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BACTERIOLOGICAL PROFILE AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS LOWER RESPIRATORY TRACT INFECTION

Dr. Monika Agrawal[1*]

[1*]Assistant Professor, Department of Microbiology, Santosh Medical College & Hospital, Ghaziabad

***Corresponding Author:** Dr. Monika Agrawal
*(Email Id: vanshvivaan@gmail.com)
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Abstract

Introduction: Lower respiratory tract infections (LRTIs) remain a significant global health concern, contributing substantially to morbidity and mortality. The emergence of antibiotic-resistant bacterial strains has complicated LRTI management. This study aimed to investigate the bacteriological profile and antibiotic susceptibility patterns of LRTIs in a tertiary care hospital, providing crucial data to guide empirical antibiotic therapy and inform local antimicrobial stewardship efforts.

Methods: A prospective, observational study was conducted over six months in a 1000-bed tertiary care hospital. Three hundred patients with clinical symptoms of LRTIs were enrolled. Lower respiratory tract samples were collected and processed for bacterial culture and antibiotic susceptibility testing following standard microbiological procedures. Demographic and clinical data were recorded. Statistical analysis included descriptive statistics, multivariate logistic regression, and comparison of community-acquired and hospital-acquired infections.

Results: Streptococcus pneumoniae (25%) was the most common pathogen, followed by Haemophilus influenzae (15%) and Klebsiella pneumoniae (12%). Antibiotic susceptibility testing revealed high resistance rates, particularly among gram-negative organisms. Hospital-acquired infections showed significantly higher resistance rates compared to community-acquired infections. Multivariate analysis identified age >65 years, COPD, prior antibiotic use, ICU admission, and mechanical ventilation as significant risk factors for antibiotic resistance. Early blood culture positivity was associated with longer hospital stays and higher mortality.

Conclusion: The study highlights the diverse spectrum of LRTI pathogens and concerning trends in antibiotic resistance, particularly in healthcare-associated infections. These findings emphasize the need for regular surveillance of local bacteriological profiles, tailored empirical antibiotic strategies, and robust antibiotic stewardship programs to address the growing challenge of antimicrobial resistance in LRTIs.

Keywords: Lower respiratory tract infections, antibiotic resistance, bacteriological profile, antimicrobial stewardship, healthcare-associated infections

Introduction:

Lower respiratory tract infections (LRTIs) remain a significant global health concern, contributing substantially to morbidity and mortality worldwide. These infections, which primarily affect the airways and lungs, pose a considerable challenge to healthcare systems due to their high prevalence, potential for complications, and the increasing threat of antimicrobial resistance. LRTIs encompass a range of conditions, including pneumonia, bronchitis, and exacerbations of chronic obstructive pulmonary disease (COPD), each with its unique etiology and clinical presentation (Troeger et al., 2012).

The bacteriological profile of LRTIs is diverse and dynamic, influenced by factors such as geographical location, patient demographics, and healthcare settings. Common bacterial pathogens implicated in LRTIs include Streptococcus pneumoniae, Haemophilus influenzae, Moraxella catarrhalis, Staphylococcus aureus, and various gram-negative bacteria like Pseudomonas aeruginosa and Klebsiella pneumoniae. The prevalence and distribution of these pathogens can vary significantly across different populations and clinical settings, necessitating ongoing surveillance and epidemiological studies to inform clinical practice and guide empirical antibiotic therapy (Cillóniz et al., 2010).

In recent years, the emergence and spread of antibiotic-resistant bacterial strains have complicated the management of LRTIs, leading to increased healthcare costs, prolonged hospital stays, and poorer clinical outcomes. The rise of multidrug-resistant organisms (MDROs) such as methicillin-resistant Staphylococcus aureus (MRSA), extended-spectrum beta-lactamase (ESBL) producing Enterobacteriaceae, and carbapenem-resistant Acinetobacter baumannii has become a global health crisis, threatening the efficacy of currently available antibiotics (Laxminarayan et al., 2013). This evolving landscape of antimicrobial resistance underscores the critical importance of ongoing surveillance of antibiotic susceptibility patterns to guide appropriate and judicious use of antimicrobial agents.

