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Original Article

Sputum bacterial profile and antibiotics sensitivity pattern in acute exacerbation of chronic obstructive pulmonary disease

Pulmonology

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ABSTRACT

Background: Constant microbiologic screening of patients with acute exacerbation of chronic obstructive pulmonary disease (AECOPD) is vital to control the possible alteration of pathogens, as well as their antibiotic resistance.

Objective: to identify sputum bacterial profile and antibiotics sensitivity in patients with AECOPD aiming to adjust antibiotics use and reduce antibiotics resistance.

Methodology: This cross-sectional study was conducted on 100 patients with AECOPD. The total and differential leucocytic count, spirometric-indices, sputum gram stain, sputum semi-quantitative culture using colony forming unit (CFU) were done for all patients. Additionally, assessments of the sensitivity of the isolated pathogenic bacterial species were done for 25 antibiotics by disk diffusion method.

Results: by sputum semi-quantitative culture 28% of the studied patients have non-pathogenic bacterial growth (i.e., growth of normal flora) and 72% have pathogenic bacterial growth. Among those with pathogenic bacterial growth the isolated bacterial species in descending order were klebsiella (40.3%), staphylococcus aureus (19.4%), pseudomonas (12.5%), streptococcal pneumoniae, E. coli (8.3% each), acinetobacter (6.9%), citrobacter (2.8%) and enterobacter (1.4%). The most predictive factors for bacterial etiology in AECOPD in descending orders were decreased blood eosinophils % (B = - 0.16), increased blood neutrophils % (B = 0.04), increased blood lymphocytes (B = 0.02), and lower FEV_1% (B = - 0.01). Levofloxacin was the most sensitive antibiotics (91.7%), followed by amikacin (88.9%), ciprofloxacin (87.5%) and gentamycin (87.5%) then imipenem (81.7%) and ofloxacin (76.4%). On the other hand, linezolid and vancomycin were the most resistant antibiotics (95.8% each), followed by clindamycin and cefotaxime (91.7% each) then colistin sulphate and tetracycline (90.3% each).

Conclusion: Gram-negative bacterial species especially klebsiella was the most prevalent organism's in AECOPD. The isolated bacterial species were sensitive mainly to quinolones, gentamycin, amikacin, and imipenem, while it was mainly resistant to clindamycin, cefotaxime, colistin sulphate, tetracycline.

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INTRODUCTION

Chronic obstructive pulmonary disease (COPD) is currently the 4th leading cause of death in the world and is projected to be the 3rd leading cause [1]. Natural history of COPD is interrupted by exacerbations, which is defined as a continuous worsening of the patients' condition from the stable state and beyond day-to-day variation that is acute in onset and mandate change in regular medications. Frequent exacerbations are coupled with an accelerated decrease of lung function, reduced physical activity, poorer quality of life, and an increased risk for mortality [2]. Numerous factors are identified to cause an acute exacerbation of COPD (AECOPD) including respiratory tract infection and environmental factors. About half of exacerbations are believed to be triggered by a bacterial infection [3].

Patients with COPD have alterations in their lung microbiome that may result in persistent infection with

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potentially pathogenic microbes, even in stages of clinical stability and associated with a higher rate of bacterial exacerbations. Patients with this infective phenotype may necessitate a personalized approach to treatment with use of short-term or long-term antibiotics therapy in adjunct to the usual COPD medications [4].

Continuous microbiologic screening of patients with AECOPD is essential to control the possible change of pathogens, as well as their level of antibiotic resistance [5]. Sputum culture is an efficient investigation to study the cause of exacerbation. In centers where there is no culture facility, simple gram stain can be performed. Information about local microbiological profile in COPD patients would improve in better choice of antibiotics for empirical therapy. Additionally, knowledge about the local bacterial profile and resistance patterns is extremely warranted to lessen the emergence of antibiotic resistance [6]. In the early treatment of patients with AECOPD, empirical antibiotic selection is very important for patient recovery. With constantly changing bacterial flora of AECOPD, choice of antibiotic should be based on the local bacterial resistance pattern. Bacterial flora of AECOPD keeps changing from time to time and choice of antibiotic depends upon the local bacterial prevalence and resistance pattern [2]. A meta-analysis study reported that bacterial infections are an important risk factor for AECOPD. In fact, after a decreasing rate of bacterial prevalence in AECOPD studies, an increasing shift is seen after 2005 and continues almost steadily [7]. Therefore, it seems that bacterial infection was noted to be more prevalent in studies published after 2005. In view of very limited data about bacteriological profile in AECOPD patients in Egypt, the present study was undertaken to identify sputum bacterial profile and antibiotics sensitivity in patients with AECOPD aiming to adjust antibiotics use and reduce antibiotics resistance.

SUBJECTS AND METHODS

Type, place, and time of the study

This cross-sectional study was conducted at chest diseases department, Al-Zahraa University Hospital, Cairo, Egypt, after approval by the institutional review board of faculty of medicine for girls (IRB 2019010171). Participation was voluntary; an informed written consent was obtained from each participant before enrolment into the study. It was conducted in period from November 2019-August 2020.

Study participants

The inclusion criteria were patients who had been diagnosed with AECOPD; 100 patients from a total of 217. Clinically, an exacerbation was defined as a worsening of respiratory symptoms that led the patient to contact health-care facilities and assessed using the Anthonisen et al.[8]criteria.The diagnosis and severity of COPD was done according to the modified criteria defined in GOLD [9](had irreversible/partially reversible airflow obstruction (post-bronchodilator $FEV_1/FVC\%$ <0.7,FEV_1<80% of percent predicted and an increase in FEV_1< 200 mL, or < 12% of baseline measurements 20 minutes after inhalation Salbutamol (400µg) given via a metered-dose inhaler).

