

Original Article

A cross-sectional study on the prevalence of multidrug-resistant clinical isolates of *Proteus* species in Northern IranMahnaz Shafaei Fallah^{1,2}, Hadi Razavi Nikoo², Aylar Jamali², Alireza Mohebbi³, Ezzat Allah Ghaemi^{1,2}¹ Laboratory Sciences Research Center, Golestan University of Medical Sciences, Gorgan, Iran² Department of Microbiology, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran³ Department of Virology, School of Medicine, Iran University of Medical Sciences, Tehran, Iran**Abstract**

Introduction: Multidrug-resistant (MDR) bacteria like *Proteus* species have led to more prolonged hospitalizations, fewer care choices, higher treatment costs, and even death. The present study aims to evaluate the prevalence of MDR *Proteus* species in clinical samples and to suggest the best therapeutic options for the MDR *Proteus* species.

Methodology: Clinical samples were collected randomly from five hospitals in Golestan Province, Iran, from February 2017 to July 2019. Disk diffusion on Mueller–Hinton agar plates were used to perform antibiotic susceptibility testing (ASTs). By using a double-disc synergy test (DDST), isolates resistant to one of the third-generation cephalosporins were examined for phenotypic extended-spectrum β -lactamase (ESBL) development. A combined double disk synergy test (CDDST) was used to identify MBL-producing isolates.

Results: 61 *Proteus* isolates, including *P. mirabilis* 44/61 (77.04%), *P. vulgaris* 7/61 (11.47%), *P. hauseri* 5/61 (8.19%), and *P. penneri* 2/61 (3.27%) were collected. Most of the isolates were obtained from urine samples. *P. hauseri* isolates were more frequent in females. Resistance to tetracycline and nitrofurantoin antibiotics was observed in most *Proteus* isolates. *P. penneri* isolates were all resistant to antibiotics. ESBL production was observed in five ceftazidime-resistant isolates ($p < 0.05$).

Conclusions: Cefepime and imipenem were found to have the lowest occurrence of antibiotic resistance among *Proteus* species, confirming that cefepime and imipenem can be used to treat *Proteus* infections.

Key words: *Proteus*; extended-spectrum β -lactamase; multidrug resistance; antimicrobial resistance.

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Introduction

Antibiotics have saved many lives and alleviated the suffering of many people worldwide. Due to the rise and growing antibiotic-resistant bacteria, scientists hope for the treatment of microbial diseases has faded quickly [1-3]. Multidrug-resistant (MDR) bacterial infections have led to more prolonged hospitalizations, fewer care choices, higher treatment costs, and even death. Hence, continuous monitoring of microbial drug resistance is crucial [4]. MDR bacteria are resistant to at least three different antibiotic families [5]. It is crucial to choose the appropriate antibiotic and determine the pattern of bacterial susceptibility to improve the effectiveness of treatment against infections caused by MDR bacteria [6].

Another form of antibiotic resistance was found in Gram-negative bacteria, which were resistant to extended-spectrum beta-lactamase (ESBL) [7,8]. ESBLs are β -lactamase hydrolyzing extended-spectrum cephalosporins, penicillin, and monobactams but not cephamycin and carbapenems. ESBLs are inhibited by

β -lactamase inhibitors, including clavulanic acid, sulbactam, and tazobactam [8-10]. The *Proteus* species belong to the order *Enterobacterales* and the *Morganellaceae* family, Gram-negative bacteria [11-13]. These organisms are found in the natural flora of humans' intestinal tracts and the soil and water, where their presence is thought to be due to fecal contamination.

Proteus mirabilis (*P. mirabilis*), *Proteus vulgaris* (*P. vulgaris*), *Proteus penneri* (*P. penneri*), *Proteus hauseri* (*P. hauseri*), and three other unidentified genomospecies 4, 5, and 6 are currently divided into five specific genera [14-16]. The urease-producing *P. mirabilis* is well-known for its ability to differentiate into elongated swarm cells and a distinctive bull's-eye pattern of motility on agar plates [14,17]. This bacterium causes wounds, gastrointestinal tract, and urinary tract infections, but it is best known for infections of the catheterized urinary tract, also known as catheter-associated urinary tract infections (CAUTI). *P. mirabilis* can induce respiratory tract infections,

bacteremia, meningitis, cystitis, acute pyelonephritis, and renal calculi [18,19]. Furthermore, proteus infection has been linked to autoimmune disorders, including rheumatoid arthritis [18]. The pathogenicity of *Proteus* species requires several virulence factors, including the mannose-resistant Proteus-like (MR/P) fimbria, mannose-resistant *Klebsiella*-like hemagglutinin (MR/K), *P. mirabilis* fimbriae (PMF) [18–20], and the urease enzyme [21].

