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Research Article

Mapping the Tribal Resistome: A Hospital-Based Surveillance of Multidrug-, Extensively Drug-, and Pandrug-Resistant Bacterial Pathogens in Bastar, Central India

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Abstract

Background: Antimicrobial resistance (AMR) poses a significant threat to global health, with multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) pathogens affecting clinical outcomes and healthcare delivery. While urban data is abundant, information on tribal populations in India is limited. Understanding regional resistance patterns is crucial for developing effective antimicrobial stewardship strategies.

Objective: This study aimed to assess the prevalence, distribution, and susceptibility patterns of MDR, XDR, and PDR bacterial pathogens in a tertiary-care hospital serving the tribal population of Bastar, Chhattisgarh, India.

Material & Method: A retrospective analysis of 1,676 culture-positive bacterial isolates from various specimens was conducted. Antimicrobial susceptibility testing was performed in accordance with Clinical and Laboratory Standards Institute guidelines, and resistance phenotypes were classified according to international criteria.

Results showed that 653 isolates (38.96%) were resistant, including 334 (19.9%) MDR, 282 (16.82%) XDR, and 27 (1.61%) PDR. Staphylococcus aureus was the most common pathogen, followed by Escherichia coli and Klebsiella species. Surgical departments had the highest burden of resistance, with pus specimens as the primary source of resistant isolates. Cell wall synthesis inhibitors, such as penicillins and cephalosporins, showed high rates of resistance, whereas imipenem and amikacin remained more effective.

Conclusion: The findings underscore the urgent need for enhanced microbiological surveillance, antimicrobial stewardship, diagnostic stewardship, and evidence-based

antibiotic policies to address the AMR threat in underserved regions of Central India.

Keywords: Antimicrobial resistance; Multidrug-resistant bacteria; Extensively drug-resistant pathogens; Pandrug resistance; Tribal health; Hospital surveillance.

Introduction

Antimicrobial resistance (AMR) has emerged as one of the greatest threats to global public health, undermining decades of progress achieved through the effective use of antimicrobial agents. The World Health Organization (WHO) recognizes AMR as one of the top ten global health threats, with resistant infections contributing significantly to increased morbidity, mortality, prolonged hospital stays, and healthcare expenditure.[1,2] India represents a major hotspot for AMR because of irrational antibiotic use, over-the-counter availability of antimicrobial agents, inadequate infection-control measures, and widespread empirical prescribing practices. Data from the Indian Council of Medical Research (ICMR) have demonstrated increasing resistance among important pathogens such as Escherichia coli, Klebsiella pneumoniae, and Staphylococcus aureus, emphasizing the need for culture-guided therapy and antimicrobial stewardship programmes.[3,4]

The emergence of multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) organisms has further complicated the management of infectious diseases. These resistant phenotypes are associated with treatment failure, increased mortality, prolonged hospitalization, and substantial economic burden worldwide.[5,6] Consequently, global initiatives such as the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) and One Health strategies advocate continuous surveillance and region-specific antibiograms to guide rational antimicrobial use and infection-control measures.[7–9]

Despite increasing evidence from urban tertiary-care centres, information regarding antimicrobial resistance among tribal populations in India remains limited. Bastar, a predominantly tribal region of Chhattisgarh, possesses unique geographical, socioeconomic, and healthcare characteristics that may influence antimicrobial consumption and resistance patterns.[10] Therefore, the present study aimed to determine the prevalence, distribution, and antimicrobial susceptibility patterns of MDR, XDR, and PDR bacterial pathogens in this underserved population, thereby contributing to evidence-based antimicrobial stewardship and regional AMR surveillance efforts.

Materials and Methods

Study setup and design: The study was conducted at Late. BRKM Government Medical College, Dimrapal, Jagdalpur, Chhattisgarh, the district capital of Bastar. Baster is a tribal district in the state of Chhattisgarh, India. It is a retrospective, observational, cross-sectional study. Isolation of MDR, XDR and PDR organisms was reported in accordance with guidelines issued by the CDC and ECDC.[5,6]

Data collection and statistical analysis: 3389 suspected patients with bodily fluid samples collected from various departments were included, of which 1676 culture-proven isolates from specimens (blood, urine, stool, CSF, peritoneal fluids, pus, and sputum) were studied retrospectively. All specimens were transported to the laboratory and cultured within 3 to 4 hours of collection.

