Section: General Medicine

Original Research Article

ANTIMICROBIAL RESISTANCE PATTERNS IN COMMUNITY-ACQUIRED INFECTIONS

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ABSTRACT

Background: Antimicrobial resistance (AMR) in community-acquired infections (CAIs) is a growing public health concern.

Materials and Methods: A retrospective study of 450 culture-positive CAI cases (Jan–Dec 2023) was conducted at Patnam Mahender Reddy Institute of Medical Sciences, Chevella, Telangana. Pathogen distribution and resistance phenotypes were analyzed.

Results: Gram-negative organisms predominated (73.6%), with Escherichia coli (37.6%) and Klebsiella pneumoniae (27.1%) as leading pathogens. ESBL prevalence was high in urinary isolates (E. coli 40.2%; K. pneumoniae 32.0%). Carbapenem resistance was observed in K. pneumoniae (13.9%) and Acinetobacter baumannii (36.4%). MRSA accounted for 30.3% of Staphylococcus aureus isolates, while macrolide resistance was noted in 30.0% of Streptococcus pneumoniae. A modest but statistically significant upward trend in carbapenem resistance among Klebsiella pneumoniae was observed (p-trend = 0.03).

Conclusion: The study demonstrates Gram-negative dominance, substantial ESBL prevalence, and emerging carbapenem resistance in CAIs. MRSA and macrolide resistance further complicate management, underscoring the need for updated empirical therapy and strengthened stewardship.

Keywords: Antimicrobial resistance, Community-acquired infections, ESBL, MRSA, Carbapenem resistance, Gram-negative pathogens, India.

INTRODUCTION

Antimicrobial resistance (AMR) has become one of the most urgent public health threats of the 21st century, undermining the effectiveness of antibiotics that were once considered the cornerstone of modern medicine.[1] The World Health Organization (WHO) has identified AMR as a global priority, warning that without coordinated action, common infections and minor injuries could once again become fatal. The Global Burden of Bacterial AMR study published in The Lancet estimated that in 2019, 4.95 million deaths were associated with bacterial AMR, including 1.27 million deaths directly attributable to resistant infections.[2] These figures highlight the scale of the crisis and underscore the disproportionate impact on low and middle income countries, particularly in South Asia, where high population density, unregulated antibiotic use, and limited surveillance infrastructure converge to accelerate resistance.

Community acquired infections (CAIs) represent a particularly concerning dimension of AMR. Unlike hospital acquired infections, which are often managed in controlled environments with access to advanced diagnostics, CAIs affect individuals outside hospital settings and frequently require empirical therapy before culture and sensitivity results are available. This practice, while clinically necessary, often results in inappropriate antibiotic use and fosters the emergence of resistant strains.[3] Urinary tract infections, respiratory tract infections, bloodstream infections, and skin and soft tissue infections are among the most common CAIs, and resistance in these domains directly impacts primary care, outpatient management, and community health outcomes.

India faces unique challenges in combating AMR. The Indian Council of Medical Research (ICMR) established the Antimicrobial Resistance Surveillance & Research Network (AMRSN) in 2018 to provide standardized national data. Reports from

AMRSN have consistently documented rising resistance rates among Escherichia coli, Klebsiella pneumoniae, and Staphylococcus aureus, pathogens that dominate both hospital and community infections.[4] Fluoroquinolone resistance in E. coli isolated from urinary tract infections has exceeded 60% in several centers, while extended spectrum beta lactamase (ESBL) production is increasingly prevalent among Gram negative organisms.[5] These findings are particularly alarming because fluoroquinolones and cephalosporins remain widely prescribed in community settings, and their declining efficacy severely limits therapeutic options.

Methicillin resistant Staphylococcus aureus (MRSA) continues to pose significant challenges in both hospital and community settings across Asia. A systematic review and meta analysis of MRSA prevalence in the Asia Pacific region reported substantial heterogeneity, with community MRSA rates ranging from 20% to 40% depending on geography and patient population.[6] The persistence of MRSA in skin and soft tissue infections complicates empirical therapy, often necessitating reliance on last resort agents such as vancomycin and linezolid. This reliance raises concerns about treatment costs, toxicity, and the potential for future resistance, further underscoring the need for rational prescribing practices.

Despite hospital based stewardship programs and national surveillance initiatives, gaps remain in community level monitoring. Prescribing practices in outpatient and semi urban settings are often guided by outdated or hospital centric data, leaving clinicians without reliable information on prevailing resistance patterns. Moreover, socioeconomic factors such as over the counter antibiotic availability, self medication, and agricultural antibiotic use exacerbate the problem. Telangana, like other Indian states, has witnessed increasing AMR trends in both urban and semi urban populations, with tertiary care centers in South India reporting high prevalence of ESBL producing Gram negative organisms in community acquired urinary tract infections. These findings emphasize the importance of localized resistance mapping, as prescribing practices must be tailored to regional epidemiology rather than national averages.

