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Corresponding Author
Muhammad Ramzan

Senior Registrar, Department of Medicine, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan

Email: Drramzanmushtaq@gmail.com

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Original Article

Prevalence, Clinical Spectrum, and Antibiotic Sensitivity Pattern of Gram-Negative Bacterial Respiratory Tract Infection in Hospitalized Adults: A Community-Based Study

Muhammad Ramzan[1],Shehlla Qadir[2],Sehrish Ijaz[3],Uzma Arshad[4],Zeemal Iqbal[5],Roha Fiaz[6]

1. Senior Registrar, Department of Medicine, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan
2. Assistant Professor, Department of Community Medicine, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan
3. Assistant Professor, Department of Pharmacology, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan
4. Associate Professor, Department of Community Medicine, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan
5. Assistant Professor, Department of Pharmacology, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan
6. Assistant Professor, Department of Medicine, Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan

Abstract

Objective: To determine the prevalence, clinical spectrum, and antibiotic sensitivity pattern of Gram-negative bacterial respiratory tract infections in hospitalized adults.

Methodology: This prospective Community-Based Study was conducted over 6 months at the Ibn-e-Siena Research Institute/Multan Medical and Dental College in Multan and included 150 adult patients with suspected respiratory tract infections.. We collected and processed respiratory samples, sputum, endotracheal aspirates, and bronchoalveolar lavage using standard microbiological techniques. We identified Gram-negative isolates and performed antibiotic susceptibility testing using the Kirby–Bauer disk diffusion method. We recorded and analyzed demographic details, presenting features, and comorbidities.

Results: We isolated Gram-negative bacteria in 102 of 150 patients (68%). Klebsiella pneumoniae was the most commonly identified organism (37.3%), followed by *Pseudomonas aeruginosa* (25.5%) and *Acinetobacter baumannii* (19.6%). Pneumonia was the most frequent clinical presentation (58.8%), followed by bronchitis and ventilator-associated pneumonia. A large proportion of patients had underlying comorbidities, diabetes mellitus (36%) and chronic obstructive pulmonary disease (28%). Antibiotic sensitivity testing revealed higher susceptibility to carbapenems such as meropenem (78%) and imipenem (75%), while resistance to commonly used antibiotics like ceftriaxone (65%) and ciprofloxacin (52%) was notable. Colistin showed the highest sensitivity (92%). Multidrug resistance was observed in 43.1% of isolates.

Conclusion: Gram-negative bacteria are a leading cause of RTI in hospitalized adults, with a high prevalence and significant association with multidrug resistance. The findings highlight the importance of surveillance of local bacterial patterns and antibiotic sensitivity to guide appropriate therapy and improve patient outcomes.

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Introduction

Respiratory tract infections (RTIs) are one of the most significant causes of morbidity and mortality among hospitalized adults worldwide. Among the many causative pathogens, Gram-negative bacteria have become a major issue because of their increasing prevalence, diverse clinical manifestations, and alarming patterns of antibiotic resistance.[1]. Although diagnostic techniques and antimicrobial therapy have improved, these infections remain a major problem in developing countries where healthcare resources may be limited.[2]. The epidemiology of respiratory tract infections has changed noticeably over the past few decades. Gram-positive organisms such as *Streptococcus pneumoniae* were considered the predominant pathogens in community-acquired infections.[3]Gram-negative bacteria such as Klebsiella *pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii,* and *Escherichia coli have* become increasingly important, especially in hospital-acquired and ventilator-related infections.[4]This change has significant clinical importance because Gram-negative pathogens are often linked with more severe disease, higher complication rates, prolonged hospital stays, as well as increased mortality.[5]The extensive use of invasive medical devices such as endotracheal tubes, ventilators, and other supportive devices can act as a channel for bacterial entry and colonization. Biofilm formation on these surfaces significantly reduces antibiotic penetration and increases bacterial survival.[6]This makes the infection more difficult to eliminate. This is particularly true in ventilator-associated pneumonia, where Gram-negative organisms are among the most commonly isolated pathogens.[7]Although advances in laboratory diagnostics, which include automated culture systems and molecular techniques, have improved pathogen detection, such facilities are not universally available.[8]In many healthcare settings, especially in resource-limited regions, clinicians must rely heavily on empirical treatment guided by local trends and clinical judgment. This further underscores the importance of prospective studies to generate accurate, context-specific data.[8]Antimicrobial resistance has now reached alarming levels globally, especially among Gram-negative bacteria.[9]The emergence of multidrug-resistant, extensively drug-resistant, and even pan-drug-resistant strains has severely limited treatment options. [7]. Resistance to carbapenems, considered highly reliable antibiotics, is increasingly reported among *Klebsiella pneumoniae* and *Acinetobacter baumannii*. Consequently, older antibiotics such as colistin are being reintroduced despite their known adverse effects.[10]Multiple factors, such as inappropriate prescribing habits, easy access to antibiotics without prescriptions, and poor adherence to treatment guidelines, often drive the development and spread of antibiotic resistance.[10]In hospital settings, the frequent use of broad-spectrum antibiotics without subsequent de-escalation contributes significantly to resistance. Antimicrobial stewardship programs aim to address these issues, but their implementation remains inconsistent, particularly in developing countries.