Specimens were inoculated onto mannitol salt agar (Difco) and streaked with a sterilised wire loop to obtain discrete colonies. Plates were incubated at 37°C for 24 h under aerobic conditions. After 24 h, culture plates were examined for colony appearance, size, colour, and morphology. Gram stain, catalase test, and coagulase test were performed. Isolates that were Gram-positive cocci, catalase-positive, and coagulated human plasma were considered S. aureus in this study.[11]

An antibiotic susceptibility test was performed on all isolates using the paper disc diffusion method. On average, 10-15 antibiotic susceptibility tests per patient were performed.

A 0.2 mL of a 12-h peptone water culture of the test organism was used to inoculate a dry, sterile nutrient agar plate. This was spread over the entire surface of the nutrient agar using a sterile glass spreader and allowed to dry for about 15 to 30 min. Antibiotic discs were placed on the agar using sterile forceps. Each disc was placed far from the others to avoid overlapping zones of inhibition. Plates with antibiotic discs were then incubated at 37°C for 24 h to observe the zones of growth inhibition produced by the antibiotics.[12] Bacteria in the culture on the left are susceptible to the antibiotic in each disc, as shown by the dark, clear rings where no bacterial growth occurs.[13]

Statistical analysis: Data were entered into the Statistical Package for the Social Sciences (SPSS) version 23 for Chicago Inc. and subjected to descriptive analyses. Associations were tested using the Chi-square test. Age was reported as mean ± SD, and differences in mean levels between genders were compared using an unpaired Student's t-test. A priori p-value of 0.05 was used throughout the analyses, and results were considered statistically significant at $p<0.05$.

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Results

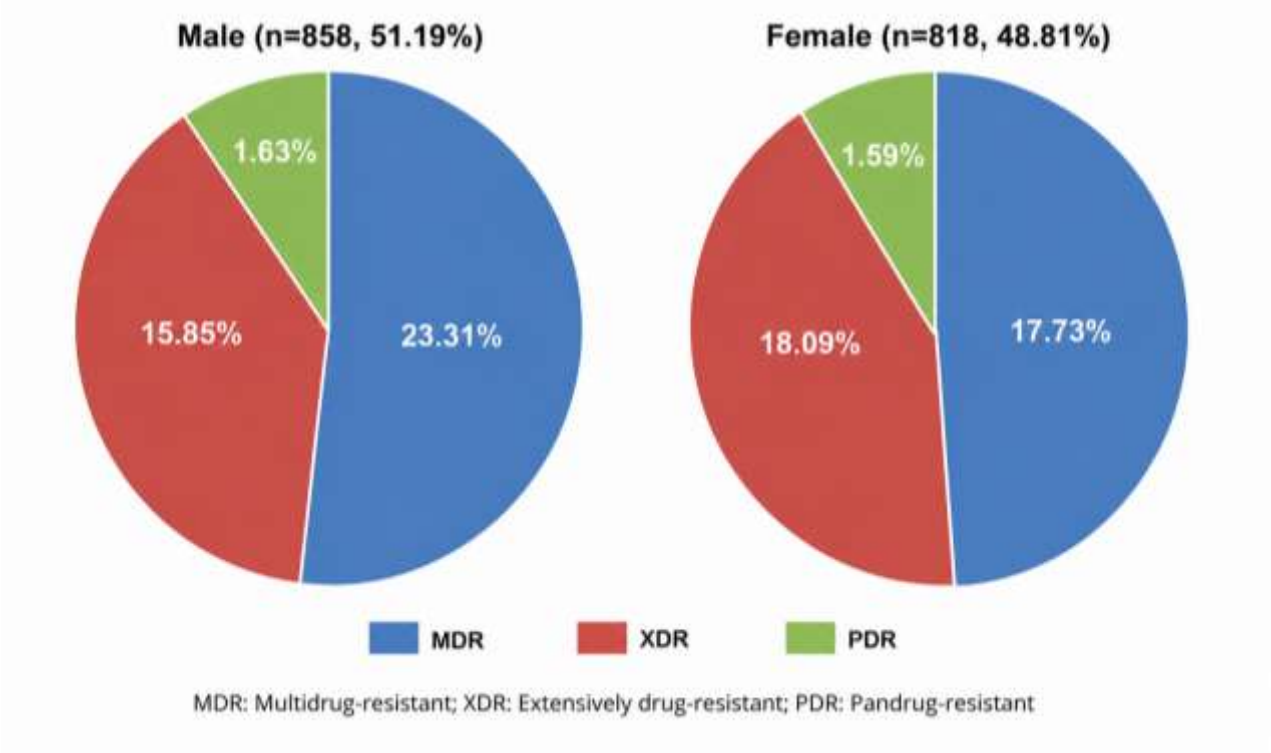
As we observed, 1676 culture-proven isolates were identified from 3389 suspected bodily fluid samples, comprising outpatients {412 (194 males & 218 females)} and inpatients {1264 (664 males & 600 females)} in the department. The mean±sd age of female patients was 27±19.65 years, compared with 32.14±21.67 years among male patients ($p<0.0001$). As illustrated in Table I, Staphylococcus aureus was predominantly isolated in both male (41.32%) and female (35.43%) patients. Secondly, Escherichia coli (15.89% males & 18.88% females) and thirdly, Klebsiella species (10.27% males & 8.62% females) were isolated. Following this, an average of 19% of patients remained isolated with Acetobacter, Citrobacter, Enterobacter, Enterococcus, Klebsiella oxytoca, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilitus, Proteus vulgaris, Staphylococcus species, Streptococcus pyrogens and Candida

