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	EMERGING ANTIMICROBIAL RESISTANCE PATTERNS IN COMMUNITY-ACQUIRED PNEUMONIA	KEY WORDS: Community-acquired pneumonia, antimicrobial resistance, bacterial pathogens, empirical therapy, antibiotic stewardship.
Dr Jakkilinki Venkata Srujan	Associate Professor, General Medicine, NRI Institute of Medical Sciences, Sangivalasa, Andhra Pradesh	
Dr Jasmine	Senior Resident, Department of General Surgery, Kalpana Chawla Government Medical College and Hospital, Karnal, Haryana	
ABSTRACT	Background: Community-acquired pneumonia (CAP) continues to be a major cause of morbidity and mortality worldwide. The growing challenge of antimicrobial resistance (AMR) among CAP pathogens has significantly impacted empirical treatment strategies and clinical outcomes. Objective: This review explores the emerging patterns of antimicrobial resistance in CAP, highlighting regional trends, mechanisms of resistance, diagnostic challenges, and implications for clinical management and public health. Discussion: The predominant bacterial pathogens in CAP include <i>Streptococcus pneumoniae</i>, <i>Haemophilus influenzae</i>, and <i>Moraxella catarrhalis</i>, with a rising incidence of resistant gram-negative organisms such as <i>Klebsiella pneumoniae</i>. Resistance mechanisms such as beta-lactamase production, efflux pumps, and genetic mutations compromise first-line therapies including beta-lactams, macrolides, and fluoroquinolones. Regional studies demonstrate varying resistance trends, with high rates reported in Asia and Africa. Diagnostic delays and empirical misuse of antibiotics exacerbate resistance. Vulnerable groups, such as pediatric and elderly patients, face unique challenges due to age-specific pharmacokinetics and comorbidities. Effective interventions include robust antibiotic stewardship, advanced diagnostics, and preventive strategies such as vaccination. Conclusion: Addressing AMR in CAP requires a multifaceted approach, combining local surveillance, targeted therapy, public health policies, and global cooperation to preserve the efficacy of current antimicrobials.	
1. INTRODUCTION	Community-acquired pneumonia (CAP) remains one of the most significant public health concerns worldwide due to its high morbidity and mortality rates. The rise in antimicrobial resistance (AMR) among pathogens responsible for CAP has compounded treatment challenges, especially in low- and middle-income countries. CAP is primarily caused by bacterial pathogens such as <i>Streptococcus pneumoniae</i>, <i>Haemophilus influenzae</i>, and <i>Moraxella catarrhalis</i>, although atypical pathogens and viruses also contribute. Empirical therapy, often guided by local resistance patterns and clinical presentation, is the standard approach; however, emerging resistance has compromised its efficacy. The increasing incidence of multidrug-resistant (MDR) strains, including resistance to commonly used agents such as beta-lactams, macrolides, and fluoroquinolones, has been well documented across different regions [1,2]. Surveillance studies have shown alarming resistance rates even in community settings, with inappropriate antibiotic use further accelerating resistance trends [3,4]. The emergence of extended-spectrum beta-lactamase (ESBL) producers and carbapenem-resistant strains among CAP pathogens is particularly worrisome, as these often necessitate more toxic or less effective alternatives. Understanding evolving resistance mechanisms and regional susceptibility profiles is essential for optimizing empirical therapy and informing public health interventions [5]. This review explores current trends, underlying mechanisms, and regional resistance patterns in CAP.	
