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Drug Resistance Patterns of Bacterial Pathogens in Adult Pneumonia Patients in a Tertiary Care Hospital

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ABSTRACT

Background: Pneumonia remains one of the leading causes of morbidity and mortality around the world, with a disproportionate burden in low- and middle-income countries such as Pakistan. Antimicrobial resistance (AMR), especially multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacteria, is becoming more common. This presents a serious obstacle to effective therapy and worsens patient outcomes.

Objective: To determine the bacteriological profile, antimicrobial resistance patterns, and distribution of MDR and XDR pathogens among adult pneumonia patients, and to evaluate their clinical characteristics.

Methodology: In the present cross-sectional study, 385 respiratory specimens were collected from adult patients with pneumonia. Pathogens were isolated and identified using Gram staining and culture using different media such as MacConkey, blood agar, and chocolate agar. Biochemical tests were performed, such as catalase and coagulase for Staphylococcus spp, Oxidase test for P. aeruginosa, and Indole, citrate, urease, and TSI.

Results: In the present study, 146 (37.9%) pneumonia patients needed intensive care management. The most affected age group was older people (> 60), accounting for 169 (43.9%). Klebsiella pneumoniae was the most commonly isolated pathogen, 126 (32.7%), followed by Pseudomonas aeruginosa, 104 (27%), and Acinetobacter baumannii, 61 (15%). Biofilm formation was observed in 182 (47.3%) of the 385 bacterial isolates from pneumonia patients.

Conclusion: The present study shows that the most common etiological agents were Gram-negative organisms, specifically Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii. These organisms also showed alarmingly high resistance rates to commonly prescribed antibiotics, such as β-lactams, tetracyclines, fluoroquinolones, and third-generation cephalosporins.

Keywords: Antimicrobial Resistance; Multidrug-resistant Bacteria; Extensively Drug-resistant Bacteria; Pneumonia

Introduction

Antimicrobial resistance among bacterial pneumonia patients continues to be a major cause of morbidity and mortality, especially in low- and middle-income countries like Pakistan. Pneumonia is the acute inflammation of the lung's parenchymal structure. when the immune system is not able to clear pathogen from the lower airways and alveoli causes the bronchioles and alveoli to become filled with inflammatory exudates and leukocytes, as a result, the blood and lungs exchange less carbon dioxide and oxygen, which leads to respiratory shortages and symptoms like coughing, sputum production, dyspnoea, chest pain, respiratory dysfunction, and in extreme situations, shock.[1] It can be categorized by mechanism (aspiration or ventilator-associated pneumonia), cause (bacterial, viral, fungal, etc.), and location of acquisition (community-acquired or hospital-acquired). Community-acquired pneumonia (CAP) is an infection acquired outside of a hospital, while hospital-acquired pneumonia (HAP) is an infection acquired after at least 48 hours of hospitalization. The bacterial pathogens that cause hospital-acquired and community-acquired pneumonia are becoming more resistant to widely used antibiotics, which makes clinical management more difficult and raises the possibility of unfavorable outcomes.[2] According to a comprehensive systematic analysis of antimicrobial resistance (AMR) in lower respiratory infections (LRI), there were approximately 20.9 deaths per 100,000 people in 2021 that were linked to AMR in LRI and approximately 5.05 deaths per 100,000 people that were directly related to AMR in LRI globally.[3] According to the latest estimates of the global burden, approximately 1.27 million deaths were due to bacterial AMR, with pneumonia being one of the main infections causing this death rate.[4] CAP is the sixth most common cause of death worldwide among adults over the age of 65. In developed countries, the incidence of CAP is 0.2 to 1.1%, and the mortality rate is 2 to 14%.[5] The leading cause of death among all nosocomial infections is hospital-acquired pneumonia. It affects 0.5 to 1.7% of hospitalized patients worldwide.[6]

Pneumonia infection spreads by aspiration, inhalation, and hematogenous transmission of pathogenic bacteria. Aspiration is a more common way for those with comorbid conditions to get Pneumonia.[7] Aging, comorbidities (such as asthma, bronchiectasis, heart disease, diabetes mellitus, immunosuppressive diseases, stroke, and chronic obstructive pulmonary disease (COPD)), past pneumonia history, immunosuppressive drugs, viral respiratory infections, and lifestyle factors (such as smoking, alcohol consumption, crowded living conditions, poor dental hygiene) are risk factors associated with pneumonia.[8,9]

Among the most common causes of atypical pneumonia are S. aureus, K. pneumoniae, H. influenzae, P. aeruginosa, M. catarrhalis, and E. coli. In contrast, the most common causes of atypical pneumonia are L. pneumophila, C. pneumoniae, and M. pneumoniae.[10,11]

Antimicrobial resistance (AMR) has increased in Pakistan due to failures in routine susceptibility surveillance, inadequate antimicrobial stewardship, and excessive antibiotic use. These days, pneumonia caused by multidrug-resistant Gram-negative bacteria (MDR-GNB) is becoming more prevalent and negatively affecting patient outcomes, suggesting a shift in infection trends toward GNB and their rapid spread, especially in hospital settings.[12] The relative frequency of these bacteria varies by region. The rise of antimicrobial resistance (AMR) in pneumonia has a significant impact on clinical outcomes, degrading antibiotic effectiveness, increasing treatment failures, extended hospitalizations, and mortality rates.[13]

Certain pneumococcal strains no longer respond to many antibiotics, such as cephalosporins, fluoroquinolones, macrolides, and penicillin.[14] In both healthcare-associated and community-acquired settings, MDR and XDR Gram-negative pathogens like Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter spp. have become more common. These pathogens are frequently linked to extended-spectrum β-lactamase (ESBL) production, carbapenem resistance, and other strong resistance mechanisms, which result in higher rates of treatment failure, longer hospital stays, and excess mortality.[15,16]

There is limited data available on the prevalence of bacterial resistance among respiratory isolates, particularly among adults with pneumonia in Khyber Pakhtunkhwa (KP). To provide information for empirical treatment and stewardship initiatives, this study aims to identify common bacterial pathogens from adult pneumonia patients and their patterns of antibiotic resistance in KP.

