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**Ministry of Higher
Education and Scientific
Research**

**A Comprehensive Analysis of the Burden of Antibiotic
Resistant Bacteria in Iraq Healthcare System
“A fifth-year graduation project “**

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Abstract

Background: Antimicrobial resistance (AMR) poses a serious threat to healthcare systems worldwide, and Iraq is no exception. This study investigates the prevalence of AMR and highlights the multidrug-resistant (MDR) bacterial challenge in Iraqi hospitals. The overuse and misuse of antibiotics, along with non-adherence to treatment guidelines, have contributed to rising resistance rates. Gram-positive and Gram-negative MDR bacteria present significant treatment challenges, necessitating new therapeutic strategies.

Method: A retrospective cross-sectional, observational study analyzing 681 bacterial culture tests over five months (Aug 2024 – Jan 2025). Data collected from six Iraqi governorates (Baghdad, Babil, Al-Qādisiyyah, Dihok, Karbala, Salah Al-Din). Hospital microbiology lab's databases (2019–2024) from both private and governmental hospitals. Included 19 bacterial types and 50 antibiotics; samples from urine, blood, vaginal, ear swab, and foot swab. Patient details such as age, disease, occupation, follow-up, and medication history were excluded.

Result: 681 samples were collected from six Iraqi governorates, with 614 (90%) being urine samples and 67 (10%) from other sources. Most samples (519) were from females, and 429 (63%) were from governmental hospitals. Cephalosporins showed the highest resistance (780 cases), while fluoroquinolones had the highest sensitivity. *Escherichia coli* was the most resistant bacteria, followed by *Staphylococcus aureus* among gram-positive bacteria. Statistical significance was observed only for bacterial resistance ($p < 0.05$).

Conclusion: Our findings underscore a worrying prevalence of antibiotic resistance across multiple dimensions: geographic regions, patient demographics, drug classes, and microbial species. The convergence of our results with global and regional data suggests that the drivers of AMR—such as antibiotic misuse, hospital transmission of resistant strains, and insufficient infection control—are indeed at play in our setting.

Keywords: antibiotic resistant bacterial resistant, bacterial culture test, Iraqi antimicrobial resistant

Introduction

Iraq is not an exception to the major harm that antimicrobial resistance (AMR) does to health care systems around the world. This study is conducted to determine the prevalence of antimicrobial resistance (AMR) and to illustrate the scope of the multidrug-resistant (MDR) problem in Iraqi hospitals (1). Worldwide, antimicrobial resistance is a major danger to healthcare. Understanding Iraq's antimicrobial resistance problems and how to address them requires a review of present practices around the prescription and usage of antibiotics (2).

The extensive clinical usage of antibiotics coincided with the emergence and early detection of antibiotic resistance (3). The Ministry of Health (MOH) of Iraq recently released a report that revealed concerning findings on antibiotic resistance in the country. According to this paper, drug-resistant strains of common bacterial infections are highly prevalent, and end-line medications like meropenem are widely resistant (4).

The overuse and misuse of antibiotics in the treatment of bacterial and non-bacterial ailments is the most prominent of several reasons that have been linked to the rising incidence of antibiotic-resistant bacteria. Ignoring recommended course durations or ultimately using over-the-counter antibiotics increases the risk of side effects and problems, encourages the development of infections that are hard to treat, and drives up treatment costs (5). Gram-positive and -negative bacteria with multidrug resistance patterns are challenging to treat, and they might not even respond to standard antibiotics. Since there are currently few new antibiotics, ineffective treatments, and ineffective preventative measures, new therapeutic alternatives and alternative antimicrobial medicines must be developed (6).

It has been demonstrated that antibiotic resistance has a negative impact on clinical and therapeutic outcomes, with repercussions ranging from treatment failures and the requirement for more costly and safe substitute medications to increased rates of morbidity and mortality, prolonged hospital stays, and elevated medical expenses (7). However, for a long time, antibiotic resistance was not a major global worry because, in the 1960s, new drug classes like methicillin and vancomycin were created, suggesting that the problem of resistance may be readily resolved by synthesizing new compounds (8). Antibiotic resistance has unfortunately spread throughout the ensuing decades as bacteria have evolved a variety of resistance mechanisms to these medications that have shielded them from their effects (9).

