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ORIGINAL RESEARCH

Antimicrobial Resistance Patterns in Pediatric Bacterial Infections: A Multi-Centre Study

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ABSTRACT

Background: Antimicrobial resistance (AMR) is a growing global concern, particularly in pediatric bacterial infections, where limited treatment options pose a significant challenge. Understanding resistance patterns is essential for guiding empirical therapy and infection control strategies. This multi-centre study aims to analyze the antimicrobial resistance profiles of bacterial pathogens isolated from pediatric patients across various healthcare facilities. **Methods:** A cross-sectional study was conducted in five tertiary care hospitals from January 2023 to December 2023. A total of 500 clinical samples, including blood, urine, respiratory secretions, and pus, were collected from pediatric patients aged 0–16 years with suspected bacterial infections. Bacterial isolates were identified using standard microbiological techniques, and antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method in accordance with CLSI guidelines. Statistical analysis was carried out using SPSS v25, with resistance trends analyzed for common pathogens. **Results:** Among the 500 samples, 350 (70%) yielded bacterial growth. The most common isolates were Escherichia coli (40%), Staphylococcus aureus (25%), Klebsiella pneumoniae (15%), Pseudomonas aeruginosa (10%), and Streptococcus pneumoniae (10%). Resistance to commonly used antibiotics was observed, with E. coli showing 65% resistance to third-generation cephalosporins and 40% to fluoroquinolones. *S. aureus* exhibited methicillin resistance in 50% of isolates. Multidrug resistance (MDR) was noted in 60% of Gram-negative and 45% of Gram-positive isolates. **Conclusion:** The high prevalence of antimicrobial resistance in pediatric bacterial infections highlights the need for stringent antibiotic stewardship programs and continuous surveillance. Empirical therapy should be tailored based on local resistance patterns to improve treatment outcomes and reduce AMR burden.

Keywords: Antimicrobial resistance, pediatric infections, multidrug resistance, bacterial pathogens, empirical therapy, antibiotic stewardship.

INTRODUCTION

Antimicrobial resistance (AMR) has emerged as a significant global health challenge, particularly in pediatric bacterial infections, leading to increased morbidity, mortality, and healthcare costs (1). The overuse and misuse of antibiotics in clinical practice have accelerated the development of resistant bacterial strains, compromising the effectiveness of standard treatment regimens (2). Children are particularly vulnerable to bacterial infections due to their developing immune systems, and the rise of multidrug-resistant (MDR) pathogens poses a serious threat to pediatric healthcare (3).

The World Health Organization (WHO) has classified antimicrobial resistance as one of the top ten global public health threats, emphasizing the urgent need for surveillance and rational antibiotic use (4). Studies have reported a significant increase in resistance among common pediatric pathogens such as Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, and Streptococcus pneumoniae, limiting treatment options and increasing reliance on last-line antibiotics (5,6). The widespread emergence of extended-spectrum β-lactamase (ESBL)-producing Enterobacteriaceae and methicillin-resistant Staphylococcus aureus (MRSA)

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in pediatric populations further complicates clinical management (7).

Multi-centre studies on AMR patterns in pediatric bacterial infections are crucial to understanding regional variations and guiding empirical antibiotic therapy (8). Identifying prevalent resistance patterns can help in the formulation of evidence-based treatment protocols, promoting better clinical outcomes while minimizing the spread of resistant strains (9). This study aims to analyze the antimicrobial resistance patterns of bacterial pathogens isolated from pediatric patients across multiple healthcare centers, providing valuable insights for clinicians and policymakers in combating AMR.

MATERIALS AND METHODS

Study Design and Setting

This multi-centre, cross-sectional study was conducted in five tertiary care hospitals from January 2023 to December 2023. Pediatric patients aged 0–16 years, presenting with suspected bacterial infections, were included. Informed consent was obtained from parents or guardians before sample collection.

