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Research Paper

Bacteriological Profile Isolated From Lower Respiratory Tract Infections and Their Antibiogram in a Tertiary Care Hospital In Jaipur, Rajasthan

Medical Microbiology

KEYWORDS : Lower respiratory tract infections, Gram-negative bacteria, Multi-drug resistance.

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ABSTRACT

Lower respiratory tract infections are the commonest health problem demanding frequent consultation and hospitalization. Moreover, emergence of multidrug resistance among organisms is an issue of increasing concern. This study was conducted to determine bacterial pathogens causing lower respiratory tract infections and their antibiogram. Lower respiratory tract secretions (sputum, pleural fluid, endo-tracheal tip, post-bronchoscopy secretion) of 760 patients were cultured, identified and antimicrobial susceptibility was performed by standard methods. Out of 760 patients, 378 were culture positive. Out of which 152 were GNB, 203 were GPC and 23 were Candida spp. The most prevalent pathogen was Streptococcus pneumoniae, Klebsiella pneumoniae and Pseudomonas aeruginosa. Gram positive isolates showed high resistance to PenicillinG while, Gram-negative isolates showed to Ampicillin. Large majority of isolated multidrug resistant organisms were found to be pathogenic. Isolation practices, antibiotic policies and effective surveillance are needed to be improved.

INTRODUCTION

Lower respiratory tract infections are the commonest health problem demanding frequent consultation and hospitalization. Carroll K.C., (2002) posited that Lower respiratory tract infections are among the most common infectious diseases of humans worldwide. Pittet D., (1994) have posited that in developing countries, acute respiratory infection (ARI) is the leading cause of morbidity and mortality in critically ill patients. Reddiah V.P., (1988) posited that in India, ARI is responsible for one million deaths. Out of these 10-15% is due to acute lower respiratory tract infections. LRTI is not a single disease but a group of specific infections each with a different epidemiology, pathogenesis, clinical presentation and outcome. Due to different resistance mechanisms spreading among respiratory pathogens and leading to multi-resistant strains their treatments are frequently difficult and also there is inadequate information from India on various Lower Respiratory Tract bacterial pathogens and their resistance patterns on hospital settings. Hence, the present study was undertaken to define the common bacterial profile in Lower Respiratory Tract Infection and to study the resistance patterns to common antibiotics and to provide empiric therapy to the clinicians in treating lower respiratory tract infections.

Material and Methods

The present study was carried out in the time span of 6 months from Jan 2015 to June 2015 in the Department of Microbiology NIMS Medical College, Jaipur. A total of 760 lower respiratory tract secretions (233 sputum, 72 endo-tracheal tip, 68 post-bronchial secretion and 5 pleural fluid) were received in diagnostic microbiology for culture and sensitivity. All specimens belonged to patients suspected of having LRTIs. Purulent portion of samples were used for making smears for gram stain and for inoculating blood agar and MacConkey agar. The specimens were cultured on Blood agar, MacConkey agar and Chocolate agar and incubated at 37°C for 18-24 hours. Identification of bacterial isolates was done by their characteristic appearance on the media, Gram's staining, motility testing (by hanging drop method), biochemical tests (Catalase, Coagulase, Indole, Methyl red, voges-proskauer, Citrate, Urease, Triple sugar iron, PPA, Oxidase test), antimicrobial susceptibility tests by Modified Kirby Bauer's disc diffusion method following the clinical laboratory standard institute (CLSI guidelines, 2014). Interpretations of results based on gram stain (< 10 squamous epithelial cells and > 25 pus cells per low power field, predominant bacteria rather than wide diversity of bacterial forms) and culture (predominant isolate). The panel of antibiotics (discs in mcg) tested was as follows: PenicillinG(PG) (10), cephoxitin (CX) (30), Ceftazidime(CT) (30), amikacin(AK) (30), azythromycin(AZ) (50), linezolid(LZ) (30), vancomycin(VA) (30), ampicillin(AMP) (10), amoxyclav (AMC) (30), cefaperazone/salbactum (CFS) (105), aztreonam(AO) (30), ciprofloxacin(CP) (5), piperacillin/tazobactum(PT) (85) and imipenem(IPM) (10).

