Original Research Article

PREVALENCE OF MULTIDRUG-RESISTANT BACTERIA IN COMMUNITY-ACQUIRED INFECTIONS: A PUBLIC HEALTH CONCERN

***Rakshita Ojha*[1], *Rajan Pathak*[2], *Rahul Chandra*[3], *Mukesh Kumar*[4]**

[1]*Assistant Professor, Department of Community Medicine, United Institute of Medical Sciences, Prayagraj, Uttar Pradesh, India.*
[2]*Assistant Professor Department of Microbiology United Institute of Medical Sciences, Prayagraj, Uttar Pradesh, India.*
[3]*Associate Professor, Department of Community Medicine, Narayan Medical College & Hospital, Sasaram, Bihar, India.*
[4]*Professor, Department of Microbiology, Netaji Subhas Medical College & Hospital, Bihta, Patna, Bihar, India.*

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Corresponding Author:
Dr Rajan Pathak,
Assistant Professor, Department of Microbiology, United Institute of Medical Sciences, Prayagraj, Uttar Pradesh, India.
Email: rajanpathak.lko@gmail.com

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ABSTRACT

Background: Multidrug-resistant (MDR) bacteria pose a significant public health threat, particularly in community-acquired infections (CAIs). The increasing prevalence of MDR pathogens complicates treatment, leading to higher morbidity, mortality, and healthcare costs. Bihar, India, with its high disease burden and widespread antibiotic misuse, is particularly vulnerable to antimicrobial resistance (AMR). **Objectives:** This study aims to assess the prevalence of MDR bacteria in CAIs in Bihar, identify the most common resistant pathogens, and evaluate contributing risk factors. The findings will inform public health strategies for AMR containment.

Materials and Methods: A cross-sectional study was conducted using microbiological data from healthcare facilities across Bihar. Clinical samples from patients with CAIs were analysed for bacterial identification and antimicrobial susceptibility. Resistance patterns were evaluated based on standard guidelines, and demographic data were correlated with infection trends.

Results: Preliminary findings indicate a high prevalence of MDR Escherichia coli, Klebsiella pneumonia, and Staphylococcus aureus in community settings. Risk factors include over-the-counter antibiotic access, poor sanitation, and limited diagnostic facilities. Resistance to beta-lactams, fluoroquinolones, and aminoglycosides was particularly prominent.

Conclusion: The study underscores the urgent need for strengthened antimicrobial stewardship, enhanced surveillance, and public awareness campaigns to curb MDR bacterial infections in Bihar. Implementing stricter regulations on antibiotic sales and improving healthcare infrastructure are critical steps to mitigate this growing crisis.

Keywords: Multidrug-resistant bacteria, community-acquired infections, antimicrobial resistance, Bihar, India, public health.

INTRODUCTION

Multidrug-resistant (MDR) bacteria have emerged as a significant global health challenge, particularly in community-acquired infections (CAIs). These infections, which occur in individuals with no recent healthcare exposure, have increasingly been linked to antibiotic-resistant pathogens, complicating treatment and leading to prolonged illness, higher healthcare costs, and increased mortality rates.[1] The prevalence of MDR bacteria in CAIs is particularly concerning in low- and middle-income countries, where antibiotic stewardship programs are often inadequate, and over-the-counter access to antibiotics contributes to resistance.[2,3] Understanding the epidemiology of MDR bacteria in community settings is crucial for developing effective public health interventions and guiding empirical antibiotic therapy.

The rise in antibiotic resistance is driven by several factors, including the overuse and misuse of antibiotics in human medicine and agriculture, poor infection control practices, and limited access to novel antimicrobial agents.[4] Pathogens such as Escherichia coli, Klebsiella pneumonia, Staphylococcus aureus, and Pseudomonas aeruginosa have demonstrated resistance to multiple antibiotic classes, making them difficult to treat outside hospital settings.[5,6] This trend has raised significant concerns for healthcare professionals and policymakers, as infections once considered manageable with first-line antibiotics now require more expensive and toxic alternatives.[7]

Bihar, one of the most populous states in India, faces unique challenges in addressing MDR bacterial infections in the community. With a high burden of infectious diseases, widespread antibiotic use without prescription, and limited microbiological diagnostic facilities, the state is particularly vulnerable to the spread of resistant pathogens.[8] This study aims to assess the prevalence of MDR bacteria in community-acquired infections in Bihar, evaluate risk factors contributing to resistance, and discuss potential public health interventions to mitigate this growing threat.

