A Study on the Microbiological Profile of Respiratory Tract Infection (RTI) in Patients Attending Gauhati Medical College & Hospital.

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ABSTRACT

Background: Respiratory tract infections (RTI's) are the most frequent infections among patients. The consequences of increased drug resistance are far reaching since bacterial infection of the respiratory tract (RT) is a major cause of death from infectious disease. **Objective:** This study was focused on obtaining a comprehensive insight into the microbial profile, its prevalence and the antibiotic susceptibility patterns of the isolates in respiratory tract infections. **Methods:** The present study was conducted in the Microbiology Department of a Teaching Government Hospital during January 2014 to June 2014. The Respiratory Tract samples were obtained from the patients (n=1376) of all the age and sex groups, with signs and symptoms suggestive of RTIs. Following culture, the isolated organisms were identified and antimicrobial sensitivity was performed by standard methods. **Results:** Out of the 1376 RT specimens evaluated, 684(49.70%) were culture positive. A Study showed predominance of Gram negative bacterial cause (67.39%) among the RTI's with *Klebsiella pneumoniae* (41.66%) as a major pathogen followed by *Candida spp* (17.39%), *Staphylococcus aureus* (12.86%), *Pseudomonas aeruginosa* (11.69%), *and E coli* (10.96%). Gram-negative organisms showed increased resistance to routinely used antibiotic. Gram positive organisms showed 100% susceptibility to vancomycin, linezolid, clindamycin, tetracycline, amoxclav and followed by their susceptibility against gentamycin, penicillin.**Conclusion:** Therefore, we can conclude that for effective management of RTI's, an ultimate and detailed bacteriological diagnosis and susceptibility testing are required to overcome the global problem of antibiotic resistance.

Keywords: Lower Respiratory Tract Infection, Antimicrobial Susceptible Pattern, Microbial Profile.

INTRODUCTION

Respiratory Tract Infection (RTI) is by large one of the leading causes of the morbidity and mortality in the world. By terminology, RTI is a term assigned not to a single disease, but to a spectrum of infections, each with a different epidemiology, clinical presentation, pathogenesis and prognosis. The etiology, signs and symptoms of respiratory diseases vary with age, sex, season, the type of population at risk and various other factors. These are commonly the first infection to occur post birth and pneumonia is quite often the final illness to occur before death. [1]

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Respiratory tract infections accounts for approximately 4.4% of all hospital admissions and around 6% of all general practitioner consultations.

They are responsible for 3 to 5% of deaths in adults .Compared to developed countries, the problem is way greater in developing countries where pneumonia is the commonest cause of hospital attendance in children and adults.[2] In India, acute lower respiratory tract infection (ARI) alone is responsible for one million deaths. Still, it needs to be mentioned that there is a lack of adequate information from India on various lower respiratory tract bacterial pathogens and their antibiogram picture in hospital settings. Additionally, the emergence of resistance to a wide range of antibiotics has drawn attention to a need for better diagnostic techniques and development of newer drugs to allow somewhat more specific therapy.[3] The etiologies of respiratory infections assume an important role in the decision making, as they form the backbone for the choice of empirical antibiotics and hospitalization measures. A number of organisms are usually implicated in their etiologies, the commonest being Gram negative bacteria,[4] followed by Gram positive organisms. Specific microbiological investigations are the need of the hour for minimizing the subsequent development of

complications and for improving the outcomes of antimicrobial therapy. The global rise in the antimicrobial resistance among the respiratory pathogens,[5] presumably due to the prophylactic and at times irrational administration of antibacterial therapy, even before the availability of the culture results, is a matter of great concern worldwide. This study has been thus undertaken in an attempt to review our current understanding on upper and lower respiratory tract infections and it has highlighted the changing trends in their occurrence and the antimicrobial susceptibility pattern of the respiratory pathogens which were isolated in Department of Microbiology, Gauhati Medical College, thereby enabling the physicians to appropriately formulate and endorse a competent and rational antibacterial policy, to further curb the incidence of the disease.

