

Article

Antimicrobial Resistance, Bacterial Pathogens, and Risk Factors for Multidrug-Resistant Hospital-Acquired Infections in Erbil City, Iraq

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Abstract:

Background: Hospital-acquired infections (HAIs) caused by multidrug resistant (MDR) bacteria are a major public health problem especially in resource-limited settings. Local data on antimicrobial resistance (AMR) are crucial to inform empirical therapy and infection prevention. **Objectives:** To identify bacterial pathogens causing HAIs, determine their AMR profiles and independent risk factors for MDR infections in a tertiary hospital in Erbil City, Iraq. **Materials and Methods:** A cross-sectional study was done at Hawler Teaching Hospital between January and June 2026. Standard microbiological methods were used to analyse 200 clinical specimens from patients with HAIs (≥48 hr after admission). Antimicrobial susceptibility testing was performed according to CLSI 2024 guidelines. MDR was defined as nonsusceptibility to at least one agent in three or more antimicrobial classes. Multivariate logistic regression was used to assess independent risk factors. **Results:** Bacterial growth was obtained in 149 of 200 specimens (74.5%). The major pathogens were *Escherichia coli* (31.5%), *Klebsiella pneumoniae* (23.5%), *Staphylococcus aureus* (21.5%), *Pseudomonas aeruginosa* (14.1%) and *Acinetobacter baumannii* (6.1%). In total, 69.1% of the isolates were MDR, with the highest rates in *K. pneumoniae* (80.0%) and *A. baumannii* (77.8%). Independent predictors of MDR infection were previous antibiotic use (AOR=4.45), ICU admission (AOR=3.92), and hospitalization >7 days (AOR=3.10). **Conclusion:** This study documented a significant burden of MDR-HAIs in Erbil City and determined modifiable clinical risk factors. The findings provide evidence to support antimicrobial stewardship, infection prevention and AMR surveillance in Iraqi healthcare settings.

Keywords: Hospital-Acquired Infections; Multidrug Resistance; Antimicrobial Resistance; Epidemiology; Infection Prevention; Iraq

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1. Introduction

Antimicrobial resistance (AMR) is one of the most serious threats to global public health in the twenty-first century. AMR has been declared a priority health crisis by the World Health Organization (WHO) and present projections estimate that drug-resistant infections could cause up to 10 million deaths per year by 2050 if present trajectories persist [1]. The most clinically important manifestations of AMR include hospital-acquired infections (HAIs), or nosocomial infections, which are defined as infections that are not present at the time of admission to the hospital and that develop after 48 hr. of hospitalization [2]. HAIs caused by multidrug resistant (MDR) organisms are associated with significant morbidity, mortality, increased hospital stay and increasing healthcare costs all over the world [1].

In high-income countries, deliberate actions such as antibiotic stewardship programs (ASPs), strict surveillance systems, and infection control protocols have resulted in measurable decreases in HAI rates [3]. However, the epidemiology of HAIs and the related AMR patterns are poorly characterized in low- and middle-income countries (LMICs) in the Middle East and North Africa (MENA) region, and the burden is still rising [4]. In this landscape Iraq and more specifically the Kurdistan Region is an under researched context. Prolonged conflict, damage to infrastructure, lack of resources and limited laboratory capacity have severely disrupted the country's health system and created conducive conditions for the emergence and spread of MDR pathogens [5].

Recent data from local Iraqi institutions point to disproportionately high resistance rates among the usual nosocomial suspects: *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*, often exceeding the rates reported by neighboring countries [6, 7]. More worryingly, carbapenem-resistant Enterobacteriaceae (CRE) and carbapenem-resistant *A. baumannii* (CRAB) are increasingly reported in Iraqi hospitals, signaling a shift towards pan-drug resistance paradigms and a significant narrowing of treatment options [8]. While the Kurdistan Region of Iraq is relatively more politically stable, it suffers from similar issues with scant local epidemiological data on HAI microbiology and AMR profiles, thus representing a critical knowledge gap.

The novelty of the present study is multi-dimensional: (i) it is one of the first comprehensive, cross-sectional microbiological surveys of HAIs from a major tertiary referral center in Erbil City, Kurdistan Region of Iraq; it includes contemporaneous (2026) AMR data on a broad panel of 16 antimicrobial agents covering all major drug classes; it quantifies MDR rates in seven bacterial species using validated CLSI-2024 criteria; and (iv) it applies multivariate logistic regression to rigorously identify independent clinical risk factors for MDR, providing actionable data for local clinicians and infection control practitioners. Locally relevant, high quality microbiological surveillance data generation is the key to guiding empirical antibiotic prescribing, updating hospital formularies and informing national AMR action plans in Iraq.

