MICROBIOLOGICAL PROFILE AND ANTIBIOGRAM OF LOWER RESPIRATORY TRACT INFECTIONS AT LAHORE GENERAL HOSPITAL, LAHORE

Muna Malik[1], Muhammad Irfan Malik[2], Fahd Kamal Akhtar[3]

[1] Department of Pathology, Ameer Ud Din Medical College/Post Graduate Medical Institute, Lahore General Hospital, Lahore – Pakistan.
[2] Department of Pulmonology, Ameer Ud Din Medical College/Post Graduate Medical Institute, Lahore General Hospital, Lahore – Pakistan.
[3] Lahore General Hospital, Lahore – Pakistan.
Address for Correspondence:
Dr. Muna Malik
Department of Pathology, Ameer Ud Din Medical College/Post Graduate Medical Institute, Lahore General Hospital, Lahore – Pakistan.
Email: mmkamboh@hotmail.com
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ABSTRACT

Objectives: To identify the microbial pathogens that are responsible for lower respiratory tract infections in a tertiary care hospital and pattern of their antimicrobial susceptibility.

Methodology: This descriptive study was carried out at Lahore General Hospital (LGH), Lahore, during January to December 2017. The lower respiratory samples i.e. sputum, broncho-alveolar lavage (BAL), tracheal secretions, endotracheal tips, tracheostomy tubes, chest drains and pleural fluid were obtained from 923 patients. The samples were collected aseptically and processed at Department of Pathology, PGMI, Lahore. The bacteria were identified according to microbiological tests and their antimicrobial susceptibility was done according to Clinical and Laboratory Standards Institute (CLSI).

Results: Total 923 samples were received, 607 were positive on culture (65.7%). The most common isolated bacteria from all these specimens were *Pseudomonas aeruginosa* 217 (35.74%). Cefoperazone-sulbactam and piperacillin-tazobactam were the most sensitive antibiotics having >70% of sensitivity. *Staphylococcus aureus* were isolated in 55 (8.73%) of specimens, out of which 73% were reported as MRSA.

Conclusion: The present study showed the microbiological pattern of bacteria in samples of LRTIs and trend of their antimicrobial susceptibility at LGH. The commonest bacterium was *Pseudomonas aeruginosa*. Cefoperazone-sulbactam and piperacillin-tazobactam were the most sensitive antibiotics.

Key Words: Lower respiratory tract infections, Antibiogram, Antimicrobial resistance, *Pseudomonas aeruginosa*

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INTRODUCTION

Lower respiratory tract infections (LRTIs) are a persistent health problem with massive burden on the society in developing countries. These infections are being the common reasons for consultation and hospitalization of patients[1,2]. Out of total hospital admissions, 4.4% of admissions are due to infections of the lower respiratory tract; 6% are presented to general practitioner for consultations and these account for 3-5% of deaths in adults[3]. Patients with LRTIs present with a wide spectrum of illness, which range from minor self-limiting infections to potentially life threatening diseases. Pneumonia is one of the foremost causes among LRTIs having increased morbidity and mortality in all age groups and often leads to the final illness before death[4]. It usually occur when the causative microorganisms reach the lower airways or pulmonary parenchyma of hosts and bypass the mechanical and other barriers of the upper respiratory tract[5].

The etiology of LRTIs according to their causative microorganisms and their antimicrobial susceptibility pattern is different. Their etiology and symptomatology depends on age group, gender, population at risk, season, healthcare facilities, immunosuppression, usage of inappropriate antimicrobials and their resistance[6-8]. The pathogenic microorganisms can be common bacteria, intracellular pathogens, fungi, viruses and parasites. Among bacteria, the commonest Gram positive bacteria are *Staphylococcus aureus & Streptococcus pneumoniae*; commonest Gram-negative bacteria are *Pseudomonas spp., Klebsiella spp., & Escherichia coli;* and Gram variable *Acinetobacter spp.* are among the commonest nosocomial infections[6]. Currently, it is no longer acceptable that antibiotics are harmless and these antibiotics may lead

to the emergence of resistant bacterial strains. From the past few decades, LRTIs present as multidrug resistant (MDR) infections and pathogenic bacteria even become Pan drug resistant (PDR) strains in hospital. Infections caused by these MDR and PDR bacteria are categorized as community-acquired pneumonia (CAP) or health care–associated pneumonia (HCAP). The HCAP is further divided into hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) happened in patients admitted in wards and ICUs respectively[9].

