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Prevalence of *blaSHV*, *blaNDM* beta-lactamase genes using multiplex PCR in clinical isolates of *Proteus mirabilis*

Najaat Ahmed Mohammed[1], Saba J. Jawad Al-Zubaidi[2]

ORCID: https://orcid.org/0000-0003-2610-189X

[1,2]College of Education for Pure Science, University of Diyala

Corresponding Email: Pbio.najatahmed@uodiyala.edu.iq[1]

saba.jasim@uodiyala.edu.iq[2]

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Abstract:

Background:

Proteus mirabilis is a Gram-negative bacterium belonging to the family Enterobacteriaceae that cause numerous diseases, including pyelonephritis, urinary stones, prostatitis, catheter-associated urinary tract infections, and diarrhea in humans. A total of 180 collected samples from different clinical sites (urine, discharge, otitis media, wounds, and vaginitis) during September 2024 to December 2024 from Baquba Teaching Hospital and Al-Batoul Maternity and Children's Hospital in Diyala Governorate/Iraq.

Aims:

This study aimed to detect *P. mirabilis* with multi drug resistance by morphological and biochemical methods and to determine some virulence factors by phenotype methods as well as detecting of genes encoding antibiotic resistance including (*blaNDM* and *blaSHV*) through multiplex PCR, in clinical samples.

Results:

Results revealed that 20 (18.18%) isolates of *P. mirabilis* were obtained. The incidence rate of isolation in females was higher than in males, 12 (60%) and 8 (40%) respectively. In this study, a higher rate of positive isolation was recorded in urine samples (65%). Also, 45% of isolates were extended spectrum beta-lactamase (ESβL) producers and 30% were Metallo beta-lactamase (MβL) producers. The most effective antimicrobial agents against all isolates are meropenem followed by Amikacin. Resistant of *P. mirabilis* for many antibiotics, especially Trimethoprim and ampicillin. Molecular detection of beta lactamase genes revealed that only 6 (30%) had *blaSHV* gene while *blaNDM* only in 7 (35%) of isolates.

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Conclusion:

P. mirabilis was resistance for many antibiotics, especially Trimethoprim and ampicillin and meropenem was the most effective followed by Amikacin. All isolates showed different rates of ESβL and MβL production and this reflect different rates of resistance genes expression such as *blaNDM* and *blaSHV.*

Keywords: *P. mirabilis*, ESßL, Metallo-ßL, *blaSHV, blaNDM,* multiplex PCR

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Introduction:

Proteus mirabilis is a major causative agent of several diseases such as pyelonephritis, urinary tract stones, prostatitis, catheter-associated urinary tract infections, and diarrhea in humans (Armbruster & Mobley, 2012). *P. mirabilis* is a medically significant organism that typically causes the majority of common nosocomial opportunistic infections, including infections of the urinary system, wounds, ears, and other area. It is listed as a medically significant nosocomial agent due to several virulence characteristics, including genes that resist antibiotics. Several nosocomial infection outbreaks and community-acquired diseases have been linked to this bacterium in various regions of the world (Alabi *et al*., 2017).

In some situations, the ESBL enzyme may be responsible for a relatively high prevalence of multidrug-resistant (MDR) strains of *P. mirabilis*. MDR may also result from genetic alterations in resistance genes or horizontal migration of resistance genes (Sfaciotte *et al.,* 2021). Misuse or non-specific use of antibiotics has led to increased levels of drug resistance and widespread distribution of different resistance genes among clinical *P. mirabilis* isolates. In addition, *P. mirabilis* has intrinsic resistance to tetracycline, tigecycline, and polymyxin (Sanches *et al*., 2023). Because of the existence of multi-resistant genes, isolates of *P. mirabilis* that produce ESBL are frequently found to be MDR. These genes allow *P. mirabilis* to endure a variety of antibiotics, including beta-lactams (Firmo *et al*., 2020).

The gene encoding New Delhi metallo-beta-lactamase-1 (*blaNDM*-1), which leads to resistance to most beta-lactam antibiotics, was identified as early as 2006, and its occurrence was initially confined to the Indian subcontinent (Yong *et al*., 2009). *blaSHV*-1 encoded enzyme (sulfhydryl variable reagent) has been shown to be active against penicillins and first-generation cephalosporins and was confirmed as part of the conjugative plasmid p453 (Liakopoulos *et al*., 2016). Allelic

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variants of this gene have recently been described, which have developed resistance to third-generation cephalosporins, monobactams and carbapenems (Poirel *et al*., 2003).