Objective

To determine the bacteriological profile, antimicrobial resistance patterns, and distribution of MDR and XDR pathogens among adult pneumonia patients, and to evaluate their clinical characteristics.

Methodology

A cross-sectional study was conducted to assess the antimicrobial resistance patterns of bacteria isolated from adult pneumonia patients. Respiratory samples were collected between January 2025 and August 2025 at Hayatabad Medical Complex, Peshawar, Khyber Pakhtunkhwa, Pakistan.

Patients aged ≥18 years, regardless of gender, who were diagnosed with pneumonia were eligible for inclusion in the study. Eligible patients were required to have chest imaging or radiographic evidence of pulmonary infiltrates

within the first 24 hours of admission, along with at least one major clinical symptom, such as cough, body temperature >37.8°C, or sputum production, or at least two minor clinical features, including dyspnoea, pleuritic chest pain, or altered mental status. Additionally, patients were required to have a white blood cell (WBC) count >12,000 cells/μL.

Patients were excluded if they had received antibiotic treatment for more than 48 hours before sample collection. Patients with neutropenia, pulmonary tuberculosis, or immunosuppressive conditions were also excluded. Furthermore, patients who were unable to provide the required clinical specimen were excluded from the study.

A total of 385 respiratory samples were collected from patients suspected of having pneumonia, as determined by Cochran's formula, and transported to the HMC laboratory for processing. Nonprobability sampling was employed in both outpatient and inpatient departments.

All adult patients (aged >18 years) admitted to HMC during the study period were included in the study population. Data were extracted from medical records and included patient demographics, culture results (blood, urine, Foley tip catheter), and antibiotic resistance trends. Data analysis was performed using SPSS version 27, and results were presented graphically.

For internal quality control measures, all respiratory specimens underwent an initial quality assessment using Gram stain microscopy to determine specimen adequacy and provide an initial indication of bacterial morphology. Each specimen was examined under a microscope before being inoculated onto standard culture media, such as chocolate agar for the isolation of fastidious respiratory pathogens like Haemophilus influenzae and Streptococcus pneumoniae, MacConkey agar for the recovery and differentiation of Gram-negative bacilli, and blood agar for the isolation of Gram-positive and fastidious organisms. Inoculated plates were incubated at 37°C under aerobic conditions for blood agar and MacConkey agar, while chocolate agar plates were incubated under a carbon dioxide atmosphere containing 5–10%. The colonies were evaluated based on morphological characteristics, hemolytic patterns, pigmentation, and odor after 24 to 48 hours of incubation to facilitate preliminary identification before further biochemical analysis.

Standard biochemical tests were used to identify the bacterial isolates after initial characterization. Tests for Gram-negative bacilli included Triple Sugar Iron agar, indole, citrate utilization, urease, motility, and oxidase; tests for Staphylococcus species included catalase and coagulase; and tests for Streptococcus species and other fastidious organisms included optochin sensitivity, bile solubility, and CAMP. The Kirby-Bauer disc diffusion method was used to test for antimicrobial susceptibility on Mueller-Hinton agar, and the results were interpreted in accordance with Clinical and Laboratory Standards Institute (CLSI) criteria. Ampicillin, amoxicillin–clavulanate, piperacillin–tazobactam, ceftriaxone, ceftazidime, cefepime, imipenem, meropenem,

