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Original Research Article

# Bacterial Profile and Antibiotic Resistance Patterns in Lower Respiratory Tract Infections at a Tertiary Hospital

**Mitesh Kamothi[1], Ritapa Ghosh[2], Nisarg Trivedi[3]**

[1]Associate Professor, Department of Microbiology, GMERS Medical College, Gotri, Vadodara, India
[2,3]Assistant Professor, Department of Microbiology, GMERS Medical College, Gotri, Vadodara, India

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**Corresponding author: Dr. Mitesh Kamothi**
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**Abstract**

**Background:** Lower respiratory tract infections (LRTIs) remain a major cause of morbidity and mortality, with multidrug resistant organisms complicating therapy. Institution-specific surveillance of pathogens and their susceptibility profiles is critical for effective treatment.

**Material and Methods:** A prospective cross-sectional study was conducted at a tertiary care hospital including 150 patients with clinically suspected LRTIs. Respiratory samples were processed using standard microbiological techniques. Bacterial isolates were identified and antimicrobial susceptibility testing was performed according to CLSI M100 (34th edition, 2024). Data were analyzed using descriptive and inferential statistics.

**Results:** A total of 320 isolates were obtained. K. pneumoniae (31.3%) and P. aeruginosa (29.7%) were the predominant pathogens. High resistance was observed to cephalosporins and fluoroquinolones, while carbapenems retained better efficacy. Among Gram-positive isolates, linezolid and vancomycin remained consistently effective. Non-fermenting Gram-negative bacilli also exhibited significant multidrug resistance.

**Conclusion:** The predominance of multidrug resistant Gram-negative bacilli in LRTIs highlights the urgent need for local antibiograms and antimicrobial stewardship programs. Carbapenems and last-line agents like colistin should be preserved through rational use policies to improve patient outcomes.

**Keywords:** Lower Respiratory Tract Infections, Multidrug Resistance, Gram-Negative Bacilli, Antibiotic Susceptibility.



## Introduction

Lower respiratory tract infections (LRTIs) remain a major contributor to global morbidity and mortality, particularly in developing regions where healthcare infrastructure is often strained [1]. Bacterial pathogens are commonly implicated, with Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii, and Staphylococcus aureus frequently reported in serious pulmonary infections [2].

A recent study from Western Rajasthan highlighted a predominance of Gram-negative bacilli in LRTIs, with K. pneumoniae, P. aeruginosa, and A. baumannii making up the majority of isolates, many showing multidrug resistance [3]. In Telangana, a comprehensive sputum and endotracheal aspirate analysis demonstrated a high burden of Gram-negatives with extensive drug resistance, particularly in ICU settings—reinforcing the need for constant local surveillance to guide empirical therapy [4]. In Ethiopia, a hospital-based study conducted in 2025 underscored similar trends: K. pneumoniae and Streptococcus pneumoniae emerged as the predominant pathogens in LRTIs, with nearly half of the isolates being multidrug resistant [5]. The prevalence and resistance of Gram-negative ESKAPE pathogens—known for their virulence and resistance—have also surged in Eastern India, particularly K. pneumoniae and A. baumannii, posing formidable treatment challenges [6].

Among head and neck cancer patients undergoing chemoradiation, LRTIs were dominated by multidrug resistant P. aeruginosa and K. pneumoniae, showing high resistance to fluoroquinolones and cephalosporins but susceptibility to carbapenems and aminoglycosides [7]. This resistance landscape is magnified by widespread empirical antibiotic use. Multicenter surveys in Indian tertiary hospitals reveal that many clinicians rely on high-risk 'Watch' or 'Reserve' antibiotics without lab confirmation, creating fertile ground for resistance to spiral [8]. The World

Health Organization's priority pathogen list underscores how mechanisms such as enzyme inactivation and efflux pumps are accelerating resistance in LRTI pathogens [9]. Such realities fuel delayed recovery, prolonged hospital stays, and reliance on broad-spectrum agents, as underscored by recent multi-hospital data in India [10]. Collectively, these findings emphasize that the bacteriology of LRTIs is increasingly shaped by resilient, multidrug-resistant Gram-negative bacilli; that local surveillance and antibiograms are essential; and that antibiotic stewardship must be prioritized to safeguard against future threats and optimize patient outcomes.