Objectives of the Study
The objective of the present study is
1. To find out the bacteriological spectrum of Respiratory Tract Infection among the patients attending our setup.
2. To determine the pattern of antibiogram of the isolates.

MATERIALS AND METHODS

The study was conducted in the Microbiology Department of Gauhati Medical College during the period from January 2014 to June 2014. The collected samples, i.e. sputum, Bronchoalveolar lavage (BAL), Tracheal aspirates and Throat swabs were obtained from the patients (1376) of all the age and sex groups, with symptoms and signs which were suggestive of RTIs. The samples were collected under aseptic precautions with as minimal contamination as possible and processed immediately following collection by the standard laboratory methods. Microscopy was performed for each sputum sample and quality of the sample was decided to use standard grading system. The samples found to be satisfactory were further processed. Organisms isolated from all the eligible samples were identified by observing the colony characteristics on the Blood agar, MacConkey agar plates and performing biochemical reactions subsequently using standard microbiological methods. The bacterial isolates were subjected to susceptibility testing by standard Kirby Bauer disc diffusion methods [6] as recommended by the Clinical Laboratory Standard Institute (CLSI) -2014. Zone diameter was measured in millimeters and interpreted as per CLSI guidelines.[7]

RESULTS

Among the 1376 samples included were Tracheal aspirate (87), Sputum (1101), Throat swabs (168) and Bronchoalveolar lavage (20). The culture result of these 1376 samples revealed that 684 (49.70%) were positive and remaining 692 (50.29%) samples either showed no growth or growth of contaminants which was considered as no growth. Of the 168 Throat swab samples 87 (51.78%) were culture positive, of the 1101 Sputum samples 547 (49.68%) were culture positive, of the 87 Tracheal aspirate samples 46 (52.87%) were culture positive and of the 20 BAL samples 4 (20%) were culture positive. [Figure 1].
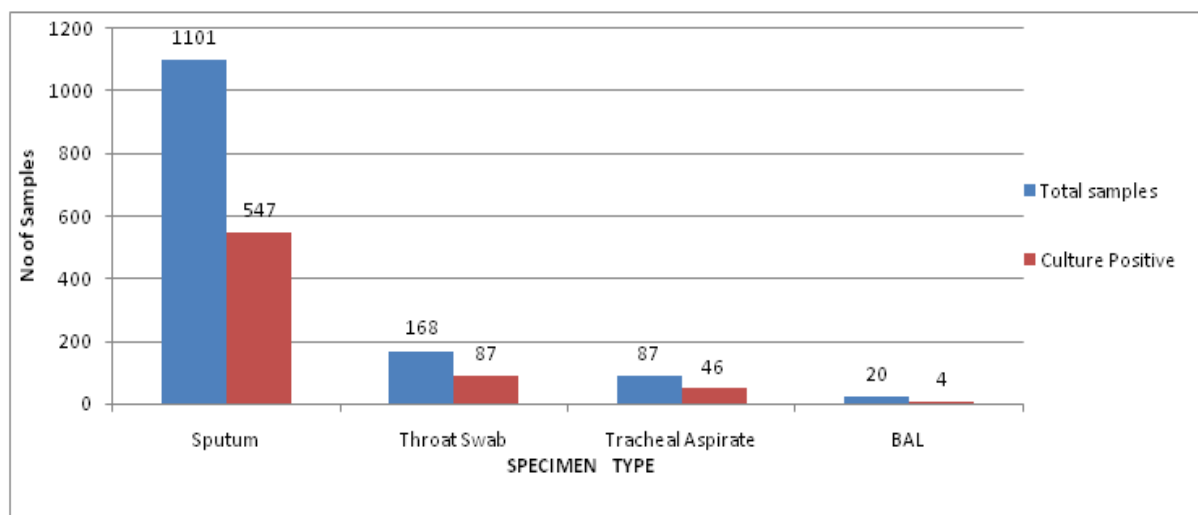

Figure 1: Culture Report of Respiratory Specimen.