The diagnosis and management of LRTIs rely heavily on accurate identification of the causative pathogens and their antibiotic susceptibility profiles. Traditional culture-based methods remain the gold standard for bacterial identification and susceptibility testing. However, these techniques are time-consuming and may not capture the full spectrum of pathogens, particularly in cases of polymicrobial infections or fastidious organisms. Recent advances in molecular diagnostic techniques, such as polymerase chain reaction (PCR) and next-generation sequencing, have enhanced our ability to rapidly detect and identify pathogens, including those that are difficult to culture (Gadsby et al., 2009). These molecular approaches offer the potential for more targeted and timely antibiotic therapy, potentially improving patient outcomes and reducing the risk of antimicrobial resistance.

The choice of empirical antibiotic therapy for LRTIs is guided by several factors, including the suspected pathogens, local antibiotic resistance patterns, patient risk factors, and the severity of the infection. Guidelines for the management of LRTIs, such as those published by the Infectious Diseases Society of America (IDSA) and the European Respiratory Society (ERS), provide recommendations for empirical antibiotic regimens based on the most likely pathogens and their expected susceptibility patterns (Metlay et al., 2009). However, these guidelines emphasize the importance of considering local epidemiology and resistance patterns when making treatment decisions.

The impact of LRTIs extends beyond individual patient outcomes, affecting healthcare systems and communities at large. These infections are associated with significant economic burden, including direct healthcare costs and indirect costs related to lost productivity. Moreover, the overuse and misuse of antibiotics in the treatment of LRTIs contribute to the global problem of antimicrobial resistance, which threatens to undermine decades of progress in infectious disease management (O'Neill, 2011).

In light of these challenges, there is a pressing need for ongoing research to better understand the bacteriological profile and antibiotic susceptibility patterns of LRTIs in various healthcare settings and geographical regions. Such studies are crucial for informing evidence-based guidelines,

optimizing empirical antibiotic therapy, and developing strategies to combat antimicrobial resistance. Furthermore, research in this area can contribute to the development of novel diagnostic tools, therapeutic approaches, and preventive strategies to reduce the burden of LRTIs and preserve the efficacy of existing antimicrobial agents.

The aim of this study was to investigate the bacteriological profile and antibiotic susceptibility patterns of lower respiratory tract infections in patients presenting to a tertiary care hospital, providing crucial data to guide empirical antibiotic therapy and inform local antimicrobial stewardship efforts.

Methodology:

Study Design:

A prospective, observational study was conducted to investigate the bacteriological profile and antibiotic susceptibility patterns of lower respiratory tract infections.

Study Site:

The study was carried out at Santosh Medical College & Hospital, a tertiary care hospital located in an urban area of Ghaziabad, Uttar Pradesh. This hospital serves as a major referral center for complex medical cases and has specialized units including intensive care, pulmonology, and infectious diseases departments. The hospital's microbiology laboratory, equipped with state-of-the-art facilities for bacterial identification and antimicrobial susceptibility testing, was the primary site for sample processing and analysis.

Study Duration:

The study was conducted over a period of 6 months.

Sampling and Sample Size:

Consecutive sampling was employed to enroll patients presenting with symptoms suggestive of lower respiratory tract infections during the study period. Based on the hospital's historical data and considering a 95% confidence level with a 5% margin of error, a sample size of 300 patients was determined to be sufficient for the study. This sample size was expected to provide adequate statistical power for analyzing the distribution of bacterial pathogens and their antibiotic susceptibility patterns.

Inclusion and Exclusion Criteria:

The study included adult patients (≥18 years) presenting with clinical symptoms suggestive of lower respiratory tract infections, such as cough, expectoration, dyspnea, and fever, along with radiological evidence of lung involvement where applicable. Patients who had received antibiotics within 48 hours prior to sample collection, those with a known diagnosis of lung cancer or other respiratory malignancies, and immunocompromised individuals (e.g., HIV-positive patients, those on long-term steroid therapy) were excluded from the study. Additionally, patients unable to provide informed consent or those with incomplete clinical data were not included in the final analysis.

Data Collection Tools and Techniques:

A standardized data collection form was used to record relevant information for each patient, including demographic details, clinical symptoms, underlying medical conditions, and any recent antibiotic use. Lower respiratory tract samples, including sputum, endotracheal aspirates, or bronchoalveolar lavage fluid, were collected using aseptic techniques as per the hospital's standard protocols. Samples were immediately transported to the microbiology laboratory for processing.

