Research Article

Microbiological profile with antibiotic resistance pattern in patients of pneumonia in Iraq

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ABSTRACT

Background: Pneumonia is the most serious infectious disease. It is broadly defined as an infection of the lung parenchyma and is clinically divided into community-acquired pneumonia and nosocomial pneumonia. In general, bacteria are the etiology of pneumonia; however, the microbial pattern, the antimicrobial sensitivity, and emerging resistant pattern differ from place to another one. The major bacteria isolated in pneumonia disease are *Klebsiella pneumonia, Streptococcus pneumonia, Haemophilus influenza,* and *Staphylococcus aureus,* particularly in association with influenza virus infection. **Methodology:** One hundred and thirty-three isolated bacteria of pneumonia disease were collected from the Teaching Laboratory of Baghdad Medical City, Al-Zafrania hospital and General Hospital Salah Al-Deen in Baghdad and Salah Al-Deen, Iraq, from May 2017 to January 2018. Bacterial isolated had been identified according to the microscopic, biochemical tests, and cultural characteristics. Later, an antimicrobial sensitivity test was done to these bacterial isolates. **Results:** Of 133 bacterial isolates from pneumonia patients, 72 (54%) of the cases were *K. pneumonia*, 35 (26%) were *S. pneumonia,* and 26 (20%) were *Moraxella catarrhalis* bacteria. **Conclusion:** Bacteriological profile is important to determine empiric treatment for pneumonia disease. *K. pneumonia* showed higher susceptibility to imipenem and higher resistance to piperacillin; *S. pneumonia* showed high susceptibility to vancomycin and high resistance to erythromycin; and *M. catarrhalis* showed higher susceptibility to cefo and higher resistance to erythromycin. Empirical antibiotic therapy can help to decrease mortality and improve the recovery of the disease.

KEY WORDS: Antibiotic resistant, Bacteriological profile, Pneumonia

INTRODUCTION

Pneumonia is the most serious infectious disease. It is broadly defined as an infection of the lung parenchyma and is clinically divided into community-acquired pneumonia and nosocomial pneumonia. In general, bacteria are the etiology of pneumonia; however, the microbial pattern, the antimicrobial sensitivity, and emerging resistant pattern differ from place to another one.[1] The major bacteria isolated in pneumonia disease are *Klebsiella pneumonia*, *Streptococcus pneumonia*, *Haemophilus influenza,* and *Staphylococcus aureus,* particularly in association with influenza virus infection. *Mycoplasma pneumoniae* infection forms a sizeable group in viral and atypical pneumonia.[2] Patients with co-existing illnesses such as diabetes mellitus, congestive heart failure, coronary artery disease, renal failure, chronic neurological disease, malignancy, and chronic liver disease have increased the incidence of pneumonia.[3] The resistant to antimicrobial drugs has been increased exponentially with the recent decades because of the broad-spectrum of antimicrobial drugs as well as more exposures to cross-infection.[4,5] The microbiological diagnosis is essential for guiding pneumonia treatment leading to an effective and target choice of antibiotic as well as decreasing the associated impact of the unnecessary use of broad-spectrum antibiotics or ineffective empiric antibiotic regimens.[6] The aim of the present study is to evaluate the microbiological profile and determine drug resistance pattern of pneumonia patients.

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MATERIALS AND METHODS

Collection and Identification of Bacterial Isolated

One hundred and thirty-three isolated bacteria were collected from the Teaching Laboratory of Baghdad Medical City, Al-Zafrania hospital and General Hospital Salah Al-Deen in Baghdad and Salah

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Al-Deen, Iraq of pneumonia patients from May 2017 to January 2018. Bacterial isolated had been identified according to the microscopic, biochemical tests, and cultural characteristics.[7]

Antimicrobial Sensitivity Test

Susceptibility testing was done using minimum inhibitory concentration breaking points. The antimicrobial agents tested were as follows: imipenem, amikacin, gentamicin, cefepime, piperacillin, vancomycin, ciprofloxacin, penicillin, tetracycline, erythromycin, cefotaxime, and augmentin. The antibiotic susceptibility test was performed according to the criteria of the Clinical and Laboratory Standards Institute (2016 guidelines).

Statistical Analysis

The data analysis was performed using the Statistical Package for the Social Sciences for Windows version 25. The ANOVA test was also used to determine the correlation of these data.

RESULTS

In this study, of the bacterial isolates were 72 (54%) *K. pneumonia*, 35 (26%) *S. pneumonia,* and 26 (20%) *Moraxella catarrhalis* bacteria [Figure 1].