The exclusion criteria were refused to participate into the study (27 patients), chest radiography showing evidence of bronchiectasis (15 patients) or pneumonia (7 patients), inability to perform spirometric test (21 patients) or reversible airway obstruction (13 patients), bad quality sputum collection (24 patients), and exacerbation or antecedent use of an antibiotic in the month prior to enrollment (10 patients) (figure 1).

Study tools

All patients were subjected to detailed medical history taken and clinical examination to diagnose AECOPD. Spirometry was performed using (FUKUDa DENSHI Spirosift SP-5000, Japan). The following parameters were recorded FEV_1% percent predicted, FVC% percent predicted, FEV_1/FVC ratio, and 25%-75% percent predicted. Spirometric-indices were calculated using the best out of three technically satisfactory performances in agreement with the European Respiratory Society [10]. Before starting empirical antibiotic therapy, blood samples were collected for total and differential leucocytic count using a hematological analyzer (Sysmex XE-21N, Kobe, Japan). The following indices were recorded; total leucocytic count (TLC)/cm^3, neutrophils %, lymphocytes %, and eosinophils %. These indices were categorized into normal, decreased or increased according to the following cutoff: 4.5-10/ cm^3 for TLC, 45-75% for neutrophils, 20-40% for lymphocytes [11], and ≥ 2% for eosinophils [12].

Within maximum 24 h of hospital admission, sputum samples were collected before beginning antibiotics treatment according to standard guideline [13]. The patients were asked to collect sputum into a universal sterile wide mouthed container with a screw cap after washing the mouth twice with water and antiseptic solution to avoid oral contamination of the sample collected. Specimens were transported to microbiology laboratory and processed within two hours. Sputum samples were examined for gram stain, semi-quantitative aerobic culture with colony forming unit (CFU).

According to the gram stain pattern, the studied AECOPD patients were classified:1) Gram-positive organisms and 2) Gram-negative organisms. Additionally, based on sputum culture and CFU count the studied patients with bacterial growth were divided into; 1) Growth of non-pathogenic organisms (either growth of normal respiratory flora or growth of other organisms with CFU < 10^4 /ml), 2) Growth of pathogenic organisms (CFU count ≥ 10^4 /ml).

