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Prevalence and Distribution of Multidrug-resistant Bacteria Isolated from Pediatric Clinical Samples

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***Abstract*—Multidrug-resistant bacterial infections (MDRIs) represent a major global health concern, contributing to increased morbidity, mortality, prolonged hospital stays, and higher healthcare costs. In Iraq, data on antimicrobial resistance among pediatric patients remain limited. This retrospective cross-sectional study assessed the prevalence and microbiological characteristics of MDRIs among hospitalized pediatric patients under 11 years of age at the Central Children's Teaching Hospital in Baghdad between March and October 2025, with confirmed positive bacterial cultures from different clinical samples, MDRIs were identified in 88.4% of patients, indicating a high prevalence. Multidrug resistance was the predominant pattern, particularly in *Escherichia coli* (96.5%) and *Klebsiella pneumoniae* (96.8%), while *Acinetobacter baumannii* was mainly extensively drug-resistant (XDR) (90.0%). Less common resistance phenotypes, including ESBL, VRE, ICR, and MRCNS, were also observed. Most isolates (76.8%) were obtained from stool and urine samples, with *E. coli* being the most frequent pathogen, whereas *A. baumannii* predominated in blood cultures. The high burden of MDR and XDR organisms underscores the urgent need for improved antimicrobial stewardship.**

***Keywords*—Multidrug resistant bacteria, Pediatric infections, Hospital-acquired infections**

I. Introduction

Antibiotics are seen as two-edged weapons because, when administered properly, they can either eradicate or prevent the growth of germs, but they can also have adverse effects, such as antimicrobial resistance (AMR). When bacteria evade the stress of antibiotic exposure by gaining genetic material, changing gene expression, or undergoing mutations, the issue of antimicrobial resistance (AMR) emerges. As a result, new strains of bacteria that are resistant to the current antibiotics arise [1-2]. The World Health Organization (WHO) listed 12 genera of Gram-negative bacteria that pose a hazard to public health in 2017 because they are resistant to several antibiotics, including *Klebsiella, E. coli, Serratia*, and *Proteus* [3]. The European Centre for Disease Prevention and Control (ECDC) and the centers for Disease Control and Prevention (CDC) did not establish an international definition of multidrug-resistant organisms (MDROs) until 2010. According to in vitro testing, MDROs are organisms that are resistant to at least one antimicrobial in three or more antibiotic classes [4]. A major hazard to public health, multidrug-resistant (MDR) organisms can have both clinical and epidemiologic repercussions. MDR, extensively drug resistant (XDR), or pandrug-resistant (PDR) resistance patterns are characteristics of MDRO. Pathogens like *Staphylococcus aureus, Enterococci, Enterobacteriaceae, Pseudomonas aeruginosa*, and *Acinetobacter* isolates that commonly cause hospital-acquired infections such bacteremia, meningitis, urinary tract infections, and soft-tissue infections are included in the MDR group [5]. Over a 11-year period, the number of strains exhibiting multidrug resistance in children has quadrupled, with *Pseudomonas aeruginosa* and *Enterobacteriaceae* showing the most resistance. These strains spread through maternal or community contact, and these initial non-invasive colorizations may act as reservoirs for subsequent widespread dissemination, including in intensive care units [6]. Numerous local investigations have examined the frequency, distribution, and resistance patterns of MDRO in pediatric populations.

Children are a particularly susceptible group of patients. About 5%–10% of infections in hospitalized children are caused by multidrug-resistant organisms (MDROs), which raises the risk of death, lengthens hospital stays, and adds to expenses [7]. In order to combat the most potent antibiotics, multidrug-resistant (MDR) bacteria have developed adaptable resistance mechanisms and an arsenal of virulence factors [8]. The development of new antibiotics that can treat multidrug-resistant illnesses has lagged behind the rise in these infections [9]. *Enterococcus faecium* (E.), *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and Enterobacter species are among the MDR bacteria that have been grouped together under the acronym "ESKAPE" due to their resistance to the bactericidal effects of traditional antibiotics [10]. Healthcare-associated infections caused by MDR bacteria have increased in frequency due to rising morbidity, death, and costs [11], and they are considered a global public health problem [12–14].