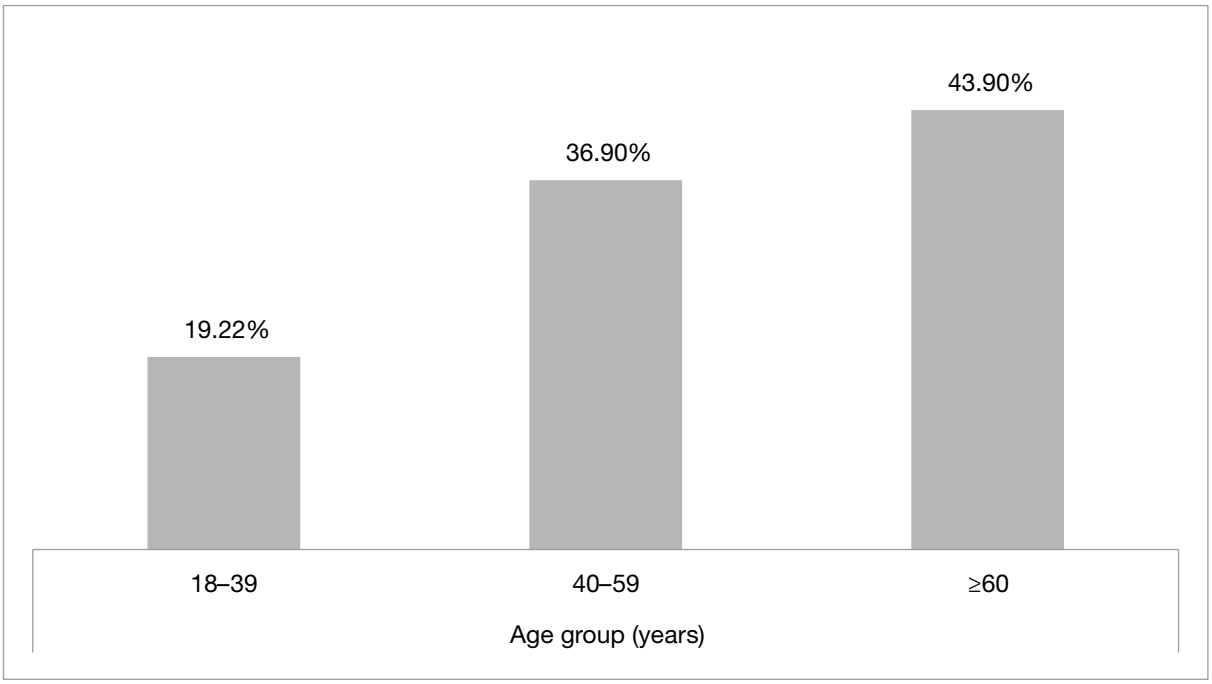


Figure 1. Age wise distribution of pneumonia positive cases

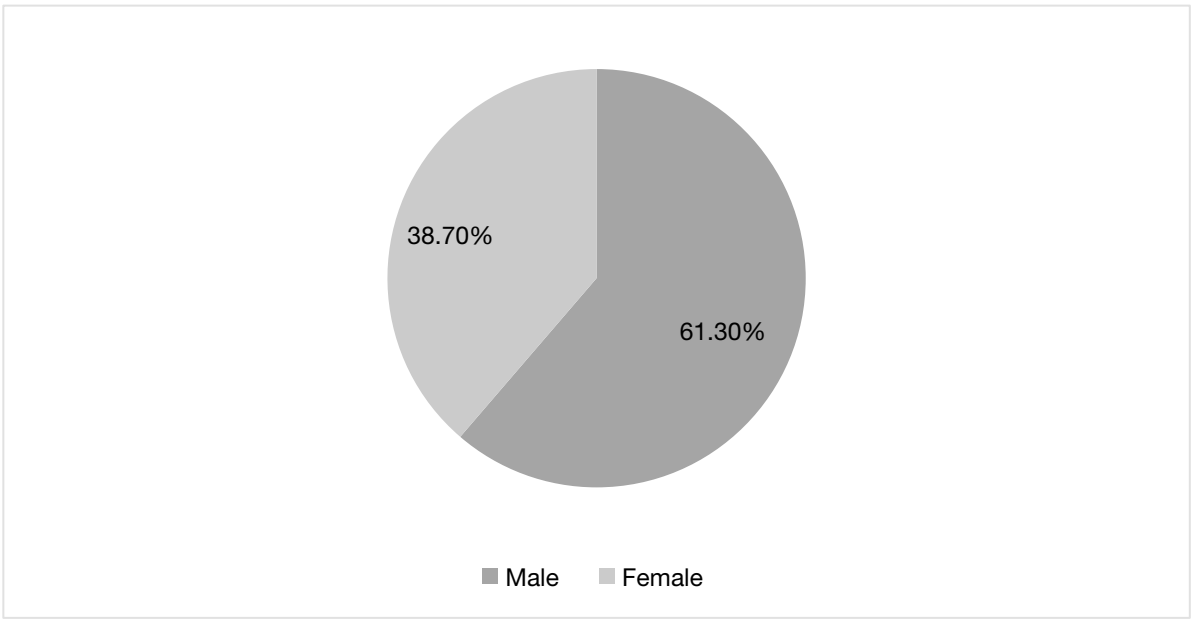


Figure 2. Gender wise distribution of pneumonia patients

ciprofloxacin, levofloxacin, amikacin, gentamicin, and colistin were among the antibiotics used to test Gram-negative isolates; penicillin, oxacillin for methicillin-resistant Staphylococcus aureus screening, erythromycin, clindamycin, tetracycline, vancomycin, and linezolid were used to test Gram-positive isolates. Reference strains (Escherichia coli ATCC 25922 and Staphylococcus aureus ATCC 25923) were tested in parallel to maintain quality assurance. International definitions were used to categorize resistance phenotypes. Multidrug-resistant (MDR) isolates were defined as resistant to at least one agent in three or more antimicrobial categories, extensively drug-resistant (XDR) isolates as non- susceptible to at least one agent in all but

