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DIAGNOSTIC VALUE OF SPUTUM CULTURE AND SENSITIVITY IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE PATIENTS AT HAYATABAD MEDICAL COMPLEX

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ABSTRACT

Background: Bacterial infection and airway colonization are clinically important in chronic obstructive pulmonary disease (COPD), particularly when patients experience worsening respiratory symptoms. Because the bacterial spectrum and antimicrobial resistance profile vary by geography and healthcare setting, local sputum-culture data are valuable for diagnostic and antimicrobial-stewardship decisions.

Objective: To assess the diagnostic value of sputum culture and sensitivity testing in COPD patients at Hayatabad Medical Complex (HMC), Peshawar, operationalized as culture yield, distribution of bacterial pathogens, and the available antimicrobial susceptibility pattern.

Methods: A hospital-based cross-sectional study was conducted in the Department of Pulmonology, HMC, from 25 January to 24 May 2025 after approval by the Research Review Board (No. 2364, dated 31 December 2024). A total of 107 hospitalized COPD patients aged 30-70 years were included. Patients with antibiotic use during the preceding two weeks, active pulmonary tuberculosis, lung carcinoma, immunocompromised status, or insufficient sputum samples were excluded. Sputum specimens were obtained by spontaneous expectoration or induction and processed in a designated reference laboratory. Data were analyzed in SPSS version 25.0. Culture yield was reported with a 95% confidence interval (CI), and associations with demographic and clinical characteristics were assessed using chi-square or Fisher exact tests as appropriate.

Results: Seventy-one of 107 sputum cultures were positive, giving a diagnostic yield of 66.4% (95% CI 57.0%-74.6%). Among positive cultures, Klebsiella pneumoniae was the most frequent isolate (22/71, 31.0%), followed by Pseudomonas aeruginosa (16/71, 22.5%), Streptococcus pneumoniae (10/71, 14.1%), Haemophilus influenzae (9/71, 12.7%), Staphylococcus aureus (6/71, 8.5%), Escherichia coli (4/71, 5.6%), and Moraxella catarrhalis (4/71, 5.6%). Reported resistance among Klebsiella pneumoniae included ceftriaxone and amoxicillin (7/22, 31.8% each), while ciprofloxacin resistance was recorded in 4/16 (25.0%) Pseudomonas aeruginosa isolates. No demographic or clinical subgroup showed a statistically significant association with culture positivity (all $p>0.05$).

Conclusion: Sputum culture identified a potentially pathogenic bacterium in approximately two-thirds of the studied COPD patients, with Gram-negative organisms predominating. Klebsiella pneumoniae and Pseudomonas aeruginosa were the leading isolates. The findings support the value of local sputum culture for organism identification and culture-guided management; however, incomplete antibiotic-specific susceptibility classification in the study dataset limits strong empirical-treatment recommendations.

Keywords	Chronic Obstructive Pulmonary Disease; Sputum Culture; Diagnostic Yield; Bacterial Pathogens; Antimicrobial Susceptibility; Antibiotic Resistance
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INTRODUCTION

Chronic obstructive pulmonary disease (COPD) is a heterogeneous, preventable and treatable respiratory disorder characterized by persistent airflow obstruction and chronic respiratory symptoms. It remains a major cause of morbidity, disability and death worldwide. Global modelling estimates continue to show a substantial disease burden, particularly among older adults and populations exposed to tobacco smoke, biomass fuels, occupational dusts and ambient air pollution.[1,2] In South Asia, COPD and chronic bronchitis are also common, although prevalence estimates vary substantially because of differences in study setting and diagnostic criteria.[3] Exacerbations and other episodes of clinical deterioration are important events in the course of COPD because they increase healthcare use and adversely affect lung function, quality of life and survival. Respiratory infections are among the most important triggers of exacerbation, and bacterial pathogens frequently identified in sputum include Haemophilus influenzae, Moraxella catarrhalis, Streptococcus pneumoniae and, particularly in more severe or hospitalized disease, Gram-negative organisms such as Pseudomonas aeruginosa and Klebsiella pneumoniae.[4,5] A prospective Asia-Pacific study has also demonstrated that airway pathogens can be detected during both stable and exacerbated COPD, emphasizing the need to interpret sputum microbiology in the clinical context.[6]