The primary objectives of this study were: (1) to determine the bacteriological spectrum of HAIs at a major tertiary care hospital in Erbil City, Iraq; (2) to assess the antimicrobial susceptibility profiles of identified pathogens against a comprehensive antibiotic panel; (3) to determine MDR rates by bacterial species; and (4) to identify demographic and clinical risk factors independently associated with MDR infections.

2. Materials and Methods

2.1. Study Design and Ethical Considerations

This cross-sectional observational study was conducted in accordance with the Declaration of Helsinki. The study protocol was approved by the Institutional Review Board (IRB) of the General Directorate of Health - Erbil, Kurdistan Region, Iraq (Approval No.: 216; 25 January 2026). Written informed consent was obtained from all participating patients or their legal guardians. Patient confidentiality was maintained throughout the study by anonymizing all data.

2.2. Study Setting

The study was conducted at Hawler Teaching Hospital in Erbil City, Kurdistan Region of Iraq, which is a major tertiary referral center serving a catchment population from all parts of Erbil governorate and its surrounding areas. The hospital houses inpatient wards for different medical and surgical specialties. These include a dedicated Intensive Care Unit (ICU), surgical wards, internal medicine and nephrology. It is one of the main referral centers for critically ill patients in the Kurdistan region.

2.3. Study Period and Sample Size

Data and specimens were collected prospectively for six months (January 2026 to June 2026). During the study period, a total of 200 clinical bacterial isolates were collected from patients diagnosed with HAIs. The sample size was calculated using the formula for cross-sectional studies with an estimated prevalence of MDR of 60% from previous Iraqi data [7] at 95% confidence level and 7% margin of error giving a minimum sample size of 188; 200 samples were collected to allow for any possible exclusions.

2.4. Inclusion and Exclusion Criteria

Patients were included if they: (i) were admitted for ≥ 48 hours prior to infection manifestation; had clinical signs and symptoms consistent with infection (fever, elevated white cell count, localized signs); and had a culture-positive specimen. Patients were excluded if: (i) infections were present at the time of admission (community-acquired); they were aged < 1 year; clinical data were incomplete.

2.5. Specimen Collection

Clinical specimens were collected by trained nursing and laboratory personnel using aseptic technique. Specimen types included midstream urine samples, wound swabs (superficial and deep), blood cultures (taken before antibiotic administration where possible), expectorated or tracheal aspirate sputum samples and catheter tip cultures. All specimens were taken to the hospital microbiology laboratory within 2 hours of collection and processed immediately on receipt.

2.6. Bacterial Identification

Specimens were inoculated on to appropriate selective and differential culture media including Blood Agar, MacConkey Agar, Mannitol Salt Agar (for *Staphylococci*) and Chocolate Agar (for fastidious organisms). Cultures were grown aerobically at 37°C for 24–48 hours. Standard microbiological methods were used for bacterial identification; colony morphology, Gram staining and conventional biochemical tests (catalase, coagulase, oxidase, urease, indole, citrate, triple sugar iron [TSI] and API identification systems [bioMérieux]).

2.7. Antimicrobial Susceptibility Testing (AST)

Antimicrobial susceptibility testing (AST) was performed on Mueller–Hinton agar by the disk diffusion method (Kirby–Bauer) in accordance with CLSI 2024 guidelines [9]. We tested sixteen antimicrobial agents that represented seven major classes: penicillins, cephalosporins, β -lactam/ β -lactamase inhibitor combinations, carbapenems, aminoglycosides, fluoroquinolones, folate pathway inhibitors, and polymyxins. Inhibition zones were interpreted as susceptible, intermediate or resistant according to CLSI criteria. Quality control was carried out using *Escherichia coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853 and *Staphylococcus aureus* ATCC 25923. MDR and XDR were defined according to the international consensus criteria proposed by Magiorakos *et al.* [10], with MDR indicating non-susceptibility to at least one agent in three or more antimicrobial classes, and XDR indicating non-susceptibility to all but two or fewer antimicrobial classes.

2.8. Data Collection

Data were collected using a structured, pre-tested data collection instrument. Variables recorded included: (A) Demographic data: age, sex, and place of residence (urban/rural); (B) Clinical variables: ICU admission (yes/no), total duration of hospital stay, prior antibiotic exposure (within the preceding 30 days), use of invasive devices (urinary catheters, central venous catheters, mechanical ventilators), history of surgical intervention, and presence of underlying chronic comorbidities (diabetes mellitus, chronic renal failure, chronic obstructive pulmonary disease, malignancy, or

immunosuppression); (C) Microbiological variables: specimen type, bacterial species identified, and complete AST profiles.

