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Molecular Characterization, Antimicrobial Resistance Profiles and Histopathological Evaluation of Proteus Mirabilis Isolated from Feline Cutaneous Wounds in Baghdad, Iraq

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ABSTRACT:

Background *Proteus mirabilis* is a non-lactose fermenting, Gram-negative rod that is a significant opportunistic pathogen in complicated skin and soft-tissue infections. Its capacity to cause wound infections in companion animals, particularly cats, raises concerns about multidrug resistance (MDR) and zoonotic transmission potential, yet data from Iraq remain scarce.

Objectives This study aims to determine the prevalence, phenotypic characteristics, multidrug resistance (MDR) profiles, virulence-associated *ure*R gene and histopathological effects of *P. mirabilis* isolated from cutaneous wounds of owned and stray cats.

Methods A total of 100 swabs (50 owned and 50 stray cats) collected from feline wounds. *P. mirabilis* isolates were identified by standard biochemical techniques and confirmed using the VITEK 2 Compact system. PCR analysis targeting the *ure*R virulence gene (225 bp) was performed on all confirmed isolates. Antimicrobial susceptibility testing was conducted to establish MDR profiles. Pathogenicity was assessed using a rabbit wound infection model. A total of 15 rabbits were randomly divided into three groups (n=5 per group): G1 (non-infected control), G2 (infected with owned cat isolates), and G3 (infected with stray cat isolates). Tissue sections were processed with haematoxylin and eosin staining for histopathological evaluation.

Results *P. mirabilis* was isolated from 13% of samples, with a higher Prevalence in stray (16%) than owned cats (10%), particularly associated with purulent abscesses. All 13 confirmed isolates were positive for the *ure*R virulence gene (225 bp). Antimicrobial susceptibility testing showed an MDR profile with resistance to ampicillin, cephalosporins, aminoglycosides and fluoroquinolones while all the isolates were still sensitive against carbapenems. Histopathological evaluations revealed that G3 induced more severe tissue damage than G2, including extensive inflammatory infiltration around necrotic areas, sluggish re-epithelialization, loss of skin appendages, irregular angiogenesis and abscess formation.

Conclusion this study provides evidence of MDR *P. mirabilis* virulence potential within feline wounds and indicates that isolates from stray cats may be more pathogenic compared to those from owned cats. As a result, a molecular diagnosis, histopathological field and culture-guided antimicrobial therapy are required to effective management of MDR wound infections in veterinary practice.

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INTRODUCTION

Feline skin and subcutaneous wounds (from superficial abrasions to deep puncture-induced abscesses) are a frequent clinical problem in veterinary medicine. Under normal conditions of wound healing a series of sequential physiological cascade is triggered, when the dermal barrier suffers extensive damage, it might have favorable conditions for colonization by opportunistic pathogens (**Takeuchi and Akira, 2010; Faccin *et al.*, 2023**). *Proteus mirabilis* is known as a member of polymicrobial flora, an established Gram-negative facultatively anaerobic uropathogen in the Enterobacteriaceae family and has become notorious battlefield opportunistic pathogen (**Funjan, 2021; Schaffer and Pearson, 2015).** Found in soil and water, as well as the gastrointestinal tracts of mammals, *P. mirabilis* quickly takes advantage of damaged tissue environments and morphs from a non-pathogenic commensal to an aggressive wound pathogen (**Ahmed, 2015**; **Drzewiecka, 2016**; **Ali and Shia, 2024**).

Environmental exposure and behavioral ecology are a major driving factor in feline wound infection epidemiological dynamics. For stray cats, exposure to environmental stressors is endless, encounter territorial aggressors regularly and can contact contaminated urban settings more frequently, which puts them at increased risk of local wound colonization compared to strictly owned cats (**Hariharan *et al.*, 2011; De Jong *et al.*, 2020; Bilan *et al.*, 2025**). Many of the virulence factors involved in tissue invasion by *P. mirabilis* during deep dermal infections (**Zuhir and Alaubydi, 2016**). Rapid expansion of the over-neutralized wound bed by hallmark swarming motility and urease production catalyzing urea hydrolysis to locally create a microenvironment with high pH and cytotoxic that can rapidly lead to necrosis while simultaneously limiting host-mediated immune clearance (**Armbruster and Mobley, 2012; Grahl *et al.*, 2021**), *ure*R is a main transcriptional activator that organizes the expression of the urease, which is a key enzyme (**Mahdi and Al-Deresawi, 2014**; **Loharch *et al.*, 2022**). While all these virulence mechanisms are in favor of bacteria concerted persistence, they also lead to significant damage of host tissue and associated inflammatory response, delay wound healing and promote abscess formation putting even higher relevance on histopathological evaluation for the real pathogenic potential of *P. mirabilis* infection (**Armbruster and Mobley, 2012; Gmiter and Kaca, 2022; Chakkour *et al.*, 2024**).

