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Antimicrobial Susceptibility in Acute Myeloid Leukemia Patients in Erbil

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ABSTRACT

Patients with acute myeloid leukemia (AML) demonstrate significant sensitivity to bacterial infections. Appropriate and efficient antibiotic treatment is essential to diminish the morbidity and mortality rate of the disease. This study aimed to determine the antibacterial susceptibility profile of bacterial isolates in AML patients in Erbil City. From August 2024 to January 2025, samples were obtained from the blood, gut, and urine of 40 AML patients at Nanakali Hospital in Erbil city. Among 40 cases of AML, 49 bacteria were isolated. Gram-negative bacteria (63.27%) were more prevalent than Gram-positive bacteria (36.73%). Most Gram-negative isolates were *Escherichia coli* (34.70%) and *Klebsiella pneumoniae* (16.43%), while *Staphylococcus hominis* (10.20%) was the most common Gram-positive. Against Gram-negative isolates, colistin (100%) showed the best antibacterial action, while vancomycin and imipenem both with percentage of 100% were most successful against Gram-positive isolates. Colistin, vancomycin, and imipenem had significant efficacy, confirming their application in therapy. Continuous surveillance of resistance is essential.

Index Terms: Acute Myeloid Leukemia, Culture Media, Effectiveness, Antibiotic Susceptibility Test

1. INTRODUCTION

Acute myeloid leukemia (AML) is a severe hematologic cancer marked by an increase in the number of myeloid precursor cells in the bone marrow, leading to inefficient hematopoiesis and consequent cytopenias [1]. The disease advances quickly, and its treatment generally entails aggressive chemotherapy protocols that further weaken the immune system, making patients extremely vulnerable to opportunistic infections, especially those induced by bacterial pathogens [2]. Infections continue to be a primary cause of morbidity and mortality in AML patients, particularly during the neutropenic phase resulting from chemotherapy [3]. The impaired integrity of mucosal barriers, neutrophil dysfunction, and the recurrent use of central venous catheters create ideal conditions for microbial translocation and bloodstream infections [4]. Bacterial pathogens, including both Gram-negative and Gram-positive types, are the most common causes of infectious and often show resistance to multidrug resistance (MDR), making treatment more difficult [5]. MDR describes the ability of microorganisms, especially bacteria, to resist the effects of various structurally and functionally different antimicrobial drugs. MDR is usually defined as not responding to at least one drug from three or more different groups of antibiotics, which greatly reduces treatment options and increases morbidity, mortality, and costs associated with healthcare [6]. Bacteria acquire MDR through many molecular processes that allow them to avoid the effects of numerous antibiotics. The primary mechanisms consist of 1 - efflux pumps, bacteria utilize membrane proteins to actively expel antibiotics from the cell, hence diminishing intracellular drug concentration. 2 - Enzymatic degradation or modification, bacteria synthesize enzymes that breakdown or chemically alter antibiotics, like β-lactamases

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that degrade β-lactam drugs. 3 - Target modification bacteria modify the antibiotic's target site by mutation or enzymatic alteration, hence diminishing drug binding efficacy. 4 - Decreased permeability mutations in porin proteins diminish the outer membrane's permeability, hence limiting antibiotic penetration [7]. Gram-negative bacilli, especially *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa,* and *Acinetobacter baumannii*, have been progressively recognized in severe neutropenic phases among AML patients [8]. Conversely, Gram-positive bacteria, including *Staphylococcus aureus*, *Enterococcus* spp., and *coagulase-negative staphylococci*, are major contributors to nosocomial infections in this group of patients [9]. The regular and widespread use of broad-spectrum antibiotics in these patients has led to an increase in MDR organisms, such as extended-spectrum beta-lactamase producers and carbapenem-resistant enterobacteriaceae. [10]. Resistance to antimicrobial agents constitutes a global health issue and presents a particularly serious risk to immunocompromised individuals, including those with hematologic malignancies. Antibiotic resistance is identified as one of the principal worldwide public health problems [11]. This problem grows more severe in low- and middle-income nations, where diagnostic capabilities are limited, infection control measures are frequently insufficient, and surveillance data are poor [12]. In Iraq, particularly in the Kurdistan Region, there is an escalating concern about the high incidence of antibiotic-resistant bacterial strains; nevertheless, comprehensive regional statistics, particularly worrying for sensitive populations such as AML patients, remain scarce [13]. Recognizing local antimicrobial susceptibility patterns is essential for directing actual antibiotic treatment, particularly in high-risk patients. Numerous studies have highlighted the necessity of local surveillance to customize antimicrobial regimens efficiently, mitigate resistance development, and enhance patient outcomes [14]. Without this data, healthcare providers might continue using general treatments that could cause resistant bacteria to develop and make treatment less effective. No comprehensive studies have been undertaken in Erbil City to evaluate the variety of bacterial isolates and their antibiotic susceptibility profiles in AML patients. This study eliminates the gap by identifying bacterial infections in AML patients in Erbil City and comparing the *in vitro* efficacy of commonly utilized antibiotics, thereby providing data to inform treatment decisions, enhance care, optimize antibiotic utilization, and mitigate infection-related mortality in this high-risk population.