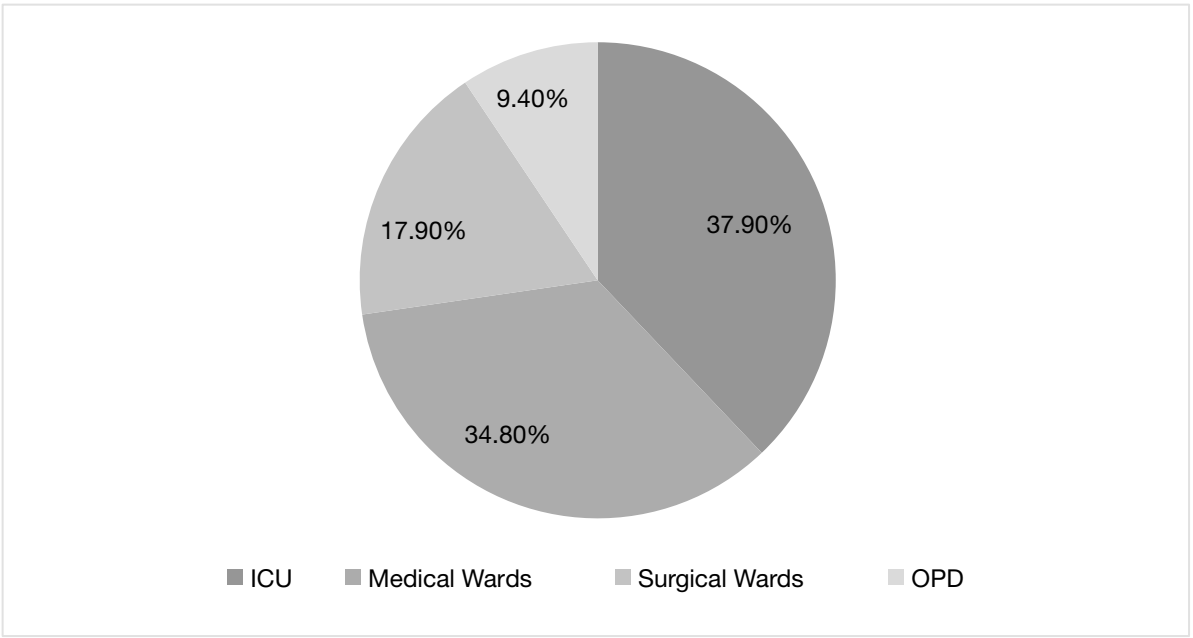


Figure 3. Pneumonia patients from different wards

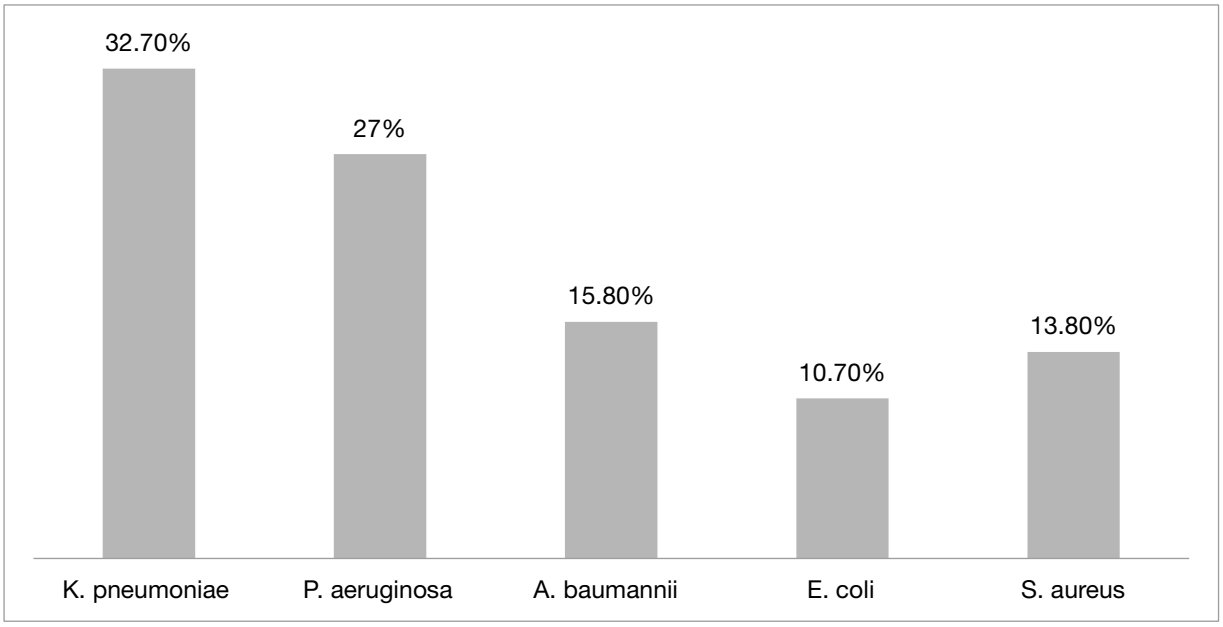


Figure 4. Graphic presentation of main bacteria isolated from Pneumonia patients

two or fewer categories, and pan-drug-resistant (PDR) isolates as showing resistance to all tested antimicrobial agents.

Results

Between January 2025 and August 2025, 385 pneumonia-positive samples were collected from patients meeting the inclusion criteria at Hayatabad Medical Complex. Samples were selected based on accessibility and availability rather than randomization. All positive samples were analyzed using SPSS version 27, and results were presented graphically.

Patients over the age of 60 accounted for the largest

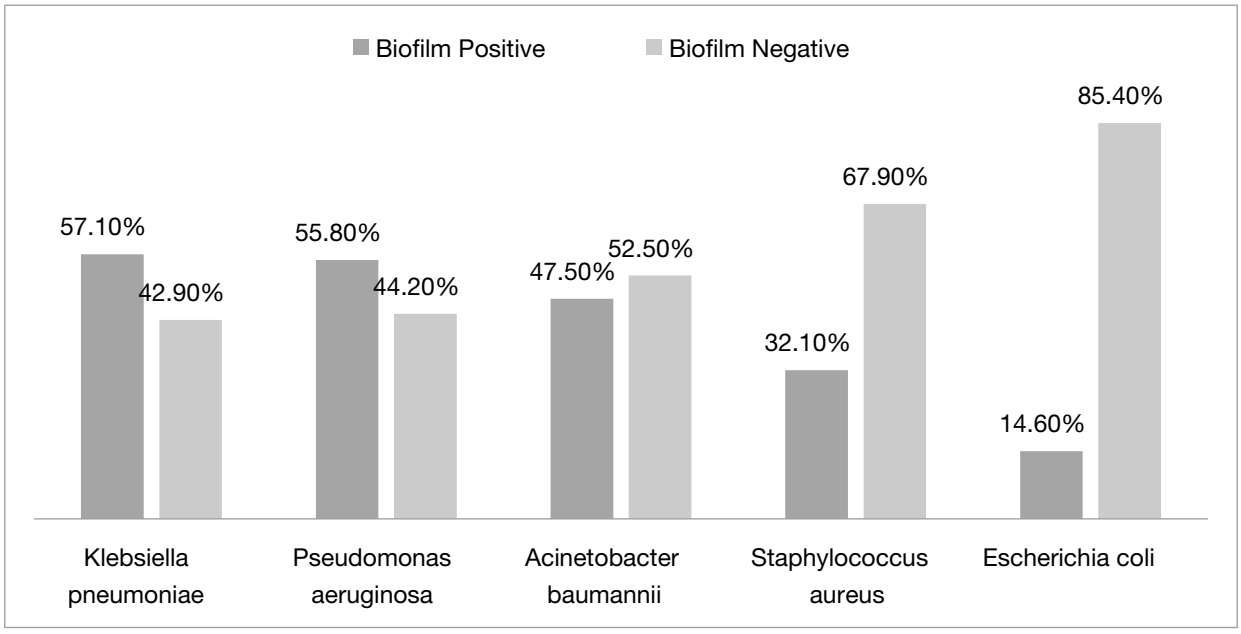


Figure.5. Represents the biofilm formation by bacteria isolated from pneumonia patients