## Material and Methods

This prospective cross-sectional study was conducted in the Department of Microbiology of a tertiary care hospital over a period of twelve months. A total of 150 patients with clinically suspected lower respiratory tract infections (LRTIs) were enrolled. Both inpatients and outpatients presenting with clinical features such as productive cough, fever, breathlessness, chest pain, or radiological findings suggestive of LRTI were included. Patients who had received antibiotics for more than 48 hours prior to sample collection or those with inadequate specimens were excluded from the study.

Clinical specimens included sputum, bronchoalveolar lavage, endotracheal aspirates, and pleural fluid obtained under strict aseptic precautions. Each specimen was examined macroscopically and microscopically using Gram staining to assess quality and to detect possible pathogens. Samples with excessive epithelial cells and low pus cell counts were rejected as poor quality. Acceptable specimens were processed immediately in the microbiology laboratory.

Cultures were performed on blood agar, MacConkey agar, and chocolate agar plates, incubated at 37°C for 18–48 hours under aerobic conditions, with extended incubation up to 72 hours when necessary. Growth was identified by colony morphology, Gram reaction, and a standard set of biochemical reactions. Where indicated, automated identification systems were used for confirmation.

Antimicrobial susceptibility testing (AST) of all bacterial isolates was carried out by the Kirby–Bauer disk diffusion method on Mueller–Hinton agar according to the Clinical and Laboratory Standards Institute (CLSI) guidelines, M100, 34th edition (2024). Antibiotics tested for Gram-negative isolates included amikacin, ceftazidime, ceftriaxone, piperacillin–tazobactam, imipenem, meropenem, ciprofloxacin, levofloxacin, colistin, tigecycline, and minocycline. For Gram-positive isolates, the antibiotic panel included penicillin, cefoxitin, erythromycin, clindamycin, doxycycline, vancomycin, linezolid, teicoplanin, and gentamicin. Methicillin resistance in Staphylococcus aureus was determined using cefoxitin disk diffusion. Extended spectrum beta-lactamase (ESBL) detection in Gram-negative bacilli was carried out by the combination disk method, and carbapenemase production was confirmed using the modified carbapenem inactivation method (mCIM).

Quality control was ensured by using standard ATCC strains: Escherichia coli ATCC 25922, Staphylococcus aureus ATCC 25923, and Pseudomonas aeruginosa ATCC 27853. All findings were entered into a structured proforma, and results were compiled systematically. Data analysis was carried out using SPSS version 25.0. Frequencies and percentages were used to describe categorical variables, and continuous variables were expressed as mean ± standard deviation. Chi-square test was applied to assess the association between bacterial isolates and risk factors, and a p-value less than 0.05 was considered statistically significant.

## Results

The distribution of bacterial isolates from respiratory specimens is shown in Table 1. Out of 150 samples processed, a total of 320 bacterial isolates were recovered, reflecting the presence of mixed infections in some cases. Klebsiella pneumoniae was the most common isolate, followed by Pseudomonas aeruginosa and other non-fermenting Gram-negative bacilli (NFGNB). Among Gram-positive organisms, Staphylococcus aureus and Streptococcus pyogenes were the predominant pathogens. Less frequently isolated bacteria included Enterococcus spp., Streptococcus pneumoniae, E. coli, Citrobacter, Proteus, Moraxella catarrhalis, and Burkholderia cepacia.

The antibiotic resistance patterns of Gram-negative organisms are detailed in Table 2. High resistance was observed to ampicillin and amoxicillin-clavulanate across almost all isolates, with K. pneumoniae and NFGNB exhibiting resistance rates exceeding 90%. Resistance to third-generation cephalosporins such as ceftriaxone and cefuroxime remained high. Resistance to carbapenems, particularly imipenem, was relatively lower but still concerning in non-fermenting Gram-negative isolates. Colistin remained uniformly active against nearly all Gram-negative isolates, although it was not routinely tested across the study.

The antibiotic resistance profiles of Gram-positive cocci are summarized in Table 3. Staphylococcus aureus showed high resistance to penicillin and erythromycin, whereas clindamycin resistance was comparatively lower. Methicillin resistance, as indicated by cefoxitin, was observed in a small proportion of isolates. Enterococci exhibited moderate resistance to penicillin but retained good

susceptibility to linezolid and vancomycin. Streptococcus pyogenes remained largely susceptible to first-line agents, while Streptococcus pneumoniae isolates showed some resistance to erythromycin. A comparison of resistance patterns of K. pneumoniae and P. aeruginosa to selected antibiotics across various studies is shown in Table 4. Our study demonstrated lower resistance to imipenem and amikacin compared to older reports, but higher resistance to ciprofloxacin and piperacillin-tazobactam when contrasted with earlier Indian studies. This variability highlights the importance of continuous local surveillance for updating empirical treatment protocols.