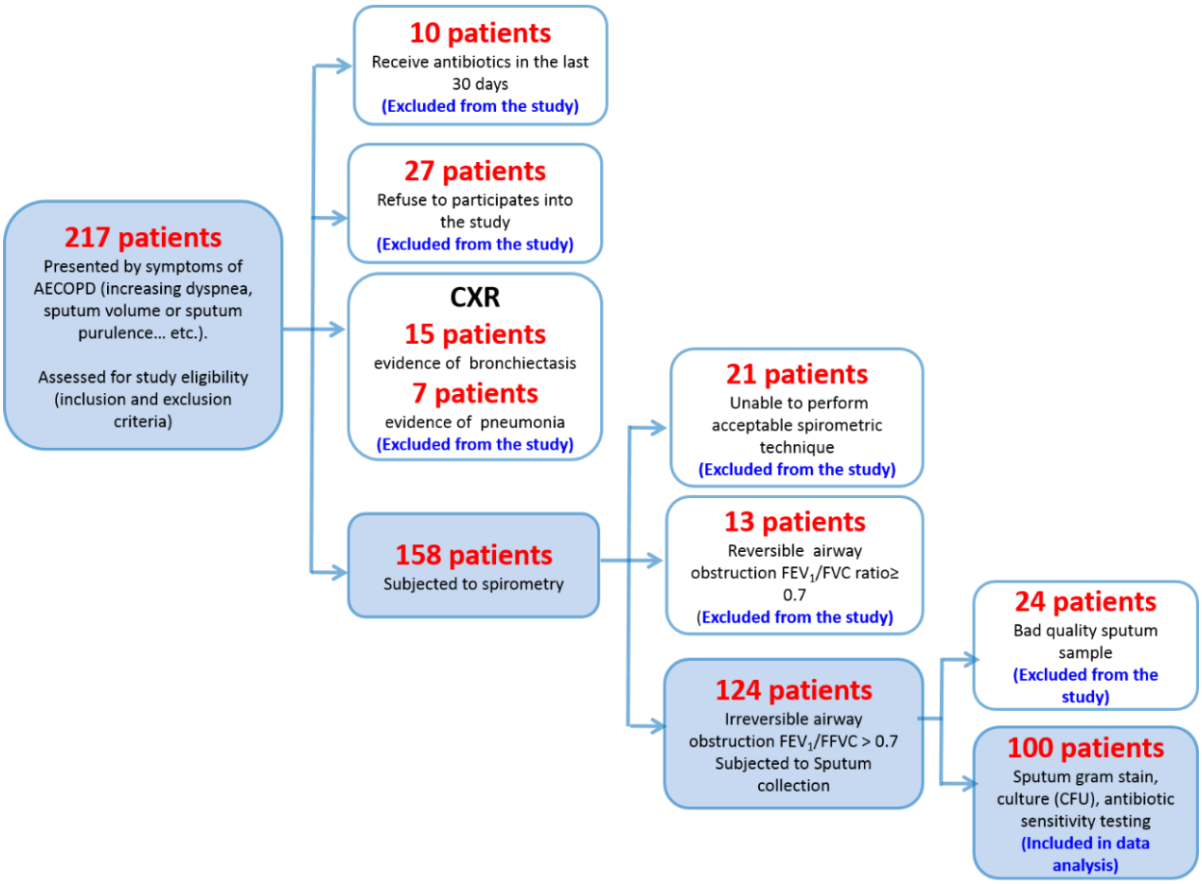


Figure (1): Flow chart for the studied participants

Moreover, antibiotic sensitivity testing using disk-diffusion method were done for the most used antibiotics in our institute. Based on the zone of inhibition around each disk the isolate was categorized as susceptible (sensitive), intermediately susceptible (moderately sensitive) or resistant. In the current study for simplicity of data presentation both susceptible (highly sensitive), and intermediate (moderately sensitive) were grouped and expressed as sensitive antibiotics while resistant one was expressed as resistant antibiotic.

Statistical analysis

The data were collected, coded, anonymized, and then analyzed by statistical package for social science (SPSS) program on windows XP version 17.0 (SPSS Inc.; Chicago, USA). Descriptive analysis was done, and the results were expressed as mean ±SD for quantitative continuous variables, and as number and percentages for qualitative (categorical and nominal) variables. Multivariate regression analysis was used to assess the most significant predictive factors for bacterial infections. The statistical significance was determined at a p-value <0.05 (confidence interval 95%).

RESULTS

The mean ±SD of age of the studied patients was 62.2 ± 7.8 with male predominance (91%). Most of studied patients (93%) were smokers with 61.4 ± 18.9 pack/year (table 1). Among the studied patents 58% have moderate COPD, 31% have severe COPD and 11% have very severe COPD (table 2). Regarding total and differential leucocytes indices, 34% of the studied patents have leukocytosis, 40% have neutrophilia, 7% have lymphocytosis, 14% have lymphopenia and 25% have eosinophilia (table 3).

Table (4) and figure (2) revealed that by gram stain; 48% of the studied patients have gram-positive organisms, and 52% have gram-negative organisms. While, by sputum culture; 28% of the studied patients have non-pathogenic organisms (growth of normal flora) and 72% have pathogenic organisms. Among the studied patients with pathogenic organisms the isolated bacterial species in descending order were klebsiella pneumonia (40.3%), staphylococcus aureus (19.4%), pseudomonas aeruginosa (12.5%), streptococcal pneumoniae and E. coli (8.3% each one), acinetobacter (6.9%), citrobacter (2.8%) and enterobacter (1.4%) (table 4 and figure 2).

Table (5) demonstrated that the most predictive factors of bacterial infection in patients with AECOPD in descending orders were decreased blood eosinophils % (p = 0.005, B = - 0.16), increased blood neutrophils % (p 0.001, B = 0.04), increased blood lymphocytes (p 0.001, B = 0.02), and lower FEV_1% (p = 0.006, B = - 0.01).

Figure (3) demonstrated that in the studied patients with AECOPD, levofloxacin was the most sensitive antibiotic (91.7%), followed by amikacin (88.9%), ciprofloxacin (87.5%) and gentamycin (87.5%) then imipenem (81.7%) and ofloxacin (76.4%). On the other hand, linezolid and vancomycin were the most resistant antibiotics (95.8% each), followed by clindamycin and cefotaxime (91.7% each) then colistin sulphate and tetracycline (90.3% each).

Table (1): Description of demographic data in the studied patients

Demographic data		AECOPD patients (n=100)
Sex	Male	91 (91%)
	Female	9 (9%)
Age (years)	Mean ±SD	62.2 ± 7.8
Smoking status	Smokers	93 (93%)
	Non-smokers	7 (7%)
Smoking (pack/year)	Mean ±SD	61.4 ± 18.9

Table (2): Spirometric indices and COPD severity of the studied patients

Spirometric-indices		AECOPD patients (n=100)
Post BD FEV_1/FVC ratio (Mean ±SD)		63.5 ± 4.5
FEV_1% (Mean ±SD)		53.2 ± 14.3
FVC% (Mean ±SD)		74.9 ± 14.8
FEF 25-75% (Mean ±SD)		51.4 ± 8.8
COPD severity	Moderate	58 (58%)
	Severe	31 (31%)
	Very severe	11 (11%)

FEV_1: forced expiratory volume in first second, FVC: forced vital capacity, FEF25-75: forced expiratory flow at 25-75 of vital capacity.

Table (3): Description of total leucocytes-indices and its status among the studied patients

Leucocytes– indices		AECOPD patients (n=100)
TLC/cm^3	Mean ±SD	9.5 ± 3.6
TLC status	Normal	66 (66%)
	Leukocytosis	34 (34%)
Neutrophils %	Mean ±SD	71.6 ± 12
Neutrophil status	Normal	60 (60%)
	Neutrophilia	40 (40%)
Lymphocytes %	Mean ±SD	27.6 ± 8.2
Lymphocytes status	Normal	79 (79%)
	Lymphocytosis	7 (7%)
	Lymphopenia	14 (14%)
Eosinophils %	Mean ±SD	2.07 ± 0.9
Eosinophils status	Normal	75 (75%)
	Eosinophilia	25 (25%)

TLC: total leucocyte count

Table (4): Classification of the studied patients according to sputum gram stain pattern and sputum bacterial culture

