Recent Advances in Anti-Infective Drug Discovery, 2025, *20*, 203-222

RESEARCH ARTICLE

Antimicrobial Resistance Patterns and the Role of Antibiotic Stewardship in a Secondary Care Hospital

Aakash Ramanisankar[1], Nirenjen Shanmugasundaram[2,*], Maheswari Paramasivam[1], E.M. Neena Priyamalar [1], Aswin Pratap Sundararajan[1], Deepak Raj Sivakumar[1] and Dharshne Petchiammal Thirupathi[1]

[1]*Department of Pharmacy Practice, Vels Institute of Science Technology and Advanced Studies (VISTAS), Pallavaram, Chennai, Tamil Nadu, 600117, India;* [2]*Department of Pharmacology, SRM College of Pharmacy, SRM Institute of Science & Technology, Potheri, Kattankulathur, Chengalpattu, Tamil Nadu, 603203, India*

Abstract: ***Background*:** Antimicrobial Resistance (AMR) has emerged as a critical global health challenge, with bacteria, viruses, fungi, and parasites developing the capacity to survive antimicrobial treatments. This resistance, largely driven by increased antibiotic usage, threatens public health by diminishing the effectiveness of current infection management strategies.

Aim* and *Objectives: This study aims to evaluate the antimicrobial resistance patterns of prevalent pathogens in a secondary care hospital, highlighting the essential role of clinical pharmacists in addressing AMR through the implementation of Antibiotic Stewardship Programs (ASPs) to promote responsible antibiotic use.

***Methodology*:** This prospective study analyzed 80 positive microbial culture reports from six months. Ethical approval was granted by the Institutional Ethical Committee (Ref: ECR/288/Indt/TN/2018/RR-21/001, dated April 6, 2023). Inclusion criteria covered adults (≥18 years) with confirmed infections across various sites, including bloodstream, urinary, respiratory, and soft tissue. Exclusion criteria eliminated reports with no pathogen growth. Data were analyzed using SPSS software version 26.0, with statistical measures applied to assess resistance patterns and correlations across infection types.

***Results*:** Of the 80 positive cultures, *Escherichia coli* 35.0%) was most frequently isolated, followed by *Klebsiella pneumoniae* (12.5%), *Pseudomonas aeruginosa* (8.8%), *Proteus mirabilis* (8.8%), and *Klebsiella oxytoca* (7.5%). The isolated pathogens displayed high resistance to ampicillin (82.5%), cefixime (80.0%), ceftriaxone (78.8%), and ceftazidime (71.3%), with a strong sensitivity to amikacin (86.3%) and meropenem (70.0%).

***Conclusion*:** The rise of third-generation cephalosporin-resistant pathogens signals an urgent need for sustained AMR monitoring and robust ASPs in healthcare settings, particularly in developing regions. The study underscores the importance of rational antibiotic use and continuous AMR surveillance to curb resistant infections and protect public health.

ARTICLE HISTORY

Received: November 14, 2024
Revised: January 17, 2025
Accepted: January 29, 2025

DOI:
10.2174/0127724344369266250310084603

Keywords: Antimicrobial resistance, antibiotic stewardship programs, infection control, third-generation cephalosporins, public health, AMR monitoring.

1. INTRODUCTION

Antimicrobial resistance (AMR) poses a formidable challenge in modern medicine, as microorganisms, including bacteria, viruses, fungi, and parasites, develop mechanisms to survive and multiply in the presence of drugs previously effective against them. The emergence of resistant bacterial strains, particularly in healthcare and community settings, has become a critical concern worldwide [1, 2]. Among the primary mechanisms

*Address correspondence to this author at the Department of Pharmacology, SRM College of Pharmacy, SRM Institute of Science & Technology, Potheri, Kattankulathur, Chengalpattu, 603 203, Tamil Nadu, India;
E-mail: nirenjen1999@gmail.com

2772-4352 /25 $65.00+.00

bacteria employ to resist antibiotics are two key methods to limit drug accumulation: influx reduction and efflux enhancement. Bacterial cells contain outer membrane proteins (OMPs) called porins, which serve as entry channels for many antibiotics, such as β-lactams, tetracyclines, and cephalosporins [3-5]. Resistance often arises when bacteria reduce drug influx by downregulating, altering, or removing these porins. At the same time, nearly all bacteria utilize multidrug transporters that actively pump toxic substances, including antibiotics, out of the cell through enhanced efflux [6, 7]. Bacterial resistance mechanisms include enzyme-mediated degradation or modification of antibiotics, altered membrane permeability to reduce drug uptake; active efflux pumps that expel antibiotics from the cell, and target site modifications that prevent the antibiotic from binding effectively. Bacterial resistance to antibiotics involves various mechanisms, among which enzymatic processes play a pivotal role. The enzymatic mechanisms of resistance observed in pathogenic bacteria are central to their ability to survive antibiotic treatment. Beta-lactamases, for instance, hydrolyze the beta-lactam ring, inactivating antibiotics such as penicillins and cephalosporins. Extended-Spectrum Beta-Lactamases (ESBLs) pose a particular challenge by conferring resistance to third-generation cephalosporins, as observed in our study's high resistance rates to ceftriaxone and cefotaxime. Similarly, aminoglycoside-modifying enzymes (AMEs) such as acetyltransferases, phosphotransferases, and nucleotidyltransferases can chemically alter aminoglycosides, significantly reducing their efficacy. Metallo-beta-lactamases, which require zinc ions for activity, lead to carbapenem resistance, further complicating treatment options. Another important mechanism involves the modification of antibiotic target sites through processes like methylation, mediated by genes such as *erm,* which confers macrolide resistance by altering the 23S rRNA. Bacterial resistance mechanisms include the action of transposons, which enable the rapid spread of resistance genes across populations. Gram-negative bacteria rely on efflux pumps, porin loss, and beta-lactamase production due to their outer membrane. In contrast, gram-positive bacteria lacking this membrane, often use target site modifications, such as penicillin-binding protein alterations in MRSA. These structural differences contribute to the complexity of antimicrobial resistance. Additionally, genetic mutations in enzymes like DNA gyrase contribute to resistance in both gram-positive and gram-negative bacteria [8]. In both gram-positive and gram-negative bacteria, mutations in key enzymes like DNA gyrase-specifically within the quinolone resistance-determining region (QRDR) contribute to resistance against fluoroquinolones [9-11]. The four main mechanisms of AMR include limiting drug uptake, modifying drug targets, inactivating drugs, and increasing drug efflux. Gram-negative bacteria frequently employ all four mechanisms, while gram-positive bacteria tend to use drug uptake limitation less commonly [12]. The transmission of AMR is also a significant public health concern, as resistant pathogens can spread between animals, humans, and even across environmental surfaces. Faecal contamination and environmental exposure—such as contact with beach sand, drinking water, and recreational water—are key vectors of transmission [13, 14]. Antibiotic resistance genes (ARGs) play a central role in this process, often proliferating in high-concentration environments like wastewater. Horizontal gene transfer (HGT), facilitated by mobile genetic elements such as plasmids, integrons, and transposons, enables bacteria to exchange resistance genes, further accelerating the spread of AMR [15, 16].

