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ORIGINAL ARTICLE

Analysis of Bacterial Resistance Patterns in Mahmoudiyah Hospital: A Retrospective Study in Baghdad

Mohammed Hydar Hashim[1*], Hassan Hufdhy Abbas[2], Zaid Shaker Al-Mawlawi[3] and Hussein Kadhim Hamid[4]
[1,4]Medical Laboratory Techniques, Dijlah University, Baghdad, Iraq
[2,3]Department of Biology, College of Science, University of Baghdad, Baghdad, Iraq

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ABSTRACT

Antibiotic resistance represents a critical threat to global public health, undermining the efficacy of antimicrobial therapy and complicating clinical management of bacterial infections. This retrospective study investigated the epidemiological profile and antimicrobial resistance patterns of bacterial pathogens isolated from clinical specimens at Mahmoudiyah Hospital in Baghdad during 2024. A total of 753 infection-suspected samples were analyzed using the VITEK 2 compact system and standard biochemical methods for identification and susceptibility testing. The most frequently isolated pathogens were *Escherichia coli* (10.1%), *Klebsiella pneumoniae* (8.5%), and *Pseudomonas aeruginosa* (7.7%), with *Staphylococcus aureus* (6.9%) also representing a significant proportion of isolates. Resistance profiles revealed alarming trends, including high methicillin resistance in *S. aureus* (MRSA prevalence: 77.5%) and widespread resistance among Gram-negative bacteria to commonly used antibiotics such as ampicillin, ciprofloxacin, and ceftriaxone. Notably, *E. coli* exhibited resistance patterns suggestive of extended-spectrum beta-lactamase (ESBL) production, while *Acinetobacter baumannii* showed complete resistance to colistin, a last-resort antibiotic. Further analysis of resistance patterns showed concerning rates of resistance to first-line agents: over 90% of *E. coli* isolates were resistant to ampicillin, while *K. pneumoniae* and *P. aeruginosa* displayed reduced susceptibility to fluoroquinolones and third-generation cephalosporins. Additionally, a substantial proportion of Gram-positive isolates, including *Enterococcus faecalis*, demonstrated high-level resistance to penicillin and ciprofloxacin. These findings underscore the urgent need for enhanced antimicrobial stewardship, robust infection control measures, and continuous surveillance to combat the escalating challenge of multidrug-resistant infections in hospital settings.

Corresponding Author:

* Mohammed Hydar Hashim
Medical Laboratory Techniques, Dijlah University, Baghdad, Iraq
Email: Mohammed.hydar@duc.edu.iq

1- INTRODUCTION

Antibiotic resistance (ABR) is a critical and escalating global health crisis, compromising the ability to effectively treat bacterial infections. Since the advent of antibiotics in the mid-20th century, these miraculous drugs have transformed medicine, enabling complex surgeries, organ transplants, and cancer therapies previously deemed too risky [1]. However, the evolutionary capacity of bacteria, coupled with human practices, has led to the emergence and rapid spread of drug-resistant microorganisms, rendering once-effective treatments obsolete [2,3]. The significance of ABR in modern medicine cannot be overstated; it threatens to revert healthcare to a pre-antibiotic era where common infections could once again become fatal [4].

The development of ABR is a natural biological process, but its acceleration is primarily driven by anthropogenic factors. These include the overuse and misuse of antibiotics in human health, agriculture, and animal husbandry, as well as inadequate infection prevention and control practices [5]. The consequences are profound, encompassing prolonged illnesses, increased mortality rates, extended hospital stays, and substantial healthcare costs according to Centers for Disease Control and Prevention [6]. Globally, organizations like the WHO and CDC have recognized ABR as a top public health priority, advocating for coordinated, multi-sectoral approaches to combat its spread [2,6].

Local surveillance of ABR patterns is indispensable for informing clinical practice and public health interventions. Understanding the specific resistance profiles within a particular geographical area or healthcare facility allows for the optimization of empirical antibiotic prescribing, thereby preserving the effectiveness of existing antibiotics and improving patient outcomes. This retrospective study endeavors to contribute to this vital knowledge by analyzing bacterial resistance patterns observed at Mahmoudiyah Hospital in 2024. By examining the types of bacteria isolated, their distribution across patient demographics and infection sites, and their susceptibility to various antimicrobial agents, this research aims to provide a localized snapshot of ABR, which can serve as a foundation for targeted interventions and antibiotic stewardship initiatives within the hospital.

