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AUDIT OF DIFFERENT BACTERIAL MICRO-ORGANISM IN ACUTE EXACERBATION OF COPD

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ABSTRACT

Objectives: To identify the frequency of bacterial pathogens in acute exacerbation of COPD. **Materials & Methods:** This cross sectional was conducted at Department of Pulmonology, Sheikh Zayed Hospital Rahim Yar Khan from August 2018 to February 2019 over the period of 6 months. A total of 162 patients of acute exacerbation of COPD of age 40-70 years and both genders were included. Patients with h/o concomitant bronchial carcinoma, pneumonia, chronic renal failure and chronic congestive failure were excluded. After taking informed written consent, a fresh sample of sputum was collected into a sterile container and was sent for culture and sensitivity. Each sample was examined and interpreted by consultant pathologist and identification of bacterial pathogens was noted. **Results:** Mean age was 57.10 ± 7.63 years. Out of the 162 patients, 112 (69.14%) were male and 50 (30.86%) were females with male to female ratio of 2.24:1. In this study, I have found the Streptococcus pneumoniae was the predominant organism isolated in 52 (32.10%) patients followed by Klebsiella pneumoniae in 38 (23.46%), Pseudomonas aeruginosa in 29 (17.90%), Moraxella catarrhalis in 23 (14.30%), Methicillin - Resistant Staphylococcus aureus in 19 (11.73%) and H. influenza in 01 (0.62%) patients of acute exacerbation COPD. **Conclusion:** This study concluded that streptococcus pneumoniae was the predominant organism isolated in patients of acute exacerbation of COPD followed by Klebsiella pneumoniae, Pseudomonas aeruginosa, Moraxella catarrhalis, Methicillin - Resistant Staphylococcus aureus and H. influenza.

KEYWORDS: Chronic obstructive pulmonary disease, bacteria, streptococcus pneumonia, Klebsiella pneumonia.

INTRODUCTION

Chronic obstructive pulmonary disease (COPD) is a chronic progressive disease which is characterized by an inexorable decline in respiratory function, exercise capacity, and health status.[1] Patient's typically has symptoms of chronic bronchitis and emphysema, but the classic triad also includes asthma. The main symptoms include shortness of breath, cough, and sputum production.[2] Patients with chronic obstructive pulmonary disease (COPD) are prone to exacerbation, which account for significant morbidity and mortality and are a key determinant of health related quality of life.[3] Globally, as of 2010, COPD affected approximately 329 million people (4.8% of the population) and is slightly more common in men than women.[4] An exacerbation of COPD is defined as an event in the natural course of the disease characterized by a change in the patient's baseline dyspnea, cough, and/or sputum that is beyond normal day-to-day variations; is acute in onset; and may warrant a change in regular medication.[5] The mortality rate for patients admitted for an acute exacerbation COPD is about 10% in-hospital, and near one third in the year after hospitalization.[6] Assessment of the severity of an exacerbation is based on the patient's medical history before the exacerbation, preexisting comorbidities, symptoms, physical examination, arterial blood gas measurements, and other pertinent laboratory tests.[7] Markers related to inflammatory processes, structural changes and systemic effects yield valuable information to compliment that provided by Forced expiratory volume in 1 second (FEV1) airflow limitation.[8] Increased levels of various inflammatory proteins such as C-reactive protein (CRP), tumor necrosis factors-α (TNF- α) and interleukin-6 (IL-6) are found in systemic circulation in COPD patients.[9] Majority of exacerbations are infectious in etiology. At least half of the COPD exacerbations are due to pathogenic micro-organisms.[10] Three classes of pathogens responsible for acute exacerbation of COPD by infecting the lower respiratory tract: respiratory viruses, atypical bacteria, and aerobic Gram-positive and Gram negative bacteria.[11,12] The proof for a bacterial infection as the inciting event for an acute exacerbation COPD comes from isolation of pathogens in lower respiratory tract secretions obtained by different techniques, isolation of new strains in such patients, the development of a pathogen strain-specific immune response and