Item		AECOPD patients (n=100)
Gram stain	Gram-positive organisms	48 (48%)
	Gram-negative organisms	52 (52%)
Sputum culture	Non-pathogenic bacterial growth	28 (28%)
	Pathogenic bacterial growth	72 (72%)

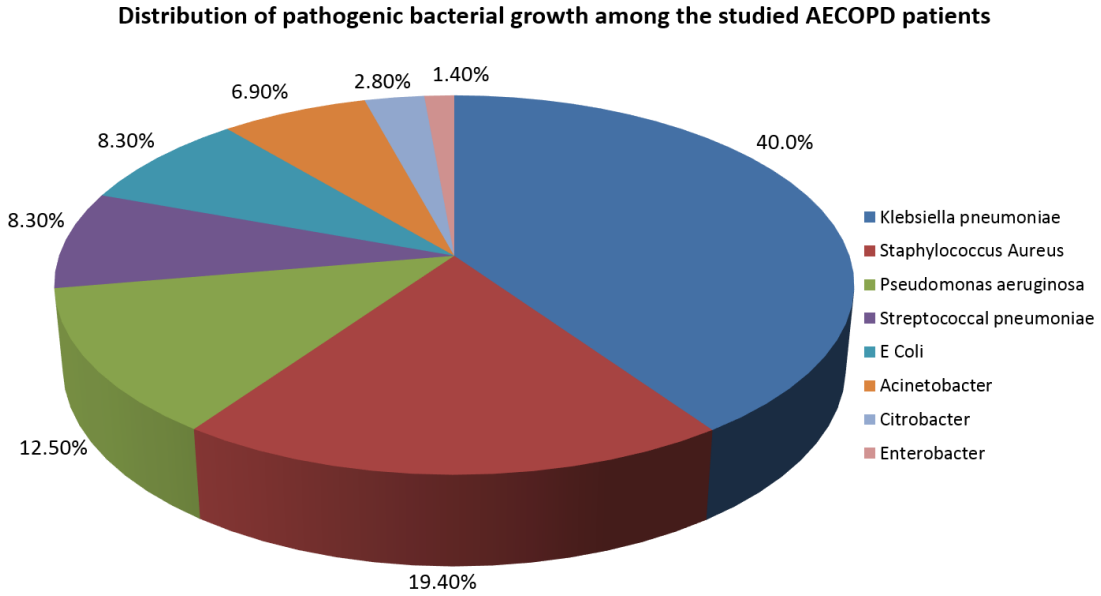
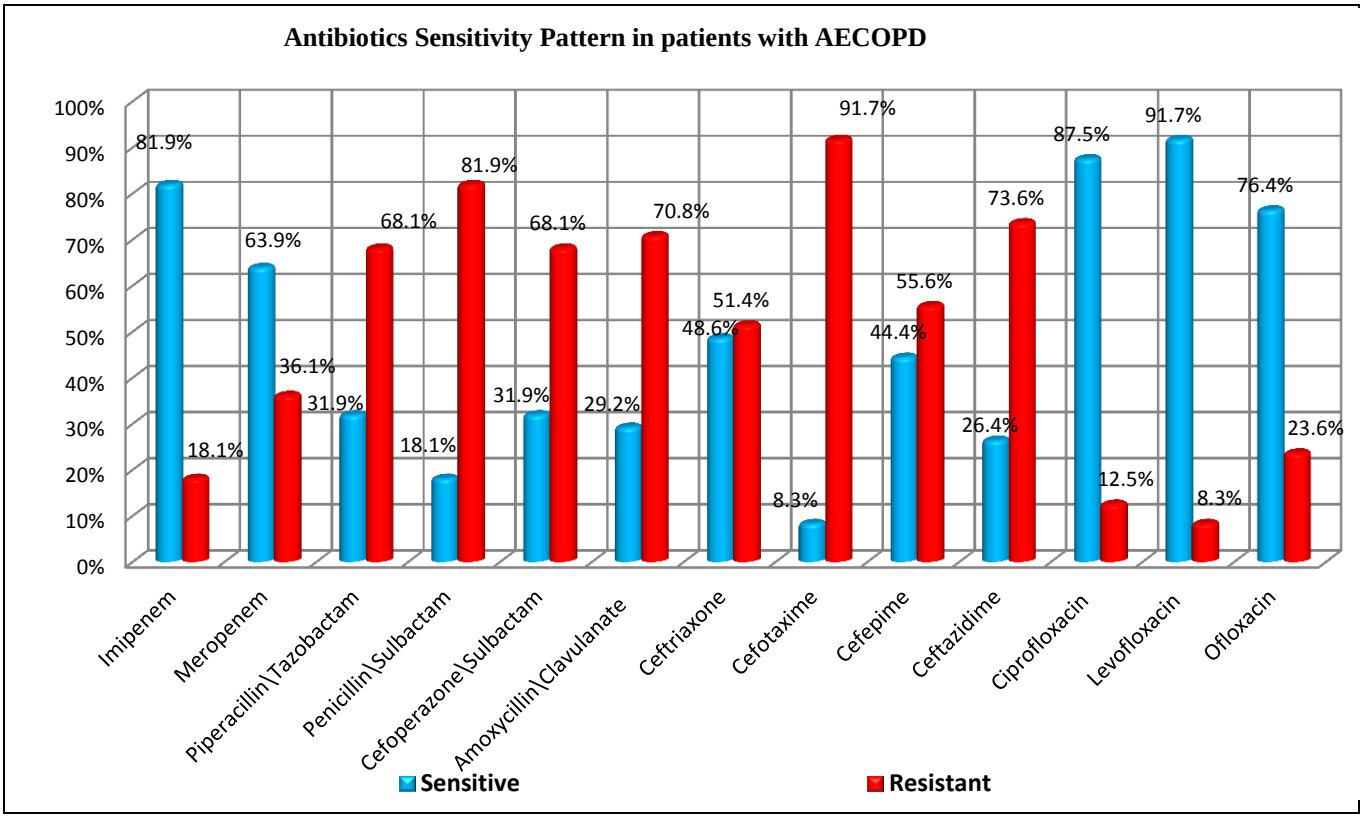


