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# COMMON PATHOGENS IN PATIENTS WITH COMMUNITY-ACQUIRED PNEUMONIA PRESENTING TO A TERTIARY CARE FACILITY

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## ABSTRACT

**Objective:** To determine the frequency of common pathogens and associated factors among patients presenting with community-acquired pneumonia (CAP) at a tertiary care facility.

**Methods:** This descriptive cross-sectional study was conducted at the Department of Pulmonology, Liaquat University of Medical and Health Sciences (LUMHS), Jamshoro/Hyderabad. A total of 150 patients aged 18–70 years diagnosed with CAP were enrolled through consecutive non-probability sampling. Sputum specimens were collected before antibiotic administration and processed for culture and pathogen identification. Demographic characteristics, comorbid conditions, smoking status, and vaccination history were recorded. Data were analyzed using SPSS version 24. Logistic regression analysis was performed to identify factors associated with Gram-negative pathogen isolation.

**Results:** The mean age of participants was 51.8 ± 14.6 years, and 92 (61.3%) were male. *Klebsiella pneumoniae* was the most frequently isolated pathogen, identified in 53 (35.3%) patients, followed by *Escherichia coli* in 23 (15.3%) and *Pseudomonas aeruginosa* in 21 (14.0%) patients. Overall, Gram-negative organisms accounted for 70.0% of all isolates, whereas Gram-positive organisms accounted for 18.0%. Diabetes mellitus, COPD, and smoking were significantly associated with Gram-negative pathogen isolation. Multivariable analysis demonstrated that diabetes mellitus (AOR: 2.4, p=0.011), COPD (AOR: 2.1, p=0.028), and smoking (AOR: 1.9, p=0.041) were independent predictors of Gram-negative infection.

**Conclusion:** Gram-negative organisms, particularly *Klebsiella pneumoniae*, were the predominant pathogens causing community-acquired pneumonia. Diabetes mellitus, COPD, and smoking were significant predictors of Gram-negative infection. These findings highlight the importance of local microbiological surveillance and tailored empirical antibiotic therapy.

**KEYWORDS:** Community-acquired pneumonia, *Klebsiella pneumoniae*, Gram-negative pathogens, sputum culture, COPD, diabetes mellitus, smoking.

## INTRODUCTION

Community-acquired pneumonia (CAP) is a prominent acute infection of the pulmonary parenchyma that occurs outside healthcare settings and is still one of the leading causes of morbidity, hospitalization, and mortality globally. Although there has been considerable progress regarding antimicrobial therapy, vaccination programs, and supportive care, community-acquired pneumonia (CAP) remains an important public health problem in both developed and developing countries (1). CAP can manifest clinically from mild disease, simplified in outpatient settings, to severe illness necessitating intensive care unit admission and mechanical ventilation. Globally, the estimated incidence of CAP (2.3 to 8.3 per thousand population-year) is heterogeneous, with higher rates among older adults and people with chronic disease conditions. CAP continues to be the most common infectious cause of mortality globally and represents an important component of healthcare resource utilization and economic burden. Pneumonia and lower respiratory tract infections are among the most important causes of mortality worldwide, with millions of deaths every year (2).

More than half of the global burden is in low- and middle-income countries, where inadequate healthcare resources, diagnostic delay, overcrowding, malnutrition, and smoking, as well as chronic medical illness, predict adverse outcomes. Pneumonia continues to be one of the most important diseases in terms of hospitalization and mortality in

South Asia. Respiratory infections remain a major public health problem in Pakistan, with pneumonia being one of the leading causes of morbidity and mortality (3). Research from Pakistan has shown the continuing burden of lower respiratory tract infections on health services and patient outcomes. Respiratory infections, especially pneumonia, are one of the most common causes of death in so-called vulnerable populations (children under 5 years and older adults), indicating that pneumonia continues to be a relevant public health problem in our country (4).

CAP is caused by a myriad of microorganisms, spanning bacterial, viral, and atypical pathogens. Streptococcus pneumoniae has traditionally been considered the leading bacterial cause worldwide; however, pathogen distribution can vary markedly by region. New evidence from South Asian nations has shown rising frequencies of Gram-negative organisms, including Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter spp, whereas viral pathogens are being progressively diagnosed using molecular diagnostics. Determining the causative pathogens accurately is crucial to the advantage of empirical antibiotic therapy and improving patient outcomes (5).