Material and Methods

This prospective Community-Based Study was conducted at the Ibn-e-Siena Research Institute/Multan Medical and Dental College, Multan, after ethical approval C-113-1071-A, dated Oct. 03, 2025. The study was conducted over 6 months, from October 2025 to May 2026. The study included adult patients admitted to the hospital with suspected respiratory tract infection. Only patients aged 18 years and above were considered eligible. The study included both male and female patients, with no gender-based restriction. A total of 150 patients were included using a non-probability consecutive sampling technique. All eligible patients admitted during the study period were considered until the required sample size was achieved. Patients were included in the study if they fulfilled the following criteria: Age ≥18 years; hospitalized patients with clinical features suggestive of respiratory tract infection, such as fever, cough, sputum production, dyspnea, or chest discomfort; radiological findings [chest X-ray or CT scan] supporting the diagnosis of respiratory infection, where applicable; microbiological evidence of Gram-negative bacterial infection obtained from respiratory samples. We excluded patients with confirmed or suspected viral respiratory infections without bacterial involvement, those already on long-term antibiotic therapy before admission, those with incomplete clinical or laboratory data, or those who refused to consent. After obtaining informed consent, we recorded detailed clinical information for each patient using a structured proforma. This included demographic details [age, gender], presenting symptoms, duration of illness, comorbid conditions [such as diabetes mellitus, chronic obstructive pulmonary

disease, chronic kidney disease], and history of prior hospitalization and previous antibiotic use. We documented clinical examination findings, including vital signs and respiratory examination. We also recorded laboratory investigations, including complete blood count, C-reactive protein [CRP], and other relevant biochemical parameters. We collected respiratory samples under aseptic conditions. These included sputum samples, endotracheal aspirates, or bronchoalveolar lavage [BAL] fluid, depending on the patient's clinical condition. We promptly transported all specimens to the microbiology laboratory for processing. We first examined samples macroscopically and microscopically to assess adequacy. We performed Gram staining for preliminary organism identification. We inoculated samples onto appropriate culture media, such as blood agar and MacConkey agar, and incubated them at 37°C for 24–48 hours. We identified bacterial growth based on colony morphology, Gram staining characteristics, and standard biochemical tests. We included only Gram-negative bacterial isolates in the final analysis. We excluded mixed growth or contaminated samples where appropriate. Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar, in accordance with standard laboratory guidelines [e.g., CLSI guidelines]. A panel of commonly used antibiotics was tested, including:

- Beta-lactams [e.g., cephalosporins]
- Carbapenems
- Aminoglycosides
- Fluoroquinolones

