

Prevalence and comparative analysis of bacterial pathogen in pus, sputum and urine samples: A prospective comparative analysis

Anuja Anil ^{1,*}, Devipriya S ¹, Gouri Krishna ¹, Akhila S Arjun ², Chitra C Nair ³ and Beena p ⁴

¹ Pharm D student Department of Pharmacy Practice, KVM College of Pharmacy, Cherthala, Kerala, India.

² Assistant professor, KVM College Of Pharmacy, Cherthala, Kerala, India.

³ Professor & HOD, Department of Pharmacy Practice, KVM College of Pharmacy, Cherthala, Kerala, India.

⁴ Principal, KVM College of Pharmacy, Cherthala, Kerala, India.

World Journal of Advanced Research and Reviews, 2026, 31(02), 437–445

Publication history: Received on 29 June 2026; revised on 06 August 2026; accepted on 08 August 2026

Article DOI: <https://doi.org/10.30574/wjarr.2026.31.2.2080>

Abstract

Objective: To compare and contrast the prevalence and antibiotic resistance pattern of bacterial isolates collected from different samples of pus, sputum and urine in a tertiary care hospital and to identify the prevalence of multidrug-resistant (MDR), extended-spectrum beta-lactamase (ESBL), and AmpC producing organisms.

Methods: A total of 170 patient cases selected using inclusion and exclusion criteria from Microbiology department over a period of 6 months. Case records were prospectively reviewed and data on age, gender, presenting complaints, number of hospital days, comorbid conditions, lab investigation data, diagnostic test, and therapeutic management were collected in a specially designed data collection form. Culture sensitivity reports were reviewed to analyse the Bacterial isolates. Bacterial strains of MDR, AmpC and ESBL were found using identification methods.

Results: The most isolated organisms included *Escherichia coli*, *Klebsiella* species, *Pseudomonas* species, and *Staphylococcus aureus*. Pus infections were more prevalent in males, whereas urine and sputum infections were more common in females. A higher prevalence of these three types of infections was observed in patients above 60 years of age. *Staphylococcus aureus* was the most frequent organism isolated from pus samples, *Klebsiella* species were predominant in sputum samples, and *E. coli* was the most common isolate in urine samples. Multidrug resistance (MDR) was detected across sputum (8.57%), pus (3.03%), and urine (6.86%) samples. Extended-spectrum beta-lactamase (ESBL) production in sputum samples were observed in *E. coli* (5.71%), while AmpC production was found in *Klebsiella* species (2.85%). In urine samples, ESBL production was detected in *E. coli* (11.76%), and AmpC production was identified in both *Klebsiella* species and *E. coli* (7.84%).

Conclusion: This study suggests the need for continuous antibiotic susceptibility studies in various clinical samples to guide effective empirical therapy and to control the spread of resistance

Keywords: AmpC; CLSI; ESBL; MDR

1. Introduction

Antimicrobial resistance develops when a microorganism is able to survive and continue to grow in the presence of antimicrobial agent at a concentration that would normally kill or inhibit its growth. In 2019, 4.95 million deaths are associated with bacterial AMR, including 1.27 million deaths attributable to bacterial resistance. From the discovery and development of antimicrobial agents the survival rate from infection is increasing day by day however with the

* Corresponding author: Anuja Anil

introduction of new antimicrobial agents, microorganisms live and develop resistance. Antimicrobial resistance has been described as one of the most serious global threat in the 21st century. However, after 1960's only few classes of antibiotics have been developed.

Most commonly identified infection in clinical practice are bacterial infections of the wound, respiratory tract, urinary tract and skin. In order to identify the causative organisms and to determine their susceptibility pattern pus, sputum, urine samples were collected. Culture and sensitivity testing help the physician to select appropriate antibiotic therapy. In pus samples *S. aureus*, *Pseudomonas aeruginosa*, and *Klebsiella* species are frequently identified while *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Streptococcus pneumoniae* are often present in sputum samples. *E. coli* was the predominant pathogen isolated from urine samples, followed by *Klebsiella* species, *Proteus* species, and *Enterococcus* species.