The World Health Organization (WHO) originally released a list of the 12 bacterial families that are the biggest threats to human health in 2017. Based on the urgency of the need to discover new medicines to tackle these infections, the WHO's list divides bacteria into three priority categories: critical, high, and medium (10). The most critical group of pathogens includes multidrug-resistant bacteria that are dangerous to patients in nursing homes and hospitals, as well as to patients whose diseases necessitate the use of medical devices such blood catheters and ventilators (11).

Acinetobacter, *Pseudomonas*, and some *Enterobacteriaceae*, including *K. pneumoniae*, *E. coli*, and *Enterobacter* species, are considered critical-priority bacteria. These organisms can cause serious and frequently deadly infectious illnesses such pneumonia and bloodstream infections, and they are resistant to several medications (12). Bacteria that are resistant to different antibiotics, including vancomycin and fluoroquinolones, such as *Staphylococcus aureus* and *Enterococcus fecium*, fall under the high priority group. *Shigella* and *Streptococcus pneumoniae* are among the microorganisms in the medium priority category; despite their potential for resistance, they can still be killed by effective antibiotics (13)

Our objective was to present an assess the prevalence and trends of antibiotic-resistant infections in Iraqi hospitals over the past five years, identify the most common antibiotic-resistant bacteria and their resistance patterns, and provide recommendations for future interventions to mitigate antibiotic resistance in Iraq.

Materials and Methods

This study employed a retrospective cross-sectional, observational design, analyzing data from hospitals and healthcare centers across Iraq. A 681 bacterial culture tests were collected over a period of five months (from august 2024 to January 2025). Six Iraqi governorates (Baghdad, Babil, Al-Qādisiyyah, Dihok, Karbala and Salah Al-Din) were included in this study.

The data were collected from the hospital's microbiology labs services database, which includes records (from 2019 to 2024) of technical procedures and laboratory urine cultures. Our study included both privet and governmental hospitals. Data included 50 types of antibiotic and 19 type of bacteria

The samples comprised in this study were obtained from both genders male and female from urine, blood, vaginal, ear swap and foot swap. Patient's information like age, disease, occupation, follow up and used medication was excluded in this study.

Statistical Analysis:

Calculation of this study was carried out by using Microsoft excel. Descriptive statistics were used. Numbers and percentages were used to express the data.

Result

Total number of sample collected was 681 from six different Iraqi governorates as presented in figure (1). Of these, 614 were urine sample (90%) and 67 were miscellaneous samples (10%). Miscellaneous samples includes (blood, vaginal biopsy, ear swap, foot biopsy). A 519 of samples were collected from female and only 162 samples related to male. Governmental hospital samples were 429 (63%) and that of private hospital 252 (37%). Characteristics of collected samples shown in (Table 1).

Table (1) Characteristics of collected samples							
Governorate	Samples No.	GENDER		Samples		Hospital	
		Male	Female	Urine	Miscellaneous	Private	Governmental
Duhok	43	0	43	43	0	43	0
Salah Al-Din	40	4	36	40	0	40	0
Baghdad	90	39	51	33	57	5	85
Babil	402	108	294	392	10	60	342
Karbala	78	0	78	78	0	78	0
Al-Qādisiyyah	28	11	17	28	0	26	2
Total	681	162	519	614	67	252	429

