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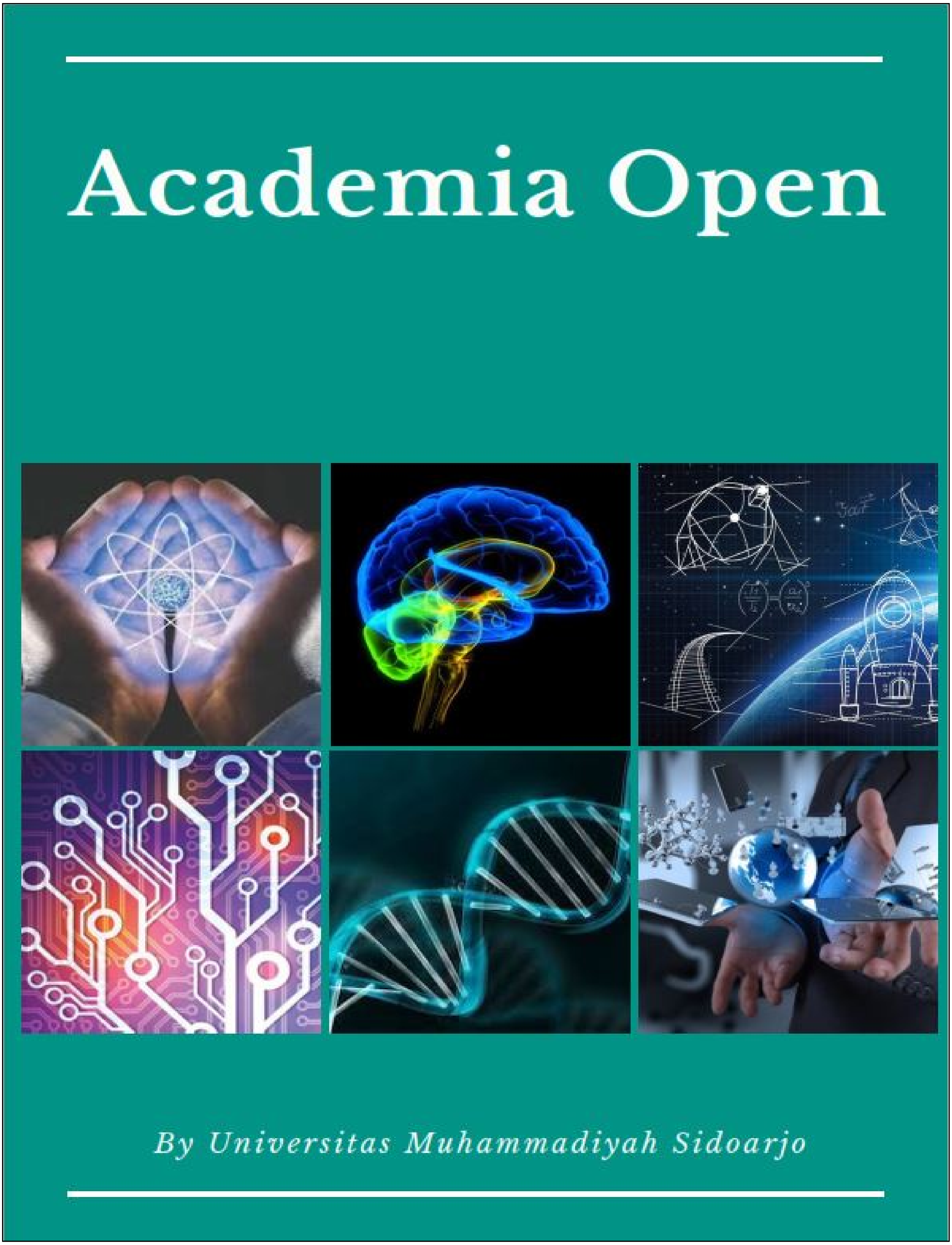

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Evaluation Of Bacterial Pathogens And Antimicrobial Resistance In Blood Isolates From Febrile Cases At Medical City Hospital In Baghdad