CAP is one of the most common causes of hospital admission in Pakistan; however, very little data are available from local centres on the microbiological profiles of patients presenting with CAP, especially from the tertiary care centre in Hyderabad. Treatment protocols are primarily designed with the help of international standards, which do not always reflect local pathogen distribution and antimicrobial resistance. To assess the frequency of common pathogens in CAP patients presenting at Liaquat University of Medical and Health Sciences (LUMHS) will provide evidence-based local epidemiological data; thereby optimizing empirical antibiotic selection, reducing inappropriate use of antimicrobials, and ultimately improving clinical outcomes. Hence, the current study was conducted to find the most common pathogens associated with community-acquired pneumonia presenting in patients attending a Tertiary care hospital at Hyderabad.

## MATERIALS AND METHODS

### Study Design and Setting

This is a cross-sectional descriptive study that took place at the Department of Pulmonology, Liaquat University of Medical and Health Sciences (LUMHS), Jamshoro/Hyderabad, Pakistan. After approvals from REU, CPSP, this study was conducted over a duration of Three months, from **1st February 2026 to 30th April 2026**, after obtaining ethical approval from the Institutional Review Board (IRB) of LUMHS (REC/-1091 date 2nd September 2025), at LUMHS, the Department of Pulmonology is a large tertiary care referral center for patients from all over urban and rural Sindh, making it a suitable place to assess the microbiological profile in community-acquired pneumonia.

### Study Population

Adults presenting to the LUMHS outpatient department or admitted to the Department of Pulmonology with a diagnosis of community-acquired pneumonia. All patients who met the operational definition of CAP and all the criteria for inclusion were invited to participate in our study. This diagnosis was made in the presence of compatible clinical signs, systemic evidence of infection, and evidence on thoracic imaging showing new pulmonary infiltrates developing before or within 48 hours of hospital admission. Patients of either sex between 18 and 70 years. Patients enrolled in the study were excluded from any diagnoses that would lead to potential confounding and misclassification, including those who: received >48 hours of antibiotics 14 days prior, had active pulmonary tuberculosis, aspiration pneumonia, healthcare-associated pneumonia versus community-acquired pneumonia; hospital-acquired pneumonia versus early ventilator-associated pneumonia (≤4 days), late ventilator-associated pneumonia (>4 days) or new pulmonary embolism; congestive heart failure; non-infectious pulmonary infiltrates.

### Sample Size and Sampling Technique

A WHO sample-size calculator was used for calculating the sample size. Considering the prevalence of Enterococcus species among community-acquired pneumonia patients as 5% (6), confidence level as 95%, and absolute precision as 3.5%, the minimum sample size required was computed to be 150 patients. Non-probability sampling was performed consecutively. All eligible patients were recruited continuously and consecutively until the target number of samples was reached. Using such a sampling technique includes every participant who meets eligibility criteria and reduces the potential for selection bias.

### Data Collection Procedure

Eligible patients were approached by the investigator once approval from the Institutional Review Board and the CPSP Research Evaluation Unit was provided. Study objectives, study procedures, and potential benefits and risks were clearly stated, ideally obtaining written informed consent prior to enrollment. The demographic data parameters comprising Age, Sex, Place of residence, and educational status were documented. Smoker status, type 2 diabetes mellitus (history), hypertension (history), chronic obstructive pulmonary disease (history), HIV/AIDS (history), chronic kidney disease (history) or not having had a transplant, requiring dialysis/chronic liver disease, taking chronic steroids, and pneumococcal vaccination and influenza vaccination were collected in detail.

Availability and validation of all comorbid conditions via the medical records, laboratory investigations, and previous treatment done wherever applicable. Before starting in-hospital antibiotic therapy to prevent altering microbiological findings, a sputum specimen was obtained from each participant. New Guidelines provide advice on how to ensure

good-quality sputum samples and reduce contamination by upper respiratory tract flora. The specimens obtained were immediately transported to the microbiology laboratory of the institute for Gram stain, culture, and pathogen identification following standard microbiological techniques.
Microbiological criteria were established to determine the prevalence of common bacterial pathogens (including Klebsiella pneumoniae, Enterococcus species, Staphylococcus aureus, Streptococcus pneumoniae, and Acinetobacter species). Gram stain morphology, colony characteristics, and standard culture methods were used for the identification of bacterial isolates. All clinical, demographic, and laboratory data were collected using a study-specific structured proforma.