In recent decades, resistance to antibiotics has increased significantly in Iran. This alarming increase has caused various researchers to conduct studies to investigate and identify antibiotic resistance [22]. According to the review of three studies conducted in the last few years in Iran, the most resistance in *Proteus* isolates was against the antibiotic cotrimoxazole. Also, the results of these studies showed high resistance to nitrofurantoin and ampicillin [23–27].

Due to the lack of knowledge of the antibiotic resistance and ESBL patterns of *Proteus* species and increased evidence of drug resistance to bacterial infection, it was aimed to evaluate the abundance distribution of MDR *Proteus* species from clinical samples. In addition, the best possible therapeutic regimen was suggested for the MDR *Proteus* species.

Methodology

Sample size and identification of Proteus species

This cross-sectional study was performed in the Department of Microbiology, Golestan University of Medical Science, Gorgan, Iran. The study was approved by the Ethics committee of Golestan University of Medical Sciences, Iran (ethical code: IR.GOUMS.REC.1397.194). All clinical samples were collected randomly with no-repeat from five hospitals, namely A, B, C, D, and F in Golestan Province, Iran, from February 2017 to July 2019.

The isolates were belonged to various sources, including urogenital, abscess, and wound swabs. All specimens were cultured on nonselective blood agar media (Merck, Darmstadt, Germany). *Proteus* species were identified by standard microbiological and biochemical methods, such as colony morphology and Gram staining, oxidase, catalase, swarming motility, indole, citrate, maltose, saccharose fermentation, urease, bile esculin, and ornithine decarboxylase. Positive *Proteus* isolates were stored in tryptic soy broth stocks (Merck, Darmstadt, Germany) with 15% glycerol at -70°C . The isolates were further confirmed by 16 sRNA gene amplification as described before [28].

Antimicrobial susceptibility test

Antibiotic susceptibility tests (ASTs) of all isolates were performed by disk diffusion method on Mueller–Hinton agar plates (Merck, Darmstadt, Germany), according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI) [29]. The antibiotics, including amikacin (30 μg), cefotaxime (30 μg), ceftazidime (30 μg), ciprofloxacin (5 μg), cotrimoxazole (25 μg), gentamicin (10 μg), imipenem (10 μg), nitrofurantoin (30 μg), nalidixic acid (30 μg), cefepime (30 μg), ceftriaxone (30 μg) and norfloxacin (10 μg) (Mast Co, Merseyside, UK) were used in disc diffusion test. Inhibition zone (IZ) diameters (mm) of each antibiotic disc on the plates were measured after 24 hours of incubation. The isolates were classified into three categories: resistant, intermediate, and susceptible. *E. coli* strain ATCC 35218 was used as a control.

Phenotypic detection of ESBL production

Each isolate resistant to one of the third-generation cephalosporins (ceftazidime, cefotaxime, and ceftriaxone) was tested for phenotypic ESBL production. A double-disc synergy test (DDST) was used for phenotypic detection of ESBL production. In brief, the isolates with 0.5 McFarland standard turbidity were cultured on Müller-Hinton agar plates. According to CLSI guidelines, ceftazidime (30 μg), cefotaxime (30 μg), and ceftriaxone (30 μg) discs were placed at a distance of 15 mm away from the amoxicillin/clavulanic acid (30 μg) that was located in the center of the plate at 37°C for 24 hours. After the incubation period, the plates with an IZ diameter > 5 mm around the amoxiclav disk compared to cephalosporins alone were considered ESBL producing isolates [4,24,29,30].

Phenotypic detection of Metallo- β -lactamase producing isolate(s)

Initial screening for the production of MBL isolates was based on carbapenem (imipenem, meropenem) resistance. In summary, imipenem-resistant isolates were evaluated by a combined double-disk synergy test (CDDST) according to the CLSI guideline. To determine MBL-producing isolates, a 0.5 McFarland turbidity suspension of imipenem-resistant isolates was cultured on Müller-Hinton agar medium. In addition, two discs of both imipenem and ceftazidime antibiotics were placed on the surface of the inoculated plate. Discs were incubated at 37°C for 24 hours by adding 8 μL of EDTA solution. Increasing the IZ around the discs (Merck, Darmstadt, Germany) compared to the

Table 1. The information of *Proteus* isolates from wards, sources, and patients.