The surge in global antimicrobial resistance presents a further complication in the clinical management of these infections. Several studies have reported that strains of multidrug-resistant (MDR) Enterobacteriaceae harboring extended-spectrum β-lactamases (ESBLs) and mobile genetic elements capable of conferring wide-ranging resistance against clinically important veterinary and human therapeutics, are more frequently isolated from companion animals than humans (**Qin *et al.*, 2015; Girlich *et al.*, 2020; Menezes *et al.*, 2024**). This concern is further supported by recent studies that reported significant antimicrobial resistance among bacterial pathogens isolated from companion animals **(Jasim and Hayyawi, 2025)**. This bacterial pathogen is important from a clinical standpoint, however localized epidemiological data about the molecular features of *P. mirabilis* in Iraqi cat populations remains scarce. Thus, this study aimed to isolation and molecular identification of *P. mirabilis* from cutaneous wounds of owned and stray cats in Baghdad, Iraq. Evaluate its antimicrobial resistance profile using automated systems, and confirm its genetic virulence potential by the targeted detection of *ure*R gene and assess the histopathological effect of selected isolated from both cat population using an a standardized rabbit wound infection model, which provides an ethically acceptable in vivo system for pathogenicity assessment

MATERIALS AND METHODS

Study Design and Sample Collection

A multi-centre, cross-sectional experimental survey was carried out in selected veterinary clinics of Baghdad, Iraq. One hundred clinical feline wound swabs were collected from 100 cats including 58 males and 42 female ranged from 6 months to 4 years old, with different types of skin lesions, including abscesses, bite wounds, post-surgical infections, and trauma. A total of 50 owned cats and 50 strays free roaming cats were used randomly; all subjects were of different sex and age. Aseptically collected deep sampled from wound bed using a sterilized transport medium swabs were immediately transferred onboard an ice box up to the Microbiology Laboratory at the College of Veterinary Medicine, University of Baghdad.

Biochemical Identification and Phenotypic Isolation

The specimens were initially streaked on to MacConkey and Blood agar (Oxoid, UK) which was incubated aerobically at 37°C for 24 h. *P. mirabilis* was presumptively identified by colony morphology, characteristic with non-lactose fermenting (NLF) colonies on MacConkey agar and distinctive swarming motility yielding a putrid odor on blood agar medium (**Atlas and Snyder**

2006). The cellular morphology was evaluated using conventional Gram staining procedures. In addition, phenotypic confirmation of selected strains was conducted by a full panel of conventional biochemical assays including Triple Sugar Iron (TSI), Urease, Phenylalanine Deaminase (PDA), Motility (SIM medium), and the IMViC series (Indole, Methyl Red, Voges-Proskauer and Citrate) (HiMedia, India).

Automated identification and antimicrobial susceptibility testing (AST)

Identification and AST were performed using VITEK 2 Compact System (bioMérieux, France). Pure colonies were suspended in sterile saline; the turbidity adjusted to a 0.5 McFarland standard with DensiChek™ turbidity meter. Inoculation of suspensions were made to Gram-negative identification cards and antimicrobial susceptibility testing card. Antimicrobial minimum inhibitory concentrations (MIC) were determined using the system's Advanced Expert System (AES) and interpreted according to Clinical and Laboratory Standards Institute guidelines (**CLSI, 2025**).