Sputum culture is inexpensive and widely available, but its diagnostic contribution varies because specimen quality, previous antimicrobial exposure, airway colonization and laboratory procedures can influence the yield. Recent studies have reported markedly different culture-positive rates and bacterial spectra across clinical settings. For example, hospital-based investigations from India, Ethiopia, Vietnam, Nepal and Pakistan have shown culture positivity ranging from approximately one-quarter to three-quarters of patients, with Gram-negative pathogens frequently prominent.[7-13] These geographic differences make local microbiological surveillance important for antimicrobial stewardship and for interpreting culture results in individual patients [14]. Published data from Khyber Pakhtunkhwa remain limited, despite the frequent clinical use of sputum culture in hospitalized COPD patients. Therefore, the present study assessed the diagnostic value of sputum culture and sensitivity testing at Hayatabad Medical Complex, Peshawar. Because no independent reference test for diagnostic accuracy was used, diagnostic value was operationalized as the proportion of sputum samples yielding a potentially pathogenic organism (diagnostic yield), the distribution of isolated bacteria, and the available antibiotic susceptibility and resistance pattern.

MATERIALS AND METHODS

A hospital-based cross-sectional study was conducted in the Department of Pulmonology, Hayatabad Medical Complex, Peshawar, from 25 January 2025 to 24 May 2025. The study was undertaken after approval from the institutional Research Review Board (approval No. 2364, dated 31 December 2024). Male and female patients aged 30-70 years with an established diagnosis of COPD were eligible. COPD was based on compatible clinical features and spirometric evidence of persistent airflow obstruction, defined as a post-bronchodilator FEV1/FVC ratio <0.70, or a previously documented spirometric diagnosis of COPD in the medical record. Patients were recruited from the inpatient pulmonology service during the study period. Patients were excluded if they had used systemic antibiotics during the preceding two weeks, had active pulmonary tuberculosis, concurrent lung carcinoma, an immunocompromised state such as HIV infection or ongoing immunosuppressive therapy, or an insufficient sputum specimen.

The primary objective was to assess the diagnostic value of sputum culture and sensitivity testing. For the purposes of this study, diagnostic value was operationalized primarily as diagnostic yield, defined as the number of sputum samples with growth of a potentially pathogenic organism divided by the total number of sputum samples collected, multiplied by 100. Secondary descriptive outcomes were the distribution of bacterial isolates and the antimicrobial susceptibility information recorded in the laboratory reports. The required sample size was 107 participants, calculated using the WHO sample-size approach for a single proportion with a 95% confidence level and 5% absolute precision, using an anticipated Haemophilus influenzae isolation proportion of 7.5% from previously available literature.

After written informed consent, demographic and clinical information was recorded on a structured pro forma. Variables included age, sex, residence, socioeconomic status, smoking history, height, weight, body mass index (BMI), duration of COPD, and comorbid diabetes mellitus, hypertension and coronary artery disease. Sputum specimens were obtained by spontaneous expectoration or sputum induction, labeled with a unique patient identifier and date, and sent to a designated reference laboratory. Samples judged insufficient by the laboratory were excluded according to the study eligibility criteria. Cultures were monitored for bacterial growth at 48 hours and again at five days, and identified organisms and the reported antimicrobial susceptibility results were transcribed to the study database. The source study dataset did not contain a complete antibiotic-testing denominator or a documented susceptibility category for every organism-antibiotic pair. Accordingly, antibiotic-specific results in this manuscript are presented transparently as the numbers recorded as sensitive, resistant, and not reported/other among all isolates of that organism. No assumption was made that an unreported isolate was either sensitive or resistant. This reporting approach prevents overestimation of susceptibility and avoids unsupported empirical antibiotic recommendations.

