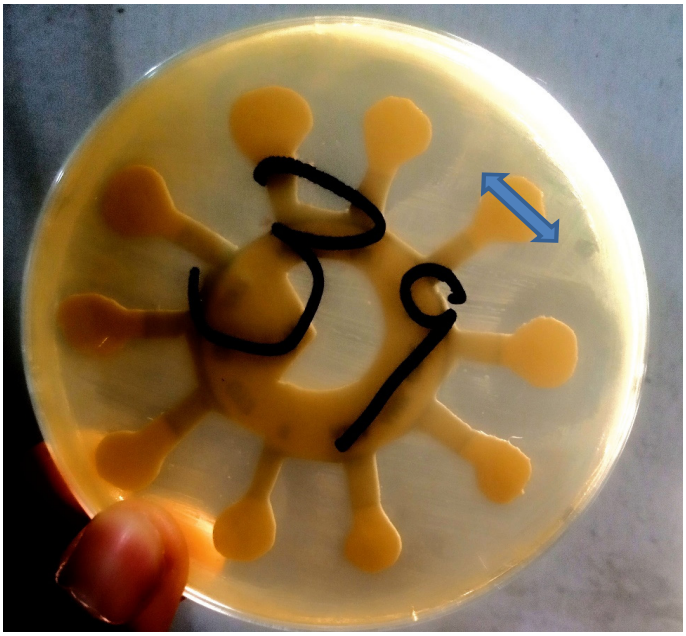

Figure 8: Blue arrows showing no zone of inhibition indicating resistance of the isolates to one of the antibiotics tested.

The results indicate that the *P. mirabilis* isolates were highly resistant to β-lactam antibiotics, including amoxicillin and cephalosporins (ceftazidime, ceftriaxone, and cefuroxime). However, Streptomycin, Ofloxacin, and to a lesser extent Cotrimoxazole and Levofloxacin, showed better antimicrobial activity against the isolates. These findings emphasize the importance of performing antimicrobial susceptibility testing before initiating treatment to ensure the selection of effective antibiotics and to reduce the spread of antimicrobial resistance.

DISCUSSION

This study revealed a 28% prevalence of *P. mirabilis* in poultry faecal samples from Gwagwalada Area Council As shown in Table 2, FCT, and this is lower than the 78.4% reported by Eze *et al.* (2020), from poultry in Lafia farms. The variations in prevalence may be due to differences in geographical location, poultry management and biosecurity practices, sample types, and the laboratory isolation and identification techniques used. These factors can significantly influence the occurrence, detection, and recovery of *Proteus mirabilis* across different studies.

The 28% prevalence obtained in this study indicates possible presence of *P. mirabilis* in the local poultry population, confirming that this pathogen is a major

concern requiring attention in Gwagwalada's poultry farms and industry. This prevalence rate is also comparable to the findings of Sanches *et al.* (2019) and Zhang *et al.* (2019), who reported prevalence rates of 32% in Brazil and 21% in China, respectively. The similarity in these findings suggests that *Proteus mirabilis* is consistently distributed across poultry production systems in different geographical regions. It also indicates that comparable management practices, environmental conditions, and husbandry systems may contribute to the persistence and occurrence of the organism worldwide.

The preliminary identification of the isolates in this study was achieved through a series of standard biochemical tests, and all 14 confirmed *Proteus mirabilis* isolates exhibited a consistent and characteristic biochemical profile: they were urease-positive, indole-negative, citrate-positive, and produced hydrogen sulfide (H_2S) on TSI agar, and this is in line with the report of Chakkour *et al.*, (2024).

This specific combination of results is a classic and reliable characteristic for *P. mirabilis*, effectively distinguishing it from other members of the Enterobacteriaceae family, such as the indole-positive *Proteus vulgaris,* as stated by O'Hara *et al.* (2000).

The antibiotic susceptibility results reveal concerning resistance patterns with significant public health implications, and this study obtained a complete resistance (100%) to all tested β-lactam antibiotics (ceftazidime, amoxicillin, ceftriaxone, and cefuroxime) which indicates widespread β-lactamase production among local *P. mirabilis* isolates, and possible indiscriminate use of the β-lactam antibiotics in routine diagnostic clinics or farms, which aligns with global reports of increasing β-lactam resistance in Enterobacteriaceae from poultry sources (Bennani *et al.*, 2020).

A high resistance rate of 71.4% was found for gentamicin, which is consistent with other Nigerian studies, such as Eze *et al.* (2021), who reported 66.7% resistance from poultry farms in Enugu State. Gentamicin is an important aminoglycoside used for treating serious systemic infections, and this high resistance observed suggests its extensive use in the poultry sector, likely for managing severe Gram-negative bacterial infections.

Streptomycin was the most effective antibiotic in this study, with a susceptibility of 71.4%, which is very different from a study in Ghana, by Frederick (2015), who reported a resistance of 61.7% from poultry meat. This variation is commonly observed and can be attributed to usage patterns of the antibiotic, as well as choice of samples. Streptomycin is an older aminoglycoside whose use has declined in favour of more potent or safer alternatives like gentamicin, and the reduced selective pressure has allowed a larger proportion of the bacterial population to remain susceptible, making it a potential option for therapy.

