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A Study on Community Acquired Bacterial Pneumonia (CAP): Characterization of Bacterial Pathogen and Antimicrobial Resistance Patterns

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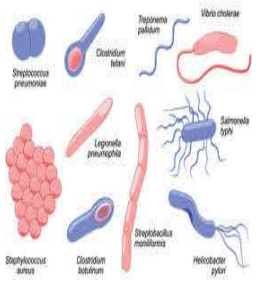

Abstract

Globally, pneumonia is a serious public health concern and a major cause of mortality and morbidity. Despite advances in antimicrobial therapies, microbiological diagnostic tests and prevention measures, pneumonia remains the main cause of death from infectious disease in the world. A key factor for managing and effectively guiding appropriate antimicrobial therapy is an understanding of the role of the different causative microorganisms in the etiology of pneumonia, since it has been shown that the adequacy of initial antimicrobial therapy is a key factor for prognosis in pneumonia. Furthermore, broad spectrum antibiotic therapies are sometimes given until microbiological results are available and de-escalation cannot be performed quickly.
In our study we found *Klebsiella* spp. as the most commonly found etiological agent of pneumonia.

Introduction

Pneumonia infection is the result of a complex process where the lower respiratory tract suffers the invasion of an infective microorganisms. It is important to know the role of the pathogenic microorganism in the etiology of pneumonia infection in order to provide adequate clinical and therapeutic management of the patient.
In children, pneumonia is the single largest infectious cause of death. Approximately 3.7 Lakh children die of pneumonia annually in India.

This study was carried out in different steps as shown below.

Materials and Methods

This study was carried out in the Department of Microbiology and Medical Technology (PGDMLT), Arts, Science and Commerce College, Kholwad, Surat, Gujarat, India, over a period of 1 year from August 2019 to November 2020.

1. Collection of different types of clinical samples (Sputum or Oropharyngeal/ Nasopharyngeal swab)

2. Cultivation of bacteria (1st day):
Gram stain and streaking of the sample on MacConkey's Agar, Blood agar and Chocolate agar plates

3. Isolation (2nd day):
Isolation, characterization and inoculation of different biochemical medias

4. Final identification of bacteria (3rd day):
Phenotypic identification of isolates (manual biochemical reactions or automation)

5. Determination of Antimicrobial susceptibility testing (AST) (3rd day):
AST for knowing antibiotic resistance pattern of isolate

6. Interpretation of results and Data analysis

Results

Table: 1:Different types of clinical samples tested:

Sample type		No. of samples
Sputum	:	134
Throat /Nasopharyngeal swab	:	16
Total Number of samples:	:	150

Table 2: Growth types from different clinical samples:

Growth type		No. of samples
Monomicrobial growth	:	115
Polymicrobial growth	:	27
No growth	:	8
Total no. of samples	:	150

Table 3: Distribution of Microbiological agents:

Isolated Etiological Agent	No.
Acinetobacter spp.	10
Candida albicans	1
Candida guilliermondii	1
Citrobacter spp.	15
E.coli	19
Enterococcus spp.	1
Klebsiella spp.	37
Nocardia spp.	1
Pseudomonas spp.	16
Proteus spp.	2
S.Pneumoniae	2
CoNS	3
No Pathogenic Growth	61
No Growth	8

Table 4: Antimicrobial resistant patter of the organisms

Antibiotic		Acinetobacter spp. (n=10) (% Resistance)	Citrobacter spp. (n=15) (% Resistance)	E.coli (n=19) (% Resistance)	Klebsiella spp. (n=37) (% Resistance)	Proteus spp. (n=2) (% Resistance)	Pseudomonas spp. (n=16) (% Resistance)
Amoxyclave (Amoxicillin/ Clavulanic acid)	AMC	10 (100%)	14 (93%)	19 (100%)	31 (84%)	1 (50%)	-
Co-Trimoxazole (Sulpha/ Trimethoprim)	COT	8 (80%)	5 (33%)	15 (79%)	21 (57%)	2 (100%)	-
Cefuroxime	CXM	8 (80%)	10 (67%)	19 (100%)	22 (59%)	1 (50%)	-
Cefoperazone	CPZ	8 (80%)	8 (53%)	18 (95%)	20 (54%)	0 (0%)	-
Piperacillin / Tazobactam	PIT	7 (70%)	6 (40%)	12 (63%)	14 (38%)	0 (0%)	3 (19%)
Gentamicin	GEN	5 (50%)	5 (33%)	5 (26%)	11 (30%)	0 (0%)	2 (12.5)
Meropenem	MRP	7 (70%)	6 (40%)	7 (37%)	12 (32%)	0 (0%)	1 (6.25%)
Levofloxacin	LE	6 (60%)	5 (33%)	13 (68%)	14 (38%)	0 (0%)	1 (6.25%)
Ciprofloxacin	CIP	8 (80%)	5 (33%)	15 (79%)	15 (41%)	0 (0%)	1 (6.25%)
Cefepime	CPM	8 (50%)	7 (47%)	18 (95%)	18 (49%)	1 (50%)	2 (12.5)
Cefoperazone/Sulbactum	CFS	4 (50%)	7 (47%)	12 (63%)	16 (43%)	0 (0%)	1 (6.25%)
Amikacin	AK	5 (50%)	5 (33%)	5 (26%)	9 (24%)	0 (0%)	2 (12.5)
Aztreonam	AT	-	-	-	-	-	8 (50%)
Colistin (Methane Sulphonate)	CL	-	-	-	-	-	5 (31.25%)
Cefotaxime (Cephotaxime)	CTX	-	-	-	-	-	8 (50%)
Ceftazidime	CAZ	-	-	-	-	-	6 (37.5%)

Discussion

Our study aimed to find out the common pathogens in a patient suffering from Community acquired pneumonia and their resistance patterns in this part of country, as etiological agent and their sensitivity and resistant patterns are different in different parts of the country.

Organisms were detected from 95% (142/150) cases. We found *Klebsiella* spp. to be the commonest etiological agent (22%). Next common bacterial pathogens were *E.coli* (11%), *Pseudomonas* spp. (9%) and *Citrobacter* spp. (9%).

We also found *S.pneumoniae* in 2 sputum samples.
Our finding were in correlation to the study carried out by Shinde et al. In their study they have also found *Klebsiella spp.* as the leading causative agent of CAP. But Mustafa S., Bahl R., Numazaki K., Ostroff SM showed in their studies that second common bacterial pathogen was *Hemophilus infulenzae.*

Conclusion

- Microbial identification of pathogens causing pneumonia is an important issue for optimum clinical management of pneumonia and is a major challenge globally, leading to expanding rate of multidrug resistant pathogens and the emergence of new pathogens.
- However, despite the effort of collecting samples in pneumonia cases, approximately 50% of the cases remain without microbiological identification using conventional methods.
- It is important to use molecular identification methods.
- We strongly recommend that conventional methods together with molecular testing, will improve the microbiological diagnosis of pneumonia, thereby improving clinical management of cases, with shorter time to antibiotic therapy, better targeted antibiotic selection, more effective de-escalation and improved stewardship for pneumonia patients.

References

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