Table-I. Gender-wise distribution of isolated microorganisms (in percentage) (n = 1,676)

Isolated microorganism	**Male** (n-858)	**Female (**n-818)
Escherichia coli	15.89%	18.88%
Klebsiella species	10.27%	8.62%
Klebsiella pneumoniae	5.62%	7.93%
Pseudomonas aeruginosa	2.44%	5.13%
Staphylococcus aureus	41.32%	35.43%
Streptococcus pyrogens	5.13%	4.43%
Others	19.3%	19.57%

Similarly, there was a significant proportion of patients who presented with multidrug, extreme and pan-drug resistance. As shown in Figure I, 200 (23.31%) of male patients were positive for MDR as compared to 145 (17.73%) female patients, but the prevalence of XDR was somewhat higher in female patients {148 (18.09%)} as compared to male patients {136 (15.85%)}. The prevalence of pan-drug resistance (PDR) was close to both genders, male (1.63%) & female (1.59%) patients.

Figure -1. Gender-wise distribution of antimicrobial sensitivity & resistance pattern (n = 1,676)



As illustrated in Table II, the suspected patient's samples were gathered from both inpatient and outpatient departments. As we observed, the commonest microorganism was isolated from the surgery department, followed by the OPD and the neonatal ICU. In the male surgical ward, the prevalence of E. coli was isolated (6.21%) and Staph. aureus was (4.89%) as compared to female surgical ward it was 1.67% (E. coli) & 4.18% (Staph. aureus), but in out-patient department (OPD), the prevalence of staph. aureus (11.58%) was more common than E. coli (5.49%). In the neonatal ICU, Staph. aureus (8.11%) was more prevalent, while the 2nd commonest isolated microorganism was Klebsiella species (2.98%).

Table-II. Departmental-wise distribution of isolated microorganism (n = 1,676)

Isolated organism from IPD & OPD								
microorganism	**Medicine**		**Surgery**		**Obstetrics & Gynaecology**	**Neonatal-ICU**	**Out Patients Department**	**Others**
	Male	Female	Male	Female				
Acetobacter	-	4 (0.24%)	-	-	2 (0.12%)	-	-	-
Candida	4 (0.24%)	12 (0.72%)	2 (0.12%)	2 (0.12%)	6 (0.36%)	30 (1.79%)	6 (0.36%)	4 (0.24%)
Citrobacter	-	-	-	-	2 (0.12%)	2 (0.12%)	-	-
Escherichia coli	10 (0.6%)	10 (0.6%)	104 (6.21%)	28 (1.67%)	20 (1.19%)	12 (0.72%)	92 (5.49%)	16 (0.95%)
Enterobacter	2 (0.12%)	-	8 (0.48%)	-	4 (0.24%)	10 (0.6%)	6 (0.36%)	2 (0.12%)
Enterococcus	8 (0.48%)	10 (0.6%)	8 (0.48%)	2 (0.12%)	4 (0.24%)	8 (0.48%)	24 (1.43%)	2 (0.12%)
Klebsiella oxytoca	4 (0.24%)	2 (0.12%)	8 (0.48%)	2 (0.12%)	4 (0.24%)	-	4 (0.24%)	8 (0.48%)
Klebsiella pneumoniae	12 (0.72%)	10 (0.6%)	26 (1.55%)	6 (0.36%)	8 (0.48%)	14 (0.84%)	18 (1.07%)	20 (1.19%)