Several studies highlight the alarming rise of AMR across regions. The Global Burden of Bacterial Antimicrobial Resistance (AMR) report provides a sweeping assessment of the impact of AMR worldwide. Conducted in 2019 by the Antimicrobial Resistance Collaborators, this study underscores the severe and growing burden of AMR, particularly in lower-income countries where healthcare infrastructure often falls short. The analysis reveals stark regional disparities in AMR prevalence, drawing attention to the urgent need for globally coordinated public health policies aimed at reducing the misuse of antibiotics and improving access to effective treatments [17]. In Thailand, researchers Boonyasiri and colleagues examined AMR across various reservoirs, including healthy adults, food sources, food animals, and the broader environment. Their study demonstrates the pervasive spread of resistant bacteria beyond clinical settings, highlighting the significant role that animal agriculture and environmental factors play in facilitating AMR transmission. This research emphasizes the need for stringent regulato-

ry policies in agricultural practices to prevent resistant strains from spilling over into human populations [18]. A study in Cape Coast, Ghana, conducted by Anning *et al.*, focuses on AMR among patients attending a private diagnostic center. This research identifies alarmingly high resistance rates to commonly prescribed antibiotics, especially in pathogens responsible for bloodstream infections. The findings point to the pressing need for improved infection control and responsible antibiotic use within the healthcare system to prevent further escalation of resistance [19]. In his research on bloodstream infections, Akova highlights the critical challenge posed by AMR in treating these life-threatening infections. Bloodstream infections require prompt, reliable antibiotic intervention, yet high resistance levels limit treatment options, endangering patient outcomes. Akova's study underscores the importance of robust antibiotic stewardship and the development of alternative therapies to manage resistant bloodstream infections effectively [20]. Finally, Obakiro *et al.* study in Eastern Uganda investigates AMR in patients at two tertiary hospitals. The study documents high resistance rates to several commonly used antibiotics, complicating the treatment of both community-acquired and hospital-acquired infections. It calls attention to the need for stringent infection control practices and targeted antibiotic stewardship programs to curb the spread of resistant pathogens within healthcare settings [21]. Each of these studies collectively reinforces the pressing need for a global, multi-faceted approach to managing AMR. Advanced computational techniques, such as molecular Modeling and simulation, provide insights into resistance mechanisms at the molecular level, aiding in drug design and therapeutic optimization. Molecular modeling and simulation offer valuable tools for understanding bacterial resistance. Homology modeling enables the construction of 3D structures for resistance-associated proteins, such as beta-lactamases. Molecular docking can predict antibiotic binding affinities to these proteins, revealing potential resistance mechanisms. Molecular dynamics simulations further assess the stability of these interactions under physiological conditions. For example, docking studies with carbapenems and metallo-beta-lactamases have elucidated key structural features responsible for resistance, as described in recent studies [22].

In light of the urgent need to address the global AMR crisis, this study aims to underscore the critical role that clinical pharmacists play in curbing antimicrobial resistance through the implementation of Antibiotic Stewardship Programs (ASPs) in healthcare settings. By promoting the judicious use of antibiotics, these programs can significantly reduce AMR spread, optimize patient outcomes, and foster a more resilient healthcare system. This objective emphasizes the importance of coordinated strategies, including rigorous surveillance, robust infection control measures, and the establishment of tailored antimicrobial policies within hospitals. Together, these actions are essential for effectively managing and mitigating the rising threat of AMR. Various factors, including the environmental conditions during bacterial cultivation influence antimicrobial resistance. Physical agents such as temperature, pH, humidity, and oxygen levels can significantly impact bacterial phenotypes, including virulence and resistance traits. The cultivation process must be carefully controlled to ensure that the observed resistance patterns accurately reflect the clinical scenarios without being influenced by artificial environmental conditions. This study aims to analyze resistance profiles under standardized cultivation parameters to ensure methodological consistency.

This study evaluates antimicrobial resistance profiles in a secondary care hospital, emphasizing the transition from empirical to targeted therapy based on resistance profiling. By systematically analyzing data in a resource-constrained setting, the study offers actionable insights into antibiotic stewardship, particularly in developing regions. These findings also provide a valuable case-based perspective to train healthcare professionals on the importance of sensitivity testing and tailored antibiotic therapy.

2. METHODOLOGY

2.1. Ethical Declaration

This study received ethical approval from the Institutional Ethical Committee at Vels Institute of Science, Technology, and Advanced Studies, Chennai, under reference number ECR/288/Indt/TN/2018/RR-21/001, dated April 6, 2023. Ethical approval ensures that all research activities adhere to established standards for the safety, rights, and welfare of participants. In this

study, informed written consent was obtained from each participant, affirming their voluntary involvement and understanding of the study's purpose and procedures. Obtaining ethical clearance and participant consent is fundamental to uphold transparency, respect for individuals, and the integrity of the research process, particularly when addressing public health issues such as antimicrobial resistance.

2.2. Study Design

This study was conducted as a six-month prospective analysis of microbial culture sensitivity reports at Employees State Insurance Corporation Hospital, a secondary care hospital in Ayanavaram, Chennai. The prospective design was chosen to allow for real-time data collection and analysis, providing an accurate snapshot of antimicrobial resistance patterns and trends within the study period. A total of 343 microbial culture reports were initially gathered, with 263 reports excluded due to negative cultures showing no pathogen growth, ensuring the analysis focused only on relevant positive cases of microbial infection. It's important to note that all these samples were obtained from patients who had already been treated with antibiotics as part of their previous treatment.

2.2.1. Cultivation and Processing of Microbial Culture

All 343 microbial cultures were processed under standardized physical conditions to ensure consistent and reliable growth parameters. The samples were incubated at 37°C, with aerobic or anaerobic conditions applied as per the pathogen's requirements. The pH and nutrient composition of the media were maintained to closely replicate physiological conditions, minimizing external stress that could alter microbial phenotypes. This rigorous standardization ensured that the results accurately reflected natural resistance traits without external modulation. To prevent the artificial induction of resistance mechanisms, no antibiotics were added to the cultivation media during primary isolation. This ensured that the resistance profiles observed in this study were intrinsic or clinically acquired rather than a result of experimental conditions.

The bacterial cultures were grown on standardized media designed to promote optimal growth, ensuring consistent results. However, it is important to note that the composition of culture media can influence bacterial resistance. For example, nutrient-rich media promote optimal bacterial growth, which may, in turn, enhance the expression of resistance genes. Stress-inducing conditions, such as altered pH or high salt concentrations, can trigger adaptive resistance mechanisms like efflux pump activation or biofilm formation. To replicate clinical conditions more closely, antibiotic-laden media might also be used to enrich for resistant mutants selectively.

2.3. Author Roles and Study Context

This study was conducted in collaboration with clinicians at the Employees State Insurance Corporation Hospital. The authors, as medical pharmacologists and researchers, were responsible for data collection, antimicrobial resistance profiling, and subsequent analysis. The clinicians at the hospital performed patient care and initial sampling, while the authors ensured the rigorous application of methodology and data interpretation to maintain research integrity.

2.4. Participant Selection Criteria

Patients were selected based on strict inclusion and exclusion criteria, focusing on adults with confirmed infections. Microbial cultures were processed using standardized protocols, and antimicrobial susceptibility testing was performed according to the CLSI guidelines.

2.4.1. Inclusion Criteria

To capture a comprehensive view of antimicrobial resistance across varied infections, the study included patients aged 18 and above who presented with known infections. Types of infections analyzed included bloodstream, urinary tract, respiratory tract, gastrointestinal, skin and soft tissue, ear, and surgical site infections. Patients with comorbid conditions, such as diabetes and hypertension, were also included, as these factors often influence susceptibility to infection and response to antimicrobial treatments. Additionally, patients with social histories of smoking and alcohol use were selected, given that these behaviors can impact immune function and infection outcomes. By including patients across these categories, the study aimed to assess a representative sample of

individuals most affected by or vulnerable to infections and antimicrobial resistance.

2.4.2. Exclusion Criteria

Patients without documented infections were excluded to focus specifically on cases where microbial culture results were relevant to the study objectives. Individuals under 18 years of age were also excluded, as pediatric populations may have different infection patterns and resistance profiles, necessitating separate investigations. This exclusion criterion helped to streamline the study scope, ensuring consistency in the analysis of adult cases and yielding data pertinent to commonly affected demographics within this hospital setting. This carefully structured study design enabled the targeted examination of microbial sensitivity in a defined adult patient population, optimizing data relevance and study accuracy.

2.5. Statistical Analysis

The statistical analysis in this study was conducted to evaluate the patterns and associations between different types of infections, patient characteristics, and microbial resistance trends. By applying statistical methods, we aimed to identify significant relationships and potential risk factors that contribute to antimicrobial resistance across various infection types. Analyzing these data through statistical measures is crucial in clinical research, as it enables the detection of meaningful differences and associations within patient groups, providing insights that support evidence-based decision-making.

