DOI: https://doi.org/10.54393/pjhs.v7i7.4097

PAKISTAN JOURNAL OF HEALTH SCIENCES
(LAHORE)
https://thejas.com.pk/index.php/pjhs
ISSN (E): 2790-9352, (P): 2790-9344
Volume 7, Issue 07 (July 2026)

Original Article

OPEN ACCESS

Bacteriology of Lower Respiratory Tract Samples with Antibiotic Susceptibility Patterns at a Tertiary Care Hospital in Karachi

Anoosha Jameel[1*], Sana Jamil[1], Yousra Pervaiz[2], Muneeba Musharraf[1] and Muhammad Ali[3]

[1]Department of Microbiology, Sindh Institute of Urology and Transplant, Karachi, Pakistan
[2]Department of Microbiology, Chughtai Lab, Karachi, Pakistan
[3]Faculty of Pharmacy, Salim Habib University, Karachi, Pakistan

ARTICLE INFO

Keywords:
Lower Respiratory Tract Infections, Antibiotic Resistance, Multidrug Resistant Organisms, Extensively Resistant Organisms, Gram-Negative Rods, Gram-Positive Cocci

How to Cite:
Jameel, A., Jamil, S., Pervaiz, Y., Musharraf, M., & Ali, M. (2026). Bacteriology of Lower Respiratory Tract Samples with Antibiotic Susceptibility Patterns at a Tertiary Care Hospital in Karachi: Bacteriology of Lower Respiratory Tract Samples with Antibiotic Susceptibility Patterns. Pakistan Journal of Health Sciences, 7(7), 103-110. https://doi.org/10.54393/pjhs.v7i7.4097

***Corresponding Author:**
Anoosha Jameel
Department of Microbiology, Sindh Institute of Urology and Transplant, Karachi, Pakistan
anooshajameel7@hotmail.com

Received Date: 9th March, 2026
1st Revision Received: 24th March, 2026
2nd Revision Received: 31st March, 2026
3rd Revision Received: 3rd April, 2026
Acceptance Date: 25th April, 2026
Published Date: 31st July, 2026

ABSTRACT

Lower respiratory tract infections are widespread in Pakistan. Determining sensitivity is crucial to combat increasing antimicrobial resistance. **Objectives:** To ascertain the prevalence of bacterial pathogens isolated in lower respiratory tract samples and the antimicrobial susceptibility patterns of these pathogens in one of the tertiary care hospitals in Karachi. **Methods:** This study was a prospective observational study that took place for six months. Three hundred and thirty-five positive respiratory samples of patients with clinical LRTIs were collected. Identification of the bacteria was conducted by the standard microbiological procedures, and the determination of antimicrobial resistance was conducted by the Kirby-Bauer disk diffusion test according to the guidelines of CLSI 2025. SPSS version 26.0 was used to analyze data. The chi-square test was applied, and a p-value <0.050 was deemed significant. **Results:** The study examined 335 culture-positive patient isolates, revealing Gram-negative rods (GNR) as the predominant pathogens (n=275), mainly *Klebsiella* spp., *Acinetobacter* spp., and *Pseudomonas aeruginosa*. Gram-positive cocci (GPC) (n=38) included *Staphylococcus aureus* and *Streptococcus pneumoniae*, while *Nocardia* was identified among gram-positive rods (n=22). Organism type significantly influenced resistance patterns (p<0.001), but specimen type did not (p=0.401). **Conclusions:** The most common LRTI pathogens were *Klebsiella* spp., *Acinetobacter* spp., and *Pseudomonas aeruginosa* that exhibited a wide spectrum of multidrug resistance. Stringent antibiotic stewardship plays a crucial role in preventing further increases in resistance.

INTRODUCTION

Lower respiratory tract infections (LRTIs) are among the common causes of morbidity and mortality and have a significant impact on the overall burden of disease in the world, as they affect people of all ages. [1]. The Global Burden of Disease (GBD) study also reveals pneumonia as the major contributor to death in the low and middle-income countries [2]. Bacterial pathogens, like *Streptococcus pneumoniae, Staphlococcus aureus, Pseudomonas aeruginosa, Klebsiella* spp., and *Acinetobacter* spp. still dominate, but their treatment has become complicated with the emergence of antimicrobial resistance (AMR) [3]. The development of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacteria is a real concern to clinicians and health officials in general [4]. Alarming trends are reported in the global surveillance of resistance: the Global Antimicrobial

