

## Antibiotic Resistance Rate among Bacterial Pathogens Isolated from Bronchoalveolar Lavage Fluid at a Tertiary Care Center in Western Uttar Pradesh, India

Sachin K Sharma<sup>1\*</sup>, Saheli Bhadra<sup>1</sup>, Tarana Sarwat<sup>1</sup>, Dalip K Kakru<sup>1</sup>

<sup>1</sup>Department of Microbiology, School of Medical Sciences & Research, Sharda University, Greater Noida (Uttar Pradesh), India

### ARTICLE INFO

#### Original Article

**Keywords:** Lower respiratory tract infections, Bronchoalveolar lavage, Antibiotic resistance, Multidrug resistance

Received: 07 Feb. 2023

Received in revised form: 25 Apr. 2023

Accepted: 03 Jun. 2023

DOI: 10.61186/JoMMID.11.2.110

#### \*Correspondence

Email: Sachinsharma1798@gmail.com

Tel: +918802577307

Fax:

© The Author(s)



### ABSTRACT

**Introduction:** Lower respiratory tract infections (LRTIs) are a common global health problem, and antibiotic resistance remains a significant concern for doctors. This study aimed to determine the prevalence of antibiotic resistance among bacterial pathogens isolated from bronchoalveolar lavage (BAL) fluid at a tertiary care center in Western Uttar Pradesh. **Methods:** A cross-sectional study was conducted from January 2021 to June 2022, in which BAL fluid samples were collected from patients attending the tertiary care center. The samples were processed for bacterial culture and antimicrobial susceptibility testing. **Results:** Out of 112 BAL samples cultured, 84 showed growths of bacterial pathogens, with 82 (97.6%) being Gram-negative bacteria and 29 (35%) of these being extended-spectrum beta-lactamase (ESBL) producers. The percentage of multiple drug-resistant (MDR) isolates was 77.38% (65/84). The Gram-negative isolates were most sensitive to imipenem, followed by ciprofloxacin, amikacin, and tetracycline. Cephalosporins and piperacillin-tazobactam showed a high resistance pattern to these bacteria. The Gram-positive isolates were susceptible to linezolid and vancomycin. **Conclusion:** The high prevalence of ESBL-producing and MDR isolates in BAL samples highlights the need for the prudent administration of antibiotics and the creation of local antibiograms to guide empirical therapy. This study provides valuable information on the antimicrobial susceptibility patterns of bacterial pathogens causing LRTIs, which can aid in developing effective treatment strategies.

### INTRODUCTION

Lower respiratory tract infections (LRTI) are a group of respiratory system inflammations that affect the trachea, bronchi, bronchioles, and alveoli, leading to the multiplication of infectious agents [1, 2]. Acute lower respiratory tract infections (ALRI) are among the most prevalent infectious diseases worldwide, causing significant morbidity and mortality in patients of all ages [1, 3]. Gram-negative bacilli (GNB) such as *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter* species, *Pseudomonas aeruginosa*, and Gram-positive organisms like *Staphylococcus aureus* and *Streptococcus pneumoniae*, are common respiratory pathogens [2]. Multidrug-resistant (MDR) Gram-negative bacteria, including extended-spectrum beta-lactamase (ESBL) producers, have become a growing concern in healthcare settings. ESBLs are enzymes that confer resistance to beta-lactam antibiotics and can lead to treatment failure and poor outcomes [4, 5, 6, 7, 8, 9].

The emergence of antibiotic resistance in respiratory infections is a significant global concern, and the misuse of antibiotics is a major contributor to resistance [11]. Moreover, the failure to de-escalate therapy based on culture and sensitivity results can also contribute to antibiotic resistance. Therefore, monitoring the epidemiology of respiratory infections is crucial to combat the rise of multidrug-resistant pathogens [11].

Bronchoalveolar lavage (BAL) is a useful diagnostic tool for diagnosing lung diseases and detecting respiratory infections. The fluid recovered from BAL can be used to identify white blood cell profiles and recover pathogens from the epithelial surface of the lower respiratory tract [12]. The bacteriological profile of pulmonary infections can vary within the same country due to differences in antibiotic use, environmental factors, and ventilation in critically ill patients. Therefore, BAL is an ideal sample

for recovering pathogens from the lower respiratory tract to guide empirical therapy [2, 12].

This study aimed to assess the prevalence of ESBL and MDR pathogens in BAL samples from a tertiary care center in Western Uttar Pradesh, India.

## MATERIAL AND METHODS

**Study design and setting.** This cross-sectional study was conducted at the Microbiology Department, Sharda Hospital, Greater Noida, India, from January 2021 to June 2022. The study included all bronchoalveolar lavage (BAL) fluid samples from the Bacteriology Laboratory.