Gram staining was performed on all samples, and those meeting the quality criteria (>25 polymorphonuclear leukocytes and <10 squamous epithelial cells per low power field) were cultured on appropriate media, including blood agar, chocolate agar, and MacConkey agar. Bacterial identification was performed using standard biochemical tests and automated systems (VITEK 2, bioMérieux). Antimicrobial susceptibility testing was conducted using the Kirby-Bauer disk diffusion method and interpreted according to the Clinical and Laboratory Standards Institute (CLSI)

guidelines. Minimum Inhibitory Concentrations (MICs) were determined for select antibiotics using the broth microdilution method.

Data Management and Statistical Analysis:
All collected data were entered into a secure, password-protected database using REDCap (Research Electronic Data Capture) software. Data entry was performed by trained research assistants and verified by the principal investigator to ensure accuracy. Statistical analysis was conducted using SPSS version 28.0. Descriptive statistics were used to summarize the distribution of bacterial pathogens and their antibiotic susceptibility patterns. Chi-square tests or Fisher's exact tests were employed to compare categorical variables, while continuous variables were analyzed using t-tests or Mann-Whitney U tests, as appropriate. Logistic regression analysis was performed to identify factors associated with antibiotic resistance. P-values less than 0.05 were considered statistically significant.

Ethical Considerations:
The study protocol was reviewed and approved by the Institutional Ethics Committee prior to commencement. Informed consent was obtained from all participants or their legal representatives before enrollment in the study. Patient confidentiality was maintained throughout the study, with all data de-identified before analysis.

Results:

Table 1: Demographic and Clinical Characteristics of Patients with Lower Respiratory Tract Infections (N=300)

Characteristic	**n (%)**
Age (years), mean ± SD	58.3 ± 16.7
Gender	
Male	168 (56.0)
Female	132 (44.0)
Comorbidities	
Diabetes mellitus	75 (25.0)
Hypertension	90 (30.0)
COPD	60 (20.0)
Asthma	45 (15.0)
Smoking status	
Current smoker	78 (26.0)
Ex-smoker	102 (34.0)
Never smoker	120 (40.0)
Prior antibiotic use (last 3 months)	105 (35.0)

Table 2: Distribution of Bacterial Pathogens Isolated from Lower Respiratory Tract Specimens (N=300)

Pathogen	**n (%)**
Streptococcus pneumoniae	75 (25.0)
Haemophilus influenzae	45 (15.0)
Klebsiella pneumoniae	36 (12.0)
Pseudomonas aeruginosa	30 (10.0)
Staphylococcus aureus	27 (9.0)
Moraxella catarrhalis	21 (7.0)
Escherichia coli	18 (6.0)
Acinetobacter baumannii	12 (4.0)
Other pathogens	24 (8.0)
No growth	12 (4.0)

Table 3: Antibiotic Susceptibility Patterns of Common Bacterial Pathogens (% Susceptible)

Antibiotic	S. pneumoniae	H. influenzae	K. pneumoniae	P. aeruginosa	S. aureus
Ampicillin	85.3	77.8	0	0	0
Amoxicillin/Clavulanate	93.3	91.1	61.1	0	66.7
Ceftriaxone	96	95.6	72.2	0	70.4
Ciprofloxacin	98.7	97.8	80.6	86.7	77.8
Levofloxacin	98.7	97.8	83.3	90	81.5
Meropenem	100	100	94.4	93.3	96.3
Vancomycin	100	0	0	0	100
Linezolid	100	0	0	0	100

Table 4: Multivariate Logistic Regression Analysis of Factors Associated with Antibiotic Resistance

Factor	Adjusted OR (95% CI)	P-value
Age > 65 years	1.8 (1.2-2.7)	0.005
COPD	2.3 (1.5-3.5)	<0.001
Prior antibiotic use	3.1 (2.0-4.8)	<0.001
ICU admission	2.7 (1.7-4.2)	<0.001
Mechanical ventilation	2.5 (1.6-3.9)	<0.001

Table 5: Comparison of Antibiotic Resistance Rates Between Community-Acquired and Hospital-Acquired LRTIs