Klebsiella species	4 (0.24%)	14 (0.84%)	24 (1.43%)	22 (1.31%)	8 (0.48%)	50 (2.98%)	18 (1.07%)	18 (1.07%)
Pseudomonas aeruginosa	2 (0.12%)	-	20 (1.19%)	8 (0.48%)	-	8 (0.48%)	4 (0.24%)	22 (1.31%)
Proteus mirabilitus	-	4 (0.24%)	16 (0.95%)	8 (0.48%)	-	-	-	6 (0.36%)
Proteus vulgaris	2 (0.12%)	-	16 (0.95%)	10 (0.6%)	-	2 (0.12%)	-	2 (0.12%)
Staphylococcus aureus	32 (1.91%)	26 (1.55%)	82 (4.89%)	70 (4.18%)	46 (2.74%)	136 (8.11%)	194 (11.58%)	56 (3.34%)
Staphylococcus species	2 (0.12%)	2 (0.12%)	14 (0.84%)	6 (0.36%)	2 (0.12%)	12 (0.72%)	14 (0.84%)	2 (0.12%)
Streptococcus pyrogens	10 (0.60%)	22 (1.31%)	4 (0.24%)	2 (0.12%)	2 (0.12%)	6 (0.36%)	32 (1.91%)	2 (0.12%)

In a comparison of departmental prevalence of antimicrobial drug sensitivity & resistance patterns in this study. We observed that the highest prevalence of MDR, XDR & PDR cases was reported from the department of surgery. In the male surgery ward, PDR was more prevalent than in other disciplines. Of the 27 patients reported during this study period, 12 were diagnosed with PDR only in the male surgical department and 4 in the female surgical department. It was quite interesting that the prevalence of drug resistance was somewhat lower in the department of internal medicine. As shown in Table III, among 1676 culture-proven isolates, 38.96% of patients had antimicrobial-resistant strains, of which 334 (19.9%) had MDR, 282 (16.82%) XDR, and 27 (1.61%) PDR ($p<0.0001$).

Table III: Department-wise Distribution of MDR, XDR and PDR Isolates (n = 1,676)

Department	MDR n (%)	XDR n (%)	PDR n (%)
Medicine (Male)	10 (0.60)	8 (0.48)	-
Medicine (Female)	20 (1.19)	28 (1.67)	-
Surgery (Male)	78 (4.65)	76 (4.53)	12 (0.72)
Surgery (Female)	38 (2.27)	28 (1.67)	4 (0.24)
Obstetrics & Gynaecology	39 (2.33)	19 (1.13)	3 (0.18)
Neonatal Intensive Care Unit (NICU)	54 (3.22)	39 (2.33)	-
Outpatient Department (OPD)	52 (3.10)	52 (3.10)	6 (0.36)
Others	53 (3.16)	32 (1.91)	2 (0.12)
Total	344 (20.52)	282 (16.82)	27 (1.61)

Others include Paediatrics, Orthopaedics, Intensive Care Unit, Emergency, and Burn Unit.

Seven samples were obtained from various departments for microorganism culture, mainly pus (most common), followed by urine and blood (Table IV). The most isolated organisms in pus were Staph. aureus (17.66%) and E. coli (7.76%), while in urine, E. coli (8.41%) and Staph. aureus (7.52%) predominated. Blood cultures yielded Staph. aureus (7.64%) and Klebsiella spp. (2.98%). The prevalence of ESKAPE organisms was high, with Staph. aureus most common across samples. Other ESKAPE bacteria included Enterococcus (3.94%), K. pneumoniae (6.8%), P. aeruginosa (3.82%), and Enterobacter (1.91%). Antimicrobial resistance was prominent, with 15 microorganisms identified (including Candida) among 1676 isolates, a prevalence of 3.93%. Notably, Klebsiella spp.

showed significant PDR (0.54%). Staphylococcus aureus was MDR, while E. coli was the dominant XDR organism. Klebsiella spp. and K. pneumoniae were also MDR and XDR (Figure II).