In order to provide urgent public health significance, this study attempts to clarify the distribution and prevalence of

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MDRO isolated from pediatric clinical specimens and evaluate related epidemiological factors.

II. MATERIALS AND METHODS

A. Study Population

Two hundred fifty pediatric patients were included in this study, comprising 58 neonates (0–28 days), 102 infants (1–11 months), 55 young children (1–2 years), 14 preschoolers (3–5 years), and 21 children aged 6–11 years. Blood, urine, stool, and throat swab samples were collected from patients admitted to the Central Children's Teaching Hospital in Baghdad, Iraq, between March 2025 and October 2025. All study cases were referred by expert consultants. The patients presented with symptoms including fever, agitation, vomiting, lethargy, diarrhea, dehydration, and poor perfusion.

B. Sample Collection

Microbiological confirmation of clinical samples from children was carried out in the microbiology laboratory of a hospital using standard laboratory methods. Samples from various body fluids and swabs were collected at different time points in 2025. All samples were inoculated into appropriate culture media, and bacterial identification and antimicrobial susceptibility testing were performed using the VITEK 2 automated system. Antibiotic susceptibility testing was conducted to evaluate the effectiveness of various antibiotics against the isolated bacterial strains. The antibiotic susceptibility profile of the recovered strains was analyzed according to the mechanism of action of the tested antibiotics. Standard procedures were strictly followed during sample collection and culture to prevent contamination.

C. Exclusion criteria

Patients with missing or incomplete data, as well as those with inconclusive bacterial culture results, were excluded from the study.

D. Ethical Clearance

After being informed about the objectives and methods of the study, each participant group's families gave their approval. The Human Development Centre Research Committee in Baghdad approved the study (No. 3320).

III. RESULTS

A total of 250 bacterial isolates were analyzed in this study. The age distribution of the participants is shown in Table 1. The majority of cases were observed in infants (1–11 months; 40.8%, n = 102) and neonates (0–28 days; 23.2%, n = 58), followed by young children (1–2 years; 22.0%, n = 55). Preschool children (3–5 years) and children/adolescents (6–11 years) accounted for 5.6% and 8.4%, respectively, indicating higher susceptibility in participants under two years of age.

TABLE 1. Age distribution of study participants.

Age Group	Frequency	Percent (%)
Neonates (0–28 days)	58	23.2
Infants (1–11 months)	102	40.8
Young Children (1–2 years)	55	22.0
Preschool Children (3–5 years)	14	5.6
Children and Adolescents (6–11 years)	21	8.4
Total	250	100.0

The distribution of bacterial species is summarized in Table 2. *Escherichia coli* was the most frequently isolated pathogen (45.6%, n = 114), followed by *Klebsiella pneumoniae* (12.4%, n = 31), *Acinetobacter baumannii* (8.0%, n = 20), *Serratia odorifera* (9.6%, n = 24), and *Staphylococcus aureus* (5.2%, n = 13). Other bacterial species, including *Raoultella ornithinolytica*, *Enterococcus faecium*, and *Pantoea agglomerans*, were less common.

TABLE 2. Frequency and percentage of bacterial isolates identified.

Diagnosed Bacteria	Frequency	Percent
Escherichia coli	114	45.6
Staphylococcus aureus	13	5.2
Klebsiella pneumoniae	31	12.4
Acinetobacter baumannii	20	8.0
Burkholderia cepacia	3	1.2
Raoultella ornithinolytica	8	3.2
Stenotrophomonas maltophilia	1	0.4
Enterococcus faecium	8	3.2
Serratia odorifera	24	9.6
Pantoea agglomerans	10	4.0
Enterococcus avium	2	0.8
Staphylococcus xylosus	3	1.2
Enterobacter cloacae	2	0.8
Proteus mirabilis	2	0.8
Enterococcus casseliflavus	1	0.4
Staphylococcus saccharolyticus	1	0.4
Enterobacter hermannii	1	0.4
Enterococcus faecalis	3	1.2
Staphylococcus haemolyticus	1	0.4
Staphylococcus hominis	1	0.4
Aeromonas hydrophila	1	0.4
Total	250	100.0