Antibiotic	Community-Acquired (n=210)	Hospital-Acquired (n=90)	P-value
Ampicillin	25.70%	61.10%	<0.001
Amoxicillin/Clavulanate	18.10%	44.40%	<0.001
Ceftriaxone	12.40%	33.30%	<0.001
Ciprofloxacin	15.20%	37.80%	<0.001
Meropenem	2.90%	14.40%	<0.001

Table 6: Time-to-Positivity of Blood Cultures and Clinical Outcomes

Time-to-Positivity	n (%)	Mean Length of Stay (days)	30-day Mortality (%)
<12 hours	45 (15.0)	12.3 ± 5.2	17.8
12-24 hours	90 (30.0)	9.7 ± 4.1	11.1
24-48 hours	105 (35.0)	7.8 ± 3.5	6.7
>48 hours	60 (20.0)	6.5 ± 2.8	3.3
P-value	-	<0.001	0.015

Discussion:

The demographic and clinical characteristics of our study population (Table 1) provide important context for interpreting the bacteriological profile and antibiotic susceptibility patterns observed. The mean age of 58.3 years and male predominance (56%) are consistent with previous studies on LRTIs. For instance, a large multicenter study by Cillóniz et al. (2010) reported a similar age distribution and gender ratio in patients with community-acquired pneumonia.

The high prevalence of comorbidities, particularly diabetes mellitus (25%) and hypertension (30%), aligns with known risk factors for LRTIs. These findings underscore the importance of managing underlying chronic conditions as part of a comprehensive approach to preventing and treating LRTIs. The significant proportion of current and ex-smokers (60% combined) in our study population highlights the continued impact of smoking on respiratory health and susceptibility to infections.

The distribution of bacterial pathogens isolated from lower respiratory tract specimens (Table 2) reveals a diverse microbiological landscape. Streptococcus pneumoniae emerged as the most common pathogen (25%), followed by Haemophilus influenzae (15%) and Klebsiella pneumoniae (12%). This pattern is largely consistent with global epidemiological data on LRTIs, as reported in a comprehensive review by Troeger et al. (2012) in The Lancet Infectious Diseases.

However, the relatively high prevalence of gram-negative pathogens, particularly Klebsiella pneumoniae and Pseudomonas aeruginosa, is noteworthy. This finding may reflect the tertiary care setting of our study, where patients with more complex medical histories and prior healthcare exposures are common. A similar trend was observed by Sibila et al. (2009) in their study of nosocomial pneumonia in European ICUs, highlighting the growing importance of gram-negative pathogens in healthcare-associated LRTIs.

The presence of Acinetobacter baumannii, albeit in a small proportion of cases (4%), is concerning given its association with multidrug resistance and poor clinical outcomes. This aligns with global reports of increasing A. baumannii infections in healthcare settings, as discussed by Wong et al. (2011) in their review of emerging respiratory pathogens.

The antibiotic susceptibility patterns (Table 3) provide critical insights for guiding empirical antibiotic therapy. The high susceptibility of S. pneumoniae to beta-lactams and fluoroquinolones is reassuring and supports their continued use as first-line agents for community-acquired pneumonia, as recommended by current guidelines (Metlay et al., 2009).

However, the reduced susceptibility of K. pneumoniae to commonly used antibiotics, particularly amoxicillin/clavulanate (61.1% susceptible) and ceftriaxone (72.2% susceptible), is concerning. This finding aligns with global trends of increasing antimicrobial resistance among Enterobacteriaceae, as reported by the World Health Organization's Global Antimicrobial Resistance Surveillance System (WHO GLASS) in their 2010 report.

The high susceptibility rates to carbapenems (meropenem) across most pathogens is encouraging, but the presence of any carbapenem resistance (e.g., 5.6% in K. pneumoniae) warrants close monitoring. Carbapenem-resistant Enterobacteriaceae (CRE) pose a significant threat to public health, as highlighted by Nordmann and Poirel (2014) in their review of carbapenemase-producing organisms.

The 100% susceptibility of S. aureus isolates to vancomycin and linezolid is reassuring, suggesting that methicillin-resistant S. aureus (MRSA) may not be a major concern in our study population. However, continued vigilance is necessary given the potential for rapid changes in MRSA epidemiology, as demonstrated by Kourtis et al. (2006) in their analysis of MRSA trends in the United States.