The increasing prevalence of resistant bacterial strains has tangled the treatment of infection leading to morbidity and mortality. One of the important mechanisms of antibiotic resistance are the production of enzymes such as Extended-Spectrum Beta-Lactamase (ESBL) and AmpC Beta-Lactamase. ESBL-producing bacteria can hydrolyse a wide range of beta-lactam antibiotics, which include third-generation cephalosporins, leading to treatment failure. Therefore, monitoring of antibiotic resistance pattern of bacterial isolates from pus, sputum and urine is crucial.

2. Methods

2.1. Study Design

A prospective comparative Study

2.2. Study Centre

Study was conducted in the Microbiology Department at SH medical Centre, Kottayam, Kerala

2.3. Study Duration

6 months

2.4. Inclusion Criteria

- Culture reports of IP patients of all ages and gender whose pus, sputum and urine samples submitted for culture and sensitivity testing
- Samples with minimum sample volume
- 3. Patients with symptoms related to the infection

2.5. Exclusion Criteria

- Contaminated samples.
- Patients with carcinogenic disease conditions.
- Patient with incomplete medical Data
- Pregnant women

Procedure: All relevant and necessary data of the patient were collected from patient's case record and microbiology department bacterial isolates were identified using standard microbiological techniques, such as Gram staining, colony morphology, and biochemical tests as per CLSI guidelines. MacConkey agar and Blood agar were the culture medium used for identification as well as C/S testing of bacteria. Patient data including age, gender, clinical details, laboratory investigations, and treatment information were recorded using an organized Data collection form. Patient confidentiality and ethical guidelines were strictly maintained throughout the entire study period.

3. Result

Table 1 Frequency and percentage distribution of culture positive samples (n =600)

Sample	No. Of Samples Collected	No. of Positive Samples	Percentage [%]
PUS	200	33	16.5
SPUTIM	200	35	17.5
URINE	200	102	51

Urine sample demonstrated the highest culture positivity (51.0%), followed by sputum (17.5%) and pus (16.5%)

3.1. Gender distribution

Table 2 Frequency and percentage distribution of positive sample based on gender N=120

Gender	Frequency	Percentage [%]
Male	76	44.70
Female	94	55.30

Among 170 positive samples cases a higher prevalence of bacterial infections in females (55%) compared to males (45%) due to hormonal fluctuations, anatomical difference, and physiological factors that can influence the immune response

3.2. Age distibution

Table 3 Frequency and percentage distribution of positive samples based on age group

AGE GROUP	FREQUENCY	PERCENTAGE (%)
0-12	9	5.29
13-20	1	0.58
21-45	11	6.47
45-60	29	17.05
>60	120	70.58

The percentage distribution of various samples across different age group , indicating that the majority (71%) occur on patient over 60 years of age .This is probably due to weakned immune system and anatomical changes of the elderly

Table 4 Frequency and percentage distribution of Bacterial isolates

ORGANISM	PUS		SPUTUM		URINE	
	Freq (n=36)	%	Freq (n=36)	%	Freq (n=36)	%
<i>E. coli</i>	4	12.12	5	14.28	57	55.88
<i>Klebsiella species</i>	5	15.15	13	37.14	19	18.62
<i>Proteus mirabilis</i>					2	1.96
<i>Pseudomonas aeruginosa</i>	2	6.06	10	28.5	15	14.70
<i>Staphylococcus aureus</i>	21	63.63	1	2.85		
<i>Streptococcus species</i>	4	12.12	5	14.28		

<i>Enterococcus species</i>			2		10	9.80
-----------------------------	--	--	---	--	----	------

- *E. coli*, *Klebsiella* species and *Pseudomonas* species were isolated from all of the three samples.
- *E. coli* was the predominant organism isolated from urine samples, *Staphylococcus aureus* was the most commonly isolated organism from pus samples, and *Klebsiella* species were the predominant organisms isolated from sputum samples

