

Antimicrobial Resistance Patterns among Bacterial Isolates from a Tertiary Care Hospital in Nagaland: A Cross-Sectional Study

Tewe U Kapfo¹, Senjele Kath², Khriekuonuo Magdaline³, Mhasesalu Tetseo⁴,
Chewete U Kapfo⁵, K Romila Chawang⁶

¹Assistant Professor, Department of Community Medicine, ²Senior Resident, Department of General Medicine, ³Senior Resident, Department of Anesthesiology, ⁴Senior Resident, Department of Orthopedics, Nagaland Institute of Medical Sciences & Research, Kohima, Nagaland, India.

⁵Consultant, Department of General Surgery, Oking Hospital and Research Clinic, Kohima, Nagaland.

⁶Consultant, Department of Obstetrics and Gynaecology, Unakoti Multispecialty Hospital, Unakoti, Tripura.

Corresponding Author: Dr. Mhasesalu Tetseo

DOI: <https://doi.org/10.52403/ijshr.20260404>

Received: 12/05/2026; Revised: 28/08/2026; Accepted: 17/10/2026

ABSTRACT

Background: Antimicrobial resistance (AMR) is a major global health challenge, particularly in developing countries, where inappropriate antibiotic use and limited surveillance accelerate its emergence. Local data on resistance patterns are essential for guiding empirical therapy.

Objective: To assess the prevalence and patterns of antimicrobial resistance among bacterial isolates in a tertiary care hospital in Nagaland, India.

Methods: This hospital-based cross-sectional study was conducted at Naga Hospital Authority Kohima from July 2024 to April 2025. Adult patients (≥ 18 years) with culture-positive bacterial isolates from specimens including blood, urine, sputum, pus, and other body fluids were included. A total of 110 bacterial isolates from 96 patients were analyzed using consecutive sampling. Data were collected from hospital

records and analyzed using descriptive statistics.

Results: Gram-negative organisms predominated (82.7%), with *Klebsiella* spp. (29.1%), *Pseudomonas* spp. (20.9%), and *Escherichia coli* (15.5%) being the most common isolates. Pus (30.2%) and urine (27.1%) were the most frequent specimen types. High resistance was observed to ampicillin (88.7%), cefuroxime (74.1%), and cefotaxime (73.2%). Ciprofloxacin showed moderate resistance (58.3%), while gentamicin demonstrated lower resistance (26.7%). Carbapenems remained largely effective, though emerging resistance was noted in *Acinetobacter* spp. Gram-positive isolates showed complete sensitivity to vancomycin and linezolid.

Conclusion: A high prevalence of AMR was observed, particularly among Gram-negative bacteria, with significant resistance to commonly used antibiotics. Strengthening antimicrobial stewardship, surveillance, and

rational prescribing practices is essential to combat AMR.

Keywords: Antimicrobial resistance, Gram-negative bacteria, Nagaland, antibiotic resistance

INTRODUCTION

Antimicrobial resistance (AMR) is a growing global health concern that arises when microorganisms such as bacteria, viruses, fungi, and parasites evolve mechanisms that enable them to withstand the effects of antimicrobial agents. This renders commonly used drugs ineffective, leading to persistent infections, increased transmission, and higher morbidity and mortality. Since the early 20th century, with the introduction of Salvarsan in 1910 and the discovery of penicillin in 1928, antimicrobials have played a transformative role in reducing infectious disease burden and improving life expectancy [1]. However, the effectiveness of these agents is now being undermined by the rapid emergence and spread of resistant organisms.

Several factors contribute to the development and dissemination of AMR, including irrational prescribing practices, over-the-counter availability of antibiotics, incomplete treatment courses, and inadequate infection control measures. In addition, the absence of robust antimicrobial stewardship programs and surveillance systems in many healthcare settings accelerates the problem [2]. AMR has been termed a “silent pandemic” due to its widespread yet often underrecognized impact on global health. It was estimated that approximately 4.95 million deaths were associated with bacterial AMR in 2019 [3], with projections suggesting that this number could rise to 10 million deaths annually by 2050 if current trends continue [4].