Data were analyzed using SPSS version 25.0. Quantitative variables were assessed for distribution using the Shapiro-Wilk test. Normally distributed variables are presented as mean ± standard deviation, while non-normally distributed variables are presented as median and interquartile range (IQR). Categorical variables are summarized as frequencies and percentages. Diagnostic yield was calculated as the proportion of positive sputum cultures among all 107 participants and is reported with a two-sided 95% Wilson confidence interval. Associations between culture positivity and baseline categorical characteristics were assessed using Fisher exact tests for 2×2 tables and the Fisher-Freeman-Halton exact approach or chi-square test for variables with more than two categories, as

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appropriate. A p-value ≤0.05 was considered statistically significant. The study was approved by the Research Review Board of Hayatabad Medical Complex. The study objectives, procedures, potential risks and benefits were explained to participants, and written informed consent was obtained before enrollment. Confidentiality was maintained by using unique study identifiers and secure electronic data handling.

RESULTS

A total of 107 COPD patients were included. The mean age was 58.9 ± 7.8 years. Males comprised 59.8% (64/107), rural residents 53.3% (57/107), and participants categorized as having low socioeconomic status 64.5% (69/107). A smoking history was present in 63.6% (68/107). Mean BMI was 24.7 ± 2.8 kg/m², while the median duration of COPD was 5.0 years (IQR 3.0-9.0). Hypertension was present in 45.8%, diabetes mellitus in 35.5%, and coronary artery disease in 20.6% (Table 1).

Table 1. Baseline demographic and clinical characteristics of COPD patients (N=107)

Characteristic	Category / summary	n (%) or summary value
Age (years)	Mean ± SD	58.9 ± 7.8
Age group	≤55 years	34 (31.8)
	56-65 years	44 (41.1)
	≥66 years	29 (27.1)
Gender	Male	64 (59.8)
	Female	43 (40.2)
Residence	Urban	50 (46.7)
	Rural	57 (53.3)
Socioeconomic status	Low	69 (64.5)
	Moderate	31 (29.0)
	High	7 (6.5)
Smoking history	Present	68 (63.6)
	Absent	39 (36.4)
BMI (kg/m²)	Mean ± SD	24.7 ± 2.8
	Normal (18.5-24.9)	57 (53.3)
	Overweight (≥25)	50 (46.7)
Duration of COPD (years)	Median (IQR)	5.0 (3.0-9.0)
	≤4 years	43 (40.2)
	5-9 years	39 (36.4)
	≥10 years	25 (23.4)
Diabetes mellitus	Yes	38 (35.5)
	No	69 (64.5)

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Characteristic	Category / summary	n (%) or summary value
Hypertension	Yes	49 (45.8)
	No	58 (54.2)
Coronary artery disease	Yes	22 (20.6)
	No	85 (79.4)

SD: standard deviation; IQR: interquartile range; BMI: body mass index; COPD: chronic obstructive pulmonary disease.

Sputum culture was positive in 71 of 107 patients, corresponding to a diagnostic yield of 66.4% (95% CI 57.0%-74.6%). Among the 71 positive cultures, Klebsiella pneumoniae was the most frequent isolate (31.0%), followed by Pseudomonas aeruginosa (22.5%), Streptococcus pneumoniae (14.1%), Haemophilus influenzae (12.7%), Staphylococcus aureus (8.5%), Escherichia coli (5.6%) and Moraxella catarrhalis (5.6%) (Table 2). The organism counts sum to 71, indicating one recorded predominant isolate per positive culture in the study dataset.

Table 2. Sputum culture yield and bacterial pathogens isolated

Outcome	n	%
Positive sputum culture	71	66.4 of all 107 samples
Negative sputum culture	36	33.6 of all 107 samples
Klebsiella pneumoniae	22	31.0 of 71 positive cultures
Pseudomonas aeruginosa	16	22.5
Streptococcus pneumoniae	10	14.1
Haemophilus influenzae	9	12.7
Staphylococcus aureus	6	8.5
Escherichia coli	4	5.6
Moraxella catarrhalis	4	5.6

Antibiotic susceptibility data were available in a non-uniform format. The largest recorded resistance proportions, calculated against the total number of isolates of each organism, were ceftriaxone and amoxicillin resistance among Klebsiella pneumoniae (7/22, 31.8% each), ciprofloxacin resistance among Pseudomonas aeruginosa (4/16, 25.0%), erythromycin resistance among Streptococcus pneumoniae (4/10, 40.0%), trimethoprim-sulfamethoxazole resistance among Haemophilus influenzae (4/9, 44.4%), and penicillin resistance among Staphylococcus aureus (3/6, 50.0%). Because a large proportion of organism-antibiotic pairs were not classified in the source dataset, the sensitive percentages shown in Table 3 should not be interpreted as complete organism-level susceptibility rates.