Evaluasi Patogen Bakteri Dan Resistensi Antimikroba Pada Isolat Darah Dari Kasus Demam Di Rumah Sakit Kota Medis Di Baghdad

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Abstract

Bacterial bloodstream infection is a critical public health issue due to its high morbidity and mortality rates. Prompt diagnosis and appropriate treatment are essential for improving patient outcomes. This study aimed to identify the bacterial composition of bloodstream infections and their antibiotic resistance patterns at Medical City Hospital, Baghdad. A cross-sectional study of 462 fever-diagnosed individuals (244 females, 218 males) conducted from July 3 to September 24, 2024, found that 96 (20.8%) had culture-positive bacteria. Staphylococcus aureus (30.21%) was the most prevalent, followed by coagulase-negative staphylococci (26.04%), Escherichia coli (10.42%), Enterobacter cloacae (8.34%), Streptococcus pyogenes (7.29%), Citrobacter spp. (6.25%), and Klebsiella spp. (5.25%). Antibiotic resistance was high, particularly to oxacillin (95.63%), ampicillin (97.79%), and gentamicin (88.54%). Multidrug resistance was identified in 87.49% of bacterial isolates, with susceptibility to cefotaxime, azithromycin, ceftriaxone, and ciprofloxacin. Notably, Gram-positive bacteria showed significant resistance to vancomycin and oxacillin (54.17%). These findings underscore the importance of routine susceptibility testing for pathogens and antibiotics to prevent the spread of resistant bacterial infections and guide effective treatment strategies.

Highlights:

1. Identify bloodstream infection bacteria, analyze antibiotic resistance patterns.
2. 20.8% culture-positive; Staphylococcus aureus most prevalent; high resistance.
3. Multidrug resistance prevalent; emphasize susceptibility testing to manage resistance.

Keywords: Bloodstream infections, Antimicrobial resistance, Multidrug, Cross-sectional research, Microbiological analysis

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Introduction

Bloodstream infections (BSI) have a major impact on the global burden of sickness and mortality, According to [1-3]. However, this problem is widespread in industrialized nations [4]. Several bacteria have been identified as the agents that cause bacteremia, and the distribution of these bacteria varies depending on the geographical region [5-7]. According to [8], these organisms transmit illnesses that result in prolonged hospitalization, increased healthcare expenditures, and an increased mortality rate

Treatment with appropriate antibiotics should be administered as soon as possible in order to effectively manage bacteremia. Nevertheless, due to antibiotic resistance in several bacterial illnesses, this problem has become an extremely important health concern, with enormous repercussions for economies and societies worldwide [9]. Investigations conducted in Ethiopia have shown a considerable incidence of bacterial drug resistance to commonly utilized antibiotics. Inadequate laboratory facilities for conducting antimicrobial drug susceptibility studies and the lack of a national guideline for antibiotic usage are the primary factors that have led to the development of this resistance. As a consequence of this, therapists use empirical ways to treat their patients, which brings to a substantial prevalence of self-treatment among individuals and animals that does not include a direct prescription from a medical professional. According to [10], accumulating these elements would establish resistance and its fast dissemination worldwide.

Several studies have demonstrated that insufficient care of bloodstream infections (BSI) results in increased patient mortality rates and the development of resistant strains to medicines [11-13]. A study done in Iraq shows that bloodstream infections BSIs are especially common in people whose immune system is compromised, for example, those recovered from critical in-care units or patients who had recent surgery [14]. It also immediately increases the difficulty of treating such diseases because of the presence of a class of drugs effectively quelling these bacteria called antimicrobial resistance AMR, aggravating mortality rates, length of hospital stay and costs. A study [15] where nearly 60% of blood samples from febrile patients in a sequence of hospitals in Baghdad confirmed resistance to multiple drugs. The factor particularly responsible for this resistance is the excessive prescribing of antibiotics in healthcare and community settings.