The burden of AMR is particularly significant in developing countries such as India, where infectious diseases remain a leading cause of morbidity. High population density, limited healthcare resources, and widespread antibiotic misuse contribute to

the rapid emergence of resistance. India has been reported to have one of the highest rates of antibiotic consumption globally [5], which further exacerbates the problem. AMR not only leads to increased mortality and prolonged hospital stays but also imposes substantial economic burdens on individuals and healthcare systems. [6]

Although national surveillance initiatives such as the Antimicrobial Resistance Surveillance and Research Network (AMRSN) have provided valuable insights into resistance patterns in various parts of India, data from the northeastern region, including Nagaland, remain limited [7]. In the absence of region-specific data, empirical treatment becomes challenging and may contribute to inappropriate antibiotic use. Therefore, the present study was undertaken to assess the prevalence and patterns of antimicrobial resistance among bacterial isolates in a tertiary care hospital in Nagaland, with the aim of generating local evidence to guide antibiotic stewardship and inform public health strategies.

Objective

To assess the prevalence and patterns of antimicrobial resistance among bacterial isolates in a tertiary care hospital.

MATERIALS & METHODS

This hospital-based cross-sectional study was conducted at the Naga Hospital Authority Kohima (NHAK), a tertiary care teaching hospital affiliated with the Nagaland Institute of Medical Sciences and Research (NIMSR), Kohima, Nagaland, India, over a period of 10 months, from July 2024 to April 2025.

The study included bacterial isolates obtained from records of patients aged ≥ 18 years whose clinical specimens were submitted for culture and yielded bacterial growth during the study period. Specimens were received from both inpatient and outpatient departments, including General Medicine, General Surgery, Obstetrics and Gynaecology, and Orthopaedics.

Inclusion Criteria

Records of adult patients (≥ 18 years) with culture-positive bacterial isolates from clinical specimens, including blood, urine, sputum, pus, and other samples such as endotracheal tube aspirates, pleural fluid, and stool, were included.

Exclusion Criteria

Records with incomplete data, contaminated samples, and duplicate isolates from the same patient were excluded.

Sample Size

The sample size was calculated based on the study conducted by Mardourian et al. [6] in Karnataka, which reported a prevalence of 45% resistance to cephalosporins. The sample size was determined using the formula:

$$n = \frac{4pq}{d^2}$$

where $p = 45\%$, $q = 55\%$, and $d = 10\%$, yielding a minimum sample size of 96 patients.

A consecutive sampling technique was employed, and all eligible isolates obtained during the study period were included. Although the minimum calculated sample

size was 96 patients, a total of 110 bacterial isolates were analyzed, as organisms from polymicrobial samples were considered separate isolates.

Data Collection

Data were retrieved from patient case records using a pre-designed semi-structured proforma. The variables collected included demographic details, type of specimen, organism isolated, and antibiotic susceptibility results. Patient confidentiality was maintained by anonymizing all records.

Handling of Polymicrobial Isolates

In polymicrobial samples, each organism was included and analyzed as a separate isolate. Therefore, the unit of analysis was bacterial isolates rather than individual patient samples

Statistical Analysis

Data were entered into Microsoft Excel and analyzed using SPSS version 21. Descriptive statistics, including frequencies and percentages, were used to summarize the data. The distribution of organisms across specimen types and antimicrobial resistance patterns was analyzed.

RESULT

Table 1. Study participants

Variable		Frequency (n)	Percentage (%)
Gender	Male	47	49
	Female	49	51
Age group (years)	≤ 20	6	6.3
	21–30	21	21.9
	31–40	11	11.5
	41–50	15	15.6
	51–60	11	11.5
	≥ 61	32	33.3

Demographic Characteristics and Specimen Distribution

A total of 96 patients were included in the study, yielding 110 bacterial isolates. Among

the participants, 49 (51%) were females and 47 (49%) were males. The majority of patients belonged to the age group ≥ 61 years (33.3%) (Table 1).

