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Diversity of Antimicrobial Resistance, and molecular characterization of *Proteus spp.* isolated from various sources

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Abstract

Proteus infections are among the most common foodborne pathogens, responsible for zoonotic diseases and food poisoning in humans. Between March and September 2023, 320 samples were collected to isolate and characterize *Proteus* spp., including 200 chicken meat samples from local markets and 120 human urine samples from hospitals in Wasit Province, Iraq. Selective media, PCR, and Vitek 2 were used for bacterial identification, along with AST testing for 20 antibiotics. Results showed that *P. mirabilis* was isolated in 25% of human samples and 13% of chicken meat samples, while *P. vulgaris* appeared in 6.6% of human samples and 4% of poultry samples. *P. mirabilis* exhibited high resistance to common antibiotics, ranging from 83.3%-100% for macrolides (Azithromycin, Erythromycin), 66.7%-83.4% for penicillin (Ampicillin, Amoxicillin-Clavulanic Acid), and 66.7% for cephalosporins (Cephalexin, Cefepime, Cefotaxime). In contrast, *P. vulgaris* showed 100% resistance to Erythromycin and Tetracycline, followed by Trimethoprim, Ampicillin, and Rifampin at 83.4% resistance. Additionally, 66.7% of isolates were resistant to Cephalexin, Nitrofurantoin, and Cefotaxime. Overall, antibiotic resistance reached 40%, largely due to genetic mutations in multiple sites of the 16 S rRNA gene, highlighting the need for continuous monitoring and control measures to curb the spread of resistant strains.

Keywords: Foodborne disease, *P. mirabilis*, *P.vulgaris*, Antibiotics.

INTRODUCTION

Poultry meat is an excellent medium for bacterial development and is known to host many bacteria that are harmful to humans (1). Raw chicken meat cuts may include food-poisoning bacteria from a variety of sources, emphasizing the significance of proper cleanliness during slaughter, handling, and cooking (2,3,4). In terms of slaughterhouse and processing plant cleanliness, the presence of pathogenic and spoilage microorganisms in chicken meat and its products is a major problem for suppliers, consumers, and public health officials worldwide(5,6). Bacterial contamination in food items is undesirable but unavoidable; it is determined by the initial bacterial load of fresh raw materials, sanitary measures during manufacture, and the time/temperature factor (7). The food contamination produced by foodborne and opportunistic pathogenic bacteria is the primary cause of diseases, and it is a danger to worldwide public health (8). *Proteus spp* is a significant food-borne zoonotic identified in the broiler breeding industry (9,10). Although the *Proteus* species recovered from chicken varies among geographic regions, *Proteus mirabilis* and *Proteus vulgaris* were the most prevalent *Proteus* serovars recovered from chicken meat. *P. mirabilis* is the considered most common pathogen, followed by *P.vulgaris*, which is less commonly isolated (11). *Proteus* is a rod-shaped Gram-negative bacterium and is renowned for its urease activity and swarming motility (12,13). It is a normal flora component in the intestinal tracts of people and animals and is found throughout the environment (14). *Proteus spp* is responsible for 90% of urinary tract infections and is classified as community-acquired infection. Elderly patients undergoing long-term catheterization have the highest *P. mirabilis* CAUTI incidence rates (15).In addition, *P. mirabilis* infections can result in bacteremia and the production of urinary stones. Given that *P. mirabilis* lives in chickens' intestinal tracts, it may be present in retail meat products as a result of fecal contamination during the slaughter process. *P.mirabilis* infection in humans may be transmitted by manipulating and consuming retail meat products (16).

The high prevalence of extensively drug-resistant foodborne *Proteus*, along with other bacteria such as *Citrobacter*, *Salmonella*, *Shigella*, and *Pseudomonas* isolated from native chicken carcasses, is a significant public health risk (17,18). This situation necessitates enhanced monitoring and heightened awareness regarding the overuse and misuse of antibiotics in humans and animals (19). The increasing application of antimicrobials to treat bacterial infections in humans and food-producing animals has led to the proliferation of antimicrobial resistance genes (20,21). The emergence and spread of multidrug-resistant (MDR) *P.mirabilis* isolates, including those producing extended-spectrum beta-lactamases (ESBLs), cephalosporinases, and carbapenemases, have raised significant concerns in recent years (22). Various virulence factors of *Proteus spp*., including sensing molecules, adhesion proteins, efflux pumps, lipopolysaccharides, and urease enzymes, play a critical role in the pathogenesis of this bacterium (23). The probability of populations developing antibiotic resistance increases with the use of antibiotics, and growing evidence indicates that the widespread non-therapeutic application of antibiotics in animals has not only accelerated the emergence of resistant bacteria but has also contributed to a higher prevalence of illnesses, increased healthcare costs, and reduced effectiveness of antimicrobial drugs (24,25). This study aimed to identify *Proteus* bacteria, as well as to conduct antimicrobial testing (AST) and analyze molecular characteristics using polymerase chain reaction (PCR) and sequencing for isolates obtained from chicken meat and humans in the Wasit Governorate of Iraq.