Klebsiella pneumoniae (41.66%) was found to be the predominant organism which was isolated, followed by Candida *spp* (17.39%), Staphylococcus *aureus* (12.86%), Pseudomonas *aeruginosa* (11.69%), E *coli* (10.96%) and Coagulase Negative Staphylococcus spp. (CONS) (1.75%) [Table 1], [Figure 2]
Pseudomonas *aeruginosa* showed maximum resistance to Ceftazidime, Piperacillin and Piperacillin-Tazobactum. [Table 2] Klebsiella

pneumoniae exhibited a higher sensitivity towards Polymixin B, Tigecycline, Imipenem, Levofloxacin, Amikacin, Gentamicin, and Amoxyclav, followed by Piperacillin-Tazobactam. However Ceftazidime and other broad spectrum antibiotics like Penicillin and Cotrimaxzole showed lower susceptibility. [Table 2]

Gram positive organisms on the other hand showed 100% susceptibility to Vancomycin and Linezolid followed by high susceptibility to Teicoplanin, Levofloxacin, Doxycycline, Amoxyclav and Gentamycin.

Table 1: Source of specimen and Microbiological cause.

Type of Specimen	No of samples tested	No of Culture positive (%)	Microorganism isolated	
Sputum	1101	547 (49.68%)	Klebsiella pneumoniae	228
			Candida spp	98
			Staphylococcus aureus	58
			Escherichia coli	75
			Serratia spp	4
			Pseudomonas spp	72
			Enterobacter spp	12
Throat Swab	168	87 (51.78%)	Klebsiella pneumonia	49
			Staphylococcus aureus	29
			Enterobacter spp	5
			Corynebacterium diphtheria	2
			Streptococcus pyogenes	2
Tracheal Aspirate	87	46 (52.87%)	Candida spp	21
			Klebsiella pneumonia	5
			Staphylococcus aureus	1
			Pseudomonas spp	7
			CONS	12
BAL	20	4 (20%)	Klebsiella pneumonia	3
			Pseudomonas spp	1
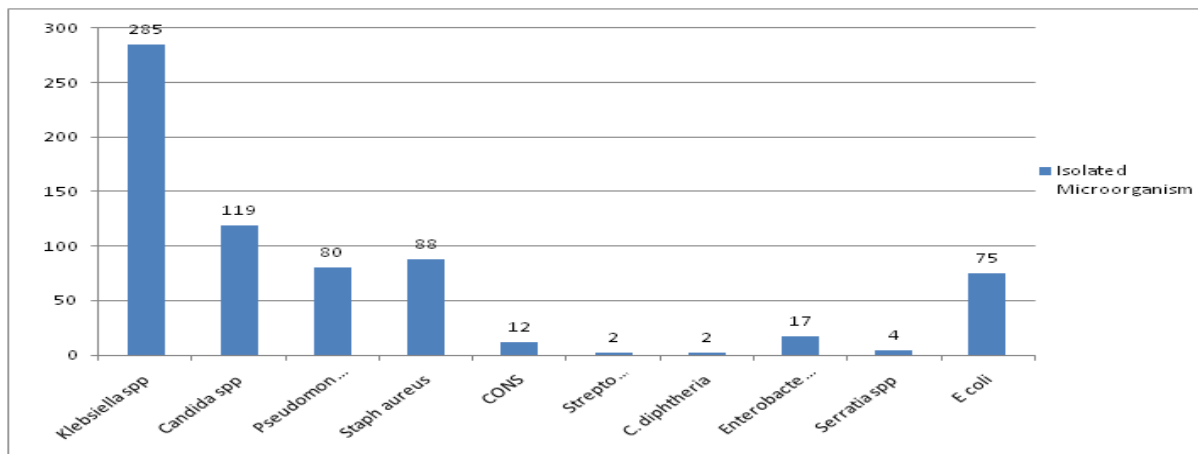
Figure 2: Diagrammatic representation of organisms isolated.
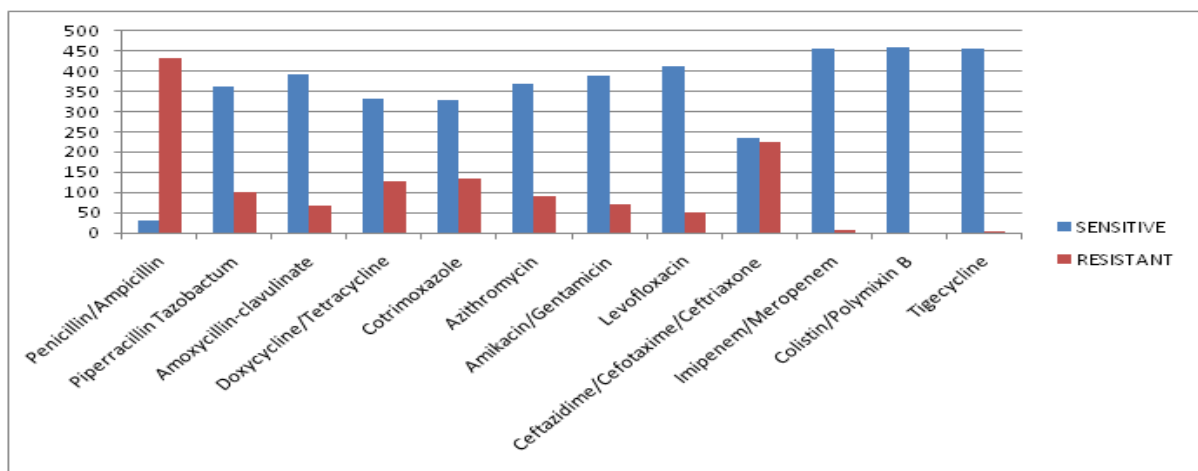
Figure 3: Antibiogram of Gram Negative Isolates.