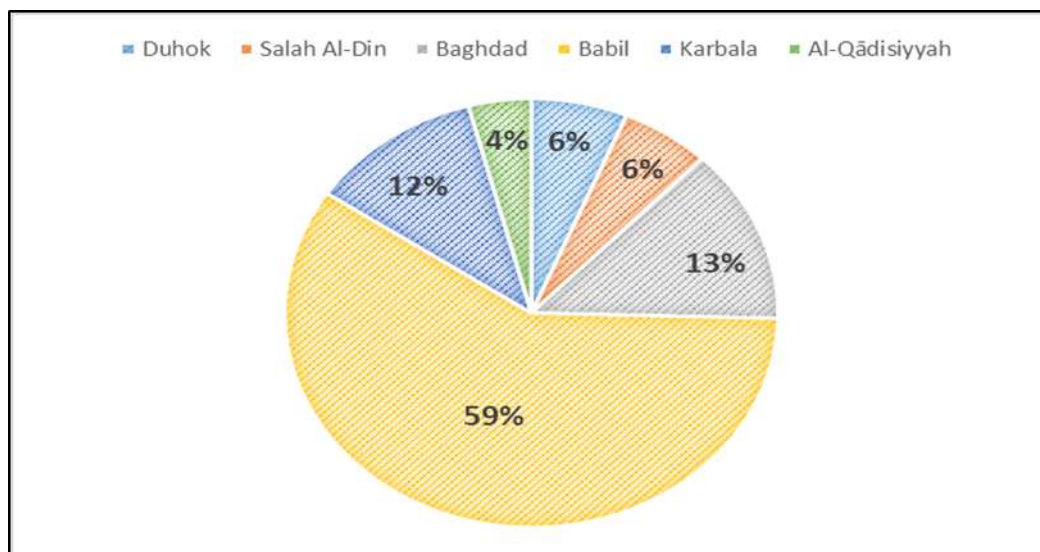


Figure (1): number of samples collected from different Iraqi governorates

A fifteen kind of antibiotic were included in this study table (2). These antibiotics were used at microbiology labs to indicate bacterial resistant and sensitivity tests.

Table (2) types of antibiotics used in bacterial culture			
No.	The Antibiotics	No.	The Antibiotics
1	Cefotaxim	26	Ticarcillin/clavulanic
2	Levofloxacin	27	Norfloxacin
3	Erythromycin	28	Vancomycin
4	Amikacin	29	Ticarcillin
5	Ciprofloxacin	30	Benzylpenicillin
6	Gentamicin	31	Oxacillin
7	Ceftriaxone	32	Ampicillin
8	Cefepime	33	Minocycline
9	Tetracycline	34	Amoxicillin
10	Aztreonam	35	Cloxacillin
11	Trimethoprim-salfamthoxazole	36	Fusidic acid
12	Nitrofurantoin	37	Rifampicin
13	Ceftazidime	38	Ampicillin/sulbactam
14	Piperacillin	39	Cefoxitin
15	Topramycine	40	Cefpodoxime
16	Ofloxacin	41	Clarithromycin
17	Imipenem	42	Cefalexin
18	Meropenem	43	Moxifloxacin
19	Cefadroxil	44	Teicoplanin
20	Augmentin	45	Colistin
21	Cefexime	46	Methicillin
22	Clindamycin	47	Ertapenem
23	Azithromycin	48	Linezolid
24	Piperacillin/Tazobactam	49	Tigecycline
25	Nalidixic acid	50	Fosfomycin

Cephalosporin is the most antibiotic class that show resistant to different types of bacteria with 780 resistant test result in all samples, while the sensitivity test show 548 as shown in figure (2). On the other hand Fluoroquinolones, exhibits more sensitivity results than other antibiotic families as presented in table (3).

In addition, the result show there is no statically significance where p- value >0.05 as mentioned in table (3).