MATERIALS AND METHODS

Ethical approval

The study was accepted and carried out in the ninth session of the Council of the College of Veterinary Medicine, University of Baghdad, on 10/1/2023, with approval No. 193 issued on 25/1/2023.

Collection of samples

From March to September 2023, 200 random chicken meat samples were collected from various local supermarkets, as well as 120 human urine samples from various clinical cases at hospitals in Wasit Governorate, Iraq, for the isolation and study of the molecular characteristics and AMR of *Proteus* isolates. The samples were stored in an ice box under strict aseptic conditions before being delivered to the meat hygiene laboratory at the University of Baghdad's Department of Public Health, College of Veterinary Medicine.

Culture Media

Proteus species were isolated and identified from Chicken meat samples according to ISO 21528-2(26). Twenty-five grams of each sample were weighed and combined in a sterile flask with 225 ml of buffered peptone water before being incubated overnight at 37°C for 18-24 hours. One milliliter of the suspension was mixed with nine milliliters of tetrathionate broth and incubated at 42°C for 18-24 hours. The samples were cultivated on two media: standard MacConkey agar, and differential agar (Hichrome UTI agar). Following the purification of *Proteus* colonies, bacterial species were identified using conventional techniques. All suspected colonies were identified using conventional biochemical followed by PCR for further confirmation.

Antibiotic Susceptibility Test

The procedure employed the Kirby-Bauer technique on Muller Hinton agar and the Vitek 2 test. The isolates were tested against 20 commonly used antibiotics, and the results were interpreted according to the Clinical and Laboratory Standards Institute 2023 (27) guidelines.

Molecular detection

PCR was used to detect *Proteus spp* from environmental and clinical samples. Cycling conditions of PCR were accomplished by adjusting the optimum temperature, time, number of cycles, denaturation,

annealing, and extension stages. The conventional PCR was done by amplifying the identity rRNA gene of *Proteus* (383 bp) using primers (-F 5′– CTGCCCGATAGAGGGGGATA –3′) and (-R 5′– GGAGTTAGCCGGTGCTTCTT –3′) that tested in the National Center for Biotechnology Information (NCBI) Genbank database and used in the current study as described by (28). Finally, the sequencing for some isolates of *Proteus* was done. Forward and reverse primers provided by Alpha DNA company, Canada were used to amplify specific DNA fragments of rRNA gene.

Sequences and phylogeny analysis

Six *Proteus spp*. PCR results for identifying specific rRNA genes and virulence factor genes were sent to Microgen/Korea for sequencing. BLAST was used to evaluate all six samples. Also, MEGA 11 software was used to evaluate and extract evolutionary history, and a phylogenetic tree was created on a scale, with branch lengths representing evolutionary distances. The maximum composite probability approach was used to compute the evolutionary distances, which were taken into account the amount of base substitutions per site.

Statistics

The Chi-squared test was used to compare isolation proportions. Additionally, the odds ratio was estimated. $P < 0.05$ indicates significance (29).

RESULTS AND DISCUSSION

Sample results were obtained using selective media, biochemical testing, and vitek2 and validated using PCR. The results showed a significant difference ($P < 0.05$) in the isolation percentage of *Proteus mirabilis* from chicken meat samples compared with human samples. The overall isolation percentage of *Proteus mirabilis* from chicken meat samples was 13% (26 out of 200 samples), compared to 25% (30 out of 120 samples) from human samples (Table 1). In contrast, there was no significant difference in the isolation percentage of *Proteus vulgaris* isolation, which was 4% (8 out of 200 samples) and 6.6% (8 out of 120 samples), respectively (Table 2). Also, the results showed that the risk factor for contamination with *Proteus mirabilis* was four times higher than that of *Proteus vulgaris* in human samples, at 25% compared to 6.6%, respectively (Table 3).

Table (1) Isolation percentage of *P. mirabilis* from different sample sources

Source of isolation	No. of samples	*P. mirabilis*	Chi-square	P-value
Chicken meat	200	26 (13%)	7.48	0.006
Human	120	30 (25%)		
Total	320	56		

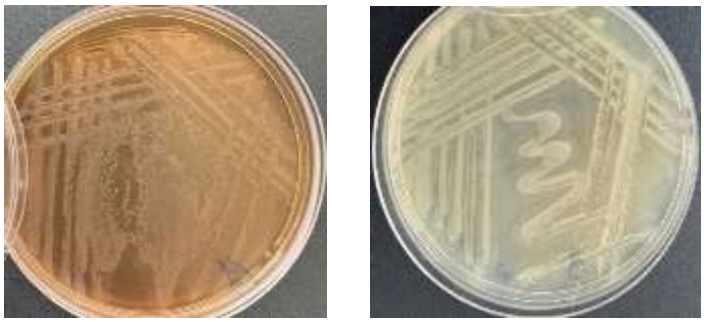
Table (2) Isolation percentage of *P. vulgaris* from different sample sources