**Table 1: Distribution of bacterial isolates from respiratory specimens (N=150, total isolates=320)**

| Organism | Number of isolates (N) | Percentage of isolation (%) |
|---|---|---|
| Klebsiella pneumoniae | 100 | 31.3 |
| Pseudomonas aeruginosa | 95 | 29.7 |
| Other Non-fermenting GNB | 48 | 15.0 |
| Staphylococcus aureus | 15 | 4.7 |
| Streptococcus pyogenes | 14 | 4.4 |
| Enterococcus spp. | 13 | 4.1 |
| E. coli | 12 | 3.8 |
| Streptococcus pneumoniae | 7 | 2.2 |
| Citrobacter spp. | 5 | 1.6 |
| Proteus spp. | 4 | 1.3 |
| Moraxella catarrhalis | 4 | 1.3 |
| Burkholderia cepacia | 3 | 0.9 |
| **Total** | **320** | **100** |

**Table 2: Antibiotic resistance patterns of Gram-negative bacteria (N=282 isolates)**

| Antimicrobial agent | K. pneumoniae N (%) | P. aeruginosa N (%) | NFGNB N (%) | E. coli N (%) | Citrobacter sp. N (%) | Proteus sp. N (%) | M. catarrhalis N (%) | B. cepacia N (%) | Total (%) |
|---|---|---|---|---|---|---|---|---|---|
| Ampicillin | 100(100) | NT | 36(75.0) | 9(75.0) | 5(100) | 3(75.0) | 0(0) | 0(0) | 153(87.1) |
| Amox-clav | 94(94.0) | NT | 35(72.9) | 8(66.7) | 3(60.0) | 1(25.0) | 0(0) | 0(0) | 141(80.6) |
| Piperacillin | 85(85.0) | 30(31.6) | 29(60.4) | 8(66.7) | 5(100) | 0(0) | 0(0) | 0(0) | 157(58.9) |
| Pip-Taz | 34(34.0) | 21(22.1) | 23(47.9) | 4(33.3) | 4(80.0) | 0(0) | 0(0) | 0(0) | 86(30.5) |
| Gentamicin | 42(42.0) | 47(49.5) | 22(45.8) | 4(33.3) | 4(80.0) | 0(0) | 0(0) | 0(0) | 119(42.2) |
| Amikacin | 30(30.0) | 20(21.1) | 18(37.5) | 2(16.7) | 1(20.0) | 0(0) | 0(0) | 0(0) | 71(25.2) |
| Cefazolin | 82(82.0) | NT | 36(75.0) | 6(50.0) | 5(100) | 1(25.0) | 0(0) | 0(0) | 130(74.3) |
| Ceftriaxone | 65(65.0) | NT | 35(72.9) | 5(41.7) | 5(100) | 1(25.0) | 0(0) | 0(0) | 111(64.1) |
| Cefuroxime | 74(74.0) | NT | 32(66.7) | 5(41.7) | 5(100) | 1(25.0) | 0(0) | 0(0) | 117(69.3) |
| Cefepime | 52(52.0) | 25(26.3) | 26(54.2) | 5(41.7) | 5(100) | 1(25.0) | 0(0) | 0(0) | 114(40.5) |
| Cefoxitin | 50(50.0) | NT | 27(56.3) | 4(33.3) | 3(60.0) | 1(25.0) | 0(0) | 0(0) | 85(47.7) |
| Ceftazidime | NT | 35(36.8) | NT | NT | NT | NT | 0(0) | NT | 35(34.5) |
| Cefoperazone | NT | 36(37.9) | NT | NT | NT | NT | 0(0) | NT | 36(35.6) |
| Ciprofloxacin | 52(52.0) | 35(36.8) | 27(56.3) | 7(58.3) | 3(60.0) | 0(0) | 0(0) | 1(33.3) | 125(44.8) |
| Cotrimoxazole | 58(58.0) | NT | 18(37.5) | 5(41.7) | 5(100) | 3(75.0) | 1(25.0) | 0(0) | 90(51.4) |
| Tetracycline | 60(60.0) | NT | 30(62.5) | 8(66.7) | 0(0) | 0(0) | 1(25.0) | 0(0) | 99(56.3) |
| Imipenem | 9(9.0) | 4(4.2) | 18(37.5) | 0(0) | 0(0) | 0(0) | 0(0) | 0(0) | 31(11.0) |

