Bacterial profile and antibiotic susceptibility in chronic obstructive pulmonary disease patients with acute exacerbation: A cross sectional study in a tertiary care hospital

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Abstract

Background: The course of Chronic Obstructive Pulmonary Disease (COPD) is characterized by intermittent exacerbations of the disease. The bacterial pathogens contribute a lot in mucus secretions and the acute exacerbations. This study was conducted to determine the bacterial profile and antibiotic susceptibility in COPD patients visiting a tertiary care hospital.

Methods: A cross sectional study was conducted in a tertiary care hospital over a period of 15 months. The sputum samples were collected from COPD patients admitted in the Pulmonology department. Purulent sputum samples were subjected to Gram staining followed by culture and antibiotic susceptibility testing according to the standard guidelines.

Result: Sputum samples from 477 COPD patients (50-85 years) were collected and significant isolates were obtained from 106 sputum samples (94 males and 14 females). The isolates were *Streptococcus pneumoniae*-22%, Mucoid *P*seudomonas *aeruginosa*-17%, *Moraxella catarrhalis*-13%, *Haemophilus influenzae*- 13%, followed by *Klebsiella pneumoniae*- 11%, Non-mucoid *Pseudomonas aeruginosa* -8%, *Stenotrophomonas maltophilia*- 7%, *Acinetobacter baumannii*- 3% and *Staphylococcus aureus* and *Group C Streptococci* 1% each. Only 2 isolates of *S. pneumoniae showed* penicillin and erythromycin resistance. The mucoid *P.aeruginosa*, the 2nd most prevalent, was susceptible to ciprofloxacin, ceftazidime and gentamicin. *M. catarrhalis* and *H. influenzae* were susceptible to amoxicillin- clavulanic acid and azithromycin. *K. pneumoniae* and Non-mucoid *P. aeruginosa* showed variable susceptibility. Isolates of *S. maltophilia* were susceptible to co-trimoxazole.

Conclusion: Susceptible strains of mucoid *P. aeruginosa* and *S. maltophilia* have also been isolated as potential pathogens. They were susceptible to fluoroquinolones and *S. tenotrophomonas maltophilia* was susceptible to co-trimoxazole also.

Keywords: Acute exacerbation, Antibiotic susceptibility, Bacterial pathogens, COPD, Fluoroquinolones

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Introduction

The role of bacterial infection in acute exacerbation of Chronic Obstructive Pulmonary Disease (COPD) have been discussed extensively.[1] The bacteria are probably significant in perpetuating the overproduction of mucus.[2] *Streptococcus pneumoniae*, Nontypeable *Haemophilus influenzae* and *Moraxella catarrhalis* have been recognized as causes of purulent exacerbations of COPD.[3] Virus infection, especially in the presence of chronic bacterial infection, is an important determinant of more severe acute exacerbations in both asthma and COPD.[4] *Staphylococcus aureus* and *Pseudomonas aeruginosa* have been found in more severe cases. The patients may need hospital admissions and antibiotic treatment during the period of exacerbations. Antibiotic does hasten recovery and improve clinical outcome.[5] However, report on the changes in the bacterial profile and the antibiotic susceptibility patterns of the most prevalent isolates are lacking in the COPD patients of this population. Hence, this study was aimed to find out the changes in the bacterial profile and the antibiotic susceptibility pattern of the isolates prevalent. The result may help the physicians to choose optimum antibiotics therapy.

Methods

A cross sectional study was conducted in a tertiary care hospital over a period of 15 months (November 2014 to January 2016). The sputum samples were collected from COPD patients attending the Pulmonology department. Purulent samples from patients (50-85 years of age) with acute exacerbation of COPD were included as the inclusion criteria whereas samples mixed with saliva and patients above the age of 85 years were excluded from the study. Purulent sputum samples were subjected to Gram staining followed by culture and antibiotic susceptibility testing. Culture was done on media like blood agar, chocolate agar and Mc Conkey agar and incubated for 48 hours at 37°C. Significance of the isolates was correlated with the Gram staining of the samples and clinical observation. Isolates were identified by using standard identification methods and antibiotic susceptibilities

were done according to the Clinical and Laboratory Standards Institute guide lines.