We measured and interpreted zones of inhibition as sensitive, intermediate, or resistant according to standard criteria. Qualitative variables included gender, type of Gram-negative organism isolated, presence of comorbidities, clinical diagnosis [e.g., pneumonia, bronchitis], and antibiotic sensitivity pattern [sensitive/resistant]. Qualitative variables included age, duration of hospital stay, and laboratory values [e.g., white blood cell count, CRP levels]. The primary outcomes included the prevalence of gram-negative bacterial respiratory tract infections, the distribution of different gram-negative organisms, the clinical spectrum of disease presentation, and antibiotic sensitivity and resistance patterns. We entered and analyzed data using SPSS version 22. We used descriptive statistics to summarize the data. We expressed continuous variables as mean ± standard deviation, and categorical variables as frequencies and percentages. Where applicable, we assessed associations between variables using appropriate statistical tests, such as the chi-square test. We considered $p < 0.05$ statistically significant.

Results

This prospective study included 150 hospitalized adult patients with suspected respiratory tract infections. We isolated Gram-negative bacterial pathogens in a significant proportion of cases. The study population spanned a wide age range. Most patients were middle-aged or elderly.

Table 1: Age Distribution of Patients, n = 150

Age Group [years]	Number of Patients	Percentage %
18–30	22	14.7%
31–50	46	30.7%
51–70	58	38.7%
>70	24	16.0%

Most patients [38.7%] were in the 51–70 years age group, indicating higher susceptibility among older adults.

Table 2: Gender Distribution

Gender	Number of Patients	Percentage %
Male	92	61.3%
Female	58	38.7%

The study population showed male predominance, with males accounting for 61.3% of cases. Of the 150 patients studied, 102 [68%] had growth of Gram-negative bacteria in respiratory samples.

Table 3: Prevalence of Gram-Negative Infection

Finding	Number of Patients	Percentage %
Gram-negative positive	102	68.0%
No Gram-negative growth	48	32.0%

Among the isolated organisms, *Klebsiella pneumoniae* was the most common, followed by *Pseudomonas aeruginosa*.

Table 4: Distribution of Isolated Organisms [n = 102]

Organism	Number	Percentage [%]
Klebsiella pneumoniae	38	37.3%
Pseudomonas aeruginosa	26	25.5%

Acinetobacter baumannii	20	19.6%
Escherichia coli	12	11.8%
Other Gram-negative bacilli	6	5.8%

Klebsiella pneumoniae emerged as the leading pathogen, accounting for more than one-third of the cases. Pneumonia was the most common clinical presentation, followed by bronchitis.

Table 5: Clinical Diagnosis in Gram-Negative Cases [n = 102]

Clinical Condition	Number	Percentage %
Pneumonia	60	58.8%
Bronchitis	22	21.6%
Ventilator-associated pneumonia [VAP]	14	13.7%
Lung abscess	6	5.9%

Pneumonia was the predominant clinical presentation, observed in more than half of the patients.

Table 6: Comorbid Conditions [n = 150]

Comorbidity	Number	Percentage %
Diabetes mellitus	54	36.0%
COPD	42	28.0%
Chronic kidney disease	18	12.0%
Hypertension	46	30.7%
No comorbidity	28	18.7%

A large proportion of patients had underlying medical conditions. Diabetes mellitus and COPD were the most frequently observed comorbid conditions. Antibiotic sensitivity testing revealed varying susceptibility patterns among Gram-negative isolates.

Table 7: Overall Antibiotic Sensitivity Pattern %

Antibiotic	Sensitive %	Resistant %
Meropenem	78%	22%
Imipenem	75%	25%
Amikacin	70%	30%
Piperacillin-Tazobactam	65%	35%
Ciprofloxacin	48%	52%
Ceftriaxone	35%	65%
Colistin	92%	8%

Carbapenems [Meropenem and Imipenem] showed relatively higher sensitivity compared to other antibiotics. Colistin showed the highest sensitivity, although its use remains limited because of toxicity concerns. A considerable proportion of isolates exhibited multidrug resistance.

Table 8: Multidrug Resistance [MDR] Pattern

Category	Number	Percentage %
MDR isolates	44	43.1%
Non-MDR isolates	58	56.9%

Approximately 43.1% of Gram-negative isolates were multidrug-resistant. Patients with Gram-negative infections had relatively longer hospital stays.