**Sample processing and identification.** The BAL fluid samples were processed according to standard bacteriological procedures. The bacterial isolates were identified by conventional biochemical assays, including catalase and oxidase, coagulase, urease, citrate, indole, MR-VP, Hugh-Leifson's oxidative fermentative test, triple sugar iron test, nitrate reduction, and amino acid decarboxylation tests.

**Antimicrobial susceptibility testing.** The Kirby Bauer disc diffusion method was used to determine antibiotic susceptibility according to the Clinical and Laboratory Standards Institute (CLSI) standards. Commercially available antibiotic disks (Himedia, Mumbai, India) were used for antimicrobial susceptibility testing, and the zone diameters were interpreted according to CLSI guidelines.

**Screening for ESBL-producing isolates.** Isolates resistant to third-generation cephalosporins were screened

for ESBL production and subjected to phenotypic confirmation.

**Phenotypic confirmation of ESBL production.** ESBL production was confirmed phenotypically using the CLSI-recommended combination disk approach, which involved the antibiotics ceftazidime and cefotaxime alone and the inhibitor clavulanic acid (30 g). ESBL producers had a 5 mm increase in the zone of inhibition around the discs containing cephalosporin plus clavulanate over the discs containing cephalosporin alone. *Pseudomonas aeruginosa* American Type Culture Collection (ATCC) 27853 was used as a positive control for ESBL, while *E. coli* ATCC 25922 was used as the negative control.

**MDR distribution.** Multiple drug resistance (MDR) was defined as an organism's antimicrobial resistance to at least one antimicrobial drug from three or more antimicrobial categories. The distribution of MDR isolates was determined based on their antimicrobial susceptibility patterns.

## RESULTS

**Study population.** Of the 112 BAL samples processed, 82 (73.21%) belonged to males and 30 (26.79%) to females. The age of the patients ranged from 16 to 85 years (Fig. 1), with the majority (n=51; 45.54%) being above 60 years of age. Of the 112 samples, 51 (45.54%) were obtained from the MICU ward, followed by 23 (20.54%) from the respiratory ward and 16 (14.29%) from the SICU ward (Fig 2).