Molecular Characterization of the *ure*R Gene

Polymerase Chain Reaction (PCR) was performed for molecular confirmation. Genomic DNA were extracted from the isolates using an extraction kit (Intron, Korea). PCR amplification was carried out in a final reaction volume of 25 µL containing 5 µL of i-Taq PCR PreMix, 1 µL each of forward and reverse primers (10 pmol/µL), 1.5 µL of template DNA, and 16.5 µL of nuclease-free distilled water. Thermal cycling conditions included an initial denaturation at 94°C for 5 min, followed by 30 cycles of denaturation at 94°C for 35 s, annealing at 58°C for 35 s, and extension at 72°C for 1 min, with a final extension at 72°C for (5 min.). Amplification was carried out using specific primers listed in which target a specific region to produce a 225 bp product **(Alatrash and Al-yasseen, 2017**). The PCR products were separated by electrophoresis in 1.5% agarose gel, visualized with RedSafe stain under UV trans illuminator.

Experimentally induced wounds in rabbits infected with the isolated identified P. mirabilis:

A rabbit wound infection model was used to assess the pathogenic potential of selected *Proteus mirabilis* isolates. Before the experiment, the rabbits were acclimatized for 3 days in the Animal House of the College of Veterinary Medicine, University of Baghdad. They were housed in plastic cages bedded with wood shavings under controlled environmental conditions (24°C with adequate ventilation). The rabbits were provided with a standard diet and drinking water ad libitum, and the cages and bedding were cleaned daily. Fifteen White New Zealand rabbits (8-10 months old, weighing 1.5 -2 kg) were divided equally into three groups: G1, the non-infected control group; G2, infected with a *P. mirabilis* isolate from owned cats; and G3, infected with a *P. mirabilis* isolate from stray cats. The rabbits received intramuscular injections of a mixture of ketamine and xylazine (**xylazine:** 5 mg/kg BW, Xyla® 2%, Interchemie, Netherlands; **ketamine:** 35 mg/kg BW, Ketamin® 10%, Dutch Farm Int., Netherlands). The rabbits were placed in sternal recumbency, and the dorsal were prepared aseptically. The surgical field was clipped, disinfected, and dried with 70% ethyl alcohol. Then, sterile surgical drapes were placed over the hair coat that was draping the operative field. A full-thickness circular excisional wound, 2 cm in diameter, was created on each rabbit using sterile surgical scissors and tissue forceps, excising the epidermis, dermis, and stratum corneum, thereby exposing the muscular fascia **(Varga Smith, 2023; Hassan, 2024).**. For the infected groups (G2 and G3), 50 µl of a bacterial suspension adjusted to Mcfarland standard No.2 (approximately equivalent to 6×10^8 CFU/ml)was applied directly to the created wounds. The clinical progression of the wounds was monitored closely over a period of 72 hours.

Histopathological evaluation:

At 3 days post-infection, the rabbits were humanely euthanized, and full-thickness skin specimens (1 × 1 cm), including the wound area, were surgically excised and immediately fixed in 10% neutral buffered formalin for 48 h. tissue samples were processed by routine methods (dehydrated with graded ethanol, cleared through xylene, embedded in paraffin, sectioned at thickness of 5 µm and stained with hematoxylin and eosin (H&E). Histopathological changes were evaluated by light microscopy (**Kim and Layton, 2019; Hashem *et al.*, 2023).**

Statistical Analysis

Methods Data were analyzed using SPSS (Version 2019). Chi-square testing was utilized to compare prevalence percentages between cat origin and wound aetiology. Statistical significance was defined as a P -value of < 0.05.

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RESULTS

Epidemiological Prevalence in Feline Wounds

Bacteriological analysis was performed for 100 feline wound specimens, a total of 13 (prevalence = 13%) were isolates of *Proteus mirabilis*. Feline lifestyle stratification indicated a higher prevalence among stray cats (16%, 8/50) than owned cats (10%, 5 /50), but this difference did not reach statistical significance ($p = 0.373$). About wound etiology, abscesses were the main source of *P. mirabilis* isolation in both cohorts represented by 61.5% of all isolates (3 owned ; 5 stray). Three isolates came from post-surgical wounds and two from bite wounds, while animal only pure traumatic open abrasions had no positive cultures (Table 1).