Table 3 provides a summary of the distribution of bacterial species and antibiotics resistance. The investigation reveals a trend of multidrug resistance (MDR) among bacterial isolates. *Escherichia coli, Klebsiella pneumoniae*, *Staphylococcus aureus*, Serratia *odorifera* and *Enterococcus faecium* are identified as MDR pathogens due to their resistance to multiple antibiotic classes with three types of

antibiotic resistance. *Acinetobacter baumannii* is highlighted as possibly extensively drug-resistant (XDR) with more than four antibiotic resistances.

TABLE 3. Distribution of antibiotics used and the bacterial results of the antibiotics.

Types of bacteria	Types of antibiotic resistance	No. of resistance categories	Classification
Escherichia coli	CTX, CRO, CIP	3	MDR
Klebsiella pneumoniae	CTX, CAZ, CIP	3	MDR
Acinetobacter baumannii	IPM, MEM, CAZ, CIP	≥4	XDR
Staphylococcus aureus	OXA, ERY, CLI	3	MDR
Serratia odorifera	AMP,AMX,CFZ	3	MDR
Enterococcus faecium	PCN,CEX	3	MDR

Abbreviations: CTX, cefotaxime; CRO, ceftriaxone; CIP, ciprofloxacin; CAZ, ceftazidime; IPM, imipenem; MEM, meropenem; OXA, oxacillin; ERY, erythromycin; CLI, clindamycin; AMP, ampicillin; AMX, amoxicillin; CFZ, cefazolin; PCN, penicillin; CEX, cephalexin; AZI, azithromycin.

Analysis of antibiotic resistance patterns (Table 4) revealed a predominance of multidrug-resistant (MDR) strains (88.4% n = 221), followed by extensively drug-resistant (XDR) bacteria (8.0% (n = 20). ESBL-producing isolates accounted for (1.6% n = 4), while VRE, ICR, and MRCNS were rare (≤1.2% each). Notably, *E. coli* and *K. pneumoniae* were predominantly MDR, whereas *A. baumannii* showed a high prevalence of XDR.

Table 4. Distribution of antibiotic resistance patterns among clinical isolates.

Antibiotic Resistance Patterns	Frequency	Percent (%)
Multidrug-Resistant (MDR)	221	88.4
Extensively Drug-Resistant (XDR)	20	8.0
Extended-Spectrum Beta-Lactamase (ESBL)	4	1.6
Vancomycin-Resistant Enterococci (VRE)	1	0.4
Inducible Clindamycin Resistance (ICR)	3	1.2
Methicillin-Resistant Coagulase-Negative Staphylococci (MRCNS)	1	0.4
Total	250	100.0

The distribution of bacterial isolates across different age groups is summarized in Fig.1. *Escherichia coli* was the most frequently isolated pathogen in all age groups, particularly among infants (1–11 months), accounting for 52 of 102 cases (51.0%), followed by young children (1–2 years; 30/55, 54.5%) and neonates (0–28 days; 16/58, 27.6%). *Klebsiella pneumoniae* was primarily observed in infants (12/102, 11.8%) and young children (9/55, 16.4%), while *Acinetobacter baumannii* was most common among neonates (13/58, 22.4%). Other pathogens, including *Staphylococcus aureus, Serratia odorifera, Raoultella ornithinolytica*, and *Enterococcus faecium*, were distributed across age groups but with lower frequencies. Overall, infants and young children accounted for the majority of bacterial infections (n = 157, 62.8%), highlighting higher susceptibility in younger age groups.

The distribution of bacterial isolates by sample type is shown in Fig.2. Stool and urine samples accounted for the majority of isolates (76.8%), with *E. coli* predominating in both (stool 51.4%, urine 60.4%). *K. pneumoniae* was also frequent in stool and urine, while *A. baumannii* was most common in blood (31.9%). *Staphylococcus aureus* was mainly isolated from blood.

