

Bacteriological profile of acute exacerbations of chronic obstructive pulmonary disease

Phani K. Reddy¹, Aruna Talatam^{2,*}, D. Pragati Rao³, S. Vineela⁴, K. Yamuna⁵

¹Associate Professor, Dept. of General Medicine, ^{2,3}Associate Professor, ^{4,5}Postgraduate, Dept. of Respiratory Medicine, NRI Medical College & General Hospital, Mangalagiri, Andhra Pradesh, India

***Corresponding Author:**

Email: arunatalatam@yahoo.com

Abstract

Introduction: Acute exacerbations of chronic obstructive pulmonary disease (COPD) influence the quality of life and account for considerable morbidity and mortality. Several factors contribute to the etiology of COPD exacerbations, of which infectious process poses a major risk. Knowledge about local bacteriological profile in COPD patients would help in better selection of antibiotic for empirical therapy thereby reducing emergence of drug resistance.

Aim and Objectives: To determine the bacteriological profile of acute exacerbations of COPD patients admitted at NRI Medical College, Guntur.

Material and Methods: All patients admitted into the hospital from January 2017 to January 2018 diagnosed to have an acute exacerbation of chronic obstructive pulmonary disease were included in the study. Sputum samples were collected prior to the initiation of antibiotic therapy and were sent for bacteriological culture and drug sensitivity. Obtained results were analysed. The procedures followed were in accordance with the ethical standards of the responsible committee on human experimentation (institutional and national).

Results: The study included 128 patients of whom sputum smear was positive for growth in 96 (75%) patients. Most common organism grown was *Klebsiella pneumoniae* (31%) followed by *Pseudomonas aeruginosa* (22%), *Candida* species (13%), *Escherichia coli* (9%). Other organisms isolated from culture were *Staphylococcus aureus*, *Burkholderia cepacia*, *Citrobacter*, *Streptococcus pneumoniae*, *Acinetobacter*, *Micrococci* and *Enterococcus* species. Simple gram's stain identified organisms in 60% of patients. Drug sensitivity patterns revealed most of the gram positive and gram negative organisms (92%) were sensitive to piperacillin-tazobactam, cefoperazone-sulbactam combinations.

Conclusion: The microbiology of acute exacerbations of COPD varies from region to region. Studies at regular intervals would assist in identifying the causative organisms thereby allowing formulating a cost effective antibiotic strategy. Antibiotic choice based on local bacteriological growth and resistance pattern reduces the emergence of drug resistance.

Keyword: Chronic obstructive pulmonary disease; Gram positive and gram negative bacteria; Antibiotic.

Introduction:

An exacerbation of Chronic Obstructive Pulmonary Disease (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 and beyond normal day-to-day variations, that is acute in onset and may warrant a change in regular medication in a patient with underlying COPD [1]. These exacerbations influence the quality of life and account for considerable mortality. Several factors contribute to the etiology of COPD exacerbations, of which infectious process poses a major risk. Other risk factors are environmental pollution, irritants and host factors. The most frequent pathogens isolated are *Haemophilus influenzae*, *Moraxella catarrhalis*, *Streptococcus pneumoniae*, *Mycoplasma pneumoniae*, and viruses [2]. Knowledge about local bacteriological profile in COPD patients would help in better selection of antibiotic for empirical therapy. This reduces the emergence of antibiotic resistance in these subset of patients.

Material and Methods:

All patients admitted at NRI general hospital from January 01, 2017 to January 01, 2018 diagnosed to have an acute exacerbation of chronic obstructive pulmonary

disease (AECOPD) according to GOLD guidelines 2018 were included in the study. After a thorough history and physical examination, blood investigations, chest radiography and pulmonary function tests were performed. We analysed for complete blood picture, viral markers and renal and liver function tests when needed. Patients with co-existent bronchiectasis or any other respiratory disease apart from COPD were excluded. Patients with history of usage of antibiotics before admission were not included in the study.

Early morning samples were collected from cases that were clinically diagnosed as AECOPD. Patients were instructed to cough deeply into a sterile container and then sent to microbiology laboratory. All the samples collected prior to the initiation of antibiotic therapy were sent for gram's stain and bacteriological culture. Adequate samples according to Bartlett grading were processed. 250-500 colony forming units (CFU) were considered significant among *Pneumococci*. In gram negative organisms even a single colony is taken as significant in adequate samples.

Drug sensitivity pattern for common antibiotics was tested. Obtained results were analyzed in percentages.

Results:

The study included 128 patients of whom sputum smear was positive for growth in 96 (75%) patients. Most common organism grown was *Klebsiella pneumoniae* (31%) followed by *Pseudomonas aeruginosa* (22%), *Candida species* (13%), *Escherichia coli* (9%). Other organisms isolated from culture were *Staphylococcus aureus*, *Burkholderiacepacia*, *Citrobacter*, *Streptococcus pneumoniae*, *Acinetobacter*, *Micrococci* and *Enterococcus species*.

In 25% of the cases no microorganisms were grown in culture suggesting prior usage of antibiotic therapy by the patient.