2.9. Statistical Analysis

Data were analyzed using IBM SPSS Statistics version 27 (IBM Corp., Armonk, NY, USA). Categorical variables were summarized as frequencies and percentages. Associations were assessed using the Chi-square or Fisher's exact test, as appropriate. Variables with $p < 0.20$ in bivariate logistic regression were included in a multivariate binary logistic regression (forced entry) to identify independent predictors of MDR. Results are presented as adjusted odds ratios (AORs) with 95% confidence intervals (CIs), and $p < 0.05$ was considered statistically significant.

3. Results

3.1. Distribution of Clinical Specimens

A total of 200 clinical specimens were obtained from 200 patients with HAIs. Urine samples were the most common specimens ($n = 80$; 40.0%), followed by wound swabs ($n = 50$; 25.0%), blood cultures ($n = 30$; 15.0%), sputum ($n = 25$; 12.5%), and catheter tip cultures ($n = 15$; 7.5%) (Table 1). The distribution of specimen types was statistically significant (Chi-square goodness-of-fit test = 54.8, $p < 0.001$ for specimen type distribution; Chi-square = 6.74, $p = 0.150$ for growth rate differences between specimen types.) reflecting the predominance of urinary tract as the most common site of HAI, consistent with global epidemiological pattern.

Table 1. Distribution and Bacterial Growth Rate of Clinical Specimens Collected from Patients with Hospital-Acquired Infections ($n = 200$)

Specimen Type	Total Samples n (%)	Positive Growth n	Growth Rate (%)
Urine	80 (40.0%)	59	73.8
Wound swabs	50 (25.0%)	43	86.0
Blood cultures	30 (15.0%)	20	66.7
Sputum	25 (12.5%)	16	64.0
Catheter tips	15 (7.5%)	11	73.3
Total	200 (100.0%)	149	74.5

Chi-square goodness-of-fit test = 54.8, $p < 0.001$

3.2. Demographic Characteristics

Of the 200 patients included, 118 (59.0%) were male and 82 (41.0%) were female, with a statistically significant sex distribution ($p = 0.011$). The mean age of participants was 48.6 ± 17.2 years. The largest age group was ≥ 60 years ($n = 47$; 23.5%), followed by the 50–59 years group ($n = 42$; 21.0%). The age distribution was statistically significant ($p = 0.003$). The majority of patients were from urban areas ($n = 142$; 71.0%) compared to rural areas ($n = 58$; 29.0%; $p < 0.001$), reflecting the largely urban referral base of the tertiary referral hospital. Complete demographic data are presented in Table 2.

Table 2. Demographic and Clinical Characteristics of Patients with Hospital-Acquired Infections (n = 200)

Variable	Category	Frequency (n)	Percentage (%)	P-value
Demographic characteristics				
Gender	Male	118	59.0	0.011
	Female	82	41.0	
Age group (years)	<20	19	9.5	0.003
	20–29	32	16.0	
	30–39	27	13.5	
	40–49	33	16.5	
	50–59	42	21.0	
	≥60	47	23.5	
Residence	Urban	142	71.0	<0.001
	Rural	58	29.0	
Clinical characteristics				
ICU admission		86	43.0	
Hospital stay >7 days		112	56.0	
Previous antibiotic exposure		124	62.0	
Catheter use		95	47.5	
Surgical intervention		68	34.0	
Chronic disease		104	52.0	

Mean age: 48.6 ± 17.2 years. Chi-square goodness-of-fit test = 31.2, $p < 0.001$ for overall clinical characteristics distribution.

3.3. Clinical Characteristics

The most common clinical risk factor was prior antibiotic exposure ($n = 124$; 62.0%), followed by prolonged hospital stay >7 days ($n = 112$; 56.0%), chronic disease comorbidity ($n = 104$; 52.0%), catheter use ($n = 95$; 47.5%), ICU admission ($n = 86$; 43.0%), and surgical intervention ($n = 68$; 34.0%). The distribution of the overall clinical profile was statistically significant ($p < 0.001$), as shown in [Table 2](#).

3.4. Bacterial Culture Positivity and Species Distribution

E. coli was the most common pathogen overall (47/149; 31.5%) and the leading uropathogen (34/59; 57.6%). *K. pneumoniae* was the most common organism isolated from sputum (7/16; 43.8%) and blood cultures (6/20; 30.0%), consistent with its role in respiratory and bloodstream HAIs. The most frequent wound pathogen was *S. aureus* (17/43; 39.5%). *A. baumannii* was isolated only from blood, wound and sputum specimens. None of the isolates were from catheter tips ($p < 0.001$ for overall distribution).