association of neutrophilic airway inflammation with bacterial isolation duringexacerbations.[12] In a study done by Rakesh G et al.[13] Streptococcus pneumoniae was the predominant organism isolated (31.10%) followed by Klebsiella pneumoniae (23.81%), Pseudomonas aeruginosa (19.14%), Moraxella catarrhalis (16.67%), Methicillin-Resistant Staphylococcus aureus (11.90%) and H.influenza in 0% patients of COPD. Knowledge of possible bacterial etiology and antibiotic sensitivity patterns of COPD exacerbations, facilitates the orientation of antibiotic treatment and reducing the high number of failures recorded with empiric treatment, which in some cases, is as high as 26%.[14] So, this study would help us to identify the frequency of bacterial pathogens in acute exacerbation of COPD in our local population. This study would provide us the local data on the pattern of bacterial pathogens in our patients with an acute exacerbation COPD and help us to design our routine practice guidelines for early recognition and proper antibiotic treatment of this condition in order to reduce the morbidity and mortality of the community.

OPERATIONAL DEFINITIONS

1. Acute exacerbation of COPD: Presence of all of the following in known COPD patients will be deemed as positive;

a. Cough, usually worse in the mornings and productive of a small amount of colorless sputum.
b. Shortness of breath (difficulty in breathing).
c. Tachypnea (breathing rate >20/min).
d. Hyper resonance on percussion.
e. Crackles (clicking, rattling, or crackling noises that may be made by one or both lungs during inhalation) on auscultation.
f. Hyperinflation of lungs on chest x-ray.
g. Presence of post bronchodilator FEV1 <50% on spirometry.

2. Bacterial pathogens: following bacterial pathogens will be noted;

1. Streptococcus pneumonia
2. Klebsiella pneumonia
3. Pseudomonas aeruginosa
4. Methicillin - Resistant Staphylococcus aureus
5. H. influenza
6. Moraxella catarrhalis

MATERIA AND METHODS

This cross sectional was conducted at Department of Pulmonology, Sheikh Zayed Hospital Rahim Yar Khan from August 2018 to February 2019 over the period of 6 months.

a. Inclusion Criteria

- All diagnosed COPD patients of <1 year duration with acute exacerbation of COPD (as per operational definitions).
- Age between 40-70 years.
- Both genders.

b. Exclusion Criteria

- Patients with concomitant bronchial carcinoma (assessed on history and medical record).
- Patients already on antibiotics or had taken antibiotics 3 weeks prior to the exacerbation.
- Patients with h/o pneumonia, congestive cardiac failure, chronic renal failure (assessed on history and medical record).
- Patients not willing to be included in the study.

RESULTS

Age range in this study was from 40 to 70 years with mean age of 57.10 ± 7.63 years. Majority of the patients 98 (60.49%) were between 56 to 70 years of age as shown in Table I. Out of the 162 patients, 112 (69.14%) were male and 50 (30.86%) were females with male to female ratio of 2.24:1 (Figure I). Mean duration of disease was 7.79 ± 3.42 months as shown in Table II. Distribution of patients according to smoking status is shown in Table II. In this study, I have found the Streptococcus pneumoniae was the predominant organism isolated in 52 (32.10%) patients followed by Klebsiella pneumoniae in 38 (23.46%), Pseudomonas aeruginosa in 29 (17.90%), Moraxella catarrhalis in 23 (14.30%), Methicillin - Resistant Staphylococcus aureus in 19 (11.73%) and H. influenza in 01 (0.62%) patients of AECOPD as shown in Table III. Stratification of bacterial pathogens with respect to age and gender are shown in Table IV & V respectively. Table VI & VII have shown the stratification of bacterial pathogens with duration of disease and smoking status respectively.

Table-I: Age distribution of patients (n=162).