2. MATERIALS AND METHODS

2.1. Data and Specimen Collecting

During the period of August 2024–January 2025, three different biological samples including blood, gut (stool), and urine from the same patient were collected from 40 AML patients at Nanakali Hospital in Erbil City from both genders (19 males and 21 females) for different age groups under or equal to 90 years (≤90 years) after patients' approval. All samples were taken in sterile containers under sterile conditions. Blood specimens were collected in blood culture bottles, gut (stool) specimens were collected in sterile stool cups, while urine specimens were collected in urine specimen containers. Later, the samples were sent to the microbiology laboratory at Nanakali Hospital for the standard cultivation method process.

2.2. Detection and Identification of Isolated Bacteria

Each sample underwent a different microbiological process. They were promptly inoculated using appropriate selective and differential media (blood agar base, cetrimide agar, eosin methylene blue agar, MacConkey agar, mannitol salt agar, Mueller–Hinton agar, and nutrient agar) at a temperature of 35–37°C for 24–48 h. Gram staining was achieved. All isolated bacteria were recognized depending on their cultural characteristics and biochemical analysis, including lipase, indole, motility, oxidase, catalase, and coagulase, manually to confirm the results using the VITEK 2 Compact System.

2.3. Antimicrobial Susceptibility Test for Isolated Bacteria

Ten different antibiotics from several classes of different modes of action on all of the bacteria that were isolated – imipenem, ceftriaxone, vancomycin, clindamycin, rifampin, ciprofloxacin, levofloxacin, amikacin, gentamicin, and colistin – were used to confirm the resistance profiles of the isolates. Results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) (CLSI, 2023) recommendations after the testing was conducted on Mueller–Hinton agar using the Kirby–Bauer disk diffusion method. After that, we confirmed the results of the resistance profile using the VITEK 2 compact system. The VITEK 2 compact system facilitated automated identification and susceptibility testing, enabling a more efficient investigation of bacterial samples. This comprehensive approach not only verified resistance patterns but also enabled the finding of potential treatment options suited to handle the particular types of bacteria identified.

2.4. Approval of Ethical Guidelines and Authorization for Participation

The local Human Research Ethics Committee at the Medical Microbiology department, Health Sciences College, Hawler Medical University-Erbil has approved and allowed the whole process carried out in this research project involving human participants, human materials, or human data (Reference number 4c/132). Every technique used during the study followed the Declaration of Helsinki, as revised in 2013, and all research subjects had written informed consent for publishing.

3. RESULTS

3.1. Distribution of AML Patients According to Age and Gender

Table 1 shows the distribution of 40 cases collected from patients with AML cancer. The distribution of cases according to different age groups showed that the highest proportions of cases were 10 (25%) belonged to the 21–30-year age groups, followed by a proportion of 5 (12.5%), which was the same proportion of four different age groups including 0–10 years, 11–20 years, 31–40 years, and 71–80 years. 41–50-year age groups had the lowest proportion 2 (5%) while no cases were recorded in the 81–90-year age group. In terms of gender distribution, male cases composed 19 (47.5%) of all samples, while females accounted for 21 (52.5%), indicating a slightly higher female proportion, as shown in Table (1). Among males, the highest proportion, 7 (17.5%) was observed in the 21–30 age group, followed by the 0–10 age group, 4 (10%), whereas female cases showed that 11–20, 31–40, and 71–80 age groups each had the highest proportion, 4 (10%). No cases of either gender were recorded in the 81–90-year age groups, as in (Table 1).