This study aims to analyze and identify gene sequences encoding antibiotic resistance, specifically *blaNDM* and *blaSHV*, using multiplex PCR. These resistance genes are concomitant with mobile genetic elements and play a crucial role in the multidrug resistance of *P. mirabilis* in clinical specimens.

Materials and Methods

Collection of samples

Samples were collected under the supervision of a specialist physician and included (180) specimens from different clinical sources including (urine, stool, otitis media, wounds, and vaginitis) from both males and females in different ages during the period from September 2024 to December 2024 at Baquba Teaching Hospital and Al-Batoul Maternity and Children's Hospital in Diyala Governorate/Iraq.

Identification of bacterial isolates

The collected specimens were streaked on McConkey media, blood agar media, and nutrient agar media, after ensuring that the patient had not taken antibiotics for at least three days for isolation and initial diagnosis. *P. mirabilis* isolates were diagnosed according to morphological features on culture media, microscopic examination (Gram's stain) and biochemical tests (Indole, Oxidase, Catalase, Urease). The diagnosis was confirmed by using VITEK2 System (Pincus, 2011).

Antibiotic susceptibility test (AST)

Antibiotic susceptibility testing of each isolate was tested against 11 antibiotics (Amikacin, Azithromycin, Ampicillin, Ceftriaxone, Ciprofloxacin, Levofloxacin, Meropenem, Gentamicin, Cefixime, Augmentin, Trimethoprim) according to Clinical and Laboratory Standards Institute (CLSI 2023) recommendations, using Kirby-Bauer disc diffusion method on Mueller-Hinton agar (MHA) and the inhibitory zones' diameters were noted.

Extended spectrum Beta lactamase production

ESβL production in *P. mirabilis* was determined by double disc synergy test (DDST) according to Patel et al. (2017).

Metallo beta lactamase production

This test was detected according to Anoar et al. (2014).

Genotypic detection of beta-lactamase genes

Twenty *P. mirabilis* isolates were subjected for amplification of two of beta-lactamase genes (*blaNDM* and *blaSHV*). Genomic DNA was extracted according manufactured company directions using a bacterial genomic DNA extraction kit (Promega/USA). The presence of *blaNDM* and *blaSHV*

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genes were screened for by PCR amplification. Primers was confirmed using the NCBI website. Primers, PCR components and program demonstrated in tables (1), (2) and (3)

Table 1: Primers used in the study

Genes	base pair sequences (5′–3′)	Product size/ bp	References
blaNDM	F: TGGCAGCACACTTCCTATC R: AGATTGCCGAGCGACTTG	488	Nasri *et al.*, 2017
blaSHV	F-AGCCGCTTGAGCAAATTAAAC R-ATCCCGCAGATAAATCACCAC	713	Hammond *et al*, 2005

Table 2: The size of the PCR mix components for amplifying genes in this study.

Name of target gene	Type of reaction	Master mix	F primer 10 pmol	R primer 10 pmol	Volume of template	Nuclease Free Water	Final volume
blaNDM	**Multiplex PCR**	**12.5 µl**	**1 µl**	**1 µl**	**5 µl**	**5.5 µl**	**25 µl**
blaSHV		**12.5 µl**	**1 µl**	**1 µl**	**5 µl**	**5.5 µl**	**25 µl**

Table 3: PCR program

Amplified gene		Primary denaturation	cycles	Denaturation	Annealing	Elongation	Final elongation
Multiplex	*SHV*	**95°C/ 3min**	**35**	**95°C/ 60sec**	**58°C/60 sec**	**72°C/40 sec**	**72°C/2min**
	NDM	**95°C/ 3min**	**35**	**95°C/ 60 sec**	**58°C/60 sec**	**72°C/40 sec**	**72°C/2min**

Results and discussion

Isolation and identification of *P. mirabilis*

Twenty isolates (18.18%) of *P. mirabilis* were identified, while other bacterial species accounted for 90 isolates (81.82%), as shown in Table (4). These findings align with several international studies, which have reported the prevalence of this bacterium to range between 5-18% among positive bacterial growth cases in clinical samples (Chakkour *et al*., 2024). However, the results of the current study disagree with those of Al-Dulaimi (2019) in Diyala, Al-Obeidi (2021) in Diyala, and Hafiz et al. (2024) in Riyadh, where the isolation rates of *P. mirabilis* were 88.88%, 8.3%, and 74.14%, respectively.