Table (1): Distribution of *P. mirabilis* isolation according to wound types in Stray cats and Owned cats:

Wound Type	stray cats	Owned cats
Post-Surgical	2/7 (28.6%)	1/14 (7.1%)
Bite	1/13 (7.7%)	1/11 (9.1%)
Traumatic	0/8 (0%)	0/10 (0%)
Abscess	5/22 (22.7%)	3/15 (20%)

$P = 0.928$ (non-significant)

Phenotypic and Biochemical Characterization

The classic morphological traits characteristic of the *P. mirabilis* were confirmed by primary culture. The isolates developed small, smooth-edged lactose non-fermenting colonies on MacConkey agar. A second subculture on blood agar exhibited a broad concentric swarming motility over the entire agar surface, with an associated intense necrotic foul smell. Both shows that by Gram staining there are pleomorphic and Gram-negative bacilli observed from microscopic examination.

A specific metabolic profile of *P. mirabilis* was established through biochemical analysis. All 13 of the isolates resulted in urease activity being positive rapidly (presenting bright pink with understand urea base), produced abundant hydrogen sulfide (H_2S) on TSI agar, alkaline slant/acid butt, and were motility-positive and phenylalanine deaminase (PDA)-positive. All isolates presented the following IMViC profile: Indole-negative, Methyl-Redd-positive, Voges-Proskauer-negative and Citrate-positive.

Identification of *P. mirabilis* isolates by Vitek® 2 compact system.

All 13 isolates were then confirmed and inactivate subjectivity associated with the visual interpretation of routine bench-top assays by automated VITEK 2 Compact System (bioMérieux, France). The system validated the phenotypic identity of the isolates as *Proteus mirabilis* with a remarkable "99% Probability" match (Bionumber: 6607734789123815). Automated biochemical profiling perfectly corroborated the conventional tests, particularly demonstrating positive reactions for a number of critical metabolites including Urease (URE), Hydrogen Sulfide (H_2S) and Ornithine Decarboxylase (ODC). Such automated expert systems could considerably improve diagnostic accuracy in veterinary microbiology. In contrast, the VITEK 2 system employs continuous, high-throughput colorimetric and fluorometric monitoring of comparable rapid complex kinetic reactions on dozens of substrates simultaneously which reduces human error and provides unprecedented reproducibility (**Pincus, 2006**).

Confirmation of Vitek® 2 and Antimicrobial Resistance by Automated Methods

All isolates were identified as *Proteus mirabilis* with a 99% probability match on VITEK 2 Compact system (Figure 1), corroborating traditional biochemical findings. Common multiresistant (MDR) phenotype [Medline] profiles were detected using automated AST profiling across the isolates. Absolute resistance (MIC ≥ 32 μg/mL) was found for broad-spectrum penicillins (ampicillin) and inhibitor combinations (amoxicillin-clavulanate). Deep resistance was also observed for third generation cephalosporins (cefotaxime, ceftazidime, cefepime) and aminoglycosides (amikacin, gentamicin), and fluoroquinolones (ciprofloxacin). Susceptibility was restricted to only carbapenems (meropenem MIC ≤ 0.06 μg/mL) and piperacillin/tazobactam. Intermediate susceptibility was observed for (imipenem MIC =2 μg/mL), indicating a highly compromised therapeutic window.

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bioMerieux Customer: **Chart Report** Printed December 26,2025 10:17:12
Patient Name: 8A Patient ID:8a
Location Physician:
Setup technologist: Laboratory Administrator(Labadmin0) Isolate Number:

Organism Quantity:

selected Organism: Proteus mirabilis

Source: wound swab

Comment:	

Identification Information	**Analysis Time:** 9 hours	**Status:** Final
Selected Organism	99% Probability **Proteus mirabilis** **Bionumber:** 6607734789123815	
ID Analysis Messages		

Susceptibility information	**Analysis Time:** 9 hours		**Status:** Final	
Antimicrobial	MIC	Interpretation	Antimicrobial	MIC	Interpretation
Ampicillin	>= 32	R	Meropenem	<= 0.06	S
Amoxicillin-Clavulanate	>= 16	R	Amikacin	>= 64	R
Piperacillin/Tazobactam	<= 4	S	Gentamicin	>= 16	R
Cefotaxime	>= 64	R	Ciprofloxacin	>= 8	R
Ceftazidime	>= 32	R	Tigecycline		
Ceftolozane/Tazobactam	>= 32	R	Colistin		
Cefepime	>= 32	R	Trimethoprim/ Sulfamethoxazole	>= 160	R
Imipenem	2	I			

AES Findings	**Last Modified:**
Confidence Level:	Consistent

Figure 1: Antimicrobial susceptibility pattern of strain Proteus mirabilis isolated from cat wound swab and Confirmatory VITEK® 2 Compact system.