Aim and Objectives

Aim

To evaluate pathogen distribution and antimicrobial resistance patterns in culture positive community acquired infections at Patnam Mahender Reddy Institute of Medical Sciences, Chevella, Telangana.

Objectives

1. To describe patient demographics and infection types.
2. To identify major pathogens and their resistance profiles (ESBL, MRSA, carbapenem resistance).
3. To assess quarterly trends in multidrug resistance.
4. To provide evidence for empirical therapy and stewardship strategies.

MATERIALS AND METHODS

Study Design and Duration

- Retrospective observational study conducted over 12 months (January 2023–December 2023).
- Retrospective design chosen to capture real-world culture-positive data, reflecting epidemiological burden without intervention bias.[7]

Study Setting

- Department of General Medicine in collaboration with Department of Microbiology.
- Patnam Mahender Reddy Institute of Medical Sciences, Chevella, Telangana.
- Microbiology laboratory equipped with automated systems for pathogen identification and antimicrobial susceptibility testing, ensuring compliance with international standards.

Study Population

- Adults aged ≥18 years presenting with CAIs.

Inclusion Criteria

- Culture-positive reports available.
- Complete antimicrobial sensitivity data.

Exclusion Criteria:

- Hospital-acquired infections.
- Pediatric cases (<18 years).
- Incomplete microbiological records.
- Age cut-off selected to minimize variability associated with pediatric resistance, which differs significantly from adult epidemiology.[8]

Sample Size and Limitations

Sample size: All eligible culture-positive CAI cases during study period.

Limitations

- Restricted to available records.
- Culture-negative infections excluded.
- Single-center design limits generalizability.
- Observational design restricts control over confounding factors (e.g., prior antibiotic exposure, comorbidities).

Specimen Collection and Processing

- Urine - urinary tract infections.
- Sputum/throat swabs - respiratory tract infections.
- Blood - bloodstream infections.
- Pus/wound swabs - skin and soft tissue infections.
- Pathogen identification: colony morphology, Gram staining, biochemical tests.
- Automated systems used for confirmation.

Antimicrobial Susceptibility Testing

- Conducted per CLSI guidelines.[9]

Methods applied:

- Kirby–Bauer disk diffusion for routine testing.
- MIC determination for selected antibiotics.

Special resistance detection:

- ESBL: double-disk synergy test.
- MRSA: cefoxitin disk diffusion.
- Carbapenem resistance: meropenem and imipenem disks.

- Quality control: CLSI-recommended reference strains.

Data Collection and Statistical Analysis

- Demographics: age, gender.
- Clinical: infection type.
- Microbiological: pathogen distribution, resistance profiles, MDR prevalence.

Statistical methods

- Descriptive statistics (percentages, proportions).
- Chi-square tests for categorical comparisons.
- 95% confidence intervals for precision.
- Graphical representation: advanced tables, bar charts, resistance trend analysis.

Ethical Considerations

- Approval obtained from Institutional Ethics Committee.
- Patient confidentiality maintained by anonymizing records.
- Study conducted in accordance with the Declaration of Helsinki.
- Informed consent waived due to analysis of existing laboratory records.

RESULTS

Demographic Characteristics

A total of 450 culture positive community acquired infection (CAI) cases were included in the study. The majority of patients were between 30 and 59 years of age (190, 42.2%), followed by those aged ≥60 years (160, 35.6%) and 18–29 years (100, 22.2%). Males accounted for 236 cases (52.4%), while females contributed 214 cases (47.6%). Respiratory infections were significantly more frequent among older adults ($p = 0.01$), whereas urinary tract infections predominated in females ($p = 0.03$).

Table 1: Demographic profile of patients (n = 450)

Variable	Category	n	Percent (%)
Age group	18–29	100	22.2
	30–59	190	42.2
	≥60	160	35.6
Gender	Male	236	52.4
	Female	214	47.6

Infection Type Distribution

Urinary tract infections (UTIs) represented the largest proportion of CAIs, with 203 cases (45.1%). Respiratory tract infections (RTIs) accounted for 113 cases (25.1%), bloodstream infections (BSIs) for 67 cases (14.9%), and skin and soft tissue infections (SSTIs) for 67 cases (14.9%). UTIs were the most common CAI overall ($p < 0.001$).