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Table (4): Isolation types and percentage

Positive growth	*P. mirabilis*	Other types of bacteria
110	20	90
100%	18.18%	81.82%

P. mirabilis isolates distribution in clinical specimens

The percentage of *P. mirabilis* among clinical samples was variable. The results showed that the highest percentage was from urine samples 13 (65%), followed by stool samples 5 (25%), and one isolation for each of otitis media and vaginitis 1 (5%) respectively, while there was no isolation from wounds as shown in Table (5).

Table (5): Distribution of isolates in clinical samples

Samples type	No. of specimens	No. of isolates
Urine	90 (50%)	13 (65%)
Stool	50 (27.78%)	5 (25%)
Otitis	15 (8.33%)	1 (5%)
Vaginal	10 (5.65%)	1 (5%)
Wounds	15 (8.33%)	0 (0%)
Total	180 (100%)	20 (100%)

In this study, a higher rate of positive isolates was recorded in urine samples, this may due to the high number of urine specimens collected than other sources. Similar finding was reported by Hafiz *et al*. (2024), who demonstrated that urine had the highest incidence of *P. mirabilis* among other clinical sources.

This is usually associated with the possession of several virulence factors that are important for causing UTIs, and these virulence factors include adhesion ability, urease production, and flagella (Filipiak *et al*., 2020).

Studies have confirmed the high percentage of proteobacteria in urine due to their natural presence in the intestinal tract, and when they move to the urethra, they lead to urinary tract infections. The presence of a urinary catheter is also an important factor in the ascent of microorganisms to the bladder due to the contact of the outer surface of the catheter tube with the urethral wall or the skin surrounding the urinary opening (Al-Dulaimi, 2019).

The current results showed that the percentage of *P. mirabilis* bacteria isolation from females 12 (60%) is higher compared to males 8 (40%) Table (6). The current study recorded the highest infection with *P. mirabilis* bacteria in females compared to males. This finding is agreed with AL-Ezzy *et al.* (2023) result, as the infection in females was higher than males by 58.3% and 41.7%,

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respectively, while it disagree with Hassan (2008) study on *P. mirabilis* bacteria in the city of Nasiriyah, as he showed that the infection in males was higher than in females by 59% and 41% respectively.

Females are more infected than males with urinary tract infections due to physiological, anatomical, hormonal and immunological differences (Mestrovic *et al.*, 2021).

Table (6): Relations between isolation and gender

Genders	No. of isolates	Percentage %
Females	12	60%
Males	8	40%
Total	20	100%

Antibiotic susceptibility test (AST)

Kirby-Bauer disk method was used to test the sensitivity of all 20 isolates under study against 11 antibiotics from different groups, most of which are used to treat multiple infections. The diameter of the inhibitory zone surrounding the disks was measured to record the results, which were then compared using AL-Ezzy *et al.* (2024). Table (7) shows the numbers and percentages of sensitive and resistant isolates toward antibiotics.

Table (7): Numbers and percentages of sensitive and resistant isolates

Antibiotic	No. of isolates (%)		
	Sensitive	Intermediate	Resistant
Cefixime	8(%20)	0 (%0)	12 (60%)
Ciprofloxacin	13(%65)	0 (%0)	7(%35)
Trimethoprim	1 (%5)	0 (%0)	19(%95)
Ceftriaxone	6(%30)	0 (%0)	14(%70)
Gentamicin	13(%65)	0 (%0)	7(%35)
Azithromycin	7(%35)	0 (%0)	13(%65)
Amoxicillin-Clavulanic acid	4(%20)	0 (%0)	16(%80)
Levofloxacin	19(%95)	0 (%0)	1 (%5)
Meropenem	20(%100)	0 (%0)	0 (%0)
Amikacin	19(%95)	0 (%0)	1 (%5)
Ampicillin	3(%15)	0 (%0)	17(%85)

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The results showed resistance to cephalosporin antibiotics, as the resistance rate of the isolates to Cefixime reached 60% and Ceftriaxone 70%. This result was disagreed from Shabeeb and Alghanimi (2018) in Karbala, as their isolates were resistant to the antibiotic at a rate of 47.3%.