**Study Outcome Measures**
The main outcome measure was the detection of specific bacterial pathogens from cultures obtained from sputum specimens collected from patients who were diagnosed with community-acquired pneumonia. Distribution of pathogens in terms of demographics and associations between isolated pathogens and clinical risk factors (diabetes mellitus, hypertension, chronic obstructive pulmonary disease, HIV/AIDS, chronic kidney disease, chronic liver disease, smoking status, (Current, former, or never smoker), chronic steroid use, and vaccination status were secondary outcomes.

**Statistical Analysis**
Data entry and analysis were conducted using the Statistical Package for Social Sciences (SPSS, version 24). Data were validated for completeness, consistency, and accuracy before being analysed. Continuous variables were tested for normal distribution with the Shapiro–Wilk test. Data, including quantitative variables such as age, were expressed as either mean ± standard deviation (if normally distributed) or median and interquartile range. The qualitative variables (gender, residence, educational status, smoking status, vaccination status) are presented as frequency and percentage, while the comorbid conditions and isolated pathogens are summarized.
We used univariate logistic regression analysis to first identify factors associated with the presence of certain pathogens. Those variables that showed a p-value of ≤0.25 in univariate analysis are then entered into a multivariable logistic regression model to adjust for confounding factors. For statistically significant predictors, adjusted odds ratios with 95% confidence intervals were calculated. Statistical significance was defined as a p-value ≤0.05 for all analyses.

**RESULTS**
A total of 150 patients diagnosed with community-acquired pneumonia (CAP) were recruited into the study. The mean age of the participants was 51.8±14.6 years, with the majority belonging to the 51–70 years age group (53.3%). There were 92 (61.3%) males and 58 (38.7%) females. Most patients resided in urban areas (56.0%), while 44.0% belonged to rural areas. Diabetes mellitus was present in 58 (38.7%) patients, hypertension in 64 (42.7%), chronic obstructive pulmonary disease (COPD) in 41 (27.3%), chronic kidney disease in 18 (12.0%), chronic liver disease in 11 (7.3%), and HIV/AIDS in 4 (2.7%) patients. Current smoking was reported by 52 (34.7%) participants. Baseline demographic and clinical characteristics of the study population are summarized in Table 1.

**Table 1. Baseline Characteristics of Patients with Community-Acquired Pneumonia (n=150)**

| **Baseline and clinical parameters** | **Frequency (%)** |
|---|---|
| **Age Group (Years)** | |
| 18–30 | 22 (14.7) |
| 31–50 | 48 (32.0) |
| 51–70 | 80 (53.3) |
| **Gender** | |
| Male | 92 (61.3) |
| Female | 58 (38.7) |
| **Residence** | |
| Urban | 84 (56.0) |
| Rural | 66 (44.0) |
| **Education Status** | |
| Illiterate | 34 (22.7) |
| Primary–Middle | 48 (32.0) |
| Secondary | 41 (27.3) |
| ≥Matric | 27 (18.0) |
| **Diabetes Mellitus** | 58 (38.7) |

| | |
|---|---|
| **Hypertension** | 64 (42.7) |
| **COPD** | 41 (27.3) |
| **Chronic Kidney Disease** | 18 (12.0) |
| **Chronic Liver Disease** | 11 (7.3) |
| **HIV/AIDS** | 4 (2.7) |
| **Current Smoker** | 52 (34.7) |
| **Pneumococcal Vaccination** | 29 (19.3) |
| **Influenza Vaccination** | 36 (24.0) |

Microbiological evaluation of sputum cultures demonstrated that *Klebsiella pneumoniae* was the most commonly isolated pathogen, identified in 53 (35.3%) patients. *Escherichia coli* was isolated in 23 (15.3%) patients, followed by *Pseudomonas aeruginosa* in 21 (14.0%) patients. *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Enterococcus* species, and *Acinetobacter* species were isolated in 10 (6.7%), 9 (6.0%), 8 (5.3%), and 8 (5.3%) patients, respectively. No significant bacterial growth was observed in 18 (12.0%) sputum specimens. The distribution of isolated pathogens is illustrated in Figure 1.