Result

A total of 760 lower respiratory tract secretions of all ages and both sexes were studied. In the present study, out of 760 samples, 378(49.7%) were culture positive, 259(34.0%) showed normal upper respiratory oral flora and 123(16.1%) showed no growth. Out of the positive culture, 203(53.7%) were GPC, 152(40.2%) were GNB and 23(6.0%) were Candida spp. respectively. The occurrence of bacterial pathogens varies with age, in that, age group ranging from 41-60years (44.4%) recorded higher isolates followed by 60-75years (29.6%) and 21-40years (19.0%) while age group 1– 20years recorded the least (6.8%). Sex related occurrence of pathogens reveals that, male 325(85.9%) subjects reported higher number of pathogens compared to females 53(14.0%). Bacterial isolates from sputum, pleural fluid, endo-tracheal tip and Post-bronchoscopy secretion were 233(61.6%), 5(1.3%), 72(19.0%) and 68(17.9%) respectively. The most common pathogen causing lower respiratory tract infection isolated was *Streptococcus pneumoniae* 104(27.5%) followed by *Streptococcus pyogenes* 46(12.1%), *Klebsiella pneumoniae* 43(11.3%), *Pseudomonas aeruginosa* 39(10.3%). Other organisms are represented in table 1.

Table:1 Distribution of micro-organisms isolated from various lower respiratory secretions.

Isolates	Sputum n=233	Pleural fluid	ET tip	Post-bronchoscopy secretion	Total (%)
Streptococcus pneumoniae	51	2	17	34	104 (27.5)
Streptococcus pyogenes	37	0	9	0	46 (12.1)
Klebsiella pneumoniae	30	0	2	11	43 (11.3)
Pseudomonas aeruginosa	12	1	18	8	39 (10.3)
Staphylococcus aureus	21	1	3	9	34(8.9)

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Escherichia coli	26	0	1	4	31(8.2)
Citrobacter spp.	17	0	6	0	23(6.0)
Enterococcus spp.	8	0	11	0	19(5.0)
Enterobacter spp.	6	0	3	0	9(2.3)
Acinetobacter spp.	2	1	2	2	7(1.8)
Candida spp.	23	0	0	0	23(6.0)

Klebsiella pneumoniae and *Pseudomonas aeruginosa* were the most prevalent (11.3% and 10.3% respectively) among the Gram-negative pathogens and *Streptococcus pneumoniae* among the Gram-positive organisms (27.5%) followed by *Streptococcus pyogenes* (12.1%) and *Staphylococcus aureus* (8.9%).

High rates of resistance to ampicillin and penicillinG were demonstrated by all GNB and GPC respectively. All GNB showed 100% susceptibility to imipenem except *Acinetobacter spp.* and among GPC 100% susceptibility to vancomycin and linezolid were obsereved. *Staphylococcus aureus* (85.2%) and *Streptococcus pyogenes* (71.7%) showed high resistance to Penicillin G but fewer isolates of *Enterococcus spp.* (32.3%) were resistant to Penicillin G. All the antibiotics showed less than 50% of resistance to all the pathogens except penicillinG (Table2). *Acinetobacter spp.* showed 100% resistance to all the antibiotics except for imipenem only for one isolate. High degree of resistance was observed among ampicillin, ciprofloxacin and amoxyclav for *Pseudomonas aeruginosa* and *Escherichia coli. K. pneumoniae*, the most prevalent pathogen, showed low susceptibility to most of the agents except cipofloxacin, amikacin and cefaperazone/salbactum. *Pseudomonas aeruginosa* also showed less than 50% of resistance to Ceftazidime, aztreonam and cefaperazone/salbactum (Table3).

Table: 2 Antibiotic resistance patterns of the GPC isolates in percentage (%) is shown

GPC	PG	CX	CT	AMC	CFS	AK	AZ	LZ	VA
Staphylococcus aureus n=34	29(85.2)	13(38.2)	7(20.5)	3(8.8)	6(17.6)	9(26.4)	11(32.3)	0	0
Enterococcus spp. n=19	11(32.3)	7(36.8)	3(15.7)	1(5.2)	0	7(36.8)	3(15.7)	0	0
Streptococcus pneumoniae n=104	53(50.9)	26(25.0)	16(15.3)	11(10.5)	16(15.3)	23(22.1)	12(11.5)	0	0
Streptococcus pyogenes n=46	33(71.7)	18(39.1)	12(26.0)	7(15.2)	12(26.0)	6(13.0)	10(21.7)	0	0