The isolates under study showed low resistance to aminoglycosides antibiotics, which include Amikacin and Gentamicin, as the resistance rate reached 5% and 35%, respectively. This result is reliable with Singla et al. (2015) finding, as the isolates showed low resistance to Amikacin antibiotic 11.4%. As for Gentamicin, this result was nearly to AL-Oqaili et al. (2017), as the isolates resistance was 54.68%.

By altering the ribosome's target site (S30), where a mutation takes place, gram-negative bacteria become resistant to aminoglycosides like amikacin and gentamicin. This results in a reduction in the antibiotic molecules' ability to pass through the membrane (Liu et al., 2023).

The resistance of the isolates to quinolones, namely ciprofloxacin and levofloxacin, was 5% and 35%, respectively. The results disagree with a previous local study by Ramatla et al. (2024), that the resistance rate to ciprofloxacin was (61.5%). The resistance rate of the isolates to Azithromycin was 65%, which is close to what Al-Obeidi (2021) found, as the resistance rate was 76%.

Meropenem was the most effective and sensitive drug against *P. mirabilis* isolates in the present study, the resistance rate of isolates to Meropenem was (0%) and the sensitivity was (100%). This result was close to Mirzaei et al. (2019) who documented that *P. mirabilis* resistance was 4.5%. The results showed that the resistance of bacteria to Ampicillin was 85%. In other study, it was recorded at 75% (Attalah *et al.*, 2020).

As for the Augmentin antibiotic, the resistance rate of the isolates under study reached 80%, Perween et al. (2016) recorded a resistance rate of 94.3% that differ from this study. The origin of resistance is due to the ability of bacteria to produce beta-lactamase enzymes such as ESβLs, which are plasmid or chromosome encoded genes, as they degrade penicillins and cephalosporins, resulting in antibiotics multi-resistance, or due to the target site modification and outer wall waste reduction (Guilfoile, 2007).

Trimethoprim showed 95% resistance; this result differed from Al-Dulaimi (2019) result which the resistance ratio for the same antibiotic was 75.7%. The reason for this resistance is due to reducing the concentration of the antibiotic inside the bacterial cell or producing a type of enzyme known as Dihydrofolate reductase, which is encoded by genes carried on the plasmid (Eliopoulos and Huovinen, 2001)

It is clear from the above that *P. mirabilis* isolates are resistant to most of the widely used antibiotics. This may be due to the bacteria adapting to the hospital environment and the continuous use of antibiotics, which allows mutations to occur in the genetic material. It has been shown that treatment with normal concentrations of antibiotics kills the bacteria present in the environment, while the bacteria inside the polysaccharide matrix remain vital and resist antibiotics, as they act as a focus for repeated infections (Ehrlich *et al.*, 2002).

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Virulence factors of *P. mirabilis*

ESβL and Metallo β-lactamase production

Double disk synergy (DDC) technique was used to test the synthesis of extended-spectrum beta-lactam enzymes, which is one of the simplest and most precise techniques. The results showed that 9 (45%) of *P. mirabilis* isolates produced these enzymes, Figure (1). Similar results were reported by Shabaan et al. (2022) that *P. mirabilis* isolates produced ESBL (51.7%). While results showed that 6 (30%) of the isolates under study were producers of the metallo-beta-lactamase enzyme.

Infections due to ESβL-producing isolates represent a critical global issue, leading to substantial rises in morbidity and death rates among hospitalized individuals. Moreover, ESβL producers exhibit cross-resistance to many other classes of antibiotics such as quinolones, aminoglycosides, and sulfa drugs (Malaki *et al*., 2022).

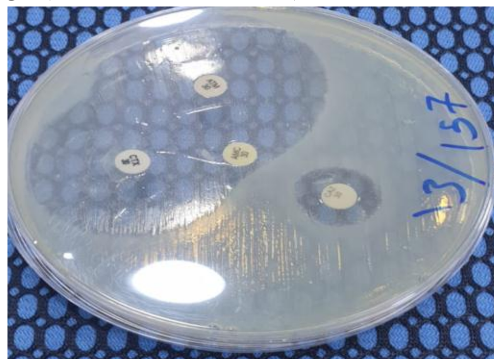

Figure 1: ß-lactamase production on Mueller-Hinton medium.