Table IV. Patient's sample-wise comparison of antimicrobial drug sensitivity & resistance (n = 1,676)

Body fluid Samples	MDR	XDR	PDR
Blood	37 (2.21%)	53 (3.16%)	-
Urine	60 (3.58%)	84 (5.01%)	2 (0.12%)
Stool	2 (0.12%)	-	-
Sputum	46 (2.74%)	25 (1.49%)	2 (0.12%)
Peritoneal fluids	-	2 (0.12%)	-
CSF	2 (0.12%)	-	-
Pus	135 (8.05%)	180 (10.74%)	23 (1.37%)

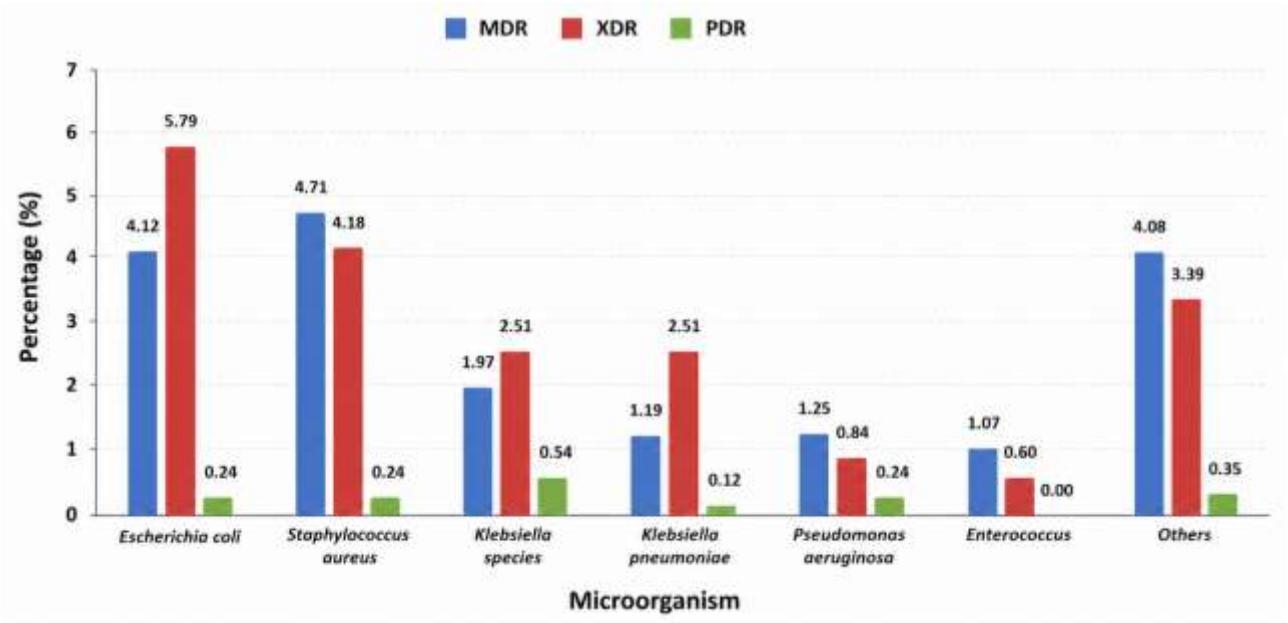
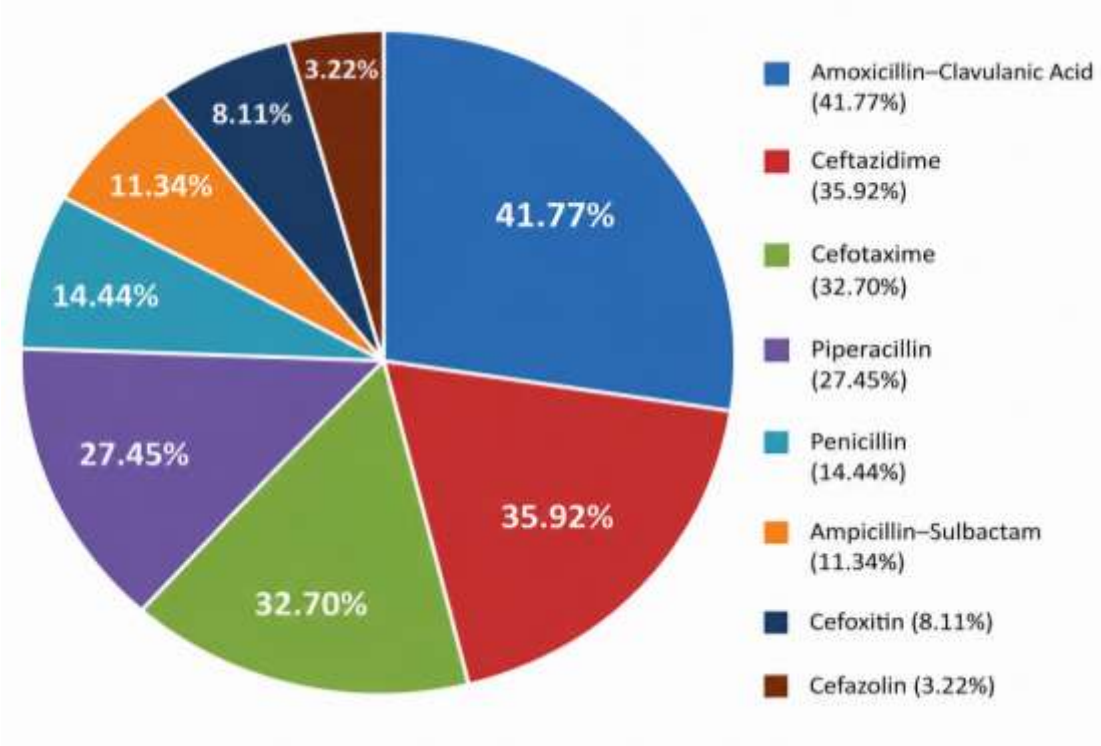