Table 2: Antibiogram pattern of all the bacterial isolates.

Antibiotic	Gram Negative Bacilli (n= 461)		Gram Positive Cocci (n=102)	
	Sensitive	Resistant	Sensitive	Resistant
Penicillin/Ampicillin	29	432	12	90
Piperracillin Tazobactum	361	100	87	15
Amoxycillin-clavulinate	393	68	93	9
Doxycycline/Tetracycline	332	129	97	5
Cotrimoxazole	328	133	88	14
Azithromycin	370	91	76	26
Amikacin/Gentamicin	389	72	81	21
Levofloxacin	412	49	94	8
Ceftazidime/Cefotaxime/Ceftriaxone	236	225	73	29
Imipenem/Meropenem	455	6	--	--
Colistin/Polymixin B	461	0	--	--
Linezolid	--	--	102	0
Vancomycin	--	--	102	0
Tigecycline	457	4	--	--
Teicoplanin	--	--	99	3
Cefoxitin screen**	--	--	65	23

** Cefoxitin screen was performed for diagnosis of MRSA strains amongst the Staphylococcus *aureus* isolates only - Antibiotic not tested for the isolate

PIC 1: C. diphtheria in Albert Stain smear under Microscope.
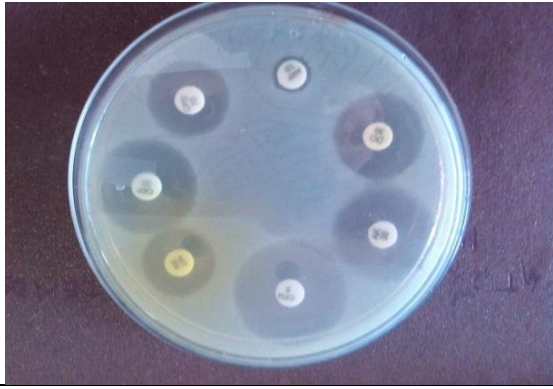

PIC 2: Hemolytic colonies of *Staphylococcus aureus*.