Our study was conducted with the aim to identify the microbial pathogens that are responsible for lower respiratory tract infections in a tertiary care hospital and chasing the rate and pattern of their antimicrobial susceptibility. The knowledge of their frequency and antimicrobial resistance pattern will help in the better clinical management of patients with LRTIs and their clinical outcome. It will also help us to draw competent outlines of the hospital antibiotic policies and regimes regarding these common and dreadful infections.

METHODOLOGY

Lower respiratory tract infections (LRTI's) are those infections, which present with symptoms comprising of cough, dyspnoea, expectoration, chest pain/discomfort and wheeze usually for a period of 7-21 days. Acute lower respiratory tract infections include bronchiolitis, acute bronchitis, influenza, community–acquired pneumonia with or without radiological signs, acute exacerbation of bronchiectasis and acute exacerbation of chronic obstructive pulmonary disease (COPD)[10]. The present descriptive study was conducted in a teaching hospital of Lahore during January 2017 to December 2017. The lower respiratory samples i.e. sputum, broncho-alveolar lavage (BAL), tracheal secretions, endotracheal tips, tracheostomy tubes, chest drains and pleural fluid were obtained from 923 patients. Patients of all age groups, both sex and having symptoms which were suggestive of LRTIs caused by bacteria e.g. fever >37˚C, productive cough, difficulty in breathing, physical finding of consolidation with chest pain and WBC count >11,500/cmm were included. Patients suffering from viral LRTIs, confirmed cases of tuberculosis and immune-compromised patients were excluded from the study.

All samples were collected aseptically and processed according to standard operating procedures of microbiology. The quality of all samples was standardized by grading system (Barlett' scoring system and Q score) and direct microscopy of the samples was done which provided initial clues about the type of bacteria, whether the material was purulent or not, i.e. ≥25 neutrophils and ≤10 squamous cells per LPF[11]. Satisfactory samples of sputum, endotracheal tips, tracheal secretions, bronchial washings and pleural fluid were processed further for culture and sensitivity. They were inoculated on blood agar and MacConkey agar with added crystal violet and incubated for 24 hours in an incubator at 37^{0}C. The cultures were read next day for any positive or negative growth. The culture was read as semi-quantitatively when growth was moderate or heavy; and quantitatively when more than 104 colony-forming units (CFU)/ml were isolated from bronchial washing[12]; and 105 CFU/ml of bacteria were isolated on culture from others samples of LRTIs[13]. The bacteria were preliminary identified on the basis of their colonial morphology, presence or absence of hemolysis on blood agar and being fermenter or non-fermenter. Then Gram's staining was done for confirmation and typing whether Gram positive or Gram-negative and cocci or bacilli. Further confirmation was done by biochemical reactions like catalase, coagulase and oxidase tests etc[14,15].

The antimicrobial susceptibility testing was done on Mueller-Hinton agar by Kirby-Bauer disc diffusion method. A 0.5 McFarland turbidity standard equivalent to bacteria suspension was prepared for inoculation and inoculated on the agar, antibiotics disc were applied and the plates were incubated at 37˚C for 24 hours and interpreted as per CLSI 2017 guidelines. The following antibiotics were used for antimicrobial susceptibility testing: ampicillin, amoxicillin-clavulanic acid, cefuroxime, ceftriaxone, ceftazidime, cefotaxime, cefipime, sulfamethoxazole trimethoprim, imipenem, meropenem, aztreonam, ciprofloxacin, levofloxacin, amikacin, gentamicin, tobramycin, piperacillin-tazobactam, cefoperazone-sulbactam. For *Acinetobacter spp,* ampicillin-sulbactam was additionally used. For Gram positive bacteria, antibiotic disk of linezolid, vancomycin, penicillin, amoxicillin-clavulanic acid, ciprofloxacin, levofloxacin, amikacin, gentamicin, tobramycin, sulfamethoxazole trimethoprim, erythromycin, azithromycin, clarithromycin, clindamycin and cefoxitin was used for identification of MRSA (CLSI 2017). MDR were considered when Gram-negative organisms were not susceptible to more than one drug in at least three antimicrobial groups[16,17]. Descriptive statistical analysis of the data were carried out by SPSS version 22. Frequencies and percentages were calculated for variables in the present study.