Finally, the crosstabulation of diagnosis and antibiotic susceptibility Fig. 3 demonstrated that MDR was the dominant resistance pattern across most species, particularly *E. coli* (96.5%) and K. pneumoniae (96.8%), whereas *A. baumannii* was primarily XDR (90.0%). Less frequent resistance types, including ESBL, VRE, ICR, and MRCNS, were observed in a small number of isolates.

Overall, the results indicate a high prevalence of multidrug and extensive drug resistance, with younger age groups most affected, and *E. coli*, K. pneumoniae, and *A. baumannii* as the leading pathogens across different sample types.

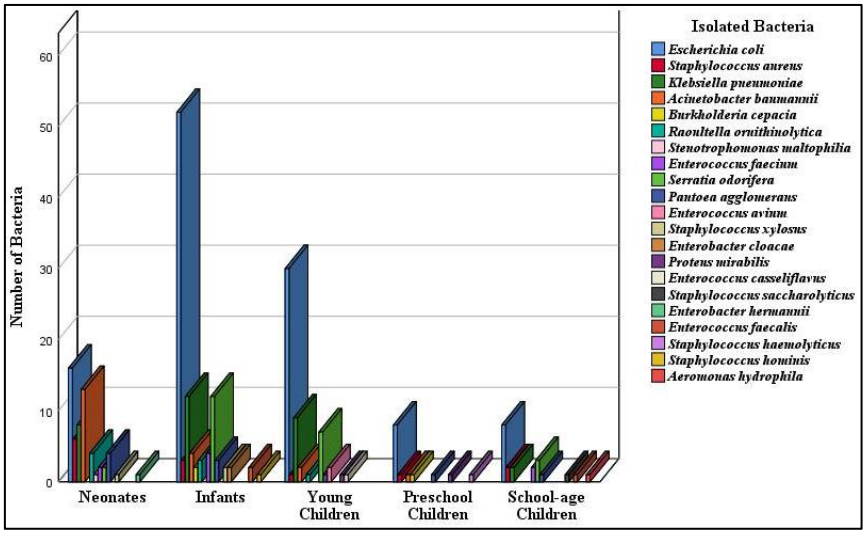

Fig. 1: Distribution of bacterial species among different age groups.

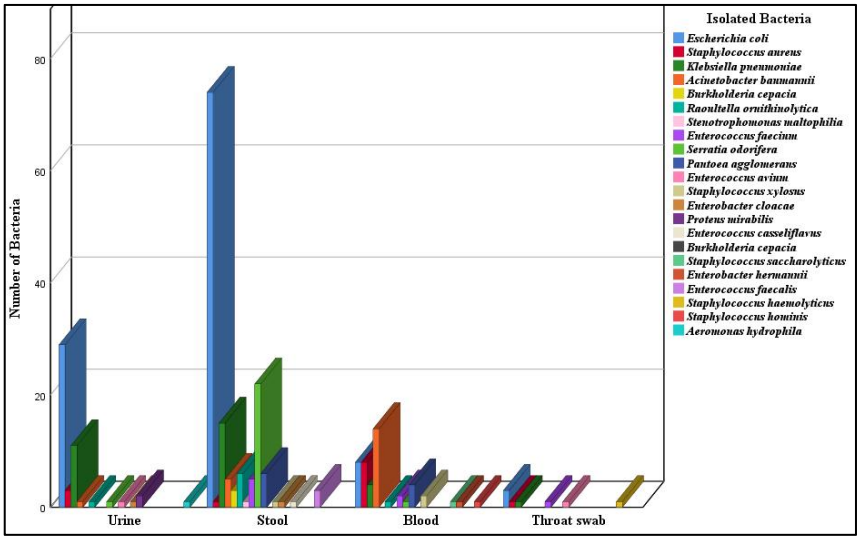

Fig. 2: Distribution of bacterial isolates according to sample type.

