

A Study on Bacteriological Profile and Antimicrobial Susceptibility Pattern of Sputum Samples in Patients with Lower Respiratory Tract Infections a Tertiary Care Hospital

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Abstract

Background & Objectives: The morbidity and mortality still remain significantly high in patients with severe lower respiratory tract infections. But data related to the offending organisms and their antibiotic sensitivity pattern is limited. Therefore, this study was designed to identify the bacterial pathogens and their antibiotic sensitivity of sputum samples in patients with severe lower respiratory tract infections which were received by Microbiology Department, between January 2015 to December 2015.

Methods: The present study was conducted during a one year period (January to December 2015). A total of 130 sputum samples were processed. All the samples were processed through Gram's stain and culture. The culture was identified by standard protocols and antibiotic susceptibility was performed by Kirby Bauer disc diffusion method.

Results and conclusion: Out of the 130 sputum culture samples, significant pathogens were isolated in 82 [63%] sputum samples. Among the isolated organisms, *Klebsiella pneumoniae* [31.7%] was the commonest isolated organism, followed by *Pseudomonas* spp [14.63%]. Majority of isolates were only sensitive amikacin, Pipracillin- tazobactam and imipenem. *Staphylococcus aureus* was isolated in 11 samples and 6 were Methicillin resistant *Staphylococcus aureus* [MRSA] which were sensitive to Vancomycin. There were a significantly high proportion of patients who were affected by drug resistant strains. Before starting empirical antibiotics on patients with moderate to severe lower respiratory tract infections, it is always advisable to obtain sputum for culture and antibiotic sensitivity test.

Keywords: *Klebsiella pneumoniae*, *Pseudomonas* sp, Sputum, MRSA, Sputum Culture.

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Introduction

Lower respiratory tract infections are among the most common infectious diseases of humans worldwide. In the United States alone, pneumonia and influenza rank as the sixth leading cause of death¹. An expanded variety of emerging pathogens likewise provides challenges for the microbiology laboratory. Overtreatment of acute uncomplicated bronchitis, which is largely due to viruses, has led to unparalleled levels of multidrug resistance among invasive pathogens. Managing patients with lower respiratory tract infections is a challenge to a clinician as they account for a greater burden of disease worldwide than ischemic heart disease, cancer, malaria or human immunodeficiency virus infection.²

The most useful clinical classification of pneumonia is according to the possible origin of infection: community acquired, hospital acquired or pneumonia in immunocompromised patients.³

Pathogenic organisms can be bacterial, viral, atypical or fungal and there is also considerable seasonal variation in some countries. A chest radiograph helps to confirm the diagnosis while sputum and blood cultures help to isolate the organism. Sputum cultures are recommended in severely ill patients with failure of antibiotic therapy.

The morbidity and mortality still remain significantly high in patients with severe lower respiratory tract infections. But data related to the offending organisms and their antibiotic sensitivity pattern is limited. Therefore, this study was designed to identify the bacterial pathogens and to review their antibiotic sensitivity in patients with lower respiratory tract infections.

Methods

The present study was conducted during a one year period (January to December 2015). A total of 130 sputum samples were processed during the study period. Repeated samples from the same patient were excluded from this study. All the 130 sputum samples were processed through Gram's stain and inoculation onto Blood agar, Chocolate agar and Mac Conkey agar. The Gram's smear was examined under low power, oil immersion and observed for the presence of polymorphs, epithelial cells and bacterial forms Sputum

samples were evaluated based on Bartlett's grading system.

The inoculated culture plates were incubated overnight at 37°C in a incubator. A Gram's stain was done the next day from the growth and examined. The organisms were identified by standard protocols and antibiotic susceptibility of recommended drugs was performed by using Kirby Bauer disc diffusion method.

The specimens yielding significant pathogenic organisms were considered as positive cultures. Those which had scanty or insignificant growths were regarded as negative and when mixed growths of significant organisms were isolated, they were counted according to the predominant growth.

Results

Out of the 130 sputum culture samples, significant pathogens were isolated in 82 [63%] sputum samples. Among the isolated organism, *Klebsiella pneumoniae* [31.7%] was the commonest isolated organism [Table: 1]. Out of the gentamicin resistant cases, 50% were sensitive to third generation cephalosporins and the rest were sensitive to second line antibiotics such as amikacin[73%], Piperacillin- tazobactam[77%] and imipenem[100%].[table-2] There were 12 samples positive for *Pseudomonas* spp[14.63%]. out of which 2 were resistant to ceftazidime and were only sensitive to imipenem or amikacin[100%]. *Staphylococcus aureus* was isolated in 11 samples and 6 were Methicillin resistant *Staphylococcus aureus* [MRSA] which were sensitive to Vancomycin.

Discussion

It is well known that *Streptococcus pneumoniae* (*Pneumococcus*) is the commonest causative organism (35%) for community acquired pneumonia⁵. But the

yield of *S. pneumoniae* from the sputum cultures of patients with bacteremic pneumococcal pneumonia is only 40%–50%, according to the studies conducted a few decades ago^{8,9}. In this study *Pneumococci* were isolated only in 4 sputum samples. This may be due to the sensitivity of this organism to antibiotics and most patients may have had antibiotics prior to hospital admission.