3.3. Pus samples (n=33)

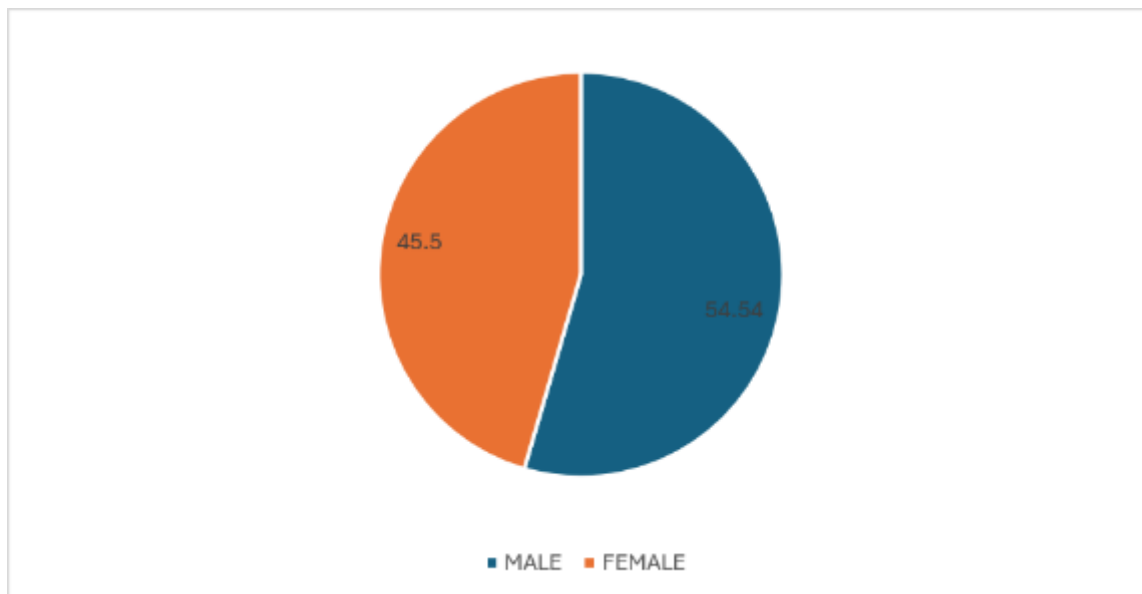


Figure 1 Frequency and percentage distribution of positive pus samples according to gender