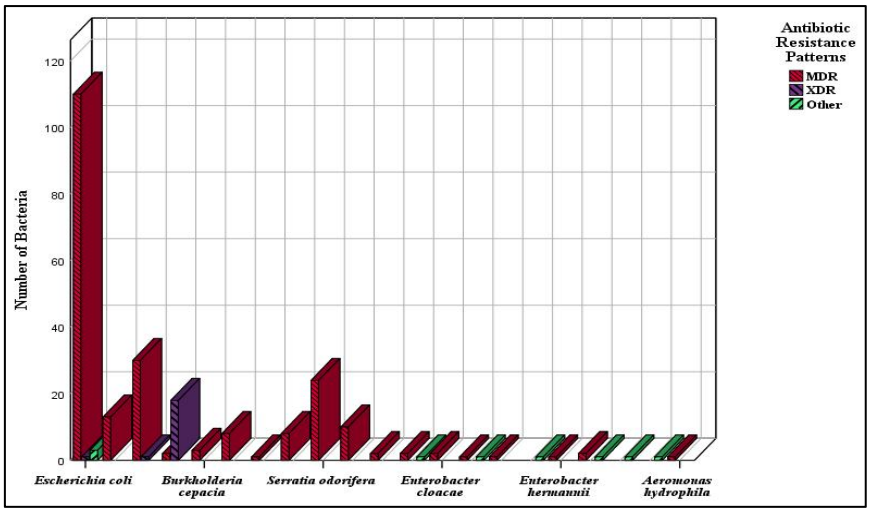

Fig. 3: Antibiotic resistance patterns by bacterial species.

IV. Discussion

MDR microorganisms have emerged and spread around the world as a result of increased antibiotic use. One of the biggest dangers to global public health and development is antimicrobial resistance (AMR). According to estimates, bacterial AMR contributed to 4.95 million fatalities worldwide in 2019 and was directly responsible for 1.27 million deaths [15].

Children have been known to develop and spread antibiotic resistance on a regular basis, and the pediatric population is susceptible to colonization by several resistant organisms [16]. According to this study, MDROs represent a serious hazard and a substantial healthcare-associated infection issue, particularly for critically pediatric patients.

Due to their wide and varied resistome, Gram negative bacteria (GNB) (Enterobacterales and non-fermenting GNB) are especially vulnerable to multidrug resistance. Through chromosomal gene changes or the horizontal transfer of resistance genes carried on vectors like plasmids, transposons, or integrons, these bacteria may acquire new resistance mechanisms in addition to their inherent resistance [17-18].

Antimicrobial drugs can be resisted by bacteria through enzymatic or non-enzymatic ways. Changes in drug targets, efflux pumps, and membrane permeability are examples of non-enzymatic processes. ESBLs and carbapenemases are two enzyme classes of great epidemiologic importance that are involved in reducing the efficacy of last-resort antimicrobials in the treatment of life-threatening illnesses among the enzymatic processes used to inactivate or hydrolyse antibiotics [8]. According to Saeedi *et al.* [19], MDRIs were found in 42% of patients and in 54.3% of positive bacterial cultures, particularly in critically sick patients referred to the Neonatal and Pediatric Intensive Care Unit,

According to a study conducted on 164 pediatric patients in Libya, 68.3% (41/60) of blood culture isolates were resistant to one or more antibiotics from three or more classes, indicating an unacceptably high multidrug resistance (MDR) rate [20]. El Zein *et al.* [21] revealed an alarming prevalence of MDROs and ESBL-producing uropathogens in urinary tract infections among hospitalised Lebanese children, reaching 68% and 45%. They reported that the primary uropathogen encountered was *Escherichia coli* (73.9%), followed by Klebsiella spp. (13.1%) and Pseudomonas spp. (4.2%).

The most prevalent resistance mechanism in Enterobacterales is the synthesis of beta lactamases, including carbapenemases, AmpC cephalosporinases, and extended-spectrum beta lactamases (ESBLs).Because their genes are found on plasmids, ESBLs are especially significant because they can spread among several Enterobacterales species with variable levels of virulence or resistance profiles [22-23].This illustrates how MDROs have expanded into community settings after first being restricted to healthcare settings.

MDROs were found in 64% of the urine cultures of children with UTIs in a cross-sectional investigation carried out in India over a one-year period [24]. In a similar vein, Parajuli *et al.* found that 65% of 739 *E. coli* isolates from three distinct populations in Nepal were resistant to at least one antibiotic [25].