Column headings are abbreviations for antibiotics, full names given in "Material and Methods"

Table: 3 Antibiotic resistance patterns of the GNB isolates in percentage (%) is shown

GNB	AMP	CT	AO	CP	AK	AMC	PT	CFS	IPM
Escherichia coli n=31	31(100)	7(22.5)	26(83.8)	29(93.5)	0	20(64.5)	0	2 (6.4)	0
Acinetobacter spp. n=7	7(100)	7(100)	7(100)	7(100)	7 (100)	7(100)	7(100)	7 (100)	6 (85.7)
Klebsiella pneumoniae n=43	42(97.6)	23(53.4)	16(37.2)	6(13.9)	3 (6.9)	27(62.7)	13(30.2)	3 (6.9)	0
Citrobacter spp. n=23	21(91.3)	13(56.5)	10(43.4)	7(30.4)	9(39.1)	11(47.8)	15(65.2)	4(17.3)	0
Enterobacter spp. n=9	9(100)	6(66.6)	4(44.4)	6(66.6)	2(22.2)	9(100)	2(22.2)	1(11.1)	0
Pseudomonas aeruginosa n=39	31(79.4)	9(23.0)	18(46.1)	29(74.3)	26(66.6)	30(76.9)	27(69.2)	11(28.2)	0

Column headings are abbreviations for antibiotics, full names given in "Material and Methods"

This study has demonstrated that major pathogens causing LRTI are *Streptococcus pneumoniae* (27.5%), *Klebsiella pneumoniae* (11.3%) and *Pseudomonas aeruginosa* (10.3%). These observations are different from the findings of Ozylimaz *et al.* (2005), and Liebowitz *et al.* (2003), where *Haemophilus influenzae* was the most prevalent pathogen followed by *Streptococcus pneumoniae* and *Moraxella catarrhalis.* In the present study 53.7 % of the isolates were GPC and 40.2% of GNB. Quite similar findings were seen in the study by Premlatha E. et al., (2014). Six percent of the specimens remained sterile on culture probably due to previous antibiotic therapy or being non representative specimens. The age group ranging from 41-60 years (44.4%) recorded higher isolation while age group 1-20 recorded the least (6.8%). This might be due to the fact that, most of the people in these age groups are more exposed to agents responsible for causing respiratory tract infections. Predominance of male over females can be explained by the fact that in our country males are exposed more to outside environment because of their more mobility as compare to females. Moreover smoking habits are more pronounced in males that constitute one of the predisposing factors for development of COPD. Imipenem was found to be a better drug for *Pseudomonas aeruginosa.*

Differences in the prevalence of antimicrobial susceptibility may be due to several factors, including different patterns of antimicrobial usages, which lead to selective pressure, as well as distribution of specific serotypes and the spread of resistant clones within certain areas.

The antimicrobial resistance among the respiratory pathogens is a major barrier interfering with an effective treatment. In our study, Gram negative bacilli showed higher resistance patterns towards ampicillin, third generation cephalosporins and beta lactam inhibitors (amoxicillin-clavulinic acid). Similar findings were reported by Goel N. et al., (2002) showing increased prevalence of drug resistance among Gram negative bacilli strains from LRTI. Antibiotic resistance can be due to frequent changing of antibiotics in prescription written by physicians, even when the causative agent of infection was not clear.

Conclusion

An increase in the predisposing conditions in recent years, like smoking, chronic alcoholism, lower immunity due to increasing age has resulted in an increased incidence of LRTIs. Indiscriminate and long-term use of antibiotics has emerged as an important predisposing factor for lower respiratory tract infections in the study, so there should be judicious use of antibiotics. We conclude that GPC were the predominant isolates of LRT infection followed by GNB. Adults, elderly and critically ill patients are at high risk for contracting lower respiratory tract infections. Imepenem were effective among all the antibiotics for Gram-negative and vancomycin and linezolid were effective among all the antibiotics for Gram-positive. The Present study also highlights the need for periodic surveillance of antimicrobial susceptibility pattern of bacterial isolates, as it would promote the judicious use of antimicrobials given to patients and thus preventing the emergence of drug resistance.

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