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Original Article

Frequency of Positive Sputum Cultures and the Microorganisms Frequently Complicating Exacerbations of COPD

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ABSTRACT

Background: Chronic obstructive pulmonary disease (COPD) remains a significant cause of global morbidity and mortality, with acute exacerbations frequently precipitated by bacterial infections. Regional variations in bacterial etiology necessitate localized studies to guide targeted therapy and prevent antimicrobial resistance. Objective: To determine the frequency of positive sputum cultures and identify the microorganisms frequently complicating exacerbations of COPD in a regional Pakistani population. Methods: This cross-sectional observational study was conducted at the Fatima Jinnah Institute of Chest Diseases, Quetta, from May to November 2024. Sixty patients presenting with acute exacerbations of COPD were consecutively recruited. Demographic, clinical, and socioeconomic data were collected, and quality-assured sputum samples were analyzed using standard microbiological techniques. Associations between sputum culture results and patient characteristics were assessed using Chi-square or Fisher's exact tests, with significance set at $p<0.05$. Results: Positive sputum cultures were observed in 70% of patients. The most frequently isolated pathogens were Pseudomonas and Moraxella, each accounting for 26.7% of positive cultures, followed by Haemophilus influenzae (25.0%), Streptococcus pneumoniae (5.0%), Staphylococcus aureus (3.3%), Haemophilus parainfluenzae (3.3%), and Acinetobacter (1.7%). Lower income was significantly associated with higher culture positivity ($p=0.027$). Conclusion: Bacterial infections play a substantial role in COPD exacerbations in this region, with Pseudomonas and Moraxella predominating. Periodic local surveillance of bacterial profiles and resistance patterns is essential to optimize antibiotic stewardship and improve patient outcomes.

Keywords: Chronic obstructive pulmonary disease, acute exacerbation, sputum culture, bacterial pathogens, antibiotic resistance.

INTRODUCTION

Chronic obstructive pulmonary disease (COPD) constitutes a major global health burden, characterized by persistent respiratory symptoms and airflow limitation resulting from airway and alveolar abnormalities, predominantly caused by chronic exposure to noxious particles or gases such as tobacco smoke or biomass combustion (1). Worldwide estimates by the World Health Organization predict that COPD will rank as the third leading cause of death by 2030, underscoring its significance as a preventable yet often progressive disease (2). The prevalence of COPD varies significantly across regions, influenced by environmental exposures, socioeconomic factors, and healthcare infrastructure, with over 65 million individuals globally estimated to suffer from moderate to severe forms of the disease (3). In Pakistan, the reported prevalence of COPD is 13.8%, further accentuating the importance of local epidemiological data to inform management strategies (4). Despite advances in pharmacological interventions, acute exacerbations remain critical events in the disease trajectory, contributing substantially to increased morbidity, mortality, and healthcare resource utilization (5).

Exacerbations of COPD are characterized by a sudden worsening of baseline respiratory symptoms such as dyspnea, cough, and sputum production, requiring changes in therapeutic management (6). These events are frequently precipitated by infections, with bacterial pathogens implicated in approximately 50-60% exacerbations, while viral infections, environmental pollutants, and unidentified triggers account for the remainder (7,8). During exacerbations, bacterial colonization in the lower airways may transition to overt infection, increasing the pathogenic burden and inflammatory response, thus necessitating antimicrobial therapy in selected patients (9). Sputum culture and microbiological profiling remain crucial diagnostic tools, as they not only facilitate accurate pathogen identification but also inform antibiotic stewardship, reducing the risk of inappropriate empiric treatment and emerging resistance (10). Gram-negative organisms such as Pseudomonas aeruginosa, Moraxella catarrhalis, and Haemophilus influenzae have been frequently implicated in acute

exacerbations, although their prevalence varies significantly across studies and geographical regions (11,12). For instance, a study in Hong Kong reported Haemophilus influenzae as the most prevalent organism in acute exacerbations, while research from India highlighted gram-negative pathogens as predominant isolates, with Pseudomonas aeruginosa representing a notable proportion (13,14). Moreover, severe exacerbations, particularly those necessitating hospitalization or intensive care, appear more frequently associated with multidrug-resistant pathogens, emphasizing the critical need for localized microbiological surveillance (15,16).

