



STUDY OF BACTERIAL PATHOGENS AND THEIR ANTIBIOGRAM IN PULMONARY SAMPLES AT A RESPIRATORY CARE CENTRE IN HYDERABAD, INDIA

Medical Microbiology

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ABSTRACT

Introduction: Lower respiratory tract infections are among the most common infectious diseases of humans worldwide and also a great challenge to the clinicians due to the increasing antimicrobial resistance. **Aim:** To identify the pathogens and their antibiotic sensitivity pattern from pulmonary samples of patients suspected to have LRTI. **Materials And Methods:** A retrospective study was conducted from August 2022 to January 2023 at a respiratory care centre. A total of 1977 samples were included. These samples were inoculated on Blood Agar and MacConkey agar. Identification of bacterial isolates was done by colony characteristics and biochemical tests. Antibiotic sensitivity was done by Kirby Bauer disc diffusion method on Mueller-Hinton agar using the appropriate antibiotic discs. **Results:** Out of 1977 samples, 68 were found to be culture positive out of which 48(70%) were from sputum sample, 8(11.7%) from bronchial wash, 11(16%) from pleural fluid and 1 (1.4%) from ETT secretion. Male patients 51(75%) were more than female patients 17(25%). In-patients 66(97%) more than outpatients 2(2.9%). Out of 66 inpatients, 60 (88.2%) were ward patients and 8(11.7%) were ICU patients. *Pseudomonas aeruginosa* 32(47%) was the most common organism isolated followed by *Klebsiella pneumoniae* 23(33.8%), *Acinetobacter* 8(11.7%), and *Staphylococcus aureus* 5(7.3%). Out of the 5 *Staphylococcus aureus*, 1 was found to be Methicillin Resistant *Staphylococcus aureus*. **Conclusion:** Bacterial isolates showed resistance to common antibiotics. Therefore, proper diagnosis and identification of the pathogenic microorganisms by culture and sensitivity test is vital for appropriate management of LRTIs.

KEYWORDS

LRTI, Bacterial Profile, Susceptibility Pattern, Respiratory Sample.

INTRODUCTION:

Lower respiratory tract infection (LRTI) is defined as the inflammation of the respiratory tract from trachea to the alveoli. It includes Pneumonia, Tracheobronchitis, Bronchitis, Bronchiectasis, Lung abscess and Empyema. LRTIs are responsible for 4.4% of all hospital admissions and 6% of all outpatient clinic [1,3,5]. LRTI is the leading cause of morbidity and mortality in critically ill patients in developing countries. LRTIs are often misdiagnosed, mistreated and underestimated due to its non-specific presentation in community or hospital setting [1]. The major respiratory pathogens are Gram-negative bacilli like *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Acinetobacter* species and Gram-positive organisms like *Staphylococcus aureus*, *Streptococcus pneumoniae* etc. The incidence and associated mortality due to LRTI can be influenced by several factors including characteristics of the population at risk, standard of health care facilities available, immunosuppressive drugs, improper antibiotic therapy, distribution of causative agents and prevalence of antimicrobial resistance[2]. The rise of antimicrobial resistance among the respiratory pathogens presumably due to the prophylactic administration of antibacterial therapy even before the availability of culture reports is a matter of potential concern worldwide[5].

Aim Of The Study: This study is conducted to identify the pathogenic micro-organisms and their antibiotic sensitivity pattern from pulmonary samples of patients suspected to have LRTI.

MATERIALS AND METHODS:

A retrospective study was conducted from August 2022 to January 2023 at a tertiary respiratory care centre, Hyderabad. A total of 1977 respiratory samples such as sputum, bronchial wash, endotracheal tube secretion and pleural fluid were received at Microbiology department from patients suspected to have LRTI in out-patients and in-patients.

Sample processing: Sputum samples were collected in a sterile wide mouth container by the patient with the instructions given by the Lab tech or nurses. Sputum samples were accepted based on Bartlett's grading.

Endotracheal tube secretions were collected by clinicians in a sterile container. Secretions were inoculated in liquid broth and solid media. Bronchial wash and pleural fluid samples were collected by clinicians in sterile container.

Direct Grams stain was done for all samples and then inoculated on Blood agar and MacConkey agar, and incubated at 37 C for 18-24 hours. All the bacterial isolated were identified using colony morphology, Gram stain and biochemical reactions according to standard recommendations. Antibiotic sensitivity of the isolated organisms was done by Kirby Bauer disc diffusion method on Mueller-Hinton agar as per Clinical Laboratory Standards Institute (CLSI) guidelines using appropriate antibiotic discs.