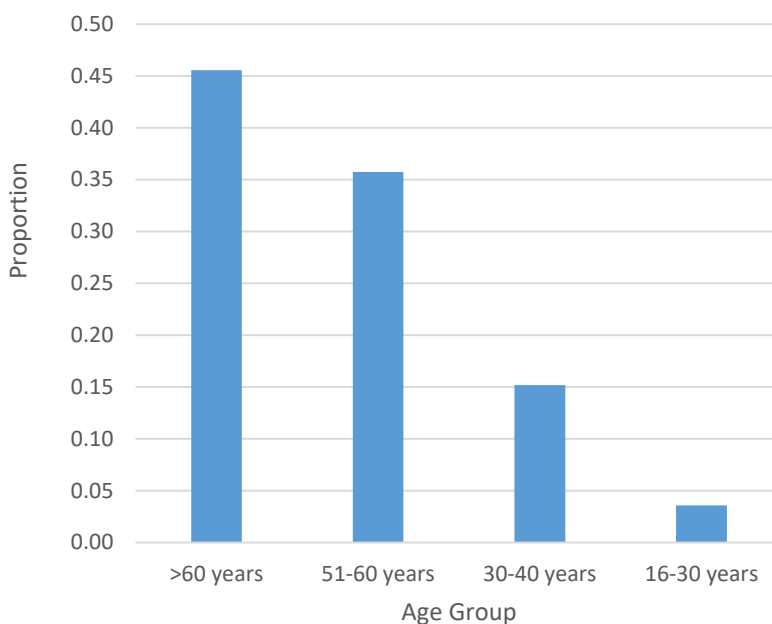


Fig. 1. Distribution of bacterial isolates by age group in the study population

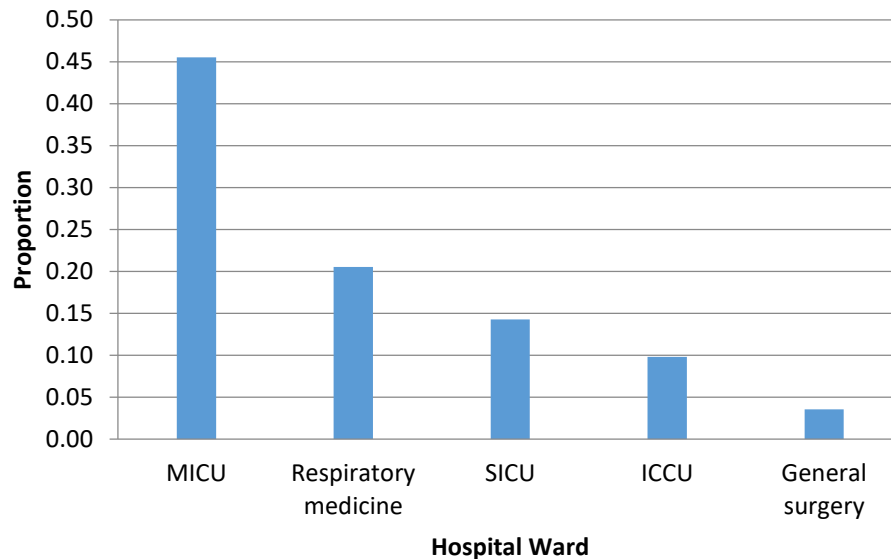


Fig. 2. Distribution of samples by ward in the study population

**Bacterial pathogens.** Of the 112 processed samples, 84 (75%) showed growth of bacterial pathogens, whereas 28 were negative. Of those 84 samples, 82 (97.6%) were Gram-negative, and 2 (2.4%) were Gram-positive. Among the Gram-negative bacteria (GNBs), *Acinetobacter* species (n=25; 29.76%) was the most frequently isolated organism, followed by *K. pneumoniae*

(n=23; 27.38%), *P. aeruginosa* (n=17; 20.24%), and *E. coli* (n=14; 16.67%). *Citrobacter* and *Enterobacter* species accounted for 2 (2.4%) and 1 (1.19%) positive samples, respectively. Of the Gram-positive cocci, one was identified as Methicillin Resistant-Coagulase Negative Staphylococcus (1.19%) and the other as Beta hemolytic Streptococcus group A (1.19%) (Fig 3).

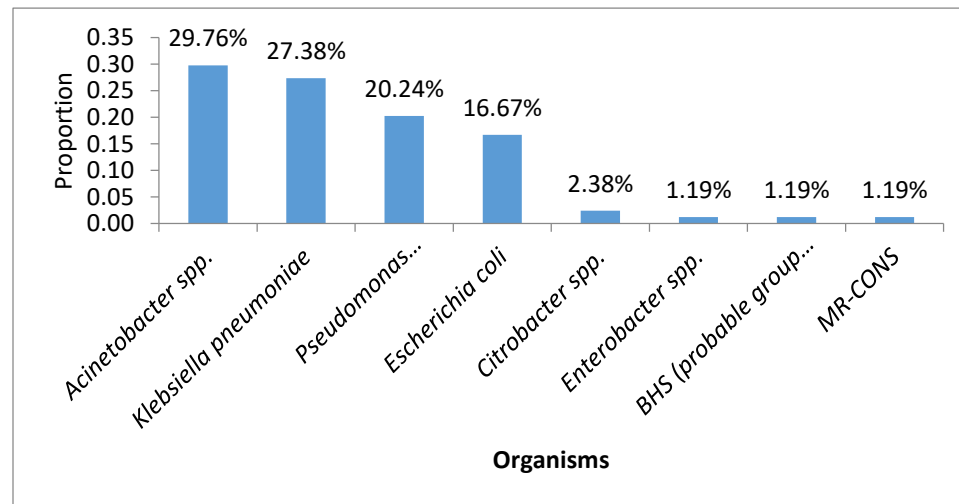


Fig. 3. Distribution of isolated bacterial pathogens

**Antimicrobial susceptibility.** A panel of 15 antibiotics was tested against the isolates. Imipenem was the most effective against all GNB isolates (43.9%), followed by amikacin (42.85%) and ciprofloxacin (39.28%). Ceftazidime was the least effective (4.87%), followed by cefotaxime (10.71%) and cefepime (13.09%). Gentamicin was 64.70% effective against *P. aeruginosa*. Vancomycin and linezolid were 100% effective against the Gram-