3.5. Antimicrobial Resistance Profile

The complete AMR profiles of all seven bacterial species against 16 antimicrobial agents are shown in [Table 3](#). Resistance to ampicillin was virtually universal among all isolates (82–100%), whereas resistance to amoxicillin-clavulanic acid ranged between 70% (*P. mirabilis*) and 95% (*A. baumannii*). Resistance rates for third generation cephalosporins (Ceftriaxone) were 60–88%, which confirms widespread ESBL (Extended-Spectrum Beta-Lactamase) production. Imipenem resistance was lowest among *E. coli* (18%) and meropenem (15%), but alarmingly high in *A. baumannii* (55 and 50%) indicating carbapenem resistant *A. baumannii* (CRAB). Colistin remained the most active agent with resistance rates of 2–25% among susceptible gram-negative organisms. The inter-species differences in resistance patterns were statistically significant (Chi-square, $p < 0.001$).

Table 3. Antimicrobial Resistance Profile (%) of Bacterial Isolates from Hospital-Acquired Infections

Antibiotic	<i>E. coli</i>	<i>K. pneumoniae</i>	<i>S. aureus</i>	<i>P. aeruginosa</i>	<i>A. baumannii</i>	<i>E. cloacae</i>	<i>P. mirabilis</i>
Ampicillin	88%	92%	100%	100%	100%	95%	82%
Amox/Clav	75%	80%	85%	90%	95%	78%	70%
Cefazolin	78%	85%	90%	88%	92%	80%	74%
Cefuroxime	70%	78%	88%	85%	90%	72%	65%
Ceftriaxone	65%	75%	85%	80%	88%	68%	60%
Ceftazidime	60%	70%	80%	75%	85%	65%	55%
Cefepime	35%	45%	60%	55%	70%	40%	30%
Pip/Tazo	30%	40%	55%	50%	65%	35%	25%
Imipenem	18%	25%	5%	30%	55%	22%	15%
Meropenem	15%	20%	5%	28%	50%	18%	12%
Amikacin	20%	30%	10%	35%	40%	22%	18%
Gentamicin	45%	55%	40%	50%	65%	48%	42%
Ciprofloxacin	60%	70%	45%	65%	75%	62%	55%
Levofloxacin	55%	65%	40%	60%	70%	58%	50%
TMP/SMX	70%	78%	50%	75%	85%	72%	68%
Colistin	2%	5%	—	10%	25%	8%	6%

Amox/Clav = Amoxicillin/Clavulanic acid; Pip/Tazo = Piperacillin/Tazobactam; TMP/SMX = Trimethoprim/Sulfamethoxazole; — = Not applicable (intrinsic resistance or not testable). Chi-square, $p < 0.001$ for inter-species resistance differences.

3.6. Multidrug Resistance Distribution

Out of 149 culture positive isolates, 103 (69.1%) were found to be MDR as per the criteria (Table 4). The highest MDR rate was detected in *K. pneumoniae* (28/35; 80.0%) followed by *A. baumannii* (7/9; 77.8%), *E. coli* (32/47; 68.0%), *P. aeruginosa* (14/21; 66.7%), *E. cloacae* (2/3; 66.7%), *S. aureus* (19/32; 59.4%), and *P. mirabilis* (1/2; 50.0%). The trend in MDR rates differed significantly among species ($p < 0.001$).

Table 4. Distribution of Multidrug-Resistant (MDR) Isolates by Bacterial Species (n = 149)

Bacterial Species	Total Isolates	MDR (n)	MDR (%)	Non-MDR (n)	P-value
<i>Escherichia coli</i>	47	32	68.0%	15	
<i>Klebsiella pneumoniae</i>	35	28	80.0%	7	
<i>Staphylococcus aureus</i>	32	19	59.4%	13	
<i>Pseudomonas aeruginosa</i>	21	14	66.7%	7	
<i>Acinetobacter baumannii</i>	9	7	77.8%	2	
<i>Enterobacter cloacae</i>	3	2	66.7%	1	
<i>Proteus mirabilis</i>	2	1	50.0%	1	
Total	149	103	69.1%	46	<0.001

MDR = Multidrug-Resistant

3.7. Risk Factors for MDR – Multivariate Analysis

Results of the multivariate logistic regression analysis are detailed in Table 5. After adjusting for all covariates, prior antibiotic use was the strongest independent predictor of MDR infection (AOR = 4.45; 95% CI: 2.10–9.42; $p < 0.001$), followed by ICU admission (AOR = 3.92; 95% CI: 1.85–8.31; $p < 0.001$), prolonged hospital stay >7 days (AOR = 3.10; 95% CI: 1.60–6.01; $p = 0.001$), catheter use (AOR = 2.35; 95% CI: 1.18–4.68; $p = 0.015$), and chronic disease (AOR = 1.88; 95% CI: 1.02–3.45; $p = 0.041$). Age ≥ 60 years did not reach statistical significance on multivariate analysis (AOR = 1.72; 95% CI: 0.95–3.11; $p = 0.072$).