DOI: https://doi.org/10.54393/pjhs.v7i7.4097

Resistance and Use Surveillance System (GLASS) of WHO has reported resistance rates of more than 50% in third-generation cephalosporin in *Klebsiella* spp. isolates in some parts of the world [5], with carbapenem resistance reported to be more than 60% in some regions of Asia and the Middle East [6]. According to reports made by the European Centre for Disease Prevention and Control (ECDC), resistance to the major antibiotics like fluoroquinolones, carbapenems, and aminoglycosides against *Pseudomonas aeruginosa* and *Klebsiella* spp. is on the rise [7]. Worldwide, antimicrobial resistance is already causing an estimated 700,000 deaths per year, and it is projected that this figure may increase unless there is a change in this situation. Hospitals, due to high levels of antibiotic utilization and high density of ill individuals, are the best breeding grounds for these formidable pathogens [8]. Pakistan is no exception, as the situation resembles these global trends with a concerning increase in the resistance of respiratory pathogens. The studies done in Karachi have established that more than 60% of the bacterial isolates on samples of lower respiratory tracts are MDR, with resistance rates among isolates of the ICUs being highly disproportionate, highlighting the critical care environments in the spread of resistant organisms [9]. A growing percentage of XDR strains is being reported. To make treatment decisions, stop the transmission of resistant strains, and reduce the load on the health sector, regular monitoring of AMR trends of respiratory pathogens is essential [4]. High disease burden and increased resistance highlight the necessity of local surveillance data. The trends on bacterial prevalence and susceptibility are usually dependent upon the geographical location, health care facility, and the patient. Thus, the current data should be used to make empirical antibiotic decisions, which should be based on the regionally specific data itself and not just on the international guidelines. Systematic surveillance of respiratory pathogens and antimicrobial profiles in the Karachi context is essential, given the high population density and healthcare needs, as it can improve patient outcomes and provide valuable information on hospital antibiotic stewardship initiatives.

Pakistan lacks multicenter surveillance data on LRTI bacteriology and antimicrobial resistance patterns, with most studies limited to single tertiary care hospitals in Karachi. No national standardized protocol exists for monitoring MDR and XDR respiratory pathogens across different regions. The current research seeks to determine the prevalence of bacterial pathogens sampled in the lower respiratory tract in a tertiary care hospital in Karachi and to determine the pattern of antibiotic susceptibility of bacteria. In addition, the study aims to determine the burden of MDR and XDR organisms among these isolates, thereby contributing crucial evidence to local and national AMR surveillance efforts.

METHODS

This prospective observational study was conducted in the Department of Microbiology, Sindh Institute of Urology and Transplant, a tertiary care center in Karachi, Pakistan, from June 2025 to November 2025. The study protocol was reviewed by the Institutional Review Board (approval No. SIUT-ERC-2025/A-568; dated 3rd June 2025), and written approval was obtained before data collection. Patient confidentiality was maintained throughout the study after obtaining consent. Positive respiratory cultures, including sputum, bronchoalveolar lavage (BAL), and endotracheal aspirates (ETT), were obtained from patients of all ages and both sexes who presented with clinical features of LRTI, such as cough, fever, dyspnea, or purulent sputum. A non-probability, consecutive sampling technique was employed. Specimens that were improperly labeled, collected in compromised containers, or that showed fungal growth or *Mycobacterium tuberculosis* bacteria were excluded. Samples from transplant recipients were also excluded to avoid confounding immunosuppression. Using the WHO sample size calculator, the required sample size was determined. Based on the previous minimum estimation of *Staphylococcus aureus* isolation, found in 8.88% of samples, with a 3% margin of error and a 95% confidence level, a total of 335 positive respiratory cultures will be required for this study [3]. All specimens were collected under strict aseptic conditions. The specimen's quality was evaluated using Bartlett's scoring system, and specimens with a score of less than 1 were rejected. Specimens were processed in the microbiology laboratory without delay. All the samples were inoculated on Blood agar (Oxoid), MacConkey agar (Oxoid), and Chocolate agar (Oxoid) and incubated at 35–37°C for 18–24 hours. Identification of bacterial isolates was done using standard microbiological tests, such as Gram staining, colony morphology, and standard biochemical analyses (e.g., oxidase, catalase, indole, citrate utilization, urease, etc.) [10]. The Kirby-Bauer disk diffusion test was used to perform antimicrobial susceptibility testing on Mueller-Hinton agar as recommended by Clinical and Laboratory Standards Institute (CLSI) 2025 guidelines [11]. The antibiotic panel included β-lactams (ampicillin, amoxicillin-clavulanate, ceftriaxone, cefepime, ceftazidime), carbapenems (imipenem, meropenem), fluoroquinolones (ciprofloxacin, levofloxacin), aminoglycosides (amikacin, gentamicin, tobramycin), and other agents such as piperacillin-tazobactam and colistin for GNR, as well as vancomycin and linezolid for GPC when indicated. Vancomycin E test strips were used to measure minimum inhibitory concentrations (MICs) of MRSA. The standard ATCC reference strains were used to control

DOI: https://doi.org/10.54393/pjhs.v7i7.4097

quality: E. coli ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, and *Staphylococcus aureus* ATCC 25923. All procedures adhered to CLSI quality control guidelines. CDC follows Magiorakos criteria for MDR and XDR bacteria. MDR Bacteria are strains that are non-susceptible to at least 1 in 3 antimicrobial categories, while XDR Bacteria are strains non-susceptible to at least 1 agent in all but 1 or 2 antimicrobial categories. Enzymes (New Delhi metallo-beta-lactamases NDM) identified in Carbapenem-resistant respiratory pathogens using the EDTA disk synergy test. Aztreonam Combination with Ceftazidime Avibactam on Carbapenem Resistant pathogens was synergetic observable in the case of double disc synergy [11].

