Journal of Neonatal Surgery
ISSN(Online): 2226-0439
Vol. 14, Issue 27s (2025)
https://www.jneonatalsurg.com

OPEN ACCESS

Antibiotic Susceptibility and Resistance Trends in Uropathogenic Bacteria: A Regional Perspective

Dr. Toufiq Ahmed[1], Dr. Shirajum Monira[2*], Dr. G M Sadik Hasan[3], Dr. Md. Masudul Karim[4], Dr. Md. Rasel Ahmad[5], Dr. Md. Immam Hossin[6], Dr. Jahidul Islam[7]

[1]Assistant professor, Department of Internal Medicine, Bangladesh Medical University, Dhaka, Bangladesh. Email: toufiqahmed@bsmmu.edu.bd. ORCID ID: 0000-0002-1355-4008

[2]Assistant professor, Department of Internal Medicine, Bangladesh Medical University, Dhaka, Bangladesh. Email: shirajum39@gmail.com. ORCID ID: 0000-0001-6500-9610

[3]Assistant professor, Department of Nephrology, Bangladesh Medical University, Dhaka, Bangladesh. Email: gmsadik28@bsmmu.edu.bd. ORCID ID: 0009-0008-5280-2159

[4]Medical officer, Department of Nephrology, Bangladesh Medical University, Dhaka, Bangladesh. Email: ORCID ID: 0009-0003-0857-0905

[5]Assistant Professor, Department of Public Health and Informatics, Bangladesh Medical University, Dhaka, Bangladesh. Email: raselbds42@bsmmu.edu.bd ORCID ID: 0009-0009-2936-0169

[6]Lecturer, Dhaka Dental College, (OSD)Director General of Health Services, Bangladesh Medical University,

Dhaka, Bangladesh, Email: bulbulbds42@gmail.com, ORCID: 0009-0002-8712-178X

[7]Associate Professor, Department of Pharmacology, Bangladesh Medical University, Dhaka, Bangladesh. Email: jahidul_islam@bsmmu.edu.bd. ORCID ID: 0000-0003-1232-6799

***Corresponding Author**

Dr. Shirajum Monira, Assistant Professor, Department of Internal Medicine, Bangladesh Medical University, Dhaka, Bangladesh

Cite this paper as: Toufiq Ahmed, Shirajum Monira, G M Sadik Hasan, Masudul Karim, Rasel Ahmad, Immam Hossin, Jahidul Islam, (2025) Antibiotic Susceptibility and Resistance Trends in Uropathogenic Bacteria: A Regional Perspective. *Journal of Neonatal Surgery*, 14 (27s), 189-195.

ABSTRACT

Background: Antimicrobial resistance (AMR) has emerged as a critical global health challenge, particularly in managing urinary tract infections (UTIs), which are among the most prevalent bacterial infections affecting individuals worldwide. ***Objective:*** This study aimed to evaluate the patterns of antibiotic susceptibility and resistance in uropathogenic bacteria isolated from clinical samples in Dhaka, Bangladesh, over one year. ***Methods:*** A cross-sectional study design was employed from July 2024 to December 2024, with clinical samples systematically collected from outpatient cases. Pathogen identification utilized standard microbiological techniques, including culture on selective media, biochemical testing, and confirmatory methods. Antibiotic susceptibility testing (AST) was performed using the Kirby Bauer disc diffusion method on Mueller–Hinton agar, following CLSI guidelines. ***Results:*** The results highlighted significant variability in resistance patterns across bacterial species. Among Escherichia coli isolates, high susceptibility was observed for imipenem (82%), nitrofurantoin (78%), and linezolid (78%), while resistance to penicillin G (35%) and fosfomycin (30%) was notable. For Klebsiella pneumoniae, meropenem (85%) and netilmicin (82%) demonstrated the highest efficacy, whereas nalidixic acid (30%) and amoxicillin (28%) exhibited substantial resistance. Acinetobacter spp. isolates showed remarkable susceptibility to moxifloxacin (85%) and cefuroxime (84%), but levofloxacin resistance (60%) emerged as a critical concern. Statistical analyses revealed significant demographic trends, with middle-aged participants (40–60 years) comprising the majority of the study population. Gender distribution showed a predominance of female participants (64.8%). Clinical symptoms, including fever (38%), urinary urgency (24%), and burning sensation (22%), were most commonly reported among patients. ***Conclusion:*** This study provides critical insights into the evolving resistance patterns of uropathogenic bacteria in a regional context.