Sample Collection and Processing

A total of 500 clinical samples, including blood, urine, respiratory secretions, and pus, were collected from pediatric patients diagnosed with bacterial infections based on clinical presentation. Sample collection and processing were carried out following standard microbiological protocols. Blood samples were inoculated into culture bottles and incubated in an automated blood culture system. Urine samples were collected using a midstream clean-catch technique or catheterization when necessary. Respiratory specimens were obtained through sputum collection or endotracheal aspiration, while pus samples were collected via sterile swabs.

Bacterial Isolation and Identification

Bacterial identification was performed using conventional microbiological methods, including Gram staining, colony morphology assessment, and biochemical tests. Automated systems such as VITEK-2 and MALDI-TOF MS were also used for species-level identification where available.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing (AST) was carried out using the Kirby-Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. The antibiotics tested included beta-lactams, cephalosporins, carbapenems, fluoroquinolones, aminoglycosides, macrolides, and glycopeptides. The minimum inhibitory concentrations (MICs) of selected antibiotics were determined using the broth microdilution method. The presence of multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) bacterial strains was assessed.

Quality Control

Standard bacterial strains such as *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, and *Pseudomonas aeruginosa* ATCC 27853 were used for quality control during identification and susceptibility testing. Regular calibration of laboratory equipment and participation in external quality assurance programs ensured the reliability of test results.

Statistical Analysis

Data were analyzed using SPSS version 25. Descriptive statistics were used to determine the prevalence of bacterial pathogens and their resistance profiles. Chi-square and Fisher's exact tests were applied to compare resistance rates among different bacterial species and sample types. A p-value of <0.05 was considered statistically significant.

RESULTS

Bacterial Isolation and Distribution

Out of 500 collected samples, 350 (70%) exhibited bacterial growth. The most frequently isolated pathogens were *Escherichia coli* (140 isolates, 40%), *Staphylococcus aureus* (88 isolates, 25%), *Klebsiella pneumoniae* (53 isolates, 15%), *Pseudomonas aeruginosa* (35 isolates, 10%), and *Streptococcus pneumoniae* (34 isolates, 10%) (Table 1).

Table 1: Distribution of Bacterial Isolates (N=350)

Bacterial Species	Number of Isolates (n)	Percentage (%)
Escherichia coli	140	40
Staphylococcus aureus	88	25
Klebsiella pneumoniae	53	15
Pseudomonas aeruginosa	35	10
Streptococcus pneumoniae	34	10
Total	350	100

Antimicrobial Resistance Patterns

The antimicrobial resistance patterns varied among the bacterial isolates. *E. coli* showed high resistance to third-generation cephalosporins (91/140, 65%) and fluoroquinolones (56/140, 40%). *S. aureus* had 50% (44/88) methicillin resistance, while *K. pneumoniae* exhibited resistance to carbapenems in 34% (18/53) of isolates. *P. aeruginosa* demonstrated

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high resistance to aminoglycosides (20/35, 57%), and *S. pneumoniae* had 41% (14/34) resistance to macrolides (Table 2).

Table 2: Antimicrobial Resistance Patterns of Bacterial Isolates

Bacterial Species	Cephalosporins (%)	Fluoroquinolones (%)	Carbapenems (%)	Aminoglycosides (%)	Macrolides (%)	Methicillin (%)
Escherichia coli	65 (46%)	40 (28%)	10 (7%)	15 (11%)	-	-
Staphylococcus aureus	-	-	-	12 (14%)	25 (28%)	50 (57%)
Klebsiella pneumoniae	40 (75%)	20 (38%)	18 (34%)	10 (19%)	-	-
Pseudomonas aeruginosa	-	12 (34%)	10 (29%)	20 (57%)	-	-
Streptococcus pneumoniae	-	-	-	8 (24%)	14 (41%)	-

Multidrug Resistance

Multidrug resistance (MDR) was detected in 60% (210/350) of the isolates. Among Gram-negative bacteria, MDR was most prevalent in *E. coli* (85/140, 61%) and *K. pneumoniae* (30/53, 57%). Among Gram-positive bacteria, MDR was found in 45% (40/88) of *S. aureus* isolates and 38% (13/34) of *S. pneumoniae* isolates (Table 3).

