

Original Research Article

Microbial patterns in acute exacerbation of chronic obstructive pulmonary disease at tertiary care

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ABSTRACT

Background: In patients experiencing acute exacerbation of chronic obstructive pulmonary disease, infections represent a prevalent cause of mortality.

Methods: This study comprised a prospective cohort analysis involving 50 AECOPD patients at a tertiary care hospital located in Cumilla. The sputum culture of these patients was assessed to detect the presence of Gram-positive and Gram-negative microorganisms. Additionally, the sensitivity and resistance patterns of these microorganisms to commonly prescribed antibiotics were investigated.

Results: From January 2023 July 2023, sputum cultures of 42% of patients yielded positive results for pathogenic microorganisms. Predominantly, gram-negative organisms such as *Klebsiella*, *Citrobacter*, *Pseudomonas*, and *Acinetobacter* were isolated. The most prevalent age group among the fifty patients was 61-80 years, constituting 70% of the sample. Subsequently, the age groups of 41-60 years and 81-100 years represented 18% and 12% of the cohort, respectively. Among clinically diagnosed COPD patients experiencing acute exacerbations, 90% were male, with the majority being smokers or exposed to passive smoking. Notably, 26% of patients had a family history of COPD. Furthermore, 97% of patients had a history of respiratory infections, with 20% experiencing upper respiratory tract infections and 80% suffering from lower respiratory tract infections, including acute bronchiolitis, pneumonia, and tracheitis.

Conclusions: *Klebsiella* exhibited relatively high susceptibility to antibiotics such as amoxicillin, azithromycin, ciprofloxacin, and cephalosporins. Conversely, *Citrobacter* and *Pseudomonas* displayed diverse susceptibility profiles, showing varying responses to different antibiotics. Additionally, *Acinetobacter* demonstrated relatively lower susceptibility to several antibiotics tested, suggesting potential challenges in its management.

Keywords: Chronic obstructive pulmonary disease, Microbial pattern, Acute exacerbation

INTRODUCTION

Obstructive pulmonary disease, comprising chronic obstructive pulmonary disease (COPD) and asthma, poses a significant global health challenge marked by

progressive airflow restriction, respiratory symptoms, and diminished quality of life.¹ Its pathogenesis is complex, involving genetic predisposition and environmental factors, with emerging evidence implicating the lung microbiome in disease onset and progression.² Recent

advancements in culture-independent techniques have unveiled diverse bacterial and fungal populations even in healthy individuals, with disruptions in these microbial profiles, known as dysbiosis, linked to various respiratory ailments, including obstructive pulmonary disease.³⁻⁵

Numerous studies have investigated how microbial profiles influence obstructive pulmonary disease, offering valuable insights into their potential roles in disease development. COPD's natural course is characterized by recurrent exacerbations marked by increased cough, purulent sputum production, and breathlessness, significantly impacting patients' lives. These exacerbations lead to higher hospitalization and mortality rates and reduced quality of life, with a majority being attributed to infectious causes.⁶ Pathogens causing acute exacerbations of COPD primarily infect the lower respiratory tract and include respiratory viruses, atypical bacteria, and aerobic Gram-positive and Gram-negative bacteria.

The findings of this study may aid in identifying microbial markers indicative of disease severity, exacerbation risk, and treatment response. Additionally, this research contributes to our broader understanding of the lung microbiome's role in obstructive pulmonary disease and its potential as a target for novel therapeutic strategies. This study seeks to illuminate microbial profiles in obstructive pulmonary disease patients, with a focus on a tertiary care hospital setting. By elucidating the connections between microbial composition and clinical parameters, we aim to advance our understanding of disease pathogenesis and potentially open avenues for personalized approaches to managing obstructive pulmonary disease.

METHODS

This study utilized an observational approach to examine the microbial compositions present in patients diagnosed with obstructive pulmonary disease at Cumilla Medical College, Cumilla, Bangladesh, within January to July 2023. Specifically, the study focused on 50 sputum samples obtained from individuals experiencing acute exacerbations of COPD, including cases of both COPD and asthma, who were consecutively recruited from a tertiary care hospital. Inclusion criteria comprised patients diagnosed with obstructive pulmonary disease, while individuals suffering from bronchial asthma, bronchiectasis, bronchial carcinoma, pneumonia, those undergoing recent antibiotic therapy, and known cases of pulmonary tuberculosis were excluded from participation. Exclusion criteria also extended to patients with histories of other significant respiratory ailments unrelated to obstructive pulmonary disease, significant comorbidities potentially affecting study outcomes, and patient's incapable of providing informed consent or participating in study procedures. All participants provided informed consent. Demographic information encompassing age, sex, and smoking history was collected from each participant, along with clinical data such as pulmonary

function test results, symptom assessments, and medication usage. Sputum samples were gathered from each participant following standardized protocols. Data was analyzed using SPSS V.25.