In a scientifically accurate manner, they presented an investigation carried out in Iraq that showed that febrile patients contain a much higher number of organisms belonging to the Gram-negative group of bacteria, especially E. coli and Acinetobacter spp. I would like to add that these organisms are frequently bactericidal and resistant to cephalosporins and carbapenems, as stated by [16]. A study [17] revealed that 45% of blood cultures obtained from febrile patients in Baghdad were positive for bacterial pathogens, with an astonishingly high resistance to beta-lactam drugs. These findings also strengthen the need for rapid assessment of bacterial pathogens and strains of resistance to AMR at the large hospitals in Iraq.

Medical City Hospital-Baghdad is a tertiary referral hospital in Iraq that provides tertiary-level care to patients with febrile age. Each of these conditions is well documented as a complication of urotoxicity associated with the use of chemotherapeutic agents in febrile patients. Determining the time of antimicrobial therapy initialization during febrile neutropenia prevention for patients with solid tumours looking for its influence on antimicrobial resistance forming. Hence, this epidemiological study, like many others, defined the hierarchy of interventions index and calendar against Bacteremia Impact Assessment and Management. Treatment for osteomyelitis in febrile children involves eradicating the cause of infection (mostly osteomyelitis destruction). Febrile patients were defined as those who presented to the health institution with extreme body temperature equal to or exceeding 38°C.

Methods

2.1 Study Design

The study was conducted among outpatients with fever from July 3 to September 24, 2024, using a prospective cross-sectional study design. Medical City Hospital, located in the heart of Baghdad, is Iraq's largest and oldest teaching hospital. Based on a probability of 15%, prevalence of 24.2% [18], precision of 5%, and confidence level of 95%, 462 were included patients with fever. The patients who received antibiotics within the previous ten days of the hospital were excluded admission from this study.

2.2 Sample Gathering

Using aseptic techniques involving 70% alcohol and 2% iodine, we collected approximately 10 ml of venous blood from adults (with some patients undergoing a single draw from one arm and others a double draw from both arms) and 2-3 ml from children. We transferred the samples into two bottles, each holding 45 ml of Brain Heart Infusion Broth (BHIB). The goal was to achieve a ratio of 5 ml of blood to 45 ml of medium, or 1:10. The blood culture was transported broth to the hospital microbiology laboratory within 30 minutes and incubated both aerobically and anaerobically at 37°C for 5-7 days.

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2.3 Microbiological Analysis

Blood culture broths were examined every day for seven days for any signs of bacterial development, such as turbidity, hemolysis, and the formation of clots. The bottles were processed using a gram stain, revealing growth evidence. Then subcultures were prepared onto blood agar, MacConkey agar, and Manitol salt agar (all manufactured by Oxoid Ltd. In the United Kingdom) and incubated at 37 °C for twenty-four hours. Blood culture broths were subjected, which showed no signs of bacterial development after seven days, to subculturing before reporting a negative result. The colony morphology, gram staining reaction, and biochemical tests [19] such as the catalase test, the coagulase test, Triple Sugar Iron agar (TSI) (OXOID, UK), citrate utilization test (BBLTM) were used, the urease test (BBLTM), and the motility indole lysine (MIL) (BBLTM) test to identify the bacterial isolates. The standard procedure was used for bacterial identification.

The API 20E test (bioMérieux Co.) was conducted to detect Enterobacteriaceae and the API 20NE test (bioMérieux Co.) to detect Pseudomonas spp. The API staph and API strept tests were used, both developed by BioMérieux, to determine the presence of Staphylococcus spp. and Streptococcus.

2.4 Antibiotic susceptibility test

A standard approach was employed to ascertain E-test MICs [20]. Muller-Hinton plates enriched with 5% sheep blood were infected with a 0.5 McFarland suspension obtained from plates. E-test strips (AB Biodisk, Solna, Sweden) were applied to each plate. Following overnight incubation at 35˚C, the MIC was determined where the growth inhibition ellipse meets the strip (table 1). The minimum inhibitory concentrations (MICs) were assessed in air and carbon dioxide (CO2). The breakpoints for categorizing susceptibility, resistance, and intermediacy for each antimicrobial agent were established according to the guidelines set out by the National Committee for Clinical Laboratory Standards (NCCLS).