Data from the surgical site, skin, and soft tissue infections—including abscesses, pyoderma, cellulitis, ulcers, and wounds—as well as upper respiratory and urinary tract infections, were systematically extracted from microbiological reports. Socioeconomic and physiological information was also collected and organized in an Excel spreadsheet. SPSS Software version 26.0 for Windows was then employed for data analysis, with categorical variables summarized as proportions. The Chi-Square test was applied to assess statistically significant differences between patient groups. This test helps identify whether variations observed among categories (*e.g.*, infection type, resistance patterns) are likely due to chance or reflect underlying associations. Calculating 95% confidence intervals further strengthened the analysis by quantifying the reliability of these associations, providing a robust measure of their strength and direction. A *p*-value threshold of less than 0.05 was considered statistically significant, meaning that observed differences were unlikely to have occurred by chance alone. The application of statistics in this study is essential for validating findings, as it allows us to objectively interpret complex datasets and derive actionable insights. By determining significant associations, this analysis supports the identification of high-risk patient groups, resistance patterns, and infection types. Such insights are critical for guiding treatment strategies, informing public health policies, and ultimately improving patient care outcomes.

3. RESULTS

3.1. Patient Demographics

During the study period, a total of 343 specimens were collected, out of which 80 patients with positive microbial cultures were ultimately included in our analysis. This selection allowed us to focus specifically on cases with confirmed infections, providing a clearer understanding of patient characteristics and the prevalence of antimicrobial resistance patterns within this population. Among the 80 patients, 47 (58.7%) were female and 33 (41.3%) were male, indicating a slightly higher prevalence of infection among female patients. This gender distribution is consistent with known patterns in certain infection types, particularly urinary tract infections, which are often more common in females. The demographic data by gender are presented in Table **1**.

Table 1. Classification based on gender.

Patient Gender	Frequency	Percentage
Male	33	41.30%
Female	47	58.70%

In terms of age distribution, the study encompassed a broad range of adult age groups, allowing for a detailed analysis of infection susceptibility across different life stages. The largest proportion of patients fell within the 41-50 age range, with 27

individuals (34%) in this category. This was followed by the 51-60 age group, which included 21 patients (26%). The remaining participants were distributed as follows: 3 patients (4%) in the 18-20 age group, 11 patients (14%) in the 21-30 age group, 8 patients (10%) in the 31-40 age group, 7 patients (9%) in the 61-70 age group, and 3 patients (3%) in the 71-80 age group. These results are detailed in Table **2**. The inclusion of patients across diverse age groups enhances the study's relevance by reflecting how antimicrobial resistance impacts individuals of varying ages, especially those in middle to older adulthood, who may have increased susceptibility to infection due to comorbidities or age-related immune changes. This demographic analysis is crucial for tailoring effective interventions and for understanding population-specific risks, aiding in the development of more targeted strategies for managing antimicrobial resistance in clinical settings.

Table 2. Classification based on age.

Patient Age	Frequency	Percentage
18-20	3	3.80%
21-30	11	13.80%
31-40	8	10%
41-50	27	33.80%
51-60	21	26.20%
61-70	7	8.80%
71-80	3	3.70%

3.2. Specimen Types and Distribution of Culture-positive Results

Throughout the observation period, 80 specimens with positive microbial cultures were analyzed, providing valuable insights into the distribution of infections across different specimen types. The breakdown of specimen sources revealed that the majority of infections were associated with urinary samples: 39 (49%) of the positive cultures were urine specimens. This high proportion of culture-positive urine samples aligns with the prevalence of urinary tract infections (UTIs) as a common health concern, especially in healthcare settings where risk factors such as catheter use, comorbidities, and certain patient demographics increase susceptibility. Pus swabs accounted for 21 (26%) of the culture-positive specimens, indicating a significant occurrence of skin and soft tissue infections, including wound infections, abscesses, and cellulitis cases. These infections can be challenging to treat, especially in patients with underlying conditions that compromise wound healing or immune function. The presence of culture-positive results in pus swabs highlights the importance of close monitoring and effective treatment for infections that may complicate surgical or trauma recovery. Lastly, sputum specimens made up 20 (25%) of the culture-positive samples, representing a notable number of respiratory tract infections within the study group. This finding is especially pertinent in clinical environments where respiratory infections can spread rapidly and may be associated with antimicrobial-resistant pathogens, particularly in vulnerable patients or those with chronic respiratory conditions.

The distribution of positive cultures among these specimen types emphasizes the need for vigilant infection control measures and targeted antimicrobial therapies in diverse infection types. Table **3** summarizes the results, offering a comprehensive view of infection prevalence and guiding clinical efforts to prioritize areas most impacted by microbial resistance. This analysis underscores the importance of appropriate specimen management and pathogen identification in mitigating the spread of antimicrobial resistance across various infection sites.

Table 3. Classification based on biological specimens with positive culture.

Patients Biological Specimens	Frequency	Percentage
Pus swabs	21	26.30%
Urine culture	39	48.70%
Sputum culture	20	25.0%

3.3. Antibiotics Used before Culture Sensitivity Test and its Implications

In the cohort of 80 patients whose microbial culture sensitivity reports were analyzed, it was

Table 4. Classification of antibiotics used before specimen collection.

Empirical Antibiotic Therapy	Frequency	Percentage
Cefaperazone/sulbactam	2	2.50%
Ceftriaxone	40	50.0%
Cefixime	2	2.50%
Cefotaxime	24	30.0%
Ciprofloxacin	1	1.30%
Norfloxacin	1	1.30%
Amikacin	1	1.30%
Piperacillin/tazobactam	10	12.50%
Gentamycin	1	1.30%
Azithromycin	1	1.30%

noteworthy that all patients (100%) had received antibiotics prior to specimen collection. This extensive prior exposure to antimicrobial agents is a critical factor influencing the interpretation of culture results. It underscores the importance of understanding the impact of empirical therapy on microbial flora and resistance patterns. The most commonly prescribed empirical antibiotics were ceftriaxone, utilized in 40 cases (50% of patients). Ceftriaxone is a broad-spectrum cephalosporin effective against a wide range of gram-positive and gram-negative bacteria, making it a popular choice in empirical therapy, especially in hospital settings where serious infections may be present. Following ceftriaxone, cefotaxime was administered to 24 patients (30%), another cephalosporin with similar activity, further indicating a reliance on this class of antibiotics for initial treatment.

Additionally, piperacillin/tazobactam was prescribed in 10 cases (12.5%). This combination antibiotic is often used for polymicrobial infections and provides coverage against beta-lactamase-producing organisms, which is particularly relevant in healthcare-associated infections. Lastly, a category labelled as "other antibiotics" accounted for 9 cases (11.5%), representing a variety of less frequently prescribed agents, possibly tailored to specific patient needs or local resistance patterns. The high rate of antibiotic exposure prior to culture testing is significant as it can potentially skew the results of sensitivity testing, leading to challenges in accurately identifying the causative pathogens and their susceptibility profiles. This highlights the critical need for careful consideration of antibiotic use in the context of microbial culture sensitivity testing, as well as the potential implications for treatment decisions. Table **4** provides a detailed breakdown of the antibiotics prescribed, allowing for a more thorough analysis of pre-treatment practices and their potential influence on the observed microbial resistance patterns in this patient population. Understanding these dynamics is essential for refining empirical treatment guidelines and fostering responsible antibiotic stewardship within clinical settings.

3.4. Pathogen Isolation and Distribution from Culture Sensitivity Tests

In our analysis of 80 positive cultures, a diverse range of pathogens were isolated, reflecting the complexity of microbial infections encountered in this patient population. The most frequently isolated pathogen was *Escherichia coli*, identified in 28 cases (35% of total isolates). This predominance is consistent with its well-known role as a leading cause of urinary tract infections (UTIs), particularly among female patients, where *E. coli* accounted for 33 cases (84.6%) of UTIs in females. This finding underscores the importance of *E. coli* as a primary target for empirical therapy in suspected UTIs, given its high prevalence in this clinical context. Following *E. coli, Klebsiella pneumoniae* was the second most commonly isolated pathogen, found in 10 cases (12.5%). Notably, 6 of these isolates (30% of *K. pneumoniae* isolates) were recovered from sputum cultures, indicating their significant

Table 5. Classification based on bacterial isolates.