DISCUSSION

Management of RTI's has been a challenge to the physicians, most recently due to the emergence of multi drug resistance.[8] The present study is an attempt to provide an insight on the prevalence and the antibiogram pattern of the respiratory pathogens which were isolated in a tertiary care hospital of Northeast India. Among the specimens processed, 554 (50.32%) sputum samples, 16 (80%) bronchoalveolar lavage, 81 (48.21%) Throat swabs and 41 (47.12%) Tracheal aspirate samples revealed no pathogens. *Klebsiella pneumoniae* was the predominant pathogen isolated from sputum 228 (41.68%), Throat swab 49 (56.32%) and BAL 3(75%) while in Tracheal aspirates Candida *spp* was the predominant pathogen isolated 21 (45.65%). Overall specimens processed showed Staphylococcus *aureus* 88 (12.86%) was the most common Gram positive bacterial isolate. Our study showed predominance of Gram negative bacterial cause (67.39%) among the RTI's. A similar finding was observed by a recent study from Nepal by SK Mishra et al who reported 84.1% occurrence. Incidentally, the same study reported Haemophilus influenzae (21%) as the most common Gram negative bacterium isolated in contrast to our study, which showed Klebsiella *pneumonia* (41.66%) as predominant Gram negative isolate. In their study, SK Mishra et al stated *Streptococcus pneumoniae* as the predominant Gram positive bacterial (8.6%) cause in contrast to the our study, which showed Staphylococcus *aureus* (12.86%) as predominant Gram positive bacterial cause.[1] Among other notable studies, V. Olugue et al.,[5] Kaul et al.,[9] and Akingbade OA[10] too found Klebsiella *pneumonia* as predominant pathogen which resonated with our study which showed similar findings. The antimicrobial resistance among the respiratory pathogens is a major issue faced by clinicians and microbiologists alike that might interfere with providing an effective treatment. This study depicts the prevalent antibiogram picture amongst the Gram negative and Gram positive respiratory pathogens which were isolated during the study, as has been shown in [Table 2].

for individual patients. The therapy should be based on an aggressive diagnostic work up and the broad spectrum antimicrobial treatment which is guided by microbiological support.

PIC 3: Modified Kirby Bauer Disc diffusion system.

In the current study Gram positive organisms showed 100% susceptibility to Vancomycin and Linezolid while possessing good susceptibility to Teicoplanin, Levofloxacin, Doxycycline, Amoxyclav and followed by their reduced susceptibility against Azithromycin, penicillin. 23 (26.13%) of the Staphylococcus *aureus* isolates were found to be Methicillin resistant (MRSA) [Table 2]. Similar findings were reported from some other investigators as well.[1,11] For Gram positive Bacterial infections Aminoglycosides and Levofloxacin are widely recommended as first line drugs for empirical treatment reserving Vancomycin and Linezolid for resistant cases. The resistance among the respiratory pathogens, especially *Pseudomonas aeruginosa* to the antimicrobial agents that have traditionally been recommended as the first line therapy, is steadily on the rise. Likewise, our study showed Gram negative isolates have maximum resistance to Ceftazidime, Piperacillin and Piperacillin tazobactum in contrast to study conducted by Ahemad M S et al.[12] which showed high susceptibility to piperacillin-tazobactum. But present study is in concordance with results found by Nidhi Goel et al.[4] In our study Amoxyclav, Amikacin and Levofloxacin had shown greater activity against *Klebsiella pneumoniae* similar to a study conducted by Bajpai et al[13] and in contrast to Ahmed et al study.[12]

CONCLUSION

The emergence of resistant strains poses a major threat to the patients globally. Inappropriate and irrational drug usage should be avoided. Owing to the increased concern which surrounds antibiotic resistance and the changing patterns of bacterial pathogens, the ongoing surveillance of disease and a regular review of the management guidelines are critical. Educational campaigns have quite sensibly tried to convince both the doctors and the general public about the need to use appropriate, evidence based antibiotic treatment policy which is based on the infective organism. Ongoing community based studies are needed to identify the best management

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