2. Common Pathogens and Shifting Etiology	The bacterial etiology of CAP varies geographically but typically includes <i>Streptococcus pneumoniae</i>, <i>Haemophilus influenzae</i>, <i>Klebsiella pneumoniae</i>, and <i>Moraxella catarrhalis</i> [6]. In recent years, surveillance data have highlighted a noticeable shift in the prevalence of these organisms, with increased isolation of gram-negative bacilli and atypical pathogens such as <i>Legionella pneumophila</i> and <i>Mycoplasma pneumoniae</i> [7]. Notably, co-infections involving multiple pathogens have also become more prevalent in CAP patients, potentially complicating diagnosis and treatment decisions [8]. Moreover, certain subpopulations—such as the elderly, immunocompromised, and those with chronic conditions—are more likely to harbor resistant organisms or	
	experience atypical presentations [9]. The use of advanced diagnostic techniques like multiplex PCR has improved pathogen identification and provided greater insight into microbial diversity in CAP [10]. However, regional variability in diagnostic access can result in inconsistent reporting and underestimation of certain pathogens. Studies have also observed seasonal and climatic influences on CAP etiology, with higher prevalence during colder months and in temperate regions [11]. The pathogen profile is thus dynamic and influenced by numerous environmental, demographic, and healthcare-related factors, all of which must be considered when assessing empirical therapy protocols.	
	3. Mechanisms of Antimicrobial Resistance in CAP Pathogens The development of resistance in CAP pathogens is driven by various genetic and biochemical mechanisms. <i>Streptococcus pneumoniae</i>, for example, exhibits resistance through alteration of penicillin-binding proteins, reducing beta-lactam efficacy [12]. Similarly, <i>Haemophilus influenzae</i> and <i>Moraxella catarrhalis</i> produce beta-lactamases, including TEM-type enzymes, which inactivate ampicillin and related drugs [13]. Macrolide resistance in <i>S. pneumoniae</i> is commonly mediated by methylation of ribosomal targets via the <i>ermB</i> gene or active efflux via <i>mefA</i> [14]. Fluoroquinolone resistance has also been reported, largely due to mutations in the <i>gyrA</i> and <i>parC</i> genes [15]. In gram-negative bacilli like <i>Klebsiella pneumoniae</i>, extended-spectrum beta-lactamases (ESBLs) and carbapenemases such as KPC and NDM enzymes confer broad resistance, complicating treatment [16]. Horizontal gene transfer via plasmids, integrons, and transposons plays a critical role in disseminating resistance elements across bacterial populations [17]. Biofilm formation is another key mechanism, particularly among hospital-adapted strains, enhancing both resistance and persistence. These molecular pathways underscore the need for ongoing genetic surveillance and molecular diagnostics to detect resistant strains early and adjust therapeutic regimens accordingly.	
	4. Global and Regional Resistance Patterns Antimicrobial resistance patterns in CAP vary significantly across countries and regions, shaped by prescribing practices, diagnostic infrastructure, and public health	
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policies. In Southwest Iran and parts of Sub-Saharan Africa, studies have identified rising resistance to first-line antibiotics such as amoxicillin and macrolides among *S. pneumoniae* and *H. influenzae* isolates [1,2,18]. Similarly, data from China have shown a growing prevalence of fluoroquinolone and cephalosporin resistance among CAP pathogens, especially in older adults and pediatric populations [13,19]. Ethiopian and Nigerian studies report concerning rates of multidrug resistance among *Klebsiella pneumoniae* and *Escherichia coli*, suggesting local reservoirs of resistance genes that may influence empirical therapy [2,11]. Surveillance networks such as the SENTRY and CARTIPS programs have provided valuable longitudinal data, highlighting resistance trends and regional deviations in susceptibility [4,20]. These variations emphasize the importance of context-specific antibiotic guidelines and the establishment of national resistance databases to inform clinical practice. Without targeted efforts to curb antimicrobial misuse and improve stewardship, resistant CAP pathogens may continue to proliferate, reducing the effectiveness of standard treatment protocols and increasing healthcare costs and morbidity.