Source of isolation	No. of samples	*P. vulgaris*	Yates' chi-square	P-value
Chicken meat	200	8 (4%)	1.12	0.28 NS
Human	120	8 (6.6%)		
Total	320	16		

Table (3) The risk factor of contamination with *Proteus spp* in human samples

Proteus spp	No. of samples	Isolation%	Odds ratio (OR)	95% Confidence Interval (CI)	P-value
P. vulgaris	120	6.6% (8)	Reference	2.04-10.67	0.0003
P. mirabilis	120	25% (30)	4.67		

All *Proteus* isolates had their genomic DNA effectively extracted, and the bands of DNA were identified on Agarose gel and examined under a UV transilluminator, revealing 100% retrieved genomic DNA. The purity and concentration of extracted DNA were evaluated directly by a Nanodrop device, which ranged from (1.75, 1.55, 1.43, 1.80, 1.77, and 1.82). The results of identifying and isolating *Proteus* species using cultural medium methods, as well as microscopic analysis, were consistent with the phenotypic traits of this bacteria. The colonies of the *P. mirabilis* and *P. vulgaris* isolates showed growth on the MacConkey agar medium with a pale color because it is a non-lactose fermenter. but They turned yellow to light brown on hi-chrome UTI agar (figures 1 and 2). A microscopic investigation of bacterial isolates belonging to the *Proteus* species was performed. Staining with Gram stain revealed that they have the shape of short rods (30).



(A) (B)

Figure (1): *Proteus mirabilis* on (A) MacConkey agar (B) Hi chrome UTI agar

(A) (B)

Figure (2): *Proteus vulgaris* on (A) MacConkey agar (B) Hi chrome UTI agar

Sequential sequencing was done for six PCR products that were isolated from chicken meat and human samples to confirm the identification of *Proteus* by amplifying the primer set of the rRNA gene. All PCR products that were sent for sequencing were registered for the first time on the NCBI under the accession numbers:(PP808498.1, PP808497.1, and PP472478.1) for a special identity of *Proteus mirabilis* also (PP9808500.1, PP808499.1, PP472479.1) for *Proteus vulgaris*. The nucleotide sequencing for 16S

RNA for *P. mirabilis* showed one nucleotide substitution was guanine to Adenine G\A in sample 3 (chicken meat) (Table 4). Also, the same table revealed that two *Proteus mirabilis* samples (isolated from chicken meat and human urine) exhibited 100% identity with the reference sequence (PP086888.1), showing no nucleotide changes. Additionally, transitions (purine-to-purine or pyrimidine-to-pyrimidine substitutions) were observed at the following positions: 298 (G\A) in *P. mirabilis* (chicken meat), and 255 (A\G). Also, 157 (G\A) in *P. vulgaris* was isolated from chicken meat and human urine samples. Furthermore, transversions (purine-to-pyrimidine or vice versa) were detected at multiple positions (355, 450, 454) in *P. vulgaris*, with changes such as C\G, A\T, and A\C. These transitions are generally less disruptive to rRNA structure compared to transversions, which may explain the retained 99% identity. Mutations were identified at several loci of the 16S rRNA gene, specifically at positions (157, 255, 298, 355, 450, 454). This indicates that the gene remains highly conserved, preserving its critical role in ribosome formation. The mutations observed are likely to affect core functionality.

Table (4) Represent type of polymorphism of *Proteus mirabilis* and *Proteus vulgaris* in 16RNA genes.

Gene: 16S ribosomal RNA gene								
No. Of sample	**Type of substitution**	**Location**	**Nucleotide**	**Source**	**Isolation source**	**Sequence ID with compare**	**Sequence ID with submission**	**Identities**
1	**-----**	**-----**	**---**	***Proteus mirabilis***	**chicken meat**	**ID: PP086888.1**	**ID: PP472478.1**	**100%**
2	**-----**	**-----**	**---**	***Proteus mirabilis***	**human Urine**	**ID: PP086888.1**	**ID: PP808497.1**	**100%**
3	**Transition**	**298**	**G\A**	***Proteus mirabilis***	**chicken meat**	**ID: PP086888.1**	**ID: PP808498.1**	**99%**
4	**Transition**	**255**	**A\G**	***Proteus vulgaris***	**chicken meat**	**ID: MH985232.1**	**ID: PP472479.1**	**99%**
5	**Transition**	**157**	**G\A**	***Proteus vulgaris***	**human Urine**	**ID: MH985232.1**	**ID: PP808499.1**	**99%**
	Transversion	**355**	**C\G**					
	Transversion	**450**	**A\T**					
6	**Transversion**	**454**	**A\C**	***Proteus vulgaris***	**chicken meat**	**ID: MH985232.1**	**ID: PP808500.1**	**99%**
	Transition	**455**	**T\C**					

Gel electrophoresis produced a DNA band of 383 (bp), indicating that the rRNA gene was successfully amplified using PCR. Lane M represents the DNA ladder, which regulates the size of DNA fragments. Lanes 1-6 show successful amplification of the rRNA gene in numerous samples, suggesting that this gene exists in all samples tested (Figure 3).