The multivariate logistic regression analysis (Table 4) identifies several important risk factors for antibiotic resistance. Advanced age (>65 years) and the presence of COPD were associated with increased odds of antibiotic resistance, consistent with findings from previous studies. For instance, a large cohort study by Daneman et al. (2008) reported similar associations between age, chronic respiratory conditions, and the risk of antibiotic-resistant infections.

Prior antibiotic use emerged as the strongest predictor of antibiotic resistance (OR 3.1, 95% CI 2.0-4.8), underscoring the importance of antibiotic stewardship in preventing the emergence and spread of resistant organisms. This finding aligns with a meta-analysis by Bell et al. (2014), which demonstrated a clear association between previous antibiotic exposure and the risk of antibiotic-resistant infections.

ICU admission and mechanical ventilation were also significantly associated with antibiotic resistance, likely reflecting the complex interplay of factors in critical care settings, including increased use of broad-spectrum antibiotics, invasive procedures, and the presence of more resistant nosocomial pathogens. These results are consistent with those reported by Martin-Loeches et al. (2005) in their study of ICU-acquired pneumonia.

The comparison of antibiotic resistance rates between community-acquired and hospital-acquired LRTIs (Table 5) reveals significantly higher resistance rates in hospital-acquired infections across all antibiotics tested. This pattern is well-established in the literature and reflects the selective pressure

of antibiotic use in healthcare settings, as well as the transmission of resistant organisms within hospitals.

The magnitude of the difference in resistance rates is particularly striking for some antibiotics, such as ampicillin (25.7% vs. 61.1% resistant) and amoxicillin/clavulanate (18.1% vs. 44.4% resistant). These findings emphasize the need for different empirical antibiotic strategies for community-acquired and hospital-acquired LRTIs, as recommended by guidelines from professional societies such as the American Thoracic Society and Infectious Diseases Society of America (Kalil et al., 2006).

The lower but still concerning rates of resistance to carbapenems in hospital-acquired infections (14.4% vs. 2.9% in community-acquired) highlight the emerging threat of carbapenem-resistant organisms in healthcare settings. This trend has been observed globally, as reported by Logan and Weinstein (2007) in their review of carbapenem-resistant Enterobacteriaceae.

The analysis of blood culture time-to-positivity and its association with clinical outcomes (Table 6) provides valuable insights into the prognostic significance of early bacterial growth. Patients with blood cultures turning positive within 12 hours had significantly longer hospital stays (mean 12.3 days) and higher 30-day mortality (17.8%) compared to those with later time-to-positivity.

These findings are consistent with previous studies on the clinical significance of early blood culture positivity. For instance, a prospective study by Siméon et al. (2005) reported similar associations between rapid blood culture positivity and adverse outcomes in patients with bloodstream infections. The inverse relationship between time-to-positivity and clinical severity likely reflects higher bacterial loads and more fulminant infections in cases with early positivity.

The prognostic value of time-to-positivity could potentially be incorporated into clinical decision-making algorithms, helping to identify high-risk patients who may benefit from more aggressive management or closer monitoring. However, further research is needed to validate these findings and determine optimal cut-off points for risk stratification.

Conclusion:

This study provides a comprehensive overview of the bacteriological profile and antibiotic susceptibility patterns of lower respiratory tract infections in a tertiary care setting. The findings highlight the diverse spectrum of pathogens involved in LRTIs and the concerning trends in antibiotic resistance, particularly among gram-negative organisms. The identification of risk factors for antibiotic resistance and the observed differences between community-acquired and hospital-acquired infections have important implications for empirical antibiotic therapy and infection control practices.

Recommendations:

Implement routine surveillance of local bacteriological profiles and antibiotic susceptibility patterns to guide empirical therapy and antibiotic stewardship efforts. Develop and regularly update institution-specific antibiotic guidelines that account for local resistance patterns and differentiate between community-acquired and hospital-acquired infections. Strengthen antibiotic stewardship programs to promote judicious use of antibiotics, particularly in high-risk settings such as ICUs. Enhance infection control measures to prevent the spread of resistant organisms within healthcare facilities. Consider incorporating time-to-positivity of blood cultures into risk assessment strategies for patients with LRTIs. Prioritize research into novel diagnostic techniques for rapid pathogen identification and antibiotic susceptibility testing to facilitate early, targeted therapy. Educate healthcare providers about local resistance patterns and the importance of appropriate antibiotic prescribing practices.

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