RESULTS

Sputum samples from fifty patients clinically diagnosed with acute exacerbations of chronic obstructive pulmonary disease (AECOPD) were examined using standard techniques. The age range of the patients in the study varied from forty to one hundred years.

Table 1: Baseline demographic characteristics.

Variables	N	%
Age distribution (years)		
41-60	9	18
61-80	35	70
81-100	6	12
Gender		
Male	45	90
Female	5	10
Family history of COPD		
Yes	13	26
No	37	74
Respiratory infections history		
UTRI	10	20
LTRI	40	80
Comorbidities		
Diabetes mellitus	18	36
Hypertension	6	12
Asthma	5	10

Among the fifty patients, the most prevalent age group was 61-80 years (70%). Following this, the next common age groups were 41-60 years (18%) and 81-100 years (12%).

Table 2: Micro-organisms isolated from sputum culture.

Type of organism	Staining	Organism	%
Pathogenic (n=21) 42%	Gram negative (n=20)	<i>Klebsiella</i>	10
		<i>Citrobacter</i>	1
		<i>Pseudomonas</i>	6
		<i>Acinobacter</i>	1
	Normal flora		2
Non pathogenic (n=29) 58%	Gram positive (n=1)	<i>Staphylococcus aureus</i>	1
	-	-	29

Of the clinically diagnosed COPD patients experiencing acute exacerbations, 45 (90%) were male, while 5 (10%) were female. Additionally, 26% of patients had a family history of COPD, while the remaining 74% did not. Furthermore, 97% of the patients had previously

experienced respiratory infections, with 20% suffering from upper respiratory tract infections (URTI) and 80%

from lower respiratory tract infections (LRTI), including acute bronchiolitis, pneumonia, and tracheitis.

Table 3: Drug sensitivity pattern of various pathogens isolated from the sputum.

Antibiotics	<i>Klebsiella</i>	<i>Citrobacter</i>	<i>Pseudomonas</i>	<i>Acinobacter</i>	Normal flora	<i>Staphylococcus</i>	Total
	N (%)	N (%)	N (%)	N (%)	N (%)	N (%)	N (%)
Amoxiclay	9 (53)	1 (6)	5 (29)	0	1 (6)	1 (6)	17 (81)
Amikacin	6 (75)	0	2 (25)	0	0	0	8 (38)
Erythromycin	5 (62.5)	1 (12.5)	1 (12.5)	0	0	1 (12.5)	8 (38)
Ampicilin	0	0	1 (100)	0	0	0	1 (5)
Amoxicilin	2 (100)	0	0	0	0	0	2 (9.5)
Azithromycin	5 (72)	0	1 (14)	0	1 (14)	0	7 (33)
Chloramphenicol	8 (53)	1 (7)	4 (27)	1 (7)	1 (7)	0	15 (71)
Gentamycin	5 (50)	1 (10)	2 (20)	1(10)	1 (10)	0	10 (48)
Doxycycline	2 (50)	1 (25)	1 (25)	0	0	0	4 (19)
Levofloxacin	7 (57.5))	1 (8.5)	1 (8.5)	1(8.5)	1 (8.5)	1 (8.5)	12 (57)
Ciprofloxacin	9 (53)	1 (6)	4 (23)	1 (6)	1 (6)	1 (6)	17 (81)
Cephadrine	5 (55)	0	3 (33)	1 (11)	0	0	9 (43)
Cefuroxime	10 (55)	1 (5)	5 (27)	1 (5)	1 (5)	0	18 (86)
Cefixime	10 (55)	1 (5)	5 (27)	1 (5)	1 (5)	0	18 (86)
Ceftriaxone	9 (56)	1(6)	4(25)	1(6)	0	1(6)	16 (76)
Ceftazidime	1 (50)	0	1 (50)	0	0	0	2 (9.5)
Imipenam	1 (50)	0	0	1 (50)	0	0	2 (9.5)
Meropenam	1 (100)	0	0	0	0	0	1 (5)
Netilmycin	0	1 (100)	0	1	0	0	1 (5)
Lomifloxacin	4 (67)	0	2 (33)	0	0	0	6 (29)
Colistin	2 (50)	0	1 (25)	0	1 (25)	0	4 (19)

All patients had received antibiotic treatment before due to respiratory infections. Diabetes mellitus was present in 18 (36%) of the 50 patients, while only 6 (12%) had a history of hypertension, and 5 (10%) had a history of asthma. The majority of patients presented with mucopurulent sputum and reported exacerbation of cough with expectoration when exposed to cold climates.