DNA extraction and purification

Twenty *P.mirabilis* isolates were subjected to amplification of virulence genes (*blaNDM* and *blaSHV gene*) based on their possession of the most potent virulence factors. Accordingly, genomic DNA was extracted using an extraction kit (Alpha DNA, USA). The concentrations and purity of DNA were measured by Nano Spectrometry. All samples had DNA concentrations ranging from (62.1-12.5) ng/µl, while the purity ranged from (1.8-1.98). DNA from six isolates was exposed to 1.5% agarose gel electrophoresis to approve the integrity of DNA. The results revealed a unique discrete band indicating successful isolation of pure DNA.

Detection of *blaNDM* and *blaSHV* gene

The results of the current study showed that 6 (30%) of the isolates had *blaSHV*, while showed that 7 (35%) of the isolates contained *blaNDM*, Figure 2.

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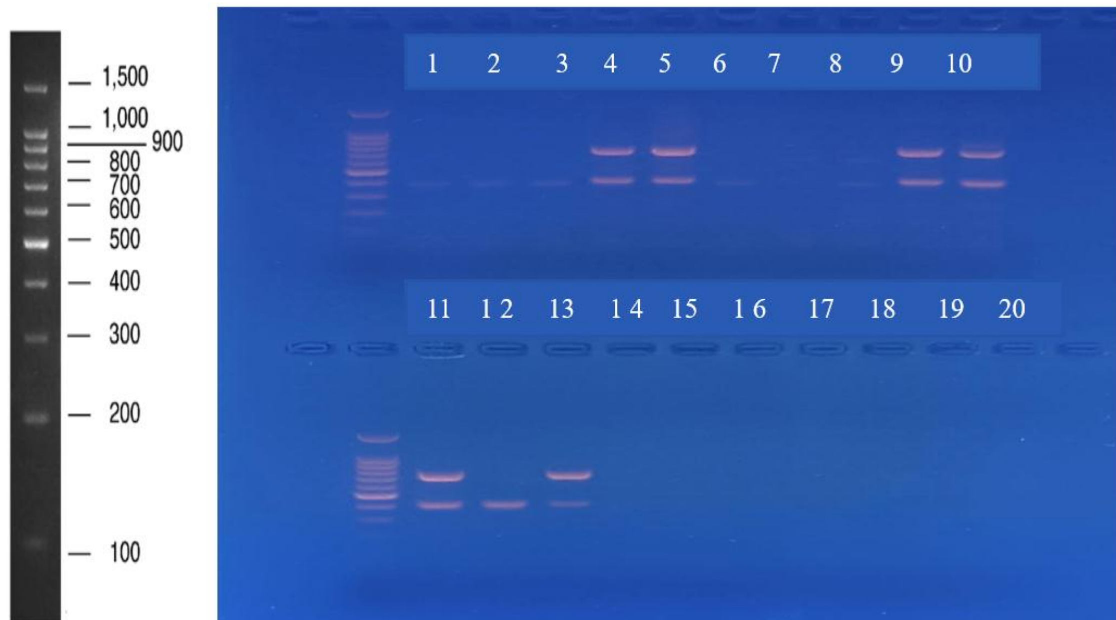

Figure (2): Agarose gel electrophoresis (1.5% agarose, 7 V/cm2 for 60 min) for A: SHV gene (amplicon 713 bp), B: NDM gene (amplicon 488 bp); size ladder 100 bp.

P. mirabilis is infamous for its capacity to aggressively spread genes of antibiotics resistance across horizontally gene transferring, and the multi-resistant isolates, comprising some carrying *blaNDM*, have caused nosocomial infections in several counties (Yang *et al*., 2022).

Over the past several years, a number of excellent publications have been published that describe the biology, genetics, and evolution of SHV β-lactamases. In addition to describing the prevalence of plasmid-associated SHV enzymes in Enterobacteriaceae and their epidemiological implications.

However, SHV enzymes did not experience the rapid spread seen in CTX-M-type variations (Canton *et al*., 2012), With increasing allele variety, they have lately been discovered in several environmental niches and in a number of Enterobacteriaceae other than the usual clinical hosts, *Klebsiella pneumoniae* and *Escherichia coli* (http://www.lahey.org/studies).