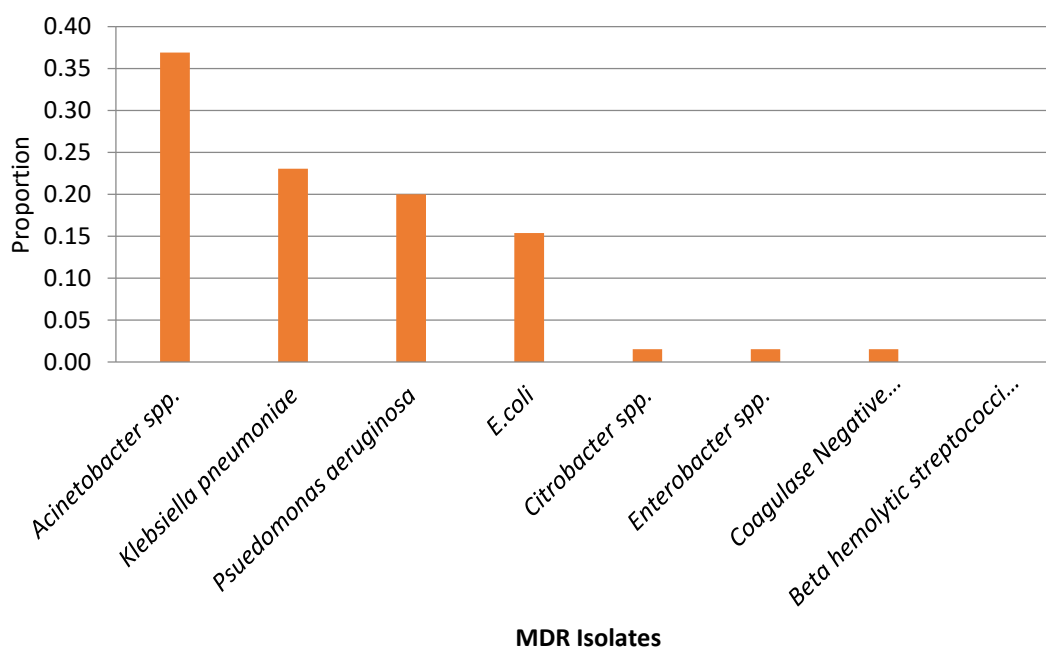
positive isolates, whereas 100% resistance was shown to cotrimoxazole (Table 1).

**Distribution of MDR isolates.** Of the 84 isolates, 65 (77.38%) were MDR, whereas the remaining 19 (22.62%) were non-MDR. Among the 65 MDR isolates, 64 were GNBs, and one was a methicillin-resistant-coagulase-negative staphylococcus species. *Acinetobacter* spp. dominated the MDR count, accounting for 36.92%

(24/65), followed by *K. pneumoniae* with 23.08% (15/65) (Fig. 4).

**Table 1.** Gram-negative isolate resistance patterns

Antibiotics	<i>Acinetobacter spp.</i> (n=25)	<i>Klebsiella pneumoniae</i> (n=23)	<i>Pseudomonas aeruginosa</i> (n=17)	<i>E. coli</i> (n=14)	<i>Enterobacter spp.</i> (n=1)	<i>Citrobacter spp.</i> (n=2)
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
<b>Amikacin</b>	24 (96%)	15 (65.2%)	9 (52.9%)	7 (50%)	1 (100%)	1 (50%)
<b>Piperacillin-tazobactam</b>	24 (96%)	20 (86.95%)	9 (52.9%)	14 (100%)	1 (100%)	1 (50%)
<b>Gentamicin</b>	23 (92%)	16 (69.5%)	6 (35.3%)	5 (35.7%)	1 (100%)	1 (50%)
<b>Tobramycin</b>	23 (92%)	22 (95.65%)	7 (41.1%)	8 (57.1%)	1 (100%)	2 (100%)
<b>Cefuroxime</b>	25 (100%)	23 (100%)	16 (94.1%)	14 (100%)	1 (100%)	1 (50%)
<b>Ceftriaxone</b>	24 (96%)	22 (95.65%)	17 (100%)	12 (85.7%)	1 (100%)	1 (50%)
<b>Cefepime</b>	23 (92%)	22 (95.65%)	13 (76.4%)	11 (78.5%)	1 (100%)	1 (50%)
<b>Ciprofloxacin</b>	21 (84%)	15 (65.2%)	6 (35.3%)	11 (78.5%)	1 (100%)	1 (50%)
<b>Tetracycline</b>	19 (76%)	12 (52.17%)	17 (100%)	12 (85.7%)	0 (0%)	1 (50%)
<b>Imipenem</b>	23 (92%)	12 (52.17%)	6 (35.3%)	3 (21.4%)	1 (100%)	1 (50%)
<b>Minocycline</b>	<b>8 (32%)</b>	-	-	-	-	-



**Fig. 4.** Frequency of multi-drug resistant organisms (MDROs) among bacterial pathogens isolated from bronchoalveolar lavage fluid

**ESBL-producing microorganisms.** Of 82 isolates, 29 (35.36%) were ESBL producers. Among those, 19 belonged to the family *Enterobacteriaceae*. Nine (39.13%) isolates of *K. pneumoniae*, 9 (64.28%) of *E. coli*, and 1 (100%) isolate of *Enterobacter spp.* were found to be ESBL producers, whereas 8 (47.06%) isolates of *P. aeruginosa* and 2 (8%) of *Acinetobacter spp.* were ESBL producers (Fig. 5).

