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Respiratory Medicine

A RETROSPECTIVE STUDY OF CLINICO-RADIOLOGICAL AND MICROBIOLOGICAL PROFILE IN CASE OF COMMUNITY ACQUIRED PNEUMONIA ADMITTED IN A TERTIARY CARE HOSPITAL.

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ABSTRACT **Background:** Community-acquired pneumonia (CAP) remains a significant cause of morbidity and mortality, particularly among hospitalized patients. Identifying the microbial profile of CAP is crucial for optimizing treatment strategies and improving patient outcomes. **Objective:** This study aims to evaluate the clinico-radiological and microbiological profile of CAP in patients admitted to a tertiary care hospital, with a focus on identifying prevalent pathogens and their distribution. **Methods:** A retrospective hospital-based study was conducted in a tertiary care centre in South India from July 2024 to December 2024. A total of 124 patients with clinico-radiological evidence of pneumonia were included. Sputum samples were analysed to determine the presence of bacterial pathogens, and statistical analysis was performed using descriptive methods. **Results:** The mean age of the study population was 55.92 years (SD ± 18.29), indicating a wide age distribution among participants. There was a female predominance, with women comprising 56.9% of the total cohort. Sputum culture results demonstrated that no pathogenic organism could be isolated in 43 cases, accounting for 33% of the study population. Among the positive cultures, Klebsiella pneumoniae emerged as the most frequently isolated pathogen, identified in 36 cases. This was followed by Acinetobacter species in 20 cases and Pseudomonas aeruginosa in 18 cases. Streptococcus pneumoniae was detected in 5 cases, suggesting a relatively lower prevalence among the typical community-acquired pathogens. In addition, methicillin-resistant Staphylococcus aureus (MRSA) and Escherichia coli were identified in a smaller subset of patients. Although less common, the presence of MRSA highlights the potential involvement of resistant organisms, which may have implications for empiric antibiotic selection and infection control practices. The detection of E. coli, while less typical in respiratory tract infections, may reflect colonization or aspiration-related infections, particularly in elderly or debilitated patients. **Conclusion:** The study highlights a shift in the microbial profile of CAP, with Klebsiella pneumoniae emerging as the predominant pathogen instead of Streptococcus pneumoniae. This shift has significant implications for empirical antibiotic therapy and antimicrobial stewardship. Continuous surveillance and region-specific treatment strategies are essential to optimize CAP management and improve clinical outcomes.

KEYWORDS :

INTRODUCTION

Community-acquired pneumonia (CAP) is a leading cause of morbidity and mortality worldwide, imposing a substantial clinical and economic burden, particularly among elderly individuals and those with comorbidities. It remains one of the most common infectious diseases requiring hospitalization and is responsible for a significant number of lower respiratory tract infection-related deaths[1]. The incidence and severity of CAP vary across different regions and are influenced by factors such as geographical location, seasonal variations, healthcare access, and host immunity[2].

The aetiology of CAP is diverse, with a range of bacterial, viral, and fungal pathogens implicated in its development. Streptococcus pneumoniae remains the most frequently identified bacterial cause, followed by atypical pathogens such as Mycoplasma pneumoniae, Chlamydophila pneumoniae, and Legionella pneumophila[3]. Gram-negative bacilli, including Klebsiella pneumoniae and Pseudomonas aeruginosa, along with Staphylococcus aureus, particularly methicillin-resistant strains (MRSA), are more commonly associated with severe cases requiring intensive care[4]. In recent years, viral pathogens such as influenza, respiratory syncytial virus (RSV), and SARS-CoV-2 have emerged as significant contributors to CAP, especially during seasonal epidemics and pandemics[5]

Despite advances in diagnostic methods, identifying the causative pathogen in CAP remains challenging. Conventional microbiological testing often has low pathogen detection rates, leading to the frequent use of empirical antimicrobial therapy[6]. This highlights the need for ongoing surveillance and research to understand regional variations in CAP aetiology, optimize antibiotic stewardship, and improve patient outcomes.

This study aims to evaluate the etiological spectrum of CAP, assess the prevalence of bacterial pathogens, and explore factors influencing pathogen distribution. By analysing microbiological trends and clinical presentations, this research seeks to enhance diagnostic accuracy and inform evidence-based management strategies for CAP.

