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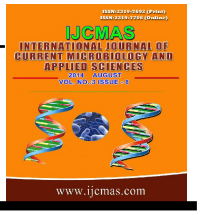

Original Research Article

Microbiological study of lower respiratory tract infections in ICU patients

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Keywords

Lower respiratory tract infections, ICU patients India.

A B S T R A C T

Introduction: Lower respiratory tract infections (LRTI) are the most common bacterial infections among patients in intensive care units (ICUs) occurring in 10-25% of all ICU patients. Aim:To study the etiology of LRTIs in ICU and antibiotic susceptibility pattern of the isolates. Material and method: Samples like sputum, endotracheal & tracheostomy tube aspirates of patients of pneumonia in ICU were collected and processed by standard microbiological techniques. Along with routine antibiotic susceptibility multidrug resistance were tested. Result: Total 151 patients were clinically suspected of LRTI, of which 43.7% patients had VAP and 18% were having pneumonia due to other causes. *P. aeruginosa* (23.8%) were the commonest isolates obtained, followed by *A. baumanii* (21.2%) and *Kl. pneumoniae* (15.2%). The most active agent against the GNB isolates was imipenem, followed by amikacin and piperacillin-tazobactum. All Gram positive isolates were susceptible to vancomycin and linezolid. Conclusion: Current knowledge of the organisms that cause LRTIs and their antibiotic susceptibility profiles are therefore necessary for the prescription of appropriate therapy.

Introduction

Lower respiratory tract infections (LRTI) are the most common bacterial infections among patients in intensive care units (ICUs) occurring in 10-25% of all ICU patients and resulting in high mortality, ranging from 22-71%. (Nidhi G. et al 2001)

LRTIs impose a serious economic burden on society, ranging from reduced output in workplaces to frequent prescription by physicians of antibiotics, even when the causative agents of infection is not bacteria (Jafari J *et al.*, 2009). In long-term hospitalised patients, bacteria from the ventilator breathing system have been implicated in the pathogenesis of ventilator associated pneumonia. (Kumari HBV et al., 2007)

However, in recent years, there has been a dramatic Report and Opinion in the year 2012 of rise in antibiotic resistance among respiratory pathogens (Imani *et al.*, 2007). Current knowledge of the organisms that

cause LRTIs and their antibiotic susceptibility profiles are therefore necessary for the prescription of appropriate therapy.

Prevalent flora and antimicrobial resistance pattern may vary from region to region depending upon the antibiotic pressure in that locality. Therefore, the present study was designed to know the bacterial profile and determine the antimicrobial resistance pattern among the aerobic GNB isolated from LRT of patients admitted to the ICU of our institute.

Materials and Methods

The study was carried out in Department of Microbiology at a tertiary care institute, Indira Gandhi Government Medical College Nagpur, from September 2010 to March 2012. In patients of Chronic obstructive pulmonary disease (COPD) and pneumonia, first morning sputum sample was collected directly into a sterile wide mouthed container and transported to laboratory according to standard protocol (Collee JG et al 1996). In microscopic examination, Sputum showing less than 10 squamous epithelial cells and more than 25 leucocytes or pus cells per low-power field confirmed the reliability of the specimen indicating that it was not contaminated with saliva. (Bartlett`s RC et al 1974) In critical care unit patients who are on ventilation for more than 48 hours, Endotrachal tube (ET) aspirates and tracheotomy tube (TT) aspirates were collected under aseptic precaution.

Samples were inoculated on 5% sheep blood agar, chocolate agar, MacConkey agar by using 4 mm Nichrome wire loop (Hi-Media, Mumbai, India). Isolates with any significant growth was identified with a detailed biochemical testing and antibiotic sensitivity testing was performed on Mueller–Hinton agar plates by Kirby—Bauer disc diffusion method. Zone diameter was measured and interpreted as per the Clinical and Laboratory Standards Institute (CLSI-2011) guidelines. Suspected extended-spectrum beta lactamases (ESBLs) producing organisms were confirmed by CLSI phenotypic confirmatory test. Detection of plasmid-mediated AmpC was done by the AmpC disk test using cefoxitin and cefotaxime disc. The isolates showing reduced susceptibility to carbapenems (imipenem and meropenem) were selected for detection of metallo-beta lactamases (MBLs) enzymes by imipenem-EDTA disk method. For quality control of disc diffusion tests ATCC control strains of *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923 and *Pseudomonas aeruginosa* ATCC 27853 strains were used.(CLSI-2011)

Results and Discussion

Table 1 shows *Pseudomonas aeruginosa* was commonest isolate followed by *Acinetobacter spp*. And *Klebseilla.* Table 2 shows that maximum gram negative bacilli (GNB) isolates were sensitive to imipenem (80.0%) followed by, amikacin (62.9%), piperacillin -tazobactum (60.0%), and Cefipime (45.7%). All isolates were resistant to ampicillin, amoxyclav, 1st generation cephalosporins.