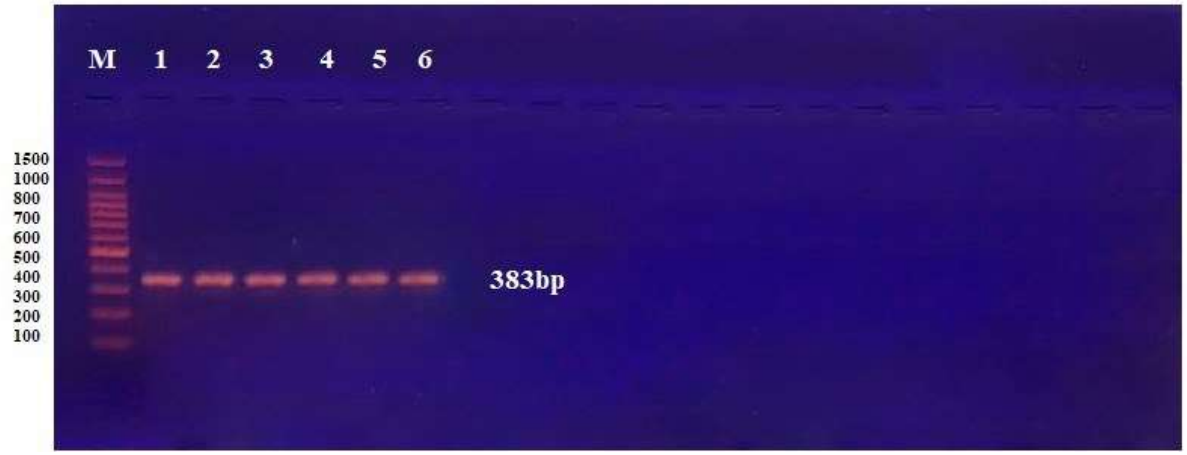


Figure (3) DNA product analysis of a 383bp rRNA gene from *Proteus spp* using 0.8% agarose gel electrophoresis at 80V for 45 minutes at room temperature (25°C).

The sequencing and similarity analysis was performed using the basic local alignment search tool (BLAST) at NCBI in comparison to global isolates, which revealed that *P.mirabilis* isolates (PP472478, PP808497, and PP808498) were completely compatible with isolates from different countries. *P. vulgaris* isolates (PP472479, PP808499, and PP808500) were 99% compatible with isolates from various countries, as shown in the phylogenetic tree (Figure 4). The phylogenetic tree genetic relationship analysis showed that the local *P.mirabilis* Iraq was closely related to NCBI-BLAST *P.mirabilis* Russia, USA, India, China, Pakistan, Iran isolate (PP086888.1, OR975996.1, OR838729.1, CP137214.1, OR030424.1, OQ780751.1) and the local *P.vulgaris* Iraq was showed closed related to NCBI-BLAST P.vulgaris Kenya, Brazil, India, China, Thailand, Turkey isolate (MH985232.1, MG027634.1, PP112209.1, KX692872.1, KP313869.1, OL597934.1) as shown in (Figure 4).

According to the AST results, *P. mirabilis* is highly resistant to the most common antibiotics at 100% erythromycin, followed by 83.4% tetracycline, azithromycin, ampicillin, rifampin, and nitrofurantoin and at a rate of 66.7% to cefepime, cephalexin, amoxicillin-clavulanicacid, and cefotaxime. Also, it showed sensitivity to meropenem, ciprofloxacin, and amikacin, at a rates of 83.3 %, and 66.6% for tricarcillin, levofloxacin, and norfloxacin with moderate sensitive (50%) to imipenem, trimethoprim, nalidix acid, and gentamycin (Figure 5). The resulting study showed that High resistance (100–83.3%) to the Macrolides group (azithromycin, erythromycin). Also, there was resistance to the penicillin group (ampicillin, amoxicillin-clavulanicacid) at 83.4-66.7% It may be due to genetic Mutations in their genes and efflux pumps are common in Enterobacteriaceae. (31) and resistance 66.7% to cefalosporins group (cephalexin, cefepime, cefotaxime).Variable resistance (33.3–83.4%) to Beta-Lactam (Amoxicillin-clavulanicacid, Cefotaxime, Ampicillin). It may be due to ESBLs (e.g., CTX-M-15) and AmpC beta-lactamases.(32).