Out of 130 culture samples, 58 sputum samples were negative for pathogens. This could be due to partially treated patients before or during the hospital stay, or these patients may be affected by viral, fungal or atypical pathogens (Table 1). Furthermore, the results of sputum bacterial cultures are strongly influenced by specimen collection, transport, rapid processing, satisfactory use of cytologic criteria, and the skill in interpretation.⁴

Out of the culture positive samples the commonest group of organisms isolated was *Klebsiella pneumoniae* [31.7%][Table:1]. In contrast, a study conducted by Maryan sotoudeh showed, *Acinetobacter* spp was the most common isolated organism [50%].

Out of the gentamicin resistant cases, 50% were sensitive to third generation cephalosporins and the rest were sensitive to second line antibiotics such as amikacin[73%], Piperacillin- tazobactam[77%] and imipenem[100%]. [table-2]

There were 12 samples positive for *Pseudomonas* spp. out of which 2 were resistant to ceftazidime and were only sensitive to imipenem or amikacin[100%]. *Staphylococcus aureus* was isolated in 11 samples and 6 were Methicillin resistant *Staphylococcus aureus* [MRSA] which were sensitive to Vancomycin.

Table 1: Organisms isolated:

Organism	NO	(%)
<i>Klebsiella pneumoniae</i>	26	31.71
<i>Pseudomonas</i> spp	12	14.63
<i>Staphylococcus aureus</i>	11	13.41
<i>Escherichia coli</i>	10	12.19
<i>Streptococcus pyogenes</i>	7	8.54
<i>Klebsiella oxytoca</i>	6	7.32
<i>Streptococcus pneumoniae</i>	4	4.88
<i>Acinetobacter baumannii</i>	2	2.44
<i>Citrobacter koseri</i>	2	2.44
<i>Enterobacter aerogenes</i>	2	2.44
TOTAL	82	100%

Table 2- Antimicrobial susceptibility pattern of isolated organisms:

Organism [n]	AK	GM	CEF	CEZ	OF	CO	CF	P	CTN	CP	IMP	PT	VAN
Klebsiella pneumoniae [26]	19 [73%]	10 [38%]	13 [50%]	14 [54%]	12 [46%]	10 [38%]	13 [50%]	-	-	-	26 [100%]	20 [77%]	-
Pseudomonas aeruginosa [12]	12 [100%]	6 [50%]	8 [67%]	10 [83%]	7 [58%]	4 [33%]	6 [50%]	-	-	-	12 [100%]	10 [83%]	-
Staphylococcus aureus [11]	9 [82%]	-	-	-	-	6 [54%]	8 [72%]	6 [54%]	6 [54%]	8 [72%]	-	-	11 [100%]
Escherichia coli [10]	7 [70%]	4 [40%]	6 [60%]	6 [60%]	5 [50%]	4 [40%]	5 [50%]	-	-	-	10 [100%]	9 [90%]	-
Streptococcus pyogenes [7]	5 [71%]	-	-	-	-	3 [43%]	5 [71%]	7 [100%]	-	7 [100%]	-	-	7 [100%]
Klebsiella oxytoca [6]	4 [67%]	3 [50%]	5 [83%]	5 [83%]	5 [83%]	3 [50%]	4 [67%]	-	-	-	6 [100%]	5 [83%]	-
Streptococcus pneumoniae [4]	3 [75%]	-	-	-	-	2 [50%]	3 [75%]	1 [25%]	-	2 [50%]	-	-	4 [100%]
Acinetobacter baumannii [2]	1 [50%]	0	1 [50%]	1 [50%]	0	0	0	-	-	-	2 [100%]	1 [50%]	-
Citrobacter koseri [2]	1 [50%]	1 [50%]	1 [50%]	1 [50%]	1 [50%]	0	1 [50%]	-	-	-	2 [100%]	2 [100%]	-
Enterobacter aerogenes [2]	2 [100%]	0	2 [100%]	2 [100%]	1 [50%]	0	1 [50%]	-	-	-	2 [100%]	2 [100%]	-

AK-Amikacin,GM-Gentamycin,CEF-Cefotaxime,CEZ-Ceftazidime,OF-Ofloxacin,CO-Cotrimoxazole,CF-ciprofloxacin,P-Penicilin,CTN-Cefoxitin,ERY-Erythromycin,CP-Cephalexin,IMP-Imipenam,PT-Piperacillin --Tazobactam,VAN-Vancomycin.

Conclusion

This study revealed that *Klebsiella pneumonia* [31.7%] was the commonest isolated organism from the sputum samples of patients suffering from lower respiratory tract infections. There were a significantly high proportion of patients who were affected by drug resistant strains.

Recommendation

Before starting empirical antibiotics on patients with moderate to severe lower respiratory tract infections, it is always advisable to obtain sputum for culture and antibiotic sensitivity test.

Conflicts of Interest: None

Source of Support: Nil

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