Molecular Detection of *ure*R

The phenotypic taxonomy was confirmed by genomic amplification using PCR. All the isolates tested successfully had a positive amplification for *ure*R that was specifically targeted. Agarose gel electrophoresis revealed a clean and discrete amplification of the expected 225 base pair PCR product, further confirming these strains have the genetic ability to tightly control expression at their urease virulence operon.

Histopathological Findings

Histopathological studies were carried out to evaluate the tissue changes caused by *Proteus mirabilis* isolates from owned and stray cats.

- Group 1 (**G1**) (control group): The skin revealed normal architecture with intact epidermis and well-organized connective tissue of dermal papilla. The scalp showed normal hair follicles and sebaceous glands The absence of severe inflammatory reaction, healthy granulation tissue formation, fibroblast proliferation, organized collagen deposition and complete re-epithelialization was observed during wound healing (**Figure 2A**).
- Group 2 (**G2**) (owned cat isolate-infected group), which had moderate changes characterized by neutrophil infiltration into the dermis. Compared to the controls, also showed significant edema and necrosis of foci (**Figure 2B**).
- Group 3 (**G3**) (stray cat isolate-infected group) showed the most advanced pathological lesions revealed severe and chronic inflammatory response associated with immature granulation tissue formation, extensive destruction of the dermis and deeper involvements in subcutaneous tissues. Also noted were an absence of skin appendages (hair follicles), abnormal formation of blood vessels (Figure 3C, and abscesses (**Figure 2D**).

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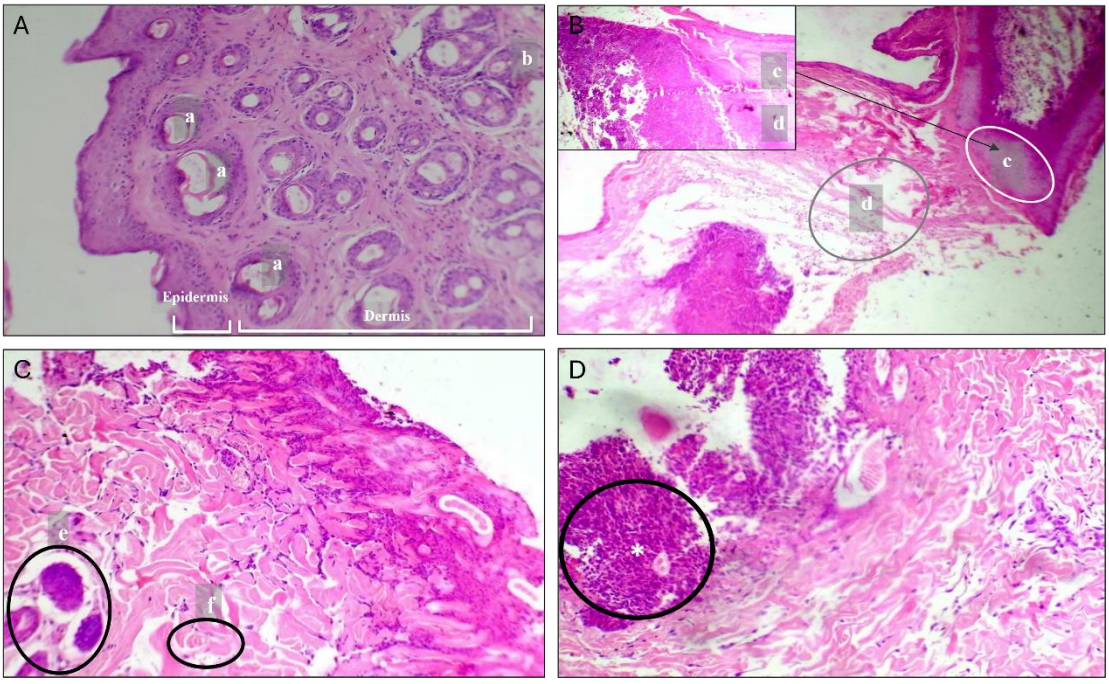