3.4. Sputum samples (n=35)

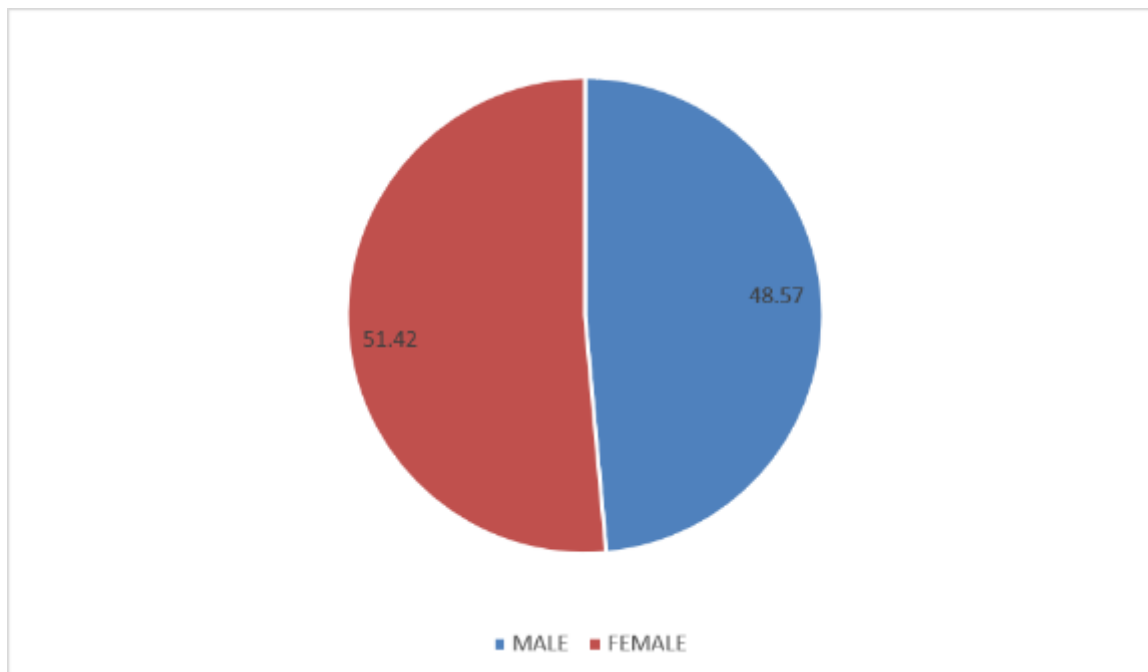


Figure 2 Frequency and percentage distribution of positive sputum samples according to gender

3.5. Urine samples (n=102)

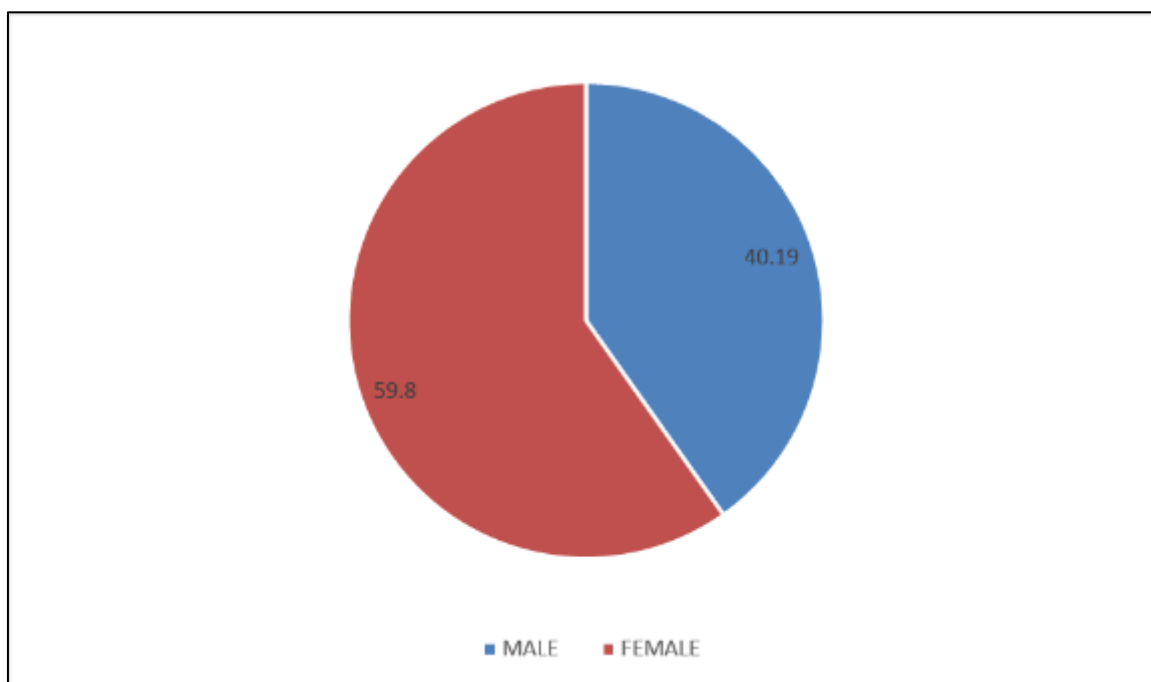


Figure 3 Frequency and percentage distribution of positive urine samples according to gender

3.6. Frequency and percentage distribution according to age group

Table 5 Frequency and percentage distribution of positive pus samples according to age group

Age group	Frequency	Percentage (%)
0-12 yrs	-	-
13-20 yrs	1	3.30
21-45yrs	4	12.12
45-60yrs	12	36.36
>60yrs	16	48.48

This table illustrates pus infection with highest proportion (49%) in the age above 60 due to age related weakened immune system and structural changes in elderly

Table 6 Frequency and percentage distribution of positive sputum samples according to age group

Age group	Frequency	Percentage (%)
0-12 yrs	2	5.71
13-20 yrs	-	-
21-45yrs	3	8.57
45-60yrs	5	14.28
>60yrs	25	71.42

The percentage distribution of respiratory tract infections across different age groups, indicating that the majority of cases (71%) occur in patients over 60 years of age.