Table 3. Recorded antibiotic sensitivity and resistance pattern among selected isolates

Organism	Antibiotic	Sensitive n (%)	Resistant n (%)	Not reported / other n (%)
Klebsiella pneumoniae (n=22)	Levofloxacin	6 (27.3)	0 (0.0)	16 (72.7)
	Ciprofloxacin	5 (22.7)	3 (13.6)	14 (63.6)
	Amikacin	4 (18.2)	0 (0.0)	18 (81.8)
	Ceftazidime	2 (9.1)	3 (13.6)	17 (77.3)

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Organism	Antibiotic	Sensitive n (%)	Resistant n (%)	Not reported / other n (%)
	Meropenem	2 (9.1)	1 (4.5)	19 (86.4)
	Ceftriaxone	0 (0.0)	7 (31.8)	15 (68.2)
	Amoxicillin	0 (0.0)	7 (31.8)	15 (68.2)
	Cefuroxime	0 (0.0)	2 (9.1)	20 (90.9)
Pseudomonas aeruginosa (n=16)	Piperacillin-tazobactam	3 (18.8)	0 (0.0)	13 (81.2)
	Meropenem	3 (18.8)	1 (6.2)	12 (75.0)
	Colistin	3 (18.8)	0 (0.0)	13 (81.2)
	Ciprofloxacin	2 (12.5)	4 (25.0)	10 (62.5)
	Levofloxacin	1 (6.2)	2 (12.5)	13 (81.2)
	Ceftazidime	0 (0.0)	2 (12.5)	14 (87.5)
Streptococcus pneumoniae (n=10)	Amoxicillin	4 (40.0)	0 (0.0)	6 (60.0)
	Levofloxacin	3 (30.0)	0 (0.0)	7 (70.0)
	Penicillin	1 (10.0)	2 (20.0)	7 (70.0)
	Erythromycin	0 (0.0)	4 (40.0)	6 (60.0)
Haemophilus influenzae (n=9)	Amoxicillin-clavulanate	4 (44.4)	0 (0.0)	5 (55.6)
	Doxycycline	3 (33.3)	0 (0.0)	6 (66.7)
	Ampicillin	0 (0.0)	3 (33.3)	6 (66.7)
	Trimethoprim-sulfamethoxazole	0 (0.0)	4 (44.4)	5 (55.6)
Staphylococcus aureus (n=6)	Vancomycin	3 (50.0)	0 (0.0)	3 (50.0)
	Clindamycin	2 (33.3)	1 (16.7)	3 (50.0)
	Penicillin	0 (0.0)	3 (50.0)	3 (50.0)

Percentages use all isolates of the relevant organism as the denominator. “Not reported / other” indicates that the source dataset did not classify those isolates as sensitive or resistant for that antibiotic; this category may include untested, undocumented or other laboratory categories and should not be interpreted as intermediate susceptibility. Antibiotic-level data were not available for Escherichia coli or Moraxella catarrhalis.

Culture positivity was then examined across baseline demographic and clinical characteristics. No statistically significant association was identified for age, gender, residence, socioeconomic status, smoking history, BMI category, duration of COPD, diabetes mellitus, hypertension or coronary artery disease (all $p>0.05$). Although the highest observed yield was among participants in the high socioeconomic category (6/7, 85.7%), the very small denominator makes this estimate imprecise and it should not be interpreted as evidence of a true subgroup difference (Table 4).