Multiplex PCR allows the simultaneous detection of several bacterial genes in a single tube by combining several primer pairs for various target sequences. Reagents and time are both saved by this method. This is a very sensitive and unique detection technique for identifying and detecting many bacterial diseases, including Enterobacteriaceae species, is multiplex PCR (Zhang et al., 2019).

Conclusions

Study revealed *P. mirabilis* resistance for many antibiotics, especially Trimethoprim and ampicillin. The most effective antibiotic against all isolates was meropenem followed by Amikacin. All isolates showed different rates of ESβL and MβL production. *P. mirabilis* isolates express different rates of resistance genes such as *blaNDM* and *blaSHV.*

P. mirabilis pathogenicity has evolved through several virulence factors that have been genetically investigated. It was found that detecting *P. mirabilis* using modern molecular methods

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represented by multiplex polymerase chain reaction (PCR) technique is much better than traditional methods due to its high sensitivity, speed, and low cost, and its result does not depend on the opinion of the person working, and it can also deal with a large number of samples at one time.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this article. The research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Authors contribution

All authors reviewed and approved the final version of the manuscript and agree to be accountable for its contents.

References

Alabi, O. S., Mendonça, N., Adeleke, O. E., & da Silva, G. J. (2017). Molecular screening of antibiotic-resistant determinants among multidrug-resistant clinical isolates of *Proteus mirabilis* from SouthWest Nigeria. *African health sciences*, *17*(2), 356-365. DOI:10.4314/ahs.v17i2.9

AL-Ezzy AIA, Areean Ibrahim Hassan Beg (2024). Phenotypic, Biochemical Identification And Antibiotic Sensitivity Pattern Of Staphylococcus Species From Urinary Tract Infections Among Female Sheep Breeders And Ewes With Special Emphasis To Methicillin And Vancomycin Resistant Staphylococcus aureus Diyala Journal for Veterinary sciences;2(1):49-57.DOI: https://doi.org/10.71375/djvs.2024.02101

AL-Ezzy AIA, Alazzawi SA, Algburi A. (2023 Multidrug Resistant Behavior Of P Mirabilis Isolated From patients Urinary Tract Infections Diyala Journal for Veterinary sci-ences;1(3):23-37. DOI: https://doi.org/10.71375/djvs.2023.01101.

AL-Dulaimi, M.TH. S. (2019). Detection of Some Virulence Genes of *Proteus mirabilis* Isolated from Different Infectious in Baquba City. MSc. Thesis, College of Science- University of Diyala.

Al-Obeidi, D. N.; Nassif, Z. M. & Mozher, A. M. (2021). MOLECULAR DETECTION OF ZAPA GENE IN *PROTEUS MIRABILIS* ASSOCIATED WITH URINARY TRACT INFECTIONS. Biochem. & Cell. Arch., 21(2). DOI: https://connectjournals.com/03896.2021.21.3865

Al-Oqaili, N. A. D.; Al-Shebli, M. K. & Almousawi, A. (2017). Antimicrobial susceptibility and molecular characterization for some virulence factors of *Proteus Mirabilis* isolated from

DJVS
Diyala Journal for Veterinary Sciences
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patients in AlQadisiyah Province/Iraq. Al-Qadisiyah J. Vet. Med. Sci., 16(2), 1-9. DOI:10.29079/vol16iss2art435

Anoar, K. A., Ali, F. A., & Omer, S. A. (2014). Detection of metallo [beta]-lactamase enzyme in some gram negative bacteria isolated from burn patients in sulaimani city, Iraq. *European Scientific Journal*, *10*(3). **DOI:** https://doi.org/10.19044/esj.2014.v10n3p%25p

Armbruster, C. E., & Mobley, H. L. (2012). Merging mythology and morphology: the multifaceted lifestyle of *Proteus mirabilis*. *Nature Reviews Microbiology*, *10*(11), 743-754. DOI: 10.1038/nrmicro2890

Chakkour, M., Hammoud, Z., Farhat, S., El Roz, A., Ezzeddine, Z., & Ghssein, G. (2024). Overview of *Proteus mirabilis* pathogenicity and virulence. Insights into the role of metals. *Frontiers in Microbiology*, *15*, 1383618. https://doi.org/10.3389/fmicb.2024.1383618

CLSI (2023). "Performance Standards for Antimicrobial Susceptibility Testing," in CLSI supplement M100, 33th ed (Wayne, PA, USA: Clinical and Laboratory Standards Institute).