## DISCUSSION

Lower respiratory tract infections pose a significant public health challenge worldwide due to their high prevalence and economic burden. Among nosocomial infections, ventilator-associated pneumonia (VAP) is the

second most common cause, contributing to 15-20% of healthcare-associated infections (HAIs) [16, 17]. VAP is also the primary cause of mortality among HAIs [18]. Hence, effective prevention and management strategies for VAP are critical to reducing the burden of HAIs and improving patient outcomes.

This study aimed to investigate the frequency and antibacterial susceptibility profile of respiratory pathogens in bronchoalveolar lavage (BAL) samples obtained from different wards and intensive care units of a tertiary care hospital. To achieve this, 112 BAL samples were collected and processed at the Microbiology Laboratory to obtain data on respiratory pathogens' prevalence and antibiotic resistance patterns.

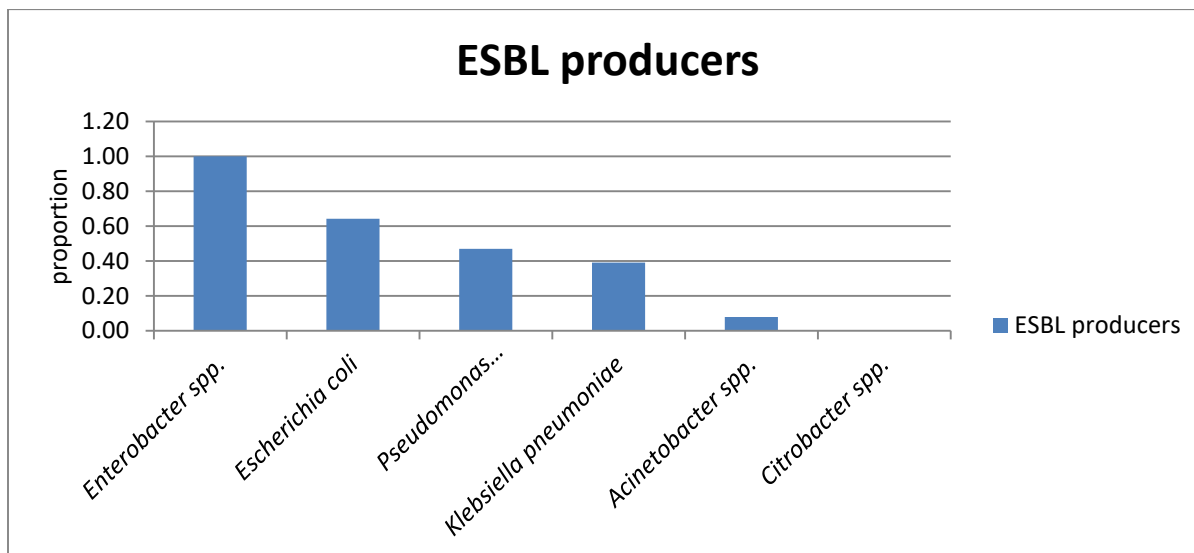


Fig. 5. Distribution of isolates based on ESBL production

The investigation included 112 bronchoalveolar lavage (BAL) samples submitted to the Microbiology Laboratory. Of these, 82 (73.2%) were obtained from male patients, whereas 30 (26.8%) were from female patients. This male predominance is consistent with findings reported in previous studies [19, 20]. Several factors could contribute to this gender disparity, including a higher prevalence of smoking, alcohol consumption, and occupational exposure to respiratory hazards among males, particularly in chronic obstructive pulmonary disease (COPD).

The highest percentage of respiratory pathogen isolates was observed in patients aged above 60 years, followed by those aged 51 to 60 years, while the lowest rate was found in the age group of 18 to 30 years. Thananki *et al.* (2018) reported that the most common age range of patients with respiratory infections was 41-60 years [19]. However, in investigations by Padmaja N *et al.* (2021) and Baishali *et al.* (2020), the majority of patients were in the 51-60 years age range [20, 21]. These discrepancies may be due to differences in study populations, such as variations in healthcare settings, geographic regions, and patient demographics.

Out of 84 growth-positive isolates in this study, 97.62% were Gram-negative, and 2.38% were Gram-positive. *Acinetobacter* spp. (30.49%) was the most frequently isolated Gram-negative pathogen, followed by *K. pneumoniae* (17.07%) and *P. aeruginosa* (14.63%). In contrast, another study reported *P. aeruginosa* (51.6%) as the predominant isolate [22]. These variations in pathogen distribution may reflect differences in patient populations, infection control practices, or geographic regions.

The most prevalent organism recovered in our study was *Acinetobacter* spp., which accounted for 29.76% of isolates. This finding is consistent with the results reported by Rajasekhar *et al.* (2006), who identified these bacteria in 30.59% of isolates [23]. In contrast,

Mohammad H Afify *et al.* (2016) reported *K. pneumoniae* (50%) as the most common pathogen, followed by *Acinetobacter* spp. (42.5%) [24].