Figure (2): Distribution of pathogenic bacterial growth among the studied AECOPD patients

Table (5): Multivariate logistic regression analysis for factors predicting bacterial infections in the in AECOPD (No. = 100)

Item	B	SE	P	95% CL	
(Constant)	0.20	1.12	0.857	- 2.03	2.44
Sex	0.15	0.21	0.475	- 0.26	0.56
Age (years)	0.00	0.01	0.447	- 0.02	0.01
Smoking (pack\year)	- 0.003	0.002	0.224	- 0.01	0.002
Comorbidities	0.01	0.01	0.658	- 0.02	0.03
Post PD FEV_1/FVC ratio	- 0.01	0.01	0.467	- 0.03	0.01
FEV_1%	- 0.01	0.004	0.006	- 0.02	- 0.004
FVC%	0.01	0.004	0.254	- 0.004	0.01
FEF 25-75%%	- 0.002	0.01	0.847	- 0.02	0.02
COPD Severity	- 0.04	0.13	0.782	- 0.29	0.22
TLC/ cm^3	- 0.02	0.02	0.261	- 0.05	0.01
TLC stats	- 0.26	0.14	0.054	- 0.53	0.01
Neutrophils%	0.04	0.004	0.001	0.03	0.05
Neutrophil status	0.10	0.11	0.358	- 0.12	0.32
Lymphocytes%	0.02	0.01	0.001	0.01	0.03
Lymphocytes status	0.08	0.04	0.07	- 0.01	0.16
Eosinophils %	- 0.16	0.06	0.005	- 0.28	- 0.05
Eosinophil status	0.20	0.11	0.088	- 0.03	0.42

B: Regression coefficient, SE: Standard error, CL: Confidence interval. FEV_1: forced expiratory volume in first second, FVC: forced vital capacity, FEF25-75: forced expiratory flow at 25-75 of vital capacity, TLC: total leucocyte count.