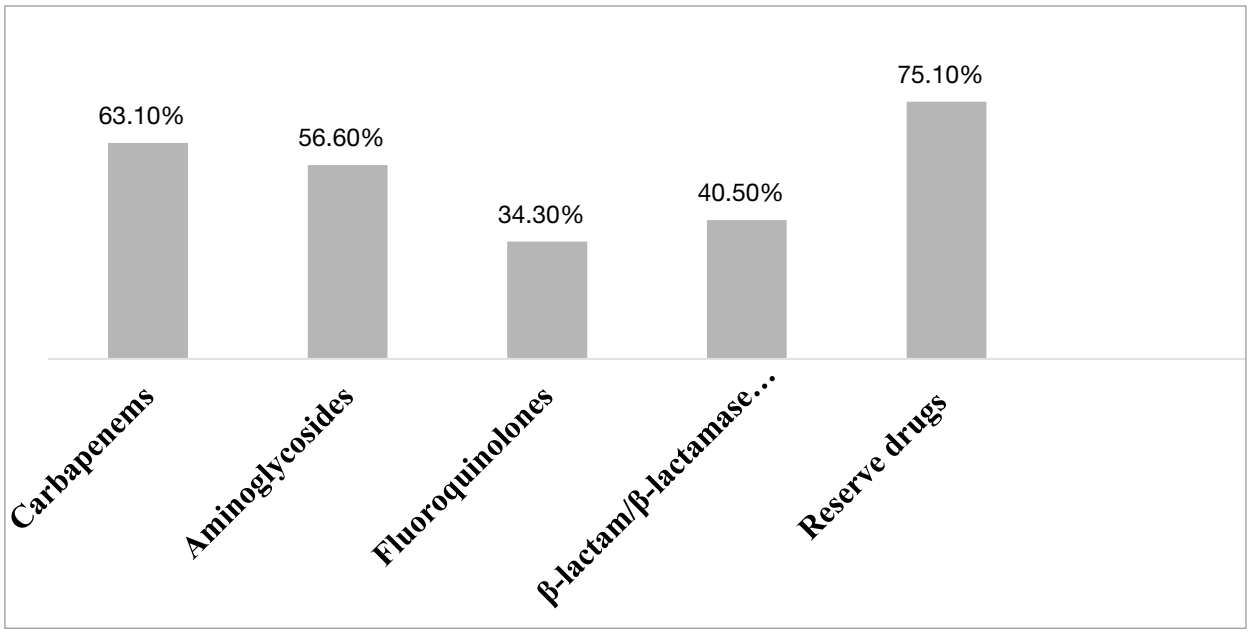
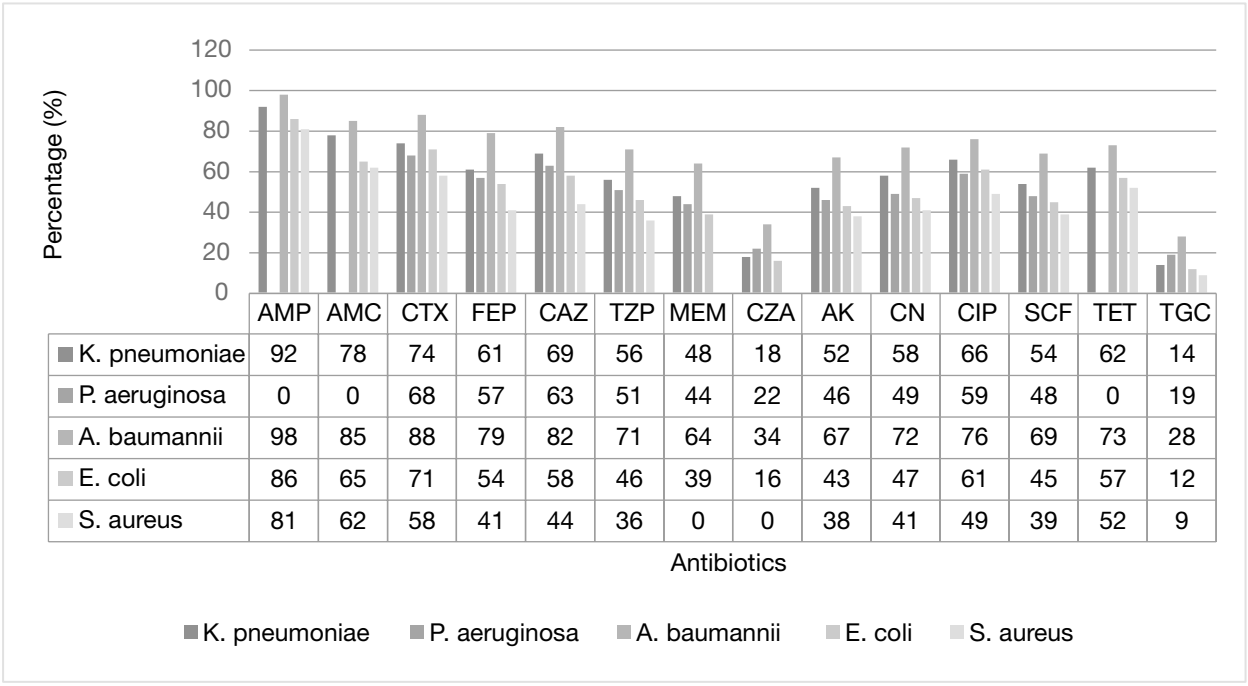


Figure 6. Resistance pattern of different antibiotic for Pneumonia patients isolates

proportion of pneumonia cases, with 169 (43.9%) of the 385 positive samples. The 40–59 age group comprised 142 cases (36.9%), while the 18–39 age group accounted for 79 cases (19.2%), as shown in Figure 1. These findings indicate that pneumonia morbidity and mortality increase with age.