Ciprofloxacin exhibited high resistance (57.1%) and the lowest susceptibility (21.4%) among the fluoroquinolones tested, and this differential resistance, where earlier-generation fluoroquinolones like ciprofloxacin show higher resistance than later generations, is a well-documented trend in antimicrobial resistance (AMR) surveillance, by the WHO (2019), which highlighted that the extensive and often indiscriminate use of early-generation antimicrobials in food animals creates a strong selective pressure for resistance.

Levofloxacin showed a much lower resistance (14.3%) compared to ciprofloxacin in this study, though a significant proportion of isolates (50.0%) were intermediate. This pattern of newer fluoroquinolones retaining efficacy against ciprofloxacin-resistant strains is observed in global poultry production, for instance, a study from broiler chickens in Egypt reported a ciprofloxacin resistance of 70%, while levofloxacin resistance was significantly lower at 20% (Elsohaby *et al.*, 2021). The higher susceptibility to levofloxacin can be attributed to its enhanced potency and the fact that it is a later-generation drug, likely experiencing less usage and thus lower selective pressure in poultry.

Ofloxacin demonstrated the best activity among the fluoroquinolones in this study, with a low resistance rate of 7.1% and a susceptibility of 50.0%, and this aligns with findings from other regions, such as a study from poultry in China, where the resistance to ofloxacin (16.3%) was substantially lower than the resistance to the older fluoroquinolones (Mo *et al.*, 2022).

Cotrimoxazole, a folate pathway inhibitor, showed moderate efficacy with 42.9% susceptibility, 35.7% intermediate, and 21.4% resistance, which is also quite low from the resistance of 60.8% that was reported by Eze *et al.* (2020). The sustained susceptibility of a significant portion of the isolates could be due to a shift in usage towards other classes of antibiotics, such as fluoroquinolones and β-lactams, reducing the selective pressure for cotrimoxazole resistance (Bennani *et al.*, 2021).

The finding that 100% of isolates demonstrated multidrug resistance is concerning and reflects the serious antimicrobial resistance crisis in Nigerian poultry production, because this universal MDR pattern exceeds rates reported in many international studies and indicates severe antimicrobial stewardship failures in the local poultry industry. The MDR patterns observed suggest complex

resistance mechanisms including multiple β-lactamase production, efflux pump overexpression, and target site modifications, and this resistance to multiple antimicrobial classes limits therapeutic options, thereby increasing treatment failure risks in both poultry and potential human infections. The resistance patterns observed, particularly to clinically important antibiotics like fluoroquinolones and β-lactams, could compromise treatment outcomes in human infections, hence the potential for horizontal gene transfer from poultry isolates to human pathogens further amplifies these concerns. There is a highly statistically significant association between antibiotic type and susceptibility category (resistant/ intermediate/ susceptible). *P. mirabilis* isolates did not respond uniformly across the ten antibiotics resistance is strongly antibiotic-dependent, with complete (100%) resistance to CTZ, AMX, CTX, and CEF, versus much lower resistance to S and OFX (7.1% each).

P. mirabilis infections, combined with widespread antibiotic resistance, impose substantial economic burdens on local farmers through increased mortality, reduced productivity, elevated treatment costs, and potential market restrictions due to food safety concerns. The resistance of *P. mirabilis* to many antibiotics as shown in this study, necessitate more expensive therapeutic alternatives or combination therapies, further increasing production costs for resource-constrained farmers in Gwagwalada, and carcass condemnation due to antibiotic residues or infection-related issues. The presence of MDR *P. mirabilis* in poultry faeces indicates potential environmental contamination through waste disposal. These resistant bacteria can persist in soil and water systems, creating reservoirs for continued resistance gene circulation and environmental exposure risks. Poor waste management practices common in some local farms may exacerbate environmental contamination, creating cyclical infection and resistance patterns within local poultry production systems.

CONCLUSION

This study demonstrated the prevalence of *P. mirabilis* (28%) from poultry faeces collected from Gwagwalada Area Council, which were characterized using conventional biochemical methods. The isolates showed varying resistance to tested antibiotics, showing a 100% resistance to the β-lactam antibiotics (ceftazidime, amoxicillin, ceftriaxone, and cefuroxime) while showing 71.4% susceptibility to Streptomycin antibiotics. The findings from this study confirms *P. mirabilis* as an important pathogen in local poultry production with substantial zoonotic potential. The resistance patterns observed pose significant risks to both animal and human health while imposing economic burdens on local farmers. These results provide baseline data essential for developing evidence-based interventions to reduce *P. mirabilis* prevalence and combat antimicrobial resistance (AMR) in Gwagwalada's poultry industry.

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NOVELTY STATEMENT

This research demonstrated the isolation and antimicrobial susceptibility testing of *Proteus mirabilis* from poultry faeces from Gwagwalada Area Council of the Federal Capital Territory, Nigeria and hence, will serve as a baseline data for further research in the study area.

AUTHOR'S CONTRIBUTION

Bridget Maria Jessica Adah carried out the Conceptualization, methodology, investigation, formal analysis and writing of manuscript. James Agbo Ameh, Samuel Mailafia, Hamza Olatunde Kazeem Olabode helped in the Supervision of the project and manuscript. Martha Echioda - Ogbole, Ebenezer Odey Odey, Owolabi Tawa Olamide and Ifeanyi Casmir Ifeanyichukwu Cajetan, were involved in the Methodology and Analysis. Emmanuel Chinonso Okafor carried out the Laboratory Investigation of the research project.

Generative AI and AI assisted technology statement

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflict of interest

The authors have declared no conflict of interest.

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