3.2. Frequency of Positive and Negative Results Across Various Sample Types

Table 2 shows the frequency of culture-positive and culture-negative results from a total of 120 biological samples obtained from patients, including 40 blood samples, 40 urine samples, and 40 gut samples. A total of 55 samples (45.8%) exhibited positive cultures, signifying bacterial growth, whereas 65 samples (54.2%) demonstrated negative cultures. Among the blood samples, 19 (47.5%) exhibited bacterial growth (culture-positive), while 21 (52.5%) showed no microbial growth (culture-negative). Urine samples exhibited the highest positivity rate, with 28 out of 40 samples (70%) demonstrating microbial growth, whereas 12 samples (30%) indicated no growth. In contrast, gut samples displayed the lowest incidence of positive outcomes, with merely 8 samples (20%) indicating bacterial growth and 32 samples (80%) producing negative culture results.

3.3. Distribution of Bacterial Species across Diverse Sample Types

A total of 49 bacterial strains were recovered from 40 patients diagnosed with AML, utilizing diverse biological materials, including blood, urine, and gut. The bacterial diversity is summarized in Fig. 1. *E. coli* was the most frequently found harmful bacterium, comprising 17 (34.70%) of the total

TABLE 1: Distribution of AML patients according to age and gender

Age groups		Gender	
Time intervals	No (%)	Male-No (%)	Female-No (%)
0–10	5 (12.5)	4 (10)	1 (2.5)
11–20	5 (12.5)	1 (2.5)	4 (10)
21–30	10 (25)	7 (17.5)	3 (7.5)
31–40	5 (12.5)	1 (2.5)	4 (10)
41–50	2 (5)	2 (5)	0 (0)
51–60	4 (10)	2 (5)	2 (5)
61–70	4 (10)	1 (2.5)	3 (7.5)
71–80	5 (12.5)	1 (2.5)	4 (10)
81–90	0 (0)	0 (0)	0 (0)
Total	40 (100)	19 (47.5)	21 (52.5)

AML: Acute myeloid leukemia

TABLE 2: Frequency of positive outcomes across various sample types

Types of samples	Growth No (%)	No growth No (%)	Total No (%)
Blood	19 (47.5)	21 (52.5)	40 (100)
Urine	28 (70)	12 (30)	40 (100)
Gut	8 (20)	32 (80)	40 (100)

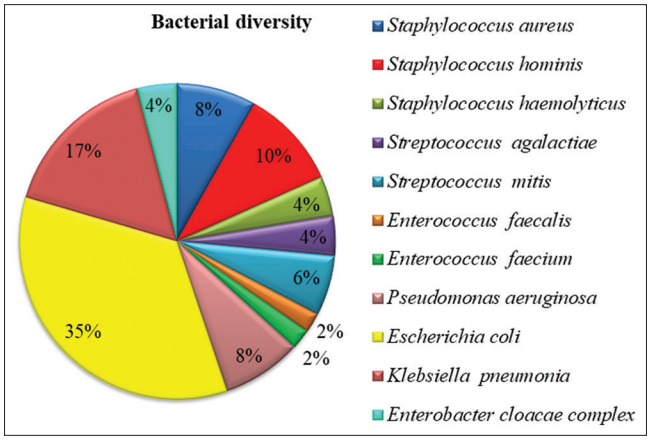

Fig. 1. Distribution of bacterial species across diverse sample types.