MATERIALS AND METHODS

The present study was a hospital-based Retrospective one conducted in the Department of Respiratory Medicine, in a tertiary care centre in South India from October 2024 to December 2024. A manual chart review of sputum culture and sensitivity (solely based on culture, no molecular diagnostic methods were done) and CT scans of patients admitted with CAP was done retrospectively. Ethical committee clearance was obtained by the institutional review board before the study (Regn, No. EC/New/INST/2023/3389 dated 31.01.2024). Consecutive sampling method was used to select the study subjects.

Inclusion Criteria

1. Patients admitted with fever, cough with sputum production, dyspnoea, or pleuritic chest pain.
2. Chest CT scan showing radiological evidence of pneumonia (e.g., consolidation, infiltrates).
3. Patients whose sputum samples were collected for culture and sensitivity analysis.
4. Patients aged ≥18 years presenting with symptoms suggestive of pneumonia.
5. Patients with no prior hospitalisation in the past 14 days.
6. Patients with complete medical records for retrospective analysis.

Exclusion Criteria

1. Hospital-Acquired Pneumonia (HAP) or Ventilator-Associated Pneumonia (VAP): Patients who developed pneumonia ≥48 hours after hospital admission.
2. Immunocompromised Patients: Individuals with HIV/AIDS, active malignancy undergoing chemotherapy, organ transplantation, or long-term corticosteroid use (>20 mg/day for ≥2 weeks).
3. Other Systemic Infections: Cases where pneumonia is secondary to another ongoing systemic infection (e.g., tuberculosis, fungal pneumonia in immunocompromised patients).
4. Recent Antibiotic Use: Patients who received broad-spectrum antibiotics within the last 48-72 hours before sample collection, which may affect microbial yield.
5. Incomplete Data: Patients with inadequate clinical, radiological, or microbiological documentation.
6. Lack of Sputum Sample: Cases where sputum samples were not obtained or were of poor quality for microbiological analysis.

Sample Size

All patient with clinic radiological evidence suggestive of pneumonia attending to the outpatient/in patient department of Respiratory medicine in our centre was selected. Sampling of the patient was by convenient method and based on inclusion and exclusion criteria as mentioned.

Sample Size: $\frac{(1.96)^2 \times 19.8 \times 80.2}{7^2}$

$= 124$

Statistical analysis was done by using Cochrane formula.

Analysis

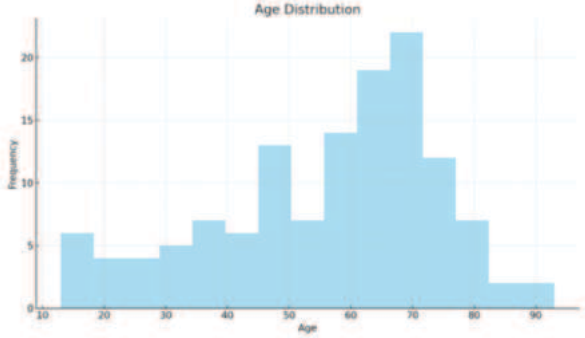
The most commonly isolated organism from sputum samples of patients exhibiting radiological findings consistent with consolidation was analyzed to assess its prevalence, clinical significance, and potential role in disease progression and management strategies. Statistical analysis was performed by using descriptive statistics.

RESULT

Patients admitted to a tertiary care hospital from October to December 2024 with CT Thorax findings indicative of consolidation were selected, and their sputum samples were analyzed for culture and sensitivity to assess the causative organisms and antibiotic susceptibility.