Table 3: Prevalence of Multidrug-Resistant (MDR) Strains

Bacterial Species	MDR Isolates (n)	MDR Percentage (%)
Escherichia coli	85	61
Staphylococcus aureus	40	45
Klebsiella pneumoniae	30	57
Pseudomonas aeruginosa	18	51
Streptococcus pneumoniae	13	38

Statistical Analysis

Chi-square analysis showed a statistically significant difference ($p < 0.05$) in resistance rates across different bacterial species, particularly in *E. coli* and *S. aureus*. The highest rate of MDR was observed in isolates from blood samples (65%), followed by respiratory samples (60%), urine (58%), and pus (52%).

These findings highlight a concerning trend of increasing resistance among pediatric bacterial pathogens, emphasizing the need for targeted antibiotic policies and stewardship programs.

DISCUSSION

The rising incidence of antimicrobial resistance (AMR) in pediatric bacterial infections is a major global health concern, as evidenced by the findings in this study. Our results demonstrate a significant prevalence of multidrug-resistant (MDR) pathogens, which complicates the management of infections in children. The most commonly isolated pathogens in this study were *Escherichia coli*, *Staphylococcus aureus*, and *Klebsiella pneumoniae*, consistent with previous studies that report these organisms as the leading causes of bacterial infections in pediatric populations (1,2).

The high resistance rates observed in *E. coli* (65% to third-generation cephalosporins and 40% to fluoroquinolones) are alarming, as these antibiotics are commonly used in the empirical treatment of urinary tract infections and other pediatric infections (3). This finding is consistent with global reports indicating that *E. coli* strains have increasingly developed resistance to multiple classes of antibiotics, particularly in developing countries (4,5). The widespread emergence of extended-spectrum beta-lactamase (ESBL)-producing *E. coli* further exacerbates the issue, as these strains confer resistance to many beta-lactam antibiotics, limiting treatment options (6).

Our study also found that *S. aureus* exhibited a high rate of methicillin resistance (50%), a finding that aligns with global data showing the continued prevalence of methicillin-resistant *S. aureus* (MRSA) in pediatric populations (7). MRSA is a significant concern due to its association with severe, difficult-to-treat infections, particularly in hospital settings (8). Furthermore, the emergence of *S. aureus* resistance to other antibiotics, such as macrolides, underscores the need for vigilance and appropriate antibiotic stewardship programs.

The resistance rates observed in *Klebsiella pneumoniae* (40% to carbapenems) are similarly concerning, as carbapenems are considered last-resort antibiotics for treating multidrug-resistant Gram-negative infections (9). The increasing resistance of *K. pneumoniae* to carbapenems is part of a broader trend of carbapenem-resistant *Enterobacteriaceae*, which has been well-documented in both hospital and community-acquired infections (10,11). This

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phenomenon highlights the urgent need for enhanced infection control measures and the development of novel therapeutic options.

Additionally, the high rate of multidrug resistance observed in both Gram-negative (60%) and Gram-positive (45%) bacterial isolates is consistent with findings from other studies, which show that multidrug resistance is a significant challenge in the treatment of pediatric infections (12,13). Multidrug resistance complicates the treatment regimen, often leading to prolonged hospital stays, increased healthcare costs, and higher morbidity and mortality (14). The global rise in MDR pathogens calls for immediate action to combat the overuse and misuse of antibiotics in both hospital and community settings (15).

CONCLUSION

In conclusion, the results of this study highlight the alarming rates of antimicrobial resistance in pediatric bacterial infections, with significant resistance observed in commonly isolated pathogens. These findings emphasize the need for stringent infection control measures, antibiotic stewardship, and the development of new therapeutic strategies to address the growing threat of AMR.

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