RESULTS:

Out of 1977 samples, 68 were found to be culture positive. Out of the 68 culture positive samples 48 (70%) were from sputum sample, 8 (11.7%) from bronchial wash, 11 (16%) from pleural fluid and 1 (1.4%) from ETT secretion. Male patients 51 (75%) were more than female patients 17 (25%). In-patients were 66 (97%) more than outpatients 2 (2.9%). Out of 66 in-patients, 60 (88.2%) were ward patients and 8 (11.7%) were ICU patients. *Pseudomonas aeruginosa* 32 (47%) was the most common organism isolated followed by *Klebsiella pneumoniae* 23 (33.8%), *Acinetobacter* species 8(11.7%) and *Staphylococcus aureus* 5 (7.3%). Out of the 5 *Staphylococcus aureus* 1 was found to be *Methicillin Resistant Staphylococcus aureus* (MRSA). Gram-negative isolates were most sensitive to Meropenem and Gentamicin, while gram positive isolates were most sensitive to Linezolid and Doxycycline (Table 1 & 2). MRSA strain was found to be sensitive to Doxycycline and Cotrimoxazole.

DISCUSSION.

In this study, LRTI was seen to be more prevalent in males 75% than females 25%. This may be due to more prevalence of associated risk factors seen in the male population like smoking, chronic alcoholism, COPD than in females. This is similar to study done from south India and western Rajasthan. [1, 2]

Inpatients 97% were more than out patients 2.9%, this could be because of nosocomial infections otherwise known as hospital acquired infections, similar observation have been shown by S. Singh et al and M Wajid et al [1,2]

In this study, Gram-negatives were more commonly isolated than Gram-positives. Similar observations have been shown in other studies done in India. The predominance of Gram-negatives may be because of waning immunity and pulmonary defence mechanism is older age group and underlying chronic diseases. Institutional care also

makes the patients more susceptible to Gram-negative pneumonia.[3]

Pseudomonas aeruginosa was the most commonly isolated organism 47%. This is similar to study done by S. Singh et al and Nasim O et al [1,6]. *Pseudomonas aeruginosa* was found to be sensitive to Meropenem, Gentamicin, Piperacillin-Tazobactam, Ciprofloxacin and Levofloxacin. Similar findings were observed by S.Singh et al. [1]

Klebsiella pneumoniae was the second most common organism isolated 33.8% and was tested to be sensitive to Meropenem, Gentamicin, Ciprofloxacin and Levofloxacin. This is in contrast to studies done in south India [3,4,5] where *Klebsiella pneumoniae* was the most common gram negative organism isolated.

Staphylococcus aureus was the most common Gram-positive bacteria isolated and was sensitive to Linezolid and Doxycycline similar to a study done in south India by M Wajid et al. and Regha IR et al. [2,5] Among the 7.2 % of gram positive isolates, one was found to be methicillin resistant *Staphylococcus aureus* (MRSA).

With the rise in hospital acquired infections, periodic analysis of types of respiratory pathogens is important in identifying respective hospital flora. A wide variety of respiratory samples are responsible for LRTI, separate studies can be carried out focussing on specific sample and their pathogens.

CONCLUSION:

This study reveals that a variety of pathogens are responsible for LRTI, Gram-negative bacteria as major pathogens. Bacterial isolates showed resistance to commonly used antibiotics like third generation Cephalosporins.

Antibiotic resistance among respiratory bacterial pathogens is alarming.

Strict implementation of antibiotic policy and stewardship has become necessary to conserve the already available antibiotics. [1]

Proper identification of the pathogens and their antibiotic susceptibility can help clinicians to choose the right antibiotic therapy and thus improve the outcome of patients and decrease antibiotic resistance.

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Conflicts of interest: there are no conflicts of interest.

Table 1: Antibiotic resistance pattern of Gram- negative organisms

Antimicrobial Agent	<i>Pseudomonas Aeruginosa</i> (n=32)	<i>Klebsiella Pneumoniae</i> (n=23)	<i>Acinetobacter</i> (n=8)
Ampicillin	16(50%)	13(56%)	4(50%)
Cefotaxime	8(25%)	7(30%)	1(12%)
Cefixime	10(3%)	1(4%)	3(37%)
Ceftriaxone	5(15%)	2(8%)	3(37%)
Ceftazidime	16(50%)	1(4%)	1(12%)
Cefipime	0(0%)	0(0%)	0(0%)
Cotrimoxazole	19(59%)	6(26%)	0(0%)
Ciprofloxacin	2(6%)	NT	0(0%)
Gentamicin	2(6%)	5(21%)	0(0%)
Meropenem	1(3%)	1(4%)	0(0%)
Piperacillin-Tazobactam	0(0%)	NT	NT

NT: not tested

Table 2: Antibiotic resistance pattern of gram-positive isolates

Antimicrobial agent	<i>Staphylococcus aureus</i>
Amikacin	1(20%)
Ampicillin	3(60%)
Azithromycin	2(40%)
Cefoxitine	1(20%)
Cotrimoxazole	0(0%)
Doxycycline	0(0%)
Gentamicin	0(0%)
Levofloxacin	2(40%)

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