RESULTS

A total of 923 samples were received and processed in the laboratory. Among these, 357 samples were received from medical units, followed by 331 from PINS, 177 from pulmonology and 58 were received from department of surgery and allied. The yield of positive culture was 607 (66%).

The most common isolated bacteria from all these specimens were *Pseudomonas aeruginosa* (n=217, 35.74%) followed by *Klebsiella pneumoniae* (n=201,

33.11%); some samples showed growth of more than one bacteria. Trend of bacteria according to different departments was as follows: from medical units *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* were equally isolated; from PINS most common isolated bacteria was *Klebsiella pneumoniae*; and from pulmonology department the most common bacterial isolate was *Pseudomonas aeruginosa*. Trend of bacteria isolated from different specimens was as follows: from tracheal secretions, ETT tips and tracheostomy tube *Klebsiella pneumoniae* was most frequently isolated; from sputum, pleural effusions *Pseudomonas aeruginosa* was most commonly isolated; and *Streptococcus pneumoniae* was commonly isolated from bronchial washings.

Our results showed that Gram-negative bacilli were least susceptible to amoxicillin-clavulanic acid (2.9-4.3%). They also showed high resistance to cephalosporin and sulfamethoxazole trimethoprim 14-40%. Except *Pseudomonas aeruginosa*, which was 63.5% susceptible to Aztreonam, *Klebsiella pneumoniae, E.coli and Acinetobacter spp*. showed high resistance to Aztreonam. *Klebsiella pneumoniae* and *E. coli* showed good response (60%) to carbapenems (imepenem and meropenem). However, *Pseudomonas aeruginosa* and *Acinetobacter spp*. were more resistan having <50% susceptibility. All bacteria were susceptible to floroquinoles and aminoglycosides; among these levofloxacin and amikacin had better susceptibility as compared to other group members. The most susceptible trend was seen with combination drugs (Cefoperazone-sulbactam and Piperacillin-tazobactam).

In our study, *Staphylococcus aureus* showed 100% susceptibility to vancomycin and linezolid, followed by aminoglycosides (51%); and 73% of *Staphylococcus aureus* of our study were reported as MRSA.