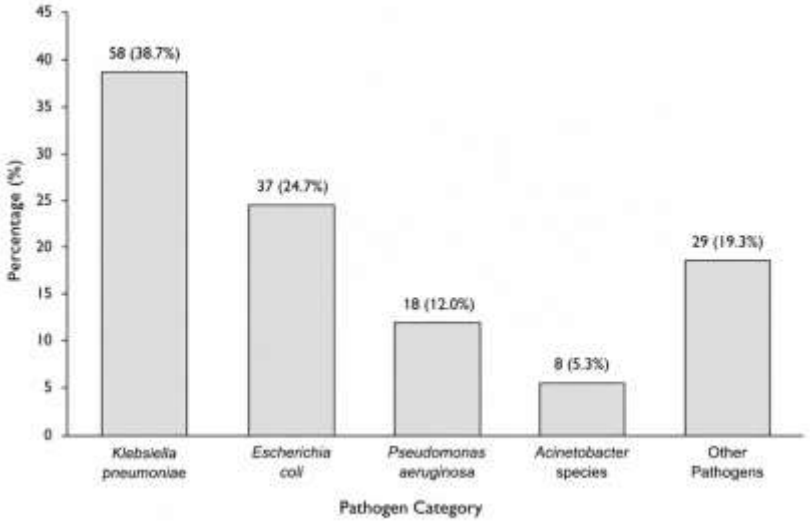


**Figure 1. Distribution of Common Pathogens Isolated from Sputum Cultures of Patients with Community-Acquired Pneumonia (n=150)**

Assessment of pathogen distribution by major comorbid conditions showed that Gram-negative organisms were more frequently isolated among patients with diabetes mellitus and COPD. *Klebsiella pneumoniae* was significantly more common among diabetic patients and those with COPD. Similarly, *Pseudomonas aeruginosa* was significantly more frequent among patients with COPD. The detailed association between major comorbid conditions and isolated pathogens is presented in Table 2.

**Table 2. Distribution of Common Pathogens According to Major Comorbid Conditions**

| Pathogen | Diabetes Mellitus (n=58) | P-value | COPD (n=41) | P-value | Hypertension (n=64) | P-value |
|---|---|---|---|---|---|---|
| Klebsiella pneumoniae | 16 (27.6) | 0.008 | 13 (31.7) | 0.012 | 21 (32.8) | 0.086 |
| Escherichia coli | 10 (17.2) | 0.043 | 5 (12.2) | 0.084 | 9 (14.1) | 0.267 |
| Pseudomonas aeruginosa | 9 (15.5) | 0.021 | 8 (19.5) | 0.017 | 8 (12.5) | 0.118 |
| Streptococcus pneumoniae | 4 (6.9) | 0.341 | 3 (7.3) | 0.427 | 4 (6.3) | 0.512 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Staphylococcus aureus | 4 (6.9) | 0.468 | 2 (4.9) | 0.591 | 3 (4.7) | 0.624 |
| Enterococcus species | 3 (5.2) | 0.537 | 2 (4.9) | 0.672 | 3 (4.7) | 0.718 |
| Acinetobacter species | 3 (5.2) | 0.291 | 3 (7.3) | 0.241 | 4 (6.3) | 0.355 |

**Data are presented as frequency (%). P-values were calculated using the Chi-square test or Fisher's exact test, as appropriate. Statistically significant associations (p<0.05)**

The prevalence of Gram-negative pathogens (*Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Acinetobacter* species) was significantly higher than that of Gram-positive pathogens. Overall, Gram-negative organisms accounted for 105 (70.0%) isolates, whereas Gram-positive organisms accounted for 27 (18.0%) isolates. No bacterial growth was observed in 18 (12.0%) patients. The microbiological profile of CAP is shown in Figure 2.