Demographic information about the patients, the type of specimen, isolated organisms, and the antibiotic susceptibility outcomes were entered into a predesigned proforma and examined with SPSS software (version 26.0, IBM Corp., Armonk, NY). The frequencies and percentages were calculated by means of descriptive statistics. Chi-square test evaluated the associations between bacteria species and patterns of antibiotic resistance ($p<0.005$ as statistically significant and $p<0.001$ reported for highly significant associations) and a confidence interval 95%. No correction for multiple testing was applied, as the analysis was exploratory in nature.

RESULTS

Out of a total of 335 positive cultures of patients, 187 (55.8%) were from males, and 148 (44.1%) were from females. The mean age of the study population was 42.85 ± 19.50 years (mean ± SD), and the participants represented a wide age range. Among these, Gram-negative rods (GNR) were the predominant group, accounting for 275 isolates (82%), while Gram-positive cocci (GPC) represented 38 isolates (11.34%). Within the GNR organisms, the most frequently isolated species was *Klebsiella* spp., found in 119 cases (43.22%), followed by *Acinetobacter* spp. in 62 cases (22.5%), and *Pseudomonas aeruginosa* in 57 cases (20.7%). Among the GPC, Staphylococcus aureus was the most common isolate, detected in 21 cases (55.3%), followed by *Streptococcus pneumoniae,* identified in 17 cases (44.7%). 22 cases of *Nocardia* were seen as gram-negative branching rods (Table 1).

Table 1: Distribution of Respiratory Pathogens in Different Sample Types

Organisms (n)	Sputum, n (%)	Tracheal Aspirate, n (%)	BAL, n (%)
Gram Negative Rods (n =275)			
Klebsiella spp. (119)	62 (52.1%)	53 (44.53%)	4 (3.36%)
Actinobacter spp. (62)	31 (50%)	29 (46.7%)	2 (3.22%)
Pseudomonas aeruginosa (57)	35 (61.4%)	19 (33.3%)	3 (5.26%)
Haemophilus influenzae (16)	16 (100%)	0	0
Stenotrophomonas (9)	8 (88.1%)	0	1 (11.1%)
Moraxella (3)	2 (66.6%)	1 (33.3%)	0
Pseudomonas species (3)	1 (33.3%)	2 (66.6%)	0
E.Coli (3)	1 (33.3%)	2 (66.6%)	0
Elizabeth meningoseptica (2)	1 (50%)	1 (50%)	0
Morganella (1)	0	1 (100%)	0
Gram Positive Cocci (n= 38)			
Staphylococcus aureus (21)	8 (38.09%)	12 (57.1%)	1 (4.7%)
Streptococcus pneumoniae (17)	15 (88.23%)	2 (11.7%)	0
Gram Positive Rods (n=22)			
Nocardia (22)	15 (68.1%)	3 (13.6%)	4 (18.1%)

Most of the respiratory pathogens were isolated from cultures of the patients falling in the age group 35- 55 years, especially *Klebsiella* spp. and *Pseudomonas aeruginosa*. *Acinetobacter* spp. was more commonly seen in the age group 15-24 years (Table 2).

Table 2: Distribution of Respiratory Pathogens in Different Age Groups and Gender

Variables	*Klebsiella* spp, n (%)	*Acinetobacter* spp, n (%)	*Pseudomonas Aeruginosa*, n (%)	*Staphylococcus Aureus*, n (%)	*Streptococcus pneumoniae*, n (%)	*Nocardia*,n (%)
Age Groups (Years)						
5-14	5 (4%)	4 (6%)	4 (7%)	2 (9%)	1 (5.8%)	0
15-24	14 (11.7%)	17 (27.4%)	6 (10.5%)	5 (23.8%)	3 (17%)	3 (13.6%)
25-34	20 (16.8%)	9 (14.5%)	5 (8.7%)	–	1 (5.8%)	5 (22.7%)
35-44	18 (15.1%)	10 (16.1%)	6 (10.5%)	5 (23.8%)	1 (5.8%)	2 (9.1%)
45-54	25 (21%)	7 (11.2%)	16 (28.1%)	4 (19.0%)	6 (35.2%)	6 (27.2%)
55-64	15 (12.6%)	9 (14.5%)	12 (21%)	4 (19.0%)	3 (17.6%)	6 (27.2%)
Above 65	22 (18.4%)	6 (9.6%)	8 (14%)	1 (4.7%)	2 (11.7%)	0
Total (100)	119 (100%)	62 (100%)	57 (100%)	21 (100%)	17 (100%)	22 (100%)
Gender						
Male	64 (53.7%)	32 (51.6%)	38 (66.6%)	16 (76.1%)	1 (64.7%)	14 (63.6%)
Female	55 (46.2%)	30 (48.3%)	19 (33.3%)	5 (23.8%)	16 (35.2%)	8 (36.3%)