Keywords: *Antibiotic Susceptibility, Antimicrobial resistance (AMR), Uropathogenic Bacteria*

INTRODUCTION

Antimicrobial resistance poses a significant threat to public health, particularly by limiting treatment options for common bacterial infections like urinary tract infections (UTIs)[1]. UTIs, characterized by bacterial growth exceeding 10^5 colony-forming units (CFU)/ml, are among the most prevalent bacterial diseases, causing significant morbidity in both outpatient and hospitalised patients, alongside respiratory and gastrointestinal infections[2]. Common causative pathogens include Acinetobacter spp., Escherichia coli, and Klebsiella pneumoniae, affecting populations in both developed and developing countries[3]. These infections result from the adherence of uropathogens to epithelial cells, leading to toxin production, inflammation, and cellular destruction [4]. Symptoms of UTIs include cystitis, urethritis, pyelonephritis, hematuria, dysuria, cloudy urine, and nocturnal enuresis[5]. The bacterial colonization and inflammatory response compromise the host's immune defences, promoting virulence and pathogenicity[6].

Uropathogenic Escherichia coli (UPEC) is the most common pathogen in urinary tract infections (UTIs), responsible for 25–50% of complicated cases and over 70% of uncomplicated ones[4]. UPEC consists of specific E. coli strains capable of surviving, colonising, and causing infections in the urinary tract. These strains produce virulence factors (VFs) and acquire antibiotic resistance genes that facilitate biofilm formation, nutrient acquisition, invasion of host cells, immune evasion, and resistance to antibiotics. The virulence factors enable UPEC to adapt to diverse environmental conditions, utilize multiple carbon sources for facultative anaerobic metabolism, and persist in the host. UPEC also constitutes approximately 20% of the female vaginal microbiota and is linked to aerobic vaginitis[7].

The rise of antibiotic resistance among uropathogenic Escherichia coli (UPEC) poses a significant challenge, limiting treatment options for UTIs. The global increase in multidrug-resistant (MDR) E. coli is particularly concerning, as UPEC's production of extended-spectrum beta-lactamases (ESBLs) enables resistance to broad-spectrum cephalosporins and monobactams. Resistance to commonly used antibiotics, including cotrimoxazole, ampicillin, nitrofurantoin, and fluoroquinolones like ciprofloxacin and levofloxacin, further complicates treatment[8].

This resistance affects both healthcare-associated and community-acquired infections, underscoring the need for ongoing monitoring of resistance patterns and risk factors. Such knowledge is crucial for developing policies and promoting responsible antibiotic use to combat MDR in UTIs.

A multicenter study conducted in Dhaka city examined antibiotic resistance patterns among bacterial isolates from outpatient cases in 2024. The findings provided baseline data to evaluate current resistance trends in the region. A network visualization of interactions among the isolated pathogens illustrates the extent and patterns of antibiotic resistance in the area.

MATERIALS AND METHODOLOGY

The study was a one-year cross-sectional investigation conducted from July 2024 to December 2024 in the Microbiology Laboratory of a recognized affiliated laboratory in Dhaka city. Clinical bacterial cultures and isolates were collected using systematic sampling methods.

Collection of Clinical Samples and Identification of Pathogens:

The study utilized convenience sampling to select samples, which included blood samples and urine samples. Patients' demographic information, including age and sex, was recorded from the registrar. Blood agar (Sigma-Aldrich) and MacConkey agar (Sigma-Aldrich) were used for pathogen isolation, with incubation performed aerobically at 37°C overnight. Pathogen identification was based on colony morphology, Gram staining, and additional biochemical tests, including catalase positivity and oxidase negativity. Bacterial isolates in this study were analyzed using standard biochemical tests and selective media, including Endo agar, MacConkey broth, Simmons citrate agar, catalase, coagulase, oxidase, and Triple Sugar Iron (TSI) agar for sugar fermentation. Additional tests included indole production, citrate utilization, urease production, and motility assays. Confirmatory testing for *E. coli* was performed using Sorbitol-MacConkey (SMAC) agar and *E. coli* O157 antiserum or latex reagents (O157 antibody-coated latex and control latex), following manufacturer-recommended protocols[9].

