Al-Turath Journal for Biology (ATJB)
Open Access Journal
Open Access Journal
ISSN Print: 3080-1265
Online : 3080-1273

Original Paper

Prevalence and Distribution of Bacterial Isolates from Blood Cultures Among Patients with Fever: A Retrospective Study

Fouad Najm Abed[1], Dalya Falah Hassan[2], Ahmed N. Abed[3], Omar Ahmed Hasson[4]

[1] Ministry of health, Al-Rusafa health Directorate, Baghdad, Iraq
[2] College of medicine, Al-Iraqia University, Baghdad Iraq.
[3] College of science for women, University of Baghdad, Baghdad, Iraq.
[4] College of Health and medical techniques, department of medical laboratories techniques, Al-Turath University, Baghdad, Iraq
Correspondence email | ahmed.najm@csw.uobaghdad.edu.iq
Received: 18/02/2026 | **Accepted**: 23/03/2026 | **Available online:** 31/03/2026 | **DOI:** https://doi.org/10.63964/atjb.2026.1.9

ABSTRACT
Bloodstream infections (BSIs) remain a critical cause of morbidity and mortality worldwide, particularly among febrile patients. Understanding the local epidemiology of bacterial isolates from blood cultures is essential for guiding empiric antimicrobial therapy and improving clinical outcomes. This study aimed to determine the prevalence, distribution, and antimicrobial susceptibility profiles of bacterial isolates recovered from blood cultures of patients presenting with fever. This retrospective cross-sectional study involved analyzing 186 blood culture records of patients presenting with fever. All blood samples were analyzed using routine microbiological procedures which involved culture of samples on suitable media, biochemical identification and antibiotic susceptibility testing (disk diffusion technique). Demographic data (age and sex) the culture result, organism identified and antibiotic susceptibility profile were retrieved and analyzed.
Of the 186 blood cultures analyzed, 33 (17.7%) yielded bacterial growth while 153 (82.3%) showed no growth. Gram-positive organisms constituted the majority of isolates at 72.7% (n=24), with *Staphylococcus haemolyticus* (n=12, 36.3%) and *Staphylococcus aureus* (n=11, 33.3%) being the predominant species. Gram-negative organisms accounted for 24.2% (n=8) of all positive cultures. Female patients comprised 55.4% of the study population and demonstrated a slightly higher culture positivity rate (18.4%) compared to males (16.8%). Notably, high rates of multidrug resistance were observed, particularly among *Staphylococcus* isolates, while vancomycin and linezolid retained full activity. The predominance of Gram-positive organisms underscores the importance of local surveillance data in guiding empiric antimicrobial therapy. The high prevalence of multidrug resistance highlights the urgent need for antimicrobial stewardship programs and continuous monitoring of resistance trends to inform treatment protocols.

KEYWORDS: *Blood culture; bacterial isolates; bloodstream infection; retrospective study; Staphylococcus aureus; Staphylococcus haemolyticus*

1. INTRODUCTION

Blood stream infections (BSIs) are among the most critical and potentially life-threatening entities in clinical medicine, with the highest associated morbidity and mortality rates and continuing to pose a considerable challenge to health systems worldwide [1]. Prompt recognition of a blood stream infection and identification of the causative pathogens by blood culture examination continue to be the gold standard for diagnosis of BSI and thus guiding targeted antibacterial therapy according to identification and sensitivities [2]. Fever is the one of the commonest reasons patients present to the physicians in primary and secondary care and physicians obtain blood cultures hoping to isolate a micro-organism, and then guide treatment accordingly [3]. The epidemiology of BSIs varies greatly by geography, institution type, and patient population, so surveillance of this aspect locally is essential to the establishment of evidence-based empiric therapy guidelines [4]. Worldwide, Gram-positive organisms have consistently been the most prevalent pathogen isolated from blood cultures (particularly *staphylococci*) and closely followed by Gram-negative bacilli (most commonly E. coli, *K. pneumoniae*, and *A. baumannii*) [5,6]. But relative prevalence of these may change depending on the proportion of nosocomial to community acquired BSI, and the composition of the patient population, and on the antibiotics prescribed locally.