Antibiotic	MIC
Amoxicillin (AM)	16 µg
Ceftriaxone (CRO)	30 µg
Azithromycin (AZM)	2 µg
Cefotaxime (CTX)	30 µg
Ciprofloxacin (CIP)	5 µg
Doxycycline (DX)	30 µg
Vancomycin (V)	30 µg
Gentamicin (G)	30 µg
Trimethoprim-sulfamethoxazole	
(TMP-SMX)	25 µg
Ampicillin (Amp)	10 µg
Imepenem (IPM)	10 µg
Oxacillin (OX)	1 µg
Chloramphenicol (C)	30 µg

Table 1. *Antibiotic Susceptibility Test and Minimum Inhibitory Concentration (MIC) Values for Bacterial Isolates*

The choice of antimicrobial drugs was based on the fact that they are easily accessible and regularly recommended for treating bacterial infections in healthcare facilities. Broth microdilution (BMD) methods were used to determine the vancomycin minimum inhibitory concentration (MIC) and disc diffusion methods to isolate vancomycin-resistant S. aureus and CoNS. Then, these bacteria were cultivated on skim milk agar and maintained at -60 °C. This was done in order to determine the MIC of vancomycin further.

2.5 Quality Control

Reference strains of E. coli (ATCC 25922) and S. aureus (ATCC 25923) were used as control strains for identification and drug susceptibility testing. We incubated some of the previously made culture material for one night for the negative control to see if any microbes had taken up residence. According to the findings of this research (Magiorakos et al. 2012), the term "multidrug resistance" refers to the simultaneous resistance to more than two different antimicrobial drugs.

2.6 Statistical Analysis

STATA version 11 (STATA Corp LP, USA) was employed to analyze the data. Categorical variables were summarised as proportions and analyzed using Pearson's Chi-Square or Fisher's exact test to investigate statistical differences among the different groups. The strength of associations was assessed by calculating odds ratios with

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their respective 95% confidence intervals (CI). A p-value of less than 0.05 was regarded as statistically significant.

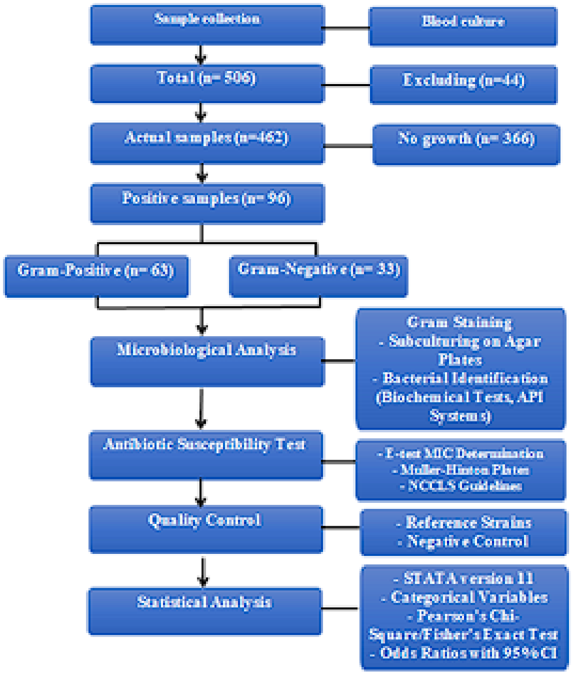

Figure 1. *The framework for this study's research*

Result and Discussion

Result

A total of 462 febrile patients from Medical City Hospital, Baghdad, were included in this study. Among these, 245 (53.67%) were women, and 214 (46.32%) were men, demonstrating a near-equal distribution across genders. The participants' ages ranged from 4 to 72 years [mean 29.67 ± 1.96 (SD)]. Interestingly, more than half of the participants, 261 (56.49%), fell within the age range of 17–35 years. This particular age group was statistically significant regarding bacterial infections, with a P-value of 0.045 ($\chi^2 = 18.473$, df = 12), indicating that younger patients were more likely to have bacterial infections than older individuals.