The findings of this study will provide valuable insights into the burden of MDR bacteria in community settings and inform local and national policies on antimicrobial resistance (AMR) containment. By highlighting key epidemiological trends, this research seeks to contribute to a broader understanding of resistance patterns and support evidence-based strategies to combat MDR bacterial infections.

MATERIALS AND METHODS

Study Design and Setting: This cross-sectional study was conducted across multiple healthcare facilities in Sasaram, Bihar, from January to June 2023. The study sites included Narayan Medical College and Hospital Sasaram, District Hospital Sasaram, Urban Health Training Centre Sasaram, and nearby Community Health Centres (CHCs) and Primary Health Centres (PHCs). These facilities were selected to ensure a representative sample of community-acquired infections in both urban and semi-urban populations.

Study Population and Sample Collection: The study included patients presenting with symptoms of bacterial infections such as urinary tract infections, respiratory infections, skin and soft tissue infections, and bloodstream infections. Inclusion criteria required patients to have no recent history of hospitalization (within the past 90 days) to confirm community-acquired status. Clinical samples—including urine, blood, sputum, and wound swabs—were collected following standard aseptic procedures from outpatient and emergency department attendees.

Bacterial Identification and Antimicrobial Susceptibility Testing (AST): Samples were transported to microbiology laboratories for bacterial culture and identification using conventional biochemical tests such as Gram staining, catalase, coagulase, oxidase tests, and biochemical reactions in triple sugar iron agar, citrate, urease, and indole tests. Antimicrobial susceptibility testing (AST) was performed using the Kirby-Bauer disk diffusion method,[9,10] and minimum inhibitory concentration (MIC) values were determined based on Clinical and Laboratory Standards Institute (CLSI) guidelines.[11] MDR was defined as resistance to at least one agent in three or more antimicrobial classes.

Data Collection and Statistical Analysis: Demographic and clinical data, including age, gender, comorbidities, and recent antibiotic use, were recorded. The prevalence of MDR bacteria was calculated as a percentage of total isolates. Associations between resistance patterns and patient characteristics were analysed using chi-square tests and logistic regression models. A p-value of <0.05 was considered statistically significant.

Ethical Considerations: Ethical approval was obtained from the institutional ethics committee of Narayan Medical College and Hospital. Written informed consent was secured from all participants, and patient confidentiality was maintained throughout the study.

RESULTS

Table 1: Sample Distribution by Region.

Region	Total Samples (n=1160)	Positive Isolates (n=750)
Narayan Medical College & Hospital Sasaram	450	290
District Hospital Sasaram	350	220
Urban Health Training Centre Sasaram	150	100
CHCs & PHCs	210	140

As shown in Table 1, the majority of samples were collected from Narayan Medical College and Hospital (n=450), which also showed the highest number of positive isolates (n=290, 64.4%). District Hospital Sasaram contributed 350 samples with 220 positives (62.9%). Urban health centres and peripheral CHCs/PHCs contributed fewer samples but demonstrated positivity rates of 66.67% and 66.67%, respectively. These findings suggest that although tertiary care facilities contributed the largest volume, positivity rates remained high across all healthcare levels, highlighting the widespread nature of community-acquired infections in Sasaram.

Table 2: Demographic and Family Data.

Demographic Parameter	Number (n=750)	Percentage (%)

Male	420	56%
Female	330	44%
Age < 18 years	180	24%
Age 18-40 years	310	41%
Age > 40 years	260	35%
Joint Family	450	60%
Nuclear Family	300	40%

Table 2 showing Males accounted for a slightly higher proportion of infections (56%) compared to females (44%). The most affected age group was 18–40 years (41%), reflecting active working-age individuals, followed by older adults >40 years (35%), and children/adolescents <18 years (24%). Interestingly, joint family settings (60%) showed higher infection prevalence compared to nuclear families (40%), suggesting possible household-level transmission dynamics and overcrowding as risk factors.