LRTI is considered as one of the most important infectious diseases in developing countries. Pneumonia is a frequent complication in patients admitted to the ICU.(Nidhi G et al 2009). In this study, maximum 60 (39.7%) LRTI infected patients were in the age group of 51-60 years. Our observation is similar with that of Meric et al, and Yehia et al who reported maximum infected patients in the age group of 45-70 years.

Table.1 Bacterial aetiology in pneumonia cases (n=151)

Isolates	**VAP (n=107)**	**Other Pneumonia (n=44)**	**Total (n=151)**
E. coli	6 (5.6%)	2 (4.5%)	8 (5.3%)
K. pneumonia	16 (14.9%)	7 (15.9%)	23 (15.2%)
K. oxytoca	0	1 (2.3%)	1 (0.7%)
C. freundii	1 (0.9%)	1 (2.3%)	2 (1.3%)
E. cloacae	1 (0.9%)	0	1 (0.7%)
P. aeruginosa	29 (27.1%)	7 (15.9%)	36 (23.8%)
A. baumannii	28 (26.2%)	4 (9.1%)	32 (21.2%)
A.lwoffi	2 (1.9%)	1 (2.3%)	3 (1.9%)
S. aureus	7 (6.5%)	2 (4.5%)	9 (5.9%)
S. pneumonia	0	2 (4.5%)	2 (1.3%)
No growth/ No significant growth	17 (15.9%)	17 (38.7%)	34 (22.5%)

Table.2 Antimicrobial sensitivity of Enterobactericeae isolate (n=35)

Drugs	***K. pneumoniae* n=`23(%)**	***K. oxytoca* n=1(%)**	***E. coli* n=8 (%)**	***C. freundii* n=2 (%)**	***E. cloacae* n=1 (%)**	**Total(n=35)**
Ampicillin	0	0	0	-	-	0
Amoxyclav	0	0	0	-	-	0
Cephalothin	0	0	0	-	-	0
Cefuroxime	0	0	1(12.5)	-	-	1(2.9)
Ceftazidime	7 (30.4)	1(100.0)	1(12.5)	1 (50.0)	1(100.0)	11 (31.4)
Cefotaxime	4 (17.4)	1 (100.0)	1(12.5)	1 (50.0)	0	7 (20)
Cefipime	8 (34.8)	1 (100.0)	4 (50.0)	2 (100.0)	1 (100.0)	19 (45.7)
Piperacillin	11 (47.8)	1(100.0)	0	1 (50.0)	1 (100.0)	14 (40.0)
Piperacillin + tazobactum	14 (60.9)	1 (100.0)	3(37.5)	2 (100.0)	1 (100.0)	21(60.0)
Imipenem	20 (86.9)	1 (100.0)	4(50.0)	2 (100.0)	1 (100.0)	28 (80.0)
Gentamicin	2 (8.7)	1 (100.0)	6 (75.0)	1 (50.0)	0	10(28.6)
Amikacin	13 (56.5)	1 (100.0)	6 (75.0)	1 (50.0)	1 (100.0)	22(62.9)
Tobramycin	4 (17.4)	0	3 (37.5)	2 (100.0)	0	9(25.7)
Ciprofloxacin	8 (34.8)	1 (100.0)	1 (12.5)	1 (50.0)	0	11(31.4)

Table.3 Antimicrobial sensitivity of nonfermenters isolate (n=71)

Drugs	*A.baumanni* n=32(%)	*A.lwoffi* n=3(%)	*P. aeruginosa* n=36 (%)	Total(n=71)
Ceftazidime	2 (6.3)	0 ()	15 (41.7)	17 (23.9)
Cefotaxime	2 (6.3)	1 (33.3)	10 (27.8)	13(18.3)
Cefipime	3 (9.4)	1 (33.3)	14 (38.9)	18(25.4)
Piperacillin	5 (15.6)	1 (33.3)	14 (38.9)	20(28.2)
Piperacillin + tazobactum	19 (59.4)	2 (66.7)	31 (86.1)	52(73.2)
Imipenem	20 (62.5)	2 (66.7)	32 (88.9)	54(76.1)
Gentamicin	7 (21.9)	1 (33.3)	17 (47.2)	25(35.2)
Amikacin	13 (40.6)	1 (33.3)	24 (66.7)	38(53.5)
Tobramycin	9(28.1)	1 (33.3)	10 (27.8)	20(28.2)
Ciprofloxacin	5 (15.6)	1 (33.3)	13 (36.1)	19(26.8)

Table.4 Antimicrobial sensitivity of gram positive cocci (n= 11)