Males constituted the majority of the study population, representing 236 cases (61.3%), compared to 149 females (38.7%), (Figure 2). These results underscore the influence of gender on the incidence of adult pneumonia.



	AMP	AMC	CTX	FEP	CAZ	TZP	MEM	CZA	AK	CN	CIP	SCF	TET	TGC
K. pneumoniae	92	78	74	61	69	56	48	18	52	58	66	54	62	14
P. aeruginosa	0	0	68	57	63	51	44	22	46	49	59	48	0	19
A. baumannii	98	85	88	79	82	71	64	34	67	72	76	69	73	28
E. coli	86	65	71	54	58	46	39	16	43	47	61	45	57	12
S. aureus	81	62	58	41	44	36	0	0	38	41	49	39	52	9

Figure 7. Resistance pattern of different antibiotic for Pneumonia patients isolates

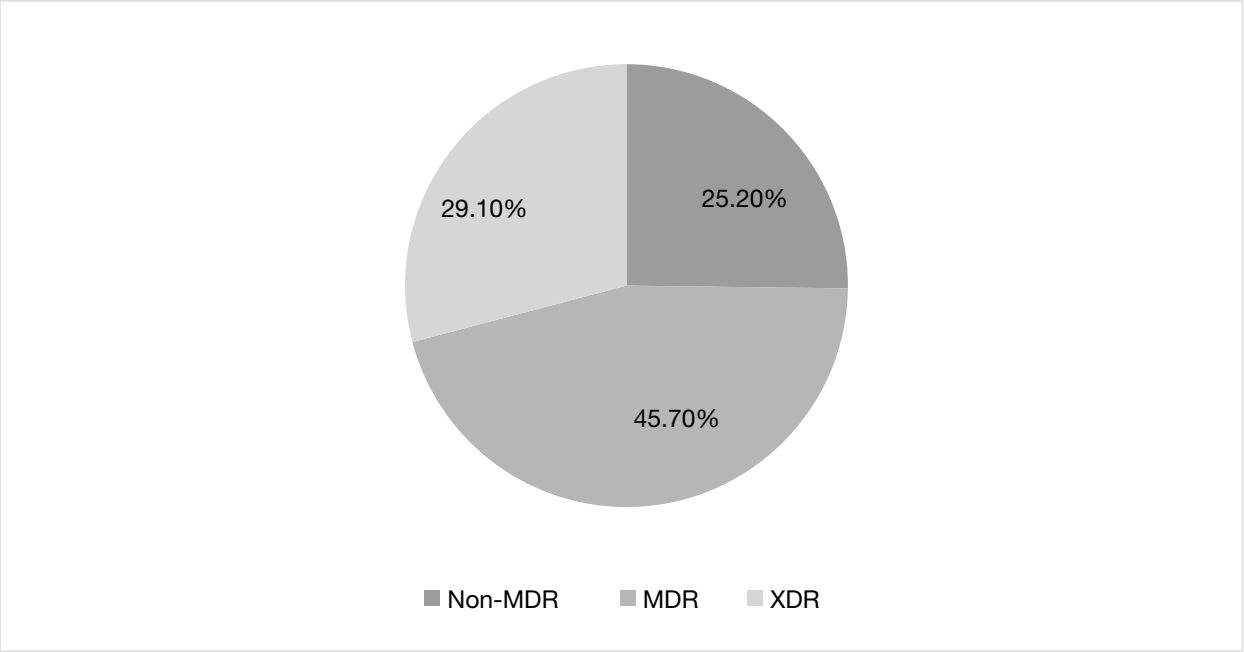


Figure 8. Adult pneumonia patients with non-multidrug-resistant (non-MDR), multidrug-resistant (MDR), and extensively drug-resistant (XDR) bacteria

The distribution of adult pneumonia patients by ward at the study location is shown in Figure 3. Due to the severity of the infection and the fact that many patients required critical care assistance, a significant number of cases were treated in the intensive care unit, 146 (37.9%). Surgical wards (69; 17.9%) and the outpatient department (36; 9.4%) reported a lower number of patients than medical wards (134; 34.8%), which accounted for more than one-third of patients (Figure 3).

The distribution of bacterial pathogens isolated from adult pneumonia patients is shown in Figure 4. The majority of the organisms were Gram-negative, with Klebsiella pneumoniae 126 (32.7%) being the most commonly isolated pathogen, followed by Pseudomonas aeruginosa 104 (27%) and Acinetobacter baumannii 61 (15%). Staphylococcus aureus 53(13.8%) made up a significant percentage of isolates among Gram-positive bacteria. The pathogen reported least frequently was Escherichia coli, 41 (10.7%). Overall, the distribution shows that Gram-negative bacteria predominate in adult pneumonia cases (Figure 4).

The biofilm-forming status of bacterial isolates from adult pneumonia patients is presented in Figure 5. Biofilm formation was observed in 182 (47.3%) of the 385 bacterial isolates from pneumonia patients. The most biofilm-producing bacteria were Klebsiella pneumoniae (57.1%), Pseudomonas aeruginosa (55.8%), and Acinetobacter baumannii (47.5%). On the other hand, Escherichia coli (14.6%) and Staphylococcus aureus (32.1%) showed reduced biofilm positivity. These results demonstrate that most Gram-negative bacteria form biofilms in pneumonia.