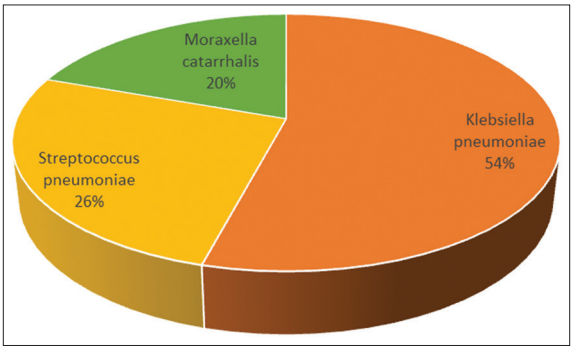

Figure 1: Distribution of isolated bacteria in pneumonia patients

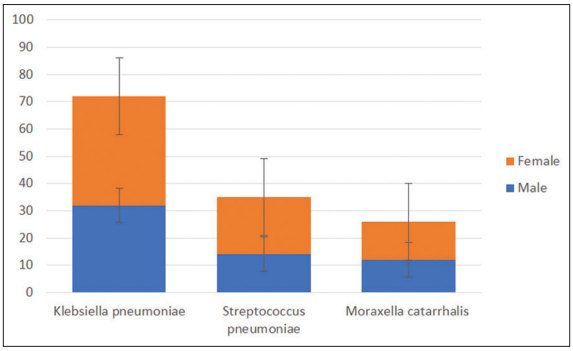

Figure 2: Distribution of the gender in isolated bacteria of pneumonia patients. Data were presented as *significant as $P < 0.05$, **highly significant as $P < 0.01$. $P = 0.017$

During this study, the majority of the patients were females (75; 56.39%) in comparison to the males (58; 43.61%) [Figure 2]. Of the participants, most of their ages were between 10 and 30 years followed by 31–45 years and older than 45 years [Figure 3].

K. pneumonia showed higher resistance to piperacillin (93.06%), following by cefepime (44.44%), gentamicin (34.72%), amikacin (26.39%), and imipenem (18.06%) [Figure 4]. *S. pneumonia* showed higher resistance to erythromycin (71.43%), tetracycline (57.14%), penicillin (25.71%), ciprofloxacin (20%), and vancomycin (11.43%) [Figure 5]. *M. catarrhalis* showed high resistance to erythromycin (73.08%), amikacin (23.08%), augmentin (19.23%), and cefo (15.38%) [Figure 6].

DISCUSSION

Pneumonia is a polymicrobial infection with high mortality rate disease.[8,9] Determining the bacterial etiology for pneumonia is very important to choose the proper treatment strategy and avoid the risk of antibiotic-resistance microorganisms treatment. In this study, the major pathogens isolated from pneumonia patients are *K. pneumonia* about 54% followed by 26% *S. pneumonia,* and 20% *M. catarrhalis* [Figure 1]. This is in accordance with Supriya *et al.,*[10]

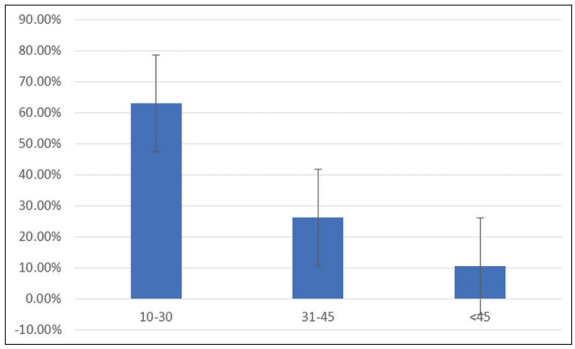

Figure 3: Distribution of age (years) among pneumonia patients. Data were presented as *significant as $P < 0.05$, **highly significant as $P < 0.01$

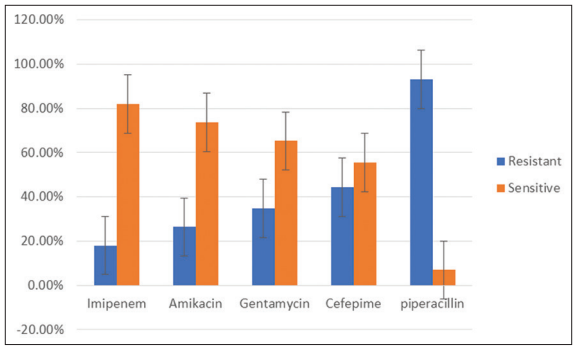

Figure 4: Antimicrobial-resistance patterns among pneumonia patients with *Klebsiella pneumonia.* Data were presented as *significant as $P < 0.05$, **highly significant as $P < 0.01$. $P = 0.637$