BSI caused by bacteria is a global and increasing public health problem, due to the increasing prevalence of antimicrobial resistance [6,7]. It is an alarming phenomenon to increasingly isolate MDR bacteria in blood cultures, thereby limiting treatment options and negatively impacting the patient, as reported for numerous other infections [8]. MRSA in *S.aureus* has shown alarming rates in much of the globe, and GNB such as *A.baumannii* have been reported to be resistant to

nearly all antimicrobials currently available [11,12]. Coagulase-negative *staphylococci* (CoNS), including *Staphylococcus haemolyticus*, represent a complex diagnostic challenge in clinical microbiology [13]. These organisms are the most common cause of blood culture contamination, yet they are also recognized as genuine pathogens in specific clinical contexts, particularly among immunocompromised patients, those with indwelling medical devices, and neonates [14]. Distinguishing true CoNS bacteremia from culture contamination would be possible with appropriate clinical correlation of number of positive culture sets, time to positivity, clinical condition of the patient etc [15,16].

Local epidemiological data though the key factor in starting empiric antimicrobials; literature on patterns of isolates, and antibiotic susceptibilities from blood cultures of different clinical settings is poor. It is even more evident in resource poor settings where microbiology diagnostic capacity is limited and antimicrobial stewardship framework is still developing [17]. It is against this background that this retrospective study of blood culture reports of febrile patients was undertaken, the purpose of which was to find out rate of culture positivity, pattern of organisms isolated, socio-demographic profile of positive culture patients and the pattern of antibiotic susceptibility of the isolated organisms.

2-MATERIALS AND METHODS

Study Design and Setting

A retrospective cross-sectional study was carried out using blood culture data collected by the Clinical Microbiology Laboratory from hospitals across Baghdad.

Sample Collection and Processing

All blood culture specimens were collected from febrile patients by routine aseptic techniques from different hospitals in Baghdad, following the recognized principles in clinical microbiology. the skin was disinfected using 70% isopropyl alcohol followed by chlorhexidine or an iodine-based antiseptic. and then left to dry before venipuncture, reducing the risk of contamination [17]. Blood samples were injected into a commercial blood culture bottle and were then transported to microbiology laboratory for incubation and processing. All blood culture bottles were incubated at 35-37 °C and then examined for microbial growth for 5-7 days after which it was reported negative.

Identification and Antimicrobial Susceptibility Testing

All positive blood cultures were sub cultured onto suitable solid media. The bacteria were identified by routine biochemical tests. Antibiotic susceptibility testing (AST) was carried out on Mueller-Hinton agar using the Kirby-Bauer disk diffusion technique on isolates based on the CLSI guidelines. The panels of antibiotics tested varied with the type of organism and they were interpreted against CLSI breakpoints as susceptible (S), intermediate (I) or resistant (R) [8][9]. The classification of multidrug-resistant (MDR), extensively drug-resistant (XDR) and pandrug-resistant (PDR) strains were based on the international expert proposal, established by Magiorakos et al. MDR strains were considered those that were resistant to at least one drug in at least three classes of antimicrobial drugs, and XDR strains, those that were susceptible to one or two classes only [10].

Statistical Analysis

Categorical variables were described using frequencies and percentages and continuous variables using the mean (SD) or median (IQR), depending on their distribution. Statistical analysis was done using IBM SPSS version 22.0, and results were considered statistically significant if two-sided P value was < 0.05.

Ethical Considerations

This study was a retrospective review of anonymized laboratory blood culture records. No direct patient contact was involved, and no identified personal information was collected, accessed or recorded.

3-RESULTS

Demographic Characteristics

A total of 186 blood culture records from febrile patients were included in this retrospective analysis. The demographic characteristics of the study population are summarized in Table 1. The majority of patients were female (103/186, 55.4%), while 83 patients (44.6%) were male. The mean age of the study population was 31.9 ± 23.0 years (range: 0.2–85.0 years), with a median age of 29.5 years. The largest proportion of patients fell within the 1–17 years age category (52/186, 28.0%), followed by the 18–39 years group (46/186, 24.7%). Patients aged 60 years and above constituted 16.6% (31/186) of the cohort, while infants under one year accounted for 6.4% (12/186).

