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Original Research

Assessment of bacterial pathogens from lower respiratory tract infections

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ABSTRACT:

Background: Lower respiratory tract infections (LRTIs) are common among patients worldwide, and the most major cause of pneumonia and bronchiolitis in hospitalization.The present study was conducted to assess bacterial pathogens from lower respiratory tractinfections. **Materials & Methods:** 75 patients of both genders were enrolled. All patients were from out-patient department (OPD), in-patient department (IPD), and intensive care unit (ICU). The respiratory tract samples (sputum, bronchoalveolar lavage [BAL], endotracheal aspirate, gastric lavage, etc.) were obtained from the patients. **Results:** Out of 75 patients, males were 42 and females were 33. Common organisms isolated were psuedomonas species in 35%, pseudomonas aeruginosa in 24%, acinetobacter species in 16%, proteus species in 5%, klebsiella species in 4%, Escherichia coli in 3%, Enterobacter aerogenes in 6% and Streptococcus pneumonia in 7%. The difference was significant (P< 0.05). The location of patients was ICU in 28, IPD in 30 and OPD in 37. Samples were bronchoalveolar lavage in 16, sputum in 52, gastric aspirate 4, ET tube in 2 and Endotracheal aspiratein 1 case. The difference was significant (P< 0.05). **Conclusion:** Common organisms in LRTI patients isolated were psuedomonas species, pseudomonas aeruginosa, acinetobacter species, proteus species, klebsiella species, Escherichia coli, Enterobacter aerogenes and Streptococcus pneumonia.

Key words: Acinetobacter species,Escherichia coli,Lower respiratory tract infections

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INTRODUCTION

Lower respiratory tract infections (LRTIs) are common among patients worldwide, and the most major cause of pneumonia and bronchiolitis in hospitalization.[1] There are 3.5 million deaths attributed to and 79 million disability-adjusted life-years lost to LRTIs which are associated with high overall morbidity and mortality in adults, especially in patients older than 70 years old.[2,3]

Etiological agents of LRTI vary geographically and timely. The problem is much greater in developing countries.[4] Recognition of the possible existence of lung microbiome has been a major recent revelation in medicine.[5] The increase in antibiotic-resistance has compromised selection of empirical treatment and choice of effective-antibiotic.[6]Overall, viruses are responsible for a large proportion of LRTIs but antibiotics are often unnecessarily prescribed for their treatment without any laboratory testing and can contribute to the emergence of antimicrobial resistance.[7] Other causes of LRTIs are bacteria: Streptococcus pneumoniae, Haemophilus influenzae, Klebsiella pneumoniae, and Staphylococcus aureus being the most common.[8]The present study was conducted to assess bacterial pathogens from lower respiratory tractinfections.

MATERIALS & METHODS

The present study comprised of 75patients of both genders. The consent was obtained from all enrolled patients.

Data such as name, age, gender etc. was recorded. All patients were from out-patient department (OPD), in-patient department (IPD), and intensive care unit (ICU). The respiratory tract samples (sputum, bronchoalveolar lavage [BAL], endotracheal aspirate, gastric lavage, etc.) were obtained from the patients. Sputum-quality of sample was assessed based on Bartlett's scoring. Satisfactory sputum samples were further processed. BAL-microscopically percentage of neutrophils with engulfed bacteria was determined, and semiquantitative analysis ≥104 colony forming

unit (CFU)/ mL was done. Endotracheal aspirate: semi quantitative analysis ≥105 CFU/ml was done. Data thus obtained were subjected to statistical analysis. P value < 0.05 was considered significant.

RESULTS

Table I Distribution of patients

Total- 75		
Gender	**Males**	**Females**
Number	42	33

Table Ishows that out of 75 patients, males were 42 and females were 33.

Table II Distribution of organisms

Organisms	Percentage	P value
Psuedomonas species	35%	0.01
Pseudomonas aeruginosa	24%	
Acinetobacter species	16%	
Proteus species	5%	
Klebsiella species	4%	
Escherichia col	3%	
Enterobacter aerogenes	6%	
Streptococcus pneumonia	7%	

Table II, graph I shows thatcommon organisms isolated were psuedomonas species in 35%, pseudomonas aeruginosa in 24%, acinetobacter species in 16%, proteus species in 5%, klebsiella species in 4%, Escherichia coli in 3%, Enterobacter aerogenes in 6% and Streptococcus pneumonia in 7%. The difference was significant (P< 0.05).