Table 7 Frequency and percentage distribution of positive urine samples according to age group

Age group	Frequency	Percentage (%)
0-12 yrs	7	6.86
13-20 yrs	-	
21-45yrs	4	3.92
45-60yrs	12	11.76
>60yrs	79	77.45

Urinary tract infections appear to be most prevalent in the age group over 60, accounting for 77% of the cases shown table.

3.7. Frequency and percentage distribution according to organism

Table 8 Frequency and percentage distribution of isolated organisms in pus sample n = 36

Type of organism	frequency	Percentage (%)
Gram positive	25	69.44
Gram negative	11	30.55

The gram-positive bacteria isolated from pus samples are *Staphylococcus aureus* (63.63%) and *Streptococcus species* (12.12%).

The gram-negative bacteria isolated from pus samples are *E. coli* (12.12%), *Klebsiella species* (15.15%) and *Pseudomonas aeruginosa* (6.06%).

Table 9 Frequency and percentage distribution of isolated organisms in sputum sample n =36

Type of organism	frequency	percentage (%)
Gram positive	8	22.22
Gram negative	28	77.77

The gram-positive bacteria isolated from sputum samples are *Enterococcus* (5.71%) and *Streptococcus* bacteria (14.28%).

The gram-negative bacteria isolated from sputum samples are *E.coli* (14.28%), *Klebsiella species* (37.14%) and *Pseudomonas aeruginosa* (28.50%).

Table 10 Frequency and percentage distribution of isolated organisms in urine samples n =103

Type Of Organism	Frequency	Percentage (%)
Gram Positive	10	9.80
Gram Negative	93	91.17

The gram-positive bacteria isolated from urine samples are *Enterococcus bacteria* (9.80%).

The gram-negative bacteria isolated from urine samples are *E.coli* (55.88%), *Klebsiella species* (18.62%), *Proteus mirabilis* (1.96%) and *Pseudomonas aeruginosa* (14.70%).

3.8. Frequency and percentage distribution of esbl, mdr, ampc strain in different samples

Table 11 Frequency and percentage distribution of ESBL, MDR and AmpC strains in pus samples n =33

Type of Organism	Frequency	Percentage (%)
ESBL	0	0
MDR	1	3.03
AmpC	0	0

Among the 33 pus samples with positive bacterial growth, one strain was found to be Multidrug resistant (MDR).

MDR is shown by *Staphylococcus aureus*.

Table12 Frequency and percentage distribution of ESBL, MDR and AmpC strains in sputum samples n=35

Type of organism	Frequency	Percentage (%)
ESBL	2	5.71
MDR	3	8.57
AmpC	1	2.85

From the 35 culture-positive sputum samples, 3 strains exhibited MDR, 2 were identified as ESBL producers, and 1 as an AmpC beta-lactamase producer.

MDR is shown by *Klebsiella species*, ESBL producers are by *E. coli*, and AmpC producer is *Klebsiella species*.

Table 13 Frequency and percentage distribution of ESBL, MDR and AmpC strains in urine samples n=102

Type of organism	Frequency	Percentage (%)
ESBL	12	11.76
MDR	7	6.86
AmpC	8	7.84

Out of a total of 102 urine samples with bacterial growth, 7 isolates exhibited multidrug resistance (MDR), 12 were extended-spectrum beta-lactamase (ESBL) producers, and 8 were AmpC beta-lactamase producers.

- MDR is shown by *E. coli* and *Klebsiella species*, *Pseudomonas aeruginosa*.
- AmpC is shown by *Klebsiella species* and *E. coli*.
- ESBL is shown by *E. coli*

4. Discussion

This research was conducted to compare and contrast the prevalence and antibiotic resistance pattern of bacterial isolates across pus, sputum and urine samples. These findings highlight the growing threat of Antimicrobial Resistance (AMR) to effective clinical management of Infectious diseases.