Bacterial Isolates	Frequency	Percentage
Escherichia coli	28	35.0%
Klebsiella pneumoniae	10	12.50%
Klebsiella oxytoca	6	7.50%
Staphylococcus aureus	4	5.0%
Staphylococcus epidermidis	2	2.50%
Pseudomonas aeruginosa	7	8.80%
Streptococcus pneumoniae	2	2.50%
Acinetobacter baumannii	2	2.50%
***Enterobacter* spp.**	2	2.50%
Citrobacter koseri	4	5.0%
Proteus mirabilis	7	8.80%
***Enterococcus* spp.**	6	7.50%

Table 6. Classification of biological specimens based on gender.

-		Type of Patients Biological Specimen Analysed			Total	*P*-value
		Pus Swabs	Sputum	Urine		
Patient Gender	Female	5	9	33	47	0.000*
	Male	16	11	6	33	
Total		21	20	39	80	

Note: *The data were analysed statistically using chi-square test.

role in respiratory infections, particularly in patients with underlying respiratory conditions. The isolation of *K. pneumoniae* is of particular concern due to its potential for antimicrobial resistance, necessitating vigilant monitoring and targeted treatment strategies. Other notable pathogens included *Pseudomonas aeruginosa* and *Proteus mirabilis*, both isolated in 7 cases (8.8%). *P. aeruginosa* is known for its association with healthcare-associated infections and is particularly challenging to treat due to its robust resistance mechanisms. Meanwhile, *P. mirabilis* was predominantly found in pus swabs, accounting for 33.3% of isolates from this specimen type, suggesting its involvement in skin and soft tissue infections.

Additionally, *Klebsiella oxytoca* and *Enterococcus spp.* were each isolated in 6 cases (7.5%), further highlighting the variety of pathogens present in the study. Lesser-known pathogens such as *Citrobacter koseri* (4 cases, 5%), *Staphylococcus aureus* (4 cases, 5%), *Staphylococcus epidermidis* (2 cases, 2.5%), *Streptococcus pneumoniae* (2 cases, 2.5%), *Acinetobacter baumannii* (2 cases, 2.5%), and *Enterobacter* spp. (2 cases, 2.5%) were also identified, demonstrating a broad spectrum of bacterial diversity among the infections studied. The results presented in Table **5** provide a comprehensive overview of the isolated pathogens, while Tables **6** and **7** further dissect the distribution of these organisms across different specimen types and patient demographics. These findings emphasize the necessity for tailored antibiotic treatment strategies, informed by the specific pathogens present and their susceptibility profiles. The high prevalence of multi-drug-resistant organisms necessitates ongoing surveillance and

Table 7. Classification of isolated pathogens based on biological specimens.

-		Type of Patients Biological Specimen Analysed			Total	*P*-Value
		Pus Swabs	Sputum	Urine		
Isolated Pathogens From Culture Sensitivity Test	Acinetobacter *baumannii*	1	0	1	2	0.000*
	Citrobacter spp.	3	0	1	4	
	Enterobacter spp.	1	0	1	2	
	Enterococcus spp.	0	0	6	6	
	Escherichia coli	2	4	22	28	
	Klebsiella oxytoca	1	2	3	6	
	Klebsiella pneumoniae	2	6	2	10	
	Proteus mirabilis	7	0	0	7	
	Pseudomonas aeruginosa	0	4	3	7	
	Staphylococcus aureus	2	2	0	4	
	Staphylococcus epidermidis	2	0	0	2	
	Streptococcus pneumoniae	0	2	0	2	
Total		21	20	39	80	

Note: *The data were analysed statistically using chi-square test.

judicious use of antibiotics to combat the rising threat of antimicrobial resistance effectively. Understanding the epidemiology of these pathogens is critical for guiding clinical decisions and optimizing patient outcomes in the face of complex infections.

3.5. Pathogen Isolation and Antimicrobial Resistance Patterns

The antimicrobial resistance patterns observed in our study provide a critical insight into the evolving landscape of pathogenic bacteria prevalent in our hospital environment. Among the isolated pathogens, *Escherichia coli* emerged as the most frequently identified organism, exhibiting alarmingly high resistance rates across multiple antibiotics. Specifically, resistance to ampicillin was observed in 96.3% of isolates, while resistance to cefixime, ceftriaxone, and cefotaxime was noted in 92.6%, 88.9%, and 85.2% of cases, respectively. Such high resistance rates underscore the urgent need for ongoing surveillance and prudent use of antibiotics, particularly in the treatment of urinary tract infections where *E. coli* is a common etiological agent. Similarly, *Klebsiella pneumoniae* demonstrated significant resistance, particularly to ampicillin (90%) and third-generation cephalosporins like cefepime and cefotaxime (70%). These findings highlight the importance of tailoring empirical therapy based on local resistance patterns, especially given the potential for *K. pneumoniae* to cause serious infections, including pneumonia and bloodstream infections. *Staphylococcus aureus*, another critical pathogen identified in our study, exhibited complete resistance (100%) to both ampicillin and ciprofloxacin. Furthermore, a high level of resistance was also noted for cefepime, ceftriaxone, cefixime, cefotaxime, and erythromycin (75%). These results are particularly concerning due to the potential for these strains to cause severe infections, compounded by the emergence of Methicillin-resistant *Staphylococcus aureus* (MRSA), found in 3.8% of our *S. aureus* isolates. In the case of *Pseudomonas aeruginosa*, resistance to a range of antibiotics was similarly troubling, with 80% of isolates resistant to amoxicillin/clavulanic acid, ampicillin, ceftriaxone, cefixime, and cefotaxime. Resistance to ceftazidime was noted in 60% of cases. *Streptococcus pneumoniae* also showed 100% resistance

to cefepime, ceftriaxone, cefixime, cefotaxime, cefuroxime, and ceftazidime, raising significant concerns regarding treatment options for infections caused by this pathogen. The resistance profiles of *Acinetobacter baumannii* and *Enterobacter* spp. were particularly alarming, with both showing near-universal resistance to the antibiotics tested, including imipenem (100%). The resistance of *Citrobacter koseri* and *Proteus mirabilis* to multiple antibiotics, including 100% resistance to ampicillin and third-generation cephalosporins, further highlights the challenge posed by these organisms. Overall, the highest resistance rates observed across all isolated pathogens were 82.5% to ampicillin, 80% to cefixime, and 78.8% to ceftriaxone and cefotaxime.

Approximately 74% of pathogens exhibited resistance to conventional antibiotic therapy, emphasizing the need for healthcare providers to reconsider their empirical treatment choices in light of these findings. Conversely, the study also identified some antibiotics with higher sensitivity rates, with amikacin showing an encouraging sensitivity of 86.3%, followed by meropenem (70%) and piperacillin/tazobactam (67.5%). This suggests that while resistance is a significant concern, certain antibiotics remain effective and should be prioritized in treatment protocols. The identification of Extended Spectrum Beta-Lactamase (ESBL) species in 17.5% of isolates and multi-drug-resistant species in 12.5% is particularly noteworthy, as these organisms pose a substantial therapeutic challenge and are often associated with worse clinical outcomes. Additionally, the presence of coagulase-negative *Staphylococcus* spp. and the identification of MRSA further underline the complexity of managing infections in our patient population. In summary, the resistance patterns outlined in this study not only reflect the current challenges in treating bacterial infections but also serve as a clarion call for the implementation of effective antibiotic stewardship programs. By closely monitoring resistance trends and adapting treatment protocols accordingly, we can better manage the risks posed by these resistant pathogens and improve patient outcomes. The results presented in Tables (**8-13**) offer crucial insights into the microbiological landscape of our institution, guiding clinicians in their decision-making processes to combat the rising tide of antimicrobial resistance effectively.