The antimicrobial susceptibility analysis demonstrated significant variability across both Gram-negative and Gram-positive respiratory isolates, with multiple comparisons showing statistical significance ($p<0.050$). Among Gram-negative

DOI: https://doi.org/10.54393/pjhs.v7i7.4097

organisms, *Klebsiella* spp. and *Acinetobacter* spp. exhibited low susceptibility to β-lactams, including ceftriaxone (~21–22%) and cefepime (~25–33%), with statistically significant differences across organisms (p<0.001). Carbapenem activity was moderate, particularly reduced in *Acinetobacter* spp. (imipenem 50%), indicating emerging resistance, although interspecies differences were not significant for some agents (p=0.978). Aminoglycosides such as amikacin showed comparatively higher efficacy, especially against *Pseudomonas aeruginosa* (84.2%; p=0.005). The sensitivity pattern for *Hemophilus influenzae* is shown. Fluoroquinolone susceptibility was low overall, particularly in *Acinetobacter* spp. (ciprofloxacin 4.8%), reflecting substantial resistance. In contrast, last-line agents polymyxin and tigecycline demonstrated consistently high susceptibility (>90%) across major Gram-negative isolates, with strong statistical significance (p<0.001). Among Gram-positive organisms, *Streptococcus pneumoniae* remained highly susceptible to β-lactams (amoxicillin and ceftriaxone ~94%; p<0.001). However, *Staphylococcus aureus* showed marked resistance, with low cefoxitin susceptibility (14.2%), indicating a high prevalence of MRSA. Vancomycin and linezolid demonstrated universal efficacy (100%), with no significant variation between organisms (p=0.735), suggesting consistent activity. The results show susceptibility patterns of GNR and GPC in respiratory samples. Among Carbapenem-resistant Gram-negative rods (n=135), NDM was seen in 75.9% of *Klebsiella* spp. isolates, 76.1% of *Acinetobacter* spp. isolates and 33.3% of *Pseudomonas aeruginosa* isolates. Ceftazidime, Avibactam, and Aztreonam showed limited activity against NDM-producing isolates separately. However, in vitro synergy between Ceftazidime – Avibactam and Aztreonam was 82% in our study. Susceptibility to agents such as colistin, doxycycline, and minocycline was variable (Table 3).

Table 3: Susceptibility Pattern of Gram-Negative Rods Isolated from Respiratory Samples

Antibiotics	*Klebsiella* spp, n (%)	*Acinetobacter* spp, n (%)	*Pseudomonas Aeruginosa*, n (%)	*Haemophilus influenza*, n (%)	*Stenotrophomonas* spp, n (%)	p-value
Amoxicillin clavulanate (30ug)	–	–	–	13 (81%)	–	<0.001
Ceftriaxone (30ug)	25 (21%)	14 (22.5%)	–	15 (93.7%)	–	<0.001
Cefepime (30ug)	30 (25.2%)	21 (33.8%)	43 (75.4%)	–	–	–
Piperacillin tazobactam	35 (29.4%)	19 (30.6%)	43 (75.4%)	–	–	<0.001
Cefoperazone	34 (28.5%)	19 (30.6%)	43 (75.4%)	–	–	0.978
Amikacin (30ug)	42 (35.2%)	17 (27.4%)	48 (84.2%)	–	–	0.005
Cotrimoxazole	30 (25.2%)	18 (29.0%)	–	7 (43.7%)	9 (100%)	<0.001
Imipenem	43 (36.1%)	31 (50%)	46 (80.7%)	–	–	0.978
Gentamicin (10ug)	52 (43.6%)	18 (29%)	–	–	–	0.868
Levofloxacin (30ug)	26 (21.8%)	5 (8.0%)	41 (71.9%)	11 (68.7%)	9 (100%)	0.963
Doxycycline	57 (47.8%)	33 (53%)	–	–	–	<0.001
Minocycline	65 (54.1%)	35 (56.4%)	–	–	9 (100%)	<0.001
Fosfomycin	61 (51.2%)	–	–	–	–	0.012
Ceftazidime-avibactam	43 (51.2%)	–	45 (78.9%)	–	–	0.087
Aztreonam	40 (33.6%)	–	47 (82.4%)	–	–	0.708
Tigecycline	105 (88.8%)	57 (91.9)	–	–	–	<0.001
Azithromycin	–	–	–	12 (75%)	–	–
Polymyxin	109 (91.6%)	58 (93.5%)	55 (96.4%)	–	–	<0.001

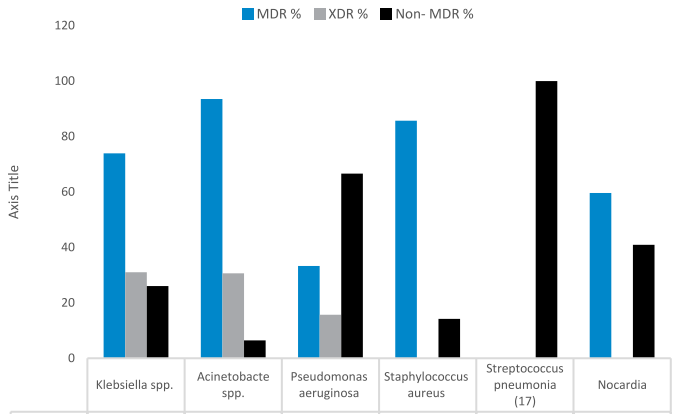
The results show susceptibility patterns of GPC in respiratory samples (Table 4).