Figure 1: Yield of culture results isolated from different specimens of LRTIs

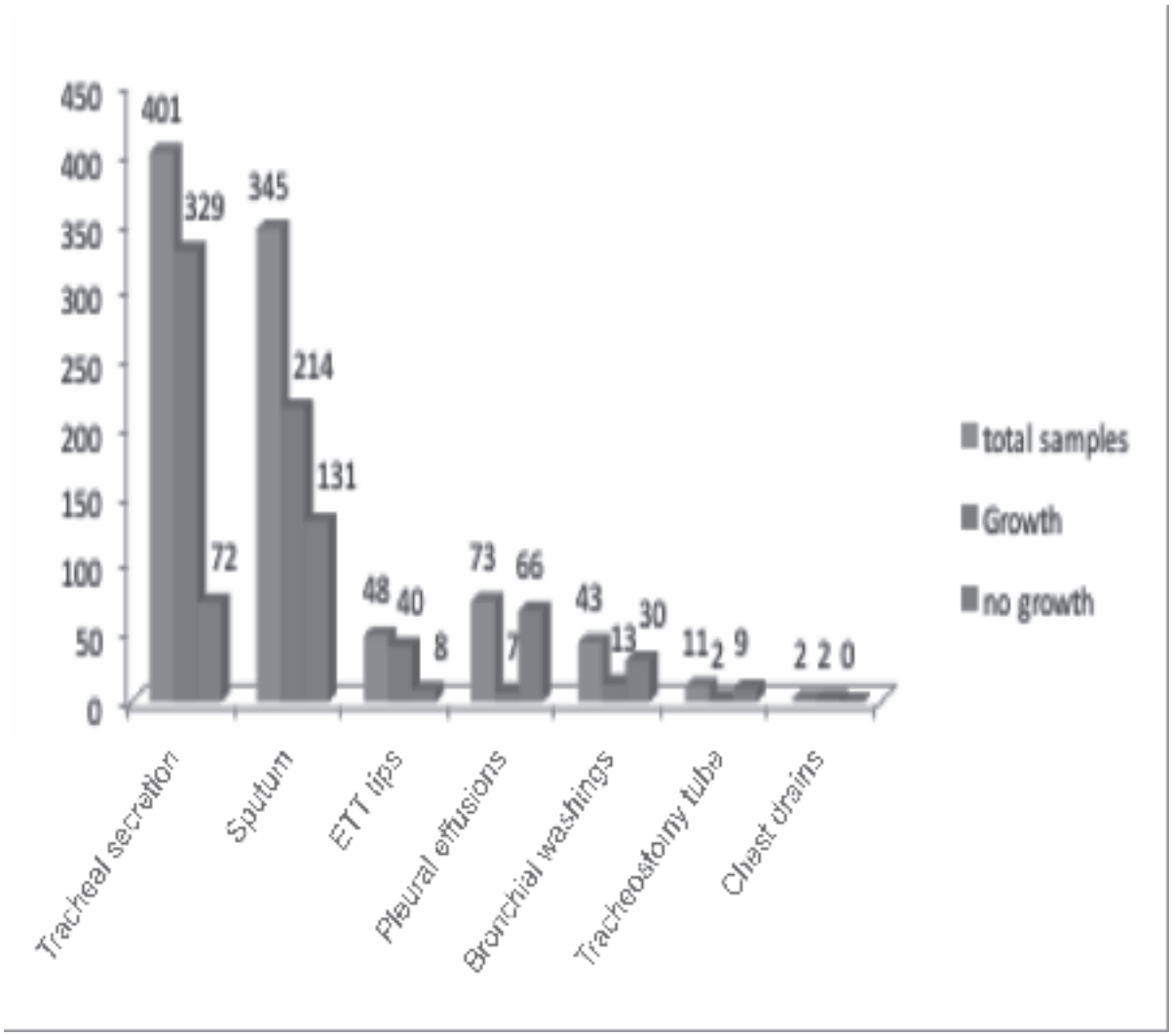

Figure 2: Frequency of bacteria isolated from different samples of LRTIs

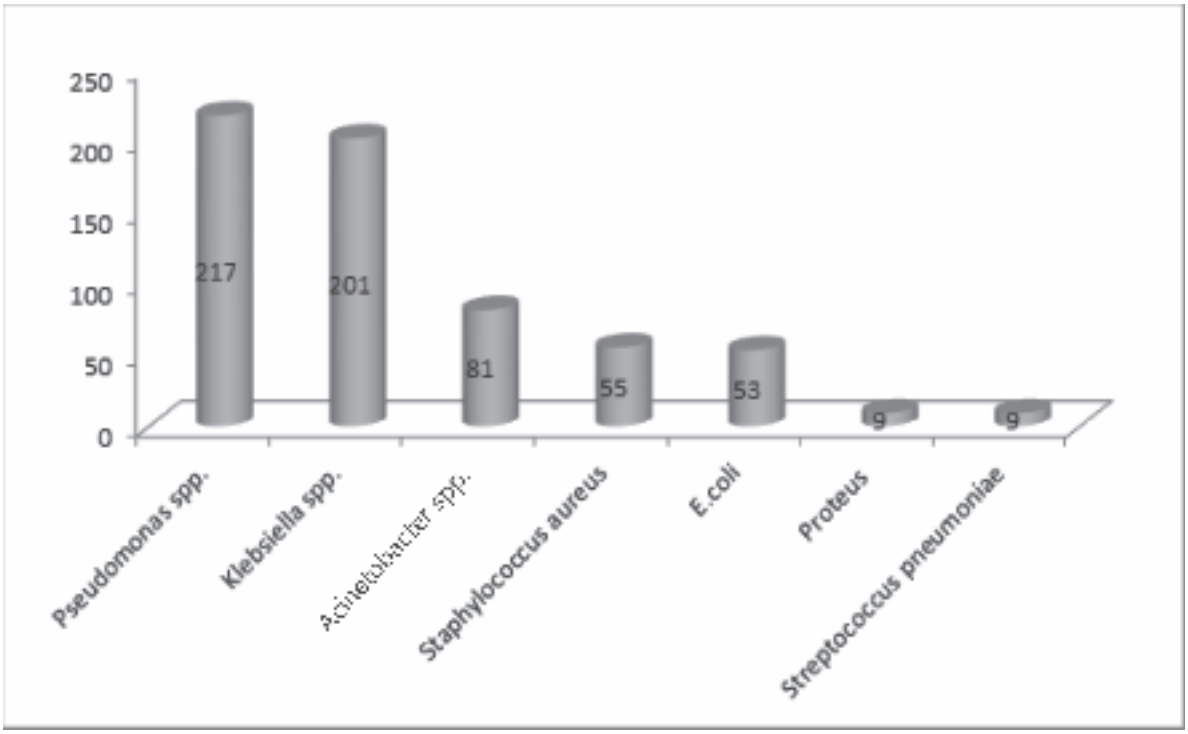

Figure 3: Antimicrobial susceptibility of Staphylococcus aureus isolated from LRTIs