isolates. *K. pneumoniae* was the second most prevalent pathogen, accounting for 8 cases (16.43%), followed by *Staphylococcus hominis* with 5 cases (10.20%), and both *P. aeruginosa* and *S. aureus*, each with 4 cases (8.16%). *Streptococcus agalactiae* and *Staphylococcus haemolyticus*, both Gram-positive bacteria, were each found in 2 (4.08%) of the total isolates. *Streptococcus mitis* was identified in 3 (6.12%). *Enterococcal* species, specifically *Enterococcus faecium* and *Enterococcus faecalis*, were infrequently observed, each representing 1 (2.04%) of the isolated pathogens. Based on the distribution of bacterial isolates among biological specimens. Blood samples tested positive for several microorganisms, including *S. aureus*, *S. hominis*, *S. mitis,* and *P. aeruginosa*. Urine samples exhibited the highest prevalence of *E. coli* and *K. pneumoniae* pathogens. Gut-related samples tested positive for *E. coli* and *the Enterobacter cloacae complex*.

The pie chart shows the distribution of bacterial species isolated across the study. *E. coli* was recognized as the predominant species, followed by *K. pneumoniae* and *S. hominis*. Additional commonly isolated bacteria comprised *S. aureus*, *P. aeruginosa*, and *S. mitis*. Species found less frequently were *S. haemolyticus*, *S. agalactiae*, *E. faecium*, and *E. faecalis*, among others. The isolates include a wide spectrum of both Gram-positive and Gram-negative bacterial pathogens, underscoring the microbial diversity among the samples.

3.4. Characterization of Various Bacterial Species on Different Types of Culture Media

For microbiological research and diagnostics, bacterial isolates must be identified and characterized. The morphological and biochemical characteristics of several bacterial species are investigated in this study utilizing a variety of culture media, such as Cetrimide agar, Eosin Methylene Blue (EMB) agar, Mannitol Salt agar, MacConkey agar, and Blood agar. With different cellular structures, including clustered cocci, short chains, diplococci, and rod-shaped forms, Gram staining was used to classify the isolates as either Gram-positive or Gram-negative bacteria. *P. aeruginosa* was selectively isolated on Cetrimide agar, *E. coli* produced distinctive metallic green colonies on Eosin Methylene Blue agar, and *S. aureus* displayed β-hemolysis on Blood agar and mannitol fermentation on Mannitol Salt agar. MacConkey agar successfully distinguished lactose fermenters such as *K. pneumoniae*, *E. coli*, and Enterobacter cloacae complex which showed red or pink colonies as shown in Table 3.

3.5. Antibiotic Susceptibility Profile for Isolated Pathogenic Bacteria

The antibiotic susceptibility profile was conducted on 18 isolated Gram-positive and 31 Gram-negative bacteria to determine their sensitivity, intermediate response, and resistance to different antibiotics. The selected antibiotics were categorized based on their mechanism of action. For Gram-positive bacteria18 bacteria were isolated, the first class of antibiotics that inhibited cell wall synthesis was classified into three groups, each containing different examples. Among those, imipenem and vancomycin were both effective to all cases of Gram-positive bacteria 18 (100%). However, ceftriaxone was not effected in 17 (94.44%) cases. The second class of antibiotics targeted protein synthesis inhibition and consisted of two groups with different antibiotics. Among those, clindamycin and rifampin showed high resistance proportions of 11 (61.11%) and 16 (88.89%), respectively. The last class of antibiotics focused on the inhibition of nucleic acid synthesis. This class included only one group with two different types of antibiotics. Among them, ciprofloxacin and levofloxacin both exhibited high resistance rates, with 14 (77.78%) and 10 (55.56%) cases, respectively. However, Levofloxacin also showed a notable proportion of sensitivity in 8 (44.44%) cases, suggesting its potential as a good treatment option. These findings are shown in Table 4. A total of 31 Gram-negative bacterial isolates were tested for antibiotic susceptibility, revealing varying levels of sensitivity and resistance across different antibiotic classes. The first class of antibiotics working on the inhibition of cell wall synthesis contains two antibiotics, imipenem and ceftriaxone. Imipenem was highly sensitive in 19 (61.29%) cases while ceftriaxone showed high resistance, with 28 (90.32%) cases being resistant. For the second class, which was inhibition of protein synthesis, aminoglycosides were used. This group contains two antibiotics, amikacin and gentamicin. Both antibiotics had the same resistance rate of 7 (22.58%) cases. Gentamicin was highly sensitive in 24 (77.42%) cases, whereas amikacin showed lower sensitivity in comparison. Another class was the disruption of the cell membrane which contained only one group. Polymyxin E like colistin was tested and showed no resistance, indicating 100% sensitivity. The last class was the inhibition of nucleic acid synthesis. Fluoroquinolones and ciprofloxacin exhibited high resistance in 29 (93.55%) cases; levofloxacin showed high sensitivity in 19 (61.29%) cases. These findings shown in Table 5 suggest that imipenem, gentamicin, polymyxin E, and levofloxacin may be more effective treatments.