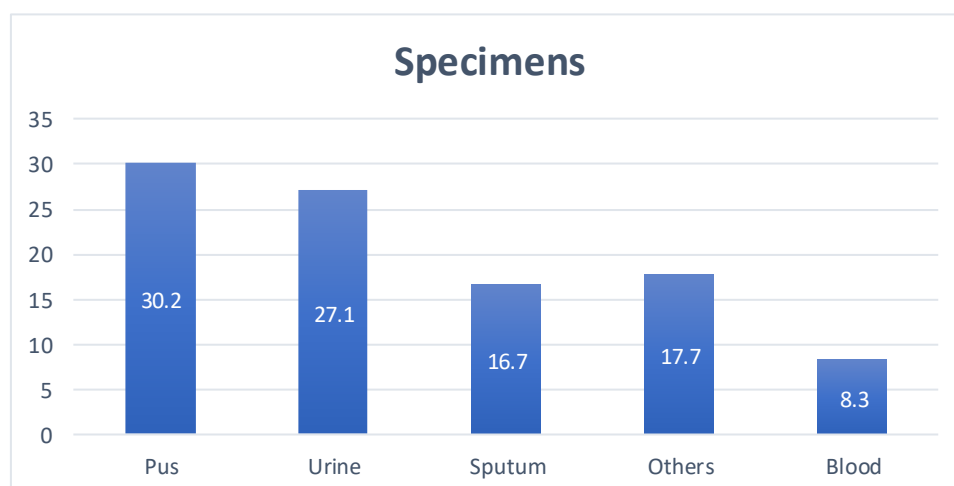


Fig. 1. Distribution of specimens

Pus (30.2%) was the most common specimen, followed by urine (27.1%), sputum (16.7%), other specimens (17.7%), and blood (8.3%) (Fig. 1).

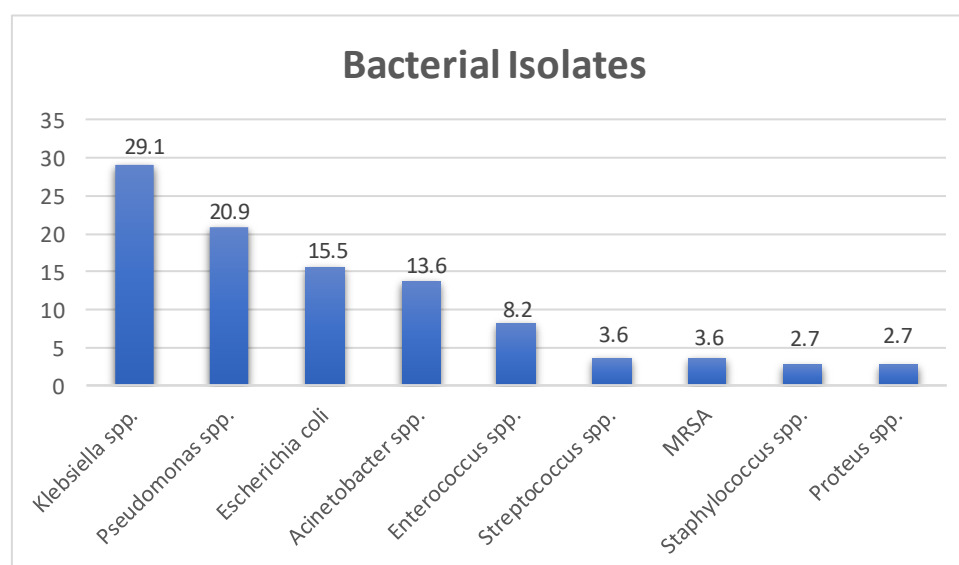


Fig. 2. Distribution of Bacterial Isolates

Gram-negative organisms predominated (82.7%). Klebsiella spp. (29.1%) was the most common isolate, followed by Pseudomonas spp. (20.9%) and Escherichia coli (15.5%) (Fig. 2).

Table 2. Distribution of Organisms Across Specimens

Organism	Blood n (%)	Urine n (%)	Sputum n (%)	Pus n (%)	Others n (%)
Klebsiella spp.	1 (3.1)	9 (28.1)	13 (40.6)	6 (18.8)	3 (9.4)
Pseudomonas spp.	5 (21.7)	4 (17.4)	3 (13.0)	8 (34.8)	3 (13.0)
E. coli	2 (11.8)	9 (52.9)	1 (5.9)	5 (29.4)	0 (0.0)
Acinetobacter spp.	0 (0.0)	0 (0.0)	0 (0.0)	7 (46.7)	8 (53.3)
Enterococcus spp.	0 (0.0)	6 (66.7)	0 (0.0)	0 (0.0)	3 (33.3)
Streptococcus spp.	0 (0.0)	1 (25.0)	1 (25.0)	1 (25.0)	1 (25.0)
MRSA	1 (25.0)	0 (0.0)	0 (0.0)	2 (50.0)	1 (25.0)
Staphylococcus spp.	0 (0.0)	0 (0.0)	0 (0.0)	2 (66.7)	1 (33.3)
Proteus spp.	0 (0.0)	1 (33.3)	0 (0.0)	2 (66.7)	0 (0.0)

The distribution of organisms varied across specimen types (Table 2). Urine samples were predominantly associated with E. coli and Enterococcus spp., while sputum

samples mainly yielded Klebsiella spp. Pus samples showed higher isolation of Pseudomonas spp. and Acinetobacter spp.