Age (in years)	No. of Patients	%
40-55	64	39.51
56-70	98	60.49
Total	162	100.0

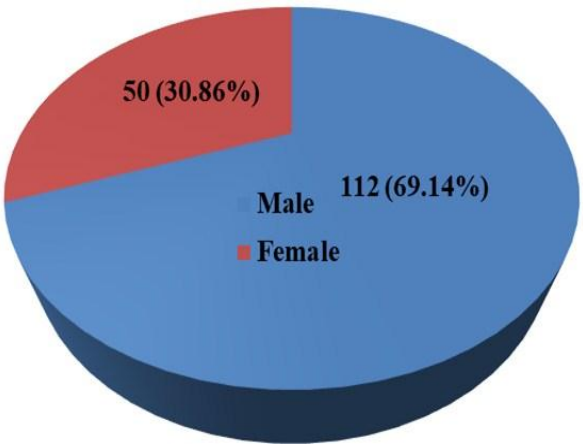

Figure-I: Distribution of patients according to gender (n=162).

Table II: Distribution of patients according to duration of disease.

Duration of disease	No. of Patients	%
≤6 months	67	41.34
>6 months	95	58.64
Mean ± SD	**7.79 ± 3.42**	

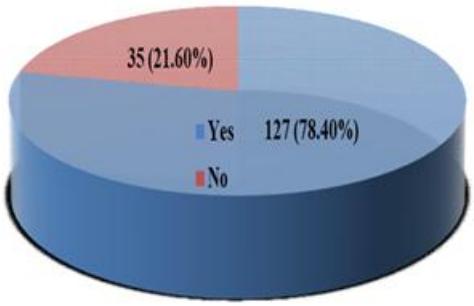

Figure II: Distribution of patients with respect to smoking (n=162).

Table III: Frequency of bacterial pathogens.

Bacterial Pathogens	Frequency (%)	
	Present	Absent
Streptococcus pneumonia	52 (32.10%)	110 (67.90%)
Klebsiella pneumoniae	38 (23.46%)	124 (76.54%)
Pseudomonas aeruginosa	29 (17.90%)	133 (82.10%)
Moraxella catarrhalis	23 (14.20%)	139 (85.80%)
Methicillin - Resistant Staphylococcus aureus	19 (11.73%)	143 (88.27%)
H. influenza	01 (0.62%)	161 (99.38%)

Table IV: Stratification of bacterial pathogens with respect to age.

		40-55 years (n=64)	56-70 years (n=98)	P-value
Streptococcus pneumonia	Yes	25 (39.06%)	27 (27.55%)	**0.125**
	No	39 (60.94%)	71 (72.45%)	
Klebsiella pneumoniae	Yes	19 (29.69%)	19 (19.39%)	**0.130**
	No	45 (70.31%)	79 (80.61%)	
Pseudomonas aeruginosa	Yes	09 (14.06%)	20 (20.41%)	**0.303**
	No	55 (85.94%)	78 (79.59%)	
Moraxella catarrhalis	Yes	07 (10.94%)	16 (16.33%)	**0.671**
	No	57 (89.06%)	82 (83.67%)	
Methicillin – Resistant Staphylococcus aureus	Yes	04 (6.25%)	15 (15.31%)	**0.337**
	No	60 (93.75%)	83 (84.69%)	
H. influenza	Yes	00 (0.0%)	01 (1.02%)	**0.418**
	No	64 (100.0%)	97 (98.98%)	

Table V: Stratification of bacterial pathogens with respect to gender.

		Male (n=112)	Female (n=50)	P-value
Streptococcus pneumonia	Yes	40 (35.71%)	12 (24.0%)	**0.140**
	No	72 (64.29%)	38 (76.0%)	
Klebsiella pneumoniae	Yes	26 (23.21%)	12 (24.0%)	**0.913**
	No	86 (76.79%)	38 (76.0%)	
Pseudomonas aeruginosa	Yes	14 (12.50%)	15 (30.0%)	**0.007**
	No	98 (87.50%)	35 (70.0%)	
Moraxella catarrhalis	Yes	18 (16.07%)	05 (10.0%)	**0.306**
	No	94 (83.93%)	45 (90.0%)	
Methicillin – Resistant Staphylococcus aureus	Yes	14 (12.50%)	05 (10.0%)	**0.648**
	No	98 (87.50%)	45 (90.0%)	

H. influenza	Yes	00 (0.0%)	01 (2.0%)	**0.133**
	No	112 (100.0%)	49 (98.0%)	

Table VI: Stratification of bacterial pathogens with respect to duration of disease.