Ninety-six bacterial strains were isolated from the patients' blood cultures, indicating that 20.8% had bacterial infections. Of these 96 isolates, 29 (30.21%) were identified as S. aureus, making it the most frequently isolated pathogen. This was closely followed by coagulase-negative staphylococci (CoNS), accounting for 25 (26.04%) bacterial isolates.

Pathogen	No. of isolates	%
n=96		
S. aureus	29	30.21%
CoNS	25	26.04%
E. coli	10	10.42%
Enterobacter cloacae	8	8.34%
S. pyogenes	7	7.29%
Citrobacter spp	6	6.25%
Klebsiella spp	5	5.21
S. paratyphi	1	1.04
P. aeruginosa	1	1.04
Bacillus cereus	1	1.04
H. influenzae	1	1.04

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Acinetobacter spp	1	1.04
Enterobacter sakazakii	1	1.04
Total	96	100%

Table 2. *Distribution of Bacterial Pathogens Isolated from Febrile Cases at Medical City Hospital, Baghdad (n=96)*

Other notable pathogens included E. coli (10.42%), E. cloacae (8.34%), and S. pyogenes (7.29%). The remaining bacterial strains, with species such as Citrobacter spp, were relatively rare. (6.25%), Klebsiella spp. (5.21%), S. paratyphi, P. aeruginosa, Bacillus cereus, H. influenzae, Acinetobacter spp., and E. sakazakii contribute only 1.04% to the overall isolates.

Although bacterial infections were more common among female participants, the difference between male and female infection rates was insignificant ($P = 0.16$, $\chi^2 = 2.01$, $df = 1$). This finding suggests that gender did not significantly determine susceptibility to bacterial infections in febrile patients. However, the age of the patients was significantly correlated with the occurrence of bacterial infections.

The antimicrobial susceptibility patterns of the bacterial isolates were tested against various commonly used antibiotics. S. aureus resisted multiple antibiotics, with 100% of isolates resistant to ampicillin, oxacillin, and amoxicillin, commonly used first-line antibiotics. Additionally, high levels of resistance were observed for gentamicin (89.66%), vancomycin (82.76%), and tetracycline (27.59%).

Pathogen	Number of drug-resistant bacterial isolates (%)											
	AM	CRO	AZM	CTX	CIP	Te	V	G	(TMP-SMX)	AMP	OX	C
S. aureus	29 (100)	4 (13.79)	5 (17.24)	7 (24.14)	5 (17.24)	8 (27.59)	24 (82.76)	26 (89.66)	12 (41.38)	29 (100)	27 (93.10)	11 (37.93)
CoNS	23 (92)	6 (24)	6 (24)	2 (8)	7 (28)	10 (40)	22 (88)	22 (88)	8 (32)	25 (100)	24 (96)	6 (24)
E. coli	10 (100)	0	NC	1 (10)	2 (50)	4 (40)	NC	8 (80)	3 (30)	9 (90)	NC	3 (30)
Enterobacter cloacae	8 (100)	1 (12.5)	NC	1 (12.5)	2 (25)	4 (50)	NC	8 (100)	2 (25)	8 (100)	NC	2 (25)
S. pyogenes	5 (71.43)	2 (28.57)	5 (71.43)	0	2 (28.57)	7 (71.43)	6 (85.71)	6 (85.71)	1 (14.29)	7 (100)	1 (14.2)	2 (28.57)
Citrobacter spp	6 (100)	0	4 (66.67	2 (33.33)	1 (16.67)	4 (66.67)	NC	5 (83.33)	2 (33.33)	5 (83.3)	NC	2 (33.33)
Klebsiella spp	5 (100)	0	0	0	0	1 (20)	NC	4 (80)	1 (20)	5 (100)	NC	1 (20)
S. paratyphi	1 (100)	0	0	0	0	0	NC	1 (100)	0	1 (100)	NC	0
P. aeruginosa	1 (100)	0	NC	0	0	0	NC	1 (100)	0	1 (100)	NC	0
Bacillus cereus	1 (100)	0	NC	0	0	0	NC	1 (100)	0	1 (100)	NC	0
H. influenzae	1 (100)	0	1 (100)	0	0	0	NC	1 (100)	0	1 (100)	NC	0
Avinetobacter spp	1 (100)	0	NC	0	0	0	NC	1 (100)	0	1 (100)	NC	0
Enterobacter sakazakii	1 (100)	0	NC	0	1 (100)	1 (100)	NC	1 (100)	0	1 (100)	NC	0
Total	92 (95.83)	13 (13.54)	21 (21.88)	13 (13.54)	20 (20.83)	37 (38.54)	52 (54.17)	85 (88.54)	29 (30.21)	94 (97.79)	52 (54.17)	27 (28.13)