3.6. Antibiotic Resistance in Isolated Pathogenic Bacterial Strain

The antibiotic resistance profile of 11 different bacterial species was estimated against a total of 10 antibiotics. The results indicate varying resistance levels among different isolates. *S. aureus* and *K. pneumoniae* exhibited the highest

TABLE 3: Characterization of various bacterial species on different types of culture media

Cetrimide agar	Mannitol salt agar	Eosin methylene blue	Nutrient agar	MacConkey agar	Blood agar	Gram stain	Cell morphology	Isolated bacteria
N. G	Round, creamy to golden, media yellow	N. G	Round, golden yellow, or creamy	N. G	Round, golden yellow β-hemolysis	G +ve	Cocci in cluster	*Staphylococcus aureus*
N. G	Round, white to off white media pink	N. G	Round, white to creamy	N. G	Round, off white, gamma hemolysis	G +ve	Cocci in cluster	*Staphylococcus hominis*
N. G	Round, white to creamy media pink	N. G	Round, creamy, or off white	N. G	Round, off white, β-hemolysis	G +ve	Cocci in cluster	*Staphylococcus haemolyticus*
N. G	N. G	N. G	Round, off white or grayish	N. G	Round, creamy, or grayish, β-hemolysis	G +ve	Diplococci short chain	*Streptococcus agalactiae*
N. G	N. G	N. G	Round, smooth, grayish	N. G	Round, off white, γ-hemolysis	G +ve	Cocci, chain	*Streptococcus mitis*
N. G	N. G	N. G	Round, gray, or cream color	N. G	Round, off white, γ-hemolysis	G +ve	Cocci, diplococcic (Pair)	*Enterococcus faecium*
N. G	N. G	N. G	Round, creamy, or grayish	N. G	Round, grayish γ-hemolysis	G +ve	Cocci, diplococci (Pair)	*Enterococcus faecalis*
Moist, smooth, greenish-blue, metallic sheen	N. G	Smooth, off white, slight sheen	Round, greenish	Smooth, round, green	Round, green, or greenish blue, γ-hemolysis	G -ve	Bacillus, single rods	*Pseudomonas aeruginosa*
N. G	N. G	Smooth, moist, greenish metallic sheen	Round, moist creamy, or grayish	Smooth, moist, pink or red	Round, off white, γ-hemolysis	G -ve	Bacillus, single rods or chain	*Escherichia coli*
N. G	N. G	Mucoid, dark pink or purple with metallic sheen	Mucoid, off white or grayish	Large moist, mucoid, pink or red	Mucoid, creamy, off-white hemolysis	G -ve	Bacillus, single rods or chain	*Klebsiella pneumoniae*
N. G	N. G	Smooth, moist, light pink	Moist, creamy, or off white	Large moist, off white to pink	Smooth, pale yellow, γ- hemolysis	G -ve	Bacillus, short chain or rods	*Enterobacter cloacae complex*

G+ve: Gram positive, G –ve: Gram negative, N.G: No growth, β-hemolysis: Beta hemolysis, γ-hemolysis: Gamma hemolysis

TABLE 4: Antibiotic susceptibility profile for isolated pathogenic Gram-positive bacteria