		≤6 months (n=67)	**>6 months (n=95)**	**P-value**
Streptococcus pneumonia	Yes	19 (28.36%)	33 (34.74%)	**0.392**
	No	48 (71.64%)	62 (65.26%)	
Klebsiella pneumoniae	Yes	17 (25.37%)	21 (22.10%)	**0.629**
	No	50 (74.63%)	74 (77.89%)	
Pseudomonas aeruginosa	Yes	12 (17.91%)	17 (17.89%)	**0.998**
	No	55 (82.09%)	78 (82.11%)	
Moraxella catarrhalis	Yes	09 (13.43%)	14 (14.74%)	**0.815**
	No	58 (86.57%)	81 (85.26%)	
Methicillin – Resistant Staphylococcus aureus	Yes	08 (11.94%)	11 (11.58%)	**0.944**
	No	59 (88.06%)	84 (88.42%)	
H. influenza	Yes	00 (0.0%)	01 (1.05%)	**0.400**
	No	67 (100.0%)	94 (98.95%)	

Table VII: Stratification of bacterial pathogens with respect to smoking.

		Yes (n=127)	**No (n=35)**	**P-value**
Streptococcus pneumonia	Yes	43 (33.86%)	09 (25.71%)	**0.361**
	No	84 (66.14%)	26 (74.29%)	
Klebsiella pneumoniae	Yes	32 (25.20%)	06 (17.14%)	**0.319**
	No	95 (74.80%)	29 (82.86%)	
Pseudomonas aeruginosa	Yes	21 (16.54%)	08 (22.86%)	**0.388**
	No	106 (83.46%)	27 (77.14%)	
Moraxella catarrhalis	Yes	18 (14.17%)	05 (14.29%)	**0.987**
	No	109 (85.83%)	30 (85.71%)	
Methicillin – Resistant Staphylococcus aureus	Yes	12 (9.45%)	07 (20.0%)	**0.086**
	No	115 (90.55%)	28 (80.0%)	
H. influenza	Yes	01 (0.79%)	00 (0.0%)	**0.598**
	No	126 (99.21%)	35 (100.0%)	

DISCUSSION

The purpose of present study was to identify the frequency of bacterial pathogens in acute exacerbation of COPD. Age range in my study was from 40 to 70 years with mean age of 57.10 ± 7.63 years. Out of the 162 patients, 112 (69.14%) were male and 50 (30.86%) were females with male to female ratio of 2.24:1. In this study, I have found the Streptococcus pneumoniae was the predominant organism isolated in 52 (32.10%) patients followed by Klebsiella pneumoniae in 38 (23.46%), Pseudomonas aeruginosa in 29 (17.90%), Moraxella catarrhalis in 23 (14.30%), Methicillin - Resistant Staphylococcus aureus in 19 (11.73%) and H. influenza in 01 (0.62%) patients of acute exacerbation COPD. In a study done by Rakesh G et al,[13] Streptococcus pneumoniae was the predominant organism isolated (31.10%) followed by Klebsiella pneumoniae (23.81%), Pseudomonas aeruginosa (19.14%), Moraxella catarrhalis (16.67%), Methicillin - Resistant Staphylococcus aureus (11.90%) and H. influenza in 0% patients of acute exacerbation COPD. Pathogenic bacteria were found in 42% of patients with acute exacerbation COPD. This could be due to declining lung function.[15] The prevalence of Gram negative isolates was 61.90%, as compared to 50% of Gram positive isolates. The Gram negative organisms were more common in the patients with the most severe lung dysfunction, whereas the Gram positive bacteria predominated in the exacerbations of the patients with the mildest degree of lung function abnormalities.[16] In a comprehensive study by Soleret al,[17] quantitative cultures of tracheobronchial aspirates (TBAs), PSB specimens and bronchoalveolar lavage fluid yielded potential pathogens and/or a positive serology in 72%of cases, including 33% that were polymicrobial S.pneumoniae, H. influenzae, and M. catarrhalis together constituted 56% of the yield while gram-negative pathogens accounted for 44% of the bacterial isolates. The presence of pathogens was clinically unpredictable. Increasingly, recent studies have reported a higher yield of pseudomonas and enterobacteriaceae in sputum specimens from patients with COPD. Pseudomonas aeruginosa isolation has been reported to increase with increasing severity of disease, and especially in association with co-morbidities, such as bronchiectasis. Organisms belonging to enterobacteriaceae have been isolated less frequently and Staphylococcus aureus is