Table 5. Multivariate Logistic Regression Analysis of Risk Factors Associated with MDR Infections

Variable	Adjusted OR	95% Confidence Interval	P-value
ICU admission	3.92	1.85 – 8.31	<0.001
Hospital stay >7 days	3.10	1.60 – 6.01	0.001
Prior antibiotic use	4.45	2.10 – 9.42	<0.001
Catheter use	2.35	1.18 – 4.68	0.015
Chronic disease	1.88	1.02 – 3.45	0.041
Age ≥60 years	1.72	0.95 – 3.11	0.072

AOR = Adjusted Odds Ratio; CI = Confidence Interval. Reference category = absence of the respective risk factor.

4. Discussion

The present cross-sectional microbiological study provides important and timely data on the bacteriological spectrum of HAIs and the alarming scale of AMR in a major tertiary care hospital in Erbil City, Kurdistan Region of Iraq. The major findings were a culture positivity rate of 74.5%, a high overall MDR prevalence of 69.1%, high resistance to ampicillin and broad-spectrum cephalosporins, emerging carbapenem resistance in Gram-negative organisms (especially *A. baumannii*), and the identification of prior antibiotic use, ICU admission and prolonged hospitalization as the leading independent risk factors for MDR.

The most common isolated bacterial isolate in this study was *Escherichia coli* (31.5%) which was in agreement with previous reports from Iraq. Mohammed *et al.* [11] reported that *E. coli* was the most frequent uropathogen in Baghdad, representing nearly one third of the urinary isolates. Also, Jalil and Al Atbee [12] reported that *E. coli* and *K. pneumoniae* were the most frequently isolated Gram-negative pathogens in urinary tract infections in Basra. A study conducted in the Kurdistan region of Iraq, also demonstrated that *E. coli* was the most common urinary pathogen isolated in long term surveillance of urine cultures in Erbil hospitals, supporting the results of the current study [13].

The overall culture positivity rate in the present study was 74.5% which is similar to that reported from tertiary-care hospitals in the Middle East. National HAI surveillance data from Saudi Arabia demonstrated a high burden of healthcare-associated infections across tertiary hospitals [14]. Similarly, studies from Turkey reported similar microbiological features and pathogen distribution in nosocomial infections [15]. Collectively, these findings support the consistency of our microbiological findings with those reported in regional healthcare settings.

The prevalence of MDR in the present study was 69.1%, suggesting a considerable burden of antimicrobial resistance that is higher than previously reported rates in high-income countries. The European Centre for Disease Prevention and Control surveillance indicates that the overall burden of multidrug-resistant pathogens is lower than in the present study [16], although antimicrobial resistance still poses a major public health problem in European hospitals. Likewise, in the Middle East and North Africa, Yang *et al.* found the highest global pooled prevalence of multidrug-resistant organisms (63.9%; 95% CI: 46.6–81.2%) [3]. These results are consistent with earlier reports from Iraqi hospitals showing high antimicrobial resistance among nosocomial Gram-negative pathogens [6].

The high prevalence of MDR *Klebsiella pneumoniae* (80.0%) in the present study is alarming and reflects the burden of antimicrobial resistance increasingly in the region. Similar findings have been reported in Iraq where studies from Erbil and Kirkuk documented widespread multidrug resistance including carbapenem resistance, and dissemination of resistance-associated genes in *K. pneumoniae* [17, 18]. The carbapenem resistance rate in the present study (20–25%) was lower than that in high-endemic

countries such as Greece. However, recent evidence suggests that carbapenem-resistant *K. pneumoniae* is still a major global health challenge [19].

The most prevalent resistance pattern was carbapenem-resistant *Acinetobacter baumannii* (50–55%), consistent with the high burden reported in Middle Eastern hospitals. Similar results have been reported in Pakistan and Algeria where widespread carbapenem-resistant, carbapenemase-producing and colistin-resistant *A. baumannii* isolates were reported [20, 21]. Carbapenem-resistant *A. baumannii* carrying *bla*OXA-23 belonging to global clones 1 and 2 have also been described in Iraq [22]. OXA-23-like and OXA-24/40-like carbapenemases are considered as important mechanisms of carbapenem resistance worldwide [23].