Table 9: Duration of Hospital Stay

Duration [days]	Number of Patients	Percentage %
<5 days	20	19.6%
5–10 days	48	47.1%
>10 days	34	33.3%

Nearly one-third of patients required hospitalization for more than 10 days.

Discussion

The present prospective study highlights the significant burden of gram-negative bacterial respiratory tract infections among hospitalized adults, with an overall prevalence of 68%. This finding is consistent with several regional and international studies that report a growing dominance of gram-negative organisms in hospital-acquired respiratory infections. For instance, Kollef et al. emphasized that gram-negative pathogens are now among the most frequently isolated organisms in intensive care units, particularly in cases of hospital-acquired and ventilator-associated pneumonia [11].In the current study, *Klebsiella pneumoniae* emerged as the most common pathogen [37.3%], followed by *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. Joseph et al. and Gales et al. reported similar findings, identifying Klebsiella species as leading causes of nosocomial respiratory infections. The predominance of these organisms may be attributed to their ability to survive in hospital environments, colonize medical equipment, and develop resistance mechanisms that enhance their persistence [12,13]. The high prevalence of *Acinetobacter* species observed in this study is also noteworthy, as these organisms have increasingly been associated with outbreaks in critical care settings [14,15,16]. Pneumonia was the most common diagnosis in clinical presentation, accounting for 58.8% of

cases. This aligns with previous studies that identified pneumonia as the primary manifestation of gram-negative respiratory infections in hospitalized patients [17,18]. Ventilator-associated pneumonia also constituted a significant proportion of cases, reflecting the role of invasive devices in predisposing patients to infection. The association between mechanical ventilation and gram-negative infections has been well documented, particularly in studies by Chastre and Fagon, who highlighted the increased risk of infection with prolonged ventilatory support [19,20]. Comorbid conditions were highly prevalent among the study population, with diabetes mellitus and chronic obstructive pulmonary disease COPD being the most common. These findings align with earlier research showing that underlying chronic illnesses compromise host immunity and increase susceptibility to infection. Diabetes, in particular, impairs neutrophil function and reduces the body's ability to combat bacterial infections, thereby facilitating colonization by opportunistic Gram-negative organisms [21]. One of the most important findings of this study is the antibiotic resistance pattern observed among the isolates. The study noted high resistance rates to commonly used antibiotics such as ceftriaxone and ciprofloxacin, while relatively better sensitivity was observed with carbapenems and colistin. These results are consistent with global trends reported by the World Health Organization WHO, 2014, which has identified antimicrobial resistance among Gram-negative bacteria as a major public health threat. The relatively high sensitivity to colistin observed in this study is similar to findings by Falagas et al., although its use remains limited because of potential nephrotoxicity and neurotoxicity [22]. This study has certain limitations that should be acknowledged. Being a single-center study, the findings may not be fully generalizable to other settings. Additionally, the study did not characterize resistance mechanisms at the molecular level, which could have provided deeper insights into antimicrobial resistance patterns. Despite these limitations, the prospective design and systematic data collection strengthen the validity of the findings.

Conclusion

Gram-negative bacteria are a leading cause of RTI in hospitalized adults, with high prevalence and a strong association with multidrug resistance. The findings highlight the importance of surveillance of local bacterial patterns and antibiotic sensitivity for appropriate therapy and improved patient outcomes.

Ethical Approval

The study was approved by the Institutional Research and Ethics Board (IREB) of the hospital under Reference No. C-113-1071-A, dated October 3, 2025, prior to the commencement of the study.

Informed Consent

We obtained written informed consent from all participants before enrolment. We informed participants and their parents or legal guardians about the study objectives, procedures, and the voluntary nature of participation. Participation was entirely voluntary.

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This study received no external funding and used available institutional resources.

Conflict of Interest

The authors declare no competing interests or conflicts of interest related to this study.

Authors' Contributions

Muhammad Ramzan: Contributed to conceptualization, study design, data collection, interpretation of findings, manuscript drafting, critical revision, and final approval. He also accepts accountability for all aspects of the work.