5. Impact of Antimicrobial Resistance on Clinical Outcomes

The emergence of resistant pathogens in CAP significantly influences clinical outcomes, including prolonged hospital stays, increased morbidity, treatment failure, and higher mortality rates. Patients infected with resistant strains often require second- or third-line agents, which may be less effective, more toxic, or costlier than standard regimens [1,5]. For instance, fluoroquinolone-resistant *S. pneumoniae* and beta-lactamase-producing *H. influenzae* have been linked to longer recovery times and the need for ICU admission in multiple regional studies [2,13]. Inappropriate initial therapy due to undetected resistance can delay clinical improvement and raise the risk of complications such as empyema or septicemia [8]. Moreover, comorbidities such as diabetes, chronic lung disease, or immunosuppression further amplify adverse outcomes when resistant organisms are involved [9]. In low-resource settings, limited access to susceptibility testing leads to empirical treatments that are often mismatched to the resistance profile, further worsening outcomes [11]. Clinical data from sub-Saharan Africa and parts of Asia demonstrate that resistance not only drives disease severity but also limits options for outpatient management, increasing hospitalization rates and economic burden [18,19]. Effective management thus requires both early pathogen detection and local resistance data to guide therapeutic decisions.

6. Diagnostic Challenges and Advances

Accurate diagnosis of CAP and its causative agents is critical for effective management, but current diagnostic methods have notable limitations. Traditional culture-based techniques are time-consuming and may yield false negatives, especially if antibiotics were administered before sampling [3,10]. Moreover, sputum samples are often contaminated with oropharyngeal flora, complicating pathogen identification. Recent advances, such as multiplex PCR, have improved sensitivity and specificity in detecting respiratory pathogens directly from clinical samples [6,17]. Molecular techniques allow for rapid identification of resistance genes, providing crucial insights for guiding therapy before culture results are available. However, these advanced methods remain underutilized in many settings due to cost, infrastructure constraints, and lack of trained personnel [20]. Serological tests and urinary antigen assays also aid in detecting atypical pathogens like *Legionella* or *Mycoplasma pneumoniae*, although their availability varies globally [7]. Point-of-care diagnostics, including rapid antigen detection and syndromic panels, hold promise for earlier detection and tailored therapy, but their implementation is still uneven. Hence, the challenge lies not

only in technological advancement but in equitable access and clinical integration. Establishing cost-effective, standardized diagnostic protocols is essential for mitigating the impact of resistance in CAP.

7. Antibiotic Stewardship in the Community Setting

Antibiotic stewardship plays a pivotal role in curbing the rise of resistance in community-acquired infections. Over-prescription of antibiotics, especially for viral or self-limiting respiratory conditions, remains widespread in outpatient and primary care settings [4,13]. Empirical treatment without microbiological confirmation often contributes to misuse, leading to selection pressure for resistant strains [19]. In many countries, antibiotics are available over the counter or prescribed without adherence to standard treatment guidelines, particularly in rural or underserved areas [2,5]. Stewardship efforts must focus on promoting rational prescribing, updating treatment protocols based on local susceptibility data, and educating both healthcare professionals and the public on responsible antibiotic use [1]. Initiatives such as delayed prescriptions, use of narrow-spectrum agents, and dose optimization have shown positive results in reducing resistance trends [16]. Integration of antimicrobial stewardship into electronic medical record systems and mobile apps can provide real-time decision support in primary care [11]. Furthermore, community-level surveillance of resistance patterns is essential for tailoring empirical therapy and preventing the spread of multidrug-resistant organisms. A multidisciplinary approach involving clinicians, pharmacists, microbiologists, and public health experts is crucial to ensure the success of these programs.

8. Pediatric and Geriatric Considerations

Special populations, particularly children and the elderly, experience distinct challenges in the management of CAP amidst rising antimicrobial resistance. In pediatric patients, *S. pneumoniae* and *H. influenzae* remain dominant, with increasing resistance to amoxicillin, macrolides, and cephalosporins posing therapeutic dilemmas [13]. Empirical therapy in children is further complicated by dosing limitations, contraindications, and concerns about long-term antibiotic exposure. Recent data from China and Ethiopia have shown rising resistance in pediatric CAP isolates, especially among outpatient populations [9]. Similarly, older adults face higher risks of infection with resistant pathogens due to age-related immunosenescence, frequent healthcare exposure, and comorbidities [7]. Studies have reported higher incidence of *Klebsiella pneumoniae* and *MDRE. coli* in elderly patients, especially those with prior antibiotic use or hospitalization [2,11]. Delayed diagnosis, polypharmacy, and atypical presentations in this group also contribute to poor outcomes. Tailored treatment strategies, informed by local resistance profiles and age-specific pharmacodynamics, are necessary. Preventive strategies, such as pneumococcal and influenza vaccination, play a significant role in reducing CAP incidence and resistance pressure in both age groups. Continued research into age-adjusted diagnostics and therapeutics is warranted.

9. Preventive Strategies and Public Health Interventions

Preventing CAP and its resistant forms requires a multifaceted public health approach. Vaccination remains one of the most effective strategies, particularly pneumococcal conjugate vaccines (PCV13, PCV15) and the influenza vaccine, both of which have demonstrated efficacy in reducing disease burden and resistance pressure [3,9]. Widespread vaccination not only decreases incidence but also indirectly reduces antibiotic use by preventing infections in the first place. Public health education campaigns focusing on hygiene, cough etiquette, and appropriate antibiotic use are essential in curbing transmission and misuse [5,13]. National surveillance programs must be expanded to monitor trends in CAP pathogens and their resistance profiles, enabling timely updates to treatment guidelines [4,18]. Additionally,

integrating resistance surveillance data into public health planning can help prioritize resources and design targeted interventions. In regions with high community resistance, preventive strategies such as improved sanitation, reduced air pollution, and smoking cessation can lower CAP incidence [2]. Strengthening primary care systems to support early diagnosis, appropriate referrals, and standardized treatment protocols is also essential. Ultimately, combating AMR in CAP demands synergy between clinical management and broader public health strategies aimed at containment and prevention.

