Letter to the Editor Regarding "A Clinicoradiological and Bacteriological Profile of Community-acquired Pneumonia in a Tertiary Care Center in Eastern India"

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Dear Editor,

We read with great interest the article titled "A Clinicoradiological and Bacteriological Profile of Community-acquired Pneumonia in a Tertiary Care Center in Eastern India" by Hati et al. [Journal of the Association of Physicians of India 2025;73(3):25–29]. The study provides valuable insights into the clinico-bacteriological landscape of community-acquired pneumonia (CAP) in the Indian context. The study focuses on a very relevant topic in today's scenario of rising cases of community-acquired pneumonia with sepsis, which manifests as a major task of managing critically ill patients. The inclusion and exclusion criteria fit the study well. Data collection has been done in a comprehensive manner. The role of procalcitonin and its utility have been highlighted, which is relevant in recent times. Comparison of Indian and international studies has been done for a broader perspective. However, we would like to highlight a few limitations that warrant consideration for future research.

1. The study offers valuable regional insights; however, the results may not be broadly applicable to the general population as they might be due to sample bias introduced by selecting participants from a single tertiary care center. In order to capture the variability in the clinical and microbiological characteristics of CAP across various hospitals and centers, multicenter studies are better.[1]
2. Although comorbidities such as diabetes and hypertension are included in the study, a comparison of the clinical severity, microbiological pattern, and biomarker levels in people with and without these illnesses has not been explained in the study. This is a lost chance to increase the therapeutic relevance of findings because comorbidities such as diabetes mellitus, chronic lung disease, and immunosuppressive status are known risk factors for severe CAP and also affect pathogen distribution and outcome.[2] Comorbidity-based outcome stratification would have provided insightful information for individualized risk assessment and management.
3. The diagnostic yield was severely limited by the study's exclusive reliance on aerobic culture techniques. This could help to explain the observed 48% culture-negative rate. A single culture method used alone may result in false negatives, overlooking possible infections. Notably, traditional aerobic cultures alone are not a reliable way to detect respiratory viruses, anaerobic bacteria, or atypical organisms (including *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, and *Legionella* spp.).[3] In order to increase the etiological yield and overall diagnostic accuracy, this constraint emphasizes the necessity of implementing other diagnostic modalities, such as anaerobic culture, polymerase chain reaction (PCR)-based multiplex panels, and BioFire respiratory panels.[4]
4. The study does not use additional validated measures like the Pneumonia Severity Index (PSI) or qSOFA; instead, it uses the CURB-65 score alone to determine the severity of pneumonia. Despite being useful and simple to use, CURB-65 may not work as well for some patient populations, especially the elderly or those with several comorbidities.[5] The PSI has been demonstrated to have better prediction accuracy for mortality and provides a more thorough risk stratification by taking into account laboratory data, age, and concomitant diseases. Multiple severity scores could help guide triage decisions more successfully and offer a more thorough picture of clinical outcomes.[6]
5. A significant limitation of the study is the absence of antibiotic resistance data for the bacterial isolates. In the context of rising antimicrobial resistance (AMR) both globally and within India, reporting susceptibility patterns is essential for guiding empirical therapy and updating clinical guidelines. Without this information, it is difficult to determine whether the identified organisms were multidrug resistant (MDR) or sensitive to standard first-line agents. Studies from India and other developing regions have documented increasing resistance to macrolides, beta-lactams, and fluoroquinolones among *Streptococcus pneumoniae* and *Klebsiella pneumoniae*, two of the most common CAP pathogens.[7] The inclusion of resistance profiles would have significantly enhanced the clinical utility of the findings and supported antimicrobial stewardship efforts.[8]
6. The study did not incorporate any advanced radiological investigations, such as computed tomography (CT) scans, relying solely on chest X-rays for evaluating pulmonary involvement. While chest radiography is widely used and accessible, it has limited sensitivity for detecting early or subtle infiltrates, small pleural effusions, or complications such as cavitation or empyema.[9] Several studies have demonstrated that chest CT offers superior diagnostic accuracy, especially in patients with equivocal or normal chest X-ray findings or when differentiating infectious from noninfectious causes of opacities.[10] The absence of CT-based imaging in this study may have led to underestimation of disease extent or misinterpretation of radiological patterns.
7. Another notable omission in the study is the lack of data on the requirement for invasive supports, such as mechanical ventilation, vasopressor therapy, or intensive care unit (ICU) admission. These outcomes are crucial for validating severity scoring systems like CURB-65 and assessing the real-world burden of severe CAP. Including such endpoints would have enhanced the study's prognostic relevance and clinical applicability.[11] Previous studies have demonstrated that markers such as procalcitonin, multilobar infiltrates, and higher CURB-65 or PSI scores correlate strongly with the need for intensive care and advanced support.[12] The absence of this information limits the interpretation of severity and treatment outcomes in the current cohort.
8. The study's microbiological assessment was limited to aerobic bacterial cultures, which likely resulted in the underrepresentation of important pathogens such as respiratory viruses, fungi, and anaerobic bacteria. These organisms are well-documented contributors to CAP, particularly among the elderly, immunocompromised patients, and those with chronic diseases.[13] The absence of diagnostic modalities like viral PCR assays, fungal cultures, or anaerobic culture techniques may have led to an

incomplete etiological profile. Notably, pathogens such as influenza viruses, respiratory syncytial virus (RSV), Aspergillus spp., and anaerobic flora involved in aspiration pneumonia could have been missed.[14] Broader microbiological testing should be considered in future studies to improve diagnostic accuracy and inform more targeted therapy.

9. The study does not provide differentiation between patients who received prior antibiotic therapy in outpatient settings or were referred from other healthcare facilities. This is an important omission, as prehospital antibiotic exposure is a well-known factor that reduces culture positivity, alters clinical presentation, and may promote the development of antibiotic-resistant organisms.[15] In many parts of India and other low- and middle-income countries, the irrational use of antibiotics—including over-the-counter availability and incomplete courses—remains a significant concern.[16] Accounting for this subgroup would have added depth to the microbiological findings and informed local antimicrobial stewardship strategies.
10. Future studies should aim to incorporate advanced molecular diagnostic tools such as multiplex PCR assays, BioFire respiratory panels, and real-time PCR (RT-PCR) to improve pathogen detection in CAP. These technologies offer significantly higher sensitivity and faster turnaround times than conventional culture, particularly in patients who are partially treated, immunocompromised, or present with atypical or viral infections.[17] Incorporation of these modalities can substantially reduce the proportion of culture-negative cases, detect coinfections, and contribute to a more comprehensive microbial profile.[18]

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