Drugs	*S. aureus* n=9 (%)	*S.pneumoniae* n=2(%)	Total n=11 (%)
Penicillin G	0	2(100.0)	2(18.1)
Cefoxitin	4(44.4)	-	4(36.3)
Erythromycin	0	1(50.0)	1(9.1)
Gentamicin	7(77.7)	-	7(63.6)
Amikacin	7(77.7)	-	7(63.6)
Tobramycin	2(22.2)	-	2(18.1)
Netillin	1(11.1)	-	1(9.1)
Rifampicin	3(33.3)	1(50.0)	4(36.3)
Ciprofloxacin	3(33.3)	2(100.0)	5(45.5)
Vancomycin	9(100.0)	2(100.0)	11(100.0)
Linezolid	9(100.0)	2(100.0)	11(100.0)
Chloramphenicol	3 (33.3)	0	3(27.3)
Tetracycline	2 (22.2)	1(50.0)	3(27.3)
Cotrimoxazole	3 (33.3)	1(50.0)	4(36.3)
Clindamycin	2 (22.2)	-	2(18.1)

Table.5 β- lactamases profile in gram negative bacilli

Gram negative bacilli	ESBL	AMP C	MBL
	Enterobacteriaceae (n=35)		All GNB (n=106)
E. coli (n=8)	2(11.1)	1 (5.6%)	0
K. pneumoniae (n=23)	4 (13.8)	2 (5.7%)	3 (13.0%)
K. oxytoca (n=1)	1(100.0)	0	0
E. cloacae (n=1)	1(100.0)	0	0
C. freundii (n=2)	0	0	0
P. aeruginosa (n=36)	-	-	4 (11.1%)
A. baumannii (n=32)	-	-	12 (37.5%)
A. lwoffi (n=3)	-	-	1 (33.3%)
Total (%)	8 (22.9%)	3 (8.6%)	20 (18.8%)

In this study, out of total 151 pneumonia cases, 107 (43.7%) were ventilator associated pneumonia (VAP) while 44 (18.0%) were pneumonia due to other causes (Table 1). Woske et al in 2001 and Jamaati et al in 2010 have reported 40.4% and 48% VAP cases respectively in their studies.

P. aeruginosa (27.1%) was the commonest isolate responsible for causing VAP, followed by *A. baumannii* (26.2%), *K. pneumoniae* (14.9%) and *S. aureus* (6.5%). Similar findings were reported by Yehia et al 2008 and Jamaati et al 2010. They also reported *P. aeruginosa* as the commonest aetiological agent in VAP infection. Woske et al in 2001 reported *S. aureus* (38%) as the commonest isolate in VAP.

In this study, we observed, 44 cases of pneumonia other than VAP (Table 1). *P. aeruginosa*, *K. pneumoniae* were the commonest isolates responsible for causing pneumonia in 15.9% cases each followed by *A. baumannii* (9.1%), *E. coli* (4.5%) and *S. aureus* (4.5%). In the present study, Table 1 shows that in pneumonia cases, aetiology can be established in 117 cases (77.5%), No significant growth was obtained in 34 cases (22.5%). 23.8% *P. aeruginosa* was commonest aetiological agent followed by 21.2% *A. baumannii* and 15.2% *K. pneumoniae* isolates.

The antibiotic sensitivity pattern of the isolates is shown in Tables 2 and 3. Most effective antibiotic for non-fermenter isolates were Imipenam 76.1% and Piperacillin-Tazobactum 73.2% while least effective antibiotic was Cefotaxime 18.3%. Enterobactericeae isolates had maximum sensitivity to Imipenem 80% and Amikacin 62.9% and complete resistance to Ampicillins, Amoxicillin and Cephalothin was observed. The pattern of antibiotic resistance recorded in this study among *P. aeruginosa*, Acinetobacter spp, *K. pneumoniae* and *E. coli* isolates is consistent with results obtained from other developing countries. (Nidhi et al 2009, OLUGBUE Vand ONUOHA S 2011 and Akingbade OA et al 2012)

All the Gram-positive isolates in our study were sensitive to Vancomycin and Linezolid. In our study, 55.6% MRSA was obtained. We observed two isolates of *S. pneumoniae,* both were sensitive to penicillin G, vancomycin, linezolid and ciprofloxacin and resistant to chloramphenicol. This result is comparable to the study done by Preeti S et al 2013 and Olugbue V and Onuoha S. 2011.

In this study, we obtained 8.6% AmpC β-lactamase and 22.9% ESBL producers in Enterobactericeae isolates and 18.8% MBL in all Gram negative bacilli (Table 5). Clinical microbiology laboratories should be extremely vigilant for the imminent detection of MBL in Imipenem resistant *Pseudomonas* spp. and *Acinetobacter* spp.

The present study has sampled a large number of imipenem-resistant *Acinetobacter* spp. isolates. In the present study, all the Imipenem-resistant isolates of *Acinetobacter* spp.*, Klebsiella* spp. *and Pseudomonas* spp. produced MBLs. The consequences of increased multidrug resistance are far reaching since bacterial infection of LRTI is a major cause of death due to infectious disease (Kumari *et al*., 2007).

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