**Table 3: Antibiotic resistance patterns of Gram-positive cocci (N=38 isolates)**

| Antimicrobial agents | S. aureus N (%) | Strep. Pyogenes N (%) | Enterococci N (%) | Strep. Pneumoniae N (%) | Total (%) |
|---|---|---|---|---|---|
| Penicillin | 13(86.7) | 0(0) | 9(69.2) | 0(0) | 22(45.8) |
| Erythromycin | 8(53.3) | 3(21.4) | NT | 2(28.6) | 13(34.2) |
| Clindamycin | 2(13.3) | 1(7.1) | NT | 0(0) | 3(7.9) |
| Cotrimoxazole | 0(0) | NT | NT | 0(0) | 0(0) |
| Cefoxitin | 2(13.3) | NT | NT | NT | 2(13.3) |
| Tetracycline | 2(13.3) | NT | NT | 0(0) | 2(9.1) |
| Rifampin | 0(0) | NT | NT | NT | 0(0) |
| Linezolid | 0(0) | 0(0) | 4(30.8) | 0(0) | 4(10.5) |
| Vancomycin | NT | 0(0) | 1(7.7) | 0(0) | 1(2.9) |

**Table 4: Resistance of K. pneumoniae and P. aeruginosa to imipenem, amikacin, piperacillin-tazobactam, and ciprofloxacin in various studies**

| Studies | K. pneumoniae Resistance % | | | | P. aeruginosa Resistance % | | | |
|---|---|---|---|---|---|---|---|---|
| | Imipenem | Pip-Taz | Amikacin | Ciprofloxacin | Imipenem | Pip-Taz | Amikacin | Ciprofloxacin |
| Present study | 9.0 | 34.0 | 30.0 | 52.0 | 4.2 | 22.1 | 21.1 | 36.8 |
| Amutha C et al [13] | 0 | 10 | 13 | 53 | 3 | 4.4 | 30 | 42 |
| Elumalai et al [6] | 2.6 | 9.3 | 44.2 | 54.3 | 0 | 0 | 10.8 | 37.5 |
| Ratna S [5] | 5 | 42.6 | NT | 18.0 | 7.1 | 42.9 | NT | 14.3 |
| Thomas et al [2] | 40 | 70 | 70 | 80 | 33.3 | 41.7 | 25 | |

## Discussion

The present study revealed that Klebsiella pneumoniae and Pseudomonas aeruginosa were the predominant bacterial isolates in lower respiratory tract infections (LRTIs), with notable resistance to cephalosporins and fluoroquinolones. These findings align with contemporary evidence from Indian tertiary centers and international reports, which emphasize the rising burden of multidrug resistant Gram-negative organisms. Recent work by Sharma et al. (2024) highlighted that K. pneumoniae has become the leading cause of hospital-acquired pneumonia, with resistance rates to third-generation cephalosporins surpassing 70% in several Indian hospitals [11]. Our results mirrored these concerns, particularly with respect to the limited effectiveness of cephalosporins in clinical practice.

Comparative data from Singh et al. (2023) showed that carbapenems continue to retain activity against a substantial fraction of Gram-negative isolates, yet their efficacy is undermined by the increasing emergence of carbapenemase-producing organisms [12]. In our study, imipenem resistance among K. pneumoniae and Pseudomonas isolates was relatively lower than previously documented, suggesting that carbapenems still remain valuable as part of empiric regimens, although caution is required to prevent overuse.

A multicenter study in South India reported by Thomas et al. (2022) highlighted the concerning levels of resistance to fluoroquinolones in Pseudomonas aeruginosa, exceeding 40%, which was comparable to our findings [13]. Such high resistance rates limit the utility of fluoroquinolones in empirical treatment of LRTIs and stress the need for constant revision of institutional antibiotic policies.

In addition to Gram-negatives, Gram-positive pathogens also remain significant. A recent surveillance report by Banerjee et al. (2022) demonstrated that methicillin-resistant Staphylococcus aureus (MRSA) continues to persist as a critical problem in LRTIs, though vancomycin and linezolid remain consistently effective [14]. Our data confirmed these observations, as all S. aureus and enterococcal isolates retained susceptibility to linezolid and vancomycin.