Antibiotic Susceptibility Testing (AST)

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar. Bacterial turbidity was standardised by comparing a suspension of pure bacterial colonies in normal saline to a 0.5 McFarland standard. The susceptibility of bacterial isolates was tested against a range of antibiotics, including:

- Beta-lactams: Ampicillin (AMP, 10 µg), amoxicillin/clavulanic acid (AMC, 30 µg), cefuroxime (CRX, 30 µg), cefixime (CXM, 30 µg), cefotaxime (CTX, 30 µg), ceftazidime (CAZ, 30 µg), penicillin (PEN, 10 IU), cloxacillin (CXC, 5 µg), and piperacillin/tazobactam (TZP, 100/10 µg).
- Carbapenems: Imipenem (IPM, 10 µg), meropenem (MEM, 10 µg), and ertapenem (ETP, 10 µg).

- Aminoglycosides: Gentamicin (GEN, 10 µg) and amikacin (AMK, 30 µg).
- Fluoroquinolones: Ciprofloxacin (CIP, 5 µg) and nalidixic acid (NAL, 30 µg).
- Other classes: Erythromycin (ERY, 5 µg), tetracycline (TET, 30 µg), trimethoprim-sulfamethoxazole (SXT, 30 µg), chloramphenicol (CHL, 30 µg), aztreonam (AZT, 15 µg), Fosfomycin (FOF, 200 µg), and colistin (CST, 10 µg).

For the detection of extended-spectrum beta-lactamases (ESBLs), the double-disk synergy test was performed using CTX, AMC, and CAZ discs. Antibiotic-impregnated discs were placed on dried Mueller–Hinton agar plates inoculated with bacterial suspensions and incubated overnight at 35°C. Inhibition zones were measured from the centre to the edges using a ruler, with *E. coli* ATCC 25922 serving as a control strain. All antibiotic discs were sourced from Becton Dickinson (BD, Sparks, MD, USA)[10].

Statistical Analysis

Data entry, validation, and analysis were conducted using SPSS version 26 and GraphPad Prism version 9.0.2. The interaction networks of isolates and antibiotic resistance were analyzed using Cytoscape version 3.8.2. Statistical significance was assessed using ANOVA and the one-sample Wilcoxon test, with a significance level set at $p = 0.05$.

RESULTS

The age distribution of participants (N = 54) is shown in Table 1. The majority of participants fell into the middle-aged categories, with 26.92% aged 40–50 years and 36.54% aged 50–60 years, both showing significantly higher proportions than expected (Z = 3.14, p = .002; Z = 5.24, p < .001, respectively). The 70–80 and 80–90 age groups had significantly lower proportions than hypothesized (1.92% each, Z = -2.31, p = .021). Other age groups did not show significant deviations.

Table 1: Age distribution of the participants in the study.

Age Group	Frequency	Percentage	Z-Statistic	P-Value
(10 – 20)	3	5.77	-1.467598771	0.142213242
(20 – 30)	3	5.77	-1.467598771	0.142213242
(30 – 40)	6	11.54	-0.209656967	0.833935414
(40 – 50)	14	26.92	3.14485451	0.001661694
(50 – 60)	19	36.54	5.241424184	1.59E-07
(60 – 70)	5	9.62	-0.628970902	0.529368106
(70 – 80)	1	1.92	-2.306226641	0.021097972
(80 – 90)	1	1.92	-2.306226641	0.021097972

Table 2 reveals that females constituted the majority of participants (64.8%), with males accounting for 35.2%. A significant overrepresentation of females was noted (Z = 2.12, p = .034).

Table 2: Distribution of gender of the participants.

Gender	Frequency	Percent	Z-test	P-value
Female	35	64.8	2.12	0.034
Male	19	35.2		
Total	54	100.0		

The occupational distribution (Table 3) showed no significant deviation from an expected equal distribution (20%) across categories. Housewives (29.6%) showed a marginal trend (Z = 1.77, p = .077), while students (24.1%) and private job holders (18.5%) demonstrated no significant differences.

Table 3: Frequencies of occupation amid participants

Occupation	Frequency	Percent	Z-Statistic	P-Value
Housewife	16	29.6	1.769076	0.076881
Student	13	24.1	0.748455	0.454186
Private Job Holder	10	18.5	-0.27217	0.785495
Businessman	8	14.8	-0.95258	0.340803
Govt. Job Holder	7	13	-1.29279	0.196085

The frequency of reported clinical features is summarized in Table 4. Fever was the most prevalent symptom (38%), significantly higher than other features (Z = 2.33, p = .01). Urgency (24%) and burning sensation (22%) were also common, though not significantly different from each other. Lower abdominal pain (7%) was significantly less frequent (Z = 5.47, p = .001).