Graph I Distribution of organisms

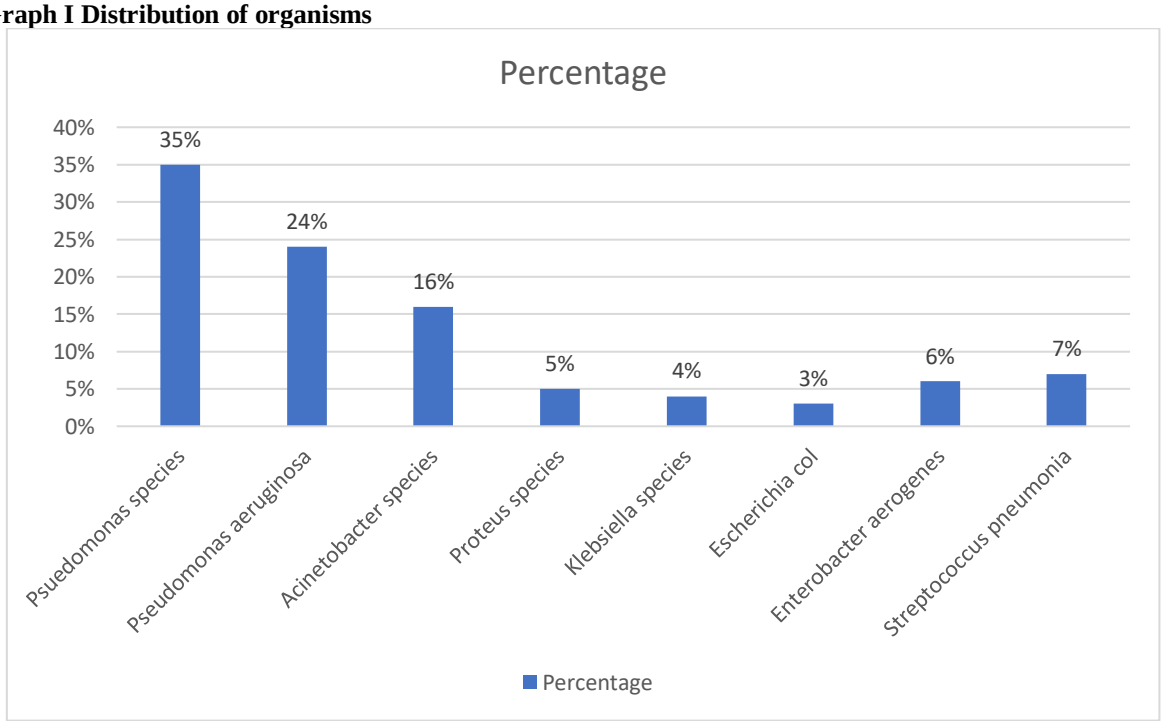
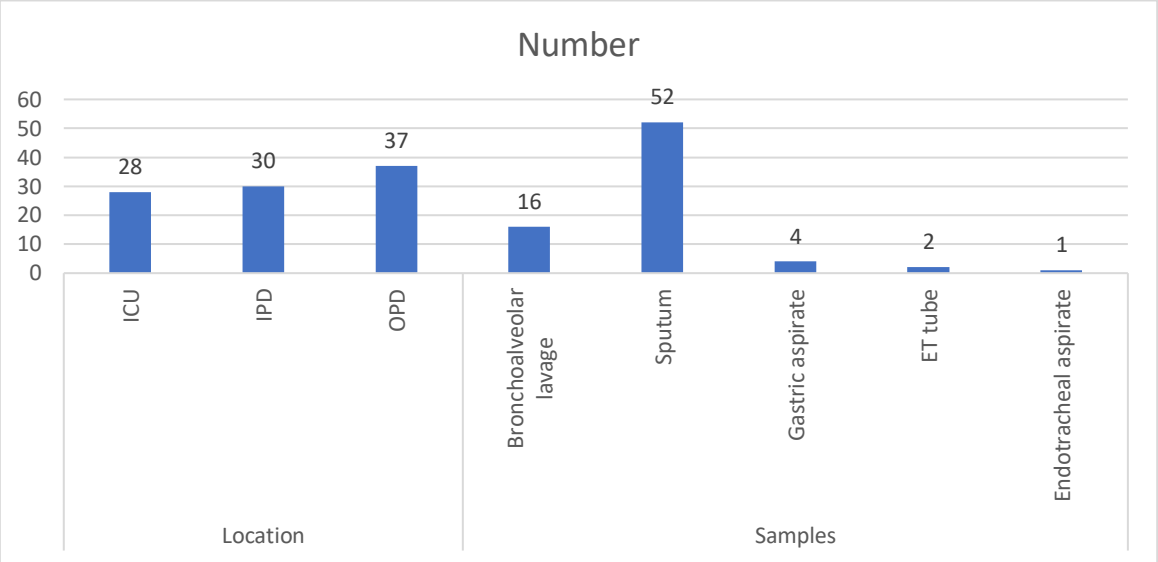