*Klebsiella* is a normal mouth flora and can be associated with pneumonia in hospitalized individuals and the elderly [25]. Therefore, its predominance in this study may be related to the predominantly older study population. In contrast, Swomya *et al.* (2014) reported *Pseudomonas* species (21.8%) as the most frequently isolated bacterium in their investigation [26].

Out of 82 Gram-negative bacterial (GNB) isolates in the present study, 64 were MDR, with 37.5% (24/64) belonging to the *Acinetobacter* spp. and 23.43% (15/64) to *K. pneumoniae*. Among the MDR-GNB, 27 were from the *Enterobacteriaceae* family. In comparison, Teklu *et al.* (2019) reported a total MDR prevalence of 68.3% among all *Enterobacteriaceae* isolates [27].

Antibiotic resistance is a significant concern in patients who have been hospitalized in intensive care units (ICUs). In this study, we observed high resistance rates to ceftriaxone among *P. aeruginosa*, *Acinetobacter* spp., and *Klebsiella* spp., with 100%, 96%, and 95.6%, respectively. These findings are consistent with those reported by other researchers, reporting resistance rates ranging from 96% to 100% for these pathogens [28, 29]. These high rates of resistance underscore the need for effective antibiotic stewardship programs and infection control measures to prevent the spread of resistant strains in ICU settings.

In this study, most Gram-negative isolates were sensitive to imipenem, ciprofloxacin, amikacin, and tetracycline. Gram-positive isolates showed 100% sensitivity to linezolid and vancomycin. These findings suggest that a combination of imipenem, ciprofloxacin, amikacin, and tetracycline may effectively treat infections caused by Gram-negative bacilli. These results are consistent with those reported by Olugbue *et al.* (2011)

[30], who found similar sensitivity patterns among Gram-negative isolates.

In our study, the prevalence of extended-spectrum beta-lactamase (ESBL)-producing *Enterobacteriaceae* was 47.5%, higher than the rates reported by earlier Ethiopian studies. Siraj *et al.* (2015) reported a prevalence of 38.4% [31], Mulualem *et al.* (2012) found a prevalence of 36% [32], Seid *et al.* (2005) reported a prevalence of 33.3% [33], and Mulisa *et al.* (2016) reported a prevalence of 25% [34]. The increased prevalence of ESBL-producing isolates highlights the urgent need for effective infection control practices and antimicrobial stewardship programs to prevent the spread of resistant strains [35].

The main extended-spectrum beta-lactamase (ESBL)-producing isolates identified in this study were *E. coli* (64.2%) and *K. pneumoniae* (39.1%), which is consistent with the findings of several other studies. Mulisa *et al.* (2016) reported ESBL prevalence rates of 51.5% for *E. coli* and 11.5% for *K. pneumoniae* [34], while Ouedraogo *et al.* (2016) found rates of 67.5% for *E. coli* and 26% for *K. pneumoniae* [36]. Rao *et al.* (2014) reported rates of 61.4% for *E. coli* and 46.2% for *K. pneumoniae* [37], and Shashwati *et al.* (2014) reported rates of 50.14% for *E. coli* and 48.27% for *K. pneumoniae* [38]. These consistent findings highlight the importance of implementing effective infection control measures and antibiotic stewardship programs to prevent the spread of ESBL-producing strains.

Our study found that 47.05% of *P. aeruginosa* strains were positive for ESBL production, consistent with a survey by Goel *et al.* (2013) [39]. They reported a 42.30% prevalence for ESBL-producing *P. aeruginosa* isolates. These results emphasize the need for effective infection control measures and judicious use of antibiotics to prevent the spread of ESBL-producing strains.

The increasing prevalence of antibiotic-resistant bacterial strains is a significant public health concern primarily attributed to the overuse and misuse of antibiotics. In the case of respiratory illnesses, antibiotics are often prescribed unnecessarily and for prolonged periods, which can promote the growth of resistant pathogens. Combination therapy, commonly used to treat respiratory diseases, can also contribute to the emergence of resistant strains. Preventing nosocomial pneumonia requires implementing effective infection control measures, such as frequent hand hygiene, patient positioning in a semi-recumbent position, and minimizing sedation. These simple steps can be crucial in preventing the spread of resistant pathogens and improving patient outcomes.

## ACKNOWLEDGMENT

The authors would like to express their heartfelt appreciation to the teachers and technical personnel of the Microbiology laboratory for their invaluable assistance. The authors received no financial support for the research.

## CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest associated with this manuscript.

## REFERENCES

- Pant S, Bhusal K R, Manandhar S. Microbiology of lower respiratory tract infection in workers of garment industry of Kathmandu. *J Col Med Sci.* 2015; 10 (3): 14-22.
- Thomas AM, Jayaprakash C, Amma GMR. The pattern of bacterial pathogens and their antibiotic susceptibility profile from lower respiratory tract specimens in a rural tertiary care centre. *J Evolution Med Dent Sci.* 2016; 5 (40): 2470-6.
- Egbe CA, Ndiokwre I C, Omoregie R. Microbiology of Lower Respiratory Tract Infections in Benin City, Nigeria. *Malaysian J Med Sci.* 2011; 18 (2): 27-31.
- Gao B, Li X, Yang F, Chen W, Zhao Y, Bai G, et al. Molecular epidemiology and risk factors of ventilator-associated pneumonia infection caused by carbapenem-resistant *Enterobacteriaceae*. *Front Pharmacol.* 2019; 10: 262.
- Cillóniz C, Dominedò C, Torres A. Multidrug resistant gram-negative bacteria in community-acquired pneumonia. *Crit Care.* 2019; 23 (1): 79.
- Sader HS, Castanheira M, Mendes RE, Flamm RK. Frequency and antimicrobial susceptibility of Gram-negative bacteria isolated from patients with pneumonia hospitalized in ICUs of US medical centres (2015–17). *J Antimicrob Chemother.* 2018; 73 (11): 3053-9.
- Rouby JJ, Sole-Lleonart C, Rello J. Ventilator-associated pneumonia caused by multidrug-resistant Gram-negative bacteria: understanding nebulization of aminoglycosides and colistin. *Intensive Care Med.* 2020; 46 (4): 766-70.
- Kidd JM, Kuti JL, Nicolau DP. Novel pharmacotherapy for the treatment of hospital-acquired and ventilator-associated pneumonia caused by resistant gram-negative bacteria. *Expert Opin Pharmacother.* 2018; 19 (4): 397-408.
- Bush K. Is it important to identify extended-spectrum betalactamase-producing isolates? *Eur J Clin Microbiol Infect Dis.* 1996; 15: 361-4.
- Sarwat T, Rastogi V, Rashid M, Chander Y. Bacteriological profile of hospital acquired infections with multidrug resistance burden and extended spectrum beta lactamase prevalence. *Int J Curr Microbiol Appl Sci.* 2018; 7 (03): 988-94.
- Regha IR, Sulekha B. Bacteriological profile and antibiotic susceptibility patterns of lower respiratory tract infections in a tertiary care hospital, Central Kerala. *IP Int J Med Microbiol Trop Dis* 2018; 4 (4): 186-90
- Meyer KC. Bronchoalveolar lavage as a diagnostic tool. *Semin Respir Crit Care Med.* 2007; 28 (5): 546-60.
- Mackie and McCartney Practical Medical Microbiology, Tests for the identification of Bacteria, 14th Edition, Delhi: Elsevier Publication 2006: 131-508
- CLSI. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing.