Table 4: Susceptibility Pattern of Gram-Positive Organisms Isolated from Respiratory Samples

Antibiotics	*Streptococcus Pneumoniae*, n (%)	*Staphylococcus Aureus*, n (%)	*Nocardia*, n (%)	p-value
Ampicillin	15 (88.2%)	–	–	<0.001
Ceftriaxone	16 (94.1%)	–	6 (27.3%)	<0.001
Cotrimoxazole	9 (52.9%)	13 (61.9%)	22 (100%)	<0.001
Ciprofloxacin	10 (58.8%)	8 (38%)	5 (22.7%)	0.151
Clindamycin	–	12 (57.1%)	–	<0.001
Erythromycin	7 (41.1%)	8 (38.09%)	–	<0.001
Cefoxitin	–	3 (14.2%)	–	<0.001
Azithromycin	7 (41.1%)	–	–	<0.001
Linezolid	17 (100%)	21 (100%)	22 (100%)	0.735
Doxycycline	–	–	16 (72.7%)	<0.001

Acinetobacter spp. showed the highest percentages of MDR and XDR pathogens among GNRs, whereas *Staphylococcus aureus* was found to be the most common MDR pathogen among GPCs. ETT showed a greater frequency of MDR and XDR while sputum and BAL showed comparable patterns (Figure 1).

DOI: https://doi.org/10.54393/pjhs.v7i7.4097



	Klebsiella spp.	Acinetobacte spp.	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumonia (17)	Nocardia
MDR %	73.9	93.5	33.3	85.7	0	59.6
XDR %	31	30.6	15.7	0	0	0
Non- MDR %	26.05	6.45	66.6	14.2	100	40.9

Figure 1: Frequency (%) of MDR, XDR, and Non – XDR in Respiratory Pathogens

DISCUSSION

This study assessed the bacteriological spectrum and antibiotic resistance patterns in LRTIs among patients at a tertiary care hospital in Karachi. The data revealed a predominant presence of Gram-negative bacteria GNRs, particularly *Klebsiella* spp., *Pseudomonas aeruginosa,* and *Acinetobacter* spp. While Gram-positive bacteria GPCs primarily *Staphylococcus aureus* and *Streptococcus pneumoniae,* were less frequent but can lead to severe infections and emerging resistance trends. Gram-negative bacteria cause LRTIs globally, particularly in hospital and ICU settings [12]. An Indonesian study indicated *Klebsiella* spp. as the commonest isolate, followed by *Pseudomonas aeruginosa,* and *Acinetobacter* spp. exhibiting substantial resistance to βlactam, cephalosporins, and fluoroquinolones, and semipermeable to carbapenems and aminoglycosides, results which are in agreement with our study [13]. Within Pakistan, similar trends have been observed. A systematic review by Bilal *et al.* reported *Klebsiella* spp. as the leading respiratory pathogen, followed by *Pseudomonas* spp. and *Acinetobacter* spp., with high resistance to cephalosporins and quinolones [14]. In contrast, *Streptococcus pneumoniae* and *Hemophilus influenzae* remain the predominant respiratory pathogens in Europe and North America, reflecting differences in healthcare settings, antibiotic usage, and patient profiles [15]. In this current research, the lower frequency of *S. pneumoniae* is probably an indication of the large numbers of hospital-acquired and ventilator-associated respiratory samples, as opposed to community-based cases. The observation that most respiratory pathogens were isolated in the 35–55year age group, particularly *Klebsiella* spp. and *Pseudomonas aeruginosa*, is consistent with regional case series demonstrating higher GNR infection rates in middle-aged and elderly cohorts because of increased co-morbidity and healthcare exposure [16]. Conversely, *Acinetobacter* spp. was more common in younger patients (15–24 years), a pattern less frequently reported in the literature and potentially reflective of localized outbreaks or demographic healthcare utilization in the current setting. Other reports have also identified substantial *Acinetobacter* isolation among young hospitalized patients, particularly in ICUs where invasive devices and prolonged stays may contribute to risk [17]. A prospective study from Egypt reported that ETT and BAL samples yielded fundamentally more resistant Gram-negative bacteria than expectorated sputum, suggesting that invasive sampling is more likely to capture hospital-adapted, drug-resistant flora [18]. Third-generation cephalosporins retained strong activity against *Haemophilus influenzae* and *Moraxella catarrhalis*, supported by data from the CHINET 2024 antimicrobial resistance surveillance network report that *H. influenzae* exhibits minimal non-susceptibility (≤0.5%) to ceftriaxone in hospital isolates, and *M. catarrhalis* continues to show high overall susceptibility profiles in respiratory samples [19]. Conversely, resistance among *Enterobacterales* to third-generation cephalosporins remains high in the nosocomial context, with resistance levels frequently exceeding 50%, and ESBL prevalence is substantial among hospital-associated isolates [20]. Carbapenem susceptibility was low among *Klebsiella* spp. and *Acinetobacter* spp. in the current study, reflecting the expanded dissemination of carbapenems such as NDM and OXA-type enzymes in tertiary hospitals. Molecular surveillance studies of carbapenem-resistant Gram-negative clinical isolates have repeatedly documented widespread carriage of genes that confer high-level resistance to carbapenems in these isolates from healthcare settings [21]. *Pseudomonas aeruginosa* was relatively more susceptible to anti-pseudomonal cephalosporins and carbapenems, with a similar trend observed in other tertiary settings, as a European surveillance study showed *Pseudomonas aeruginosa* exhibiting greater susceptibility to ceftazidime and cefepime relative to carbapenem-resistant Enterobacterales and non-fermenters. However, the resistance rates can be changed but heavily depend on local antibiotic use and infection control practices [22, 23]. Aminoglycosides such as amikacin and tobramycin are fairly active against Gram-negative isolates, consistent with established literature, which positions these agents as important components of combination therapy for severe Gram-negative pneumonia [24]. Among Gram-positive organisms, *Staphylococcus aureus* exhibited high rates of multidrug resistance, aligning with regional and international reports where MRSA remains a frequent MDR isolate in respiratory samples [26]. *Streptococcus pneumoniae* showed high susceptibility to ampicillin and