Figure 2: Representative histopathological sections in rabbit skin wounds following experimental infection with *Proteus mirabilis*. (A) G1 control group showing normal epidermis, dermis, hair follicles (a), and sebaceous glands (b) (H&E stain, 20X). (B) G2 showing inflammatory cell infiltration, tissue necrosis (c), and edema (d) (H&E stain, 4x and 20X). (C) G3 showing destruction of skin appendages (f) and irregular angiogenesis (e) (H&E stain, 20X). (D) G3 showing abscess formation in the subcutaneous tissue (asterisk) (H&E stain, 40X).

DISCUSSION

This study indicates that *P. mirabilis* are prominent pathogens of opportunistic nature, complicating feline soft tissue injuries in Baghdad, Iraq. The 13% overall isolation rate is consistent with more recent regional surveillance, for example the 18.33% prevalence described in feline wounds by **Rashied *et al.* (2023).** The 16% of isolates from stray cats versus 10% from owned cats endemic epidemiology recovering reinforces the need to bridge behavioral ecology to infectious disease. The systemic immunity is undoubtedly bypassed by continuous environmental exposure, nutritional stress and high frequency of territorial conflicts that are integral to lifestyle as a stray feline which allows the perennial inoculation of soil-borne and enteric pathogens directly to open abrasions (**Hariharan *et al.*, 2011; De Jong *et al.*, 2020**).

P. mirabilis strong preference for closed abscesses (the source of the majority of isolates) is an ideal reflection of its pathophysiological niche. Feline territorial fights cause penetrating wounds that deliver a diverse microbiota within deeper strata of the subcutis. The main seal for dermal barrier, which in turn rapidly establishes a hypoxic and devitalized microenvironment (**Kožár *et al.*, 2018; Faccin *et al.*, 2023**). Under purulent, closed air conditions such that for example the facultative anaerobes *P. mirabilis* explicitly commandeer physiological repair mechanisms into an indefinite cycle of necrotizing inflammation (**Eze *et al.*, 2014; Seo *et al.*, 2015; Bilan *et al.*, 2025**). Moreover, its association with post-surgical infections further reinforces its position as a potentially catastrophic perioperative contaminant and a pathogen capable of colonizing surgical incisions when environmental sanitation or localized postoperative care is compromised (**Gulaydin *et al.*, 2024**).

The classic in vitro swarming motility and biochemical profile is more than just a diagnostic signature; it is an essential virulence factor. Swarming is an exceedingly well-coordinated form of differentiation whereby short vegetative swimmer cells rapidly differentiate into long, hyper-flagellated swarmer cells (**Manos and Belas, 2006; Armbruster and Mobley, 2012**). This multicellular migration allows the pathogen to quickly spread through wet wounds, skipping localized phagocytosis and creating stable biofilms (**Drzewiecka, 2016**). At the same time, high-level expression of the urease enzyme (regulated by a master transcriptional activator, *ure*R which was amplified in all our isolates) facilitates rapid hydrolysis of urea to release vast quantities

of ammonia. This extreme localized alkalinization causes direct cell death, triggers necrosis in tissues and inhibits the function of the macrophages of the host (**Coker *et al.* 2000; Zhang *et al.*, 2012; Mora and Arioli, 2014; Al-Khalidy and Aburesha, 2023**).

