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BACTERIOLOGICAL PROFILE AND ANTIBIOGRAM PATTERN OF LOWER RESPIRATORY TRACT INFECTIONS IN A TERTIARY CARE HOSPITAL IN NORTHERN INDIA



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3. Professor, Department of Microbiology, NIMS Medical College, NIMS University, Jaipur, Rajasthan. Abstract

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Objectives. The present study was conducted to determine the bacterial aetiology and their antimicrobial susceptibility pattern of lower respiratory tract infections so as to update the clinicians in the various antimicrobial alternatives available in the treatment. Methods. 60 sputum samples from patients with lower respiratory tract infections were collected in time span of six months. Bacterial pathogens were isolated from sputum specimens, and subjected to antibiotic susceptibility testing, using standard bacteriologic techniques. Results. Out of the 60 cases, only 46 had an established bacterial aetiology. The most prevalent pathogen was Klebsiella pneumoniae followed by Staphylococcus aureus and Pseudomonas aeruginosa. Gram positive organisms showed 100% susceptibility to vancomycin, linezolid and levofloxacin. While, Gram negative isolates showed high susceptibility with aztreonam, imipenam. colistin. piperacillin/tazobactum and cefoparazone/sulbactum. Conclusions. For effective management of LRTIs bacteriological diagnosis and antibiotic susceptibility pattern is indispensable.

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INTRODUCTION

Respiratory tract infection is one of the most important infectious diseases worldwide. This infection is the leading cause of morbidity and mortality in critically ill patients in developing countries ^[1]. Respiratory tract infections are usually contracted through air and by direct contact ^[2].

In India, acute lower respiratory tract infection (ARI) is responsible for one million deaths. There is inadequate information from India on various lower respiratory tract bacterial pathogens and their resistance patterns in hospital settings. In addition, the emergence of resistance as a major problem has drawn attention to a need for better diagnostic techniques and newer drugs to allow more specific therapy ^[3].

At present the therapy for communityacquired lower respiratory tract infections (LRTI) is often empirical, and how to choose an effective antimicrobial agent is a new challenge to the clinicians, as the composition and the resistance to antimicrobial agents of infectious pathogens was changing frequently. The knowledge of likely prevalent strains along with their antimicrobial resistance pattern will help in better management of patients and framing the antibiotic policy.⁽⁴⁾

Hence, the present study was undertaken to define the common bacterial profile in lower respiratory tract infection (LRTI) and to study their antibiotics sensitivity pattern.

MATERIALS AND METHODS

The present study was carried out in the time span of 6 months from Aug 2012 to 2013 in the Department Jan of Microbiology NIMS Medical collage Jaipur. The study included 60 patients of all age group who had clinically evident lower respiratory tract infections. The Patients first morning sputum sample was collected directly into a sterile wide mouthed container and transported to the laboratory according to standard protocol^[5].

Sputum sample were inoculated on blood agar, chocolate agar and macconkey's agar. After 18-24 hours incubation plates were examined for colony characteristics and further identification of bacterial isolates was done by established methods ^[6]. Antibiotic sensitivity was performed by Kirby- Bauer disc diffusion method as recommended by NCCLS ^[7]. The

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antibiogram of each confirmed isolate was studied and susceptibility results were compiled.

RESULTS AND DISCUSSION

Out of 60 patients presented clinically as Lower Respiratory tract infection, the positive culture diagnosis could be possible in 46 cases (36 for single pathogen and 10 for mixed infections) in the present study.

The preponderance of males was seen in present study as among the total number cases studied males were 33 (55%) and females were 13 (21.66%). This could be due to more prevalent associated risk factors (e.g. Smoking, chronic alcoholism,) of pneumonia seen in males than females. Similar findings were reported by other investigators ^[8, 9].

In the present study maximum number of patients 23 (38.33%) were from 21-40 age group, followed by 12 (20%) patients from 41-60 years age group, then 8 (13.33%) were >60 years. Least infection rate was observed in 1-20 years age group (5%). Similar prevalence of infection in higher age group was reported by Christopher et. al ^[9]. People within this age group may have lower immunity due to age or other ailments that may compromise the

immune system, which may explain the high prevalence observed in this study.

The commonest pathogen causing Lower respiratory tract infection in present study was *Klebsiella pneumoniae* (Table 1). This is comparable with findings of Supriya et. al. who reported *Klebsiella pneumonia* to be commonest bacterial isolate ^[10].

The other organisms isolated were Staphylococcus aureus, Pseudomonas aeruginosa, Coagulase negative staphylococcus, Streptococcus pyogenes, Enterococcus sp. Citrobacter freundii, Proteus mirabilis and Escherichia coli. 2 strains of Candida albicans were also isolated. Similar results were obtained by A. M. El-Mahmood et. al. and SK Mishra et. al. separately in their studies ^[3, 10].

The *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* was commonest organism causing lower respiratory tract infection in hospitalized patients whereas among outpatients *Staphylococcus aureus* is the commonest organism causing lower respiratory tract infection in the present study. Similar findings were reported by Supriya et. al. ^[11].