Given that up to 30% of children infections in Southern Europe and Asia are caused by bacteria resistant to two or more medications, an increase in multidrug-resistant (MDR) diseases is especially concerning [26]. According to reports, MDROs are responsible for a 20% increase in children's hospital stays and a 40% rise in hospital-acquired mortality [27].

V. Conclusion

The high prevalence of multidrug-resistant (MDR) bacteria, particularly among *Escherichia coli*, represents a significant concern in the pediatric population. *E. coli* was the most frequently isolated pathogen and was predominantly recovered from urine and stool samples, suggesting that urinary tract and gastrointestinal infections are major causes of hospital admission among pediatric patients. These findings highlight the increasing burden of antimicrobial resistance in children and emphasize the urgent need to strengthen infection control strategies and implement targeted antimicrobial stewardship programs in pediatric healthcare settings.

Conflict of interest

Authors declare that they have no conflict of interest.

REFERENCES

[1] U. Theuretzbacher, "Accelerating resistance, inadequate antibacterial drug pipelines and international responses," *International Journal of Antimicrobial Agents*, vol. 39, pp. 295–299, 2012, doi: 10.1016/j.ijantimicag.2011.12.006.

[2] J. M. Munita and C. A. Arias, "Mechanisms of antibiotic resistance," *Microbiology Spectrum*, vol. 4, pp. 481–511, 2016, doi: 10.1128/microbiolspec.VMBF-0016-2015.

[3] A. Bryce et al., "Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis," *The Lancet*, vol. 399, pp. 629–655, 2022, doi: 10.1016/S0140-6736(21)02724-0.

[4] A. P. Magiorakos et al., "Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions," *Clinical Microbiology and Infection*, vol. 18, pp. 268–281, 2012, doi: 10.1111/j.1469-0691.2011.03570.x.

[5] S. Qureshi et al., "Prevalence and risk factors associated with multidrug-resistant organism carriage among pediatric patients at admission in a tertiary care hospital of a developing country: a cross-sectional study," *Qureshi et al. BMC Infectious Diseases*, vol. 21, 2021, doi: 10.1186/s12879-021-06275-5.

[6] Q. Yang et al., "Antimicrobial susceptibility among Gram-negative isolates in pediatric patients in Latin America, Africa-Middle East, and Asia from 2016–2020 compared to 2011–2015: ATLAS surveillance results," *Journal of the Pediatric Infectious Diseases Society*, vol. 12, pp. 459-470, 2023, doi: 10.1093/jpids/piad055.

[7] M. T. Murray, M. P. Beauchemin, N. Neu, and E. L. Larson, "Prior antibiotic use and acquisition of multidrug-resistant organisms in hospitalized children: a systematic review," *Infection Control & Hospital*

Epidemiology, vol. 40, no. 10, pp. 1107–1115, 2019, doi: 10.1017/ice.2019.215.

[8] M. Ahmadi, R. Ranjbar, P. Behzadi, and T. Mohammadian, "Virulence factors, antibiotic resistance patterns, and molecular types of Klebsiella pneumoniae clinical isolates," *Expert Review of Anti-infective Therapy*, vol. 20, no. 3, pp. 463–472, 2022, doi: 10.1080/14787210.2022.1990040.

[9] P. D. Tamma and A. J. Hsu, "Defining the role of novel β-lactam agents in carbapenem-resistant Gram-negative organisms," *Journal of the Pediatric Infectious Diseases Society*, vol. 8, no. 3, pp. 251–260, 2019.

[10] D. M. P. De Oliveira et al., "Antimicrobial resistance in ESKAPE pathogens," *Clinical Microbiology Reviews*, vol. 33, p. e00181-19, 2020.

[11] E. J. McGrath and B. I. Asmar, "Nosocomial infections and multidrug-resistant bacterial organisms in pediatric intensive care units," *Indian Journal of Pediatrics*, vol. 78, no. 2, pp. 176–184, 2011.

[12] M. Girona-Alarcón et al., "Device-associated multidrug-resistant bacteria surveillance in critically ill children: 10 years of experience," *Acta Paediatrica*, vol. 110, no. 1, pp. 203–209, 2021.