The histopathological assessment in the experimental rabbit-induced wound model further reinforced the molecular and phenotypic data through real tissue damaging potential mediated by isolated *P. mirabilis* strains. Owned cat isolates (G2) caused moderate pathological changes in the wounds in comparison to control group such as inflammatory cells infiltration, edema, necrotic changes, and delayed re-epithelialization (**Chakkour *et al.*2024**)

These data confirm that virulence determinants (urease activity, swarming motility, biofilm formation and extracellular enzymes) can subvert normal wound repair mechanisms of *P. mirabilis* (**Armbruster and Mobley, 2012; Gmiter and Kaca, 2022**). Stray cat isolates (G3) also had significant distinctions regarding the aggressiveness of their histopathological lesions based on greater neutrophilic infiltration, destruction of skin appendages, irregular angiogenesis and chronic inflammation after inducing wounds compared with either owned feline isolates (G2) or the control group (G1). G3 showed higher pathological severity and may be related to the environmentally exposed condition on free-roaming cats, which possibly allows a longer period for bacterial adaptation and expression of virulence. These findings were consistent with the relationship between feline outdoor lifestyle and bacteria pathogenic potential and wound severity (**Hariharan *et al.*, 2011; De Jong *et al.*, 2020; Faccin *et al.*, 2023**), the use of Vitek® 2 Compact system has given strong technologic assistance for longtime microbiological data, Accurate automated confirmation in the clinical setting is important to reduce taxonomic confusion of members from the Proteeae tribe as they move away from presumptive phenotypic identification (**Miller *et al.*, 2018**; **Hasan *et al.*, 2023; Mahmood, 2025)**. Most of the biochemical markers, particularly Urease and H2S (99% probability) imply that the feline isolates have a homogenous metabolic fingerprint. Rapid identification is essential for appropriate clinical intervention, since acute and irreversible tissue damage caused by P. mirabilis can occur if therapy is delayed by initial misidentification (**Pincus 2006**).

Vitek®2 system determined an antibiotic susceptibility profile revealed a challenging antimicrobial resistance pattern. Antibiotic susceptibility of *P. mirabilis* isolates has varied across studies **(Al-Nabhani and Shami, 2023; Mohsin and Al-Rubaii, 2023; Muthanna Muwafaq and Bahaa Abdullah Laftaah, 2024)**. In the present study , the complete resistance against ampicillin, amoxicillin-clavulanate and newer generation cephalosporins (eg, cefotaxime, ceftazidime) was phenotypically attributed to the production of Extended-Spectrum β-Lactamases (ESBLs) or AmpC enzymes (**Qin *et al.*, 2015; De Curraize *et al.*, 2020**), Though **Rashied *et al.* (2023)** reporting full gentamicin susceptibility in their cat collection while in our study were resistant to this aminoglycoside at high levels and strongly reflect a rapid local change of antibiotic-resistant profiles despite. Some veterinary will refrain from using fluoroquinolones as first line agents with consequences for resistant urogenital infections; this is the dangerous zoonotic burden that needs urgent attention and makes CLSI validated culture-directed use essential (**CLSI, 2025; Faccin *et al.*, 2023**).

CONCLUSION

The study indicated that *Proteus mirabilis* is a significant opportunistic pathogen in cat cutaneous wound infections in Baghdad, Iraq. With a higher prevalence trend observed among stray cats compared to owned cats. All isolated strains exhibited MDR profiles. Thus, antimicrobial susceptibility testing and culture-guided therapy are of the highest importance in veterinary practice. Histopathological findings, combined with the detection of the *ure*R virulence gene in all isolates, support the pathogenic potential of *P. mirabilis* as a causative agent of soft tissue infections. In conclusion, these findings reinforce the role of antimicrobial resistance and bacterial virulence factors in tissue pathogenicity, indicating the importance of continuous molecular surveillance and rational antimicrobial prescribing to prevent treatment failure and the potential dissemination of MDR pathogens.

ETHICAL CONSIDERATIONS

Compliance with ethical guidelines: This study was approved by the Ethics Committee of the College of Veterinary Medicine, University of Baghdad, Baghdad, Iraq (Code: P.G/710).

Funding: This study was extracted from the master's thesis of Aya Oday Abdulqader, approved by the Department of Microbiology, College of Veterinary Medicine, University of Baghdad, Baghdad, Iraq.

Authors' contributions: All authors contributed equally to the conception and design of the study, data collection and analysis, interception of the results and drafting of the manuscript. Each author approved the final version of the manuscript for submission.

Conflict of interest: The authors declared no conflict of interest.

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