Result

477 sputum samples were studied during a period of 15 months. Among the total samples collected, significant isolates were obtained from 106 sputum samples. Among the 106 samples, 92 were from male and remaining was from female patients (Fig. 1). The distribution of age and the number of cases is given in Fig. 2. The number of bacterial infection in acute exacerbation cases was more in the age group of 60-65 years, whereas the age group 50-55 years showed minimum number (Fig. 3). Among the total isolates identified, *S. pneumoniae* was found to be the most prevalent (22%), while the second most prevalent was Mucoid *P. aeruginosa* (17%) (Fig. 4). The other isolates were *M. catarrhalis*-13%, *H. influenzae*- 13%, followed by *Klebsiella pneumoniae*- 11%, Non-mucoid *P. aeruginosa* 8%, *Stenotrophomonas maltophilia*- 7%, *Acinetobacter baumannii*- 3%. The *Staphylococcus aureus* and *Group C Streptococci* were 1% each.

Only 2 isolates of *S. pneumoniae showed* penicillin and erythromycin resistance. The mucoid *P. aeruginosa*, the 2nd most prevalent, was susceptible to ciprofloxacin, ceftazidime and gentamicin. *M. catarrhalis* and *H. influenzae* were susceptible to amoxicillin- clavulanic acid and azithromycin (Table 1). *K. pneumoniae* showed variable and Non-mucoid *P. aeruginosa* showed high susceptibility (Table 2). Isolates of *S. maltophilia* were susceptible to co-trimoxazole and levofloxacin/ciprofloxacin.

Table 1: Distribution of antibiotic susceptibility of isolates

Name of the Isolate	Penicillin		Erythromycin		Azithromycin		Amoxy-Clavu		Total
	S	R	S	R	S	R	S	R	
S. pneumoniae	21	2	21	2	21	2	-	-	23
M. catarrhalis	-	-	14	0	14	0	14	0	14
H. influenzae	-	-	14	0	14	0	14	0	14

S- Susceptible; R-Resistant

Table 2: Distribution of antibiotic susceptibility of isolates

Name of the Isolate	Ceftazidime		Ceftriaxone		Gentamicin		Piperacillin		Ciprofloxacin		Total
	S	R	S	R	S	R	S	R	S	R	
Mucoid P. aeruginosa	18	0	-	-	18	0	18	0	18	0	18
Non-mucoid P. aeruginosa	7	1	-	-	8	0	8	0	8	0	8
K. pneumoniae	-	-	4	8	7	5	-	-	3	9	12