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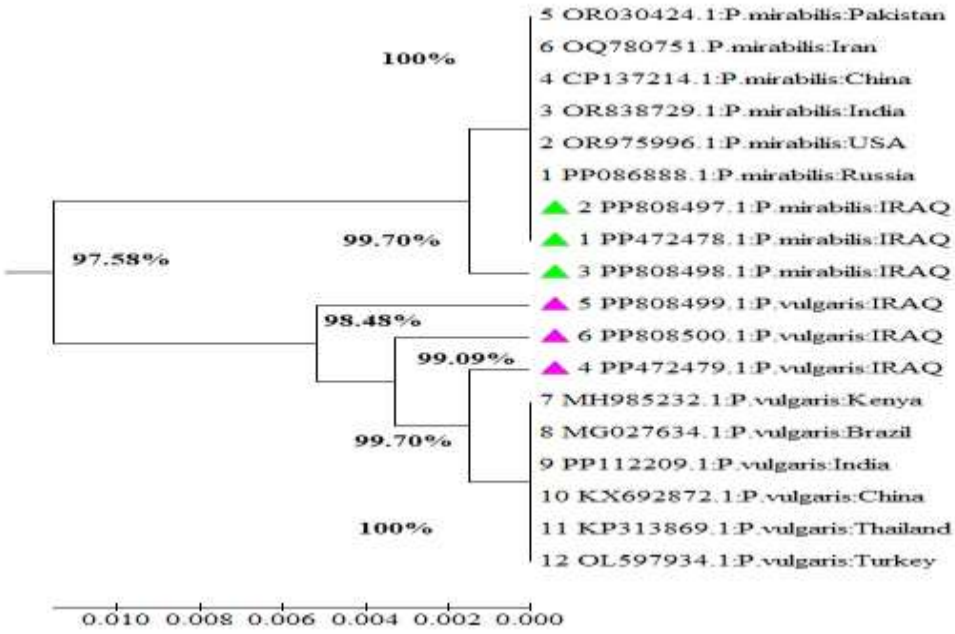
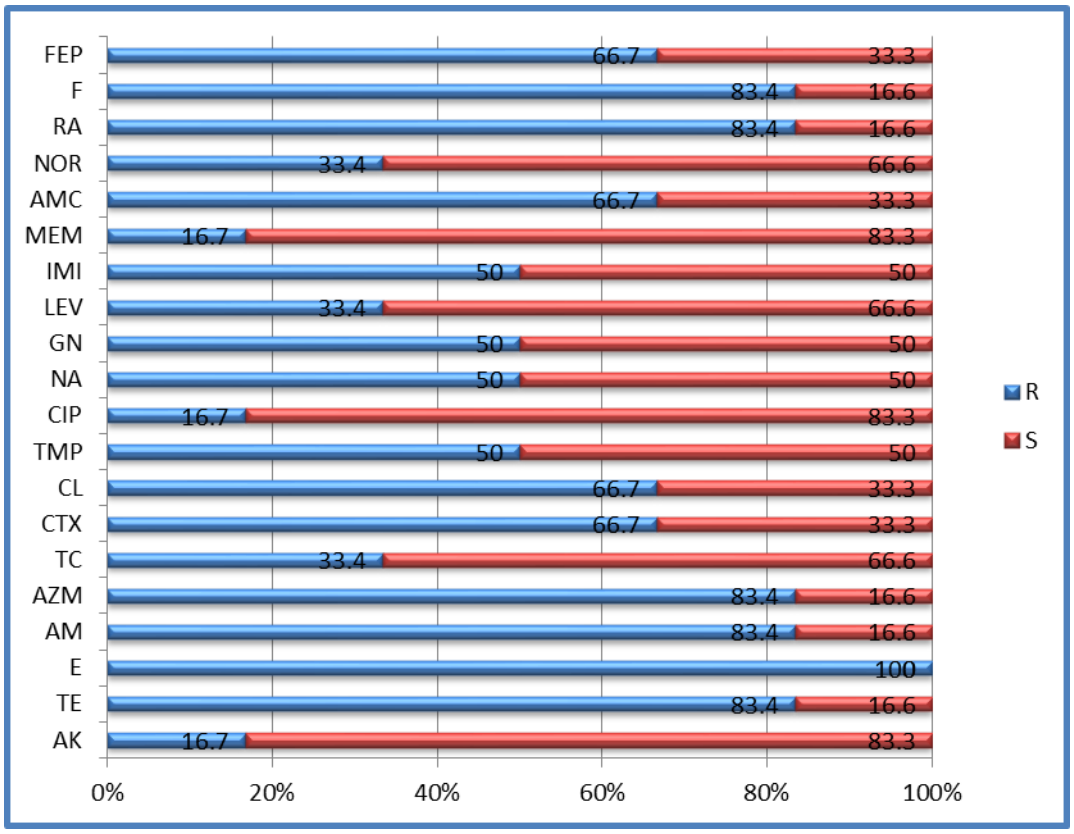