Table 3: Risk Factors Associated with MDR Infections.

Risk Factor	Number of Patients (n=750)	Percentage (%)
Recent antibiotic use	420	56%
Self-medication/OTC purchase	310	41%
Poor sanitation practices	280	37%
Comorbidities (e.g., DM, HTN)	190	25%
Low socioeconomic status	340	45%

Table 3 shows, recent antibiotic use was the most common risk factor (56%), followed by self-medication with OTC antibiotics (41%). Poor sanitation practices were reported in 37% of cases, suggesting environmental contributors. Comorbidities such as diabetes and hypertension were present in 25% of cases, indicating increased vulnerability in chronically ill patients. Low socioeconomic status was also an important determinant (45%), reinforcing the role of health disparities in AMR..

Table 4: Prevalence of MDR Bacteria.

Bacterial Isolate	Total Isolates (n=750)	MDR Isolates (%)
Escherichia coli	280	75%
Klebsiella pneumonia	190	65%
Staphylococcus aureus	140	50%
Pseudomonas aeruginosa	90	45%
Acinetobacter spp.	50	40%

As shown in table 4, E. coli was the most frequently isolated pathogen (37.3% of isolates), with an alarming MDR rate of 75%, underscoring its dominant role in CAIs. K. pneumonia accounted for 25.3% of isolates, with 65% MDR prevalence. S. aureus was the third most common (18.7%), half of which were MDR strains, including MRSA. Opportunistic pathogens such as P. aeruginosa and Acinetobacter spp. were less frequent but still showed significant resistance (45% and 40%, respectively). The high prevalence of MDR E. coli and K. pneumonia parallels national and international reports on CAIs.

Table 5: Antibiotic Resistance Patterns of Major Pathogens.

Antibiotic Class	E. coli (n=280)	K. pneumonia (n=190)	S. aureus (n=140)	P. aeruginosa (n=90)	Acinetobacter spp. (n=50)
Beta-lactams	78%	72%	55%	65%	70%
Cephalosporins	74%	70%	48%	60%	68%
Carbapenems	22%	28%	12%	40%	45%
Aminoglycosides	65%	62%	50%	55%	60%
Fluoroquinolones	80%	76%	58%	62%	65%
Tetracyclines	52%	48%	40%	35%	50%
Glycopeptides	NA	NA	28% (MRSA)	NA	NA
Sulfonamides	68%	63%	42%	50%	55%
Polymyxins	10%	12%	NA	20%	25%

Resistance to first-line agents such as ampicillin and cephalosporins was alarmingly high (>70% in E. coli and K. pneumonia). Fluoroquinolone resistance was also widespread across pathogens. Aminoglycosides showed slightly better activity but resistance remained high (40–66%). Carbapenem resistance was lower compared to other classes but still significant (28–38%), raising concern about last-resort antibiotic effectiveness. Notably, 12% of S. aureus isolates showed reduced susceptibility to vancomycin, suggesting emergence of VISA strains in the community. (Table 5) These patterns highlight the diminishing therapeutic options for CAIs in Sasaram.

DISCUSSION

The present study provides a comprehensive analysis of multidrug-resistant (MDR) bacterial pathogens isolated from community-acquired infections (CAIs) in Sasaram, Bihar. Out of 1160 clinical samples collected across multiple healthcare facilities, 750 yielded positive isolates, of which a large proportion demonstrated multidrug resistance. The data confirm that MDR organisms are not confined to hospital environments but are increasingly emerging in the community, reflecting an escalating public health crisis in low-resource settings such as Bihar.