3.6. Post-culture Sensitivity Antibiotic Prescriptions: Tailoring Therapy to Resistance Patterns

Following the analysis of culture sensitivity test results, a targeted approach was adopted in prescribing antibiotics for patients with confirmed infections. The objective was to ensure the most effective treatment by utilizing antibiotics that demonstrated sensitivity against the isolated pathogens, thus enhancing the chances of a favorable clinical outcome. Among the antibiotics prescribed, piperacillin/tazobactam emerged as the most frequently utilized option, accounting for 26.3% of prescriptions. This broad-spectrum antibiotic is particularly valuable in treating infections caused by various gram-negative bacteria. It is a suitable choice given the high prevalence of resistant organisms identified in our study. Piperacillin/tazobactam's effectiveness against beta-lactamase-producing strains further underscores its role as a critical component of empirical therapy, especially in settings where multi-drug-resistant pathogens are common. Amikacin was the second most prescribed antibiotic, representing 25% of the cases. As an aminoglycoside, amikacin is known for its potent activity against a wide range of aerobic gram-negative bacteria, including *Pseudomonas aeruginosa*. Its use in this context is particularly warranted, given the high levels of resistance observed in other antibiotics for pathogens prevalent in our patient population. By prioritizing amikacin, clinicians can harness its efficacy against resistant strains, thereby improving treatment outcomes. Additionally, imipenem, a member of the carbapenem class, was prescribed in 12.5% of cases. Imipenem is renowned for its broad-spectrum activity and stability against many beta-lactamases, making it an invaluable agent in the treatment of serious infections caused by resistant bacteria. The decision to include imipenem in therapy regimens reflects a strategic choice aimed at addressing the substantial resistance patterns identified in pathogens such as *Klebsiella pneumoniae* and *Acinetobacter baumannii*. These prescribing trends emphasize the importance of utilizing culture-sensitivity data to guide antibiotic therapy. By moving away from broad-spectrum empirical therapy towards more precise treatment based on laboratory findings, healthcare providers can not only improve individual patient outcomes but also contribute to the broader goal of combating antimicrobial resistance. Such targeted therapy can

Table 8. Antimicrobial resistance pattern among bacterial isolates.

Antibiotics/ Isolated Pathogens	*Escherichia coli* n = 27 (%)	*Klebsiella pneumonia* n = 10 (%)	*Klebsiella oxytoca* n = 6 (%)	*Staphylococcus aureus* n = 4 (%)	*Staphylococcus epidermidis* n = 2 (%)	*Pseudomonas aeruginosa* n = 5 (%)
Amoxycillin/ clavulanic acid	33.30	40	66.70	25	-	80
Ampicillin	96.30	90	83.30	100	100	80
Cefepime	85	70	33.30	75	100	20
Co-trimoxazole	55.60	30	16.70	-	-	40
Ceftriaxone	88.90	60	66.70	75	100	80
Cefixime	92.60	60	66.70	75	100	80
Cefotaxime	85.20	70	66.70	75	100	80
Cefuroxime	37	10	33.30	-	-	40
Ciprofloxacin	70.40	20	33.30	100	50	20
Norfloxacin	63	10	16.70	-	50	40
Ceftazidime	85.20	60	50	50	100	60
Meropenem	7.40	-	-	-	-	-
Amikacin	3.70	20	-	-	-	-
Piperacillin/ Tazobactam	11.10	20	16.70	25	-	-
Gentamycin	25.90	30	-	50	-	20
Nitrofurantoin	11.10	-	50	-	-	-
Chloramphenicol	-	40	33.30	-	-	-
Imipenem	18.50	10	50	-	50	20
Clindamycin	-	-	-	-	50	-
Erythromycin	-	-	-	75	50	40

Table 9. Antimicrobial resistance pattern among less common bacterial isolates identified in the study.

Antibiotics/ Isolated Pathogens	*Streptococcus pneumonia* n = 2 (%)	*Acinetobacter baumannii* n = 1 (%)	*Enterobacter* spp. n = 2 (%)	*Citrobacter koseri* n = 4 (%)	*Proteus mirabilis* n =7(%)	*Enterococcus* spp. n = 6 (%)
Amoxycillin/ clavulanic acid	50	-	100	100	28.60	-
Ampicillin	50	100	100	100	100	16.70
Cefepime	100	100	100	100	100	33.30
Co-trimoxazole	-	100	-	100	85.70	100
Ceftriaxone	100	100	100	100	100	66.70
Cefixime	100	100	100	100	100	66.70

(Table 9) contd…

Antibiotics/ Isolated Pathogens	*Streptococcus pneumonia* n = 2 (%)	*Acinetobacter baumannii* n = 1 (%)	*Enterobacter* spp. n = 2 (%)	*Citrobacter koseri* n = 4 (%)	*Proteus mirabilis* n =7(%)	*Enterococcus* spp. n = 6 (%)
Cefotaxime	100	100	100	100	100	66.70
Cefuroxime	100	100	50	50	71.40	-
Ciprofloxacin	50	-	-	100	57.10	66.70
Norfloxacin	50	-	-	50	-	16.70
Ceftazidime	100	100	100	100	100	33.30
Meropenem	-	-	-	25	-	-
Amikacin	50	-	-	-	-	16.70
Piperacillin/tazobactam	50	-	50	50	-	-
Gentamycin	50	100	-	50	29	50
Nitrofurantoin	-	-	-	-	-	-
Chloramphenicol	-	-	-	-	85.70	16.70
Imipenem	-	-	100	50	14.30	-
Clindamycin	-	-	-	-	-	50
Erythromycin	-	-	-	-	-	83.30

Table 10. Classification of frequently resistant antibiotics.

Antibiotic Resistant Patterns	Frequency	Percentage
Amoxycillin/Clavulanic acid	31	38.80%
Ampicillin	66	82.50%
Cefepime	56	70.0%
Co-trimoxazole	38	47.50%
Ceftriaxone	63	78.80%
Cefixime	64	80.0%
Cefotaxime	63	78.80%
Cefuroxime	26	32.50%
Ciprofloxacin	42	52.5%
Norfloxacin	26	32.50%
Ceftazidime	57	71.30%
Meropenem	3	3.80%
Amikacin	5	6.30%
Piperacillin/tazobactam	11	13.80%
Gentamycin	22	27.50%
Nitrofurantoin	6	7.50%
Chloramphenicol	13	16.30%
Imipenem	16	20.0%
Cefaperazone/sulbactam	2	2.50%
Clindamycin	4	5.0%
Erythromycin	11	13.80%
No significant resistance	4	5.0%

Table 11. Classification of highly sensitive antibiotics.

Antibiotic Sensitivity Patterns	Frequency	Percentage
Amoxycillin/Clavulanic acid	45	56.30%
Ampicillin	9	11.30%
Cefepime	19	23.80%
Co-trimoxazole	35	43.80%
Ceftriaxone	10	12.50%
Cefixime	9	11.30%
Cefotaxime	15	18.80%
Ciprofloxacin	27	33.80%
Norfloxacin	13	16.30%
Ceftazidime	16	20.0%
Meropenem	56	70.0%
Amikacin	69	86.30%
Piperacillin/tazobactam	54	67.50%
Gentamycin	52	65.0%
Nitrofurantoin	27	33.80%
Chloramphenicol	16	20.0%
Imipenem	37	46.30%
Cefaperazone/sulbactam	1	1.30%
Clindamycin	5	6.30%
Erythromycin	3	3.80%
Azithromycin	2	2.50%
Vancomycin	13	16.30%
Poly Myxin B	7	8.80%
Cloxacillin	2	2.50%
Colistin	5	6.30%

Table 12. Classification of resistant species among isolated pathogens.

Resistance to Empirical Therapy	Frequency	Percentage
Resistant spp.	59	73.80%
Non-Resistant spp.	21	26.30%

Table 13. Classification based on Bacterial characteristics among isolated pathogens.

Bacterial Characteristics	Frequency	Percentage
Extended spectrum beta-lactamase spp.	14	17.50%
Methicillin-resistant *Staphylococcus aureus*	3	3.80%
Multi-drug resistant spp.	10	2.50%
Coagulase negative *Staphylococcus* spp.	1	1.30%
Normal significant growth spp.	52	65.0%

Table 14. Classification of antibiotics used after specimen collection.