Figure II: Commonest isolated pathogens with their resistance patterns (n-1676)

Most cell synthesis inhibitors exhibited higher resistance rates compared to sensitive patterns. As shown in Figure III, the highest resistance was observed against amoxicillin–clavulanic acid (41.77%), followed by ceftazidime (35.92%), cefotaxime (32.70%), and piperacillin (27.45%), indicating significant resistance to β-lactam antibiotics and third-generation cephalosporins. In contrast, cefazolin (3.22%), cefoxitin (8.11%), and ampicillin–sulbactam (11.34%) exhibited lower rates of resistance. Meanwhile, Imipenem, Chloramphenicol, Co-trimoxazole, and Amikacin demonstrated higher sensitivity rates rather than resistance.

Figure III: Distribution of Resistance Patterns Among Major β-Lactam Antibiotics (n = 1,676)



Discussion

Staphylococcus aureus was the predominant pathogen, accounting for 642 of 1,676 culture-positive specimens (38.27%). Among these, 151 isolates showed resistance to multiple antibiotics. The prevalence of MDR, XDR, and PDR phenotypes among S. aureus was 12.14%, 10.74%, and 0.62%, respectively. Additionally, 100 of the 151 resistant isolates (66.22%) were vancomycin-resistant (VRSA). While concerning, confirmation with MIC-based methods and molecular testing is needed to verify true resistance.[22,23] Gandra et al. reported increasing trends of MRSA and other resistant Gram-positive pathogens in India from 2008 to 2014, underscoring the rising antimicrobial resistance in healthcare. Thati et al. found VRSA strains in ICUs in Hyderabad, all previously identified as MRSA.[16] Menezes et al. also noted the emergence of VISA in southern India, highlighting the growing threat of glycopeptide resistance.[17]

The antimicrobial resistance profile of Staphylococcus aureus in the present study revealed maximum resistance to ciprofloxacin (35.82%), amoxicillin–clavulanic acid (35.51%), co-trimoxazole (28.97%), piperacillin (20.56%), and ofloxacin (20.56%). These findings suggest widespread exposure to broad-spectrum antimicrobial agents and underscore the importance of antimicrobial stewardship programmes and evidence-based prescribing practices in reducing unnecessary antibiotic use and preserving antimicrobial effectiveness.[1,9]

Escherichia coli was the second most common pathogen, accounting for 292 of 1,676 culture-positive isolates (17.42%). Among these, 170 isolates (58.21%) exhibited antimicrobial resistance, including 23.63% MDR, 33.21% XDR, and 1.36% PDR. Gandra et al. documented increasing resistance among

Escherichia coli isolates in India, particularly against third-generation cephalosporins, reflecting the growing challenge of antimicrobial resistance nationwide.[15] The higher prevalence observed in the present study suggests regional variations in microbial epidemiology and antimicrobial utilisation patterns.