CONCLUSION

The growing antimicrobial resistance in community-acquired pneumonia presents a critical challenge to global public health. Shifts in pathogen profiles, rising multidrug resistance, and diagnostic limitations complicate effective management. Resistance trends vary regionally, emphasizing the need for localized surveillance and evidence-based empirical therapy. Strengthening antibiotic stewardship, improving diagnostic access, and promoting preventive strategies such as vaccination are essential to curb resistance. Special consideration for vulnerable populations, including children and the elderly, is vital. A coordinated approach involving clinicians, microbiologists, and public health systems is imperative to contain resistance, optimize outcomes, and ensure the continued efficacy of existing antimicrobial agents.

REFERENCES

- Hassanzadeh, S., Khoramrooz, S. S., Mazloomirad, F., Sharifi, A., Roustaei, N., Gholamnezhad, M., & Jamshidnejad, E. (2023). Bacterial profile and their antimicrobial resistance patterns among patients with community-acquired pneumonia in southwestern Iran. *Iranian Journal of Microbiology*, 15(3), 343–349. <https://doi.org/10.18502/ijm.v15i3.12894>
- Assefa, M., Tigabu, A., Belachew, T., & Tessema, B. (2022). Bacterial profile, antimicrobial susceptibility patterns, and associated factors of community-acquired pneumonia among adult patients in Gondar, Northwest Ethiopia: A cross-sectional study. *PLOS ONE*, 17(2), e0262956. <https://doi.org/10.1371/journal.pone.0262956>
- Farajzadeh Sheikh, A., Rahimi, R., Meghdadi, H., Alami, A., & Saki, M. (2021). Multiplex polymerase chain reaction detection of *Streptococcus pneumoniae* and *Haemophilus influenzae* and their antibiotic resistance in patients with community-acquired pneumonia from southwest Iran. *BMC Microbiology*, 21, 343. <https://doi.org/10.1186/s12866-021-02408-7>
- Pfaller, M. A., & Jones, R. N. (2002). Gatifloxacin phase IV surveillance trial (TeqCES study): Report of pathogens isolated and susceptibility patterns in community-acquired respiratory tract infections. *Diagnostic Microbiology and Infectious Disease*, 44(1), 77–84. [https://doi.org/10.1016/s0732-8893\(02\)00446-7](https://doi.org/10.1016/s0732-8893(02)00446-7)
- Mazloomirad, F., Hassanzadeh, S., Sharifi, A., Nikbakht, G., Roustaei, N., & Khoramrooz, S. S. (2021). Identification and detection of pathogenic bacteria from patients with hospital-acquired pneumonia in southwestern Iran; evaluation of biofilm production and molecular typing of bacterial isolates. *BMC Pulmonary Medicine*, 21, 408. <https://doi.org/10.1186/s12890-021-01773-3>
- Kurutepe, S., Ececi, T., Ozgen, A., Biçmen, C., Celik, P., Akto, u Özkan, S., & Sürcüoğlu, S. (2012). Investigation of bacterial etiology with conventional and multiplex PCR methods in adult patients with community-acquired pneumonia. *Mikrobiyoloji Bulteni*, 46(4), 523–531.
- Wang, Z., Ji, W., Guo, H. B., Tao, Y. Z., & Ding, Y. F. (2011). Comparative studies on the composition and antibiotic-resistance of pathogenic bacteria between children with community-acquired and hospital-acquired pneumonia. *Zhonghua Yu Fang Yi Xue Za Zhi*, 45(3), 211–216.
- Sun, H., Chen, L., Chen, X., Jia, X., Li, N., Liu, W., ... & Zhang, J. (2016). Antimicrobial susceptibility of community-acquired respiratory tract pathogens isolated from class B hospitals in China during 2013 and 2014. *Zhonghua Jie He He Hu Xi Za Zhi*, 39(1), 30–37.
- Luan, Y., Sun, Y., Duan, S., Zhao, P., & Bao, Z. (2018). Pathogenic bacterial profile and drug resistance analysis of community-acquired pneumonia in older outpatients with fever. *Journal of International Medical Research*, 46(11), 4596–4604. <https://doi.org/10.1177/0300060518786915>
- Gotfried, M. H. (2001). Epidemiology of clinically diagnosed community-acquired pneumonia in the primary care setting: Results from the 1999–2000 respiratory surveillance program. *American Journal of Medicine*, 111(Suppl 9A), 25S–29S. [https://doi.org/10.1016/s0002-9343\(01\)01028-2](https://doi.org/10.1016/s0002-9343(01)01028-2)
- Hamde, F., Chala, B., Bekele, M., Shenkutie, A. M., Abubeker, R., & Tafess, K. (2024). Isolation and antimicrobial resistance patterns of bacterial pathogens from community-acquired pneumonia at Adama Hospital Medical College, Adama, Ethiopia. *Journal of Tropical Medicine*, 2024, 8710163. <https://doi.org/10.1155/2024/8710163>
- Hirai, J., Kinjo, T., Koga, T., Haranaga, S., Motonaga, E., & Fujita, J. (2020). Clinical characteristics of community-acquired pneumonia due to *Moraxella catarrhalis* in adults: A retrospective single-centre study. *BMC Infectious Diseases*, 20, 821. <https://doi.org/10.1186/s12879-020-05564-9>
- Sun, H. L., Yang, Q. W., Xu, Y. C., Wang, H., Xie, X. L., Chen, M. J., ... & He, L. (2009). Resistance study of community respiratory pathogens isolated in China from 2005 to 2007. *Zhonghua Yi Xue Za Zhi*, 89(42), 2983–2987.
- Yohannes, H., Belachew, T., Assefa, M., Getaneh, E., Zeray, H., Kegne, A., ... &