Despite extensive international research on the bacteriology of COPD exacerbations, there exists a paucity of region-specific data for Balochistan, Pakistan. Given differences in environmental exposures, healthcare-seeking behaviors, and antibiotic usage patterns, it is essential to delineate the local bacteriological landscape to optimize empiric therapy and reduce the burden of antimicrobial resistance. Additionally, socioeconomic determinants such as income, literacy levels, and occupational exposure may influence the risk of bacterial infections in this population, yet remain insufficiently studied. Recognizing these gaps is crucial, as appropriate antibiotic selection based on local pathogen prevalence and sensitivity profiles can substantially improve clinical outcomes and reduce hospital admissions (17,18).

MATERIALS AND METHODS

This cross-sectional observational study was conducted at the Pulmonology Department of the Fatima Jinnah Institute of Chest Diseases (FJICD) in Quetta, Pakistan, between 3 May 2024 and 4 November 2024. The study aimed to assess the frequency of positive sputum cultures in patients experiencing acute exacerbations of chronic obstructive pulmonary disease (AECOPD) and to identify the predominant microorganisms involved in these episodes. Ethical approval for the study was obtained from the Institutional Review Board of FJICD, and written informed consent was secured from all participants prior to their enrolment, ensuring voluntary participation and confidentiality in accordance with the Declaration of Helsinki (19).

Eligible participants included adult patients of either gender aged ≥18 years who presented to the Emergency Department, outpatient department, or inpatient services of the FJICD with a clinical diagnosis of AECOPD, characterized by a recent increase in baseline symptoms such as dyspnea, cough, and sputum production requiring a change in treatment. Patients were excluded if they had active pulmonary tuberculosis, confirmed bronchiectasis, malignancy, recent antibiotic use within the previous 14 days, or were unable to produce an adequate sputum sample for analysis. Recruitment followed a consecutive sampling strategy whereby all eligible patients during the study period were approached for inclusion until the predetermined sample size was achieved.

Upon presentation, patients were interviewed and examined by a pulmonologist who documented demographic variables including age, sex, marital status, education level, occupation, monthly household income, and clinical history details such as duration of COPD diagnosis, duration of treatment, smoking history measured in pack-years, biomass exposure history, and the presence of comorbidities like diabetes mellitus, hypertension, ischemic heart disease, facial paralysis, hepatitis C, or tuberculosis. Biomass exposure was defined as routine exposure to smoke from sources such as firewood, dung, or crop residue used for cooking or heating. Each participant was instructed to provide an early morning sputum sample collected in a sterile, wide-mouthed, leak-proof container, ensuring minimal contamination with oral flora, and samples were immediately transported to the institutional microbiology laboratory under cold chain conditions for culture and sensitivity analysis (20).

Sputum specimens were assessed microscopically for adequacy using Gram stain to ensure a high-quality sample, defined as the presence of >25 polymorphonuclear leukocytes and <10 epithelial cells per low power field, before proceeding to culture. Samples were cultured on blood agar, chocolate agar, and MacConkey agar plates and incubated at 37°C for 24-48 hours under aerobic conditions. Microbial identification was performed using standard biochemical tests, colony morphology, and Gram stain characteristics, and results were further confirmed using an automated identification system when necessary. Bacterial isolates were classified according to species, and antibiotic sensitivity patterns were determined via the Kirby-Bauer disc diffusion method, interpreted per Clinical and Laboratory Standards Institute (CLSI) guidelines (21).

The primary outcome variable was the presence of a positive sputum culture, defined as significant growth of a pathogenic organism, while secondary outcomes included the distribution of specific bacterial species among positive cultures. To address potential confounding, stratification was performed by age groups, gender, marital status, educational attainment, occupation, income, duration of illness, duration of treatment, smoking status, and biomass exposure. The sample size of 60 patients was determined based on the expected proportion of positive sputum cultures from previous regional studies, allowing for adequate precision and statistical power for subgroup analysis (22).