Ehrlich, G. D.; Veeh, R.; Wang, X.; Costerton, J. W.; Hayes, J. D.; Hu, F. Z.; Daigle, B. J.; Ehrlich, M. D. and Post , J. C. (2002). Mucosal biofilm formation on middle-ear mucosa in the chinchilla model of otitis media. JAMA. 287(13):1710-1715.
DOI: 10.1001/jama.287.13.1710

Eliopoulos, G. M. and Huovinen, P.(2001). Resistance to Trimethprim-Sulfamethoxazole. Clincal Infection Disease. 32(11) :1608-1614. DOI: 10.1086/320532

Filipiak, A.; Chrapek, M.; Literacka, E.; Wawszczak, M.; Głuszek, S.; Majchrzak, M. ... & Adamus-Białek, W. (2020). Pathogenic factors correlate with antimicrobial resistance among clinical *Proteus mirabilis* strains. Front. Microbiol., 11, 579389. DOI: 10.3389/fmicb.2020.579389

Firmo, E. F., Beltrão, E. M. B., da Silva, F. R. F., Alves, L. C., Brayner, F. A., Veras, D. L., & Lopes, A. C. S. (2020). Association of blaNDM-1 with blaKPC-2 and aminoglycoside-modifying enzyme genes among Klebsiella pneumoniae, *Proteus mirabilis* and Serratia marcescens clinical isolates in Brazil. *Journal of Global Antimicrobial Resistance*, *21*, 255-261.
DOI: 10.1016/j.jgar.2019.08.026

Guilfoile, G. (2007). Deadly disease and epidemics Antibiotic Resistant Bacteria. Chelser House publisher, World Health organization. 10 -119.

Hafiz, T. A.; Alghamdi, G. S.; Alkudmani, Z. S.; Alyami, A. S.; AlMazyed, A.; Alhumaidan, O. S., ... & Alotaibi, F. E. (2024). Multidrug resistant *Proteus mirabilis* infections and clinical outcome at tertiary hospital in Riyadh, Saudi Arabia. Inf. Drug Res., 571-581. DOI: 10.2147/IDR.S448335

Hammond, D. S., Schooneveldt, J. M., Nimmo, G. R., Huygens, F., & Giffard, P. M. (2005). bla(SHV) Genes in *Klebsiella pneumoniae*: different allele distributions are associated with different promoters within individual isolates. *Antimicrobial agents and chemotherapy*, *49*(1), 256–263. doi: 10.1128/AAC.00359-07

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Liakopoulos, A., Mevius, D., & Ceccarelli, D. (2016). A review of SHV extended-spectrum β-lactamases: neglected yet ubiquitous. *Frontiers in microbiology*, *7*, 1374. https://doi.org/10.3389/fmicb.2016.01374

Liu, L.; Dong, Z.; Ai, S.; Chen, S.; Dong, M.; Li, Q.; ... & Peng, G. (2023). Virulence-related factors and antimicrobial resistance in *Proteus mirabilis* isolated from domestic and stray dogs. Front. Microbiol., 14, 1141418. https://doi.org/10.3389/fmicb.2023.1141418

Mestrovic, T.; Matijasic, M.; Peric, M.; Paljetak, H.C.; Baresic A, and Verbanac, D. (2021). The role of gut, vaginal, and urinary Microbiome in urinary tract infections: From Bench to Bedside. Diagnostics, 11, 7-19. DOI: 10.3390/diagnostics11010007

Mirzaei A.; Habibi M.; Bouzari S.; et al. (2019). Characterization of antibiotic- susceptibility patterns, virulence factor profiles and clonal relatedness in *Proteus mirabilis* isolates from patients with urinary tract infection in Iran. Inf. Dr. Resist; 12:3967–79. DOI: 10.2147/IDR.S230303

Nasri E, Subirats J, Sanchez-Melsio A, Mansour HB, Borrego CM, Balcázar JL (2017) Abundance of carbapenemase genes (*blaKPC, blaNDM* and *blaOXA*-48) in wastewater effluents from Tunisian hospitals. Environ Pollut 229:371-4. DOI: 10.1016/j.envpol.2017.05.095

Patel, J.B., Weinstein, M., Eliopoulos, G., Jenkins, S., Lewis, J., Limbago, B., Mathers, A.J., and Mazzulli.T. (2017). M100 Performance standards for antimicrobial susceptibility testing. United State: Clinical and Laboratory Standards Institute (CLSI), p.240.