Age Analysis

The age distribution is shown in the chart below:



In the study age of the patient ranged from 22 years to 85 years with a mean of 55.92 and standard deviation of 18.29 which suggests that ages can vary quite a bit from the average of 56 years, ranging from younger (13 years) to older (93 years) individuals. A histogram of age distribution was plotted, showing a relatively normal distribution with a slight skew towards older ages. (fig 1)

Gender Analysis

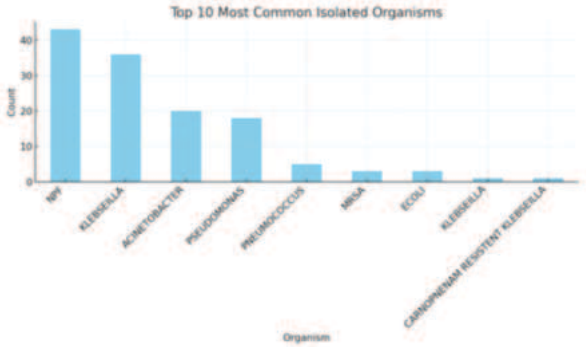
In this study it was found that 74 (56.9%) were females and 56 (43.1%) were males. A pie chart was created, showing that females are the majority in this study, constituting a little over half of the dataset. (Table 2).

Gender Distribution

Gender	Count
F	74
M	56

Analysis of Isolated Organisms

The bar chart below represents the most common isolated organisms:

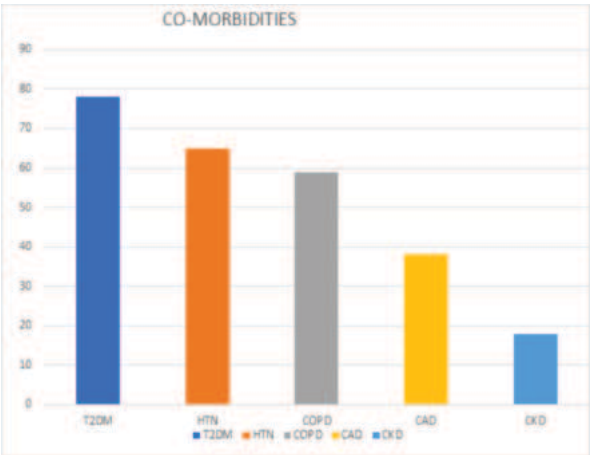


The organisms isolated from individuals were also analysed, revealing that no organism was detected in 43 individuals (43% of the total), constituting the majority of cases. Klebsiella was isolated in 36 individuals, making it the most common organism. Other organisms included Acinetobacter (20), Pseudomonas (18), and Pneumococcus (5), with some rarer organisms such as MRSA and E. coli also observed in smaller numbers. The organisms were categorized as either normal flora (NPF) or pathogenic species (like Klebsiella, Acinetobacter, etc.). A bar chart was created to visually compare the frequencies of the most common organisms. (fig 3).

Comorbidities

In our study, Type 2 Diabetes Mellitus (T2DM) and Hypertension were the most common comorbidities, reflecting a substantial burden of chronic health conditions among the study population. Of the 124 patients analysed, 78 had T2DM and 65 had Hypertension. Other notable comorbidities included Chronic Obstructive Pulmonary Disease (COPD), present in 59 patients, and coronary artery disease (CAD), observed in 38 patients. Chronic Kidney Disease (CKD) was the least prevalent, affecting 18 patients. (fig4)

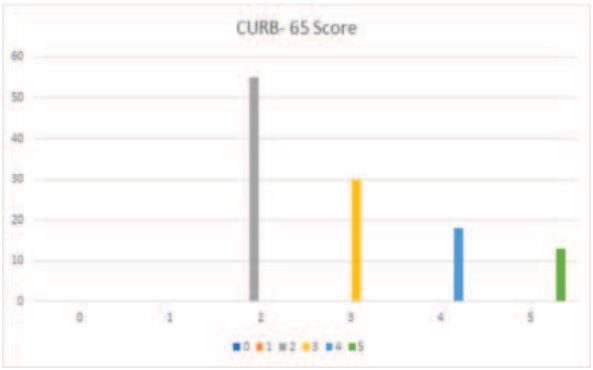
The bar chart represents the Comorbidities found in our study population



CURB 65 Scoring

The CURB 65 score chart depicts the distribution of scores ranging from 0 to 5. The highest bar is at score 2, with over 55 occurrences. There is noticeable presence of cases at score 3 which is the second most frequent, indicating severe pneumonia in significant number of patient (30), likely requiring intensive treatment. Score 4 (18) and score 5 (13) have very few instances, pointing to the presence of severe CAP cases, but not the predominant profile

The bar chart representing CURB 65 score among our study population



DISCUSSION

Community acquired pneumonia remain a leading cause of morbidity and mortality worldwide, particularly among young children, the elderly, and individuals with underlying health condition. This study offers a thorough understanding of the causes of CAP in hospitalized patients at our centre. Accurate diagnostic testing enhances clinical outcomes both directly, by enabling personalized antibiotic management, and indirectly, by providing essential epidemiological data that informs initial empirical therapy. The present study was a hospital-based study where 130 patients fulfilling inclusion criteria were included.