Table 2: Distribution of infection types (n = 450)

Infection type	Cases (n)	Percent (%)
UTI	203	45.1
RTI	113	25.1
BSI	67	14.9
SSTI	67	14.9

Pathogen Distribution

Gram negative organisms accounted for 73.6% of isolates, with Escherichia coli (169, 37.6%) and Klebsiella pneumoniae (122, 27.1%) being the most common. Gram positive organisms comprised 26.4% of isolates, dominated by Staphylococcus aureus (66, 14.7%) and Streptococcus pneumoniae (40, 8.9%). This Gram negative predominance was statistically significant ($p < 0.001$).

Table 3: Pathogen Distribution by Infection Type (n = 450)

Pathogen	UTI	RTI	BSI	SSTI	Total
Escherichia coli	136	0	28	5	169
Klebsiella pneumoniae	55	51	10	6	122
Staphylococcus aureus	0	0	22	44	66
Streptococcus pneumoniae	0	40	0	0	40
Pseudomonas aeruginosa	8	11	0	12	31
Acinetobacter baumannii	0	11	0	0	11
Enterococcus spp.	4	0	0	0	4
Other Gram-negatives	0	0	7	0	7
Total	203	113	67	67	450

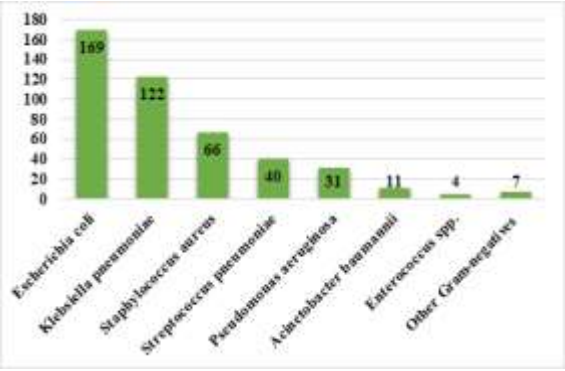

Figure 1: Pathogen distribution in community-acquired infections

Interpretation: Community-acquired infections in this cohort (n = 450) were dominated by Gram-negative organisms. Escherichia coli (169 cases) and Klebsiella pneumoniae (122 cases) together accounted for more than half of all isolates. Among Gram-positive pathogens, Staphylococcus aureus (66 cases) and Streptococcus pneumoniae (40 cases) were less frequent. Non-fermenters such as Pseudomonas aeruginosa (31 cases) and Acinetobacter baumannii (11 cases) appeared in smaller numbers, while Enterococcus spp. (4 cases) and other Gram-negative organisms (7 cases) contributed minimally. Overall, Gram-negative bacteria comprised approximately 73.6% of the total isolates, underscoring their predominance in community-acquired infections.

Antimicrobial Resistance Patterns

Resistance analysis revealed high fluoroquinolone resistance in E. coli (110, 65.1%) and cephalosporin resistance in K. pneumoniae (67, 54.9%). ESBL production was detected in 68 E. coli isolates (40.2%) and 39 K. pneumoniae isolates (32.0%). Carbapenem resistance was observed in 17 K. pneumoniae isolates (13.9%) and 4 A. baumannii isolates (36.4%). Among Gram positive organisms, MRSA was identified in 20 S. aureus isolates (30.3%), while macrolide resistance was noted in 17 (25.8%). S. pneumoniae exhibited macrolide resistance in 12 cases (30.0%) and penicillin non susceptibility in 8 cases (20.0%).

Table 4: Resistance phenotypes (n = 450)

Pathogen	Total (n)	Key resistance	Count (%)	MDR (%)
Escherichia coli	169	Fluoroquinolone-R 110 (65.1)	ESBL-producing 68 (40.2)	40.2
Klebsiella pneumoniae	122	Cephalosporin-R 67 (54.9)	Carbapenem-resistant 17 (13.9)	35.2
Staphylococcus aureus	66	MRSA 20 (30.3)	Macrolide-R 17 (25.8)	30.3
Streptococcus pneumoniae	40	Macrolide-R 12 (30.0)	Penicillin non-susceptible 8 (20.0)	—
Pseudomonas aeruginosa	31	Aminoglycoside-R 12 (38.7)	—	25.8
Acinetobacter baumannii	11	Carbapenem-resistant 4 (36.4)	—	36.4

Among 450 isolates, E. coli (n = 169) showed high fluoroquinolone resistance (65.1%) with ESBL in 40.2%. K. pneumoniae (n = 122) had cephalosporin resistance (54.9%) and carbapenem resistance (13.9%). S. aureus (n = 66) exhibited MRSA (30.3%) and macrolide resistance (25.8%), while S. pneumoniae (n = 40) showed macrolide resistance (30.0%) and penicillin non-susceptibility (20.0%). Non-fermenters contributed notably: P. aeruginosa (38.7% aminoglycoside resistance) and A. baumannii (36.4% carbapenem resistance).