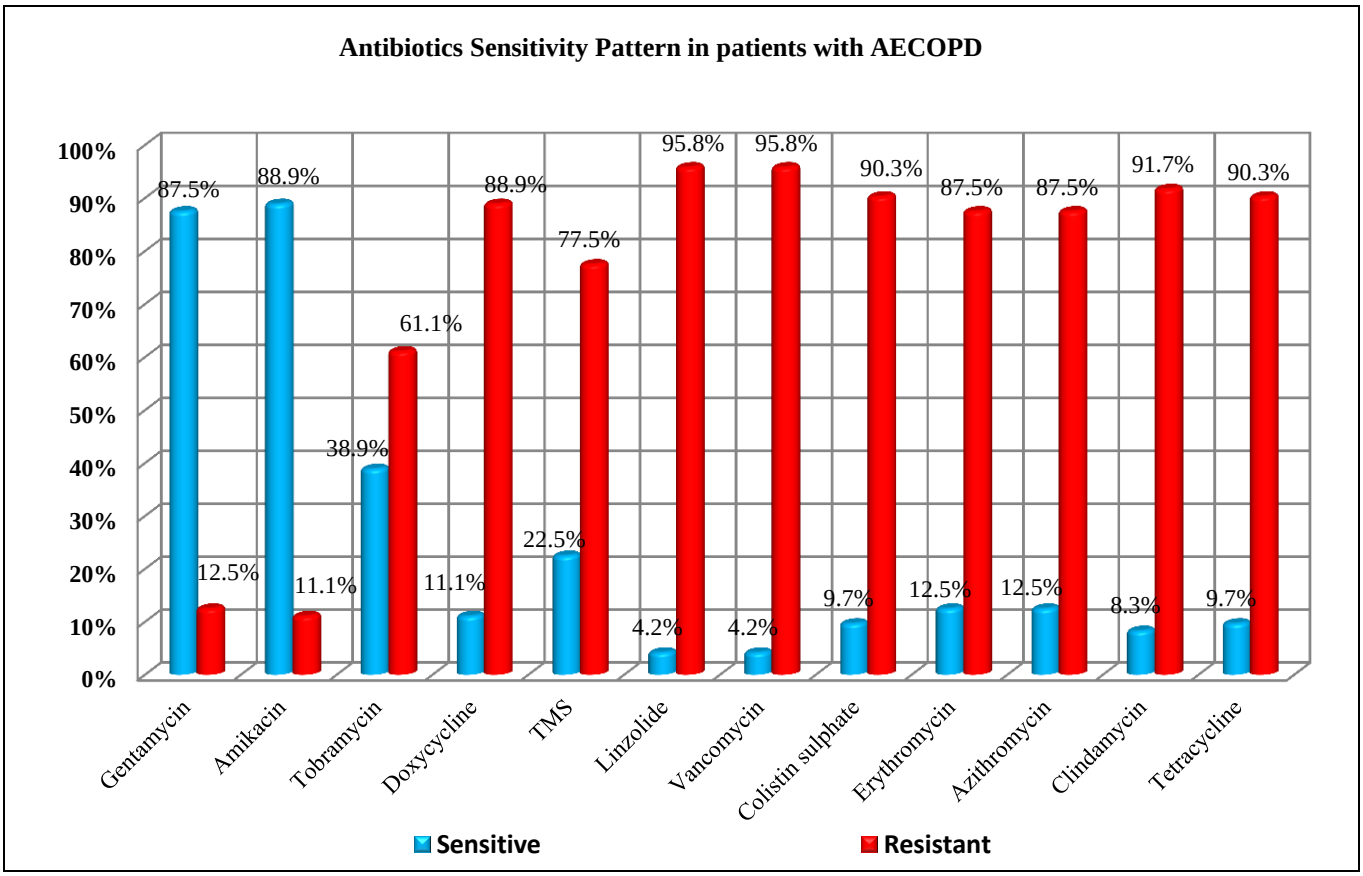


Figure (3): Antibiotics sensitivity pattern in AECOPD patients with bacterial growth

DISCUSSION

Exacerbations add to burden of COPD disease leading to increased morbidity and mortality[6].Bacterial flora of AECOPD keeps varying from time to time and choice of antibiotic depends upon the local bacterial prevalence and resistance pattern[2].Because sputum bacterial culture services are either not accessible or are not sufficiently utilized particularly in outpatients setting in our country, it is better to identify the pattern of bacterial flora and their antibiotic susceptibility pattern of a certain geographical region. Thus, we aimed to identify sputum bacterial profile and antibiotics sensitivity in patients with AECOPD aiming to adjust antibiotics use and reduce antibiotics resistance.

In the current study by using sputum culture 28% of the studied patients have non-pathogenic bacterial growth (growth of normal flora) and 72% have pathogenic bacterial growth. This means that bacterial infection is the responsible etiological agents in high proportion of AECOPD patients. A complex host–pathogen interaction in the airways determines the outcome of each new bacterial strain acquisition in COPD, and the balance between host defense and pathogen virulence determines the level of proliferation of the pathogen, which, in turn, determines the increase in airway inflammation. Large increases in airway inflammation in bacterial infections result in greater physiological changes, with subsequent changes in symptoms to be identified as an AECOPD[14].Since lung microbiome dysbiosis is a major cause of chronic respiratory complications that can disturb homeostasis in the lung resulting in lung inflammation and infection[15].Similarly, Mangla et al. [16]reported that a total 72% of AECOPD patients had positive sputum culture and in 28 % of patients no organisms were isolated. Erkan et al. [17] reported that an infectious agent was identified in 61.3% of patients, either serologically or with sputum culture. Many other studies reported lower prevalence of bacterial etiology in AECOPD;50% [18], 48.7 % [2], 47.22% [19],37%[20], and 34.7% [21]. Moghoofei et al. [7] in their meta-analysis reported that he overall estimation of the prevalence of bacterial infection in AECOPD was 49.59%. This variation in the relative incidence of isolated bacteria in studies may be attributed to patient's inclusion criteria and used sputum culture techniques.

Among our studied patients with pathogenic bacterial growth there was predominance of gram-negative bacteria as the isolated bacterial species in descending order were K. pneumonia (40.3%), S. aureus (19.4%), P. aeruginosa (12.5%), S. pneumoniae and E. coli (8.3% each), acinetobacter (6.9%), citrobacter (2.8%) and enterobacter (1.4%). Similar results were reported in Egypt and India with predominance of gram-negative bacteria with K. pneumonia, P. aeruginosa and acinetobacter reported as the most common isolates followed by S. aureus [22][23][24]. Additionally, klebsiella pneumonia was the most common isolates [25]. Moreover, one previous study reported approximately the same prevalence of P. aeruginosa (10.1%) [21]. Kuwal and Joshi [19] found that the P. aeruginosa was the most predominant organism (38.23%) followed by *klebsiella* (29.41%), *S. aureus* (23.53%), *S. pneumoniae* (5.88%) and *acinetobacter* (2.94%). Mangla et al. [16] reported that 32% of cases were found to be infected with pseudomonas species, 12% of streptococcus pneumoniae, 6% streptococcus pyogenes, 8% klebsiella pneumoniae, 4% E. coli, 6% H. influenza. Saad et al. [26] reported that the bacteria isolated were H. influenzae in 42 cases, pseudomonas in 37 cases, S. pneumoniae in 18 cases, and acinetobacter in 14 cases. Sharma et al. [2] reported that collectively, gram-negative bacteria were the predominant etiological agent (35.7%). However, S. pneumoniae was the most common isolated organism (13%), among gram-negative bacteria, E. coli (9.4%) was the most isolated organism followed by acinetobacter (8.1%), P. aeruginosa (7.5%) and klebsiella (6.3%). Several previous studies have implicated P. aeruginosa and klebsiella as the most common organisms responsible for AECOPD, E. coli and acinetobacter species have not yet been reported in studies as a major etiological risk for AECOPD [25]]27].