DOI: https://doi.org/10.54393/pjhs.v7i7.4097

amoxicillin, which parallels some community pneumonia data, though rising macrolide resistance has been documented globally, with azithromycin susceptibility now <60% in many regions [26], which is also consistent with our study findings. The predominance of MDR and XDR among *Acinetobacter* spp. in this study reflects their well-recognized propensity for accumulating resistance. Extensive resistance in *Acinetobacter* spp. has been reported in multiple ICU surveillance series, often associated with prolonged ventilation and invasive device use [18]. The high prevalence of NDM among carbapenem-resistant *Klebsiella* spp. and *Acinetobacter* spp. isolates in our study are consistent with molecular epidemiology studies from the Indian subcontinent, where NDM has effectively displaced other carbapenamases in many tertiary hospitals [6]. Both ceftazidime avibactam and aztreonam showed limited standalone activity against NDM producers and emphasized the need for combination strategies [27]. Although synergy between ceftazidime avibactam and aztreonam has been detected in selective studies, the high synergism rate (82%) observed in this study suggests that the combination of Ceftazidime avibactam and Aztreonam may provide a reliable treatment option for severe infections caused by NDM-producing organisms [28].

This prospective observational study provides a snapshot of resistance patterns and does not include full genotypic profiling, clinical outcomes, or prior antibiotic exposure. Despite these constraints, it offers valuable local data to guide empirical therapy and stewardship. Overall, the statistically significant differences observed for most antibiotics highlight distinct resistance patterns among organisms, emphasizing the need for targeted therapy. It is high time to make stringent policies for combating antibiotic resistance; otherwise, the clinical implications of AMR will take over, leading to treatment failure, limited therapeutic options, longer hospital stays, higher healthcare costs, and unmanageable infections.

CONCLUSIONS

This study highlights the predominance of respiratory pathogens like *Klebsiella* spp., *Acinetobacter* spp., *Pseudomonas Aeruginosa*, *Staphylococcus aureus*, and *Streptococcus pneumoniae*. The high prevalence of MDR and XDR isolates highlights the importance of effective antimicrobial stewardship.

Authors' Contribution

Conceptualization: AJ
Methodology: AJ, SJ, YP
Formal analysis: MM
Writing and Drafting: AJ, SJ, YP, MM, MA
Review and Editing: AJ, SJ, YP, MM, MA

All authors approved the final manuscript and take responsibility for the integrity of the work

Conflicts of Interest

All the authors declare no conflict of interest.

Source of Funding

The authors received no financial support for the research, authorship, and/or publication of this article.

REFERENCES

[1] Vos T, Lim SS, Abbafati C, Abbas KM, Abbasi M, Abbasifard M *et al.* Global Burden of 369 Diseases and Injuries in 204 Countries and Territories, 1990–2019: A Systematic Analysis for the Global Burden of Disease Study 2019. The Lancet. 2020 Oct; 396(10258): 1204-22.

[2] Infections GB. Antimicrobial Resistance, C. Global, Regional, and National Incidence and Mortality Burden of Non-COVID-19 Lower Respiratory Infections and Aetiologies, 1990-2021: A Systematic Analysis from the Global Burden of Disease Study 2021. Lancet Infectious Diseases. 2024; 24(9): 974-1002. doi: 10.1016/S1473-3099(24)00176-2.

[3] Raghubanshi BR and Karki BM. Bacteriology of Sputum Samples: A Descriptive Cross-Sectional Study in a Tertiary Care Hospital. Journal of the Nepal Medical Association. 2020 Jan; 58(221): 24. doi: 10.31729/jnma.4807.