Bacterial isolates' resistance profiles showed significant variation across antibiotic classes, as shown in Figure 6. Resistance to reserve drugs, such as colistin and tigecycline, was highest (75.1%), followed by aminoglycosides (56.6%) and carbapenems (63.1%). Fluoroquinolones showed relatively lower resistance rates (34.3%), while β-lactam/β-lactamase inhibitor combos showed moderate resistance (40.5%). These results highlight the limited therapy choices for adult pneumonia patients and show a troubling level of resistance even to last-line medicines.

AMP: Ampicillin, AK: Amikacin; AMC: Amoxicillin/ Clavulanic Acid,

TZP: Piperacillin/Tazobactam, CTX: Cefotaxime, CAZ: Ceftazidime, MEM: Meropenem, FEP: Cefepime, CZA: Ceftazidime/Avibactam, CN: Gentamicin, CIP: Ciprofloxacin, SCF: Sulbactam/Cefoperazone, TGC: Tigecycline, TET: Tetracycline.

Bacterial isolates had a significant burden of drug resistance, according to an analysis of antimicrobial resistance phenotypes, as shown in Figure 7. Extensively drug-resistant organisms made up 29.1% of cases, but nearly half of the isolates (45.7%) were categorized as multidrug-resistant. Just 25.2% of the isolates were still non-MDR. The significant incidence of MDR and XDR microorganisms highlights an essential medical problem in the treatment of adult pneumonia.

The distribution of bacterial isolates based on their antibiotic class susceptibility is shown in Figure 8.

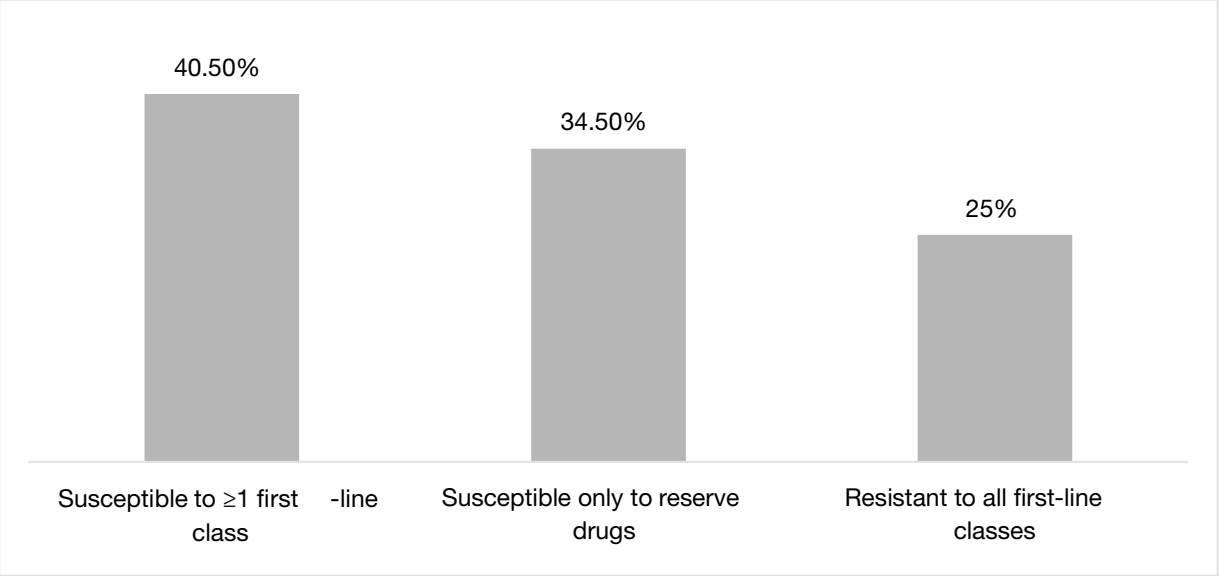


Figure 9. Percentage distribution of bacterial isolates susceptible to first-line antibiotics, susceptible only to reserve drugs, and resistant to all first-line antibiotic classes among adult pneumonia patients

Although 34.5% of isolates showed only susceptibility to reserve antibiotics, such as tigecycline and colistin, 40.5% of isolates remained sensitive to at least one first-line antibiotic class. Unexpectedly, 25.0% of isolates exhibited resistance to every first-line antibiotic class that was examined.

Discussion

This study provides a comprehensive analysis of the microbiological profile, antibiotic resistance patterns, and biofilm-forming capacity of bacterial pathogens responsible for pneumonia in adult patients at Hayatabad Medical Complex. The findings reveal a substantial burden of multidrug-resistant (MDR) and extensively drug-resistant (XDR) isolates, with a predominance of Gram-negative bacteria such as Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii. Alarmingly high resistance rates were observed for commonly prescribed first-line antibiotics, including cephalosporins, fluoroquinolones, and β-lactam/β-lactamase inhibitor combinations, while susceptibility was largely retained for a limited number of reserve drugs. Nearly half of the isolates demonstrated biofilm-forming capacity, which is associated with increased antibiotic resistance and chronic infection. These results underscore the growing challenge of managing drug-resistant pneumonia in adult patients and highlight the urgent need for enhanced antimicrobial stewardship, ongoing resistance surveillance, and evidence-based treatment strategies, particularly in resource-limited healthcare settings.