The results of low levels of colistin resistance (2–25%) in Gram negative bacteria are encouraging and are consistent with reports from neighbouring countries. Low resistance in *Escherichia coli* and *Klebsiella pneumoniae* but much higher rates in *Acinetobacter baumannii* have been reported in previous studies [24]. Despite the development of resistance, colistin remains an important treatment option for MDR Gram negative infections. Resistance in 25 % of *A. baumannii* is a clinical concern and highlights the need for continued antimicrobial stewardship and surveillance.

Our findings are consistent with previous studies identifying prior antibiotic exposure as a major modifiable risk factor for MDR healthcare-associated infections. Prior antibiotic use was an independent predictor of MDR Gram-negative infections in Saudi Arabia (OR = 5.50) [25] and of healthcare-associated MDR *Klebsiella pneumoniae* infections among ICU patients [26]. These findings are consistent with the role of antibiotic selective pressure in the emergence and persistence of MDR pathogens.

ICU admission was found to be an independent risk factor for MDR infection (AOR = 3.92) probably because of intensive exposure to antibiotics, frequent use of invasive devices, critical illness, and a greater opportunity for cross-transmission of resistant pathogens. These results are in line with a recent multicenter study from Tunisia, which also found ICU admission as an independent predictor of MDR healthcare-associated infections (AOR = 3.61) [27].

Duration of hospital stay >7 days (AOR = 3.10) and urinary catheter use (AOR = 2.35) were significant independent predictors of MDR infection in the present study. These findings are consistent with multinational prospective studies demonstrating that prolonged hospitalization and urinary catheter utilization are major risk factors for healthcare-associated infections and supporting the implementation of catheter bundle protocols and early removal of invasive devices to reduce infection risk [28].

There are several strengths of the present study, including the utilization of a validated standardized methodology (Kirby-Bauer/CLSI 2024), a comprehensive 16-antibiotic panel, rigorous multivariate analysis, and to our knowledge, the most comprehensive HAI-focused AMR survey from the Erbil-Kurdistan Region published to date. Limitations include single-center design limiting generalizability, absence of molecular resistance characterization (ESBL, carbapenemase genotyping), cross-sectional methodology precluding causal inference, and possible selection bias from only culture-positive cases. Further multicenter studies on molecular epidemiology and whole-genome sequencing are needed to fully characterize AMR mechanisms in the Kurdistan Region.

5. Conclusions

This study demonstrated a high burden of MDR hospital-acquired infections in a tertiary care hospital in Erbil City, Kurdistan Region of Iraq, with an overall prevalence of 69.1%. Gram-negative pathogens predominated (*K. pneumoniae*, *E. coli*, *P. aeruginosa*, and *A. baumannii*) with high levels of resistance to aminopenicillins, cephalosporins and fluoroquinolones; *A. baumannii* was emerging carbapenem resistant. Carbapenems and colistin remained the most active agents, while the main modifiable risk factors included

prior use of antibiotics, ICU admission and long hospital stay. The results emphasize the critical need for strategies in antimicrobial stewardship, carbapenem-sparing, enhanced infection prevention and control, regional AMR surveillance and expanded molecular diagnostics. One Health approach involving clinical, veterinary, environmental and policy interventions is needed to tackle MDR in Iraq.

Author Contributions

AHM: Conceptualization, Methodology, Investigation, Formal analysis, Data curation, Writing – original draft, Writing – review and editing. The author has read and approved the final version of the manuscript.

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Institutional Review Board Statement

The study was conducted in accordance with the Declaration of Helsinki. It was approved by the Institutional Review Board of the General Directorate of Health - Erbil, Kurdistan Region, Iraq (Approval No. 216; 25 January 2026).

Informed Consent Statement

Informed consent was obtained from all subjects involved in the study.

Data Availability Statement

The data presented in this study are available on request from the corresponding author.

Conflicts of Interest

The author declares no conflict of interest.