Table 3. Percentage Resistance to Commonly Used Antibiotics among Gram-negative Organisms

Antibiotic	Escherichia coli (n=17)	Klebsiella spp. (n=32)	Pseudomonas spp. (n=23)	Acinetobacter spp. (n=15)	Proteus spp. (n=3)
Ampicillin	88.2	93.8	87	100	66.7
Cefotaxime	70.6	75	73.9	86.7	66.7
Ceftazidime	76.5	78.1	69.6	80	66.7
Ciprofloxacin	64.7	62.5	60.9	73.3	33.3
Gentamicin	35.3	40.6	47.8	53.3	33.3
Amikacin	11.8	25	30.4	40	0
Piperacillin–Tazobactam	41.2	46.9	43.5	50	33.3
Imipenem	0	3.1	8.7	20	0
Meropenem	0	6.3	8.7	26.7	0

Antimicrobial susceptibility analysis of Gram-negative isolates (Table 3) revealed high resistance to beta-lactam antibiotics, particularly ampicillin and cephalosporins, along with moderate resistance to

fluoroquinolones. Aminoglycosides and carbapenems demonstrated relatively better activity, although Acinetobacter spp. showed emerging resistance.

Table 4. Percentage Resistance to Commonly Used Antibiotics among Gram-positive Organisms

Antibiotic	Enterococcus spp. (n=9)	MRSA (n=4)	Streptococcus spp. (n=4)	Staphylococcus spp. (n=3)
Ampicillin	77.8	—	—	—
Ciprofloxacin	55.6	—	50	33.3
Gentamicin	22.2	—	—	—
Penicillin	100	100	0	0
Erythromycin	50	50	50	0
Clindamycin	50	50	0	0
Vancomycin	0	0	0	0
Linezolid	0	0	0	0

Among Gram-positive isolates (Table 4), high resistance to penicillin and moderate resistance to macrolides and clindamycin were observed. Notably, all isolates were sensitive to vancomycin and linezolid.

Overall Antimicrobial Resistance Pattern

A high prevalence of antimicrobial resistance was observed across commonly used antibiotics. Ampicillin exhibited the highest resistance (88.7%), followed by cefuroxime (74.1%) and cefotaxime (73.2%). Moderate resistance was noted for ciprofloxacin (58.3%) and cotrimoxazole (55.4%), while amoxicillin-clavulanate showed resistance in 51.9% of isolates.

Among the tested antibiotics, gentamicin demonstrated the highest sensitivity (66.7%), followed by ciprofloxacin (38.8%) and amoxicillin-clavulanate (31.5%). Cephalosporins showed relatively low

sensitivity overall, with cefotaxime (22.5%) and cefuroxime (14.8%). Ampicillin exhibited the lowest sensitivity (11.3%), indicating limited clinical utility.

DISCUSSION

The present study highlights a high burden of antimicrobial resistance (AMR) among bacterial isolates in a tertiary care setting in Nagaland, with Gram-negative organisms predominating (82.7%). This finding is consistent with multicentric Indian surveillance data reported by Veeraraghavan et al. [8], where Gram-negative bacilli, particularly Klebsiella spp., Pseudomonas spp., and Escherichia coli, were the leading pathogens exhibiting significant resistance patterns. The predominance of Klebsiella spp. (29.1%) in this study aligns with the observations of Podschun and Ullmann [9], who described Klebsiella as a major

nosocomial pathogen, especially in respiratory and wound infections.

The higher proportion of elderly patients (≥ 61 years) in this study may have contributed to increased infection rates, as ageing is associated with immunosenescence and increased healthcare exposure, as described by Gavazzi and Krause [10]. The predominance of pus and urine samples suggests a higher burden of skin and soft tissue infections and urinary tract infections, comparable to findings reported by Dasgupta et al. [11] in tertiary care intensive care settings.