Species	Ward				Mean age	Gender		Source					Total
	Urology	Outpatient	ICU	Burn		Male	Female	Urine	Wound	Abscess	Tracheal	Vaginal	
<i>P. mirabilis</i>	0	38	8	1	31.5 ± 16.72	17	30	38	3	3	2	1	47
<i>P. vulgaris</i>	3	3	0	1	35.5 ± 16	3	4	6	1	0	0	0	7
<i>P. hauseri</i>	0	5	0	0	49 ± 14.94	1	4	5	0	0	0	0	5
<i>P. penneri</i>	0	2	0	0	45 ± 6	1	1	2	0	0	0	0	2
Total	3	48	8	2	34 ± 17.1	22	39	51	4	3	2	1	61

initial state. The discs with IZ ≥ 8 mm were considered MBL producing isolates [29–31].

Statistical analysis

The data analysis was performed by SPSS software version 16.0 (SPSS Inc., Chicago, IL, USA). Categorical and continuous quantitative variables were analyzed by Pearson's Chi-squared and independent samples *t*-tests. A $p \leq 0.05$ was considered significant with a 95% confidence interval (CI).

Results

Characterization of *Proteus* isolates

A total of 61 *Proteus* isolates were collected. The most prevalent species have belonged to *P. Mirabilis* 44/61 (77.04%), *P. vulgaris* 7/61 (11.47%), *P. hauseri* 5/61 (8.19%), and *P. penneri* 2/61 (3.27%). 36/61 (59%) isolates were recovered from females, and the remaining 25/61 (41%) were from males. The mean patient was 34 years (1 to 74 years old).

P. hauseri was more common in older patients (mean 49 years) (Table 1). *P. penneri*, *P. hauseri* isolates, *P. vulgaris* (86%), and *P. mirabilis* (80.85%) species were isolated from urine. *P. hauseri* isolates were more frequent in females (4/5). Interestingly, *P. hauseri* and *P. penneri* isolate was commonly detected from outpatients, while 57% of *P. vulgaris* isolated were inpatients (Table 1).

Antibiotic susceptibility test

As shown in Table 2, resistance to tetracycline and nitrofurantoin antibiotics was observed in the most *Proteus* isolates. All *P. mirabilis* isolates were resistant

to nitrofurantoin. Only one isolate of *P. mirabilis* was sensitive to tetracycline. Surprisingly, none of the *P. penneri* isolates were resistant to the four families of antibiotics. Accordingly, *P. penneri* species were more sensitive to antibiotics among the *Proteus* species. Unlike *P. penneri* isolates, antibiotic resistance was more common among *P. vulgaris* isolates, but in general, no significant relationship was observed between antibiotic resistance and type of *Proteus* species ($p > 0.05$). Further information is provided in Table 2.

ESBL and Metallo-β-lactamase

From 16 isolates resistant to ceftazidime, ceftriaxone, or both, 5/16 (31.25%) produced ESBL, of which four isolates were *P. mirabilis*, and one isolate was *P. hauseri* (Figure 1). Three isolates producing ESBL were isolated from urine, and the other two isolates were isolated from wounds and trachea. No metallo-β-lactamase producing isolates were observed in imipenem-resistant cases. However, the frequency of resistance to imipenem, gentamicin, ceftazidime, ciprofloxacin, chloramphenicol, cefepime, cefotaxime, and ampicillin was higher in ESBL-producing isolates. A significant correlation was found between ESBL production and resistance to ciprofloxacin, ampicillin, cefepime, and cefotaxime ($p < 0.001$).

Discussion

Proteus spp infects humans due to its numerous virulence factors, such as the enzyme urease, flagella, fimbriae, biofilm formation, and produce toxins such as hemolysin and mirabilysin [19]. Therefore, assessments

Table 2. Antibiotic susceptibility of clinical isolates of *Proteus* species.