Table III Assessment of parameters

Parameters	Variables	Number	P value
Location	ICU	28	0.17
	IPD	30	
	OPD	37	
Samples	Bronchoalveolar lavage	16	0.01
	Sputum	52	
	Gastric aspirate	4	
	ET tube	2	
	Endotracheal aspirate	1	

Table III, graph II shows that location of patients was ICU in 28, IPD in 30 and OPD in 37. Samples were bronchoalveolar lavage in 16, sputum in 52, gastric aspirate 4, ET tube in 2 and Endotracheal aspirate in 1 case. The difference was significant (P< 0.05).

Graph II Assessment of parameters



DISCUSSION

Lower respiratory tract infections (LRTIs) are major cause of morbidity and mortality globally. LRTI is a broad terminology surrounding different clinical presentations and aetiologies, which may vary according toage and season among others.[9]The elderly have an increased risk of developing LRTIs compared to young adults.[10] Furthermore, it is also reported that children admitted with LRTIs had more severe respiratory disease and a longer recovery period even a quarter of them suffering respiratory sequelae. Antibiotics are commonly used to treat LRTIs, but clinical management of LRTIs is difficult due to antibiotic resistance.[11]Microbiological cultures of respiratory tract and blood specimens provided clinically relevant information concerning the identity and analysis of microorganisms with their susceptibility to antibiotics.[12]The present study was conducted to assess bacterial pathogens from lower respiratory tractinfections.

We found that out of 75 patients, males were 42 and females were 33.Tao et al[13] in total, 1,775 lower respiratory tract samples were received. Total 769 bacterial pathogens were isolated from cases of VAP, HAP, CAP, COPD, and cystic fibrosis. Pseudomonas species was the commonest isolate (31%), followed by Klebsiella pneumonia (21.3%), Acinetobacter species (17.5%), Escherichia coli (15.4%), and Staphylococcus aureus (5%). Others include Group A β-hemolytic Streptococcus, Burkholderiacepacia complex, Stenotrophomonas maltophilia, and Nocardia. Gram-negative organisms showed increased resistance to routinely used antibiotics. Gram-positive organisms showed 100% susceptibility to vancomycin, linezolid, and clindamycin.

We observed that common organisms isolated were psuedomonas species in 35%, pseudomonas aeruginosa in 24%, acinetobacter species in 16%, proteus species in 5%, klebsiella species in 4%, Escherichia coli in 3%, Enterobacter aerogenes in 6% and Streptococcus pneumonia in 7%.Trenholme et al[14] in their study 4,161 positive culture samples out of 18,798 different specimens from LRTI patients were analyzed for pathogen incidence and antibiotic sensitivity. Among the respiratory tract cultures, the frequency of Gram-negative bacterial strains was higher than Gram-positive bacterial strains. Pseudomonas aeruginosa was the dominant pathogen in both the adult respiratory ward (21.49%) and RICU (975), whereas Staphylococcus aureus (19.19%) was the most common bacterium in the pediatric ward. Among the blood cultures, Gram-positive bacteria remained the major microorganisms involved in LRTIs, and the most frequent pathogen was Staphylococcus epidermidis (n = 59, 47.20%) in the pediatric ward and Staphylococcus aureus (21.8%) in adult respiratory ward. However, Gramnegative bacteria were the main pathogens in the RICU, of which Klebsiella pneumoniae (27.57%) is the most prevalent. Pseudomonas aeruginosa of LRTI patients remained highly susceptible (>70%) to routine antibiotics in pediatric ward.