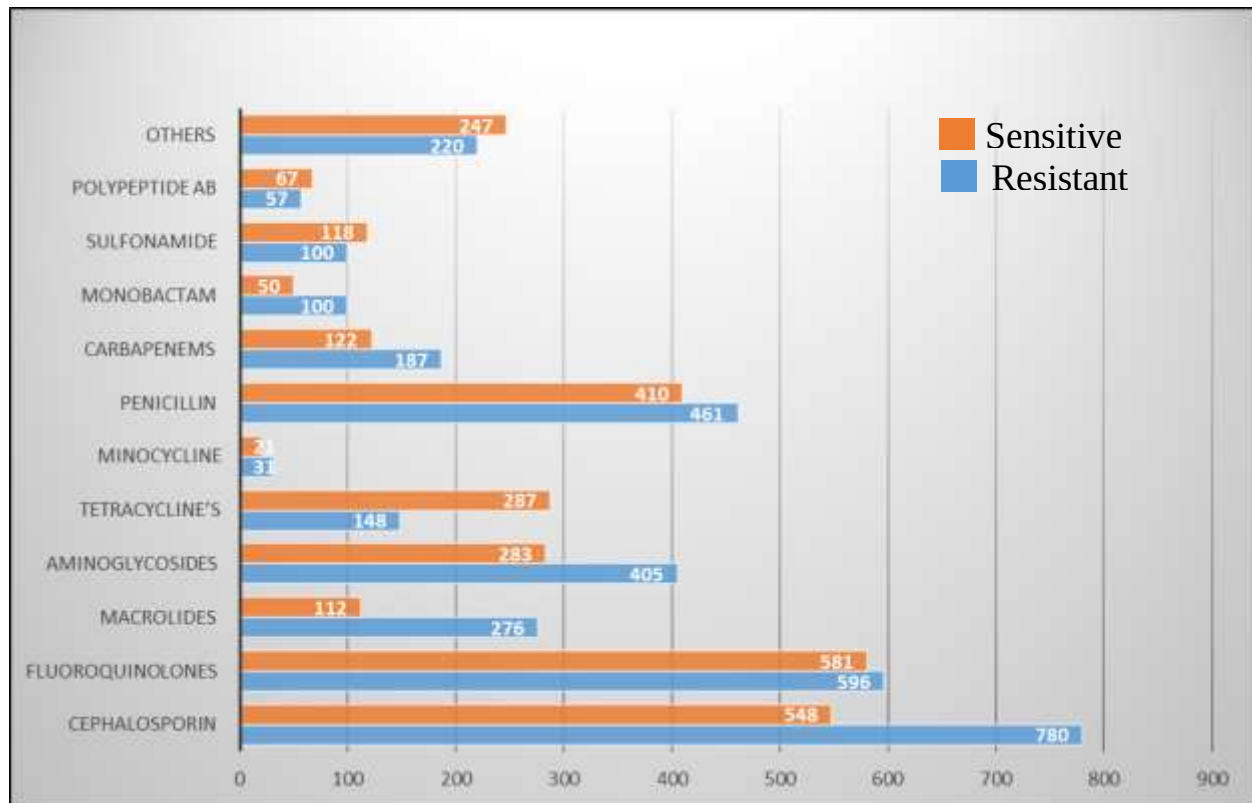


Figure (2): antibiotics sensitivity culture's test results

Table (3): test results of antibiotic				
No.	antibiotics	R	S	P-value
1	Cephalosporin	780	548	0.076
2	Fluoroquinolones	596	581	
3	Macrolides	276	112	
4	Aminoglycosides	405	283	
5	Tetracycline’s	148	287	
6	Minocycline	31	21	
7	Penicillin	461	410	
8	Carbapenems	187	122	
9	Monobactam	100	50	
10	Sulfonamide	100	118	
11	Polypeptide Ab	57	67	
12	Others	220	247	
R: resistant , S: sensitive				

Where Fosfomycin is the least one that reveal resistant but there is no sensitivity test result. However the result show there is no statically significance where p- value >0.05 as presented in table (4).

Table (4): test results of miscellaneous classes of antibiotic				
No.	Antibiotic	R	S	P-value
1	Nitrofurantoin	100	82	0.321
2	Clindamycin	61	54	
3	Fusidic acid	21	5	
4	Rifampicin	21	22	
5	Colistin	9	17	
6	Linezolid	3	22	
7	Tigecycline	3	45	
8	Fosfomycin	2	0	
R: resistant , S: sensitive				

For bacteria, Escherichia Coli is the most bacteria that revealed a resistant to different types of antibiotics, while for gram positive bacteria Staphylococcus Aureus is more resistant than other, figure (3) presented bacterial culture tests of collected samples. A p-value was <0.05 that means a statically significance as presented in table (5).