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References

- [1] Murray CJ, Ikuta KS, Sharara F, Swetschinski L, Aguilar GR, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet*. 2022;399(10325):629–655. [https://doi.org/10.1016/S0140-6736\(21\)02724-0](https://doi.org/10.1016/S0140-6736(21)02724-0).
- [2] World Health Organization. Global Report on Infection Prevention and Control. Geneva: WHO; 2022. Available at: <https://www.who.int/publications/i/item/9789240051164>
- [3] Yang X, Li X, Qiu S, Liu C, Chen S, Xia H, et al. Global antimicrobial resistance and antibiotic use in COVID-19 patients within health facilities: a systematic review and meta-analysis of aggregated participant data. *J Infect*. 2024;89(1):106183. <https://doi.org/10.1016/j.jinf.2024.106183>.
- [4] Hassoun-Kheir N, Stabholz Y, Kreft JU, de la Cruz R, Romalde JL, Smets BFA, et al. Comparison of antibiotic-resistant bacteria and antibiotic resistance genes abundance in hospital and community wastewater and their correlations with clinical data. *Sci Total Environ*. 2020; 15; 743:140804. <https://doi.org/10.1016/j.scitotenv.2020.140804>.
- [5] Al-Tawfiq JA, Laxminarayan R, Mendelson M. How should we respond to the emergence of plasmid-mediated colistin resistance in humans and animals? *Int J Infect Dis*. 2017; 54:77–84. <https://doi.org/10.1016/j.ijid.2016.11.415>.
- [6] Ali SM, Soor TAH, Ahmed GA, Mhdin GA, Othman GA, Faiq SM. Distribution and molecular characterization of antibiotic-resistant *Pseudomonas aeruginosa* in hospital settings of Sulaymaniyah, Iraq. *Pol J Microbiol*. 2024;73(4):467–473. <https://doi.org/10.33073/pjm-2024-037>
- [7] Raouf FEA, Benyagoub E, Alkhudhairy MK, Akrami S, Saki M. Extended-spectrum beta-lactamases among *Klebsiella pneumoniae* from Iraqi patients with community-acquired pneumonia. *Rev Assoc Med Bras*. 2022;68(6):833–837. <https://doi.org/10.1590/1806-9282.20220222>
- [8] Al-Sheboul SA, Al-Moghrabi SZ, Shboul Y, Atawneh F, Sharie AH, Nimri LF. Molecular Characterization of Carbapenem-Resistant *Acinetobacter baumannii* Isolated from ICU Patients in Jordanian Hospitals. *Antibiotics (Basel)*. 2022;11(7):835. <https://doi.org/10.3390/antibiotics11070835>