Gram's stain (Fig. 3) revealed presence of organisms in 60% of cases with highest percentage constituted by gram negative bacilli followed by gram positive cocci. In few cases candida species with pus cells were also identified.

Majority of patients were males (95%) and in the age group above 50 years. All the male patients were smokers.

Among the bacteria, there were 10 types of strains, out of which 7 strains belonged to gram-negative

bacteria (77.78%) and 3 belonged to gram-positive group (22.22%).

In *Pneumococci* the colony forming units ranged from 250-500.

Antibiotic sensitivity pattern revealed that *piperacillin - tazobactam* was sensitive to majority of the organisms (92%) excluding candida. In few cases with *klebsiella*, *acinetobacter*, *burkholderia* (7%) resistance to *piperacillin- tazobactam* was present. But they were sensitive to *meropenem*, *dorepenem*, *colistin* and *tigecycline*. Only one case with *acinetobacter* was panresistant to all drugs. Sensitivity to *cefoperazone – sulbactam* combination was almost similar to *piperacillin - tazobactam* combination. Quinolones were effective in 70% of patients with resistance present in 25% patients infected with gram negative organisms and 5% of patients infected with gram positive organisms. *Amoxicilline* was resistant to 40% of the patients having gram positive organisms. Among three patients with *staphylococcus aureus* one was resistant to all drugs except *linezolid*. Against gram negative organisms *amikacin*, *gentamicin* was sensitive in 95% cases.

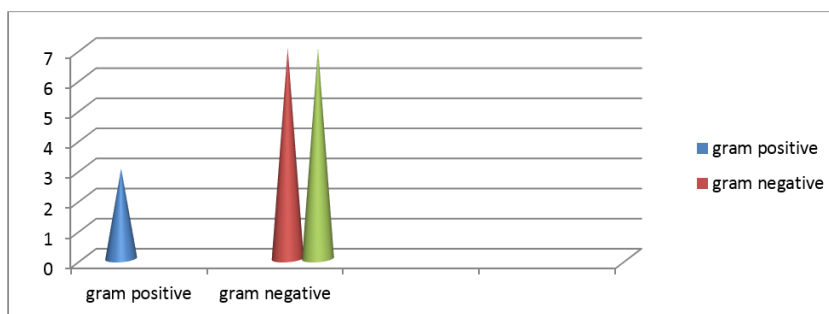


Fig. 1: Bacteriological strains

Table 1: Bacteriological profile

Organism isolated	Number	Percentage
<i>Klebsiella</i>	30	31.25
<i>Pseudomonas</i>	22	23
<i>Candida</i>	15	15.6
<i>E.coli</i>	9	9.3
<i>Acinetobacter</i>	5	5.2
<i>Streptococcus pneumonia</i>	5	5.2
<i>Staphylococcus aureus</i>	3	3.1
<i>Enterobacter cloacae</i>	2	2.08
<i>Enterococci</i>	2	2.08
<i>Bukholderia</i>	2	2.08
<i>Citrobacter</i>	1	1

Table 2: Antibiotic sensitivity pattern against both positive and gram negative organisms

Antibiotics	No. of isolates	Percentage
<i>Piperacillin –tazobactam</i>	75	92%
<i>Cefoperazone-sulbactam</i>	74	92%
<i>Levofloxacin</i>	56	70%
<i>Amoxicillin</i>	7	6.6%
<i>Amikacin</i>	57	95%

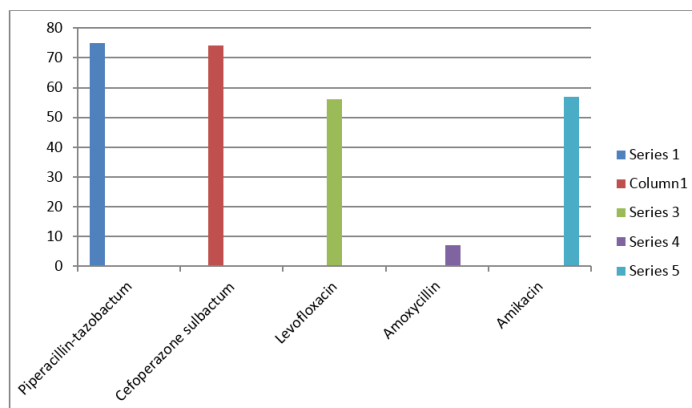


Fig. 3: Antibiotic sensitivity pattern against both positive and gram negative organisms

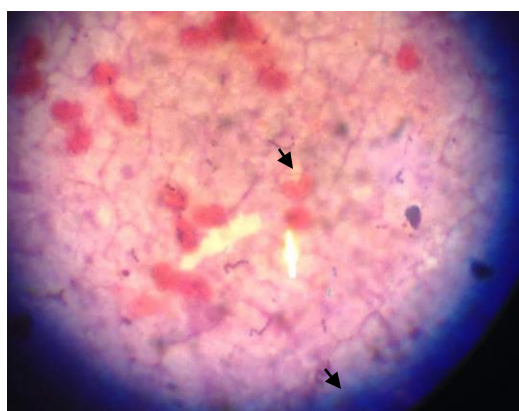


Fig. 4: Smear showing plenty of pus cells (arrow), gram positive cocci arranged in pairs and chains