Classification according to the mechanism of action	Groups	Antibiotics	Interpretation		
			Sensitive (%)	Inter-mediate (%)	Resistance (%)
Inhibition of cell wall synthesis	Beta-lactam (carbapenem)	Imipenem	18 (100)	/	/
	Beta-lactam (cephalosporin)	Ceftriaxone	1 (5.56)	/	17 (94.44)
	Glycopeptide	Vancomycin	18 (100)	/	/
Inhibition of protein synthesis	Lincosamides	Clindamycin	7 (38.89)	/	11 (61.11)
	Rifamycin	Rifampin	2 (11.11)	/	16 (88.89)
Inhibition of nucleic acid synthesis	Fluoroquinolones	Ciprofloxacin	/	4 (22.22)	14 (77.78)
	Fluoroquinolones	Levofloxacin	8 (44.44)	/	10 (55.56)

Number of Gram-positive bacteria=18

TABLE 5: Antibiotic susceptibility profile for isolated pathogenic Gram-negative bacteria

Classification according to the mechanism of action	Groups	Antibiotics	Interpretation		
			Sensitive (%)	Inter-mediate (%)	Resistance (%)
Inhibition of cell wall synthesis	Beta-lactam (Carbapenem)	Imipenem	19 (61.29)	1 (3.23)	11 (35.48)
	Beta-lactam (cephalosporin)	Ceftriaxone	3 (9.68)	/	28 (90.32)
Inhibition of protein synthesis	Aminoglycoside	Amikacin	21 (67.74)	3 (9.68)	7 (22.58)
	Aminoglycoside	Gentamicin	24 (77.42)	/	7 (22.58)
Disruption of cell membrane	Polymyxin E	Colistin	31 (100)	/	
Inhibition of nucleic acid synthesis	Fluoroquinolones	Ciprofloxacin	2 (6.45)	/	29 (93.55)
	Fluoroquinolones	Levofloxacin	19 (61.29)	/	12 (38.71)

Number of Gram-negative bacteria=31

resistance, with 6 out of 10 antibiotics (60%) showing ineffectiveness. *S. hominis*, *S. mitis*, *E. faecium*, *E. coli*, and *Enterobacter cloacae* demonstrated resistance to 5 antibiotics (50%). *Staphylococcus haemolyticus* and *P. aeruginosa* showed intermediate resistance, with 4 antibiotics (40%) being ineffective. *S. agalactiae* and *E. faecalis* exhibited the lowest resistance rates, with only 3 antibiotics (30%) showing ineffectiveness. This was indicated for multidrug-resistant bacteria; most of those bacteria were resistant to more than three antibiotics. This is all summarized in Table 6.

TABLE 6: Antibiotic resistance in isolated pathogenic bacterial strain

Isolated bacteria	Number of antibiotic resistances (Total number of antibiotics=10) (%)
Staphylococcus aureus	6 (60)
Staphylococcus hominis	5 (50)
Staphylococcus haemolyticus	4 (40)
Streptococcus mitis	5 (50)
Streptococcus agalactiae	3 (30)
Enterococcus faecium	5 (50)
Enterococcus faecalis	3 (30)
Escherichia coli	5 (50)
Pseudomonas aeruginosa	4 (40)
Klebsiella pneumoniae	6 (60)
Enterobacter cloacae	5 (50)