In contrast, Gad and Agmy [28]in upper Egypt found that the predominant isolates in 376 patients with AECOPD were H. Influenzae (32%), streptococcus pneumonia (30%), M. catarrhalis (14%), klebsiella pneumoniae (10%) and chlamydia pneumoniae (7%). Bisenova and Yergalieva [29] found that the etiological structure of sputum showed that streptococcus pneumoniae (40.4%) and M. catarrhalis (16.0%) were the most common pathogens from the total amount of isolates, S. aureus – 4.5%, P. aeruginosa (2.6%), streptococcus pyogenes (4.8%), candida albicans (1.6%), enterococcus (5.0%). Some studies in different countries reported that S. pneumoniae, H. influenzae or M. catarrhalis were the predominant isolates then come the gram-negative bacteria in AECOPD [4][17][18][30][31][32]. While Tanriverdi et al. [20] found that the most frequently isolated bacteria were H. influenzae (26.7%), pseudomonas (22.2%), streptococcus pneumonia (18.5%). Moreover, Ma et al. [33]and ElFeky et al. [34] reported predominance of S. pneumoniae, H. influenzae and M. catarrhalis in community-based outpatients and gram-negative bacilli from hospitalized patients. Moghoofei et al. [7] in their meta-analysis reported that the most common isolated pathogens were including H. influenzae, S. pneumoniae, klebsiella pneumoniae, S. aureus, M. catarrhalis, A. baumannii, and P. aeruginosa. This discrepancy in the incidence of isolated bacterial species in different studies may be related to different patient inclusion criteria and different sputum culture techniques.

The increased blood neutrophils% as a significant predictive for bacterial infections in our study (p 0.001, B = 0.04) may be explained by the fact that bacterial exacerbations induce neutrophilic inflow into the bronchial lumen. Subsequent activation and degranulation of the inflowed neutrophils in the lumen releases considerable amounts of proteolytic enzymes in the bronchi. The clinical correlates of this inflammatory process are increased secretions and bronchial obstruction, which is the cardinal symptoms of increased dyspnea, sputum production and sputum purulence [7]. Similarly, Sethi [35] reported that the neutrophilic airway inflammation is associated with isolation of bacterial pathogens from sputum. Sharma et al. [2] found that both leukocytosis and neutrophilia was noticed in patients with sputum bacterial growth. In contrast, the decreased blood eosinophils is a significant predictive factor for bacterial infection in our study (p = 0.005, B = - 0.16), may be attributed to the previously reported inverse relationship between eosinophils and bacterial infections, as blood eosinophil counts are known to be decreased during severe bacterial infection [36].On the other hand, bacterial infections are proven to cause eosinopenia and thepatients with eosinophils ≤2% may have greater bacterial colonization in the airways[37].

The lower FEV_1% (severity of COPD) as a significant predictive factor for bacterial growth in our studied patients (p = 0.006, B = - 0.01), may be attributed to that severe COPD is associated with structure changes in the airways, beside frequent hospital admission, both factors increase susceptible to colonization with potentially pathogenic organism especially gram-negative organisms. On the other hand, bacterial infection, increase sputum production and airways inflammation with subsequent increase of airways obstruction with more worsening of FEV_1%. Similar result was reported in previous studies as COPD severity was an important determinant of microorganism type, with gram-negative bacilli being associated with more severe cases [33][34][17]. Sharma et al. [2] found that the growth percentage of a pathogenic organism was found to be highest (71.4%) in severe obstruction followed by moderate obstruction (55.9%) and least (35.2%) in mild obstruction cases (p = 0.004). Kuwal and Joshi [19] found that the gram-negative bacteria were dominating in patients with stage III and stage IV COPD. Abdallah et al. [32] found that FEV_1<35 % were significantly associated with negative-gram bacteria. The identification of the predictive factors in this study could represent the first step in the development of a prediction paradigm for bacterial etiology in AECOPD. However, this potential model will require to undergo external confirmation with larger patient cohorts from several centers.

In our study we found that the most sensitive antibiotics were levofloxacin, followed by amikacin, ciprofloxacin, and gentamycin, then imipenem and ofloxacin. On the other hand, the most resistant antibiotics were linezolid and vancomycin, followed by clindamycin and cefotaxime, then colistin sulphate and tetracycline. This higher resistance rate could be due to injudicious use of antibiotics during previous COPD exacerbations, with subsequent development of antibiotics resistance. The excessive use of antibiotics contributes significantly to increasing bacterial resistance and increased medical costs and the risk of drug-related adverse events [38]. Similarly, Gad and Agmy [28]in upper Egypt found a higher sensitivity for moxifloxacin, levofloxacin, macrolides, and cefipime. A higher rate of resistance was recorded for tetracycline, first or second generations cephalosporins and gentamicin. Erkan et al. [17] noted poor efficacy of penicillin, ampicillin, amoxicillin-clavulanic acid, tetracycline, and erythromycin to most prevalent respiratory pathogens. In contrast, ciprofloxacin seems to be the most efficient drug for all microorganisms. Mangla et al. [16] found that the isolated organisms were most commonly sensitive to piperacillin and tazobactam, amikacin, azithromycin, ciprofloxacin. Moreover, Sharma et al. [2] found that S. pneumoniae, H. influenzae and M. catarrhalis were sensitive to fluoroquinolones, cephalosporins, aminoglycoside and piperacillin-tazobactam. However, gram-negative bacteria showed significant resistance to the above antibiotic groups. Colistin and Polymyxin B were the only effective antibiotics against all the isolated organisms.