Multidrug resistance (MDR), defined as resistance to ≥1 drug in ≥3 antimicrobial classes, was observed in 40.2% of E. coli, 35.2% of K. pneumoniae, 30.3% of S. aureus, 25.8% of P. aeruginosa, and 36.4% of A. baumannii.

Quarterly MDR Trends

Quarterly analysis showed that ESBL prevalence in E. coli remained stable across the year (17 cases per quarter). Carbapenem resistance in K. pneumoniae increased modestly (Q1–Q4: 4, 4, 4, 5; p trend = 0.03). MRSA prevalence in S. aureus remained consistent (5 cases each quarter), while MDR in P. aeruginosa was stable (2 cases per quarter).

Table 5: Quarterly MDR trends (n = 450)

Pathogen phenotype	Q1	Q2	Q3	Q4	Total
E. coli ESBL	17	17	17	17	68
K. pneumoniae Carb-R	4	4	4	5	17
S. aureus MRSA	5	5	5	5	20
P. aeruginosa MDR	2	2	2	2	8

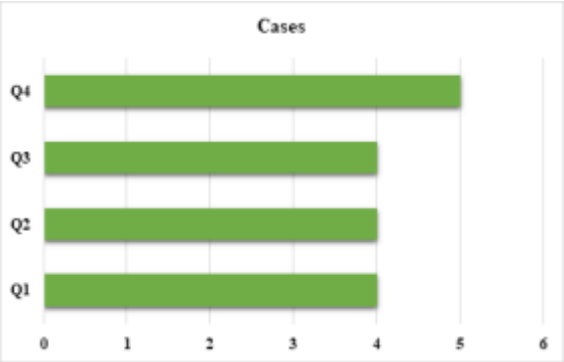

Figure 2: Line chart showing quarterly carbapenem resistance in Klebsiella pneumoniae

Interpretation: The quarterly distribution of cases remained stable across Q1 to Q3, with each quarter reporting 4 cases. A modest increase was observed in Q4, which recorded 5 cases. This pattern suggests consistent case occurrence throughout the year, with a slight rise in the final quarter

In summary, Gram negative organisms dominated CAIs, with E. coli and K. pneumoniae showing high levels of fluoroquinolone and cephalosporin resistance, respectively. ESBL prevalence was concentrated in urinary isolates, while carbapenem resistance in K. pneumoniae demonstrated a rising trend. MRSA burden was notable in SSTI, and macrolide resistance in S. pneumoniae complicated respiratory infection management. These findings highlight the urgent need for localized antimicrobial stewardship and updated empirical therapy guidelines in South India.

DISCUSSION

The present study highlights the predominance of Gram negative organisms in community acquired infections, with Escherichia coli and Klebsiella pneumoniae accounting for the majority of isolates. This finding is consistent with national surveillance reports, which have documented similar pathogen distribution patterns in India during recent years.[10]

The high prevalence of extended-spectrum beta lactamase (ESBL) production among urinary isolates underscores the growing challenge of empirical therapy, as third generation cephalosporins and fluoroquinolones are increasingly ineffective in community settings.[11]

Carbapenem resistance in K. pneumoniae and Acinetobacter baumannii observed in this study is particularly concerning, as these agents are often considered last line therapies. The modest but statistically significant upward trend in carbapenem resistance among K. pneumoniae suggests early signals of community dissemination, which has been reported in other regional studies.[12] In contrast, methicillin resistant Staphylococcus aureus (MRSA) prevalence remained stable, aligning with Asia Pacific data that indicate persistent but plateaued MRSA rates in skin and soft tissue infections.

Overall, these findings emphasize the urgent need for antimicrobial stewardship programs that extend beyond hospital boundaries into community practice. Empirical therapy guidelines must be updated to reflect local resistance trends, particularly the high burden of ESBL and the emergence of carbapenem resistance. Strengthening surveillance systems and incorporating molecular characterization of resistance mechanisms will be critical to mitigate the growing threat of AMR in India.

Limitations

- This study was retrospective in design.
- It was conducted at a single-center.
- Molecular resistance testing was not performed.