Perween, N.; Prakash, S. K. and Bharara,T.(2016). Prevalence of Multidrug-Resistant and Extensively Drug-resistant Proteus, Providencia and Morganella Species in Burn Wound Infection. International Journal of Scientific Study. Vol 3 (11) :154-156. DOI: 10.11648/j.ijidt.20210602.14

Pincus, D. H. (2011). Microbial Identification Using The Biomérieux Vitek® 2 System. BioMérieux, *Inc. Hazelwood, MO, USA*. 1: 1-32.

Poirel L, Decousser JW, Nordmann P. Insertion sequence ISEcp1B is involved in expression and mobilization of a blaCTX-M β-lactamase gene. Antimicrob Agents Chemother 2003; 47: 2938-45. doi: 10.1128/AAC.47.9.2938-2945.2003

Ramatla, T.; Ramaili, T.; Lekota, K.; Mileng, K.; Ndou, R.; Mphuthi, M.; ... & Thekisoe, O. (2024). Antibiotic resistance and virulence profiles of *Proteus mirabilis* isolated from broiler chickens at abattoir in South Africa. Vet. Med. Sci., 10(2), e1371. DOI: 10.1002/vms3.1371

Sanches, M. S.; Silva, L. C.; Silva, C. R. D.; Montini, V. H.; Oliva, B. H. D. D.; Guidone, G. H. M.; ... & Rocha, S. P. D. (2023). Prevalence of Antimicrobial Resistance and Clonal Relationship in ESBL/AmpC Producing *Proteus mirabilis* isolated from Meat products and Community-acquired urinary tract infection (UTI-CA) in Southern Brazil. Antibiotics, 12(2), 370. DOI: 10.3390/antibiotics12020370

Sfaciotte, R. A. P., Parussolo, L., Melo, F. D., Wildemann, P., Bordignon, G., Israel, N. D., ... & Ferraz, S. M. (2021). Identification and characterization of multidrug-resistant extended-spectrum beta-lactamase-producing bacteria from healthy and diseased dogs and cats

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admitted to a veterinary hospital in Brazil. *Microbial Drug Resistance*, *27*(6), 855-864. DOI: 10.1089/mdr.2020.0043

Shabeeb, B. T.; Alghanimi, Y. K.; and Ahmed, M. M. (2018). Molecular and Bacteriologic Study of â-lactam Resistance *Proteus mirabilis* associated with Urinary Tract Infection in Holy Karbala province, Iraq. Journal Research, 10(3), 549-555.

Singla, P.; Sangwan, J.; Garg, S. and Chaudhary, U. (2015). Prevalence and Antibiogram of Multidrug resistant Uropathogenic Isolates of *Proteus mirabilis* in a Teaching Tertiary Care Hospital. International Journal of Current Microbiology Applied Sciences. 4(12): 675-682.

Yang, L.; He, H.; Chen, Q.; Wang, K.; Lin, Y.; Li, P.; Li, J.; Liu, X.; Jia, L.; Song, H.; et al. Nosocomial Outbreak of Carbapenemase-Producing *Proteus mirabilis* With Two Novel *Salmonella* Genomic Island 1 Variants Carrying Different bla_{NDM-1} Gene Copies in China. *Front. Microbiol.* 2022, *12*, 800938. DOI: 10.3389/fmicb.2021.800938

Yong, D., Toleman, M. A., Giske, C. G., Cho, H. S., Sundman, K., Lee, K., & Walsh, T. R. (2009). Characterization of a new metallo-β-lactamase gene, *bla NDM*-1, and a novel erythromycin esterase gene carried on a unique genetic structure in *Klebsiella pneumoniae* sequence type 14 from India. *Antimicrobial agents and chemotherapy*, *53*(12), 5046-5054. DOI: 10.1128/AAC.00774-09

Zhang, J., Xu, Y., Ling, X., Zhou, Y., Lin, Z., Huang, Z., Guan, H., Xiao, Y., Xu, W., Kan, B. (2019). Identification of diarrheagenic Escherichia coli by a new multiplex PCR assay and capillary electrophoresis. Molecular and Cellular Probes. DOI: 10.1016/j.mcp.2019.101477