Among the 124 patients in the study population, the mean age was 55.92 years, with ages ranging from 22 to 85 years. The distribution of gender showed a slightly higher proportion of females compared to males, indicating a subtle female predominance in the study group.

In this study, Among the 124 patients, 74 (56.9%) were female, while 56 (43.1%) were male. The higher proportion of female patients could indicate an increased predisposition to pulmonary infections among females or differences in healthcare-seeking behaviour. Sputum culture results showed that no organism was isolated in 43 individuals (33%), suggesting either non-infectious causes of consolidation or low bacterial loads. Among the detected organisms, Klebsiella pneumoniae was the most common pathogen, isolated in 36 cases. Historically, Streptococcus pneumoniae has been recognized as the predominant bacterial pathogen in CAP. However, our study indicates a notable shift in microbial aetiology, with Klebsiella pneumoniae emerging as the most frequently isolated organism. Among the 124 patients analysed, Streptococcus pneumoniae was found in only 5 cases. This transition may be attributed to regional variations, changes in antibiotic prescribing patterns, and an increasing prevalence of antimicrobial resistance. A similar study by Saeed Shohar and Daniel M in 2020 reported Streptococcus as the most frequently isolated organism in patients with CAP, followed by Haemophilus, Staphylococcus aureus, and Gram-negative bacilli. This contrasts with the microbial pattern observed in our study, highlighting a notable difference in the distribution of causative organism[7]. Additionally, the predominance of Gram-negative organisms, including Acinetobacter and Pseudomonas, further underscores the evolving microbial landscape of CAP in hospitalized patients. In this study Acinetobacter (20 cases), Pseudomonas aeruginosa (18 cases), and Streptococcus pneumoniae (5 cases) were also notable isolates. Less frequently identified organisms included Methicillin-resistant Staphylococcus aureus (MRSA) and Escherichia coli (E. coli), which were each isolated from the sputum samples of individual patients.

According to the study conducted by Shah in India, 43 individuals with CT suggestive of consolidation, no organism was isolated. Klebsiella was isolated in 36 patients, making it the most common organism. Other organisms included Acinetobacter (20), Pseudomonas (18), and Pneumococcus (5), with some rarer organisms such as MRSA and E. coli also observed in smaller numbers[8]. This correlates with a previous study done by Bashir Ahmed Bacteriological and clinical profile of Community acquired pneumonia in hospitalized patients found that 71 cases no etiological cause was obtained. Pseudomonas aeruginosa was the commonest pathogen, followed by Staphylococcus aureus (7/29), Escherichia coli (6/29), Klebsiella spp. (3/29), Streptococcus pyogenes (1/29), Streptococcus pneumoniae (1/29) and Acinetobacter spp. This study provides valuable insights into the microbiological profile of patients presenting with radiological evidence of consolidation. The predominance of Gram-negative pathogens, particularly Klebsiella and Acinetobacter, has significant implications for empirical antibiotic selection. Given the presence of resistant strains, antimicrobial stewardship programs should be strengthened to optimize treatment outcomes[9]

In a similar study done by Vikram B Vikhe - A Study on the Aetiology and Clinical Manifestations of Community-Acquired Pneumonia in Adults in Western India, Sputum cultures showed growth in 65 cases (65%), with Klebsiella pneumoniae being the most prevalent pathogen in 28 cases (43%), followed by Streptococcus pneumoniae in 18 cases (28%). This study highlights the clinical profile and rising aetiology of K. pneumoniae in CAP in adults in Western India, particularly in the elderly.[10]