Antibiotics	<i>P. mirabilis</i> , n (%)	<i>P. vulgaris</i> , n (%)	<i>P. hauseri</i> , n (%)	<i>P. penneri</i> , n (%)	Total, n (%)	Sig.
Ampicillin	11 (23.40)	0 (0.00)	0 (0.00)	2 (40.00)	13 (21.31)	0.20
Cefoxitin	10 (21.27)	0 (0.00)	0 (0.00)	0 (0.00)	10 (16.40)	0.20
Cefazolin	12 (25.53)	4 (57.10)	0 (0.00)	2 (40.00)	18 (29.50)	0.20
Ceftazidime	8 (17.02)	2 (28.60)	0 (0.00)	2 (40.00)	12 (19.67)	0.20
Cefotaxime	7 (14.89)	2 (28.60)	0 (0.00)	3 (60.00)	12 (19.67)	0.20
Cefepime	5 (10.63)	2 (28.60)	0 (0.00)	1 (20.00)	8 (13.11)	0.50
Imipenem	7 (14.89)	2 (28.60)	0 (0.00)	0 (0.00)	9 (14.75)	0.40
Gentamicin	8 (17.02)	1 (14.30)	0 (0.00)	0 (0.00)	9 (14.75)	0.60
Ciprofloxacin	6 (12.76)	2 (28.60)	0 (0.00)	1 (20.00)	9 (14.75)	0.60
Cotrimoxazole	15 (31.93)	2 (28.60)	0 (0.00)	1 (20.00)	18 (29.50)	0.60
Chloramphenicol	18 (38.29)	3 (42.90)	0 (0.00)	2 (40.00)	23 (37.70)	0.50
Nitrofurantoin	47 (100)	6 (85.80)	1 (50.00)	3 (60.00)	57 (93.44)	0.001
Tetracycline	46 (97.87)	7 (100.00)	2 (100.00)	5 (100.00)	60 (98.36)	0.90

of antibiotic resistance and ESBL patterns of *Proteus* species is crucial for suggesting correct antibiotic regimen. *Proteus* is a known bacterial genus that causes urinary tract infections and is more likely to be isolated from urine than other sources [18,19]. Most of the *Proteus* species were isolated from urinary tract samples in the present study. This finding was consistent with the previous reports [30,32,33].

As a result, *P. mirabilis* was the most prevalent isolate, followed by *P. vulgaris*, *P. Hauseri*, and *P. penneri*. Similar results are also reported from Iran [30]. One of the exciting findings was the identification and isolation of *P. hauser* by biochemical diagnosis. The bacterium was differentiated from *P. vulgaris* in 2000 by doctor Hauser. *P. hauseri* is indole positive but negative for salicin and esculin tests. These tests are the distinguishing feature of *P. hauseri* from *P. vulgaris*. Due to the similarity to *P. vulgaris*, accurate statistics of *P. hauseri* frequency in the world have not been reported.

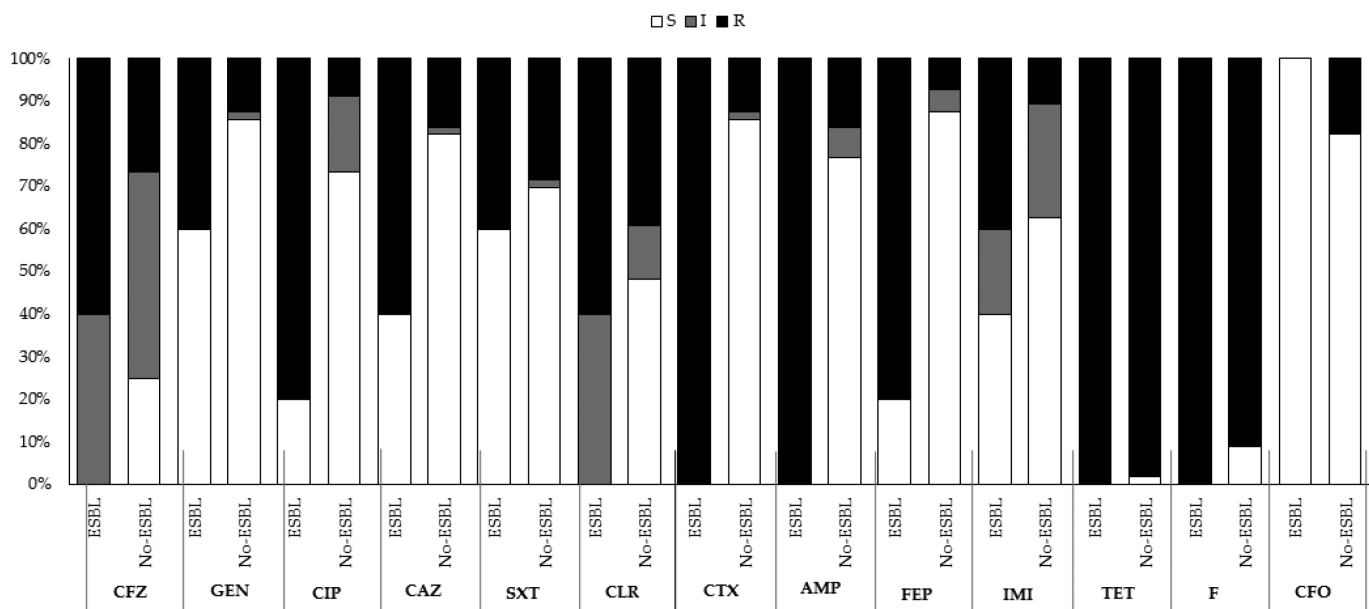
Women are more prone to urinary tract infections because they have a shorter bladder outlet than men and a shorter distance to the anus. As expected, most isolates were obtained from women, which has been the subject of many studies in other parts of the world and Iran [34–36]. Moreover, most *Proteus* isolates were found in hospitalized patients, while *P. penneri* and *P. hauseri* isolates and a large portion of *P. mirabilis* isolates were obtained from outpatients. *Proteus* is an opportunistic bacterium, and one of the most critical risk factors for infections is an extended hospital stay and the use of a catheter [19]. Due to these reasons, the