Burden of MDR Pathogens in the Community: Our results demonstrate that Escherichia coli (75% MDR) and Klebsiella pneumoniae (65% MDR) were the most prevalent resistant Gram-negative isolates, followed by Staphylococcus aureus (50% MDR), Pseudomonas aeruginosa (45%), and Acinetobacter spp. (40%). These findings align with national surveillance data showing E. coli and K. pneumoniae as the predominant MDR pathogens in both community and hospital infections.[12] A recent ICMR-AMR surveillance report revealed resistance rates exceeding 70% for fluoroquinolones and third-generation cephalosporins in Enterobacteriaceae isolated from outpatients, which is consistent with our observations.[13]

Antibiotic Resistance Profiles: Fluoroquinolone resistance was alarmingly high, affecting 80% of E. coli and 76% of K. pneumonias isolates. Fluoroquinolones, particularly ciprofloxacin and levofloxacin, are widely used empirically for urinary tract and respiratory infections in India due to their oral availability and broad spectrum. Their indiscriminate use has led to widespread resistance, as similarly reported in North India and Nepal, where resistance exceeded 70% in community isolates.[14,15] The mechanism is often linked to mutations in the quinolone resistance-determining region (QRDR) and plasmid-mediated quinolone resistance genes such as qnr, which have been reported widely in South Asia.[16]

Beta-lactam resistance was also prominent, with >70% resistance rates in E. coli and K. pneumonias. This is likely mediated by extended-spectrum beta-lactamases (ESBLs), particularly blaCTX-M genes, which are now the dominant ESBL type in India.[17] ESBL-producing Enterobacteriaceae severely restrict treatment options, often necessitating carbapenem use. Worryingly, carbapenem resistance was observed in K. pneumonias (28%) and Acinetobacter spp. (45%), reflecting emerging carbapenemase producers in the community. Comparable findings were reported in a multicentre study from India, where 20–30% of K. pneumonias from outpatient settings were carbapenem-resistant.[18] This is particularly concerning given carbapenems are last-line agents, and their failure leaves polymyxins as one of the few therapeutic options.

Among Gram-positive isolates, Staphylococcus aureus accounted for 140 isolates, with 50% demonstrating multidrug resistance. Methicillin-resistant S. aureus (MRSA) constituted 28% of total isolates, paralleling rates reported in South India and Bangladesh, where MRSA prevalence in CAIs ranged between 25–30%.[19,20] MRSA strains also demonstrated glycopeptide resistance (28%), suggesting the presence of vancomycin-intermediate S. aureus (VISA). The emergence of VISA strains in the community is rare but has been increasingly reported worldwide,[21] raising concerns about treatment options for skin and soft tissue infections in the outpatient setting.

Non-fermenting Gram-negative bacilli presented another layer of concern. Pseudomonas aeruginosa showed 45% MDR prevalence, with resistance to aminoglycosides and cephalosporins exceeding 50%. Similarly, Acinetobacter spp. displayed high resistance to carbapenems (45%) and even polymyxins (25%). National data from India mirror these findings, with >40% carbapenem resistance in Acinetobacter isolates even from community-acquired infections.[22] Polymyxin resistance, though still low, has serious implications as it represents the final therapeutic barrier for MDR Gram-negative infections. The detection of such resistance in community isolates suggests possible horizontal gene transfer of mcr plasmid-mediated resistance, a phenomenon reported in several Asian countries.[23]

Risk Factors Driving Resistance: Analysis of demographic and risk factor data provides insight into the drivers of MDR infections. The majority of cases occurred in adults aged 18–40 years, who are more likely to self-medicate and purchase antibiotics without prescriptions. In Bihar, studies have shown that more than 60% of antibiotics are dispensed without medical oversight, fuelling misuse.[24] Family structure also appeared relevant, with joint families (60%) more commonly affected than nuclear families, suggesting that overcrowding and shared facilities may facilitate transmission of resistant pathogens. These findings resonate with similar studies from Uttar Pradesh and rural Bihar, where larger households were independently associated with higher rates of MDR bacterial carriage.[25]

Over-the-counter availability of antibiotics was another key factor. Our results support findings from South India and Nepal, where unrestricted access to antibiotics, especially fluoroquinolones and cephalosporins, was strongly associated with resistance development in community pathogens.[26] Furthermore, lack of adequate sanitation and limited access to clean drinking water in Sasaram may have compounded the spread of resistant Enterobacteriaceae, as environmental reservoirs often contribute significantly to AMR propagation.[27]

Comparative Global Perspective: The resistance rates observed in Sasaram are not unique but reflect broader global patterns. A multicentre Chinese study reported >75% fluoroquinolone resistance in E. coli and nearly 30% carbapenem resistance in K. pneumonias, closely paralleling our results.[28] Similarly, in Africa, studies from Nigeria and Kenya reported MDR rates of >60% in Enterobacteriaceae, attributing them to rampant self-medication and unregulated drug markets.[29,30] These parallels highlight that AMR is a global challenge transcending geographical boundaries, though its impact is disproportionately severe in low- and middle-income countries (LMICs) due to weak regulatory frameworks.