Among the three clinical specimens, urine samples showed the highest culture positivity (51%), followed by sputum (17.5%) and pus (16.5%). This higher positivity in urine samples is consistent with the high prevalence of urinary tract infections in hospital and community settings, particularly among elderly individuals and females. The predominance of infections in patients above 60 years of age may be attributed to age-related decline in immune function, multiple comorbidities, frequent hospitalization, and increased exposure to invasive procedures.

The most frequently isolated organisms were *E.Coli*, *Klebsiella species*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* etc. The predominant one found in pus samples was *Staphylococcus aureus* (63.63%), while *Klebsiella species* (37.14%) and *E.Coli* (55.88%) in sputum and urine respectively. Gender-wise analysis revealed that pus infections were slightly more common among males, whereas urine and sputum infections were more frequent among females. The higher incidence of urinary tract infections in females can be explained by anatomical factors such as a shorter urethra and its proximity to the perianal region, which facilitate bacterial colonization. The predominance of wound infections among males may be associated with greater occupational exposure, trauma, and skin injuries.

A considerable proportion of isolates exhibited multidrug resistance, reflecting the increasing burden of antimicrobial resistance in tertiary care hospitals. The high prevalence of ESBL- and AmpC-producing organisms observed in this study further highlights the need for routine surveillance and appropriate antimicrobial stewardship interventions.

The emergence of resistant Gram-negative organisms observed in this study reflects the growing global challenge of antimicrobial resistance. Excessive antibiotic consumption, inappropriate empirical prescribing, prolonged hospitalization, and inadequate infection-control practices are recognized contributors to this problem. Periodic monitoring of resistance trends and development of institution-specific antibiograms are therefore essential to optimize empirical antibiotic therapy and reduce the spread of resistant pathogens.

The study has certain limitations. It was conducted in a single tertiary care hospital over a relatively short duration with a limited sample size, which may restrict the generalizability of the findings. Molecular characterization of resistance genes responsible for ESBL and AmpC production was not performed, and patient-related risk factors associated with multidrug resistance were not evaluated. Future multicentre studies involving larger populations and molecular techniques would provide a more comprehensive understanding of antimicrobial resistance patterns and their epidemiology.

Overall, the findings of this study reinforce the need for routine culture and antimicrobial susceptibility testing, rational antibiotic prescribing, strict infection prevention measures, and continuous antimicrobial stewardship programmes. Such interventions are essential to preserve the effectiveness of existing antibiotics and improve patient outcomes in tertiary care settings.

5. Conclusion

The present study evaluated the prevalence and antimicrobial resistance patterns of bacterial isolates obtained from pus, sputum, and urine samples in a tertiary care hospital. The findings demonstrated that Gram-negative bacteria were the predominant pathogens, with *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Proteus* species accounting for the majority of isolates, while *Staphylococcus aureus* was the most common Gram-positive organism. A substantial proportion of isolates exhibited multidrug resistance, including ESBL- and AmpC-producing strains, highlighting the increasing burden of antimicrobial resistance in clinical practice.

The comparative analysis of bacterial isolates from pus, sputum, and urine samples highlights the variability in pathogen distribution and resistance profiles among different types of clinical infections. These findings emphasize the importance of specimen-specific microbiological diagnosis and susceptibility testing to ensure appropriate antimicrobial selection. Strengthening antimicrobial stewardship Programmes, promoting rational antibiotic use, and implementing effective infection prevention and control measures are essential to reduce the burden of multidrug-resistant organisms and improve patient outcomes in tertiary care settings.

Compliance with ethical standards

Acknowledgements

We express our sincere gratitude to the Department of Microbiology of SH Medical center Kottayam Kerala for granting permission to conduct the study and our Guide Dr. Akhila S Arjun her valuable assistance during data collection and our parents for constant support through our journey. Special appreciation is extended to the faculty members, laboratory personnel, and all those who contributed directly or indirectly to the successful completion of this research.