prevalence of this bacterium was expected to be higher in hospitalized patients than in outpatients. Accordingly, therapeutic approaches in these patients are crucial.

Since *Proteus* species are inherently resistant to nitrofurantoin and tetracycline [37,38], the results showed a high degree of resistance to these antibiotics (91% and 98% to nitrofurantoin and tetracycline, respectively). Unlike other *Proteus* species, *P. penneri* isolates were more sensitive to nitrofurantoin. Antibiotic resistance has been seen in various forms among Gram-negative bacteria. Resistance to broad-spectrum β -lactams is one type of resistance that has become a global problem among Gram-negative bacilli [39]. As a result, ESBL production was detected in only 8.2% of isolates, falling within the reported range of 0 to 11.8% for ESBL-producing *Proteus* isolates [24,30,40]. Furthermore, the finding was lower than that reported for other parts of the world, such as Japan (45.6%), India (48.86%), and Taiwan [32,41,42].

Antibiotic resistance was detected among ESBL isolates to imipenem, gentamicin, ciprofloxacin, ceftipime, cefotaxime, chloramphenicol, and ampicillin. There was also concurrent resistance between ciprofloxacin, ampicillin, cefotaxime, and ceftipime. Some investigations have found a link between ESBL production and ciprofloxacin resistance [24]. The ESBL-producing gene could be on a chromosome or a plasmid. Many genes conferring resistance to aminoglycosides, trimethoprim-sulfamethoxazole, and fluoroquinolones have been found on the plasmid harboring the ESBL gene. The

Figure 1. ESBL production by *Proteus* isolates. The figure shows the sensitivity of *Proteus* isolates to different types of antibiotics.



association between the simultaneous existence of these genes and being ESBL in *Klebsiella* was explored in one study, and it was found to be statistically significant. Another reason for this synchrony could be changing the bacterium's outer membrane proteins. Mutations at the nan locus in Gram-negative bacteria are linked to ciprofloxacin resistance and the presence of ESBL enzymes [43-44].

Conclusions

In imipenem-sensitive bacteria, metallo β -lactamase production was not found. This shows that imipenem could treat *Proteus* species that produce metallo β -lactamases. Furthermore, cefepime and imipenem were found to have the lowest occurrence of antibiotic resistance among *Proteus* species, confirming that cefepime and imipenem can be used to treat *Proteus* infections.