The resistance profile of Escherichia coli showed particularly high rates of resistance to third-generation cephalosporins, including ceftazidime (63.01%) and cefotaxime (61.64%), consistent with previous reports from India.[15] Resistance to ciprofloxacin (51.36%), co-trimoxazole (42.46%), amoxicillin–clavulanic acid (41.09%), and piperacillin (39.72%) was also substantial. The emergence of extended-spectrum β-lactamase (ESBL)-producing Escherichia coli has become a major global therapeutic challenge, especially in low- and middle-income countries.[24] Saravanan and Raveendaran reported a high burden of antimicrobial resistance in a tertiary-care hospital setting, with substantial resistance to co-trimoxazole, fluoroquinolones, penicillins, and cephalosporins, findings that are comparable to those observed in the present study.[18] Conventional diagnostic microbiology literature also indicates that highly resistant E. coli isolates increasingly require reserve antimicrobial agents for effective treatment.[11]

Klebsiella spp. (13.60%) and Klebsiella pneumoniae (7.94%) together constituted the third most common group of bacterial pathogens, accounting for 361 of 1,676 isolates. Among these, 52.53% of Klebsiella spp. and 55.65% of K. pneumoniae isolates exhibited antimicrobial resistance. Previous Indian studies have similarly documented a substantial burden of resistant Klebsiella infections in tertiary-care hospitals.[15,18,20] In the present study, Klebsiella spp. contributed the highest proportion of PDR isolates, accounting for nine of the twenty-seven PDR cases, whereas two PDR cases were associated with K. pneumoniae. The World Health Organization has classified carbapenem-resistant Klebsiella pneumoniae among the highest-priority pathogens requiring urgent research and development of novel antimicrobial agents and therapeutic strategies.[25]

An important observation was that XDR phenotypes were more common than MDR among Klebsiella spp. and K. pneumoniae. Similar international findings include those of Zhang et al., who highlighted the rising prevalence of carbapenem-resistant Enterobacteriaceae in China and the challenges they pose.[19] Basak et al. showed E. coli and K. pneumoniae are major contributors to MDR, while Pseudomonas aeruginosa is a key contributor to XDR infections.[20] Mohapatra et al. found a high prevalence of XDR and PDR Gram-negative bacilli in eastern India, indicating an increasing burden of resistant pathogens in healthcare.[21]

About 39% of bacterial isolates were antimicrobial-resistant, with many showing MDR, XDR, and PDR traits. Unlike in urban Indian studies, where Gram-negative bacilli are common, Staphylococcus aureus was the predominant resistant pathogen in this tribal group. Resistance was high to cell wall synthesis inhibitors such as penicillins and cephalosporins, indicating widespread antibiotic misuse. Imipenem, amikacin, chloramphenicol, and co-trimoxazole showed better activity and should be used based on culture and sensitivity results.[1,2,9]

The findings of the present study are consistent with the Global Research on Antimicrobial Resistance (GRAM) project, which identified AMR as one of the leading causes of infectious disease-related mortality worldwide, particularly in low-resource settings lacking effective surveillance systems and antimicrobial stewardship programmes.[26] The present investigation, therefore, underscores the urgent need for continuous microbiological surveillance, hospital infection-control measures, diagnostic stewardship, and rational antimicrobial use in tribal healthcare institutions. Development of region-specific antibiograms and organism-directed narrow-spectrum therapy may substantially reduce the further emergence and dissemination of resistant pathogens in this vulnerable population.[3,9,10]

Conclusion

This study highlights a concerning burden of antimicrobial resistance among tribal communities in Bastar, where nearly 40% of culture-positive isolates exhibit MDR, XDR, or PDR. The main resistant pathogens identified are Staphylococcus aureus, Escherichia coli, and Klebsiella species, with penicillins and cephalosporins exhibiting the highest resistance levels. The rising incidence of XDR and PDR strains, especially among Gram-negative bacteria, threatens effective clinical treatment. To address this, strengthening antimicrobial stewardship, encouraging targeted narrow-spectrum therapies, limiting inappropriate broad-spectrum antibiotic use, and ongoing training for healthcare providers are crucial. Urgent coordinated efforts at the institutional and national levels are necessary to maintain the efficacy of current antimicrobials and prevent the global spread of resistance.