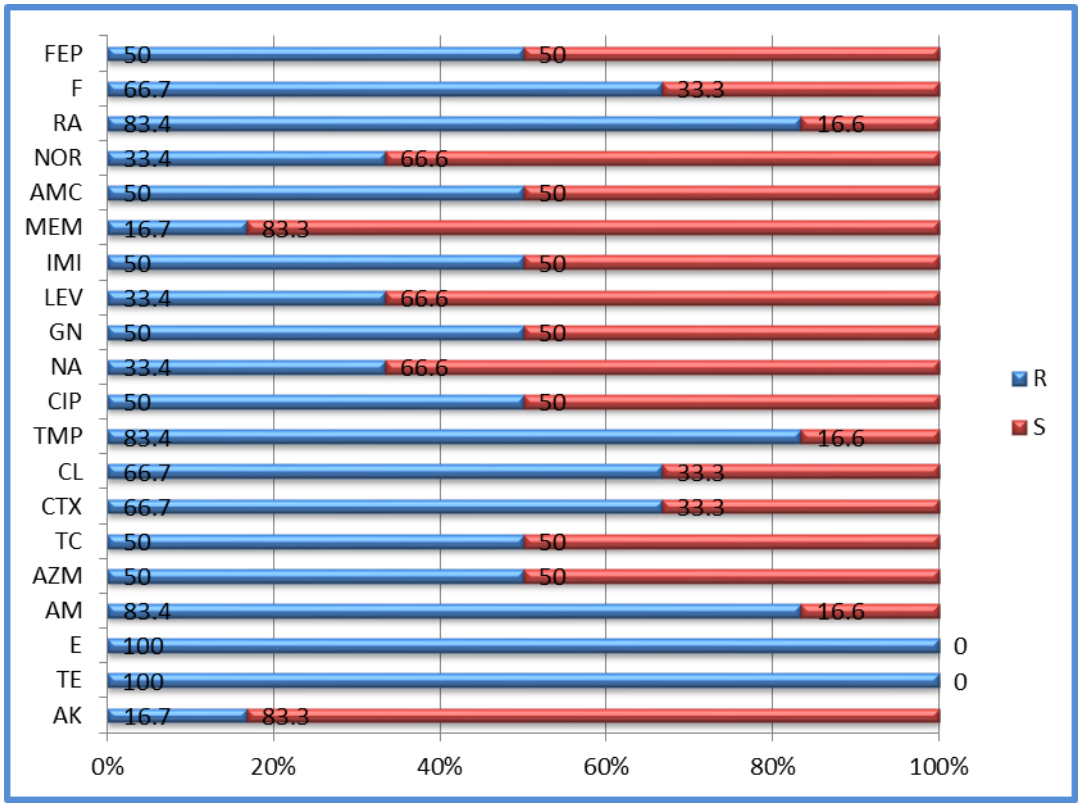
Figure (4) The comprehensive phylogenetic tree of the 16S rRNA sequences from NCBI database and sequences from the tested samples



S= Sensitive; R: resistant

Figure (5) Shows the susceptibility of *P.mirabilis* to several antibiotics

P. vulgaris isolates resisted erythromycin and tetracycline (100%), followed by trimethoprim, ampicillin, and rifampin (83.4%). In addition, 66.7% were resistant to cephalexin, nitrofurantoin, and cefotaxime. Figure (6) shows that *Proteus vulgaris* was susceptible to meropenem and amikacin (83.3%), nalidixic acid, levofloxacin, and norfloxacin (66.6%). The study revealed that the overall percentage of antibiotic resistance in our study was 40% (8/20) based on AST results for human and chicken isolates, in compression the overall sensitivity was 25% (5/20).



S= Sensitive; R: resistant

Figure (6) Shows the susceptibility of *P.vulgaris* to several antibiotics

These results showed variation in the serotypes of *proteus* may attributed to the source of isolation and the location of the sampling. Also, mutation and horizontal gene transfer like conjugation or transformation led to new serotypes. This variation may be due to the source of isolation and the location of the sampling. Additionally, it may arise from mutation and horizontal gene transfer, such as conjugation or transformation, which can lead to new serotypes. Dalia, (33) indicated that the serological variation may be due to the location of sampling, the timing of sample collection, geographic climate, age, immunity of humans or chickens, drug consumption, and hygienic restrictions, which may be linked to the relative differences in results between different places, while Sanches *et al.*, (34) pointed out the significant incidence of *proteus spp*. could be attributed to poor hygiene practices during slaughter, scalding, de-feathering, evisceration, and carcass cutting. These processes enable the cross-contamination of healthy, clean birds with diseased or infected corpses, and eventually with humans. Inadequate veterinary control may also result in the slaughter of sick birds and the spread of illnesses. Contamination of fresh chicken meat with different food pathogens may occur due to many improper hygiene and personal faults that occurred during different slaughtering, storage, transportation, and handling processes, such as contaminated water, gastrointestinal contamination, air, dust, sewage, and food or on food equipment, environmental surfaces (35).