We found that location of patients was ICU in 28, IPD in 30 and OPD in 37. Samples were bronchoalveolar lavage in 16, sputumin 52, gastric aspirate 4, ET tube in 2 and endotracheal aspiratein 1 case.Rahbar et al have shown the isolation of Burkholderiacepaciacomplexas 4.66% of all the nonfermenters isolated from different types of specimens (respiratory, blood, urine, wound, etc.). Rahbar et al[15] iin their study 141 adult patients with

LRTIs were enrolled. Among the participants, 46.8% were positive for at least one bacterium. Streptococcus pneumoniae and Haemophilus influenzae were the most detected bacteria with 14.2% (20/141) followed by Klebsiella pneumoniae, 9.2% (13/141), Staphylococcus aureus, 7.1% (10/141), and Moraxella catarrhalis, 4.3% (6/141). Bacterial coinfection accounted for 23% (14/61) with Haemophilus influenzae being implicated in 19.7% (12/61). The diagnostic performance of RT-PCR for bacteria detection (43.3%) was significantly different from that of culture (17.7%). Only Streptococcus pneumoniae detection was associated with empyema by RT-PCR.

CONCLUSION

Authors found that common organisms in LRTI patients isolated were psuedomonas species, pseudomonas aeruginosa, acinetobacter species, proteus species, klebsiella species, Escherichia coli, Enterobacter aerogenes and Streptococcus pneumonia.

REFERENCES

1. Panda S, Prema NB, Ramani TV. Lower respiratory tract infection –Bacteriological profile and antibiogram pattern. Int J Cur Res Rev 2012;4:149-55.
2. Akingbade OA, Ogiogwa JI, Okerentugba PO, Innocent-Adiele HC, Onoh CC, Nwanze JC, et al. Prevalence and antibiotic susceptibility pattern of bacterial agents involved in lower respiratory tract infections in Abeokuta, Ogun State, Nigeria. Report Opinion 2012;4:25-30.
3. Chawla K, Vishwanath S, Munim FC. Nonfermenting gram-negative bacilli other than Pseudomonas aeruginosa and Acinetobacter spp. causing respiratory tract infections in a tertiary care center. J Glob Infect Dis 2013;5:144.
4. Ahmed NH, Hussain T, Biswal I. Antimicrobial resistance of bacterial isolates from respiratory secretions of ventilated patients in a multi-specialty hospital. Avicenna J Med 2015;5:74.
5. Sethi S. Infectious etiology of acute exacerbations of chronic bronchitis. Chest 2000;117:380-5.
6. ElKorashy RIM, El-Sherif RH. Gram negative organisms as a cause of acute exacerbation of COPD. Egyptian J Chest Dis Tuberc2014;63:345-9.
7. Malini A, Deepa EK, Gokul BN, Prasad SR. Nonfermenting gram-negative bacilli infections in a tertiary care hospital in Kolar, Karnataka. J Lab Physicians 2009;1:62.
8. Shah BA, Singh G, Naik MA, Dhobi GN. Bacteriological and clinical profile of Community acquired pneumonia in hospitalized patients. Lung India 2010;27:54.
9. Refdanita, R., Radji, M., Aribinuko, N., and Pauline, E. The sensitivity pattern of microorganisms against antibiotics at the intensive care unit of Fatmawati Hospital Jakarta 2001–2002. Makara J Health Res. 2010;8, 41–48.
10. Shi, T., McLean, K., Campbell, H., and Nair, H. Aetiological role of common respiratory viruses in acute lower respiratory infections in children under five years: a systematic review and meta-analysis. J. Glob. Health. 2015;5:010408.
11. Ghanshani, R., Gupta, R., Gupta, B. S., Kalra, S., Khedar, R. S., and Sood, S. Epidemiological study of prevalence, determinants, and outcomes of infections in medical ICU at a tertiary care hospital in India. Lung India. 2015;32:441–448.
12. Goel, N., Chaudhary, U., Aggarwal, R., and Bala, K. Antibiotic sensitivity pattern of gram-negative bacilli isolated from the lower respiratory tract of ventilated patients in the Intensive care unit. Indian J. Crit. Care Med. 2009;13, 148–151.
13. Tao, L., Hu, B., Rosenthal, V. D., Gao, X., and He, L. (2011). Deviceassociated infection rates in 398 intensive care units in Shanghai, China: international nosocomial infection control consortium findings. Int. J. Infect. Dis. 2011;15:774–780.
14. Trenholme, A. A., Byrnes, C. A., McBride, C., Lennon, D. R., Chan-Mow, F., Vogel, A. M., et al. Respiratory health outcomes 1 year after admission with severe lower respiratory tract infection. Pediatr. Pulmonol. 2013;48: 772–779.
15. Rahbar M, Mehragan H, Haji Ali Akbari N. Prevalence of drug resistance in nonfermenter gram-negative bacilli. Iran J Pathol2010;5:90-6.