The distribution of organisms across specimens revealed expected trends, with *E. coli* and *Enterococcus* spp. predominating in urine samples and *Klebsiella* spp. predominating in sputum samples. These findings are consistent with established etiological patterns of urinary tract infections described by Flores-Mireles et al. [12] and respiratory infections reported by Singla et al. [13]. The high isolation of *Acinetobacter* spp. in pus and other specimens is concerning, as highlighted by Peleg et al. [14], given its ability to persist in hospital environments and its multidrug-resistant nature.

A key finding of this study was the high resistance to beta-lactam antibiotics, particularly ampicillin (88.7%) and cephalosporins ($>70\%$). This pattern suggests widespread production of extended-spectrum beta-lactamases (ESBLs), consistent with findings reported by Paterson and Bonomo [15]. Moderate resistance to fluoroquinolones (58.3%) further limits oral treatment options, reflecting overuse and misuse of these agents, as discussed by Ventola [16].

Encouragingly, aminoglycosides such as gentamicin showed relatively lower resistance (26.7%), and carbapenems retained good activity against most Gram-negative organisms. However, the resistance pattern observed in *Acinetobacter* spp., particularly against carbapenems, is concerning and warrants close surveillance. Carbapenem-resistant *Acinetobacter* has

been identified as a critical priority pathogen by the World Health Organization, as elaborated by Tacconelli et al. [17].

Among Gram-positive organisms, universal sensitivity to vancomycin and linezolid is reassuring and consistent with findings reported by Kaur and Chate [18]. However, high resistance to penicillin and moderate resistance to macrolides and clindamycin indicate limited therapeutic options. The presence of methicillin-resistant *Staphylococcus aureus* (MRSA), as described by Chambers and DeLeo [19], further emphasizes the need for stringent infection control practices.

Overall, the high resistance rates observed in this study may be attributed to irrational antibiotic use, lack of antimicrobial stewardship programs, and inadequate infection control practices. Similar trends have been reported globally, as emphasized by Laxminarayan et al., [2] where antibiotic misuse remains a major driver of AMR.

Limitations

This study has certain limitations. Being a single-Centre hospital-based study, the findings may not be generalizable to other healthcare settings or the wider community. As this was a record-based cross-sectional study, the analysis depended on the completeness and accuracy of existing laboratory and clinical records, making it susceptible to missing data and information bias. Important clinical variables such as prior antibiotic exposure, duration of hospital stay, comorbidities, and treatment outcomes were not assessed. In polymicrobial samples, each organism was analyzed as a separate isolate, which may have led to overrepresentation of certain pathogens and resistance patterns.

CONCLUSION

This study showed a high burden of antimicrobial resistance among bacterial isolates in a tertiary care hospital in Nagaland, with Gram-negative organisms predominating. High resistance was observed to commonly used antibiotics,

particularly beta-lactams and fluoroquinolones, while aminoglycosides and carbapenems remained relatively effective. The resistance pattern observed in *Acinetobacter* spp., especially against carbapenems, is a matter of concern and warrants close surveillance.

The findings highlight the need for antimicrobial stewardship, rational antibiotic prescribing, regular antibiogram-based surveillance, and strengthened infection prevention and control measures. Further multicentric studies are recommended to better understand regional antimicrobial resistance trends.

Declaration by Authors

Ethical Approval: Approved

Acknowledgement: None

Source of Funding: None

Conflict of Interest: The authors declare no conflict of interest.

Creative Commons Attribution License 4.0

This is an open-access article published under the terms of the Creative Commons Attribution 4.0 International License (CC BY 4.0).