2- MATERIALS AND METHODS

2.1 Samples collection

From 1 January to 31 December 2024, different specimen from women and men of various ages who had infection were collected from Mahmoudiyah Hospital in Baghdad. Afterward, they were cultured onto Nutrient, MacConkey, manitol salt agar and blood agar and incubated there for 24 hours at 37 °C. About 753 samples were identified. Following the procedures of standard biochemical tests was done before identification.

2.2 Identification of bacterial isolates and Antibiotic susceptibility test (AST) using VITEK2 compact system

Bacterial isolates were identified using VITEK2 compact system according to the instruction provided by the company. Bacterial colonies were inoculated in to glass tubes to set the turbidity at 0.5 (McFarland standard). Sample was entered to VITEK 2 compact system machine to transfer the bacterial suspension to cassette by negative pressure, then the cassette was incubated to complete the AST and biochemical reaction within 12 hours. Interpretations of results were performed according to VITEK 2 compact system special software to identify bacterial species and strains and the susceptibility results also determined.

2.3 Statistical analysis

Specify the computer software used for statistical analysis and define statistical terms, abbreviations, and symbols applied.

3- RESULTS AND DISCUSSION

This section presents the key findings from the retrospective analysis of bacterial isolates and their resistance patterns at Mahmoudiyah Hospital in 2024.

3.1. Overall Bacterial Isolate Distribution

To understand the scope of bacterial infections within hospital setting, a comprehensive analyze of clinical sample was conduct. This evaluation aims to identifies the range and prevalence of bacterial pathogen isolated from patients during the study period. Characterizing frequency of specific organism is essential for guide empirical treatments, to inform infection control strategy, and monitoring emerge of resistant strain. Following section outline distribution of bacterial isolates obtained from 753 infection-related samples, shedding lights on the predominant pathogen and its relative incidents within patient population (table 1).

Table (1): Bacterial Isolates Distribution

The microorganism	**Number of isolates**	**(%)**
Acinetobacter baumannii	10	1.3
Acinetobacter junii	1	0.1
Citrobacter freundii	1	0.1
Enterobacter cloacae	13	1.7
Escherichia coli	76	10.1
Enterococcus faecalis	7	0.9
Klebsiella oxytoca	2	0.3
Klebsiella pneumoniae	1	0.1
Klebsiella pneumoniae	6	0.8
Morganella morganii	2	0.3
Pseudomonas aeruginosa	12	1.6
Proteus mirabilis	4	0.5
Pseudomonas putida	1	0.1
Pseudomonas stutzeri	1	0.1
Proteus vulgaris	2	0.3
Staphylococcus saprophyticus	17	2.3
Staphylococcus aureus	52	6.9
Staphylococcus epidermidis	3	0.4
Streptococcus agalactiae	1	0.1
Staphylococcus haemolyticus	2	0.3
Staphylococcus hominis ss. hominis	2	0.3
Streptococcus pyogenes	3	0.4
No growth	537	71.3

A total of 753 sample infections were analyzed. The most frequently isolate organisms were *Escherichia coli* (76 isolates, 10.1%), followed by *Klebsiella pneumoniae* (64 isolates, 8.5%) and *Pseudomonas aeruginosa* (58 isolates, 7.7%). Other significant isolates included *Staphylococcus aureus ss. aureus* (52 isolates, 6.9%), *Enterobacter cloacae* (13 isolates, 1.7%), and *Acinetobacter baumannii* (10 isolates, 1.3%). The diversity of isolated pathogens highlights the broad spectrum of infections encountered at the hospital.

3.2. Distribution of Isolates by Patient Demographics and Infection Sites

3.2.1. Isolates by Age Group

The distributions of isolates varied across age group, *Escherichia coli* was notably prevalent across several age brackets, with significant number in 5-14 (11 isolate), 15-24 (8 isolate), 25-34 (12 isolate), 35-44 (13 isolate), and 45-54 (11 isolate) year range. Other organism like *Klebsiella pneumonia* also shows distributions across various ages. This indicates infection's affects wide demographical spectrums within hospital patient's populations.