Definite Antibiotic Therapy	Frequency	Percentage
Linezolid	1	1.30%
Cefaperazone/sulbactam	1	1.30%
Ceftriaxone	5	6.30%
Cefotaxime	9	11.30%
Ciprofloxacin	1	1.30%
Meropenem	1	1.30%
Amikacin	20	25.0%
Piperacillin/tazobactam	21	26.30%
Gentamycin	8	10.0%
Nitrofurantoin	2	2.50%
Imipenem	10	12.50%
Azithromycin	2	2.50%

help preserve the efficacy of critical antibiotics and reduce the risk of further resistance development. The post-culture sensitivity antibiotic regimen exemplifies a shift towards evidence-based medicine, where specific susceptibility patterns inform the choice of antibiotics. This approach not only maximizes the likelihood of therapeutic success but also aligns with current best practices in antimicrobial stewardship, ultimately enhancing patient care and mitigating the impact of antibiotic resistance in the clinical setting. The data presented in Table **14** further illustrate these prescribing patterns and their implications for clinical practice.

3.7. Patient Outcomes Following Antibiotic Therapy

The evaluation of patient outcomes is a critical component of our study, providing insight into the effectiveness of both empirical and definitive antibiotic therapies administered to the cohort of 80 patients with positive culture results. Each patient received initial empirical antibiotic therapy, followed by a tailored approach based on culture sensitivity reports, allowing us to assess the impact of these strategies on clinical outcomes. Among the patients assessed, a notable 60% reported a positive response to definitive therapy, reflecting a favorable clinical outcome characterized by resolution of infection symptoms and overall improvement in health status. This high percentage underscores the importance of utilizing culture sensitivity data to guide antibiotic selection, ensuring that the prescribed therapies align with the resistance patterns of the isolated pathogens. The effective switch to targeted antibiotics is critical in managing infections, especially in settings marked by significant antimicrobial resistance. In contrast, 13.8% of patients experienced intermediate outcomes. This group included individuals whose clinical responses were mixed; while some improvements were noted, they did not achieve complete resolution of symptoms. Factors contributing to these intermediate outcomes may include the severity of the infection, the presence of underlying comorbidities, or delayed response to therapy due to the initial use of less effective empirical treatments. Recognizing this subgroup is essential for understanding the complexities of treating infections in a resistant bacterial landscape. Alarmingly, 70% of patients experienced poor outcomes during the empirical antibiotic therapy phase. This high rate indicates the inadequacy of initial treatment choices, likely due to the prevalence of resistant organisms that were not effectively targeted by the empirical therapies prescribed. This finding emphasizes the critical need for prompt and accurate microbiological diagnostics, as well as the necessity of refining empirical treatment protocols based on local resistance patterns. The reliance on empirical therapy, while necessary in some cases, underscores the potential for suboptimal outcomes,

Table 15. Classification based on patient's outcome.

Patients Outcomes	Frequency			Percentage		
	Good Feedback of Results	Intermediate Feedback of Results	Poor Feedback of Results	Good Feedback of Results	Intermediate Feedback of Results	Poor Feedback of Results
During empirical therapy	10	14	56	12.50%	17.50%	70.0%
-	Good Feedback of Results	Intermediate Feedback of Results	No change in Empirical therapy	Good Feedback of Results	Intermediate Feedback of Results	No change in Empirical therapy
During definite therapy	48	11	21	60.0%	13.80%	26.20%

particularly in an era of rising antimicrobial resistance. The data presented in Table **15** encapsulate these outcomes, providing a clear visual representation of the differential responses to empirical *versus* definitive antibiotic therapies. The stark contrast in patient outcomes serves as a powerful reminder of the importance of timely culture and sensitivity testing, as well as the necessity for healthcare providers to remain vigilant in monitoring and adjusting treatment plans based on emerging data.

The analysis of patient outcomes demonstrates that while empirical therapies may frequently fail to provide adequate treatment responses in a landscape of antibiotic resistance, transitioning to culture-guided definitive therapy significantly enhances patient outcomes. These findings not only highlight the efficacy of targeted antibiotic use but also reinforce the urgent need for ongoing education and training in antibiotic stewardship practices to ensure optimal patient care. By continuously evaluating and adapting treatment strategies based on resistance patterns and patient feedback, healthcare providers can significantly improve clinical outcomes in the face of escalating antimicrobial resistance.

4. DISCUSSION

The study conducted on antimicrobial resistance patterns and patient outcomes in a cohort of 80 patients with confirmed infections sheds light on critical aspects of clinical practice, particularly in the face of increasing antimicrobial resistance. This research was driven by the urgent need to understand the demographic and clinical factors associated with infections in our healthcare environment, as well as the implications of empirical antibiotic therapy and resistance patterns on patient outcomes. The cultivation of bacteria under controlled physical conditions is critical to accurately assessing antimicrobial resistance patterns. In this study, standardized parameters such as temperature (37°C), pH, and oxygen availability were maintained to provide optimal conditions for microbial growth while preventing environmental stress-induced phenotypic changes. Prolonged sublethal antibiotic exposure during cultivation can induce adaptive resistance mechanisms, such as overexpression of efflux pumps or modification of target sites. Conversely, the absence of selective pressure in controlled cultivation can lead to the attenuation of resistance traits over successive generations due to a lack of fitness advantage. These phenomena underscore the importance of methodological rigor in AMR studies, as inconsistent cultivation conditions can lead to misleading conclusions about resistance or susceptibility. By adhering to standardized cultivation protocols, this study ensures that the resistance profiles obtained reflect clinically relevant scenarios, thereby providing reliable data for guiding antibiotic stewardship programs. Future studies could explore how slight variations in cultivation conditions might influence resistance phenotypes, further enhancing our understanding of AMR dynamics.

The composition of bacterial culture media plays a crucial role in the expression of antimicrobial resistance. In nutrient-rich environments, bacteria grow optimally, which can enhance the expression of resistance genes, particularly under conditions of selective pressure. Stress-inducing conditions, such as low pH or high salt concentrations, can activate adaptive resistance mechanisms, including the overexpression of efflux pumps or biofilm formation. These mechanisms are known to confer resistance to multiple classes of antibiot-

ics and are often observed in clinical settings. Furthermore, antibiotic-laden media can be used to select resistant mutants, a critical consideration when investigating the development of resistance *in vitro*. The media used in this study was selected to ensure reproducibility, but future studies should consider how variations in media composition might impact resistance expression in different bacterial species.

One of the most striking findings from the results is the high prevalence of infections in females, particularly related to urinary tract infections (UTIs). The data indicating that 58.7% of the patients were female aligns with established trends in infectious disease epidemiology, where UTIs disproportionately affect women due to anatomical and physiological factors. This emphasizes the necessity for clinicians to maintain a high index of suspicion for UTIs in this demographic, thus allowing for prompt diagnosis and treatment. The diverse age distribution of the patient population also highlights the importance of considering age-related susceptibility to infections when formulating treatment strategies. The distribution of culture-positive results was dominated by urinary specimens, which accounted for nearly half of the positive cultures. This finding underscores the relevance of UTIs as a significant health concern, particularly in settings where factors such as catheter use and co-morbidities may heighten the risk of infection. The notable number of pus swabs and sputum cultures further indicates the diverse spectrum of infections prevalent in the patient population, necessitating targeted infection control measures. A critical observation in the study was the complete prior antibiotic exposure among the patient cohort, with 100% receiving antibiotics before culture testing. This factor complicates the interpretation of resistance patterns, as previous antibiotic use can skew the results and limit the identification of the true susceptibility profile of pathogens. The results highlight the need for careful antibiotic stewardship practices and the consideration of the impact of empirical therapy on microbial flora. The study identified a concerning prevalence of multidrug-resistant organisms, with *E. coli* and *Klebsiella pneumoniae* exhibiting alarmingly high resistance rates to commonly used antibiotics. For instance, resistance to ampicillin reached 96.3% among *E. coli* isolates. Such high resistance rates necessitate a reevaluation of empirical treatment protocols and underscore the importance of tailoring therapy based on local resistance data. The emergence of methicillin-resistant *Staphylococcus aureus* (MRSA) in the patient cohort further emphasizes the need for continuous surveillance and adaptation of treatment strategies to combat resistant pathogens effectively. Patient outcomes following antibiotic therapy demonstrated the importance of transitioning from empirical to definitive therapy based on culture sensitivity results. A significant 60% of patients achieved a favorable clinical outcome following targeted therapy, highlighting the effectiveness of tailoring antibiotic treatment to the susceptibility profiles of isolated pathogens. However, the 70% poor outcome rate during the empirical therapy phase signals the inadequacies of initial treatment choices in a setting marked by significant antimicrobial resistance.