Shehlla Qadir, Sehrish Ijaz, Uzma Arshad: Contributed to study design, data collection, data curation, literature review, data interpretation, manuscript revision, and final approval. They also accept accountability for all aspects of the work.

Zeemal Iqbal, Roha Fiaz: Contributed to conceptualization, study supervision, clinical assessment, interpretation of findings, and critical revision of the manuscript for important intellectual content. She also approved the final version and accepts accountability for all aspects of the work.

All authors reviewed and approved the final version of the manuscript and agreed to be accountable for all aspects of the work in accordance with the ICMJE authorship criteria.

References

1. Panickar A, Manoharan A, Anbarasu A, Ramaiah S. Respiratory tract infections: an update on the complexity of bacterial diversity, therapeutic interventions and breakthroughs. Arch Microbiol. 2024;206(9):382. doi: 10.1007/s00203-024-04107-z.

2. Ferrer R, Soriano A, Cantón R, Del Pozo JL, García-Vidal C, Garnacho-Montero J, et al. A systematic literature review and expert consensus on risk factors associated with infection progression in adult patients with respiratory tract or rectal colonization by carbapenem-resistant Gram-negative bacteria. Rev Esp Quimioter. 2022;35(5):455-67. doi: 10.37201/req/062.2022.

3. Klompas M, Branson R, Cawcutt K, Crist M, Eichenwald EC, Greene LR, et al. Strategies to prevent ventilator-associated pneumonia, ventilator-associated events, and nonventilator hospital-acquired pneumonia in acute-care hospitals: 2022 update. Infect Control Hosp Epidemiol. 2022;43(6):687-713. doi: 10.1017/ice.2022.88.

4. Rosenthal VD, Yin R, Rodrigues C, Myatra SN, Divatia JV, Biswas SK, et al. Multinational prospective cohort study over 18 years of the risk factors for ventilator-associated pneumonia in 9 Asian countries: INICC findings. Am J Infect Control. 2023;51(7):751-7. doi: 10.1016/j.ajic.2022.11.005.

5. Gunalan A, Sastry AS, Ramanathan V, Sistla S. Early- vs late-onset ventilator-associated pneumonia in critically ill adults: comparison of risk factors, outcome, and microbial profile. Indian J Crit Care Med. 2023;27(6):411-5. doi: 10.5005/jp-journals-10071-24465.

6. Di Pilato V, Willison E, Marchese A. The microbiology and pathogenesis of nonfermenting Gram-negative infections. Curr Opin Infect Dis. 2023;36(6):537-44. doi: 10.1097/QCO.0000000000000969.

7. Semet C. The ongoing challenge of ventilator-associated pneumonia: epidemiology, prevention, and risk factors for mortality in a secondary care hospital intensive care unit. Infect Prev Pract. 2023;5(4):100320. doi: 10.1016/j.infpip.2023.100320.

8. Zhu D, Zhao Q, Guo S, Bai L, Yang S, Zhao Y, et al. Efficacy of preventive interventions against ventilator-associated pneumonia in critically ill patients: an umbrella review of meta-analyses. J Hosp Infect. 2024;145:174-86. doi: 10.1016/j.jhin.2023.12.017.

9. Li W, Cai J, Ding L, Chen Y, Wang X, Xu H. Incidence and risk factors of ventilator-associated pneumonia in the intensive care unit: a systematic review and meta-analysis. J Thorac Dis. 2024;16(9):5518-28. doi: 10.21037/jtd-24-150.

10. Li Q, Zhou X, Yang R, Shen X, Li G, Zhang C, et al. Carbapenem-resistant Gram-negative bacteria (CR-GNB) in ICUs: resistance genes, therapeutics, and prevention—a comprehensive review. Front Public Health. 2024;12:1376513. doi: 10.3389/fpubh.2024.1376513.

11. Ochoa P, Rico Mendoza A, Molano D, Masclans JR, Parada-Gereda HM. Risk factors and outcomes of ventilator-associated pneumonia: an updated systematic review and meta-analysis. BMC Pulm Med. 2025;25(1):453. doi: 10.1186/s12890-025-03932-2.