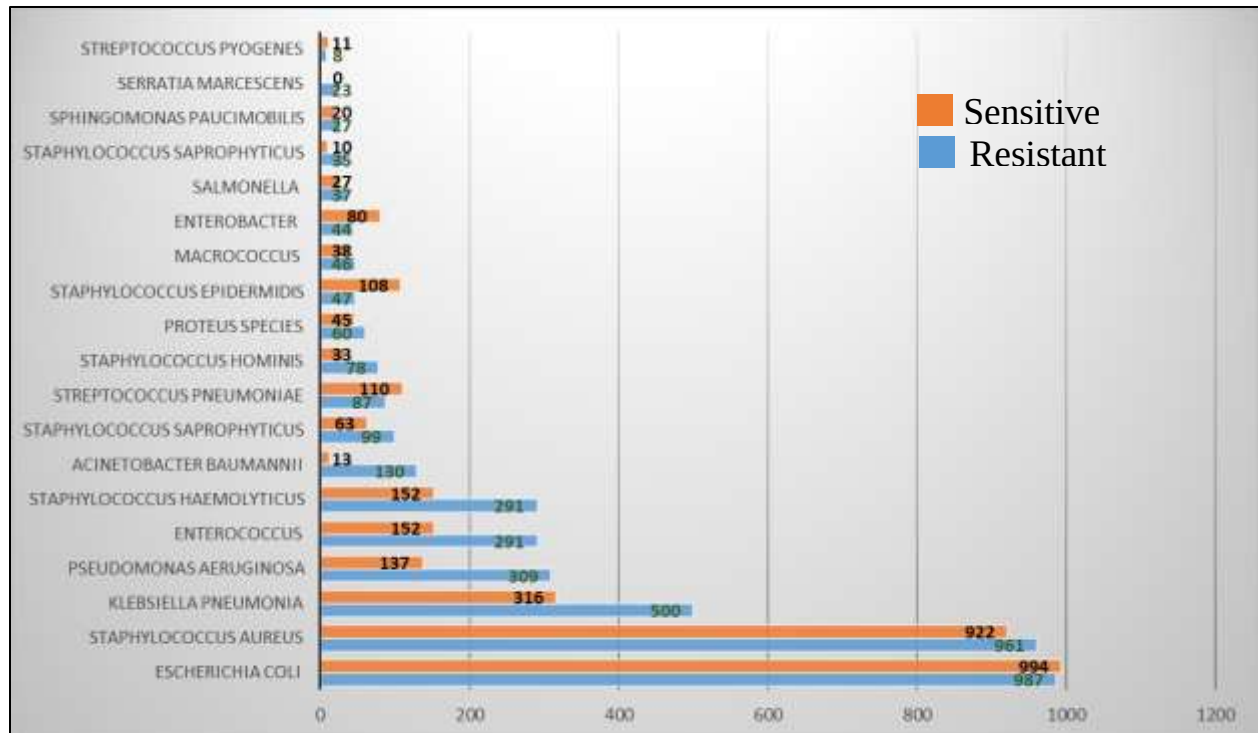


Figure (3): bacterial culture tests of collected samples

Table (5): types of bacteria					
No.	Bacteria	Type	R	S	P-value
1	Escherichia Coli	G -Ve	987	994	0.0078
2	Staphylococcus Aureus	G +Ve	961	922	
3	Klebsiella Pneumonia	G -Ve	500	316	
4	Pseudomonas Aeruginosa	G -Ve	309	137	
5	Enterococcus	G +Ve	291	152	
6	Staphylococcus Haemolyticus	G +Ve	291	152	
7	Acinetobacter Baumannii	G -Ve	130	13	
8	Staphylococcus Saprophyticus	G +Ve	99	63	
9	Streptococcus Pneumoniae	G +Ve	87	110	
10	Staphylococcus Hominis	G +Ve	78	33	
11	Proteus Species	G -Ve	60	45	
12	Staphylococcus Epidermidis	G +Ve	47	108	
13	Macrococcus	G +Ve	46	38	
14	Enterobacter	G -Ve	44	80	
15	Salmonella	G -Ve	37	27	
16	Staphylococcus Saprophyticus	G +Ve	35	10	
17	Sphingomonas Paucimobilis	G -Ve	27	20	
18	Serratia Marcescens	G -Ve	23	0	
19	Streptococcus Pyogenes	G +Ve	8	11	
R: resistant , S: sensitive					