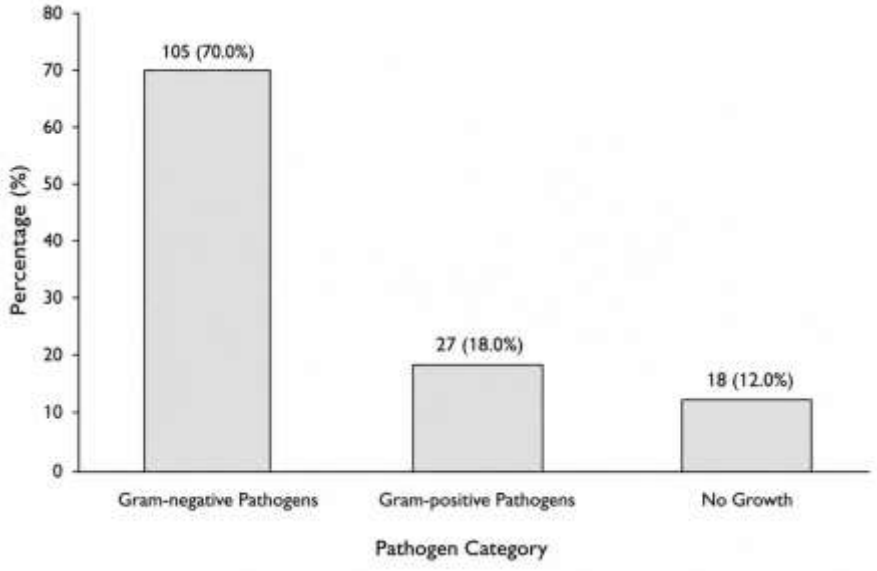


**Figure 2. Distribution of Gram-Negative and Gram-Positive Pathogens Among Patients with CAP (n=150)**

Multivariable logistic regression analysis was performed to identify factors associated with Gram-negative bacterial isolation. Diabetes mellitus, COPD, and current smoking emerged as independent predictors of Gram-negative infection. Patients with diabetes mellitus had 2.4-fold higher odds of Gram-negative bacterial isolation compared with non-diabetic patients (AOR: 2.4; 95% CI: 1.2–4.8; p=0.011). Similarly, COPD (AOR: 2.1; 95% CI: 1.1–4.3; p=0.028) and current smoking (AOR: 1.9; 95% CI: 1.0–3.8; p=0.041) were significantly associated with Gram-negative pathogen isolation. The results of multivariable analysis are presented in Table 3.

**Table 3. Multivariable Logistic Regression Analysis for Predictors of Gram-Negative Pathogen Isolation**

| Variable | Adjusted Odds Ratio (95% CI) | P-value |
|---|---|---|
| Diabetes Mellitus | 2.4 (1.2–4.8) | 0.011 |
| COPD | 2.1 (1.1–4.3) | 0.028 |
| Current Smoking | 1.9 (1.0–3.8) | 0.041 |
| Hypertension | 1.2 (0.6–2.5) | 0.563 |
| Chronic Kidney Disease | 1.4 (0.5–3.9) | 0.481 |
| Age >50 years | 1.3 (0.7–2.6) | 0.394 |
| Male Gender | 1.2 (0.6–2.3) | 0.522 |

Adjusted odds ratios (AORs) and 95% confidence intervals (CIs) were obtained using multivariable logistic regression analysis. Variables entered into the model included age, gender, diabetes mellitus, hypertension, chronic obstructive pulmonary disease (COPD), chronic kidney disease, and smoking status. A p-value ≤0.05 was considered statistically significant.

Further subgroup analysis demonstrated that *Klebsiella pneumoniae* remained the predominant pathogen across all age groups and was particularly common among patients aged above 50 years (43.8% vs. 25.7%, p=0.018). In

contrast, *Streptococcus pneumoniae* was more frequently isolated among younger patients aged below 50 years (10.0% vs. 4.3%, p=0.041). Smokers exhibited a significantly higher prevalence of *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* compared with non-smokers (53.8% vs. 30.6%, p=0.006). Table 4.

**Table 4. Association of Age Group and Smoking Status with Common Pathogens in Community-Acquired Pneumonia (n=150)**

| Risk factors | Klebsiella pneumoniae n (%) | Streptococcus pneumoniae n (%) | Pseudomonas aeruginosa n (%) | P-value |
|---|---|---|---|---|
| Age ≤50 years (n=70) | 18 (25.7) | 7 (10.0) | 7 (10.0) | |
| Age >50 years (n=80) | 35 (43.8) | 3 (4.3) | 14 (17.5) | 0.018 |
| Smokers (n=52) | 28 (53.8) | 2 (3.8) | 11 (21.2) | |
| Non-smokers (n=98) | 30 (30.6) | 8 (8.2) | 10 (10.2) | |

## DISCUSSION

The current study aimed to identify the prevalence of the most common pathogens from patients presented in a tertiary care hospital with community-acquired pneumonia (CAP). Klebsiella pneumoniae was the most common pathogen isolated in 53 (35.3%) patients, followed by Escherichia coli in 23 (15.3%) patients and Pseudomonas aeruginosa in 21 (14.0%). Gram-negative organisms were responsible for the majority (n = 105, 70.0%) of all isolates, compared with Gram-positive organisms accounting for only 27 (18.0%) isolates combined. The present study findings show a dominance of Gram-negative pathogens in the local population, indicative of an evolving microbiological pattern seen with community-acquired pneumonia. Vikhe VB and colleagues, in a similar study done in India, found that Klebsiella pneumoniae was detected on approximately 35% of CAP cases (7). Similarly, increasing frequencies of Gram-negative organisms among hospitalized CAP patients have been reported from studies conducted in Pakistan (8) and other South Asian countries (9-11). The resemblance could be due to similar healthcare systems, extensive empiric antibiotic use, a large burden of diabetes mellitus, and the lethargic nature of presentation in the health facilities. On the contrary, studies from the United States and Europe have shown Streptococcus pneumoniae to be the most predominant pathogen with an approximate range of 20–30% in CAP (12, 13). These discrepancies may be attributed to higher pneumococcal vaccination coverage, better infection control measures, and more rigorous antimicrobial stewardship programmes among developed countries.