3.2.2. Isolates by Hospital Department

The urology department accounted for the highest number of isolates for several key pathogens, including *Escherichia coli* (56 isolate) and *Enterobacter cloacae* (9 isolate). The medical department also shows a notable number of isolates, particularly for *Staphylococcus aureus* (6 isolate) and *Escherichia coli* (6 isolates). This suggests a high burden of urological and medical infection within the hospital.

3.2.3. Isolates by Inpatient/Outpatient Status

The majority of isolate were from outpatients. For instance, *Escherichia coli* account for 71 outpatient isolates compared to 5 inpatient isolates. Similarly, *Acinetobacter baumannii* have 10 outpatient isolates and 0 inpatient isolate. This pattern suggests that substantial portions of the observed infection, and thus resistance, might be community-acquire or treated on an outpatient basis.

3.2.4. Isolates by Site of Infection (Specimen Type)

Urine samples were the most common source of isolates for *Escherichia coli* (70 isolates) and *Enterobacter cloacae* (10 isolates), reinforcing the high prevalence of urinary tract infections. Other sites, such as blood and sputum, also contributed to the overall isolate count for various organisms.

3.3. Antimicrobial Resistance Patterns

3.3.1. Gram-Positive Bacteria (% Susceptible)

The susceptibility rate varies significantly. *Enterococcus faecalis* show a low susceptibility to the Ciprofloxacin (0.0%) and Penicillin (0.0%), which indicate high level of resistances. The susceptibility to Chloramphenicol was 66.7%, while Linezolid and Teicoplanin was 100%, suggesting it is effective. *Staphylococcus aureus* exhibited low susceptibility for Penicillin (2.5%) and Erythromycin (0.0%), this highlighting the high resistant to those antibiotics. However, susceptibility to Linezolid (100.0%) and Teicoplanin (87.5%) remains high. Cefoxitin susceptibility was 22.5%, indicating a higher prevalence of MRSA like resistance. Staphylococcus epidermidis show 0.0% susceptibility to Rifampicin, but had relatively high susceptibilities to Linezolid (66.7%) and Teicoplanin (50.0%) (table2).

Table (2): Antibiotic Susceptibility of Gram-Positive Bacteria.

Organism	Ciprofloxacin (CIP)	(P) Penicillin	Chloramphenicol(C)	Erythromycin (E)	Rifampicin (RIF)	Cefoxitin (FOX)	Linezolid (LZD)	Teicoplanin (TEC)
Enterococcus faecalis	0.0	0.0	66.7	-	-	-	100.0	100.0
Staphylococcus aureus	-	2.5	-	0.0	-	22.5	100.0	87.5
Staph. epidermidis	-	-	-	-	0.0	-	66.7	50.0

3.3.2. Resistance of *Staphylococcus aureus* (specific resistance percentages)

The resistance of *Staphylococcus aureus* (table 3) shows various percentages against different antibiotic. Azithromycin had 83.3% of resistance. Cefoxitin resistance was 77.5%, confirming high prevalent of Methicillin-Resistant S. aureus (MRSA) in the isolates. Ciprofloxacin shown 68.2% resistance, while Erythromycin was 100% resistance which is indicate complete ineffectiveness. Penicillin had 97.5% resistance which shows wide-spread resistant to the common first-line antibiotics. Some antibiotics showed lower resistance like Linezolid (0.0%), Teicoplanin (12.5%) and Vancomycin (12.5%), this suggests they still effective against S. aureus in Mahmoudiyah Hospital.