uncommon except when the infections are hospital-acquired. Atypical organisms, such as Mycoplasma pneumoniae and Chlamydia pneumoniae have rarely been isolated.[18,19] This is in contrast to their higher frequency as pathogens in community-acquired pneumonias. In another study, sputum culture for pathogenic bacteria was positive in 44 cases (55%) and no bacterial growth was seen in 37 (45%) cases. Gram negative bacilli were more isolated than Gram positive cocci. The commonest isolate was Klebsiella pneumoniae 26 (59%), followed by Pseudomonas aeruginosa 7 (15%), Staphylococcus aureus 6 (13.6%), Streptococcus pneumoniae 3 (6.8%) and Streptococcus pyogenes 2 (4.5%). The drug sensitivity reveals that the gram negative isolates were sensitive to Amikacin (100%) followed by quinolones like Levofloxacin and Ofloxacin. Staphylococcus aureus was sensitive to Amikacin, Ciprofloxacin and Cefoperazone.[14]

In a retrospective review of records of nearly 500episodes of acute exacerbation COPD in hospitalized patients inTaiwan,[20] Klebsiella pneumoniae and P. aeruginosa were the most common sputum pathogens with the former being more commonly isolated from mild COPD and the latter associated with a poorer clinical outcome. In a prospective study in a small sample of patients with severe COPD followed up for one year, out of a total of188 sputum samples, 128 episodes yielded a single pathogen while 42 episodes were polymicrobial. The most frequent pathogen isolated was P. aeruginosa followed by H. influenzae, S. pneumoniae, M. catarrhalis and S. aureus. Pseudomonas aeruginosa was the most frequent pathogen in patients with a single as well as multiple exacerbations.[21] Monsoet al,[22] using PSB cultures obtained H. influenza and S. pneumoniae in concentrations exceeding 103 colony-forming units/ milliliter (CFU/mL) in 25% of patients with stable disease. Miravitlles et al,[23] recently reported that almost half of the population of ambulatory moderate-to-very severe COPD patients were colonized with potential pathogens and presented with more severe dyspnoea and a darker color of sputum. However, results are also seen in an Indian study by Chawla et al,[24] P.aeruginosa was the predominant isolate (25.92%) amongst the hospitalized patients followed by S.pneumoniae and Acinetobacter spp (18.51% each), Klebsiella spp. And M.catarrhalis (14.80% each). An analysis of individual bacterial species showed that isolation of M. catarrhalis and S. pneumoniae was associated with a significant increase in the frequency of exacerbations whereas H. influenzae, P. aeruginosa, and Gram-negative bacilli were not. However, as can be seen from these data, the majority of visits at which a pathogen was detected were not associated with an exacerbation. Therefore, acquisition of bacterial infection in a COPD patient does not automatically result in an exacerbation and it is likely that there are both host and pathogen factors that determine the outcome of bacterial infection. Further studies are needed to identify the key factors that determine the outcome of bacterial infection in COPD.[1]

CONCLUSION

This study concluded *that* Streptococcus pneumoniae was the predominant organism isolated in patients of acute exacerbation of COPD followed by Klebsiella pneumoniae, Pseudomonas aeruginosa, Moraxella catarrhalis, Methicillin - Resistant Staphylococcus aureus and H. influenza. So, we recommend that there should be early recognition of the bacterial pathogen for proper antibiotic treatment of this condition in order to reduce the morbidity and mortality of the community.

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