The observed transition from Streptococcus pneumoniae to Klebsiella pneumoniae as the predominant pathogen in community-acquired pneumonia (CAP) can be attributed to several key factors: Widespread use of pneumococcal-targeted antibiotics (e.g., penicillin, cephalosporins, and macrolides) may have contributed to a decline in Streptococcus pneumoniae prevalence. Empirical use of broad-spectrum antibiotics, including β-lactam/β-lactamase inhibitors and carbapenems, may have favoured the survival of multidrug-resistant (MDR) Klebsiella pneumoniae. Klebsiella pneumoniae has demonstrated higher levels of antimicrobial resistance, particularly against cephalosporins and carbapenems. The rise in extended-spectrum beta-lactamase (ESBL)-producing and carbapenem-resistant Klebsiella pneumoniae strains has made it a clinically significant pathogen in respiratory infections.

Patients who had received antibiotics before sample collection could have altered pathogen detection, particularly leading to an underestimation of Streptococcus pneumoniae and overrepresentation of resistant Gram-negative bacteria like Klebsiella pneumoniae. The lack of bronchoalveolar lavage (BAL) may have limited the detection of true lower respiratory tract pathogens. Patients with diabetes, COPD, chronic kidney disease, or alcohol use disorder are more susceptible to Klebsiella pneumoniae, potentially skewing results. Some patients diagnosed with CAP may have had prior healthcare exposure (e.g., nursing home residents, frequent hospital visitors), leading to an increased likelihood of Gram-negative infections rather than typical CAP pathogens.

The 33% of culture-negative cases in our study could be attributed to prior antibiotic use or limitations of conventional culture methods. Molecular diagnostics such as PCR-based panels or next-generation sequencing, as advocated by Jain et al. in the CDC EPIC study (2015), may provide more comprehensive pathogen detection in future investigations. Our study highlights a shifting microbial profile in community-acquired pneumonia (CAP) within our tertiary care setting in South India. Our findings differ significantly from large-scale Western data. For example, the EPIC study conducted by Jain et al. (2015) in the United States reported Streptococcus pneumoniae as the most common bacterial pathogen (5%) and human rhinovirus and influenza virus as the most frequently detected overall. Interestingly, a causative organism was not identified in nearly 62% of the cases, despite the use of comprehensive molecular diagnostics. This finding is consistent with the 33% of culture-negative cases observed in our study and underscores the diagnostic limitations posed by conventional culture methods[11].

In our study cohort, a considerable number of patients presented with comorbidities known to influence the progression and outcomes of respiratory illnesses. Specifically, diabetes mellitus was present in 78 patients, hypertension in 65, coronary artery disease (CAD) in 59, and chronic kidney disease (CKD) in 18. The high burden of comorbidities in our study population likely contributed to the overall disease severity and resource utilization. These findings highlight the importance of a multidisciplinary approach in managing respiratory patients, especially those with systemic involvement. It is also worth noting that the co-existence of multiple comorbidities may have synergistic effects, further amplifying the risk of adverse outcomes. Future studies focusing on stratifying risk based on comorbidity burden may help tailor therapeutic strategies and improve prognostication.

The CURB-65 scoring system, a validated tool for assessing the severity of community-acquired pneumonia and guiding

hospitalization decisions, was applied to our study population. The score distribution revealed that 55 patients had a CURB-65 score of 2, 30 patients scored 3, 18 patients scored 4, and 13 patients had the maximum score of 5. This distribution reflects a considerable burden of moderate to severe disease in our cohort.

Patients with a CURB-65 score of 2 or more are typically considered for inpatient management due to the increased risk of mortality and complications. Notably, nearly half of our patients fell into the higher risk categories (scores ≥3), highlighting the severity of illness at presentation. A score of 3 or more has been associated with a significantly higher 30-day mortality rate and often necessitates intensive monitoring, and in some cases, ICU care. The high proportion of patients with elevated CURB-65 scores likely correlates with the high prevalence of comorbidities observed in our study—such as diabetes, hypertension, CAD, and CKD—all of which can influence vital signs, renal function, and mental status, thereby affecting the overall score. This further emphasizes the complex interplay between underlying systemic illnesses and acute respiratory conditions. These findings underscore the importance of early severity assessment using standardized tools like CURB-65, which can aid in triage, predict outcomes, and guide clinical decision-making. Incorporating such scoring systems into routine assessment can enhance the precision of care delivery, especially in resource-limited settings.