Disclosure of conflict of interest

The authors declare that there are no financial or non-financial conflicts of interest regarding the publication of this Research

Statement of ethical approval

The study was approved by the Institutional Ethics Committee

Statement of informed consent

Written informed consent was obtained from all study participants prior to enrolment

References

- [1] World Health Organization. Antimicrobial resistance. Fact sheet. 2020 [cited 2025 Jun 15]. Available from: <https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance>
- [2] Murray CJ, Ikuta KS, Sharara F, Swetschinski L, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet*. 2022;399(10325):629-655. doi:10.1016/S0140-6736(21)02724-0.
- [3] Centers for Disease Control and Prevention. Antibiotic resistance threats in the United States, 2019. Atlanta (GA): US Department of Health and Human Services; 2019.
- [4] Ventola CL. The antibiotic resistance crisis: part 1: causes and threats. *P T*. 2015;40(4):277-283.
- [5] National Centre for Disease Control. Integrated Disease Surveillance Programme. New Delhi: NCDC; 2021.
- [6] Aminov RI. A brief history of the antibiotic era: lessons learned and challenges for the future. *Front Microbiol*. 2010;1:134. doi:10.3389/fmicb.2010.00134.
- [7] Davies J, Davies D. Origins and evolution of antibiotic resistance. *Microbiol Mol Biol Rev*. 2010;74(3):417-433. doi:10.1128/MMBR.00016-10.
- [8] Paterson DL, Bonomo RA. Extended-spectrum beta-lactamases: a clinical update. *Clin Microbiol Rev*. 2005;18(4):657-686. doi:10.1128/CMR.18.4.657-686.2005.
- [9] Jacoby GA. AmpC beta-lactamases. *Clin Microbiol Rev*. 2009;22(1):161-182. doi:10.1128/CMR.00036-08.
- [10] World Health Organization. Global priority list of antibiotic-resistant bacteria to guide research, discovery and development of new antibiotics. Geneva: World Health Organization; 2017.
- [11] Brook I. Microbiology and management of soft tissue and muscle infections. *Int J Surg*. 2008;6(4):328-338. doi:10.1016/j.ijsu.2007.07.001.
- [12] Bowler PG, Duerden BI, Armstrong DG. Wound microbiology and associated approaches to wound management. *Clin Microbiol Rev*. 2001;14(2):244-269. doi:10.1128/CMR.14.2.244-269.2001.
- [13] Jain S, Williams DJ, Arnold SR, Ampofo K, Bramley AM, Reed C, et al. Community-acquired pneumonia requiring hospitalization among U.S. children. *N Engl J Med*. 2015;372(9):835-845. doi:10.1056/NEJMoa1405870.
- [14] Medina M, Castillo-Pino E. An introduction to the epidemiology and burden of urinary tract infections. *Ther Adv Urol*. 2019;11:1756287219832172. doi:10.1177/1756287219832172.
- [15] Gupta K, Hooton TM, Naber KG, Wullt B, Colgan R, Miller LG, et al. International clinical practice guidelines for the treatment of acute uncomplicated cystitis and pyelonephritis in women. *Clin Infect Dis*. 2011;52(5):e103-e120. doi:10.1093/cid/ciq257.
- [16] Yilmaz NO, Agus N, Bozcal E, Oner O, Uzel A. Detection of plasmid-mediated AmpC beta-lactamase in Enterobacteriaceae by a novel phenotypic method. *Indian J Med Microbiol*. 2013;31(1):53-59. doi:10.4103/0255-0857.108723.
- [17] Bush K, Bradford PA. Epidemiology of beta-lactamase-producing pathogens. *Clin Microbiol Rev*. 2020;33(2):e00047-19. doi:10.1128/CMR.00047-19.
- [18] Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 30th ed. CLSI supplement M100. Wayne (PA): CLSI; 2020.
- [19] Livermore DM. Beta-lactamases in laboratory and clinical resistance. *Clin Microbiol Rev*. 1995;8(4):557-584. doi:10.1128/CMR.8.4.557.
- [20] Coudron PE. Inhibitor-based methods for detection of extended-spectrum beta-lactamases. *Clin Microbiol Rev*. 2005;18(4):760-768. doi:10.1128/CMR.18.4.760-768.2005.