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References

- Dandachi I, Sokhn ES, Dahdouh EA, Azar E, El-Bazzal B, Rolain JM, Daoud Z (2018) Prevalence and characterization of multi-drug-resistant Gram-negative bacilli isolated from Lebanese poultry: a nationwide study. *Front Microbiol* 9: 550. doi: 10.3389/fmicb.2018.00550.
- Tyers M, Wright GD (2019) Drug combinations: a strategy to extend the life of antibiotics in the 21st century. *Nat Rev Microbiol* 17: 141-155. doi: 10.1038/s41579-018-0141-x.
- Tanko N, Bolaji RO, Olayinka AT, Olayinka BO (2020) A systematic review on the prevalence of extended-spectrum beta lactamase-producing Gram-negative bacteria in Nigeria. *J Glob Antimicrob Resist* 22: 488-496. doi: 10.1016/j.jgar.2020.04.010.
- Yazdansetad S, Alkhudhairy MK, Najafpour R, Farajtabrizi E, Al-Mosawi RM, Saki M, Jafarzadeh E, Izadpour F, Ameri A (2019) Preliminary survey of extended-spectrum β -lactamases (ESBLs) in nosocomial uropathogen *Klebsiella pneumoniae* in north-central Iran. *Heliyon* 5: e02349. doi: 10.1016/j.heliyon.2019.e02349.
- Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT, Monnet DL (2012) Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect* 18: 268-281. doi: 10.1111/j.1469-0691.2011.03570.x.
- Mesaros N, Nordmann P, Plésiat P, Roussel-Delvallez M, Van Eldere J, Glupczynski Y, Van Laethem Y, Jacobs F, Lebecque P, Malfroot A, Tulkens PM, Van Bambeke F (2007) *Pseudomonas aeruginosa*: resistance and therapeutic options at the turn of the new millennium. *Clin Microbiol Infect* 13: 560-78. doi: 10.1111/j.1469-0691.2007.01681.x.
- Sivaraman GK, Rajan V, Vijayan A, Elangovan R, Prendiville A, Bachmann TT (2021) Antibiotic resistance profiles and molecular characteristics of extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* and *Klebsiella pneumoniae* isolated from shrimp aquaculture farms in Kerala, India. *Front Microbiol* 12: 622891. doi: 10.3389/fmicb.2021.622891.
- Castanheira M, Simner PJ, Bradford PA (2021) Extended-spectrum β -lactamases: an update on their characteristics, epidemiology and detection. *JAC Antimicrob Resist* 3: dlab092. doi: 10.1093/jacamr/dlab092.
- Rawat D, Nair D (2010) Extended-spectrum β -lactamases in Gram Negative Bacteria. *J Glob Infect Dis* 2: 263-274. doi: 10.4103/0974-777x.68531.
- De Angelis G, Del Giacomo P, Posteraro B, Sanguinetti M, Tumbarello M (2020) Molecular mechanisms, epidemiology, and clinical importance of β -lactam resistance in *Enterobacteriaceae*. *Int J Mol Sci* 21: 5090. doi: 10.3390/ijms21145090.
- Fallah MS, Mohebbi A, Yasaghi M, Ghaemi EA (2021) CRISPR-Cas systems in *Proteus mirabilis*. *Infect Genet Evol* 92: 104881. doi: 10.1016/j.meegid.2021.104881.
- Girlich D, Bonnin RA, Dortet L, Naas T (2020) Genetics of acquired antibiotic resistance genes in *Proteus* spp. *Front Microbiol* 11: 256. doi: 10.3389/fmicb.2020.00256.
- Bonnin RA, Girlich D, Jousset AB, Gauthier L, Cuzon G, Bogaerts P, Haenni M, Madec JY, Couvé-Deacon E, Barraud O, Fortineau N, Glaser P, Glupczynski Y, Dortet L, Naas T (2020) A single *Proteus mirabilis* lineage from human and animal sources: a hidden reservoir of OXA-23 or OXA-58 carbapenemases in Enterobacteriales. *Sci Rep* 10: 9160. doi: 10.1038/s41598-020-66161-z.
- Drzewiecka D (2016) Significance and roles of *Proteus* spp. bacteria in natural environments. *Microb Ecol* 72: 741-758. doi: 10.1007/s00248-015-0720-6.
- O'Hara CM, Brenner FW, Miller JM (2000) Classification, identification, and clinical significance of *Proteus*, *Providencia*, and *Morganella*. *Clin Microbiol Rev* 13: 534-546. doi: 10.1128/CMR.13.4.534-546.2000.
- Dai H, Lu B, Li Z, Huang Z, Cai H, Yu K, Wang D (2020) Multilocus sequence analysis for the taxonomic updating and identification of the genus *Proteus* and reclassification of *Proteus* genospecies 5 O'Hara et al. 2000, *Proteus cibarius* Hyun et al. 2016 as later heterotypic synonyms of *Proteus terrae* Behrendt et al. 2015. *BMC Microbiol* 20: 152. doi: 10.1186/s12866-020-01844-1.
- Pearson MM, Rasko DA, Smith SN, Mobley HL (2010) Transcriptome of swarming *Proteus mirabilis*. *Infect Immun* 78: 2834-2845. doi: 10.1128/IAI.01222-09.
- Christopher M (2016) AMLS *Proteus mirabilis* and urinary infections. *Physiol Behav* 176: 100-106. doi: 10.1128/microbiolspec.UTI-0017-2013.
- Armbruster CE, Mobley HLT, Pearson MM (2018) Pathogenesis of *Proteus mirabilis* infection. *EcoSal Plus* 8: 10.1128/ecosalplus.ESP-0009-2017. doi: 10.1128/ecosalplus.esp-0009-2017.
- Wasfi R, Hamed SM, Amer MA, Fahmy LI (2020) *Proteus mirabilis* biofilm: development and therapeutic strategies. *Front Cell Infect Microbiol* 10: 414. doi: 10.3389/fcimb.2020.00414.
- Grahl MVC, Uberti AF, Broll V, Bacaicoa-Caruso P, Meirelles EF, Carlini CR (2021) *Proteus mirabilis* urease: unsuspected