Table 3. *Bacterial organisms tested for antibiotic susceptibility in blood cultures taken from feverish patients at Baghdad's Medical City Hospital. (NC: Not compatible)*

Pathogen	Number of drug-resistant bacterial isolates (%)											
	S	R+1	R+2	R+3	R+4	R+5	R+6	R+7	R+8	R+9	R+10	R+11

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S. aureus	1 (3.45)	-	-	1 (3.45)	3 (6.9)	6 (20.69	7 (24.14)	6 (20.69)	3 (6.9)	1 (3.45)	1 (3.45)	-
CoNS	1 (4)	-	-	3 (12)	7 (28)	2 (8)	6 (24)	3 (12)	2 (8)	1 (4)	-	-
E. coli	-	-	-	-	-	4 (40)	2 (10)	2 (10)	2 (10)	-	-	-
Enterobacter cloacae	-	-	-	-	1 (12.5)	3 (37.5)	3 (37.5)	1 (12.5)	-	-	-	-
S. pyogenes	-	-	-	1 (14.29)	2 (28.57)	2 (28.57)	2 (28.57)	-	-	-	-	-
Citrobacter spp	-	-	-	-	2 (33.33)	1 (16.67)	1 (16.67)	1 (16.67)	1 (16.67)	-	-	-
Klebsiella spp	-	-	-	-	2 (40)	1 (20)	1 (20)	1 (20)	-	-	-	-
S. paratyphi	-	-	-	-	-	-	1 (100)	-	-	-	-	-
P. aeruginosa	-	-	-	-	-	-	-	1 (100)	-	-	-	-
Bacillus cereus	-	-	-	1 (100)	-	-	-	-	-	-	-	-
H. influenzae	-	-	-	-	-	-	1 (100)	-	-	-	-	-
Acinetobacter spp	-	-	-	-	-	-	-	1 (100)	-	-	-	-
Enterobacter sakazakii	-	-	-	-	-	1 (100)	-	-	-	-	-	-
Total	2 (2.08)	-	-	6 (6.25)	17 (17.71)	20 (20.83)	20 (20.83)	16 (16.67)	8 (8.33)	2 (2.08)	1 (1.04)	-

Table 4. *Bacterial bacterial MDR patterns in the blood of feverish patients admitted to Medical City Hospital, Baghdad*

Discussion

Dissemination of MRSA strains into the general population has now emerged as one of the primary objectives in controlling infectious diseases. A study [21] summarizes this observation, stating that MRSA is responsible for most hospital-acquired infections in advanced and low-income countries. This study found that S. aureus was completely resistant to ampicillin and oxacillin. This is in line with a larger trend of MRSA, which is a major cause of complicated and hard-to-treat bloodstream infections.

Similarly, staphylococci that do not produce coagulase (CoNS), often regarded as less pathogenic than S. aureus, have garnered attention as real pathogens, particularly in the context of nosocomial infections and patients with immunocompromised conditions. Also, [22] disclosed that CoNS are common in hospital-acquired infections in intravascular devices and prosthetic implants.

The resistance profiles of the CoNS in this study agree.

All the isolates in the previous studies were 100% resistant to ampicillin, oxacillin, and other beta-lactam antibiotics like vancomycin and gentamicin. In a similar study, [23] also found a high level of CoNS prevalence in urinary tract infections and reported high rates of resistance to vancomycin and beta-lactam antibiotics. Researchers have also found that Commensal CoNS dominates a large proportion of blood infection clinics that excessively use broad-spectrum antibiotics, highlighting the opportunistic pathogenic features of CoNS.