The findings of our study highlight a significant burden of chronic comorbidities among patients diagnosed with community-acquired pneumonia (CAP), with Type 2 Diabetes Mellitus and Hypertension being the most prevalent. This comorbidity profile is clinically relevant when considering initial empirical antibiotic therapy, particularly in light of the 2019 IDSA/ATS guidelines for the management of CAP. According to these guidelines, the presence of comorbidities such as diabetes, chronic respiratory diseases (e.g., COPD), and cardiovascular conditions (e.g., CAD) necessitates a broader spectrum of empirical antibiotic coverage. For outpatients with such comorbidities, a combination of amoxicillin/clavulanate with either a macrolide or doxycycline, or monotherapy with a respiratory fluoroquinolone, is recommended. In the inpatient setting, a beta-lactam (e.g., ceftriaxone) in combination with a macrolide, or monotherapy with a respiratory fluoroquinolone, is advised. Our study did not consistently reflect stratification of empirical therapy based on such risk profiles, indicating a potential area for improvement in antimicrobial stewardship. Furthermore, empirical coverage for MRSA or Pseudomonas aeruginosa—while essential in high-risk patients—should be guided by prior microbiologic data or specific risk factors, which were not routinely assessed in our cohort. Incorporating such risk-based decision-making into routine practice could help optimize antibiotic use and minimize resistance.

Lastly, the IDSA/ATS guidelines emphasize re-evaluating antibiotic therapy at 48–72 hours based on clinical response and microbiological findings, as well as favouring shorter courses of therapy (typically 5–7 days) for clinically stable patients. Implementing these practices could further enhance patient outcomes and support antibiotic stewardship efforts in our setting.

Community acquired pneumonia is a major public health concern, with Streptococcus pneumoniae traditionally recognized as the leading causative agent. However, our study findings indicate a shift in microbial prevalence, with klebsiella pneumoniae emerging as the most frequently isolated organism. The predominance of klebsiella pneumoniae in our study could be influenced by multiple factors, including regional variations in pathogen distribution, differences in study population characteristics, prior antibiotic exposure affecting microbial flora. Therefore, clinician should remain vigilant about Klebsiella pneumoniae as the potential pathogen in CAP, particularly in high-risk groups.

Limitations

1. The finding is based on data from a single institution, which may limit the generalizability of results to other region or population.
2. A larger sample may be needed to validate the observed shift in pathogen prevalence and strengthen statistical significance.
3. The study relied on sputum cultures, which may yield false negative results due to prior antibiotic use or difficulty obtaining high quality sample.
4. The study did not assess viral or atypical organism, which are significant contributors to CAP
5. A detailed antimicrobial resistance profile of Klebsiella pneumoniae was not included, limiting insights into optimal treatment strategies.
6. Bronchoalveolar lavage (BAL) was not performed, which could have provided more accurate lower respiratory tract samples for pathogen identification.
7. Polymerase chain reaction (PCR) for bacterial and viral pathogen detection was not conducted, which may have limited the detection of fastidious or non-culturable organisms.

CONCLUSION

Our study highlights a notable shift in the microbial aetiology of community acquired pneumonia, with Klebsiella pneumoniae emerging as the predominant pathogen instead of traditionally common Streptococcus pneumoniae. This finding suggests potential changes in infection patterns, possibly influenced by regional factors, patient demographics, and antibiotic resistance trends. Given Klebsiella pneumonia's potential for severe infections and drug resistance, continuous monitoring is essential. This highlights the need for continuous surveillance, tailored antibiotic strategies, and further research to optimize CAP management and improve patient outcomes.

Moreover, the clinical and radiological correlation observed in this study underscores the value of a comprehensive diagnostic approach, especially in resource-limited settings. The role of CURB-65 scoring as a prognostic tool was validated, aiding in early identification of high-risk patients who may benefit from more intensive care. Given the limitations inherent to a single-centre, hospital-based study, larger multicentric studies with molecular diagnostic tools are warranted to better characterize the evolving epidemiology of CAP. Future research should also explore host immune responses and novel biomarkers for early and accurate diagnosis, which could ultimately improve patient outcomes and reduce healthcare costs.

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