Discussion

Antibiotic resistance among bacterial pathogens has emerged as one of the most pressing global public health challenges. The World Health Organization (WHO) reports that bacterial antimicrobial resistance (AMR) was directly responsible for approximately 1.27 million deaths worldwide in 2019, underscoring its severe impact (World Health Organization, 2023) . Misuse and overuse of antibiotics in human medicine are primary drivers of this crisis (World Health Organization, 2023) , and conflict-affected regions such as Iraq face additional pressures that exacerbate the problem (14) . The present study evaluated the patterns of antibiotic resistance across various provinces, patient demographics, and hospital types, providing important insights into the epidemiology of resistant infections in our setting. In the following discussion, we examine our findings in light of the broader literature, addressing the distribution of samples, the spectrum of antibiotics tested, resistance levels to different antibiotic classes, and the resistance profiles of key bacterial species.

Sample Distribution by Province, Gender, and Hospital Type of our results detailed the distribution of clinical isolates across different provinces, patient genders, and hospital types. We observed that the majority of samples originated from Babil province and Baghdad, together accounting for a large portion of isolates. This skewed distribution likely reflects the concentration of healthcare facilities and population density in those provinces, as well as referral patterns that centralize laboratory services in larger urban centers . It also suggests that antibiotic resistance is not confined to a single region, but rather is a widespread issue, echoing the findings of a multi-province surveillance study in Iraq that reported pervasive AMR across the country (15).

Regarding gender, our sample included approximately 24% male and 76% female patients. This proportion may be influenced by the types of infections sampled; for instance, urinary tract infections (often caused by *Escherichia coli*) are more common in females, whereas bloodstream and respiratory infections (involving pathogens like *Staphylococcus aureus* or *Klebsiella pneumoniae*) can be more frequent in older male patients (Bra16) . Indeed, some epidemiological studies indicate that men have a higher incidence of infections with antimicrobial-resistant bacteria than women , which could contribute to the sex distribution observed. Nevertheless, women generally receive more antibiotic prescriptions over their

lifetime than men (17), potentially accelerating resistance development in communities.

The type of hospital was another factor in sample distribution. We noted that 63% of isolates came from governmental (public) hospitals, compared to 37% from private hospitals. Patients in larger tertiary-care hospitals often have more severe or refractory infections and prior antibiotic exposures, which is associated with a higher likelihood of multidrug-resistant organism isolation . Our findings align with the expectation that referral and teaching centers encounter more drug-resistant infections due to the concentration of complicated cases and greater antibiotic use intensity (14) . Overall, the distribution of samples underscores that antibiotic resistance is a system-wide issue, affecting diverse patient groups and healthcare settings, and necessitates a coordinated regional response.

Antibiotics Tested and Their Clinical Relevance: Our study evaluated bacterial susceptibility to a panel of antibiotics spanning multiple classes. These included beta-lactam antibiotics such as penicillins and cephalosporins, fluoroquinolones, aminoglycosides, macrolides, and others. This selection reflects the antibiotics commonly used in clinical practice for treating infections caused by the organisms under study. For example, third-generation cephalosporins (e.g., ceftriaxone) and fluoroquinolones (e.g., ciprofloxacin) are frequently employed as first-line or empirical treatments for serious Gram-negative infections , while macrolides (e.g., azithromycin or erythromycin) are important for respiratory pathogens and certain Gram-positive infections . Aminoglycosides (such as gentamicin and amikacin) are often used in combination therapy for severe infections due to their broad spectrum and bactericidal activity. We also included representatives of other classes, such as sulfonamides (trimethoprim-sulfamethoxazole) and carbapenems, which are reserved as last-resort drugs for multidrug-resistant organisms . By testing this wide array of antibiotics, the study aimed to capture resistance patterns comprehensively. It is notable that many of these agents fall into the WHO “Watch” or “Reserve” categories, meaning they should be used judiciously to minimize further resistance development (WHO, 2019). The chosen panel thus provides insight into which current therapies remain effective and which have diminished utility due to resistance.