Table 4: Represents clinical features presented by the patients

Clinical Feature	Frequency	Percent	Z-value	P-value
Fever	42	38		
Urgency	26	24	2.33	0.01
Burning sensation	24	22	2.65	0.00
Lower abdominal pain	8	7	5.47	0.001
Generalized weakness	2	2		
Vomiting	2	2		
Incontinence	2	2		
Dysuria	1	1		
Hematuria	1	1		
Loin pain	1	1		
Recurrent fever	1	1		
Total	110	100		

The antimicrobial susceptibility patterns of ***Acinetobacter spp***. reveal significant variability among antibiotics. High susceptibility rates were observed for Moxifloxacin, Cefuroxime, Ceftazidime (85%), and Imipenem (75%). Moderate susceptibility was noted for Amikacin (60%) and Meropenem (62%). Levofloxacin exhibited the highest resistance rate (60%) and low susceptibility (15%), indicating limited efficacy. Ofloxacin and Ceftriaxone showed moderate susceptibility (45% and 60%, respectively). These findings highlight the necessity of tailoring antibiotic therapies based on susceptibility data to improve treatment outcomes and address rising resistance.

Table 5: Acinetobacter Antimicrobial Susceptibility and Resistance Patterns

Antibiotic name	R (%)	I (%)	S (%)	R 95% CI	S 95% CI
Amikacin	25	15	60	20.0-30.0	50.0-70.0
Meropenem	30	8	62	25.0-35.0	55.0-70.0
Levofloxacin	60	25	15	55.0-65.0	10.0-20.0
Ofloxacin	35	20	45	30.0-40.0	40.0-50.0
Ceftriaxone	10	30	60	5.0-15.0	55.0-65.0
Moxifloxacin	5	10	85	2.0-8.0	80.0-90.0
Cefuroxime	15	1	84	10.0-20.0	80.0-88.0
Ceftazidime	10	5	85	5.0-15.0	80.0-90.0
Imipenem	20	5	75	15.0-25.0	70.0-80.0

The antimicrobial susceptibility patterns for ***E. coli*** reveal varied efficacy among antibiotics. High susceptibility rates were observed for Imipenem (82%), Nitrofurantoin, Linezolid, and Cefixime (all 78%). Moderate susceptibility was noted for Amikacin and Gentamicin (65%), as well as Amoxiclav (67%). Fosfomycin showed 58% susceptibility with a resistance rate of 30%. Penicillin G had the highest resistance (35%) and the lowest susceptibility (53%). These findings emphasize the importance of susceptibility data to guide effective treatment strategies for *E. coli* infections.

Table 6: *E.Coli Spp* Antimicrobial Susceptibility and Resistance Patterns

Antibiotic name	R (%)	I (%)	S (%)	R 95% CI	S 95% CI
Fosfomycin	30	12	58	20.0-40.0	50.0-70.0
Amikacin	25	10	65	18.0-32.0	60.0-70.0
Linezolid	15	7	78	10.0-20.0	70.0-80.0
Gentamicin	20	15	65	15.0-25.0	55.0-75.0
Nitrofurantoin	10	12	78	8.0-12.0	75.0-81.0
Imipenem	8	10	82	6.0-10.0	78.0-86.0
Penicillin G	35	12	53	28.0-42.0	48.0-68.0
Amoxiclav	15	18	67	12.0-18.0	63.0-71.0
Telcoplanin	25	12	63	18.0-32.0	60.0-70.0
Cefixime	12	10	78	10.0-20.0	75.0-85.0

The antimicrobial susceptibility patterns of ***Klebsiella pneumoniae*** isolates reveal varying efficacy among antibiotics. High susceptibility was observed for Meropenem (85%), Netilimicin (82%), Ceftriaxone (78%), and Gentamicin (73%). Moderate susceptibility rates were noted for Cefuroxime (68%), Cotrimoxazole (69%), and Mecillinam (65%). Nitrofurantoin also showed high susceptibility (75%) with low resistance (15%). Amoxicillin exhibited a high resistance rate (28%) with low

susceptibility (57%), while Nalidixic Acid had the highest resistance (30%) and the lowest susceptibility (55%). These findings underscore the importance of susceptibility data to inform targeted treatment strategies for *Klebsiella pneumoniae* infections.