4. DISCUSSION

This study's findings offer essential insights into the antimicrobial susceptibility patterns of AML patients in Erbil, Iraq, while also emphasizing significant similarities with global antimicrobial resistance trends. The significant frequency of Gram-negative bacteria (63.27%), especially *E. coli* (34.70%) and *K. pneumoniae* (16.43%), reflects trends noted in other areas where these pathogens predominantly cause infections in immunocompromised individuals. A multicenter European investigation showed analogous data, indicating that Enterobacteriaceae constituted 58% of bloodstream infections in patients with hematological malignancies [8]. The prevalence of these organisms likely indicates their capacity to inhabit the gastrointestinal tract and translocate after mucosal damage generated by chemotherapy, a feature well-documented in neutropenic patients [3]. The prevalence of Gram-positive isolates is 36.73%, with *S. hominis* at 10.20%, consistent with U.S. hospital findings indicating that *coagulase-negative staphylococci* comprised 31% of nosocomial bloodstream infections in cancer patients. The prevalence of *P. aeruginosa* (8.16%) is particularly alarming because of its inherent resistance mechanisms and correlation with adverse outcomes in neutropenic individuals. This discovery aligns with Italian data indicating that *P. aeruginosa* is the etiological agent in 12% of Gram-negative infections inside hematological units [15]. The antibiotic resistance patterns identified in this study indicate both regional particularities and global alarming tendencies. The notably elevated resistance to ceftriaxone (90.32% in Gram-negative isolates) surpasses the rates documented in adjacent Middle Eastern nations, where resistance to third-generation cephalosporins varies from 60% to 75% [13]. The ciprofloxacin resistance incidence of 93.55% significantly exceeds the 65% reported in Chinese hematological centers [16]. Potentially indicating variations in antibiotic prescribing policies and infection control protocols. The total sensitivity to colistin (100%) and the significant efficiency of imipenem (61.29%) against Gram-negative isolates align with findings from European studies, where these antibiotics are considered last-resort choices [17]. The 35.48% resistance to imipenem is concerning and exceeds the 15–20% resistance rates documented in Western Europe, indicating the emergence of carbapenem resistance in our region that requires urgent attention. The 100% susceptibility of Gram-positive isolates to vancomycin and imipenem is promising and aligns with global trends, since these antibiotics continue to be fundamental in managing resistant Gram-positive infections [6]. The elevated resistance rates to rifampin (88.89%) and ciprofloxacin (77.78%) indicate

the repercussions of extensive prophylactic usage, akin to trends noted in Indian cancer centers, where fluoroquinolone resistance escalated to 80% after the introduction of routine prophylaxis [12]. The patterns of MDR are notably concerning, since 60% of *S. aureus* and *K. pneumoniae* isolates exhibit resistance to six or more classes of antibiotics. This surpasses the 40–50% MDR rates documented in Turkish hematological patients [5] and nears the 70% resistance shown in certain Indian studies [12]. situating our region among those with the most acute resistance challenges worldwide. Various causes may contribute to these concerning resistance patterns. The absence of effective antimicrobial stewardship programs in Iraqi hospitals, along with the accessibility of over-the-counter antibiotics, undoubtedly contributes to the misuse of antibiotics [13]. Moreover, the scarcity of infection management resources in our environment may promote the propagation of resistance strains, as evidenced in other resource-limited settings [12]. The elevated incidence of extended-spectrum β-lactamase-producing Enterobacteriaceae, indicated by ceftriaxone resistance rates, aligns with global patterns but is more pronounced in our location. These findings possess significant clinical ramifications. The elevated resistance rates to frequently employed antibiotics such as ceftriaxone and ciprofloxacin indicate that they should be discontinued for empirical usage in our context. Treatment guidelines ought to account for local resistance trends, potentially prioritizing combination therapy or novel medicines when accessible. The sustained efficacy of colistin, however promising, prompts apprehension over the necessity of increased utilization of this last-resort antibiotic, thereby hastening the emergence of resistance [17]. The study's shortcomings comprise its single-center methodology and limited sample size, potentially impacting generalizability. The absence of molecular characterization of resistance mechanisms hinders a comprehensive knowledge of resistance transmission patterns. Subsequent research should integrate genomic techniques to pinpoint individual resistance genes and clonal affiliations, as demonstrated in European institutions [18].

This study indicates significantly elevated antibiotic resistance rates among AML patients in Erbil, surpassing other international reports. The results highlight the critical necessity for extensive antimicrobial stewardship initiatives, improved infection control protocols, and investment in swift diagnostic technologies. Given the substantial regional variation in resistance patterns, our findings underscore the necessity of local surveillance to inform treatment plans. The circumstances necessitate prompt measures to conserve the remaining effective antibiotics and avert a post-antibiotic era in hematological malignancies.

5. CONCLUSION

This study highlights the bacterial diversity and antibiotic resistance in AML patients in Erbil. *E. coli* and *K. pneumoniae* were the most common isolates. High resistance to ceftriaxone, ciprofloxacin, and rifampin was observed, while colistin, imipenem, and vancomycin remained effective. The findings stress the need for local antimicrobial stewardship, regular surveillance, and improved infection control. In the absence of national data, this research fills a critical gap and calls for molecular studies to guide future treatment and policy.

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