Animals are a key source of this pathogen's transmission to humans because contamination of chicken carcasses with intestinal flora is widespread when the carcasses are placed in a chiller for washing and

cooling in the slaughterhouse (36). The results of this study agreed with Amani (37), who reported that the percentage of *P. mirabilis* isolation was higher than that of *P. vulgaris*, which was (20%, and 11.0%) respectively. The results were also consistent with Alsherees *et al.* (38), who reported that *P.mirabilis* had the highest percentage, reaching 78.6%, and with Feglo *et al*., (39), who reported that the percentage of *P. mirabilis* isolation was (61.5%) while *Proteus vulgaris* was (30.5%). The results of AST for chicken meat and human samples in this study agreed with (40). It was shown that 67.7% and 58% of the isolates were resistant to cefepime and cefotaxime, respectively. Also, agreed with Huda and Sanaa, (41). Who found cefepime resistance was 83.3%. multiple generations of antibiotics, such as third or fourth-generation cephalosporins, are primarily responsible for the emergence and spread of multidrug resistance in gram-negative bacteria, which can lead to infections that cause morbidity and mortality. Careful handling of these antibiotics may be able to prevent or reduce the establishment or spread of multidrug-resistant Gram-negative bacteria (42).

P. mirabilis and *P. vulgaris* showed resistance to ampicillin at the rate of 83.4%. This finding is consistent with Serry *et al* (43), who reported a resistance rate of 85.1%. Regarding Amoxicillin and clavulanic acid, the results indicated most *P. mirabilis* and *P. vulgaris* isolates were resistant at 66.7% and 50%, respectively. Similar findings were reported by Huda and Sanaa (41) and Roshna *et al*., (44) , with rates of 69% and 65.62%, respectively. The cause of resistance can be traced back to *P. mirabilis* capacity to produce broad-spectrum beta-lactase enzymes (ESβLs), which encode a chromosomal or plasmid if it analyzes penicillins and sporins. This ability has led to multiple antibiotic resistance or altered target sites and decreased outer wall permeability (45). Moreover, it can be because of the flow mechanisms that drive the antagonists within the cell outside (46). The emergence of multidrug resistance strains that are resistant to many of the antimicrobial agents tested may be due to ampicillin, amoxicillin, and cephalothin being considered the most commonly prescribed antibiotics in hospitals, as well as the most easily available in the market without a prescription, and were also very inexpensive. The widespread usage and more frequently antimicrobial medications led to a general rise in the formation of resistant bacteria (47). This antibiotic's high resistance rate is attributable to its widespread usage, particularly in children, for treating tonsil and middle ear infections, as well as general respiratory infections (48). What makes the situation worse is the administration of antibiotics without expert medical, as well as not completing the appropriate treatment courses and discontinuing taking antibiotics when the patient's first indications of improvement occur (49).

The relatively high sensitivity to imipenem may be attributable to the drug's rare use this antimicrobial agent's exposure is limited due to its high cost, low tolerability, and scarcity. As a result, to reduce the possibility of germs developing resistance, this medicine should be used carefully and prudently (50). Gram-negative bacteria develop resistance to aminoglycosides such as amikacin and gentamicin through mechanisms that are altered in the target site (30S) of the ribosome, where a mutation occurs; additionally, the mutation may result in a decrease in the permeability of antibiotic molecules across membrane (51,52). Alternatively, active flow systems or modifying the permeability of the outer wall modify the antibiotic's molecular structure, resulting in a loss of effectiveness (53). The high resistance of *P.mirabilis* isolates to Ciprofloxacin may be due to a genetic mutation that causes a change in the target site, preventing the antibiotic from attaching to it, or it may be due to an increase in flow systems (54). Resistance to Ciprofloxacin may be caused by one of three methods of quinolone resistance: mutations that alter drug targets, mutations that lower drug accumulation, and plasmid-mediated genes that protect cells from quinolone lethal. These genes are typically discovered in Enterobacteriaceae and alter the dynamics of the development and acquisition of quinolone resistance (55,56).