DISCUSSION

The data tables of our study outline the distribution of various organisms isolated from sputum samples, their Gram staining characteristics, and their respective drug sensitivity patterns. These findings offer crucial insights into the prevalence of pathogens and their susceptibility to different antibiotics, which are imperative for guiding effective treatment strategies in respiratory infections. Firstly, the Gram staining results reveal a predominance of Gram-negative organisms among the pathogenic isolates, with *Klebsiella*, *Citrobacter*, *Pseudomonas*, and *Acinobacter* being the most prevalent. This aligns with the common etiology of respiratory infections, where Gram-negative bacteria frequently play a significant role, especially in hospitalized or immunocompromised individuals. Notably, *Staphylococcus aureus* was the only Gram-positive organism identified, albeit in a small percentage among the pathogenic isolates. Regarding drug sensitivity patterns, the data highlight variations in

antibiotic susceptibility among different pathogens. For instance, *Klebsiella* exhibited relatively high susceptibility to antibiotics like amoxicillin, azithromycin, ciprofloxacin, and cephalosporins. Conversely, *Citrobacter* and *Pseudomonas* showed diverse susceptibility profiles, with varying responses to different antibiotics. Additionally, *Acinobacter* displayed relatively lower susceptibility to several antibiotics tested, indicating potential challenges in its management. Similar studies carried out in several places and we compared their findings with our data. The contribution of Smith et al was to document the pattern of initial antibiotic prescribing in acute exacerbations of chronic obstructive pulmonary disease in a hospital setting where all episodes of acute exacerbation of COPD, as diagnosed by the admitting doctor, in one hospital in the period January to May 1996, were identified.⁷ The purpose of Narayanagowda et al was to analyse the hospital data on AECOPD in patients with special reference in males and female cases, the pathogens involved, antibiotic susceptibility pattern. The sputum specimen was collected using sterile sputum cups and subjected to Gram's stain, culture and biochemical reactions.⁸ Again, Sharan et al determined the bacteriology of acute exacerbations of chronic obstructive pulmonary disease in hospitalized patients in the institution and their antibiotic susceptibility pattern to formulate cost effective antibiotic strategy and reducing the emergence of drug resistance.⁹ In developing country like India acute exace-

rbations of chronic obstructive pulmonary disease is common in adults more than 50 years of age due to smoking habits and high indoor pollution.

The course of chronic obstructive pulmonary disease is characterized by intermittent exacerbations of the disease.¹⁰ Suseela et al was conducted to determine the bacterial profile and antibiotic susceptibility in COPD patients visiting a tertiary care hospital.¹¹ Susheela et al focused on microbiological pattern in acute exacerbation of COPD a retrospective study at MIMS, Mandya. 60 patients admitted with acute exacerbation are included.¹² Acute exacerbation is a common problem in the usual course of chronic obstructive pulmonary disease. Acute exacerbation a prominent feature of COPD, is a major entity altering the course of the disease. Cases of acute exacerbation of COPD satisfying the eligibility criteria were included. Chronic obstructive pulmonary disease is a major cause of chronic morbidity and mortality world-wide.¹³

Mussema et al study bacterial isolates and antibacterial resistance patterns in a patient with acute exacerbation of chronic obstructive pulmonary disease in a tertiary teaching hospital, southwest Ethiopia.¹⁴ Furthermore, the resistance patterns observed in the normal flora underscore the importance of differentiating between true pathogens and colonizing organisms to avoid unnecessary antibiotic use. It's noteworthy that certain antibiotics, such as amoxicillin, demonstrated considerable efficacy against normal flora, indicating potential utility in empiric treatment regimens.

Interestingly, the data also highlight some notable findings regarding specific antibiotics. For instance, the high susceptibility of *Klebsiella* to amikacin and gentamicin suggests the potential effectiveness of aminoglycosides in treating infections caused by this organism. Similarly, the relatively high resistance of *Citrobacter* to cephalosporins warrants attention, emphasizing the importance of antibiotic stewardship and empirical therapy considerations.

CONCLUSION

The importance of continuous surveillance of antimicrobial resistance patterns to guide empirical therapy and minimize the emergence of resistant strains. Clinicians should consider local epidemiological data, along with individual patient factors, when selecting appropriate antibiotic regimens. Additionally, efforts to promote judicious antibiotic use and infection control measures are essential in combating antimicrobial resistance and optimizing patient outcomes in respiratory infections.

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