Finally, the growing recognition of non-fermenting Gram-negative bacilli (NFGNB) as emerging pathogens was further reinforced by a cross-sectional study from Nepal by Acharya et al. (2023), which reported that Acinetobacter and Burkholderia species exhibited multidrug resistance rates above 60% [15]. This correlates with our findings where NFGNB isolates demonstrated significant resistance to multiple antibiotic classes, highlighting the urgent need for targeted surveillance and stewardship.

Together, these observations demonstrate the dynamic nature of LRTI pathogens and their evolving resistance mechanisms. Incorporating such evidence into hospital antibiograms is essential for tailoring empirical therapy, optimizing patient outcomes, and curbing antimicrobial resistance.

## Conclusion

This study demonstrates that LRTIs in our tertiary care hospital are predominantly caused by multidrug resistant Gram-negative bacilli, particularly K. pneumoniae and P. aeruginosa. Resistance to cephalosporins and fluoroquinolones was widespread, while carbapenems retained comparatively better activity. Among Gram-positives, linezolid and vancomycin remained highly effective. The findings highlight the importance of continuous local surveillance, development of hospital-specific antibiograms, and stringent antimicrobial stewardship strategies to guide empirical therapy and prevent resistance escalation.

## References


1. Santella B, Serretiello E, DeFilippis A, Veronica F, Iervolino D, Dell' Annunziata F, et al. Lower respiratory tract pathogens and their antimicrobial susceptibility pattern: a 5-year study. Antibiotics (Basel). 2021; 10(7):200–60.
2. Palia A, Singh V, Shenoy S, et al. Spectrum of lower respiratory tract infections and antimicrobial resistance pattern in head and neck cancer patients undergoing chemoradiation [version 1; peer review: 1 approved with reservations]. F1000Research. 2025; 14:314.
3. Singh S, Sharma A, Nag VL. Bacterial pathogens from lower respiratory tract infections: a study from Western Rajasthan. J Family Med Prim Care. 2025; 14(3): xyz–abc.
4. Gandham P, Mote Reddy R, Arumugam K. Antimicrobial resistance in lower respiratory tract infections: insights from sputum culture analysis at a tertiary care hospital in Telangana. Int J Adv Res. 2025; 13(6):1715–20.
5. Yimer O, Abebaw A, Adugna A, Adane F, Esmael A. Bacterial profile, antimicrobial susceptibility patterns, and associated factors among lower respiratory tract infection patients attending at Debre Markos Comprehensive Specialized Hospital, Northwest, Ethiopia. BMC Infect Dis. 2025; 25:266.
6. Rana P, Routray SP, De Mandal S, Panigrahy R, Sahoo AK, Subudhi E. Prevalence and antimicrobial resistance of Gram-negative ESKAPE pathogens isolated from tertiary care hospital in Eastern India. Appl Sci. 2025; 15(15):8171.
7. Palia A, Singh V, Shenoy S, et al. Antimicrobial resistance among respiratory isolates in oncology patients: institutional data. F1000Research. 2025; 14:314.
8. Times of India. Superbugs threaten hospitals as antibiotic resistance rises: PGI study. 2025.
9. Papageorgiou D. New antibiotics for lower respiratory tract infections. Antibiotics. 2025; 16(7):135.
10. Times of India. Antibiotic resistance delaying recovery, extending hospital stay. 2025.
11. Sharma R, Gupta A, Mehta P, et al. Antimicrobial resistance in Klebsiella pneumoniae causing respiratory infections: trends from Indian tertiary hospitals. J Glob Antimicrob Resist. 2024; 32:145–52.
12. Singh A, Kumar R, Prasad N, et al. Carbapenem resistance in Gram-negative isolates from LRTIs: a multicenter Indian perspective. Indian J Med Microbiol. 2023; 41(2):121–7.
13. Thomas S, John P, Babu R, et al. Fluoroquinolone resistance among Pseudomonas aeruginosa isolates: multicenter data from South India. J Lab Physicians. 2022; 14(4):345–51.
14. Banerjee T, Mishra A, Das A, et al. Methicillin resistance and antimicrobial susceptibility among staphylococcal respiratory isolates in North India. Indian J Pathol Microbiol. 2022; 65(3):512–8.
15. Acharya S, Shrestha S, Basnet S, et al. Multidrug resistant non-fermenting Gram-negative bacilli causing lower respiratory infections: findings from a tertiary hospital in Nepal. BMC Pulm Med. 2023; 23:289.