Data were coded and entered into SPSS version 24.0 (IBM Corp., Armonk, NY, USA) for statistical analysis. Continuous variables such as age, duration of diagnosis, duration of treatment, pack-years of smoking, and biomass exposure were summarized using mean ± standard deviation (SD) or median with interquartile range (IQR) based on distribution normality. Categorical variables, including gender, education, occupation, marital status, income, smoking status, biomass exposure, comorbidities, and sputum culture results, were presented as frequencies and percentages. Associations between categorical variables and sputum culture positivity were examined using the Chi-square test or Fisher's exact test as appropriate, considering a p-value <0.05 statistically significant. Post-stratification analyses were performed to explore differences in the prevalence of specific bacterial pathogens across demographic and clinical subgroups. All analyses were conducted under double-entry verification to ensure data accuracy and reproducibility (23).

RESULTS

A total of 60 patients presenting with acute exacerbation of chronic obstructive pulmonary disease were enrolled in the study, with a median age of 62.5 years (IQR 18). The majority of participants were male, comprising 85% (n=51), while females represented 15% (n=9). Regarding marital status, 97% of patients were married. Educational attainment varied among participants, with 46.7% having no formal

education, 25% educated up to class 1-8, 15% between class 9-12, and 13.3% possessing education above class 12. Employment status showed that 33.3% were employed, while 66.7% were unemployed, with reasons for unemployment including disability due to illness (21.7%), unavailability of jobs (3.3%), housework (15%), and retirement (26.7%). A monthly household income of ≤20,000 PKR was reported by 70% of participants. Comorbid conditions were present in 33.3% of patients, with hypertension being the most prevalent at 21.7%, followed by diabetes mellitus (10%), ischemic heart disease (10%), facial paralysis (1.7%), hepatitis C (1.7%), and tuberculosis (1.7%). Concerning smoking status, 68.3% were ex-smokers, 20% were current smokers, and 11.7% had never smoked. Biomass exposure was reported by 25% of patients, while 6.7% disclosed additional substance use beyond smoking. Table 1 summarizes the baseline characteristics and clinical features of the study population.

Table 1. Baseline Characteristics of Patients with Acute Exacerbation of COPD (N=60)

Variable	Frequency (%) / Median (IQR)
Age (years)	62.5 (18)
Gender	
• Male	51 (85.0)
• Female	9 (15.0)
Marital Status	
• Married	58 (96.7)
• Unmarried	2 (3.3)
Education Level	
• No education	28 (46.7)
• Class 1-8	15 (25.0)
• Class 9-12	9 (15.0)
• > Class 12	8 (13.3)
Employment Status	
• Employed	20 (33.3)
• Unemployed	40 (66.7)
Monthly Income ≤20,000 PKR	42 (70.0)
Comorbidities Present	20 (33.3)
• Hypertension	13 (21.7)
• Diabetes Mellitus	6 (10.0)
• Ischemic Heart Disease	6 (10.0)
Smoking Status	
• Current smoker	12 (20.0)
• Ex-smoker	41 (68.3)
• Never smoked	7 (11.7)
Biomass Exposure	15 (25.0)
Additional Substance Use	4 (6.7)

Table 2. Distribution of Microorganisms in Positive Sputum Cultures (N=42)

Microorganism	Frequency (%)
Pseudomonas	16 (26.7)
Moraxella	16 (26.7)
Haemophilus influenzae	15 (25.0)
Streptococcus pneumoniae	3 (5.0)
Staphylococcus aureus	2 (3.3)
Haemophilus parainfluenzae	2 (3.3)
Acinetobacter	1 (1.7)

Among the 60 patients studied, 42 (70%) demonstrated positive sputum cultures. The organisms most frequently isolated were Pseudomonas and Moraxella, each accounting for 26.7% of positive cultures, followed by Haemophilus influenzae in 25%, Streptococcus pneumoniae in 5.0%, Staphylococcus aureus in 3.3%, Haemophilus parainfluenzae in 3.3%, and Acinetobacter in 1.7% of cases. The distribution of microorganisms among culture-positive patients is detailed in Table 2.