[4] Reynolds D, Burnham JP, Vazquez Guillamet C, McCabe M, Yuenger V, Betthauser K *et al.* The Threat of Multidrug-Resistant/Extensively Drug-Resistant Gram-Negative Respiratory Infections: Another Pandemic. European Respiratory Review. 2022 Dec; 31(166): 220068. doi: 10.1183/16000617.0068-2022.

[5] Ajulo S and Awosile B. Global Antimicrobial Resistance and Use Surveillance System (GLASS 2022): Investigating the Relationship Between Antimicrobial Resistance and Antimicrobial Consumption Data Across the Participating Countries. Plos One. 2024 Feb; 19(2): e0297921. doi: 10.1371/journal.pone.0297921.

[6] Jayathilaka N, Shehana S, Nakkawita D, Senaratne T. Prevalence and Molecular Epidemiology of Carbapenem Resistance in Asia: A Systematic Review and Meta-Analysis. Systematic Reviews. 2025 Jun; 14(1): 123. doi: 10.1186/s13643-025-02776-

DOI: https://doi.org/10.54393/pjhs.v7i7.4097

5.

[7] Piotrowski M, Alekseeva I, Arnet U, Yücel E. Insights into the Rising Threat of Carbapenem-Resistant Enterobacterales and Pseudomonas Aeruginosa Epidemic Infections in Eastern Europe: A Systematic Literature Review. Antibiotics. 2024 Oct; 13(10): 978. doi: 10.3390/antibiotics13100978.

[8] Fong IW. Antimicrobial Resistance: A Crisis in the Making. New Antimicrobials: For the Present and the Future. 2023 May: 1-21. doi: 10.1007/978-3-031-26078-0_1.

[9] Ali Z, Mumtaz N, Naz SA, Jabeen N, Shafique M. Multi-Drug-Resistant Pseudomonas Aeruginosa: A Threat of Nosocomial Infections in Tertiary Care Hospitals. Journal of the Pakistan Medical Association. 2015; 65(12): 12-6.

[10] Boury N, Siegesmund A, Kushner DB, Smyth DS, Allen ME, Frazier A *et al.* Updated ASM Curriculum Guidelines Describe Core Microbiology Content to Modernize the Framework for Microbiology Education. Journal of Microbiology and Biology Education. 2024 Dec; 25(3): e00126-24. doi: 10.1128/jmbe.00126-24.

[11] Schuetz AN, Ferrell A, Hindler JA, Humphries R, Bobenchik AM. Overview of Changes in the Clinical and Laboratory Standards Institute Performance Standards for Antimicrobial Susceptibility Testing: M100 32nd and 33rd Editions. Journal of Clinical Microbiology. 2025 Sep; 63(9): e01623-23. doi: 10.1128/jcm.01623-23.

[12] Lamichhane A, Sapkota S, Khadka S, Adhikari S, Thapa A, Rana JC *et al.* Incidence of ESBL-producing Gram-Negative Bacteria of Lower Respiratory Tract Infection in Bharatpur Hospital, Nepal. Anti-Infective Agents. 2021 Oct; 19(5): 14-21. doi: 10.2174/2211352518999200520081129.

[13] Singh G, Loho T, Yulianti M, Aditianingsih D, Zakiyah LF, Masse SF *et al.* Factors Associated with Antibiotic Resistance and Survival Analysis of Severe Pneumonia Patients Infected with Klebsiella Pneumoniae, Acinetobacter Baumannii, and Pseudomonas Aeruginosa: A Retrospective Cohort Study in Jakarta, Indonesia. SAGE Open Medicine. 2024 Aug; 12: 20503121241264097. doi: 10.1177/20503121241264097.

[14] Bilal H, Khan MN, Rehman T, Hameed MF, Yang X. Antibiotic Resistance in Pakistan: A Systematic Review of the Past Decade. BioMed Central Infectious Diseases. 2021 Mar; 21(1): 244. doi: 10.1186/s12879-021-05906-1.

[15] Goretzki SC, Van der Linden M, Itzek A, Hühne T, Adelmann RO, Ala Eldin F *et al.* Outbreak of Severe Community-Acquired Bacterial Infections from Streptococcus Pyogenes, Streptococcus Pneumoniae, Neisseria Meningitidis, and Haemophilus Influenzae Among Children in North Rhine-Westphalia (Germany), October to December 2022. medRxiv. 2023 Sep: 2023-09. doi: 10.1101/2023.09.14.23295531.

[16] Almouwlid A, Albenasy K, Kamel Y, Abdelmoktader A, Alaidarous M, Abdel-Hadi A. Incidence and Antibiotic Susceptibility of Gram-Negative Bacteria Associated with Chest Infections in Intensive Care Unit Patients from a Selected Hospital in the Kingdom of Saudi Arabia. BioMed Research International. 2025; 2025(1): 5283526. doi: 10.1155/bmri/5283526.