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Table 4. Sputum culture yield stratified by baseline demographic and clinical characteristics (N=107)

Characteristic / category	Positive culture n/N (%)	Negative culture n/N (%)	p-value
Age: ≤55 years	22/34 (64.7)	12/34 (35.3)	0.966
Age: 56-65 years	30/44 (68.2)	14/44 (31.8)	
Age: ≥66 years	19/29 (65.5)	10/29 (34.5)	
Gender: Male	44/64 (68.8)	20/64 (31.2)	0.538
Gender: Female	27/43 (62.8)	16/43 (37.2)	
Residence: Urban	34/50 (68.0)	16/50 (32.0)	0.838
Residence: Rural	37/57 (64.9)	20/57 (35.1)	
Socioeconomic status: Low	44/69 (63.8)	25/69 (36.2)	0.595
Socioeconomic status: Moderate	21/31 (67.7)	10/31 (32.3)	
Socioeconomic status: High	6/7 (85.7)	1/7 (14.3)	
Smoking history: Present	48/68 (70.6)	20/68 (29.4)	0.288
Smoking history: Absent	23/39 (59.0)	16/39 (41.0)	
BMI: Normal (18.5-24.9)	37/57 (64.9)	20/57 (35.1)	0.838
BMI: Overweight (≥25)	34/50 (68.0)	16/50 (32.0)	
COPD duration: ≤4 years	29/43 (67.4)	14/43 (32.6)	0.966
COPD duration: 5-9 years	26/39 (66.7)	13/39 (33.3)	
COPD duration: ≥10 years	16/25 (64.0)	9/25 (36.0)	
Diabetes mellitus: Yes	26/38 (68.4)	12/38 (31.6)	0.832
Diabetes mellitus: No	45/69 (65.2)	24/69 (34.8)	
Hypertension: Yes	33/49 (67.3)	16/49 (32.7)	1.000
Hypertension: No	38/58 (65.5)	20/58 (34.5)	
Coronary artery disease: Yes	16/22 (72.7)	6/22 (27.3)	0.615
Coronary artery disease: No	55/85 (64.7)	30/85 (35.3)	

P-values are exact tests based on the tabulated counts (Fisher exact for 2×2 comparisons; Fisher-Freeman-Halton exact approach for multi-category comparisons). No comparison reached the prespecified significance level of p≤0.05.

DISCUSSION

The present study found a sputum culture yield of 66.4% among 107 hospitalized COPD patients at Hayatabad Medical Complex. This means that approximately two-thirds of the submitted specimens yielded a potentially pathogenic bacterium. The 95% confidence interval of 57.0%-74.6% also demonstrates that, while the point estimate is relatively high, considerable sampling uncertainty remains. The finding is broadly comparable with other recent hospital-based studies in which culture positivity varied

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substantially according to population, specimen criteria, prior antibiotic exposure and laboratory methods. Mussema et al. reported a culture-positive rate of 69.2% among patients with AECOPD in Ethiopia, while Danish et al. reported 74.5% in a Pakistani cohort.[8,12] A recent study from Khyber Teaching Hospital, Peshawar, reported a yield of 71.7% in AECOPD patients.[13] By contrast, a 2023 study of elderly Vietnamese inpatients reported a lower rate of 25.1%, illustrating the influence of setting and case selection on culture yield.[9] Klebsiella pneumoniae was the most frequent isolate in the present study, accounting for 31.0% of positive cultures, followed by Pseudomonas aeruginosa at 22.5%. The predominance of these Gram-negative organisms is consistent with several recent hospital-based studies. Mood et al. found Pseudomonas aeruginosa and Klebsiella pneumoniae among the most common isolates in hospitalized AECOPD patients, while Danish et al. reported Klebsiella pneumoniae (34.1%) and Pseudomonas aeruginosa (24.4%) as the two leading pathogens.[7,12] Studies from Vietnam have likewise documented prominent Gram-negative organisms, including Klebsiella and Pseudomonas, among patients with exacerbated COPD.[9,10] These similarities support the clinical relevance of Gram-negative respiratory pathogens in hospitalized COPD populations, although the exact spectrum varies geographically.