- [9] Clinical and Laboratory Standards Institute. Performance Standards for Antimicrobial Susceptibility Testing, 34th Edition. Wayne, PA: CLSI; 2024. CLSI Supplement M100. <https://clsi.org/shop/standards/m100/>
- [10] Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect.* 2012;18(3):268–281. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>.
- [11] Mohammed EJ, Hasan KC, Allami M. Phylogenetic groups, serogroups and virulence factors of uropathogenic *Escherichia coli* isolated from patients with urinary tract infection in Baghdad, Iraq. *Iran J Microbiol.* 2022;14(4):445–457. <https://doi.org/10.18502/ijm.v14i4.10230>. PMID: 36721510; PMCID: PMC9867636.
- [12] Jalil MB, Al Atbee MYN. The prevalence of multiple drug resistance *Escherichia coli* and *Klebsiella pneumoniae* isolated from patients with urinary tract infections. *J Clin Lab Anal.* 2022;36(9): e24619. <https://doi.org/10.1002/jcla.24619>.
- [13] Assafi MS, Ali FF, Polis RF, Sabaly NJ, Qarani SM. An epidemiological and multidrug resistance study for *E. coli* isolated from urinary tract infection (three years of study). *Baghdad Sci. J.* 2022;19(1):13. <https://doi.org/10.21123/bsj.2022.19.1.0007>
- [14] Alsheddi F, Humayun T, Alsaffar M, Aldecoa YS, Alshammari WH, Aldalbehi FZ, et al. National Healthcare-Associated Infections Report 2022 - Saudi Arabia. *J Infect Public Health.* 2023;16(11):1769–1772. <https://doi.org/10.1016/j.jiph.2023.07.007>.
- [15] Madran B, Genç Z, Keske Ş, Sargın-Altunok E, Menekşe Ş, Akpınar A, et al. Healthcare-Associated Infection Rates in Türkiye (2014–2023): A Systematic Review and Meta-Analysis. *Infect Dis Clin Microbiol.* 2025;7(1):17–26. <https://doi.org/10.36519/idcm.2025.470>.
- [16] Zarb P, Coignard B, Griskeviciene J, Muller A, Vankerckhoven V, Weist K, et al. The European Centre for Disease Prevention and Control pilot point prevalence survey of healthcare-associated infections and antimicrobial use. *Euro Surveill.* 2012;17(46):20316. <https://doi.org/10.2807/ese.17.46.20316-en>.
- [17] Ahmed ZS, Mawlood AH. Molecular characterization of efflux pump and porin related genes in multidrug resistance *Klebsiella pneumoniae* isolates recovered from Erbil hospitals. *J. Univ. Babylon Pure Appl. Sci.* 2023 ;31(2):115–27. <https://doi.org/10.29196/jubpas.v31i2.4665>.
- [18] Abdullah IT, Hasib FA, Mohammad FI. Studying the prevalence of multidrug resistant *Klebsiella pneumoniae* in Kirkuk city. *NTU J. Agric. Vet. Sci.* 2023 ;3(4). <https://doi.org/10.56286/ntujavs.v3i4.724>.
- [19] Lin XC, Li CL, Zhang SY, Yang XF, Jiang M. The Global and Regional Prevalence of Hospital-Acquired Carbapenem-Resistant *Klebsiella pneumoniae* Infection: A Systematic Review and Meta-analysis. *Open Forum Infect Dis.* 2023;11(2): ofad649. <https://doi.org/10.1093/ofid/ofad649>.
- [20] Taj Z, Rasool MH, Khurshid M, Aslam B, Qamar MU. Insights into the Intersection of Biocide Resistance, Efflux Pumps, and Sequence Types in Carbapenem-Resistant *Acinetobacter baumannii*: A Multicenter Study. *Pathogens.* 2023;12(7):899. <https://doi.org/10.3390/pathogens12070899>.
- [21] Bouali A, Bendjama E, Cherak Z, Mennaai M, Kassah-Laouar A, Rolain JM, et al. Distribution of carbapenemase-producing and colistin resistant *Acinetobacter baumannii* isolates in Batna hospitals, Algeria. *BMC Infect Dis.* 2025;25(1):825. <https://doi.org/10.1186/s12879-025-11198-6>.
- [22] Wajid Odhafa M, Al-Kadmy I, Pourmand MR, Naderi G, Asadian M, Ghourchian S, et al. The context of blaOXA-23 gene in Iraqi carbapenem-resistant *Acinetobacter baumannii* isolates belonging to global clone 1 and global clone 2. *BMC Res Notes.* 2024;17(1):300. <https://doi.org/10.1186/s13104-024-06890-w>.
- [23] Müller C, Reuter S, Wille J, Xanthopoulou K, Stefanik D, Grundmann H, et al. A global view on carbapenem-resistant *Acinetobacter baumannii*. *mBio.* 2023;14(6): e0226023. <https://doi.org/10.1128/mbio.02260-23>.
- [24] Hadavand F, Khelghati F, Seifi A, Afhami S, Esmailpour N, Alizadeh M, Moradnejad P, Seilakhori FN, Nasiri MJ. Colistin resistance among multidrug-resistant gram-negative bacteria in Iran: a systematic review and meta-analysis. *Novelty in Biomedicine.* 2025 ;13(2):105–18. <https://doi.org/10.22037/nbm.v13i2.46666>.
- [25] Althaqafi A, Yaseen M, Farahat F, Munshi A, Al-Amri A, Essack SY. Risk Factors for Infection with Multidrug-Resistant Gram-Negative Bacteria in a Tertiary Care Hospital in Saudi Arabia: A Case-Control Study. *Cureus.* 2023;15(4): e37291. <https://doi.org/10.7759/cureus.37291>.
- [26] Migliara G, Baccolini V, Isonne C, Cianfanelli S, Di Paolo C, Mele A, et al. Prior Antibiotic Therapy and the Onset of Healthcare-Associated Infections Sustained by Multidrug-Resistant *Klebsiella pneumoniae* in Intensive Care Unit Patients: A Nested Case-Control Study. *Antibiotics (Basel).* 2021 Mar 15;10(3):302. <https://doi.org/10.3390/antibiotics10030302>.
- [27] Balhi S, Boughattas S, Ben Rejeb M, Ben Cheikh A, Haddad N, Trabelsi A, et al. Trends and risk factors of multidrug-resistant hospital-acquired infections in a Tunisian university hospital: repeated point prevalence surveys, 2023–2025. *Antimicrob Steward Healthc Epidemiol.* 2026 ;6(1): e169. <https://doi.org/10.1017/ash.2026.10424>.
- [28] Rosenthal VD, Yin R, Brown EC, Lee BH, Rodrigues C, Myatra SN, et al. Incidence and risk factors for catheter-associated urinary tract infection in 623 intensive care units throughout 37 Asian, African, Eastern European, Latin American, and Middle Eastern nations: Multinational prospective research of INICC. *Infect Control Hosp Epidemiol.* 2024; 45:567–575. <https://doi.org/10.1017/ice.2023.215>.