- non-enzymatic properties relevant to pathogenicity. *Int J Mol Sci* 22: 7205. doi: 10.3390/ijms22137205.
22. Mehtarpour M, Takian A, Eshrati B, Jaafaripooyan E (2020) Control of antimicrobial resistance in Iran: the role of international factors. *BMC Public Health* 20: 873. doi: 10.1186/S12889-020-09006-8.
 23. Fazeli H, Moghim S, Zare D (2018) antimicrobial resistance pattern and spectrum of multiple-drug-resistant enterobacteriaceae in Iranian hospitalized patients with cancer. *Adv Biomed Res* 7: 69. doi: 10.4103/abr.abr_164_17.
 24. Mirzaei A, Habibi M, Bouzari S, Asadi Karam MR (2019) Characterization of antibiotic-susceptibility patterns, virulence factor profiles and clonal relatedness in proteus mirabilis isolates from patients with urinary tract infection in Iran. *Infect Drug Resist* 12: 3967-3979. doi: 10.2147/IDR.S230303.
 25. Tabatabaei A, Ahmadi K, Shabestari AN, Khosravi N, Badamchi A (2021) Virulence genes and antimicrobial resistance pattern in *Proteus mirabilis* strains isolated from patients attended with urinary infections to tertiary hospitals, in Iran. *Afr Health Sci* 21: 1677-1684. doi: 10.4314/ahs.v21i4.22.
 26. Esfahanian F, Mobasherizadeh S, Baradaran A, Abbasi Baghbaderani S, Naimi A, Nouri S, Rostami S (2022) Prevalence of antibiotic resistance in *Enterobacteriaceae* among the patients hospitalized in Al-Zahra hospital, Isfahan, Iran. *J Prev Epidemiol*. doi: 10.34172/jpe.2022.23166.
 27. Mirzaei B, Babaei R, Bazgir ZN, Goli HR, Keshavarzi S, Amiri E (2021) Prevalence of *Enterobacteriaceae* spp. and its multidrug-resistant rates in clinical isolates: A two-center cross-sectional study. *Mol Biol Rep* 48: 665-675. doi: 10.1007/S11033-020-06114-X.
 28. Tajbakhsh E, Tajbakhsh S, Khamesipour F (2015) Isolation and Molecular detection of gram negative bacteria causing urinary tract infection in patients referred to Shahrekord hospitals, Iran. *Iran Red Crescent Med J* 17: e24779. doi: 10.5812/ircmj.17(5)2015.24779.
 29. Deshmukh DG, Damle AS, Bajaj JK, Bhakre JB, Patwardhan NS (2011) Metallo- β -lactamase-producing clinical isolates from patients of a tertiary care hospital. *J Lab Physicians* 3: 93-97. doi: 10.4103/0974-2727.86841.
 30. Malekjamshidi MR, Shahcheraghi F, Feizabadi MM (2011) Detection and PFGE analysis of ESBL-producing isolates of *Proteus* species isolated from patients at Tehran hospitals. *Med Sci Monit* 16: BR327-32.
 31. Dogonchi AA, Ghaemi EA, Ardebili A, Yazdaneshtad S, Pournajaf A (2018) Metallo- β -lactamase-mediated resistance among clinical carbapenem-resistant *Pseudomonas aeruginosa* isolates in northern Iran: A potential threat to clinical therapeutics. *Ci Ji Yi Xue Za Zhi* 30: 90-96. doi: 10.4103/tcmj.tcmj_101_17.
 32. Kanayama A, Kobayashi I, Shibuya K (2015) Distribution and antimicrobial susceptibility profile of extended-spectrum β -lactamase-producing *Proteus mirabilis* strains recently isolated in Japan. *Int J Antimicrob Agents* 45: 113-8. doi: 10.1016/j.ijantimicag.2014.06.005.
 33. Biendo M, Thomas D, Laurans G, Hamdad-Daoudi F, Canarelli B, Rousseau F, Castelain S, Eb F (2005) Molecular diversity of *Proteus mirabilis* isolates producing extended-spectrum beta-lactamases in a French university hospital. *Clin Microbiol Infect* 11: 395-401. doi: 10.1111/j.1469-0691.2005.01147.x.