S- Susceptible; R-Resistant

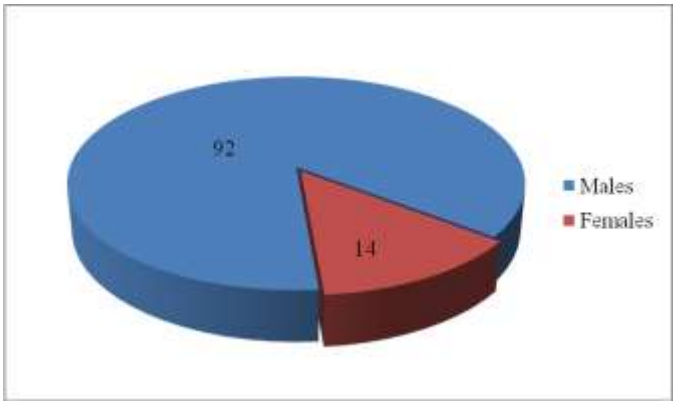

Fig. 1: Distribution of gender

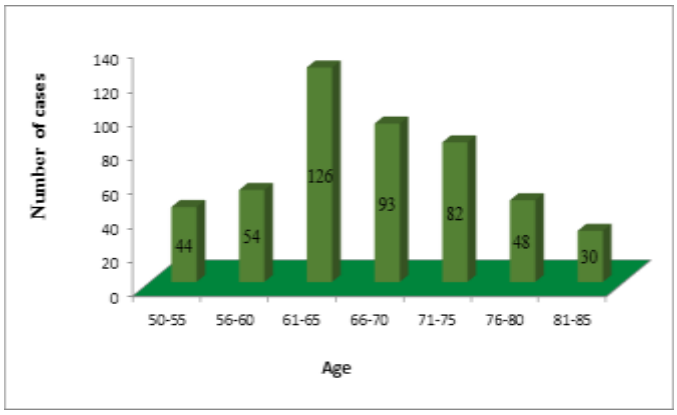

Fig. 2: Distribution of cases among the age

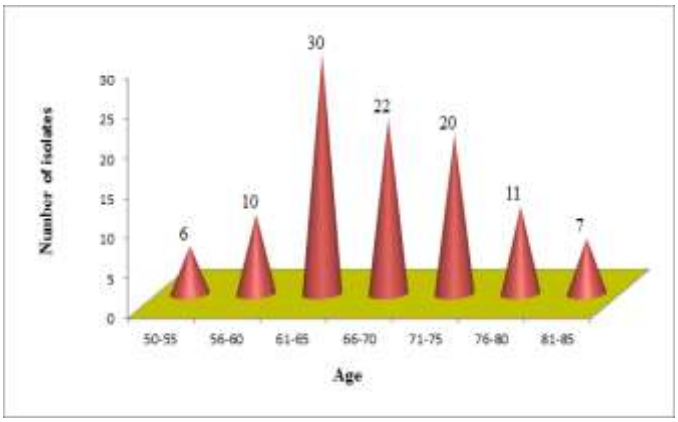

Fig. 3: Distribution of isolates among the age

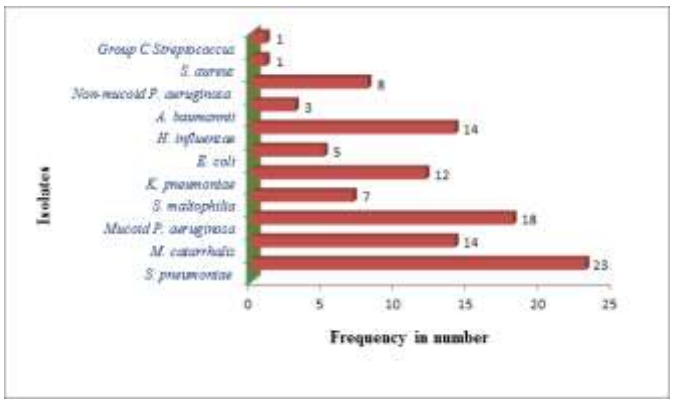

Fig. 4: Frequency of different isolates

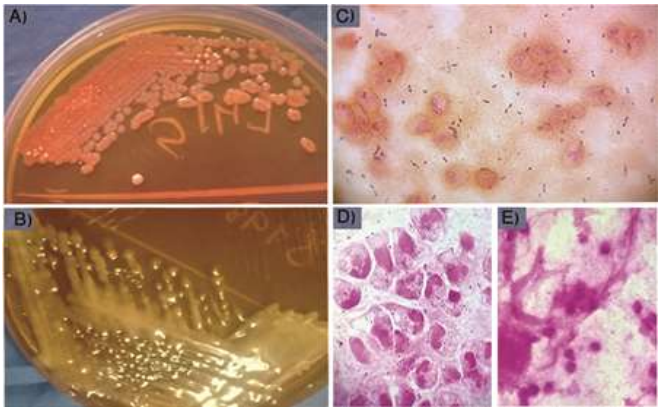

Fig. 5: Photographs showing culture of A) *S. maltophilia* B) Mucoid *Pseudomonas*; and Gram smear of sputum with C) *Pneumococci* D) Intracellular *M. catarrhalis* and E) H. *influenzae*

Discussion

Infections can cause acute decompensation and it is the most common identifiable cause of death in COPD patients.[6] Chronic colonization of the airways and sputum with unencapsulated strains of *H. influenzae* and *S. pneumoniae* occurs in at least one half of the patients.[1] Incidence of other bacteria like *M. catarrhalis* is also increasing. According to previous studies, the bacterial infection has got a significant role in the acute exacerbation.[2] If the infection persists, chronic inflammation may cause lung damage. Though the bacterial infection is responsible for half of the exacerbations, it is not easy to differentiate these patients from those who are uninfected. Therefore, the antibiotics have to be given more often than is strictly necessary.[2] The culture and susceptibility of sputum samples may help a lot to identify those who need antibiotics.