<https://creativecommons.org/licenses/by/4.0>

REFERENCES

- Hutchings MI, Truman AW, Wilkinson B. Antibiotics: past, present and future. *Curr Opin Microbiol.* 2019; 51:72-80. doi: 10.1016/j.mib.2019.10.008.
- Laxminarayan R, Duse A, Wattal C, Zaidi AKM, Wertheim HFL, Sumpradit N, et al. Antibiotic resistance—the need for global solutions. *Lancet Infect Dis.* 2013;13(12):1057-98. doi:10.1016/S1473-3099(13)70318-9.
- Antimicrobial Resistance Collaborators. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet.* 2022;399(10325):629-55. doi:10.1016/S0140-6736(21)02724-0.
- O'Neill J. Tackling drug-resistant infections globally: final report and recommendations. London: Review on Antimicrobial Resistance; 2016.
- Kariuki S, Kering K, Wairimu C, Onsare R, Mbae C. Antimicrobial resistance rates and surveillance in Sub-Saharan Africa: where are we now? *Infect Drug Resist.* 2022; 15:3589-3609. doi:10.2147/IDR.S342753.
- Mardourian M, Lyons H, Brunner JR, Edwards MK, Lennox A, Mahadevaiah S, et al. Prevalence of antimicrobial resistance in urine, blood, and wound pathogens among rural patients in Karnataka, India. *Antimicrob Steward Healthc Epidemiol.* 2023;3(1): e91. doi:10.1017/ash.2023.162.
- Gandra S, Tseng KK, Arora A, Bhowmik B, Robinson ML, Panigrahi B, et al. The mortality burden of multidrug-resistant pathogens in India: a retrospective, observational study. *Clin Infect Dis.* 2019;69(4):563-570. doi:10.1093/cid/ciy955.
- Veeraraghavan B, Jesudason MR, Prakash JAJ, Anandan S, Sahni RD, Pragasam AK, et al. Antimicrobial susceptibility profiles of gram-negative bacteria causing infections collected across India during 2014-2016: study for monitoring antimicrobial resistance trend report. *Indian J Med Microbiol.* 2018; 36(1):32-36. doi: 10.4103/ijmm.IJMM_17_415.
- Podschun R, Ullmann U. *Klebsiella* spp. as nosocomial pathogens: epidemiology, taxonomy, typing methods, and pathogenicity factors. *Clin Microbiol Rev.* 1998;11(4):589-603. doi:10.1128/CMR.11.4.589.
- Gavazzi G, Krause KH. Ageing and infection. *Lancet Infect Dis.* 2002;2(11):659-66. doi:10.1016/S1473-3099(02)00437-1.
- Dasgupta S, Das S, Chawan NS, Hazra A. Nosocomial infections in the intensive care unit: incidence, risk factors, outcome and associated pathogens. *Indian J Crit Care Med.* 2015;19(1):14-20. doi:10.4103/0972-5229.148633.
- Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary tract infections: epidemiology, mechanisms, and treatment options. *Nat Rev Microbiol.* 2015;13(5):269-284. doi:10.1038/nrmicro3432.
- Singla A, Kumar N, Chaudhary P, Mamoria VP. Prevalence and antimicrobial susceptibility pattern of bacterial agents involved in lower respiratory tract infection at a tertiary care hospital, Jaipur, Rajasthan, India. *Natl J Lab Med.* 2021;10(4):M006-M009. doi: 10.7860/NJLM/2021/48829.2528
- Peleg AY, Seifert H, Paterson DL. *Acinetobacter baumannii*: emergence of a

- successful pathogen. Clin Microbiol Rev. 2008;21(3):538-82. doi:10.1128/CMR.00058-07.
15. Paterson DL, Bonomo RA. Extended-spectrum beta-lactamases: a clinical update. Clin Microbiol Rev. 2005;18(4):657-86. doi:10.1128/CMR.18.4.657-686.2005.
 16. Ventola CL. The antibiotic resistance crisis: part 1: causes and threats. P T. 2015;40(4): 277-283.
 17. Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, et al. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis. Lancet Infect Dis. 2018;18(3):318-327. doi:10.1016/S1473-3099(17)30753-3.
 18. Kaur DC, Chate SS. Study of antibiotic resistance pattern in methicillin resistant *Staphylococcus aureus* with special reference to newer antibiotic. J Glob Infect Dis. 2015;7(2):78–84. doi:10.4103/0974-777X.157245
 19. Chambers HF, DeLeo FR. Waves of resistance: *Staphylococcus aureus* in the antibiotic era. Nat Rev Microbiol. 2009;7(9): 629-41. doi:10.1038/nrmicro2200.

How to cite this article: Kapfo TU, Kath S, Magdaline K, Tetseo M, Kapfo CU, Chawang KR. Antimicrobial resistance patterns among bacterial isolates from a tertiary care hospital in Nagaland: a cross-sectional study. *Int. J. Sci. Healthc. Res.* 2026; 11(4): 33-40. DOI: <https://doi.org/10.52403/ijshr.20260404>