On the other hand, within the resistant isolates studied in E. coli and E. cloacae genera, it is possible to distinguish those carrying resistance patterns characteristic of the more general epidemiological trend of resistance seen with Gram-negatives. For instance, E. coli exhibited 100% resistance to amoxicillin and ampicillin. Furthermore, the bacteria exhibited a high level of amikacin resistance (80%) and a mid-range sensitivity to trimethoprim-sulfamethoxazole (90%). In addition, [24] documented these stress or sulfamethoxazole resistance attributes of E. coli bloodstream infections in India. Firstly, the prevalence of these resistant E. coli strains is rising, leading to an increased prescription of amoxicillin and ampicillin. Concerns about the waning effectiveness of fluoroquinolones

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and third-generation cephalosporins against nosocomial Gram-negative infections have led to the reported resistance towards ciprofloxacin and cefotaxime. Similarly, we observed 100% resistance to amoxicillin, ampicillin, and trimethoprim-sulfamethoxazole in the E. cloacae isolates of this study, and we also scored these results in E. cloacae bloodstream infections in Latin America. [25]

Despite the limited measures currently available to combat it, Gram-negative bacteria are exhibiting an alarming global increase in AMR. The phenomenon of carbapenem resistance in Enterobacteriaceae and P. aeruginosa has appeared in many recent reviews. However, [26] focused on the increasing cases of carbapenem-resistant Enterobacter cloacae in inpatient and outpatient settings. It is worth mentioning that P. aeruginosa showing ciprofloxacin resistance in the present study adds another twist to the issues encountered in managing Gram-negative bacterial infection. It's important to note [27] that implementing paid placement services has significantly increased the prevalence of fluoroquinolone-resistant P. aeruginosa. This level has been consistently low over the past ten years. The study noted that MDR strains, primarily E. coli, E. cloacae, and Citrobacter spp., were present in some of these gram-negative isolates. This mirrors the global crisis of AMR, where unnecessary or inappropriate prescribing, and especially the use of antibiotics, has led to the emergence of superbugs.

Additionally, the distribution of multidrug-resistant (MDR) strains is worrisome. This study confirms the presence of pathogen-specific resistance, but it is concerning overall. Of 96 bacterial isolates, 95.83% resisted at least one antibacterial agent, and most resisted several antibiotic classes. This aligns with the findings of [28], which highlighted the increasing prevalence of multidrug-resistant (MDR) strains of bacteria, particularly in healthcare-associated infections and community-acquired infections. These and other factors lead authors to emphasize that most bloodstream infections today, caused by S. aureus, Coagulase-negative staphylococci (CoNS), and gramme-negative bacilli, are multidrug-resistant, making them difficult to treat and contributing to increased rates of morbidity and mortality. [29] also said that the main reason MDR [multiple drug resistant] organisms are appearing in healthcare facilities is because of the heavy use of antibiotics in these places, especially in septic intensive care units and surgical wards. These conclusions suggest that the global health crisis resulting from increased civil infections by MDR bacteria only scratches the surface.

This study reveals that many S. aureus and coagulase-negative staphylococci (CoNS) resist vancomycin, a commonly used last-resort antibiotic for Gram-positive infections. The study found vancomycin resistance in 82.76% of the S. aureus isolates and 88% of the CoNS isolates submitted to pneumonia disease. It would appear that vancomycin-resistant staphylococci (VRS) may be in the early stages of emerging within this population. This is in line with other global reports since [30] indicated an increasing percentage of S. aureus and CoNS, which showed resistance to vancomycin, especially among patients who have been on heavy antibiotics for a while. [31] S. pyogenes became more resistant to vancomycin, making it harder to control Gram-positive infections that spread quickly. The urge to have VRS outbreaks is quite alarming because these germs cause few effective treatment options for infection; hence, new antibiotics are needed.