Discussion:

Acute exacerbation based on winnipeg criteria includes increased breathlessness, sputum volume and sputum purulence [3]. Exacerbations add to burden of the disease leading to increased morbidity and mortality. Though there are several trigger factors infections pose a major risk. High concentrations of bacteria are present in lower airways in majority of patients with exacerbations. Respiratory viruses (*Influenza*, *Para influenza*, *Rhinovirus*, *Corona virus*, *Adenovirus* & *RSV*), atypical bacteria (*Mycoplasma pneumoniae* & *Chlamydia pneumoniae*) and aerobic gram positive & gram negative bacteria are commonly associated with COPD acute exacerbations [4].

Sputum culture was positive in 75% of cases in our study. The most common pathogen isolated was *Klebsiella pneumoniae* followed by *Pseudomonas aeruginosa*, *Candida sps*, *E coli*, *Acinetobacter* unlike other studies where *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Mycoplasma pneumoniae*, *Moraxella catarrhalis* were commonly implicated [5]. Rakesh G *et al* found in their study that *Streptococcus pneumoniae* was commonest 38.10% followed by *Klebsiella* (23.81%), *Pseudomonas aeruginosa* (19.14%), *Moraxella catarrhalis* (16.67%) and *Methicillin resistant Staphylococcus aureus* (11.9%)

[6]. These isolates included both monobacterial and polymicrobial growth. In a study done by Prakhar sharma, *Streptococcus pneumoniae* was the most common organism isolated but collectively the most predominant organisms were gram negative bacteria [7]. We could not investigate the role of atypical organisms in our patients because of lack of availability of serological tests.

Klebsiella pneumoniae and *Acinetobacter spp.* were the most common isolates in patients with mild to moderate COPD admitted to the respiratory ICU and to the ward. *Acinetobacter spp.*, however, was the most common isolate in patients with severe to very severe COPD in a study done by Khalid Eid *et al* [8]. Our results also agree with those of Hui *et al*. [9], who found that *Klebsiella spp.*, *P. aeruginosa*, and *Acinetobacter spp.* constitute a large proportion of pathogens identified in patients with AECB.

In an Indian study by Anand Patel [10], *Streptococcus pneumoniae* (59%) was found to be the commonest isolate contrary to our study. Our study is in concordance with a study by Madhavi *et al* [11] who had found *Klebsiella pneumoniae* as the most common organism. Chawla *et al* [12] reported *Pseudomonas aeruginosa* as the most common organism.

Local microbial profile is almost similar to the bacteriological profile noted in our study. In Kaliparambil Sugathan Roshni *et al* [13] gram negative bacteria were isolated commonly in COPD patients. However in a study by Rao D S *Streptococcal pneumoniae* was the most common organism isolated. [14] Rao *et al* [15] found in their study that *Klebsiella pneumoniae* was the most common organism isolated (22%) followed by *Streptococcus pneumoniae*, *Pseudomonas*, *Haemophilus* and *Staphylococcus aureus*.

In studies done by Sharma *et al* [16] and Madhu *et al* [17] *Klebsiella pneumoniae* was the most common organism causing acute exacerbations in COPD patients in last two decades. Gram negative organisms were the most predominantly isolated organisms in a study by M f Aleemullah *et al* [18] (62.3%), Gram positive bacteria in 37.61% and mixed infections in 15.6% patients.

MiravittlesM *et al* [19] found that *Haemophilus influenzae* was the most common organism isolated followed by *P. Aeruginosa*, *Streptococcus pneumoniae* and *Moraxella catarrhalis*.

Antibiogram in our study revealed that *piperacillin-tazobactam* is highly effective with sensitivity of 92% which is not in concordance with the study done by Prakhar sharma *et al* [7] which showed much higher resistance to the above drug (37.6%). Similar to our study the combination of *piperacillin-tazobactam* combination was highly effective in a study done by Anand K Patel [10]. Rakesh *et al* also showed in their study that *piperacillin-tazobactam* was sensitive to most of the organisms [6]. Newer *quinolones levofloxacin* and *moxifloxacin* showed significant resistance (44.2% and 37.6% respectively) in the study done by Prakharsharma *et al* [7] results of which are nearer to our study. Sensitivity to *cefoperazone – sulbactam* combination was almost similar to piperacillin-tazobactam combination in our study which is in agreement with the study done by Anand K patel. [10] Rao D S *et al* found in their study that most of the organisms were sensitive to *Amikacin*, *Gentamycin* and *Amikacin* [14].

Conclusion:

Bacterial pathogens play an important role in acute exacerbations of COPD. Sputum culture is an effective investigation to study the etiology of exacerbation. In centres where there is no culture facility simple gram stain can be done. Information about the local bacteriological profile and resistance patterns is highly warranted to reduce the emergence of antibiotic resistance. Such studies are regularly required to prevent morbidity and mortality.

Conflicts of interest: Nil

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