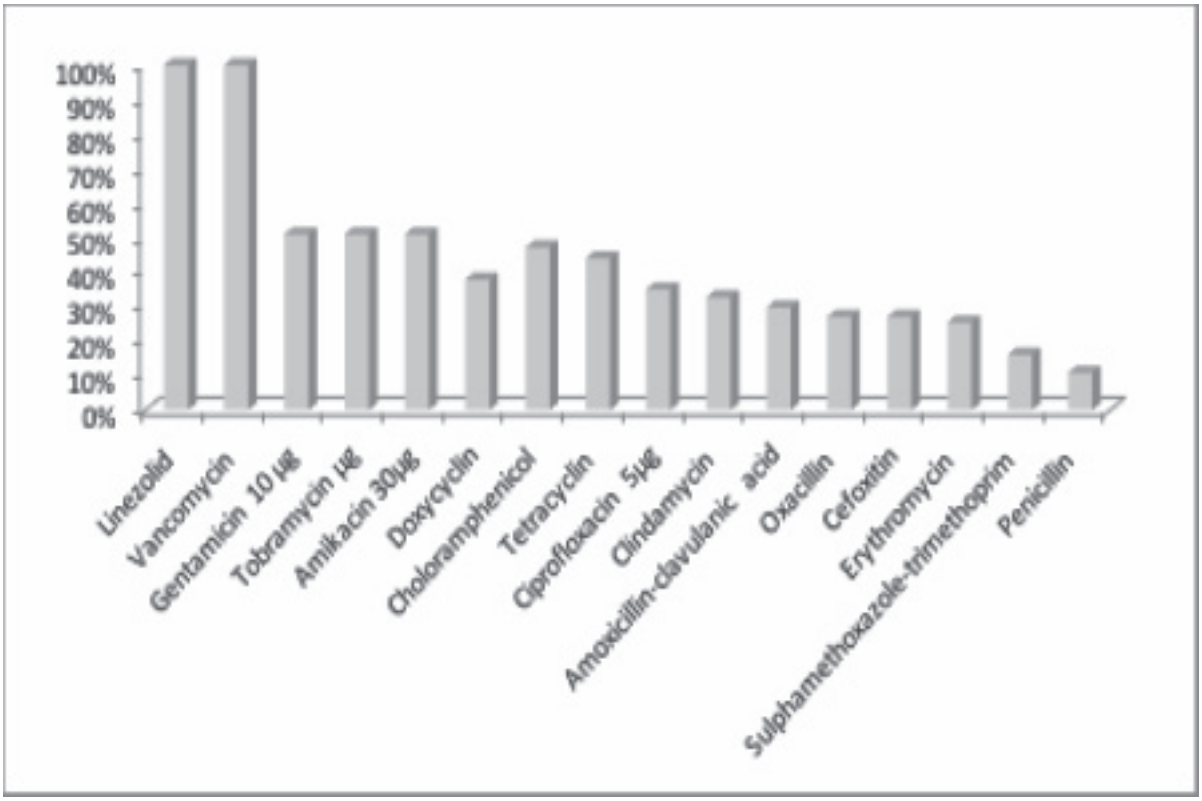

Table 1: Antimicrobial susceptibility pattern

Antibiotics	Percentage of Sensitivity			
	Klebsiella Spp.	***Pseudomonas Spp.***	***Acinetobacter Spp.***	***E. coli***
Amoxicillin-clavulanic acid 30µg	2.9%	--	--	4.3%
Ceftazidime 30µg	13.9%	29.4%	24.6%	13.2%
Cefotaxime 30µg	16.9%	--	28.3%	16.9%
Ceftriaxone 30µg	14%	--	19%	13.5%
Cefuroxime 30µg	16.9%	--	15.9%	16%
Cefepime 30µg	34.3%	51.1%	41.9%	22.6%
Cefoperazone-sulbactam	66.6%	71.2%	69.1%	67.9%
Sulfamethoxazole trimethoprim	16.4%	--	10.2%	20.7%
Aztreonam	31.3%	63.5%	30.8%	33.9%
Gentamicin 10 µg	64.2%	62.6%	59.2%	67.9%
Tobramycin µg	57.3%	55.7%	56.7%	52.8%
Amikacin 30µg	56.7%	69.5%	65.4%	77.3%
Ciprofloxacin 30 µg	48.7%	58.5%	34.5%	26.4%
Levofloxacin 30	62.6%	66.3%	53.0%	47.1%
Imepenem	50.7%	48.3%	37%	64.1%
Meropenem	53.2%	53.9%	38.2%	67.9%
Piperacillin-tazobactam	66.1%	78.3%	82.7%	73.5%
Piperacillin	--	42.3%	33.3%	--
Ampicillin-sulbactam	--	--	44.4%	--

DISCUSSION

The bacteriological diagnosis of LRTIs is usually challenging, as the specimens used for investigation are contaminated by the microbes which exist in the upper respiratory tract, as a result the need for sophisticated invasive procedures is required[2]. In our study, LRTIs was more common among males 726 (78.6%), this is similar to the findings of Sarkar et al[18]. They linked this with more prevalence of smoking as well as profession related to smoke among males. In our study, the most common specimen received was of tracheal secretions followed by sputum. In contrast to this, sputum was most common specimen of LRTIs in other studies[7].

Most of the specimens received in our laboratory showed positive culture growth. This result is also consistent with other studies conducted by Ravichitra et al[9]. The highest yield of positive culture was isolated from tracheal secretions in our study, which is also in accordance to Khan et al 6 and Mishra et al[7]. In our study, *Pseudomonas aeruginosa* was the commonest bacterium isolated, which is similar to the study conducted by Saxena et al[19]. The knowledge of etiology of pathogens in patients of lower respiratory tract infections will be helpful for the empirical drug choice[19]. According to WHO, common infections e.g. pneumonia are increasingly