One of the earlier studies suggested a small but statistically significant improvement due to antibiotic therapy in patients with exacerbations of COPD.[5] Nontypeable *H. influenzae*, *M. catarrhalis*, and *S. pneumoniae* are the most common causes of exacerbations and *Chlamydia pneumoniae* can be responsible for a small proportion.[3] Many studies show *H. Influenzae* as the prevalent oranism.[2] In our study, out of 106 isolates (22%) were *S. pneumoniae* followed by Mucoid *P. aeruginosa* (17%). The pneumoccus is frequently recovered from the sputum of patients with chronic bronchitis even in the absence of clinical infection.[3] But in the present study the growth of *S. pneumoniae*could be correlated with the Gram smear appearance of the samples where this was the sole organism present.

According to Yang X et al.[7] the isolation rate was *S. pneumoniae* (10%), *P. aeruginosa* (10%), *H. influenzae* (7%), *M. catarrhalis* (7%), and *K. pneumoniae* (7%). In our study, the nonmucoid *P. aeruginosa* was 8% only. The mucoid *P. aeruginosa* is usually considered a pathogen associated with cystic fibrosis.[8] In our study this organism was second among the isolates. While mucoid *P. aeruginosa* is reported in severe cases of COPD, the *S. maltophilia* have been seen as the nosocomial pathogens.[9,10] These two also may be listed as potential pathogens in the acute exacerbation. Sethi et al.[11] could find the aquisiton of new strains of pathogenic bacteria in the exacerbation of COPD. From a study from Thaiwan, the predominant bacteria were *K. pneumoniae* (19.6%), *P. aeruginosa* (16.8%) and *H. influenzae* (7.5%), followed by *Acinetobacter baumannii* (6.9%).[12] In the present study the isolation of *K. pneumoniae and A.baumannii* were 11 and 3%, respectively. These isolates were multidrug resistant.

The role of antibiotic treatment like macrolides was studied by Targowski and Jahnaz-Rozyk.[13] We could also find that the isolates of *H. influenzae* and *M. catarrhalis* were susceptible to macrolide like azithromycin. This agrees with a study by Hetal.[14] The patients with serious co-morbid conditions or advanced structural lung disease require treatment with new more potent agents. The knowledge of the patterns of antimicrobial resistance in the respiratory pathogens will help to prevent treatment failures.[15] So the bacteriological analysis of the sputum samples in exacerbation is essential. A study by Russo and Aprile suggest that the benefit of antimicrobial therapy in acute exacerbations of COPD may be related to exacerbation severity.[16] Fluoroquinolones exhibit low resistance, good activity levels and high respiratory penetration, and they are particularly well suited for shorter-course, higher-dose regimens in selected.[17] The present study showed 17% of Mucoid *P. aeruginosa* with good susceptibility to fluoroquinolones like ciprofloxacin. Additionally 3% of drug resistant *A. baumanni* was also been isolated, may be hospital pathogen.

Optimal and effective antimicrobial therapy for acute exacerbation episodes can significantly diminish healthcare costs and maintain quality of life in the elderly patient.[18] In our study we could see that the majority of the patients were in the age group of 60-65. By microbiologically evaluating these patients they can be provided with good healthcare and they can lead a

quality life. The limited number of patients and short period of study are the major limitations of this study. This warrant a multicentre study to establish the suitable antibiotic regimen for the bacterial isolates found in the COPD patients.

Conclusion

Bacteriological study of the sputum samples could found that beyond the conventional pathogens other agents like Mucoid *P. aeruginosa* and *S. maltophilia* also been responsible for exacerbation of COPD. Only two of twenty three isolates of *S. pneumoniae* were resistant to penicillin. *M. catarrhalis*, and *H. influenzae* were susceptible to azithromycin and amoxicillin-clavulanic acid. Mucoid *P. aeruginosa* was found susceptible to ciprofloxacin and *S. maltophilia* to co-trimoxazole and ciprofloxacin.

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