Resistance Levels to Different Antibiotic Classes: The susceptibility testing results reveal alarming resistance rates across multiple antibiotic classes. **Cephalosporins:** A high proportion of isolates were resistant to cephalosporins, particularly extended-spectrum cephalosporins. For instance, over half of Enterobacteriaceae isolates were resistant to third-generation cephalosporins, indicating widespread production of extended-spectrum β -lactamases (ESBLs) that inactivate these drugs. This finding is consistent with reports from Iraq and the region, where ESBL-producing *E. coli* and *Klebsiella* are prevalent in both community and hospital settings (18). **Penicillins and β -lactam/ β -lactamase inhibitors:** These also showed diminished efficacy; notably, ampicillin had an extremely high resistance rate (often >90%), rendering it essentially ineffective against most Gram-negative isolates. Oxacillin (used as a surrogate for methicillin) was similarly ineffective against *S. aureus* in our samples, underscoring a high prevalence of MRSA (methicillin-resistant *S. aureus*).

Fluoroquinolones: We found substantial resistance to fluoroquinolones like ciprofloxacin and levofloxacin; approximately half of all isolates were non-susceptible to fluoroquinolones. Such high fluoroquinolone resistance is a growing global concern. For context, many regions now report >50% of *E. coli* from complicated infections are fluoroquinolone-resistant (T19). Overuse of fluoroquinolones has likely driven the selection of mutants with target-site alterations and efflux pump mechanisms, as well as plasmid-mediated resistance factors. **Macrolides:** Resistance to macrolides (e.g. erythromycin) was notably high among Gram-positive organisms in our study. In our *S. aureus* isolates, macrolide resistance was common (reflecting the presence of the MLSB resistance phenotype). This mirrors findings elsewhere; for example, nearly 60% of *S. aureus* isolates in one Iraqi study were resistant to erythromycin (Al-Mathkhury et al., 2023). Similarly, *Streptococcus pneumoniae* (though not a focus of our analysis) is known to exhibit substantial macrolide resistance in many regions.

Aminoglycosides: While aminoglycosides such as gentamicin and amikacin retained activity against some organisms, we still observed significant resistance in certain isolates (just under 60% of tested isolates were resistant). This is concerning because aminoglycosides are often key second-line agents. However, their continued effectiveness against a fraction of isolates is somewhat reassuring, suggesting these drugs can still be useful in combination therapy for certain multidrug-resistant infections. **Carbapenems:** For the carbapenem antibiotics tested, most

Enterobacteriaceae remained susceptible, aligning with our finding that all ESBL-producers were inhibited by imipenem or meropenem .

Nonetheless, we observed a few instances of carbapenem resistance, particularly in non-fermenters like *Pseudomonas* and *Acinetobacter*. Carbapenem-resistant *Acinetobacter baumannii* and *P. aeruginosa* are categorized by WHO as critical priority pathogens due to their ability to evade nearly all available antibiotics. The emergence of any carbapenem resistance in our setting is therefore a grave warning sign. Other classes: We also noted patterns such as high resistance to trimethoprim-sulfamethoxazole among Gram-negative rods, and to clindamycin among staphylococci (often linked with macrolide resistance via inducible MLS_B mechanisms). Tetracycline resistance was likewise prominent in both Gram-negative and Gram-positive groups, reflecting the long-standing use of that class. In summary, the resistance levels observed across these antibiotic classes highlight that many first-line and even second-line antibiotics are losing efficacy. This necessitates urgent attention to antibiotic stewardship and the development of new therapeutic strategies, as also suggested by global health authorities (WHO, 2024) .