CONCLUSION

This study of 450 culture positive community acquired infections provides critical insights into the local antimicrobial resistance (AMR) landscape. Gram negative organisms, particularly Escherichia coli and Klebsiella pneumoniae, were the predominant pathogens, with high rates of fluoroquinolone and cephalosporin resistance. Extended spectrum beta lactamase (ESBL) production was substantial in urinary isolates, while carbapenem resistance in K. pneumoniae showed a modest but significant upward trend. Gram positive organisms contributed notably through methicillin resistant Staphylococcus aureus (MRSA) and macrolide resistant Streptococcus pneumoniae, underscoring the multifaceted nature of AMR in community settings.

The findings emphasize the urgent need for updated empirical therapy guidelines that reflect local resistance profiles. High ESBL prevalence limits the utility of commonly prescribed agents, while emerging carbapenem resistance threatens the effectiveness of last line therapies. MRSA and macrolide resistance further complicate the management of skin and respiratory infections. Strengthening antimicrobial stewardship programs, expanding surveillance to include molecular characterization, and promoting rational antibiotic use in both hospital and community practice are essential steps to mitigate the growing AMR burden.

In conclusion, this study highlights the importance of localized resistance mapping to guide empirical therapy and public health strategies. By integrating surveillance data into clinical decision making, healthcare providers can improve patient outcomes while slowing the progression of resistance in the community.

REFERENCES

1. Torumkuney, D., Poojary, A., Shenoy, B., Nijhara, P., Dalal, K. and Manenzhe, R., 2022. Country data on AMR in India in the context of community-acquired respiratory tract infections: links between antibiotic susceptibility, local and international antibiotic prescribing guidelines, access to

medicine and clinical outcome. Journal of Antimicrobial Chemotherapy, 77(Supplement_1), pp. i10-i17.
2. Laxminarayan, R. and Chaudhury, R.R., 2016. Antibiotic resistance in India: drivers and opportunities for action. PLoS medicine, 13(3), p. e1001974.
3. Singh, A., Amod, A., Pandey, P., Bose, P., Pingali, M.S., Shivalkar, S., Varadwaj, P.K., Sahoo, A.K. and Samanta, S.K., 2022. Bacterial biofilm infections, their resistance to antibiotics therapy and current treatment strategies. Biomedical Materials, 17(2), p.022003.
4. Ranjbar, R. and Alam, M., 2023. Antimicrobial Resistance Collaborators (2022). Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Evidence-based nursing.
5. Kannian, P., Mahanathi, P., Ashwini, V., Vaishnavi, M. and Priya, C., 2021. Carbapenem–resistant gram-negative bacilli are predominantly multidrug or pan-drug resistant. Microbial Drug Resistance, 27(8), pp.1057-1062.
6. BHARDWAJ, N., 2022. Analyzing and comparing the antibiotic resistance pattern of Uropathogenic microorganism isolates of suspected UTI patients from OPD and IPD (Doctoral dissertation, APEEJAY STYA UNIVERSITY).
7. Pierce, V.M. and Mathers, A.J., 2022. Setting antimicrobial susceptibility testing breakpoints: a primer for pediatric infectious diseases specialists on the Clinical and Laboratory Standards Institute approach. Journal of the Pediatric Infectious Diseases Society, 11(2), pp.73-80.
8. Satlin, M.J., Lewis, J.S., Weinstein, M.P., Patel, J., Humphries, R.M., Kahlmeter, G., Giske, C.G. and Turnidge, J., 2020. Clinical and Laboratory Standards Institute and European Committee on Antimicrobial Susceptibility Testing position statements on polymyxin B and colistin clinical breakpoints. Clinical Infectious Diseases, 71(9), pp. e523-e529.
9. Humphries, R., Tamma, P.D. and Mathers, A.J., 2022. Disk correlates for revised Clinical and Laboratory Standards Institute Enterobacterales piperacillin-tazobactam MIC breakpoints. Journal of clinical microbiology, 60(5), pp. e00243-22.
10. Kumar, P., Kumar, D., Gautam, V., Singh, S. and Fadhil Pratama, M.R., 2025. Antimicrobial Resistance a Global Burden-Mechanisms, Current Insights, and Future Directions. Bulletin of Pharmaceutical Sciences Assiut University, 48(1), pp.523-545.
11. Sandaradura, I., 2022. Precision antimicrobial therapy: the application of therapeutic drug monitoring in critical illness (Doctoral dissertation, University of New South Wales (Australia)).
12. Goltz, J., 2022. Investigating Factors Associated with Extended-Spectrum Beta-Lactamase-Producing Enterobacteriaceae Colonization and/or Infection in Humans: A One Health Approach (Doctoral dissertation, University of Guelph).