Streptococcus pneumoniae, Haemophilus influenzae and Moraxella catarrhalis were also identified. These organisms are well-recognized airway pathogens in COPD, and prospective Asia-Pacific data have demonstrated an association between the presence or acquisition of H. influenzae and M. catarrhalis and exacerbation events.[6] The pathogen distribution in this study should nevertheless be interpreted in light of the study design: participants were hospitalized patients with COPD, but the original dataset did not document a standardized acute-exacerbation definition for every participant. Therefore, direct comparison with studies restricted to formally defined AECOPD should be made cautiously. The antibiotic findings indicate clinically relevant recorded resistance, particularly ceftriaxone and amoxicillin resistance among Klebsiella pneumoniae and ciprofloxacin resistance among Pseudomonas aeruginosa. Recent studies from the region and other low- and middle-income settings similarly report substantial resistance among Gram-negative respiratory isolates.[8-13] However, the present dataset does not provide complete antibiotic-level test denominators or a full susceptible-intermediate-resistant classification for each isolate. For this reason, the revised analysis deliberately avoids concluding that specific antibiotics had high overall susceptibility simply because a small number of isolates were recorded as sensitive. Instead, the results demonstrate the need for culture-guided interpretation and better standardized local antibiogram reporting.

None of the examined demographic or clinical variables was significantly associated with culture positivity. Smoking history showed a numerically higher yield among smokers (70.6%) than non-smokers (59.0%), and coronary artery disease was associated with a numerically higher yield, but neither difference was statistically significant. Likewise, the high observed yield among the small high-socioeconomic-status subgroup was based on only seven participants. These findings indicate that the current sample does not support using the recorded demographic variables alone to predict which patients will have a positive culture. The study has practical local relevance. Sputum culture remains a relatively accessible diagnostic tool and can help identify potentially pathogenic organisms in selected COPD patients, particularly those receiving hospital care. Current COPD management frameworks emphasize individualized assessment and appropriate antibiotic use rather than indiscriminate antimicrobial treatment.[1,4,5] The local predominance of Klebsiella pneumoniae and Pseudomonas aeruginosa in this study supports maintaining awareness of Gram-negative pathogens while using culture and susceptibility information whenever clinically appropriate. At the same time, culture results must be interpreted alongside symptoms, sputum characteristics, disease severity and the possibility of chronic airway colonization.

This study has several limitations. First, it was conducted at a single tertiary-care hospital and included only 107 patients, which limits generalizability to other institutions, community settings and stable outpatient COPD populations. Second, the source dataset did not document a standardized acute-exacerbation definition for every participant; therefore, the cohort should not be described as an AECOPD-only population. Third, sputum culture can identify airway colonization as well as infection, and the dataset did not contain quantitative culture thresholds or a cytologic sputum-quality measure that would allow these possibilities to be differentiated more precisely. Fourth, the detailed laboratory platform, culture media, antimicrobial susceptibility method, breakpoint standard and complete susceptible-intermediate-resistant results were not captured in the study dataset used for this manuscript. Consequently, organism-antibiotic pairs that were not explicitly recorded as sensitive or resistant were retained as “not reported/other,” and empirical antibiotic rankings were intentionally avoided. Fifth, molecular pathogen detection and resistance-gene characterization were not performed, and viral pathogens were not assessed. Finally, the study did not compare clinical outcomes between culture-guided and empirical treatment strategies. Future multicenter prospective studies should use standardized sputum-quality criteria, explicit AECOPD definitions, complete CLSI- or EUCAST-based susceptibility reporting, and longitudinal clinical outcomes.

CONCLUSION

Sputum culture demonstrated a diagnostic yield of 66.4% (95% CI 57.0%-74.6%) among hospitalized COPD patients at Hayatabad Medical Complex. Klebsiella pneumoniae was the most common isolate, followed by Pseudomonas aeruginosa, Streptococcus pneumoniae and Haemophilus influenzae. Recorded resistance was notable for ceftriaxone and amoxicillin among Klebsiella pneumoniae and for ciprofloxacin among Pseudomonas aeruginosa. No demographic or clinical subgroup was significantly associated with culture positivity. These findings support the use of sputum culture as a locally informative tool for pathogen identification and culture-guided antimicrobial decision-making, while highlighting the need for complete and standardized susceptibility reporting before drawing strong conclusions about empirical antibiotic choice.

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