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References:

1. World Health Organization. Global antimicrobial resistance and use surveillance system (GLASS) report 2025. Geneva: World Health Organization; 2025.
2. World Health Organization. Antimicrobial resistance. Geneva: World Health Organization; 2024.
3. Indian Council of Medical Research. Antimicrobial Resistance Surveillance and Research Network (AMRSN) annual report 2024. New Delhi: ICMR; 2025.
4. Indian Council of Medical Research. National treatment guidelines for antimicrobial use in infectious diseases. New Delhi: ICMR; 2023.
5. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT, Monnet DL. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18(3):268–81.
6. Centers for Disease Control and Prevention; European Centre for Disease Prevention and Control. Antimicrobial resistance definitions and surveillance recommendations. Atlanta: CDC; Stockholm: ECDC; 2011.
7. World Health Organization. Global antimicrobial resistance and use surveillance system (GLASS): implementation manual. Geneva: World Health Organization; 2023.
8. Velazquez-Meza ME, Galarde-López M, Carrillo-Quiróz B, Alpuche-Aranda CM. Antimicrobial resistance: One Health approach. Vet World. 2022;15(3):743–49.
9. Walia K, Ohri VC, Madhumathi J, Ramasubramanian V. Policy document on antimicrobial stewardship practices in India. Indian J Med Res. 2019 Feb;149(2):180–184.
10. One Health Trust. India ResistanceMap: antimicrobial resistance in India. Boston: One Health Trust; 2025.
11. Forbes BA, Sahm DF, Weissfeld AS. Bailey and Scott's diagnostic microbiology. 14th ed. St. Louis: Elsevier; 2017.
12. Kirby WMM, Bauer AW, Sherris JC, Turck M. Antibiotic susceptibility testing by a standardized single disk method. Am J Clin Pathol. 1966;45(4):493–96.
13. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 35th ed. Wayne, PA: CLSI; 2025.
14. Rice LB. Federal funding for the study of antimicrobial resistance in nosocomial pathogens: no ESKAPE. J Infect Dis. 2008;197(8):1079–81.
15. Gandra S, Mojica N, Klein EY, Ashok A, Nerurkar V, Kumari M, et al. Trends in antibiotic resistance among major bacterial pathogens isolated from blood cultures tested at a large private laboratory network in India, 2008–2014. Int J Infect Dis. 2016;50:75–82.
16. Thati V, Shivannavar CT, Gaddad SM. Vancomycin resistance among methicillin-resistant Staphylococcus aureus isolates from intensive care units of tertiary care hospitals in Hyderabad. Indian J Med Res. 2011;134:704–08.
17. Menezes GA, Harish BN, Sujatha S, Vinothini K, Parija SC. Emergence of vancomycin-intermediate Staphylococcus aureus in southern India. J Med Microbiol. 2008;57(Pt 7):911–12.

18. Saravanan R, Raveendaran V. Antimicrobial resistance pattern in a tertiary care hospital: An observational study. J Basic Clin Pharma. 2013 Jun;4(3):56–63.
19. Zhang R, Liu L, Zhou H, Chan EW, Li J, Fang Y, Chen S. Nationwide surveillance of clinical carbapenem-resistant Enterobacteriaceae in China. EBioMedicine. 2017 Jun;20:181–187.
20. Basak S, Singh P, Rajurkar M. Multidrug resistant and extensively drug resistant bacteria. J Pathog. 2016;2016:4065603.
21. Mohapatra DP, Prasanna AS, Saha S, Jena J, Debata NK. Extensively drug-resistant and pandrug-resistant Gram-negative bacteria in a tertiary-care hospital in Eastern India: A 4-year retrospective study. J Glob Antimicrob Resist. 2018 Dec;15:246–249.
22. Cong Y, Yang S, Rao X. Vancomycin-resistant Staphylococcus aureus infections: a review of case updating and clinical features. J Adv Res. 2020 Jan;21:169–176.
23. McGuinness WA, Malachowa N, DeLeo FR. Vancomycin resistance in Staphylococcus aureus. Yale J Biol Med. 2017;90(2):269–281.
24. Moolchandani K, Sastry AS, Deepashree R, Sistla S, Harish BN, Mandal J. Antimicrobial resistance surveillance among intensive care units of a tertiary care hospital in Southern India. J Clin Diagn Res. 2017 Feb;11(2):DC01–DC07.
25. World Health Organization. WHO bacterial priority pathogens list, 2024: bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance. Geneva: World Health Organization; 2024.
26. Murray CJL, Ikuta KS, Sharara F, Swetschinski L, Aguilar GR, Gray A, Han C, Bisignano C, Rao P, Wool E, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Lancet. 2022;399(10325):629–655.