[13] A. H. Uc-Cachón et al., "High prevalence of antimicrobial resistance among Gram-negative bacilli in ICUs at a tertiary-care hospital in Yucatán, Mexico," *Medicina*, vol. 55, no. 9, p. 588, 2019.

[14] D. C. Zaha et al., "Recent advances in investigation, prevention, and management of healthcare-associated infections: multidrug-resistant strain colonization and risk factors in a university hospital ICU," *BioMed Research International*, vol. 2019, p. 2510875, 2019.

[15] Antimicrobial Resistance Collaborators, "Global burden of bacterial antimicrobial resistance in 2019: systematic analysis," *The Lancet*, vol. 399, pp. 629–655, 2022, doi: 10.1016/S0140-6736(21)02724-0.

[16] J. P. Roy et al., "Emerging pathogens and resistance mechanisms shaping future pediatric antimicrobial resistance," *Journal of Pure and Applied Microbiology*, vol. 19, no. 2, pp. 834–847, 2025, doi: 10.22207/JPAM.19.2.46.

[17] M. Sarshar, P. Behzadi, D. Scribano, A. T. Palamara, and C. Ambrosi, "Acinetobacter baumannii: an ancient commensal with weapons of a pathogen," *Pathogens*, vol. 10, no. 4, p. 387, 2021, doi: 10.3390/pathogens10040387.

[18] P. Behzadi, Z. Baráth, and M. Gajdács, "A narrative review on the microbiology, virulence and therapeutic prospects of multidrug-resistant Pseudomonas aeruginosa," *Antibiotics*, vol. 10, no. 1, p. 42, 2021, doi: 10.3390/antibiotics10010042.

[19] F. A. Saeedi et al., "Multidrug-resistant bacterial infections in pediatric patients hospitalized at King Abdulaziz University Hospital, Jeddah, Saudi Arabia," *Children*, vol. 11, p. 444, 2024, doi: 10.3390/children11040444.

[20] G. Ali, "Antibiotic resistance patterns and multidrug-resistant bacteria in pediatric patients: a retrospective study," *AlQalam Journal of Medical and Applied Sciences*, vol. 5, pp. 810–815, 2025.

[21] Z. El Zein et al., "The challenge of multidrug resistance in hospitalized pediatric patients with urinary tract infections," *Frontiers in Cellular and Infection Microbiology*, vol. 15, p. 1570405, 2025, doi: 10.3389/fcimb.2025.1570405.

[22] C. A. Moxon and S. Paulus, "Beta-lactamases in Enterobacteriaceae infections in children," *Journal of Infection*, vol. 72, suppl., pp. S41–S49, 2016, doi: 10.1016/j.jinf.2016.04.021.

[23] M. Mahony, B. McMullan, J. Brown, and S. E. Kennedy, "Multidrug-resistant organisms in pediatric urinary tract infections," *Pediatric Nephrology*, vol. 35, pp. 1563–1573, 2020, doi: 10.1007/s00467-019-04316-5.

[24] S. S. Roul, L. Priyadarshini, and S. K. Pradhan, "Risk factors of multidrug-resistant urinary tract infection in children: a cross-sectional study," *Research & Reviews: Pediatrics*, vol. 23, pp. 16–20, 2022, doi: 10.4103/rrp.rrp_11_22.

[25] N. P. Parajuli et al., "High rates of multidrug resistance among uropathogenic E. coli in children and analysis of ESBL producers from Nepal," *Antimicrobial Resistance & Infection Control*, vol. 6, p. 9, 2017, doi: 10.1186/s13756-016-0168-6.

[26] A. M. Algammal et al., "AMR patterns and virulence of emerging multidrug-resistant Edwardsiella tarda in Nile tilapia and African catfish," *Aquaculture*, vol. 548, p. 737643, 2022.

[27] N. Y. Abo et al., "The impact of antimicrobial stewardship in children in low- and middle-income countries: a systematic review," *Pediatric Infectious Disease Journal*, vol. 41, no. 3S, pp. S10–S17, 2022.