- Tigabu, A. (2023). Pathogenic bacteria recovered from Gene X-pert tuberculosis-negative adult patients in Gondar, Northwest Ethiopia. *BMC Pulmonary Medicine*, 23(1), 197. <https://doi.org/10.1186/s12890-023-02500-w>
- Casellas, J. M., Gilardoni, M., Tome, G., Goldberg, M., Ivanovic, S., Orduna, M., ... & Montero, J. M. (1999). Comparative in-vitro activity of levofloxacin against isolates of bacteria from adult patients with community-acquired lower respiratory tract infections. *Journal of Antimicrobial Chemotherapy*, 43(Suppl C), 37–42. https://doi.org/10.1093/jac/43.suppl_3.37
- Wang, H., Liu, Y. L., Chen, M. J., Xu, Y. C., Sun, H. L., Yang, Q. W., ... & Hu, B. J. (2012). Antimicrobial susceptibility of community-acquired respiratory tract pathogens isolated from adults in China during 2009 and 2010. *Zhonghua Jie He He Hu Xi Za Zhi*, 35(2), 113–119.
- Demars, Y., Braham, T., Rotzinger, D. C., Brouillet, R., Jaton, K., Opota, O., ... & Boillat-Blanco, N. (2022). Utility of polymerase chain reaction in nasopharyngeal swabs for identifying respiratory bacteria causing community-acquired pneumonia. *Microbiology Spectrum*, 10(3), e0037922. <https://doi.org/10.1128/spectrum.00379-22>
- Liu, Y. N., Chen, M. J., Zhao, T. M., Wang, H., Wang, R., Liu, Q. F., ... & Ying, K. J. (2006). A multicentre study on the pathogenic agents in 665 adult patients with community-acquired pneumonia in cities of China. *Zhonghua Jie He He Hu Xi Za Zhi*, 29(1), 3–8.
- Worku, M., Belay, G., & Tigabu, A. (2022). Bacterial profile and antimicrobial susceptibility patterns in cancer patients. *PLOS ONE*, 17(4), e0266919. <https://doi.org/10.1371/journal.pone.0266919>
- Pfaller, M. A., Ehrhardt, A. F., & Jones, R. N. (2001). Frequency of pathogen occurrence and antimicrobial susceptibility among community-acquired respiratory tract infections in the respiratory surveillance program study: Microbiology from the medical office practice environment. *American Journal of Medicine*, 111(Suppl 9A), 4S–12S. [https://doi.org/10.1016/s0002-9343\(01\)01025-7](https://doi.org/10.1016/s0002-9343(01)01025-7)