Resistance Profiles of Key Bacterial Species: Table 5 summarized the resistance patterns for the major bacterial species isolated in our study, including *E. coli*, *K. pneumoniae*, *S. aureus*, *P. aeruginosa*, and others. Gram-negative rods: *Escherichia coli* was the most frequently isolated Gram-negative species and showed high levels of resistance to multiple antibiotics. Many *E. coli* isolates were resistant to penicillins, fluoroquinolones, and trimethoprim-sulfamethoxazole, consistent with the global spread of multidrug-resistant *E. coli* in both community and hospital infections. A large subset were ESBL-producing, explaining their nearly uniform resistance to cephalosporins . This aligns with prior local reports identifying *E. coli* as one of the most drug-resistant pathogens in Iraq, especially in urinary tract infections (20). *Klebsiella pneumoniae* was another predominant Gram-negative pathogen, notable for both its frequency and its resistance. *K. pneumoniae* isolates in our study often produced ESBLs and, worryingly, some showed reduced susceptibility to carbapenems – indicative of possible carbapenemase production. A surveillance study spanning multiple Iraqi provinces found *K. pneumoniae* to be the most common Gram-negative bacterium and a major contributor to MDR infections . Our findings support this; *Klebsiella* not only was common but also tended to be resistant to more drug classes than *E. coli*, underscoring its reputation as an urgent threat (CDC, 2019). *Proteus mirabilis* was sporadically isolated and tended to have

a resistance profile similar to *E. coli* (e.g. high fluoroquinolone and sulfonamide resistance, but relative retention of nitrofurantoin susceptibility in urinary isolates).

Gram-positive cocci: *Staphylococcus aureus* was the most prominent Gram-positive organism in our sample set. We identified a high proportion of MRSA among these isolates, as evidenced by oxacillin resistance. These MRSA strains also frequently carried resistance to macrolides and lincosamides, as expected from co-selection of resistance determinants. The persistence of MRSA is a global concern; for example, the United States still reports MRSA comprising around 40% of *S. aureus* infections in recent years (21). In our context, the ubiquity of MRSA (with a few isolates showing reduced susceptibility to vancomycin) raises alarms about diminishing therapeutic options for staphylococcal infections. In addition, although few in number, *Enterococcus faecium* isolates in our study included some vancomycin-resistant strains (VRE), reflecting the increasing presence of resistant enterococci in healthcare settings and aligning with global trends in rising VRE prevalence.

Non-fermenters and others: Non-fermenting Gram-negatives like *Pseudomonas aeruginosa* and *Acinetobacter* spp. were less common in our sample, but they pose significant treatment challenges. *P. aeruginosa* isolates showed resistance to many first-line antipseudomonal agents (such as ceftazidime and ciprofloxacin), though most remained susceptible to amikacin and colistin. *Acinetobacter*, while only isolated in low numbers, displayed multidrug resistance including at least one carbapenem-resistant strain. This pattern mirrors global trends for these opportunistic pathogens, which are often associated with hospital-acquired infections and have intrinsic resistance mechanisms. Their presence in our study, even at low prevalence, is concerning because infections caused by these bacteria are difficult to treat and have high morbidity. Collectively, the species-specific analysis highlights that both the commonly encountered bacteria (*E. coli*, *S. aureus*, *Klebsiella*) and the less frequent but high-risk pathogens (*Pseudomonas*, *Acinetobacter*, *Enterococcus*) are contributing to the AMR burden. Each requires targeted control strategies, and our data underscore the importance of ongoing surveillance to inform such strategies.

Conclusion

Our findings underscore a worrying prevalence of antibiotic resistance across multiple dimensions: geographic regions, patient demographics, drug classes, and microbial species. The convergence of our results with global and regional data suggests that the drivers of AMR—such as antibiotic misuse, hospital transmission of resistant strains, and insufficient infection control—are indeed at play in our setting.

Recommendations

Immediate actions are needed to mitigate this trend. Strengthening antibiotic stewardship programs in hospitals, enforcing regulations on antibiotic dispensing to curb over-the-counter misuse, and enhancing infection prevention measures are critical steps. Our results also point to the need for continuous surveillance regular AMR monitoring and the development of national antibiotic guidelines are essential to manage the crisis.

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