Stratified analysis revealed that the rate of positive sputum cultures was not significantly associated with age groups (p=0.142), gender (p=0.813), marital status (p=0.346), education level (p=0.538), or employment status (p=0.999). However, there was a statistically significant association between lower household income (≤20,000 PKR) and higher sputum culture positivity (p=0.027). Additionally, patients with longer duration of diagnosis (>5 years) exhibited significantly lower rates of positive sputum cultures compared to those with shorter disease duration (p=0.017), and sputum positivity was significantly less common in patients with treatment duration exceeding five years (p=0.010). No statistically significant associations were observed between sputum culture positivity and smoking status (p=0.192), other substance use (p=0.952), or biomass exposure (p=0.329). These findings are presented in Table 3.

Further stratification of specific bacterial isolates showed no statistically significant differences across age groups for Pseudomonas (p=0.149), Haemophilus influenzae (p=0.55), Moraxella (p=0.785), Streptococcus pneumoniae (p=0.635), Staphylococcus aureus

(p=0.923), Haemophilus parainfluenzae (p=0.923), or Acinetobacter (p=0.281). Table 4 provides the detailed distribution of bacterial isolates by age group.

Table 3. Frequency of Positive Sputum Cultures by Demographic and Clinical Factors (N=60)

Factor	Positive Culture n (%)	Negative Culture n (%)	p-value
Age ≤ 60 years	17 (40.5)	11 (61.1)	0.142
Age > 60 years	25 (59.5)	7 (38.9)	
Male	36 (85.7)	15 (83.3)	0.813
Female	6 (14.3)	3 (16.7)	
Married	40 (95.2)	18 (100.0)	0.346
Unmarried	2 (4.8)	0 (0.0)	
No Education	22 (52.4)	6 (33.3)	0.538
Employed	14 (33.3)	6 (33.3)	0.999
Monthly Income ≤ 20,000 PKR	33 (78.6)	9 (50.0)	0.027*
Duration of diagnosis > 5 yrs	4 (9.5)	7 (38.9)	0.017*
Duration of treatment > 5 yrs	2 (25.0)	6 (75.0)	0.010*
Current Smoker	6 (14.3)	6 (33.3)	0.192
Biomass Exposure	9 (21.4)	6 (33.3)	0.329

*Statistically significant ($p < 0.05$)

Table 4. Distribution of Specific Microorganisms by Age Groups among Positive Cultures (N=42)

Microorganism	Age ≤ 60 yrs n (%)	Age > 60 yrs n (%)	p-value
Pseudomonas	5 (17.9)	11 (34.4)	0.149
Haemophilus influenzae	8 (28.6)	7 (21.9)	0.550
Moraxella	7 (25.0)	9 (28.1)	0.785
Streptococcus pneumoniae	1 (3.6)	2 (6.3)	0.635
Staphylococcus aureus	1 (3.6)	1 (3.1)	0.923
Haemophilus parainfluenzae	1 (3.6)	1 (3.1)	0.923
Acinetobacter	1 (3.6)	0 (0.0)	0.281

DISCUSSION

This study offers valuable insights into the bacteriological profile of acute exacerbations of chronic obstructive pulmonary disease in the population of Quetta, Pakistan, revealing a high frequency of positive sputum cultures in 70% of patients. The predominance of Pseudomonas and Moraxella, each contributing to 26.7% of positive cultures, underscores the shifting landscape of bacterial pathogens implicated in exacerbations and suggests a pattern differing from earlier reports where Haemophilus influenzae was frequently the leading isolate (24). The prominence of Pseudomonas in our findings aligns with studies conducted in India and Korea, where Pseudomonas aeruginosa emerged as a significant pathogen, particularly in patients with advanced disease severity or prior hospitalizations, indicating potential colonization evolving into infection under exacerbation triggers (25,26). However, while our observed prevalence of Pseudomonas at 26.7% is comparable to the 23.9–38.2% range reported in some Asian cohorts, it is notably higher than the 6.3% reported in a Hong Kong study, emphasizing regional variability likely influenced by differences in environmental exposures, healthcare practices, and antimicrobial usage patterns (27,28).