12. Rosenthal VD, Memish ZA, Bearman G. Preventing ventilator-associated pneumonia: a position paper of the International Society for Infectious Diseases, 2024 update. Int J Infect Dis. 2025;151:107305. doi: 10.1016/j.ijid.2024.107305.

13. Rongrungruang Y, Plongla R, Pleumkanitkul S, Hantrakun V, Khawcharoenporn T. Etiology of hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) in tertiary-care hospitals in Thailand: a multicenter, retrospective cohort study. Infect Drug Resist. 2025;18:351-61. doi: 10.2147/IDR.S492299.

14. Khalil KA, Alsultan M, Daher NA. Microbial profile and antimicrobial resistance patterns in ventilator-associated pneumonia (VAP): a cross-sectional study from Syria. J Postgrad Med. 2025;71(1):7-14. doi: 10.4103/jpgm.jpgm_565_24.

15. Hussain Z, Naim A, Fatima A, Karim A, Uddin F, Shams S. Distribution of MBL and serine-β-lactamase-producing pathogens in ventilator-associated pneumonia: insights into MDR and XDR strains. Iran J Microbiol. 2025;17(5):761-72. doi: 10.18502/ijm.v17i5.19885.

16. Hussain Z, Farooqui F, Ibrahim A, Baig S. Patients and surfaces: integrated clinical-environmental surveillance of MDR Gram-negative bacteria in critical-care units (Karachi, 2024–2025). Microorganisms. 2025;13(12):2762. doi: 10.3390/microorganisms13122762.

17. Kerimoglu E, Catak T, Kilinc A. Evaluation of infections caused by carbapenem-resistant Pseudomonas aeruginosa, Acinetobacter baumannii, and Klebsiella pneumoniae in an intensive care unit: a retrospective study. Antibiotics (Basel). 2025;14(7):700. doi: 10.3390/antibiotics14070700.

18. Nguyen QP, Pham NT, Tran VG. Characteristics and trends of antibiotic resistance in several Gram-negative bacteria responsible for pneumonia in intensive care patients in Northern Vietnam, 2022–2024. IJID Reg. 2025;16:100709. doi: 10.1016/j.ijregi.2025.100709.

9. Colaneri M, Montrucchio G, Scaglione G, Monti G, Tricella G, Genovese C, et al. Incidence, microbiology, and mortality of ventilation-associated pneumonia in a large Italian cohort of critically ill patients: results from the PROSAFE project. Clin Microbiol Infect. 2025;31(9):1491-9. doi: 10.1016/j.cmi.2025.05.026.

20. Wunderink RG, Matsunaga Y, Ariyasu M, Clevenbergh P, Echols R, Kaye KS, et al. Cefiderocol versus high-dose, extended-infusion meropenem for the treatment of Gram-negative nosocomial pneumonia (APEKS-NP): a randomized, double-blind, phase 3, non-inferiority trial. Lancet Infect Dis. 2021;21(2):213-25. doi: 10.1016/S1473-3099(20)30731-3.

21. Bassetti M, Echols R, Matsunaga Y, Ariyasu M, Doi Y, Ferrer R, et al. Efficacy and safety of cefiderocol or best available therapy for the treatment of serious infections caused by carbapenem-resistant Gram-negative bacteria (CREDIBLE-CR): a randomized, open-label, multicentre, pathogen-focused, descriptive, phase 3 trial. Lancet Infect Dis. 2021;21(2):226-40. doi: 10.1016/S1473-3099(20)30796-9.

22. Torre-Cisneros J, Almirante B, De La Fuente Martos C, Rascado P, Salavert Lletí M, Sánchez-García M, et al. Effectiveness and safety of cefiderocol treatment in patients with Gram-negative bacterial infections in Spain in the early access program: results of the PERSEUS study. Eur J Clin Microbiol Infect Dis. 2025;44(6):1375-90. doi: 10.1007/s10096-025-05108-6