Similar to our study, another study conducted in the United States found that pneumonia was most common in those aged 60 and older, followed by those between the ages of 40 and 59.[17] Effective pathogen elimination in the elderly respiratory tract is affected by immune senescence, an age-related decline in immune function marked by decreased innate and adaptive immunity, lower mucociliary clearance, weakened antigen presentation, and lowered antibody synthesis.[18] Along with immunological changes, structural changes in the aging lung, such as reduced lung elasticity, impaired cough reflex sensitivity, and poor mucociliary clearance, make it more difficult for inhaled pathogens to be removed, promoting microbial colonization and infection.[19] Additionally, frailty syndromes and chronic comorbid illnesses (such as diabetes, cardiovascular disease, and chronic obstructive pulmonary disease) are often more prevalent in people over 65, which further reduces immunological tolerance and physiological balance.[20,21]

Consistent with our findings, a study conducted in Muzaffargarh, Punjab in 2023 demonstrated a higher prevalence among males compared to females.[22] Consistent with our results, another study carried out in Dir, KP in 2017 reported a higher prevalence among males compared to females.[23] Biological and behavioral variables interact in a complicated way to cause this sex gap. Due to the immunomodulatory effects of estrogen and the presence of two X chromosomes, which carry several immune-related genes that may improve pathogen recognition and clearance, females frequently exhibit stronger immune responses.[24] These biological

explanations include differences in innate and adaptive immunity. Males, on the other hand, typically have greater testosterone levels, which have been associated with immunosuppressive effects and poorer inflammatory responses, which could reduce their capacity to eradicate lung infections successfully.[25,26] The variation may be made worse by behavioral and lifestyle factors; males are known to be more susceptible to lower respiratory tract infections due to higher rates of smoking, alcohol consumption, occupational exposures, and delayed healthcare-seeking behaviors.[27]

Our study is in line with another study carried out in Japan in 2021, which reported that intensive care units accounted for over one-third of pneumonia patients, followed by patient management in medical wards.[28] Due to the severity of the illness, the existence of conseq-uences like respiratory failure, septic shock, hypercapnia, which is associated with longer hospital stay, acute respiratory distress syndrome (ARDS), and related comorbidities, requires mechanical ventilation and needs to be managed in an intensive care unit (ICU), which worsens the outcomes. All of these conditions were found to be strongly linked to increased mortality in patients with severe pneumonia in an intensive care unit (ICU).[29,30] Moreover, underlying comorbid conditions such as diabetes, hypertension, and chronic lung disease have been linked to more severe pneumonia requiring ICU treatment.[31]

Similar to our study, another multicenter study conducted in Ethiopia in 2021 found that K. pneumoniae is the most common isolate in adult pneumonia cases.[32] In a recent study from a tertiary care hospital in Pakistan in 2025, P. aeruginosa and A. baumannii were similarly identified as predominant pathogens in ventilator-associated and ICU-acquired pneumonia.[15]

The majority of the isolates from our study were Gram-negative; P. aeruginosa accounted for the most common cause of pneumonia. This distribution is consistent with prior research in Nepal in 2021, especially for ventilator-associated and hospital-acquired pneumonia, where most isolates were Gram-negative. In one ICU study, most respiratory isolates were P. aeruginosa, A. baumannii, and K. pneumoniae. Biofilm production was common among these infections, particularly P. aeruginosa and A. baumannii, which correlated with multidrug-resistant profiles.[33] Klebsiella pneumoniae was the most common pneumonia pathogen in our study, indicating its aggressiveness, opportunistic character, and ability to survive in both hospital and community settings, especially among elderly and critically ill patients. K. pneumoniae has many virulence factors that help it spread and persist in the lower respiratory tract, such as a thick polysaccharide capsule that prevents phagocytosis and antibody destruction, siderophores that aid in iron acquisition, type 1 and type 3 fimbria adhesins that improve adherence to respiratory epithelium, and the capacity to form biofilms that shield it from host defenses and antibiotic penetration. These virulence characteristics not only increase pathogenicity but also contribute to its success as a cause of pneumonia.[34,35] The oropharyngeal mucosa is colonized by the opportunistic pathogen K. pneumoniae. People with compromised immune systems, advanced age, hospital environment, and contaminated equipment may also increase the risk of drug-resistant pneumonia. may become infected.[36]

In this study, pneumonia-associated pathogens showed high levels of antimicrobial resistance, which is consistent with a recent clinical study from Karachi, Pakistan in 2025, indicating that Klebsiella species and Acinetobacter baumannii dominate among Gram-negative bacteria resistant to carbapenems and colistin.[37] Similar results from clinical isolates reported in Khyber Pakhtunkhwa in 2025, where hypervirulent strains of K. pneumoniae showed over 90% resistance to ampicillin and significant resistance to other commonly used drugs, are reflected in the high resistance rates to first- and second-line agents such as ampicillin, cephalosporins, fluoroquinolones, and aminoglycosides observed in our study.[35] Critical resistance genes like bla_{NDM-5}, bla_{NDM-1}, and $bla_{OXA-232}$ are present in a high percentage of carbapenem-resistant strains. Additionally, traditional β-lactamases like $bla_{CTX-M-15}$ are also common, which facilitates resistance to broad-spectrum cephalosporins and related agents. Rapid horizontal gene transfer and the growth of multidrug-resistant clones are made possible by the frequent combination of these resistance determinants on mobile genetic elements. Multidrug-resistant (MDR) and extensively drug-resistant (XDR) strains of bacteria result from the overuse and misuse of antibiotics, particularly for respiratory infections without microbiological confirmation.

Conclusion

This study highlights a significant public health concern: antibiotic-resistant bacterial pathogens are a major cause of adult pneumonia in Pakistan. The most common etiological agents identified were Gram-negative organisms, particularly Klebsiella pneumoniae, Pseudo-monas aeruginosa, and Acinetobacter baumannii, all of which exhibited high resistance rates to frequently prescribed antibiotics, including β-lactams, tetracyclines, fluoroquinolones, and third-generation cephalosporins. Pathogens isolated from intensive care units demons-trated extensive drug resistance (XDR) phenotypes in substantial proportions, and multidrug resistance (MDR) was also prevalent. Study limitations include the absence of molecular characterization of resistance mechanisms (such as ESBLs, carbapenemases, or methicillin resistance genes) and the single-center design, which may restrict the generalizability of the findings to other

hospitals or regions in Pakistan.

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