Our study reports that among the 80 patients analyzed, infections were more prevalent in females, with urinary tract infections (UTIs) being the most common type. This trend aligns with findings from Saravanan and Raveendaran in 2013 [23], which also observed a higher incidence of UTIs in females, likely due to anatomical and physiological factors. Additionally, our study included a predominance of patients in the 41-50 and 51-60 age groups, which supports findings in other studies indicating that middle-aged and older adults are more susceptible to infections, often due to comorbidities and age-related immune changes. These demographic insights are critical for developing targeted antimicrobial resistance (AMR) interventions for high-risk age groups. In our study, urine samples accounted for nearly half of the positive cultures, with pus swabs representing 26% and sputum samples 25%. The high prevalence of UTI-causing pathogens, particularly *Escherichia coli* (*E. coli*), reflects established infection trends observed in studies like that of Handa *et al.* in 2024 [24], where *E. coli* was also predominant, especially among female patients. Both studies underscore the importance of addressing AMR in UTIs, given their frequent occurrence in clinical settings.

Additionally, the prevalence of *Klebsiella pneumoniae* in respiratory samples resonates with findings from studies like that of Saini *et al.*, which observed shifts in respiratory pathogen re-

sistance patterns, particularly during the COVID-19 pandemic [25]. Our study revealed alarming resistance levels in *E. coli* to commonly prescribed antibiotics such as ampicillin (96.3%) and third-generation cephalosporins (up to 92.6% resistance), consistent with rising resistance trends documented by Saravanan, Handa [23, 24]. The elevated resistance to cephalosporins in *E. coli* and *Klebsiella pneumoniae* highlights the need to reassess empirical therapies in our hospital and similar settings. Studies by Saini *et al.* in 2021 [25] have also highlighted this trend, particularly noting increased cephalosporin resistance in the pandemic and post-pandemic periods, likely driven by elevated antibiotic use. *Staphylococcus aureus* in our study exhibited 100% resistance to both ampicillin and ciprofloxacin, echoing concerns across multiple studies where Methicillin-resistant *Staphylococcus aureus* (MRSA) rates have risen. These findings underline the ongoing challenge posed by resistant Staphylococcus strains in healthcare-associated infections and emphasize the necessity of enhanced infection control measures. A notable finding in our study was the improvement in patient outcomes when shifting from empirical to culture-guided antibiotic therapy. Piperacillin/tazobactam and amikacin, both demonstrating high sensitivity rates in our study, proved to be effective choices. This finding aligns with studies by Handa *et al.* and Saini *et al.* [24, 25], where targeted therapies were associated with better patient outcomes than empirical treatments. These results reinforce the value of culture sensitivity testing in optimizing antibiotic selection and improving treatment efficacy, especially in settings with high AMR prevalence. The resistance mechanisms of gram-negative and gram-positive bacteria differ due to their structural and genetic characteristics. In gram-negative bacteria, the outer membrane acts as a barrier to many antibiotics, and resistance is often mediated by porin channel modifications that limit drug influx. Efflux pumps further reduce intracellular antibiotic concentrations, while beta-lactamase enzymes degrade beta-lactam antibiotics, including penicillins and cephalosporins. These mechanisms collectively make gram-negative bacteria highly resistant to many antibiotic classes. On the other hand, gram-positive bacteria lack an outer membrane but rely on enzymatic processes and genetic adaptations for resistance. Target site modifications are particularly prominent; for instance, the alteration of penicillin-binding proteins (PBPs) in MRSA confers resistance to beta-lactam antibiotics. Additionally, the methylation of 23S rRNA by erm genes confers resistance to macrolides. The absence of an outer membrane makes gram-positive bacteria less reliant on efflux mechanisms but equally challenging to treat due to their adaptability. These differences underscore the importance of tailored therapeutic approaches based on the bacterial group and resistance profile, as highlighted in our findings. For instance, the high resistance to ceftriaxone observed in gram-negative isolates aligns with beta-lactamase activity, while resistance in gram-positive isolates may be due to PBP modification.

Although the resistance patterns observed align with known trends, this study's systematic approach in a secondary care hospital highlights its novelty. The clinical impact of resistance profiling after empirical therapy underscores the importance of transitioning to targeted therapy, particularly in resource-limited settings where such analyses are rarely conducted systematically. These findings offer practical strategies for improving antibiotic stewardship programs and reducing antimicrobial resistance globally. This study is clinically impactful as it reinforces the importance of culture and sensitivity testing in guiding antibiotic therapy, particularly in patients with infections caused by resistant organisms. The findings provide a clear rationale for improving diagnostic practices and refining empirical treatment guidelines based on local resistance patterns. From a social perspective, the implications of this research extend beyond individual patient care; it emphasizes the need for public health initiatives aimed at promoting responsible antibiotic use and enhancing awareness of antimicrobial resistance. Moreover, this study differentiates itself from other research in the field by providing a comprehensive analysis of pathogen distribution, resistance patterns, and clinical outcomes in a defined patient population within a specific healthcare setting.

The study also serves as a training tool for healthcare professionals, illustrating the significance of antimicrobial resistance profiling in optimizing therapy. By presenting real-world data from a diverse patient population, it emphasizes the role of sensitivity testing in clinical decision-making, providing a framework for educational

and institutional practices. By presenting detailed demographic data and linking it to resistance patterns and treatment outcomes, the study contributes valuable insights to the existing literature. It guides prescribers in making informed treatment decisions. For prescribers, the study underscores the necessity of adhering to evidence-based guidelines informed by local resistance data and emphasizes the importance of targeted antibiotic therapy. For the public, it highlights the pressing issue of antimicrobial resistance, promoting awareness of the risks associated with inappropriate antibiotic use and encouraging collaboration between healthcare providers and patients to foster responsible antibiotic stewardship. This study not only illuminates the current landscape of antimicrobial resistance and its clinical implications but also serves as a clarion call for continued research and education in this critical area. By adopting a proactive and informed approach to antimicrobial therapy, healthcare providers can significantly enhance patient outcomes while contributing to the global effort to combat the rising tide of antibiotic resistance. The findings align with global AMR goals outlined by the WHO, which advocate for the systematic monitoring of antimicrobial resistance. By demonstrating the benefits of targeted therapy over empirical treatments, this study provides a case-based perspective that can inspire similar efforts in other institutions. The approach outlined here can guide resource-constrained settings to implement effective antibiotic stewardship programs.

CONCLUSION

This study highlights the critical issue of antimicrobial resistance among isolated pathogens in hospitalized patients. *Escherichia coli* emerged as the most frequently isolated pathogen, followed by *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, and *Klebsiella oxytoca*. Alarmingly, we observed high resistance rates to essential antibiotics, including ampicillin, cefixime, ceftriaxone, and ciprofloxacin, while maintaining sensitivity to amikacin, meropenem, piperacillin/tazobactam, and gentamicin. The significant resistance to third-generation cephalosporins underscores the urgent need for robust monitoring of both community-acquired and hospital-acquired infections. We advocate for genetic characterization of these pathogens to enhance infection control strategies in healthcare settings. This research equips clinicians with vital information to guide antibiotic selection tailored to local resistance patterns, reinforcing the importance of effective antimicrobial stewardship. Addressing the challenge of antimicrobial resistance requires ongoing vigilance, targeted interventions, and collaborative efforts to safeguard patient health and improve clinical outcomes.

AUTHORS' CONTRIBUTIONS

The authors confirm their contribution to the paper as follows: study conception and design: AR, NPE; data collection: APS; validation: MP, DPT; visualization: DRS; draft manuscript: NS. All authors reviewed the results and approved the final version of the manuscript.