E. coli is an uncommon cause of acute lower respiratory tract infection and in this study, they comprised of 1.8% of the

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total cases. It is in agreement with findings of other investigators who reported 5.8% and 6.9% prevalence of *E. coli* in separate studies ^[12, 10]. Only 2 isolates of *Proteus mirabilis* were isolated from hospitalized patients in this study. This organism is an opportunistic pathogen and causes lower respiratory tract infection.

Identification of polymicrobial infection is very important for treatment strategies ^[11]. In the present study, incidence of mixed infections was 16.6% which is consistent with the fact that incidence of mixed infections does not usually exceed 30%.

Candida albicans were isolated from 2 samples (3.63%) in the present study. Jha et. al. also isolated *Candida species* 30 (12.2%) in their study^[13].

In present study Gram positive organisms showed 100% susceptibility to vancomycin, linezolid and levofloxacin followed by their susceptibility against gentamycin, amikacin, erythromycin, clindamycin, co-trimoxazole, ofloxacin, tetracycline, amoxicillin and ceftriaxone (Table 2). There are similar reports from other investigators ^[11, 14]. The lactose fermenting gram negative bacilli organism showed 100% susceptibility to aztreonam, imipenam, colistin, piperacillin/tazobactum and cefoparazone/sulbactum. more than 50% resistance was found against cefepime, amikacin, ciprofloxacin, ceftriaxone and ofloxacin. High resistance of 86.7% was observed against co-trimoxazole and ceftazidime (Table 3). According to other investigators colistin was found to be the most effective drug against all types of Gram-negative bacteria followed by Imipenem^[15].

Pseudomonas aeruginosa showed 100% susceptibility to aztreonam and imipenem then the followed by susceptibility against piperacillin/tazobactam, netilmycin, cefoparazone/sulbactam, tobramycin, amikacin, ciprofloxacin, ceftazidime, gentamycin and least sensitive to cefoparazone (Figure 1). There are similar reports from other investigators ^[10, 14, 15].

Thus the present study concludes that the aztreonam, piperacillin/tazobactum and cefoparazone/sulbactum were effective among the antibacterial for empiric treatment for Gram negative bacterial respiratory tract infections reserving imipenam and colistin for life threatening infections. For Gram positive Bacterial

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infections	amiı	noglycosides	and	selection of the appropriate antibacterial		
levofloxacin	are	recommended	for	therapy should be based on the organisms		

empirical treatment reserving vancomycin and Linezolid for resistant cases. The which are isolated and on the emerging resistance to the conventional therapies.

Table 1

Microbial Profile of lower respiratory tract infections

Microbial Isolate	IPD	OPD	Total	Percentage
Klebsiella pneumoniae	07	08	15	27.27 %
Staphylococcus aureus	04	09	13	23.63%
Pseudomonas aeruginosa	08	03	11	20 %
Coagulase Negative Staphylococcus	00	04	04	7.27 %
Citrobacter freundii	02	00	02	3.63 %
Candida albicans Sp.	00	02	02	3.63%
Enterococcus spp.	02	00	02	3.63 %
Streptococcus pyogenes	00	03	03	5.45%
Proteus mirabilis	02	00	02	3.63 %
Escherichia coli	01	00	01	1.8%

Table 2

Percentage susceptibility Pattern of Gram positive Cocci (GPC) to the selected antimicrobial Agents

Antimicrobial	Staphylococcus	Coagulase	Streptococcus	Enterococcus
Agents	aureus	Negative	pyogenes	
		Staphylococcus		
A section at s	02.2.0/	75.0/	100.0/	100.0/
Аткаст	92.3 %	/5 %	100 %	100 %
Ceftriaxone	30.7 %	50 %	00 %	00 %
Clindamycin	61.6 %	50 %	00 %	00 %
Erythromycin	77.7 %	75 %	100 %	100 %
Gentamycin	92.3 %	100 %	100 %	100 %
Vancomycin	100 %	100 %	100 %	100 %
Co-Trimoxazole	61.6 %	25 %	100 %	00 %
Tetracycline	53.8 %	25 %	66.6 %	00 %
Amoxicillin	46.4 %	100 %	100 %	100 %
Ofloxacin	53.8 %	75 %	00 %	00 %
Linezolid	100 %	100 %	100 %	100 %
Levofloxacin	100 %	100 %	100 %	100 %

Table 3

Percentage susceptibility pattern of Gram negative Bacilli to the selected antimicrobial agents.

Antimicrobial Agents	Klebsiella	Escherichia	Citrobacter	Proteus
	pneumonia	coli	spp.	mirabilis
Amikacin	40 %	100 %	00 %	00 %
Ciprofloxacin	33.3 %	100 %	100 %	00 %
Aztreonam	100 %	100 %	100 %	100 %
Imipenam	100 %	100 %	100 %	100 %
Ceftazidime	13.3 %	100 %	100 %	00 %
Piperacillin/tazobactum	100 %	100 %	100 %	100 %
Cefoperazone/Sulbactum	100 %	100 %	100 %	100 %
Co-Trimoxazole	13.3 %	00 %	100 %	00 %
Cefepime	46.6 %	100 %	100 %	00 %
Ceftriaxone	20 %	100 %	50 %	50 %
Colistin	100 %	100 %	100 %	100 %
Ofloxacin	20%	00 %	100 %	00 %



Figure 1: The antimicrobial susceptibility pattern of Pseudomonas species.

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