[17] Almoghrabi Y, Daghistani H, Niyazi HA, Niyazi HA, AbdulMajed H, Juma NA *et al.* Epidemiological and Clinical Insights into Acinetobacter baumannii: A Six-Year Study on Age, Antibiotics, and Specimens. International Journal of General Medicine. 2024 Dec: 5715-25. doi: 10.2147/IJGM.S489514.

[18] Maebed AZ, Gaber Y, Bakeer W, Dishisha T. Microbial Etiologies of Ventilator-Associated Pneumonia (VAP) in Intensive Care Unit of Beni-Suef University's Hospital. Beni-Suef University Journal of Basic and Applied Sciences. 2021 Jul; 10(1): 41. doi: 10.1186/s43088-021-00130-x.

[19] Guo Y, Ding L, Han R, Yin D, Wu S, Yang Y *et al.* Antimicrobial Resistance Profile of Clinical Isolates from Hospitals Across China: CHINET 2024 Surveillance Report. One Health Advances. 2025 Oct; 3(1): 23. doi: 10.1186/s44280-025-00092-0.

[20] Borcan AM, Rotaru E, Radu G, Costea EL, Borcan CA, Olariu MC *et al.* Resistance Trends in Klebsiella pneumoniae Strains Isolated from Bloodstream Infections in a Tertiary Care Hospital over a Period of 7 Years. Microorganisms. 2025 Oct; 13(11): 2451. doi: 10.3390/microorganisms13112451.

[21] Shahid M, Ahmad N, Saeed NK, Shadab M, Joji RM, Al-Mahmeed A *et al.* Clinical Carbapenem-Resistant Klebsiella Pneumoniae Isolates Simultaneously Harboring bla NDM-1, bla OXA Types and Qnrs Genes from the Kingdom of Bahrain: Resistance Profile and Genetic Environment. Frontiers In Cellular and Infection Microbiology. 2022 Oct; 12: 1033305. doi: 10.3389/fcimb.2022.1033305.

[22] Karlowsky JA, Lob SH, DeRyke CA, Hilbert DW, Wong MT, Young K *et al.* In Vitro Activity of Ceftolozane-Tazobactam, Imipenem-Relebactam, Ceftazidime-Avibactam, and Comparators Against Pseudomonas Aeruginosa Isolates Collected in United States Hospitals According to Results from the SMART Surveillance Program, 2018 to 2020. Antimicrobial

DOI: https://doi.org/10.54393/pjhs.v7i7.4097

Agents and Chemotherapy. 2022 May; 66(5): e00189-22. doi: 10.1128/aac.00189-22.

[23] Rodríguez-Baño J, Gutiérrez-Gutiérrez B, Machuca I, Pascual A. Treatment of Infections Caused by Extended-Spectrum-Beta-Lactamase-, Ampc-, and Carbapenemase-Producing Enterobacteriaceae. Clinical Microbiology Reviews. 2018 Apr; 31(2): 10-128. doi: 10.1128/CMR.00079-17.

[24] Tamma PD, Aitken SL, Bonomo RA, Mathers AJ, Van Duin D, Clancy CJ. Infectious Diseases Society of America Guidance on the Treatment of Extended-Spectrum β-Lactamase Producing Enterobacterales (ESBL-E), carbapenem-resistant Enterobacterales (CRE), and Pseudomonas aeruginosa with Difficult-to-Treat Resistance (DTR-P. aeruginosa). Clinical Infectious Diseases. 2021 Apr; 72(7): e169-83. doi: 10.1093/cid/ciaa1478.

[25] Turner NA, Sharma-Kuinkel BK, Maskarinec SA, Eichenberger EM, Shah PP, Carugati M *et al.* Methicillin-Resistant Staphylococcus aureus: An Overview of Basic and Clinical Research. Nature Reviews Microbiology. 2019 Apr; 17(4): 203-18. doi: 10.1038/s41579-018-0147-4.

[26] Anderson R and Feldman C. The Global Burden of Community-Acquired Pneumonia in Adults, Encompassing Invasive Pneumococcal Disease and the Prevalence of Its Associated Cardiovascular Events, with a Focus on Pneumolysin and Macrolide Antibiotics in Pathogenesis and Therapy. International Journal of Molecular Sciences. 2023 Jul; 24(13): 11038. doi: 10.3390/ijms241311038.

[27] Idrees EK, Aldriwesh MG, Alkhulaifi MM, Alghoribi MF. Systematic Review of Multidrug-Resistant Klebsiella Pneumoniae in the Arabian Peninsula: Molecular Epidemiology and Resistance Patterns. Frontiers in Microbiology. 2025 Jan; 16:1 489317. doi: 10.3389/fmicb.2025.1489317.

[28] Falcone M, Daikos GL, Tiseo G, Bassoulis D, Giordano C, Galfo V *et al.* Efficacy of Ceftazidime-Avibactam Plus Aztreonam in Patients with Bloodstream Infections Caused by Metallo-B-Lactamase–Producing Enterobacterales. Clinical Infectious Diseases. 2021 Jun; 72(11): 1871-8. doi: 10.1093/cid/ciaa586.