LIST OF ABBREVIATIONS

AMEs = Aminoglycoside-modifying Enzymes

AMR = Antimicrobial Resistance

ARGs = Antibiotic Resistance Genes

ASPs = Antibiotic Stewardship Programs

ESBLs = Extended-spectrum Beta-lactamases

MRSA = Methicillin-resistant *Staphylococcus aureus*

OMPs = Outer Membrane Proteins

PBPs = Penicillin-binding Proteins

QRDR = Quinolone Resistance-determining Region

UTIs = Urinary Tract Infections

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

This study received ethical approval from the Institutional Ethical Committee at Vels Institute of Science, Technology, and Advanced Studies, Chennai, India, under reference number ECR/288/Indt/TN/2018/RR-21/001, dated April 6, 2023.

HUMAN AND ANIMAL RIGHTS

All procedures performed in studies involving human participants were in accordance with the ethical standards of institutional and/or research committees and with the 1975 Declaration of Helsinki, as revised in 2013.

CONSENT FOR PUBLICATION

Informed written consent was obtained from each participant.

STANDARDS OF REPORTING

STROBE guidelines were followed.

AVAILABILITY OF DATA AND MATERIALS

All the data and supporting information are provided within the article.

FUNDING

None.

CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

ACKNOWLEDGEMENTS

The authors are thankful to the management of Vels Institute of Science, Technology and Advanced Studies (VISTAS, SRM Institute of Science and Technology (SRMIST), and the Physicians, Nursing staff, and Patients of ESI Hospital, Ayanavaram for extending their Support towards the successful completion of research work.

REFERENCES

[1] Salam MA, Al-Amin MY, Salam MT, *et al.* Antimicrobial resistance: A growing serious threat for global public health. Healthcare 2023; 11(13): 1946. http://dx.doi.org/10.3390/healthcare11131946 PMID: 37444780

[2] Prestinaci F, Pezzotti P, Pantosti A. Antimicrobial resistance: A global multifaceted phenomenon. Pathog Glob Health 2015; 109(7): 309-18. http://dx.doi.org/10.1179/2047773215Y.0000000030 PMID: 26343252

[3] Ghai I, Ghai S. Understanding antibiotic resistance *via* outer membrane permeability. Infect Drug Resist 2018; 11: 523-30. http://dx.doi.org/10.2147/IDR.S156995 PMID: 29695921

[4] Delcour AH. Outer membrane permeability and antibiotic resistance. Biochim Biophys Acta Proteins Proteomics 2009; 1794(5): 808-16. http://dx.doi.org/10.1016/j.bbapap.2008.11.005 PMID: 19100346

[5] Ghai I. A barrier to entry: Examining the bacterial outer membrane and antibiotic resistance. Appl Sci 2023; 13(7): 4238. http://dx.doi.org/10.3390/app13074238

[6] Fernández L, Hancock REW. Adaptive and mutational resistance: Role of porins and efflux pumps in drug resistance. Clin Microbiol Rev 2012; 25(4): 661-81. http://dx.doi.org/10.1128/CMR.00043-12 PMID: 23034325

[7] Li XZ, Plésiat P, Nikaido H. The challenge of efflux-mediated antibiotic resistance in Gram-negative bacteria. Clin Microbiol Rev 2015; 28(2): 337-418. http://dx.doi.org/10.1128/CMR.00117-14 PMID: 25788514

[8] Munita JM, Arias CA. Mechanisms of antibiotic resistance. Microbiol Spectr 2016; 4(2): 481-511. http://dx.doi.org/10.1128/microbiolspec.VMBF-0016-2015 PMID: 27227291

[9] Kherroubi L, Bacon J, Rahman KM. Navigating fluoroquinolone resistance in Gram-negative bacteria: A comprehensive evaluation. JAC Antimicrob Resist 2024; 6(4): dlae127. http://dx.doi.org/10.1093/jacamr/dlae127 PMID: 39144447

[10] Spencer AC, Panda SS. DNA gyrase as a target for quinolones. Biomedicines 2023; 11(2): 371. http://dx.doi.org/10.3390/biomedicines11020371 PMID: 36830908

[11] Hooper DC, Jacoby GA. Mechanisms of drug resistance: Quinolone resistance. Ann N Y Acad Sci 2015; 1354(1): 12-31. http://dx.doi.org/10.1111/nyas.12830 PMID: 26190223

[12] Reygaert WC. An overview of the antimicrobial resistance mechanisms of bacteria. AIMS Microbiol 2018; 4(3): 482-501. http://dx.doi.org/10.3934/microbiol.2018.3.482 PMID: 31294229

[13] Nappier SP, Liguori K, Ichida AM, Stewart JR, Jones KR. Antibiotic resistance in recreational waters: State of the science. Int J Environ Res Public Health 2020; 17(21): 8034. http://dx.doi.org/10.3390/ijerph17218034 PMID: 33142796

[14] Graham DW, Bergeron G, Bourassa MW, *et al.* Complexities in understanding antimicrobial resistance across domesticated animal, human, and environmental systems. Ann N Y Acad Sci 2019; 1441(1): 17-30. http://dx.doi.org/10.1111/nyas.14036 PMID: 30924539

[15] Zhuang M, Achmon Y, Cao Y, *et al.* Distribution of antibiotic resistance genes in the environment. Environ Pollut 2021; 285: 117402. http://dx.doi.org/10.1016/j.envpol.2021.117402 PMID: 34051569

[16] Michaelis C, Grohmann E. Horizontal gene transfer of antibiotic resistance genes in biofilms. Antibiotics 2023; 12(2): 328. http://dx.doi.org/10.3390/antibiotics12020328 PMID: 36830238

[17] Murray CJL, Ikuta KS, Sharara F, *et al.* Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. Lancet 2022; 399(10325): 629-55. http://dx.doi.org/10.1016/S0140-6736(21)02724-0 PMID: 35065702

[18] Boonyasiri A, Tangkoskul T, Seenama C, Saiyarin J, Tiengrim S, Thamlikitkul V. Prevalence of

antibiotic resistant bacteria in healthy adults, foods, food animals, and the environment in selected areas in Thailand. Pathog Glob Health 2014; 108(5): 235-45. http://dx.doi.org/10.1179/2047773214Y.0000000148 PMID: 25146935

[19] Anning AS, Baah E, Buabeng SD, *et al.* Prevalence and antimicrobial resistance patterns of microbes isolated from individuals attending private diagnostic centre in Cape Coast Metropolis of Ghana. Sci Rep 2022; 12(1): 14282. http://dx.doi.org/10.1038/s41598-022-18595-w PMID: 35995932

[20] Akova M. Epidemiology of antimicrobial resistance in bloodstream infections. Virulence 2016; 7(3): 252-66. http://dx.doi.org/10.1080/21505594.2016.1159366 PMID: 26984779

[21] Obakiro SB, Kiyimba K, Paasi G, *et al.* Prevalence of antibiotic-resistant bacteria among patients in two tertiary hospitals in Eastern Uganda. J Glob Antimicrob Resist 2021; 25: 82-6. http://dx.doi.org/10.1016/j.jgar.2021.02.021 PMID: 33662642

[22] Tabasi M, Maghami P, Amiri-Tehranizadeh Z, Reza S.M, Chamani J. New perspective of the ternary complex of nano-curcumin with β-lactoglobulin in the presence of α-lactalbumin: Spectroscopic and molecular dynamic investigations. J Mol Liq 2023; 392: 123472. http://dx.doi.org/10.1016/j.molliq.2023.123472

[23] Saravanan R, Raveendaran V. Antimicrobial resistance pattern in a tertiary care hospital: An observational study. J Basic Clin Pharm 2013; 4(3): 56-63. http://dx.doi.org/10.4103/0976-0105.118797 PMID: 24808672

[24] Handa VL, Patel BN, Bhattacharya DA, Kothari RK, Kavathia DG, Vyas BRM. A study of antibiotic resistance pattern of clinical bacterial pathogens isolated from patients in a tertiary care hospital. Front Microbiol 2024; 15: 1383989. http://dx.doi.org/10.3389/fmicb.2024.1383989 PMID: 38694800

[25] Saini V, Jain C, Singh NP, *et al.* Paradigm shift in antimicrobial resistance pattern of bacterial isolates during the COVID-19 pandemic. Antibiotics 2021; 10(8): 954. http://dx.doi.org/10.3390/antibiotics10080954 PMID: 34439004