caused by resistant bacteria and these MDR pathogens are responsible for poor prognosis[21,22]. In our study, current antibiotics used to treat LRTIs showed high rate of resistance. The most multi-drug resistant bacteria of LRTIs was *Acinetobacter spp*. This is consistent with the study conducted by Saha who reported huge resistance of *Acinetobacter spp.* against large group of antibiotics. The most susceptible antibiotics among Gram-negative bacteria were beta lactam along with beta lactamase inhibitors e.g. cefoperzone-sulbactam and piperacillin–tazobactam, having almost 70% susceptibility followed by aminoglycosides and carbapenems having more than 60% of susceptibility; similar observations were reported by Kombade et al[23]. The resistant strains, including MDR and extensively drug resistant (XDR), were an alarming trend. Some super bugs were resistant to all antimicrobials except colistin and tigecycline[25].

In the present study, 73% *Staphylococcus aureus* were MRSA. Tripathi et al[4] also reported *Staphylococcus aureus* as second most common bacteria that has emerged as a secondary opportunist in LRTIs. In our

study, small number of *Streptococcus pneumoniae* were isolated from LRTIs specimens that could be due to the hospital-based data.

CONCLUSION

Our study showed current scenario of bacterial etiology and antibiogram of LRTIs in a tertiary care hospital of Lahore. Pseudomonas aeruginosa was the most common bacteria isolated in our study from clinical specimens. Most of the pathogens were highly resistant to common antibiotics.

RECOMMENDATIONS

The bacterial antibiogram will be helpful to develop a policy for antibiotics prescription and to minimize antibiotics resistance among the infections of lower respiratory tract. The proper identification of etiological agents and their susceptibility pattern is very useful for health professionals for rational use of antibiotic therapy and improve treatment outcome of LRTIs.

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CONTRIBUTORS

MM conceived the idea, planned the study and drafted the manuscript. MIM and FKA helped acquisition of data, did statistical analysis and critically revised the manuscript. All authors contributed significantly to the submitted manuscript.