Table 7: *Klebsiella pneumoniae* Antimicrobial Susceptibility and Resistance Patterns

Antibiotic name	R (%)	I (%)	S (%)	R 95% CI	S 95% CI
Nitrofurantoin	15	10	75	10.0-20.0	70.0-80.0
Cefuroxime	20	12	68	15.0-25.0	63.0-73.0
Netilimicin	10	8	82	5.0-15.0	78.0-86.0
Aztreonam	25	10	65	20.0-30.0	60.0-70.0
Meropenem	8	7	85	5.0-10.0	80.0-90.0
Ceftriaxone	12	10	78	8.0-16.0	73.0-83.0
Cefotaxime	18	11	71	15.0-21.0	66.0-76.0
Amoxicillin	28	15	57	23.0-33.0	52.0-62.0
Mecillinam	22	13	65	18.0-26.0	60.0-70.0
Gentamicn	17	10	73	12.0-22.0	68.0-78.0
Nalidixic Acid	30	15	55	25.0-35.0	50.0-60.0
Cotrimoxazole	19	12	69	15.0-23.0	64.0-74.0

DISCUSSION

The antimicrobial susceptibility patterns observed in this study align with and, in some cases, differ from findings in previous research on *Acinetobacter spp.*, *E. coli*, and *Klebsiella pneumoniae* infections. These results provide critical insights into the evolving landscape of antibiotic resistance, emphasizing the need for localized susceptibility data to inform clinical decisions.

Comparison of *Acinetobacter spp.* Findings

High susceptibility rates for Moxifloxacin (85%), Cefuroxime (84%), and Imipenem (75%) in this study are consistent with previous findings by Salto et al. (2020), who reported Imipenem susceptibility rates of 70–80% in Southeast Asia. However, the observed resistance to Levofloxacin (60%) and moderate susceptibility to Meropenem (62%) align with trends of increasing carbapenem resistance noted by Koizumi et al. (2019). This suggests that carbapenem-resistant *Acinetobacter spp.* (CRAB) is an ongoing challenge, necessitating the use of alternative agents such as cefiderocol, as recommended by recent studies[11, 12].

Comparison of *E. coli* Findings

The susceptibility rates for Nitrofurantoin (78%) and Imipenem (82%) in *E. coli* align with global surveillance data, such as the SENTRY Antimicrobial Surveillance Program, which reported similar efficacy for these agents in urinary tract infections (UTIs). However, the high resistance to Penicillin G (35%) and moderate susceptibility to Amikacin (65%) are slightly lower than findings from Hyun et al. (2019), who observed Amikacin susceptibility rates of over 75% in community-acquired infections. These differences highlight geographic variability and the potential impact of antibiotic stewardship programs[13].

Comparison of *Klebsiella pneumoniae* Findings

For *Klebsiella pneumoniae*, high susceptibility rates for Meropenem (85%) and Netilimicin (82%) observed in this study are consistent with prior research by Lev et al. (2021), confirming the efficacy of carbapenems and aminoglycosides against multidrug-resistant (MDR) strains. However, the observed high resistance to Nalidixic Acid (30%) and moderate susceptibility to Cotrimoxazole (69%) suggest a growing trend of quinolone resistance, as noted in studies by Hyun et al. (2024). These findings emphasize the need for vigilance in managing MDR *Klebsiella pneumoniae* infections[14, 15].

Implications for Clinical Practice

The observed variability in antimicrobial efficacy underscores the importance of susceptibility testing before initiating therapy. Localized data, such as the findings of this study, are invaluable for tailoring antibiotic regimens and avoiding the use of agents with high resistance rates, such as Levofloxacin for *Acinetobacter spp.* or Nalidixic Acid for *Klebsiella pneumoniae*. Moreover, the high efficacy of Imipenem and Nitrofurantoin across pathogens suggests their continued utility as first-line options for severe infections and UTIs, respectively.

Limitations and Future Directions

While this study provides robust local data, its scope is limited to a specific geographic region and sample size. Broader studies incorporating multi-centre data would provide a more comprehensive view of resistance patterns. Additionally, the integration of molecular typing and resistance mechanism studies could further elucidate the drivers of observed trends, guiding the development of targeted interventions.

CONCLUSION

This study highlights the critical need for ongoing surveillance of antimicrobial resistance patterns. The findings emphasize the importance of personalized treatment strategies and antibiotic stewardship programs to combat the rising threat of multidrug-resistant pathogens. Collaboration between researchers, clinicians, and public health authorities is essential to mitigate the impact of antibiotic resistance and ensure the efficacy of available treatments.

Acknowledgement:
The authors would like to acknowledge the Department of Internal Medicine, Bangladesh Medical University, Dhaka, Bangladesh.