P.mirabilis and *P.vulgaris* had 33.4% resistance to both antibiotics Norofloxacin and Levofloxacin. The resistance of both species may be attributed to genetic mutations, extracellular drug delivery, or horizontal gene transfer. The last reason is the most dangerous, as it enables bacteria to acquire new traits, including antibiotic resistance genes, either through direct cell-to-cell contact via a conjugation pilus, transfer of plasmids (small circular DNA), transposable elements carrying resistance genes (57), or transfer of beta-lactamase enzymes (e.g., ESBLs) transformation, and gene conversion, making antibiotic-

resistant bacteria a major challenge in modern medicine (58). The current study found Tetracycline resistance of 83.4% from *P. mirabilis* and 100% of *P. vulgaris*. Furthermore, the current results show that 83.4% of the *P. mirabilis* isolates are resistant to Nitrofurantion. These findings are consistent with those of Sayal *et al*., (59) and Hussein *et al*., (60) who observed resistance rates of 90% and 80%, respectively. At the same time, 66.7% of the isolates of *P. vulgaris* were resistant to Nitrofurantoin. Several causes are responsible for the rise in antimicrobial resistance rates, including the overuse and misuse of antibiotics by the general public and healthcare professionals (61). According to Wellington *et al*., (62), insufficient surveillance systems and reliance on unreliable microbiological methods also led to the incorrect prescription of antibiotics. However, overuse of antibiotics poses a serious risk as it leads to the establishment and spread of multidrug-resistant strains of both pathogenic and non-pathogenic organisms, which can be spread to people through the food chain. The main reason for concern is the sudden increase in resistance formation and transmission. Testing isolated microorganisms for antibiotic resistance has thus become a global interest for effective treatment and control measures (63). Furthermore, the results showed that the inappropriate and indiscriminate administration of these antibiotics, which increases the incidence of *Proteus* infection, increases the resistance of *P. mirabilis* and *P.vulgaris* to certain antibiotics over time. This may be due to the bacteria finding new ways to resist, such as producing β-lactamases or transferring genetic elements containing the genes for these enzymes. Several mutations in the genes responsible for these enzymes have increased their resistance to antibiotics, especially extended-spectrum β-lactamases (ESBLs). This may be due to other mechanisms, such as changing the target site or altering access to the target site by changing antibiotic-binding proteins (64,65).

In conclusion, this study discovered the presence of *Proteus spp*. genetic alterations, which resulted in changes in the bacteria's molecular characteristics and antibiotic resistance. It also revealed commonalities between NCBI sequences identified in Iraq and other countries. These similarities could be caused by the importation of goods such as chicken meat, which may include proteus bacteria serovars, or by the entry of sick or infected persons, notably foreign workers and military personnel. This could result in the spread of these bacterial strains from other countries to Iraq.

التوصيف الجزيئي وتنوع مقاومة مضادات الميكروبات لبكتريا *Proteus* المعزولة من مصادر متعددة

صفا جبار مظهر باحث شتاق طالب عبدالواحد أستاذ مساعد

فرع الصحة العامة- كلية الطب البيطري- جامعة بغداد

المستخلص

تعد عدوى *Proteus* من أكثر مسببات الأمراض المنقولة عن طريق الغذاء شيوعًا والمسؤولة عن العدوى الحيوانية المنشأ والتسمم الغذائي لدى البشر. تم جمع 320 عينة لعزل وتوصيف Proteus spp. بين مارس وسبتمبر 2023، شملت 200 عينة لحم دجاج من الأسواق المحلية و120 عينة بول بشري من مستشفيات محافظة واسط، العراق. استُخدمت الأوساط الزرعية الانتقائية واختبارات PCR و Vitek 2 لتحديد الأنواع البكتيرية، إضافةً إلى اختبار AST باستخدام 20 مضادًا حيويًا. كشفت النتائج عن انتشار وعزل نوعين هما *P.mirabilis* بنسبة 25٪ من العينات البشرية و13٪ من لحم الدجاج والثانية *P.vulgaris* بنسبة 6.6% من البشر و4% من لحم الدجاج. ووفقًا لنتائج تحليل AST، اظهرت عزلات *P. mirabilis* مقاومة عالية للمضادات الحيوية الأكثر شيوعًا حيث تراوحت بين 83.3%-100% لمجموعة الماكروليدات (أزيثروميسين، إريثروميسين) و66.7%-83.4% للبنسلين(أمبيسيلين، أموكسيسيلين-حمض الكلافولانيك) ، مع 66.7% مقاومة للسيفالوسبورينات (سيفالكسين، سيفيبيم، سيفوتاكسيم) . في المقابل، أبدت عزلات *P. vulgaris* مقاومة بنسبة 100% للإريثروميسين والتتراسيكلين، وبنسبة 83.4% للتريميثوبريم، والأمبيسلين، والريفامبين. بالإضافة إلى ذلك، أظهرت مقاومةً للسيفاليكسين بنسبة 66.7% ، والنيتروفورانتوين، والسيفوتاكسيم، نستنتج من ذلك أن المقاومة الإجمالية للمضادات الحيوية بلغت 40% ويعزى ذلك إلى حدوث طفرات وراثية في عدة مواقع من جين 16 S rRNA مما يؤكد الحاجة إلى مراقبة انتشار هذه الأنواع المقاومة واتخاذ تدابير للحد منها.

الكلمات المفتاحية: الأمراض المنقولة بالغذاء، *P. mirabilis*، *P. vulgaris*، المضادات الحيوية.

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