- Twenty-Fourth Informational Supplement CLSI: Document M100-S28. Wayne, PA, 2020
15. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect.* 2012; 18 (3): 268-81.
  16. Afshari A, Pagani L, Harbarth S. Year in review 2011: Critical care- infection. *Crit Care.* 2012; 16 (6): 244.
  17. Hunter JD. Ventilator associated pneumonia. *BMJ.* 2012; 344: e3325.
  18. Eybpoosh S, Eshrati B. Nosocomial infection surveillance system in Iran: structures, processes and achievements. *Iran J Epidemiol.* 2019; 15 (1): 105-15.
  19. Thananki R, K.N, R., Unguturu, S. Bacteriological Analysis of Broncho Alveolar Wash of Patients with Suspected Pneumonia Cases. *Int J Med Sci Clin Invent.* 2018; 5 (11): 4178-81.
  20. Padmaja N, Rao V. Bacteriological profile and antibiogram of bronchoalveolar lavage fluid from patients with respiratory tract infections at a tertiary care Hospital. *Indian J Microbiol Res.* 2021; 8 (2): 119-22.
  21. Baishali D, Dina R. Bacteriology of chronic respiratory diseases in a tertiary care hospital in Assam. *Int J Health Res Med Leg Pract.* 2020; 6 (2): 34-8.
  22. Adhikari S, Regmi RS, Pandey S, Paudel P, Neupane N, Chalise S, et al. Bacterial etiology of bronchoalveolar Lavage fluid in tertiary care patients and antibiogram of the isolates. *J Inst Sci Technol.* 2021; 26 (1): 99-106.
  23. Rajasekhar T, Anuradha K, Suhasini T, Lakshmi V. The role of quantitative cultures of non-bronchoscopic samples in ventilator associated pneumonia. *Indian J Med Microbiol.* 2006; 24 (2): 107-13.
  24. Afify MH, Shaheen EA, El-Dahdouh SS, El-Feky HM. Comparison between bronchoscopic BAL and non-bronchoscopic BAL in patients with VAP. *Egypt J Chest Dis Tuberc.* 2016; 65 (1): 113-9.
  25. Vivek KU, Kumar N. Microbiological profile of bronchoalveolar lavage fluid in patients with chronic respiratory diseases: a tertiary care hospital study. *Int J Med Res Rev.* 2016; 4: 330-4.
  26. Sowmya, Bhat S, Saralaya V. Spectrum of bacteria isolated from bronchoalveolar lavage in a tertiary care centre. *J Evol Med Dent Sci.* 2014; 3 (28): 7950-4.
  27. Teklu DS, Negeri AA, Legese MH, Bedada TL, Woldemariam HK, Tullu KD. Extended-spectrum beta-lactamase production and multi-drug resistance among *Enterobacteriaceae* isolated in Addis Ababa, Ethiopia. *Antimicrob Resist Infect Control.* 2019; 8: 39.
  28. Veena Kumari HB, Agarathna SN, Chandramuki A. Antimicrobial resistance pattern among Aerobic gram negative bacilli of Lower Respiratory Tract Specimens of Intensive Care Unit in a Neuro centre. *Indian J Chest Allied Dis.* 2007; 49 (1): 19-22.
  29. Sofianou DC, Constandinidis TC, Yannacou M, Anastasiou H, Sofianos E. Analysis of risk factors for Ventilator associated pneumonia in a multidisciplinary intensive care unit. *Eur J Clin Microbiol Infect Dis.* 2000; 19 (6): 460-3.
  30. Olugbue V, Onuoha S. Prevalence and antibiotic sensitivity of bacterial agents involved in lower respiratory tract infections. *Int J Biol Chem Sci.* 2011; 5 (2): 774-81.
  31. Siraj SM, Ali S, Wondafrash B. Extended-spectrum  $\beta$ -lactamase production in *Klebsiella pneumoniae* and *Escherichia coli* at Jimma University specialized hospital, south-west, Ethiopia. *Mol Microbiol Res.* 2015; 5 (1): 1-9.
  33. Seid J, Asrat D. Occurrence of extended spectrum  $\beta$ -lactamase enzymes in clinical isolates of *Klebsiella* species from Harar region, eastern Ethiopia. *Acta Trop.* 2005; 95 (2): 143-8.
  34. Mulisa G, Selassie L, Jarso G, Shiferew T, Zewdu A, Abebe W, et al. Prevalence of extended Spectrum Beta-lactamase producing *Enterobacteriaceae* : a cross sectional study at Adama hospital, Adama, Ethiopia. *J Emerg Infect Dis.* 2016; 1 (1): 1-6.
  35. Eybpoosh S, Mostaan S, Gouya MM, Masoumi-Asl H, Owlia P, Eshrati B, et al. Frequency of five *Escherichia Coli* pathotypes in Iranian adults and children with acute diarrhea. *PLoS One.* 2021; 16 (2): e0245470.
  36. Ouedraogo A-S, Sanou M, Kissou A, Sanou S, Solaré H, Kaboré F, et al. High prevalence of extended-spectrum  $\beta$ -lactamase producing *Enterobacteriaceae* among clinical isolates in Burkina Faso. *BMC Infect Dis.* 2016; 16: 326.
  37. Rao SP, Rama PS, Gurushanthappa V, Manipura R, Srinivasan K. Extended-Spectrum Beta-lactamases producing *Escherichia coli* and *Klebsiella pneumoniae*: a multi-centric study across Karnataka. *J Lab Physicians.* 2014; 6 (1): 7-13.
  38. Shashwati N, Kiran T DA. Study of extended-spectrum  $\beta$ -lactamase producing *Enterobacteriaceae* and antibiotic coresistance in a tertiary care teaching hospital. *J Nat Sci Biol Med.* 2014; 5 (1): 30-5.
  39. Goel V, Hogade SA, Karadesai SG. Prevalence of extended-spectrum betalactamases, AmpC beta-lactamase, and metallo-beta-lactamase producing *Pseudomonas aeruginosa* and *Acinetobacter baumannii* in an Intensive Care Unit in a tertiary care hospital. *J Sci Soc.* 2013; 40 (1): 28-31.

**Cite this article:**

Sharma SK, Bhadra S, Sarwat T, Kakru DK. Antibiotic Resistance Rate among Bacterial Pathogens Isolated from Bronchoalveolar Lavage Fluid at a Tertiary Care Center in Western Uttar Pradesh, India. *J Med Microbiol Infect Dis*, 2023; 11 (2): 110-116. DOI: 10.61186/JoMMID.11.2.110.