 34. Amiri P, Pournajaf A, Shavalipour A, Tayebi Z, Goudarzi H, Eslami G, Hashemi A, Gholami M (2015) Evaluation of antimicrobial resistance in the beta-lactamase producing *Escherichia Coli* isolated from urinary tract infection in the patients referring to Taleghani Hospital of Tehran. *Tabari Biomed Stu Res J* 1:11-19.
 35. Molazade A, Gholami M S, Shahi A, Najafipour S, Mobasheri F, Ashraf Mansuri JA, Somaie J (2014) Evaluation of antibiotic resistance pattern of isolated gram-negative bacteria from urine culture of hospitalized patients in different wards of Vali-Asr Hospital in Fasa during the years 2012 and 2013. *J Fasa Univ Med Sci* 4: 275-283.
 36. Acheampong DO, Feglo PK (2011) Empirical treatment of neonatal sepsis by *Klebsiella*: A case study at Komfo Anokye Teaching Hospital (KATH), Ghana. *Eur J Exp Biol* 1: 18–22.
 37. Mirzaei A, Nasr Esfahani B, Raz A, Ghanadian M, Moghim S (2021) From the urinary catheter to the prevalence of three classes of integrons, β -lactamase genes, and differences in antimicrobial susceptibility of *Proteus mirabilis* and clonal relatedness with Rep-PCR. *Biomed Res Int* 2021: 9952769. doi: 10.1155/2021/9952769.
 38. Hrbacek J, Cermak P, Zachoval R (2020) Current antibiotic resistance trends of uropathogens in central europe: survey from a tertiary hospital urology department 2011-2019. *Antibiotics* 9: 630. doi: 10.3390/antibiotics9090630.
 39. Exner M, Bhattacharya S, Christiansen B, Gebel J, Goroncy-Bermes P, Hartemann P, Heeg P, Ilschner C, Kramer A, Larson E, Merkens W, Mielke M, Oltmanns P, Ross B, Rotter M, Schmuthausen RM, Sonntag HG, Trautmann M (2017) Antibiotic resistance: What is so special about multidrug-resistant Gram-negative bacteria? *GMS Hyg Infect Control* 12: Doc05.
 40. Saffar H, Asgari Niaraki N, Ghahroudi Tali A, Baseri Z, Abdollahi A, Yalfani R (2016) Prevalence of AmpC β -lactamase in clinical isolates of *Escherichia coli*, *Klebsiella spp.*, and *Proteus mirabilis* in a tertiary hospital in Tehran, Iran. *Jundishapur J Microbiol* 9: e39121. doi: 10.5812/jjm.39121.
 41. Pandey JK, Narayan A, Tyagi S (2013) Prevalence of *Proteus* species in clinical samples, antibiotic sensitivity pattern and ESBL production. *Int J Curr Microbiol Appl Sci* 2: 253-261.
 42. Wang JT, Chen PC, Chang SC, Shiau YR, Wang HY, Lai JF, Huang IW, Tan MC, Lauderdale TL, TSAR Hospitals (2014) Antimicrobial susceptibilities of *Proteus mirabilis*: a longitudinal nationwide study from the Taiwan surveillance of antimicrobial resistance (TSAR) program. *BMC Infect Dis* 14: 486.
 43. Rajivgandhi G, Maruthupandy M, Ramachandran G, Priyanga M, Manoharan N (2018) Detection of ESBL genes from ciprofloxacin resistant Gram-negative bacteria isolated from urinary tract infections (UTIs). *Frontiers in Laboratory Medicine* 2: 5-13. doi: 10.1016/j.flm.2018.01.001.
 44. Sohn KM, Kang CI, Joo EJ, Ha YE, Chung DR, Peck KR, Lee NY, Song JH (2011) Epidemiology of ciprofloxacin resistance and its relationship to extended-spectrum β -lactamase production in *Proteus mirabilis* bacteremia. *Korean J Intern Med* 26: 89-93. doi: 10.3904/kjim.2011.26.1.89.

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