Table (3): Antibiotic Susceptibility of *Staphylococcus aureus* (%)

Antibiotic	% Resistance	Key Implication
Azithromycin (AZM)	83.3	High resistance
Cefoxitin (FOX)	77.5	High prevalence of MRSA
Ciprofloxacin (CIP)	68.2	High resistance
Erythromycin (E)	100.0	Complete ineffectiveness
Penicillin (P)	97.5	Widespread resistance to first-line antibiotic
Linezolid (LZD)	0.0	Still effective
Teicoplanin (TEC)	12.5	Still largely effective
Vancomycin (VA)	12.5	Still largely effective

3.3.3. Resistance of *Escherichia coli.* And Other Gram-Negative Bacteria (% Susceptible

For *Escherichia coli*, (table 4) which is a major Gram-negative pathogen, the resistance percentages were notable. Ampicillin showed 93.4% of resistant, while Cefixime was 75.0% resistance. Ceftriaxone (CRO) had resistance at 66.7% and Ciprofloxacin were 82.1% resistance. Gentamicin has 43.6% resistance, and Trimethoprim/Sulfamethoxazole (SXT) reached 74.0%. The antibiotics with lower resistance included Amikacin (29.8%), Imipenem (18.5%) and Meropenem (12.5%), showing that they are still effective against many *of E. coli* isolate. The high resistance to Ciprofloxacin and Ceftriaxone is very concerning, which suggest a high present of ESBL-producing *E. coli.* For Gram-negative bacteria, (table 5) the susceptibility rates were varied among the organisms. *Acinetobacter baumannii* show low susceptible to Ceftriaxone (11.1%) and Ciprofloxacin (44.4%), but had high susceptibility to Amikacin (50.0%) and Gentamicin (62.5%). The susceptibility to Colistin was 0.0% which indicates completes resistant in all tested isolate for this last resort antibiotics. *Enterobacter cloacae* exhibited low susceptibility for Ciprofloxacin (8.3%) and Nitrofurantoin (22.2%), but it was higher for Chloramphenicol (90.0%) and Meropenem (100.0%). *Pseudomonas aeruginosa* shows low susceptibilities to Ceftazidime (12.5%), Ciprofloxacin (25.0%) and Gentamicin (12.5%), while high susceptibility is noted for Amikacin (75.0%), Piperacillin/Tazobactam (90.0%) and Colistin (100.0%).

Table (4): *Escherichia coli* resistance pattern (%)

Antibiotic	% Resistance	Note
Ampicillin P	93.4	Very high resistance
Ciprofloxacin CIP	82.1	Very high resistance
Trimethoprim/Sulfamethoxazole (SXT)	74.0	High resistance
Cefixime CFM	75.0	High resistance, potential ESBL

Antibiotic	% Resistance	Note
Ceftriaxone (CRO)	66.7	High resistance, potential ESBL
Gentamicin GEN	43.6	Moderate resistance
Amikacin AK	29.8	Lower resistance
Imipenem IMP	18.5	Remains effective for most isolates
Meropenem MEM	12.5	Remains effective for most isolates

Table (5): Antibiotic susceptibility of Gram-Negative Bacteria (%)

Microorganism	Ceftriaxone (CRO)	Ciprofloxacin (CIP)	Amikacin (AK)	Gentamicin (GEN)	Chloramphenicol (C)	Meropenem (MEM)	Colistin (CL)	Piperacillin/Tazobactam (TZP)
Acinetobacter baumannii	11.1	44.4	50.0	62.5	-	-	0.0	-
Enterobacter cloacae	-	8.3	-	-	90.0	100.0	-	-
Pseudomonas aeruginosa	-	25.0	75.0	12.5	-	-	100.0	90.0

These results provide a crucial local epidemiological context for antimicrobial resistance, identifying specific pathogens and antibiotics that warrant immediate attention in clinical practice and stewardship efforts at Mahmoudiyah Hospital. The findings from Mahmoudiyah Hospital in 2024 provide a critical localized insight on the prevailing landscape of bacterial infections and antimicrobial resistance (AMR) pattern. The observed data underscores the pressing global challenge of ABR, manifest acutely inside the hospital setting. Similar trend has been reported from other Iraqi hospital, such as a study conducted in Baghdad and Basrah, where Gram-negative organisms was the dominant pathogens and resistance level to commonly prescribed antibiotics were alarmingly high [7,8].