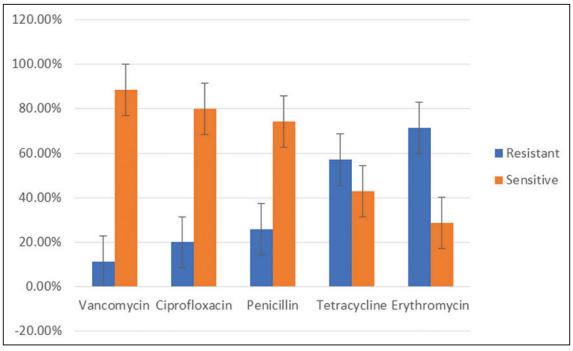

Figure 5: Antimicrobial-resistance patterns among pneumonia patients with *Streptococcus pneumonia.* Data were presented as *significant as $P < 0.05$, **highly significant as $P < 0.01$. $P = 0.322$

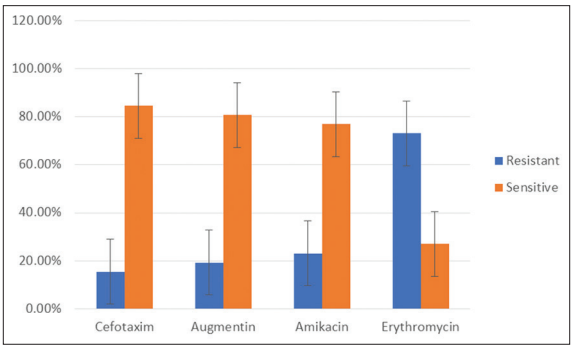

Figure 6: Antimicrobial-resistance patterns among pneumonia patients with *Moraxella catarrhalis.* Data were presented as *significant as $P < 0.05$, **highly significant as $P < 0.01$. $P = 0.290$

Song *et al.,*[11] and Acharya *et al.*[12] However, these results differ from Khalil *et al.*

K. pneumonia (Gram-negative capsule bacterium) showed higher resistance to piperacillin (93.06%) and less resistance to imipenem (18.06%). Bajpai *et al.,*[13] Assunção *et al.,*[14] and El-Sokkary *et al.,* in their study,[15] published analogous data. The main resistance of *K. pneumonia* is due to the expression of extended-spectrum ß-lactamases (ESBLs) that confers resistance against cephalosporins, penicillins, monobactams, and the expression of carbapenemases, which confers resistance against all β-lactams including carbapenems. In addition, the capsule of *K. pneumonia* (a polysaccharide matrix that coats the cell) is essential for the virulence and hypervirulent of this bacterium. However, these represent challenges in the management and treatment, especially in Asian countries (where most of the cases are reported).[16,17]

In this study, *S. pneumonia* (Gram-positive bacterium) showed higher resistance to erythromycin (71.43%) and less resistance to vancomycin (11.43%), and this is in accordance with the studies of Al-Muhairi *et al.*[18] and Shah *et al.*[19] and in contrast to the study of Mahendra *et al.*[20] The high resistance of this bacterium to macrolide (71.43%) and fluoroquinolone (20%) antibiotics increased recently than recent years 27.8% and 0.9% in 2002–2003 and 26.2% and 1.3% in 2003–2004[21] may because of the easy availability of the these drugs to treat suspected cases of bacterial pneumonia.

M. catarrhalis in this study showed high resistance to erythromycin (73.08%) and less resistance to cefotaxime (15.38%). The resistance of this bacterium to augmentin (amoxicillin-clavulanate) (19.23%) is increased than 0.25% in 2002–2004.[21]

Pneumonia is a polymicrobial infection with multidrug resistance disease. The guideline for pneumonia disease treatment is using beta-lactams (ceftriaxone, cefotaxime, ampicillin/sulbactam, and piperacillin/tazobactam) alone or in combination with macrolide or fluoroquinolone. The combination of fluoroquinolone and clindamycin should be preferred in allergy cases if present.[22] Local resistance should be considered while evaluating the potential efficacy of antimicrobial treatment. As the antibiotic resistance increases with time, drug efficacy changed during the disease progression.

CONCLUSION

Pneumonia is an infectious disease with high prevalence and mortality worldwide. Determining the bacteriological profile can help to choose the best antibiotics that target specific pathogens and improve antibiotic resistance crisis, especially multidrug resistant and ESBLs.

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