Public Health Implications: The implications of these findings are profound. MDR organisms in community settings threaten the effectiveness of standard empirical therapies for common infections such as urinary tract infections, pneumonia, and skin infections. Patients often require hospitalization and intravenous therapy when oral options fail, increasing both costs and morbidity. In regions like Sasaram with limited healthcare infrastructure, this may lead to increased mortality. Moreover, the spread of carbapenem- and polymyxin-resistant strains outside hospital environments suggests that the last therapeutic lines are under threat even before patients reach tertiary care facilities.

The results strongly emphasize the need for antimicrobial stewardship at the community level. Restricting over-the-counter antibiotic sales, enforcing prescription-only policies, and promoting rational prescribing practices are crucial first steps. Public awareness campaigns about the dangers of self-medication, coupled with improved diagnostic facilities, could reduce unnecessary antibiotic use. Additionally, expanding microbiological surveillance to rural healthcare centres would help track resistance trends and inform treatment guidelines.

In conclusion, the high prevalence of MDR bacteria in community-acquired infections in Sasaram reflects a broader global trend, necessitating immediate intervention. By adopting a multifaceted approach that includes policy changes, healthcare education, strengthened diagnostic capabilities, and stringent antibiotic regulations, the burden of MDR bacterial infections can be mitigated effectively. Future research should focus on longitudinal surveillance studies, assessing the effectiveness of intervention programs, and exploring alternative therapeutic strategies such as bacteriophage therapy and novel antimicrobial compounds. Addressing MDR at both the local and global levels require coordinated efforts to preserve the efficacy of existing antibiotics and ensure better public health outcomes.

Limitations: This study has several limitations. First, the sample size was limited to healthcare facilities in Sasaram, which may not be representative of the entire region of Bihar. Second, due to resource constraints, molecular characterization of resistance genes was not performed, which could have provided deeper insights into the mechanisms of resistance. Third, reliance on hospital-based data may have led to an underestimation of MDR bacterial prevalence in asymptomatic carriers within the community. Additionally, socioeconomic and behavioural factors influencing antibiotic use were not extensively analysed, which may have impacted the interpretation of risk factors.

Recommendations: Addressing the high prevalence of multidrug-resistant (MDR) bacteria in community-acquired infections in Sasaram requires urgent, coordinated policy action. Enforcement of strict regulations to curb over-the-counter antibiotic sales, coupled with strengthened antimicrobial stewardship programs and adherence to evidence-based prescribing guidelines, is critical. Expanding microbiological diagnostic capacity at primary and secondary healthcare levels will reduce empirical misuse of broad-spectrum antibiotics, while community-wide education campaigns must target irrational self-medication practices. Integration of sanitation improvements, vaccination, and infection prevention measures into public health programs will further limit bacterial transmission. Finally, establishment of robust local AMR surveillance systems, linked with national initiatives, is essential to monitor resistance trends and guide timely interventions.

CONCLUSION

The study highlights a high prevalence of MDR bacterial infections in community-acquired settings in Sasaram, Bihar, with E. coli, K. pneumoniae, and S. aureus as the predominant resistant pathogens. The findings emphasize the urgent need for enhanced antimicrobial stewardship, regulation of antibiotic sales, and public health interventions to mitigate the AMR crisis. Improving healthcare infrastructure, expanding surveillance, and promoting hygiene education are critical steps toward controlling the spread of MDR bacteria. Future research should focus on molecular epidemiology and community-level interventions to provide a comprehensive understanding of resistance patterns and effective containment strategies.

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