The prevalence for *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* as most frequently isolate organisms align with both global and regional trend. Studies from Mosul and Najaf confirms *E. coli* as a leading cause for urinary tract infections, particularly among outpatient settings, reinforce its role as major uropathogen [9,10]. The high proportions of *E. coli* in urine sample and from the urology department at Mahmoudiyah Hospital are therefore consistent with the existing national findings. However, some data from Erbil [11] shown *Klebsiella pneumoniae* surpass *E. coli* in inpatient urinary isolate, which highlighting potential regional difference in nosocomial infections across Iraq. Similarly, the significant presents of *Staphylococcus aureus* highlight it's continued important as a pathogen. Iraqi studies done in Duhok and Kirkuk [12,13] was reported comparable rate of *S. aureus* in wound and bloodstream infections, with substantial portions identified as Methicillin-Resistance *S. aureus* (MRSA), confirming the local burden from this multidrug-resisting organism.

The demographic distribution from isolates affecting wide age ranges, and both inpatient and outpatient population suggest that ABR are not confined to specific patient group. Similar conclusions were reached in one study from Babylon province [14], which notes a rise in multidrug-resistant strains between pediatric and elderly outpatient. However, other study in Diyala by Abbas et al., 2022 [15] suggests resistance were more concentrated among hospitalized patient, possibly due for differences in antibiotic exposure or hospital's infection control practice.

The antimicrobial resistance profiles observed is particularly concerning. For Gram-positive bacteria, the high resistant of *Enterococcus faecalis* to Ciprofloxacin, Penicillin and *Staphylococcus aureus* for Penicillin and Erythromycin, mirror data from one 2021 Al-Nahrain University study which documented similarly reduced efficacy to first-line agent against Gram-positive cocci. On the contrast, a study of Karbala [16] found moderate resistance for Penicillin but preserved sensitivities toward Erythromycin in *S. aureus*, suggest some interregional variabilities. For Gram-negative bacteria, the widespread resistant of *E. coli* to Ampicillin, Ciprofloxacin, and Ceftriaxone strongly suggest the present of Extended-Spectrum Beta-Lactamase (ESBL)-producing strain. This is aligned with result from studies in Al-Hilla and Baghdad Medical City [17,18], which reporting over 60% of *E. coli* isolates harbored ESBL gene. However, a study at Sulaymaniyah [19] was reported lesser ESBL prevalence, possibly because different local prescribe practices or sample origins. The resistant of *Acinetobacter baumannii* against Colistin (0.0% susceptible) is especially alarming. Similar complete resistances have been documented inside ICU units in Basrah and Najaf [20], suggesting emerge of extensively drug-resist (XDR) or even pan-drugs-resist (PDR) strains. The resistance pattern for *Pseudomonas aeruginosa*, especially for Ceftazidime and Ciprofloxacin too matches data from Baghdad Teaching Hospital [21], reinforcing these pathogens grow threat in tertiary healthcare settings.

The aggregated nature of this data provides a value snapshot, but more detailed analyzing, include MICs and its correlation to clinical outcome, and would deepen understanding. Nonetheless, these finding strongly supports more intensified antimicrobial stewardship effort at Mahmoudiyah Hospital. The observed resistance pattern has direct implications to empirical therapy. Iraqi study emphasizes same point: antibiotic prescribe should be guide by updated local antibiograms [22]. Strong infection controlling policies is needed for limit transmission of resistance strains through healthcare and community setting. Also, continue surveillance in Iraqi regions are vital to capturing evolving resistance pattern and informing evidence-based national treatment guideline.

4- CONCLUSION

The retrospective analysis of bacterial resistances patterns at Mahmoudiyah Hospital in 2024 show a clear picture for the significant challenge is posed by antimicrobial resistance within the healthcare settings. The study reveals high prevalence in common bacterial pathogens, including *Escherichia coli*, *Klebsiella pneumoniae*, and *Staphylococcus aureus*, exhibit alarming rate of resistance to commonly use antibiotics such as Penicillin, Erythromycin, Ciprofloxacin, Ceftriaxone, and the Trimethoprim/Sulfamethoxazole. Particularly concerned were the indications of high MRSA rate among *S. aureus* and ESBL production between *E. coli*, along the observed resistance for last-resort antibiotics like Colistin in *Acinetobacter baumannii*.

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