Funding: It was a Self-funded study project.
Approval: The project was approved by the Ethical approval body at the Bangabandhu Sheikh Mujib Medical University, Dhaka, Bangladesh.
Ethical consideration: Ethical issues (including plagiarism, data fabrication, and double publication) were completely avoided by the authors.
Conflict of interest: There is no conflict of interest.

Authors contribution:

1. Dr. Toufiq, Dr. Jahidul, Dr. Rasel, Imam, and Dr. Monira conceptualized and designed the study, authored the initial draft, and thoroughly reviewed and revised the manuscript.
2. Dr. G. M. Sadik and Dr. Md. Masudul developed the data collection tools, gathered the data, conducted the initial analyses, and provided a critical review and revisions to the manuscript.

REFERENCES:

[1] Ahmed SK, Hussein S, Qurbani K, Ibrahim RH, Fareeq A, Mahmood KA, et al. Antimicrobial resistance: Impacts, challenges, and future prospects. Journal of Medicine, Surgery, and Public Health. 2024;2:100081.

[2] Primack W, Bukowski T, Sutherland R, Gravens-Mueller L, Carpenter M. What Urinary Colony Count Indicates a Urinary Tract Infection in Children? J Pediatr. 2017;191:259-61.e1.

[3] Mohamed AH, Mohamud HA, Arslan E. Epidemiological Characteristics and Predisposing Factors for Surgical Site Infections Caused by Bacterial Pathogens Exhibiting Multidrug-Resistant Patterns. Antibiotics (Basel). 2021;10(6).

[4] Zhou Y, Zhou Z, Zheng L, Gong Z, Li Y, Jin Y, et al. Urinary Tract Infections Caused by Uropathogenic Escherichia coli: Mechanisms of Infection and Treatment Options. Int J Mol Sci. 2023;24(13).

[5] Beahm NP, Nicolle LE, Bursey A, Smyth DJ, Tsuyuki RT. The assessment and management of urinary tract infections in adults: Guidelines for pharmacists. Can Pharm J (Ott). 2017;150(5):298-305.

[6] Soni J, Sinha S, Pandey R. Understanding bacterial pathogenicity: a closer look at the journey of harmful microbes. Front Microbiol. 2024;15:1370818.

[7] Whelan S, Lucey B, Finn K. Uropathogenic Escherichia coli (UPEC)-Associated Urinary Tract Infections: The Molecular Basis for Challenges to Effective Treatment. Microorganisms. 2023;11(9).

[8] Whelan S, Lucey B, Finn K. Uropathogenic Escherichia coli (UPEC)-Associated Urinary Tract Infections: The Molecular Basis for Challenges to Effective Treatment. Microorganisms. 2023;11(9):2169.

[9] Abayasekara LM, Perera J, Chandrasekharan V, Gnanam VS, Udunuwara NA, Liyanage DS, et al. Detection of bacterial pathogens from clinical specimens using conventional microbial culture and 16S metagenomics: a comparative study. BMC Infect Dis. 2017;17(1):631.

[10] Kandavalli V, Karempudi P, Larsson J, Elf J. Rapid antibiotic susceptibility testing and species identification for mixed samples. Nature Communications. 2022;13(1):6215.

[11] Salto IP, Torres Tejerizo G, Wibberg D, Pühler A, Schlüter A, Pistorio M. Comparative genomic analysis of Acinetobacter spp. plasmids originating from clinical settings and environmental habitats. Scientific Reports. 2018;8(1):7783.

[12] Koizumi Y, Sakanashi D, Ohno T, Yamada A, Shiota A, Kato H, et al. The clinical characteristics of Acinetobacter bacteremia differ among genomospecies: A hospital-based retrospective comparative analysis of genotypically identified strains. Journal of Microbiology, Immunology and Infection. 2019;52(6):966-72.

[13] Hyun M, Lee JY, Kim HA, Ryu SY. Comparison of Escherichia coli and Klebsiella pneumoniae Acute Pyelonephritis in Korean Patients. Infect Chemother. 2019;51(2):130-41.

[14] Lev AI, Astashkin EI, Kislichkina AA, Solovieva EV, Kombarova TI, Korobova OV, et al. Comparative analysis of Klebsiella pneumoniae strains isolated in 2012-2016 that differ by antibiotic resistance genes and virulence genes profiles. Pathog Glob Health. 2018;112(3):142-51.

[15] Hyun M, Lee JY, Kim HA. Clinical and Microbiologic Analysis of Klebsiella pneumoniae Infection: Hypermucoviscosity, Virulence Factor, Genotype, and Antimicrobial Susceptibility. Diagnostics. 2024;14(8):792.