A lower percentage of isolates were resistant to ceftriaxone (13.79%), azithromycin (17.24%), and ciprofloxacin (17.24%).

Similarly, CoNS isolates demonstrated significant resistance patterns. All CoNS isolates, like S. aureus, were completely resistant to ampicillin and oxacillin. They were also very resistant to vancomycin (88%), gentamicin (88%), and tetracycline (40%). Interestingly, CoNS isolates showed higher resistance to azithromycin (24%) and ceftriaxone (24%) compared to S. aureus.

E. coli demonstrated 100% resistance to amoxicillin and ampicillin among the Gram-negative bacteria. E. coli also exhibited high levels of resistance to gentamicin (80%) and trimethoprim-sulfamethoxazole (90%). In comparison, resistance to cefotaxime (50%) and ciprofloxacin (40%) was moderate.

All isolates (100%) resist amoxicillin and ampicillin for E. coli. We also observed high resistance rates for gentamicin (100%) and trimethoprim-sulfamethoxazole (100%). In comparison, resistance to ciprofloxacin and tetracycline was moderate at 50% each. E. cloacae exhibited lower resistance to ceftriaxone (12.5%) and cefotaxime (12.5%).

S. pyogenes showed high resistance to vancomycin (85.71%) and gentamicin (85.71%), while Citrobacter spp. demonstrated resistance to gentamicin (83.33%) and trimethoprim-sulfamethoxazole (83.33%). Klebsiella spp., although less prevalent, exhibited 100% resistance to amoxicillin and ampicillin, with moderate resistance to gentamicin (80%) and trimethoprim-sulfamethoxazole (80%).

The overall prevalence of multidrug-resistant (MDR) bacterial strains was notable. Of the 96 bacterial isolates, 92 (95.83%) demonstrated resistance to at least one antibiotic, and most isolates exhibited resistance to multiple antibiotics. For S. aureus, the most common MDR pattern involved resistance to seven antibiotics (24.14%), followed by resistance to six antibiotics (20.69%). CoNS exhibited similar MDR patterns, with the most frequent resistance profile involving resistance to five antibiotics (28%), followed by resistance to six antibiotics (24%).

For Gram-negative bacteria, 40% of E. coli isolates resisted six antibiotics. In comparison, 37.5% of E. cloacae isolates were resistant to five or six antibiotics. Citrobacter spp. and Klebsiella spp. followed similar trends, with

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Citrobacter spp. Exhibiting resistance to five antibiotics in 33.33% of cases and Klebsiella spp. Exhibiting resistance to four antibiotics in 40% of cases.

The single S. paratyphi isolate was resistant to amoxicillin, ampicillin, and trimethoprim-sulfamethoxazole. In contrast, the P. aeruginosa isolate was resistant to amoxicillin, ampicillin, and ciprofloxacin. Similarly, H. influenzae was resistant to amoxicillin, ampicillin, and cefotaxime.

Conclusion

This study provides critical insights into the bacterial pathogens responsible for bloodstream infections among febrile patients at Medical City Hospital in Baghdad, revealing a substantial challenge posed by multidrug resistance. Among the 96 culture-positive cases, Staphylococcus aureus and coagulase-negative staphylococci (CoNS) were the most frequently isolated pathogens, followed by Escherichia coli and Enterobacter cloacae. The alarming discovery that 87.49% of bacterial isolates exhibited multidrug resistance underscores the pressing need for careful antimicrobial stewardship. High resistance was observed to commonly used antibiotics such as oxacillin (95.83%), ampicillin (97.79%), and gentamicin (88.54%). At the same time, certain drugs like cefotaxime, azithromycin, ceftriaxone, and ciprofloxacin retained better efficacy. The resistance of Gram-positive bacteria to vancomycin and oxacillin further complicates treatment strategies, highlighting the importance of continuously monitoring antimicrobial resistance patterns. This study emphasizes the urgent need for regular susceptibility testing and judicious antibiotic use to prevent the further emergence and spread of resistant bacterial strains, ensuring better clinical outcomes for patients suffering from bloodstream infections.

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