Moraxella's substantial role as a pathogen, equalling that of Pseudomonas in this cohort, mirrors the observations of some European studies but contrasts with data from certain Asian centers where Moraxella catarrhalis accounted for a lower proportion of exacerbations (29). This discrepancy may reflect local epidemiological nuances, including climate, crowding, and smoking behaviors, which modulate airway microbiota composition. Haemophilus influenzae accounted for 25% of positive cultures in our study, consistent with its recognized pathogenic role globally, although its prevalence fell short of the dominant proportions exceeding 30% reported in prior regional analyses (30). Streptococcus pneumoniae, Staphylococcus aureus, Haemophilus parainfluenzae, and Acinetobacter were less frequent isolates, collectively comprising less than 15% of positive cultures. The relatively low isolation rate of Streptococcus pneumoniae, at 5.0%, echoes findings from Hong Kong and European studies where pneumococcal prevalence has declined, possibly reflecting broader vaccine coverage and changes in microbial ecology due to widespread antibiotic use (27,31).

The significant association between low household income and increased sputum culture positivity in this study introduces a socioeconomic dimension rarely explored in bacteriological profiles of COPD exacerbations. Lower-income patients may experience delayed access to healthcare, suboptimal baseline disease management, and greater exposure to environmental pollutants, collectively predisposing them to bacterial infections with pathogens such as Pseudomonas and Acinetobacter, which were notably more prevalent in this subgroup (32). This finding highlights an important health disparity, suggesting that socioeconomic determinants should be integrated into risk stratification models to guide empiric antibiotic choices and public health interventions. Additionally, the association between shorter duration of COPD diagnosis and treatment with higher rates of sputum positivity might indicate that patients in earlier disease stages, potentially with less optimized therapy or unrecognized comorbidities, are more susceptible to bacterial exacerbations, warranting closer surveillance during early disease management (33). Although this study provides robust microbiological data specific to the Balochistan region, several limitations merit consideration. The sample size, while adequate for initial exploration, may limit the

generalizability of findings to the broader Pakistani population, particularly in diverse urban and rural contexts. Furthermore, the cross-sectional design precludes assessment of causality or long-term outcomes associated with specific pathogens. The absence of detailed antibiotic susceptibility data within this analysis limits the immediate translation of findings into therapeutic recommendations, though this remains a critical avenue for future research. Additionally, factors such as prior antibiotic use, vaccination status, and specific comorbidity profiles were not analyzed in depth, which could have nuanced impacts on pathogen prevalence and resistance patterns.

Nonetheless, the strengths of this study lie in its prospective data collection, rigorous sputum sample quality assessment, and comprehensive demographic profiling, which together enhance the reliability of pathogen identification and the observed associations with socioeconomic factors. These findings underscore the necessity of incorporating localized bacteriological surveillance into clinical guidelines for managing acute COPD exacerbations. Such efforts are particularly relevant in settings with constrained resources, where empiric antibiotic selection must balance efficacy with stewardship to curb rising antimicrobial resistance. Future research should expand upon these results by integrating antimicrobial sensitivity patterns, assessing the clinical outcomes associated with specific pathogens, and exploring the role of biomarkers, such as inflammatory mediators or oxygen saturation levels, as adjuncts in identifying bacterial exacerbations (34,35). This multidimensional approach would facilitate precision medicine strategies tailored to regional epidemiology, ultimately improving outcomes and resource utilization in COPD care.

CONCLUSION

This study revealed that 70% of patients presenting with acute exacerbations of chronic obstructive pulmonary disease had positive sputum cultures, with Pseudomonas and Moraxella emerging as the most frequently isolated pathogens, followed by Haemophilus influenzae, Streptococcus pneumoniae, Staphylococcus aureus, Haemophilus parainfluenzae, and Acinetobacter, underscoring a significant bacterial contribution to exacerbation episodes in this regional population and highlighting the need for periodic local surveillance of microbial profiles and resistance patterns to inform targeted antibiotic therapy, reduce antimicrobial resistance, and optimize clinical outcomes, while future research should further elucidate pathogen-specific impacts on disease progression and therapeutic responses to enhance evidence-based management strategies for COPD.

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