The incidence of Escherichia coli (15.3%) and Pseudomonas aeruginosa (14.0%) we reported in the present study was also considerable. We identified similar frequencies previously reported by tertiary care centers in Pakistan (14), India (15), and America (16). The comparatively high burden of these pathogens compared to Western studies may be due to a higher prevalence of chronic disease, environmental exposure, multiple contacts with healthcare systems, and inappropriate use of antibiotics, which favor colonization by Gram-negative organisms.

In the present study, it is important to note that Streptococcus pneumoniae was infrequently isolated in only 10 (6.7%) patients. Similarly, Staphylococcus aureus and Enterococcus species were obtained from 9 (6.0%), and 8 patients (5.3%), respectively. These frequencies are lower than those seen in many European and North American studies, where pneumococcus is still the most dominant pathogen (17). But that was not the case with a recent study conducted in Pakistan and neighbouring countries, which have also reported similar reductions in pneumococcal isolation. To explain these differences, we hypothesize that it could be due to pre-hospital broad-spectrum antibiotic exposure, variable diagnostic methodology, and evolving pathogen epidemiology favoring Gram-negative organisms.

In terms of demographic characteristics, the majority are older than 50 years old, with 80 (53.3%) patients; more men constitute the study population —92 (61.3%). These results are in line with reports from Pakistan (18), India (19), and Brazil (20) that also showed CAP generally affects older males (33% to 94%). Older people exhibit reduced immune response and a higher prevalence of co-morbid diseases; men are more often affected by smoking and work-related respiratory exposure.

In 58 (38.7%) patients, diabetes mellitus was recorded, and this disease was shown to be an independent risk factor for the isolation of Gram-negative pathogens. Klebsiella pneumoniae was the isolate in 16 (27.6%) of diabetic patients, and Pseudomonas aeruginosa was isolated from 9 (15.5%). Diabetes mellitus was also a significant independent risk factor for Gram-negative infection, with an adjusted odds ratio of 2.4 (95% CI: 1.2–4.8). A meta-analysis conducted recently showed very similar results. Hyperglycemia impairs neutrophil function, alters cellular immunity, and promotes bacterial proliferation, which results in a higher incidence of Gram-negative infections (21).

Chronic obstructive pulmonary disease, 41 (27.3%) patients, a significant predictor of isolation of a Gram-negative pathogen. In patients with COPD, Klebsiella pneumoniae and Pseudomonas aeruginosa were the most frequently isolated, at 13 (31.7%) and 8 (19.5%), respectively. COPD nearly doubled the odds of Gram-negative infection (AOR: 2.1, 95% CI: 1.1–4.3). Similar observations have been reported from studies done in China (22). This association might be due to structural lung damage, chronic airway inflammation, and recurrent antibiotic exposure.

Current smoking was observed in 52 (34.7%) cases, and with the addition of confounding factors, it remained independently associated with Gram-negative bacterial infection (AOR: 1.9, 95% CI: 1.0-3.8). Compared with non-

smokers, smokers had significantly higher frequencies of Klebsiella pneumoniae (53.8% vs. 30.6%, p=0.006) and Pseudomonas aeruginosa, where these data are provided (50 years (43.8% vs 25.7%, p=0.018), while Streptococcus pneumoniae was isolated more often among younger patients (10.0% vs 4.3%, p=0.041). These findings are in parallel with the reports from China (23) and India (24) that older age was a significant risk factor for harboring Gram-negative organisms in patients due to multiple comorbidities and immune decline with aging.

## CONCLUSION

*Klebsiella pneumoniae* was the most common pathogen causing community-acquired pneumonia, with Gram-negative organisms accounting for the majority of isolates. Diabetes mellitus, COPD, and smoking were significant predictors of Gram-negative infection. These findings highlight the need for local microbiological surveillance and risk-based empirical antibiotic selection to improve the management of community-acquired pneumonia.

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