As contamination by upper airway secretions which may frequently harbors potential pathogens is a main concern in sputum culture, therefore, the main strength of the current study is that we did semi-quantitative culture with CFU and culturing only good quality sputum. However, our study has some limitations that should be mentioned; First, viral and atypical bacteria were not evaluated in the current study, we would prefer to evaluate them, but the technical and financial obstacles prevented us from studying these agents. Second, the study was carried out at only one center in Egypt. Lastly, the small sample size limited the analysis of specific factors per organism.

CONCLUSIONS

Acute exacerbation of COPD is frequently associated with bacterial infections as 72% of patients with AECOPD have pathogenic bacterial growth. Gram-negative bacterial species were the most prevalent isolated organisms. The most common isolated organisms were klebsiella pneumonia, S. aureus, P. aeruginosa. Regarding antibiotics sensitivity, the quinolones, amikacin, gentamycin, and imipenem were the most sensitive antibiotics. While linezolid, vancomycin, clindamycin, and cefotaxime were the most resistant antibiotics**.** Therefore, we recommend that to improve and adjust antibiotics therapy it seems logical to evaluate the bacterial profile of AECOPD in a region

from time to time alongside with the antibiotic resistance pattern of the bacterium. Moreover, judicious use of antibiotics based on sputum culture and antibiogram seems to be the safest approach to prevent antibiotics resistance.

Future direction

- Periodic studies to detect possible pathogens and their antibiotic susceptibility pattern would help in formulating a cost-effective antibiotic policy lessening the development of drug resistance.
- A confirmation of our findings in a large international cohort of AECOPD is attractive.

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الملخص العربي

النمط البكتيري في البصاق ونمط الحساسية للمضادات الحيوية في التفاقم الحاد لمرض ضيق الشعب الهوائية المزمن

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ملخص البحث

الخلفية : المسح الجرثومي (البكتيري) المستمر لمرضى التفاقم الحاد لضيق الشعب الهوائي المزمن يُعد ضرورة للسيطرة على التغيرات المحتملة للجراثيم (للبكتيريا) ومقاومتها للمضادات الحيوية.

الهدف : التعرف على النمط البكتيرى في البصاق، وحساسيتها للمضادات الحيوية في مرضى التفاقم الحاد لضيق الشعب الهوائي المزمن بهدف (ضبط- تعديل- ترشيد) استخدام المضادات الحيوية والحد من المقاومة لها.

الطرق : تم تنفيذ هذه الدراسة المقطعية العرضية على 100 من مرضى التفاقم الحاد لضيق الشعب الهوائي المزمن، حيث تم عمل الفحوصات التالية: لكل مريض عدد كرات الدم البيضاء الكلى والنوعى، مؤشرات/ نسب مقياس التنفس، فحص البصاق بصبغة غرام، مزرعة البصاق الهوائية الشبه كمية واستخدام عدد وحدات المستوطنات البكتيرية، بالإضافة إلى تقييم حساسية الفصائل البكتيرية المعزولة ل25 مضاد حيوي باستخدام طريقة الانتشار القرصي.

النتائج: باستخدام مزرعة البصاق الكمية وُجِد أن 28% من المرضى المنوطين بالدراسة لديهم نمو بكتيريا غير ضارة، بينما 72% لديهم نمو بكتيريا ضارة، ومن بين هؤلاء الذين لديهم نمو بكتيريا ضارة تم عزل الفصائل البكتيرية التالية مرتبة تنازليا: كليبسيلا (40.3٪) ، المكورات العنقودية الذهبية (19.4٪) ، الزائفة الزنجارية (12.5٪) ، المكورات الرئوية العقدية، الإشريكية القولونية (8.3٪ لكل منهما)، الأسنتوبكتر 6.9)٪(، ستروبكتر (2.8٪) والأنتيروبكتر(1.4٪). ومن العوامل التنبؤية لوجود بكتيريا في مرضى التفاقم الحاد لضيق الشعب الهوائي المزمن نقص خلايا الحمضات بالدم، زادة خلايل النتروفيل بالدم، و نقص اقصى معدل للزفير في الثانية الأولى. بالنسبة لحساسية الميكروب للمضات الحيوية وجد أن ليفوفلوكساسين أكثر المضادات الحيوية حساسية (91.7 %)، يليه أميكاسين (88.9% و سيبروفلوكساسين وجنتاميسين (87.5% لكلا منهما)، ثم ايميبينيم (81.7%) و أوفلوكساسين (76.4%)، وعلى الصعيد الآخر يعتبر لينيزوليد وفانكوميسين أكثر المضادات الحيوية مقاومة (95.8% لكلا منهما) ، يليه كليندامايسين وسيفوتاكسيم (91.7% لكلا منهما) ثم كوليستين سلفات وتيتراسيكلين (90.3%لكلا منهما).

الاستنتاجات: تعد فصائل البكتيريا السالبة لصبغة غرام وخاصة كليبسيلا هي الأكثر انتشارا في مرضى التفاقم الحاد لضيق الشعب الهوائي المزمن، و أظهرت فصائل البكتيريا المعزولة حساسية للمضادات الحيوية التالية: لينيزوليد، فانكوميسين، كينولونز، جنتاميسين، أميكاسين، ايميبينيم، بينما أظهرت مقاومة للمضادات الحيوية التالية (كليندامايسين وسيفوتاكسيم وكوليستين سلفات و تيتراسيكلين).

الكلمات المفتاحية: التفاقم الحاد لمرض ضيق الشعب الهوائية المزمن، فصائل البكتيريا ، حساسية المضادات الحيوية، الحساسية البكتيرية.

الباحث الرئيسي

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