Table 1. Demographic Characteristics of the Study Population (N = 186)

Characteristic	Category	n (%)
Sex	Female	103 (55.4)
	Male	83 (44.6)
Age Group	<1 year	12 (6.4)
	1–17 years	52 (28.0)
	18–39 years	46 (24.7)
	40–59 years	45 (24.2)
	≥60 years	31 (16.6)
Diagnosis	Fever	185 (99.5)
	Dehydration	1 (0.5)

Blood Culture Positivity Rate

A total of 186 blood cultures were isolated and studied. Growth occurred in 33 (17.7%) of the cultures and the remaining 153(82.3%) cultures showed no growth. While there was a small difference between gender proportions of patients who had culture positive growth; female patients19/103 (18.4%) compared to male patients 14/83 (16.8%); this was not significant ($p>0.05$). Table 2 shows the breakdown of age groups who had culture positive growth; these were highest in patients aged 40-59 years and ≥ 60 years, so there was a pattern of highest culture positivity in older adults.

Table 2. Distribution of Positive Blood Cultures by Age Group

Age Group	Total (n)	Positive, n (%)	Positivity Rate (%)
<1 year	12	2	16.6
1–17 years	52	9	17.3
18–39 years	46	6	13.0
40–59 years	45	9	20
≥60 years	31	7	22.5
Total	186	33	17.7

Distribution of Bacterial Isolates

The prevalence of bacterial species identified from positive blood cultures is illustrated in Table 3. Gram-positive bacteria were found to be most prevalent, representing 72.7% (24/33) of all positive isolates, and *Staphylococcus haemolyticus* was the organism most frequently isolated representing 36.3% (12/33) of all positive cultures followed closely by Staphylococcus aureus representing 33.3% (11/33). One isolate of *Enterococcus faecalis* (3.0%) was identified. 24.2% (8/33) of all positive cultures were Gram-negative and *Escherichia coli* was the most frequently identified Gram-negative organism 9.1% (3/33) with *Acinetobacter baumannii* identified in 6.1% (2/33) of cases and single isolates were identified for *Klebsiella pneumoniae* and *Enterobacter spp*. (3.0% each) and anaerobic bacteria identified once (3.0%). Since the analysis only utilized laboratory records and did not distinguish true bloodstream infections from contaminating coagulase-negative *Staphylococcus strains*, the high rate of *S. haemolyticus* reported in this study may overestimate the true rate of bacteremia, as a significant portion of these isolates likely represent blood culture contamination**.**

Table 3. Distribution of Bacterial Isolates from Positive Blood Cultures (N = 33)

Organism	Gram Classification	N	% of Total
S. haemolyticus	Gram-positive	12	36.3
S. aureus	Gram-positive	11	33.3
E. faecalis	Gram-positive	1	3.0
Subtotal Gram-positive		24	72.7
E. coli	Gram-negative	3	9.1
A. baumannii	Gram-negative	2	6.1
K. pneumoniae	Gram-negative	1	3.0

Organism	Gram Classification	N	% of Total
Enterobacter spp.	Gram-negative	1	3.0
B. cepacia	Gram-negative	1	3.0
Subtotal Gram-negative		8	24.2
Anaerobic bacteria	Other	1	3.0
Total		33	100.0

Antimicrobial Susceptibility Patterns

***Staphylococcus aureus* Isolates.** Out of the 11 isolates of *S. aureus*, we had AST data for 8 isolates. Resistant for oxacillin showed (3/8, 37.5%) and out of 8 isolates 5 isolates were resistant to erythromycin (62.5%), clindamycin (75.0%) and tetracycline (62.5%). All tested isolates remained fully susceptible to vancomycin (100%), linezolid (100%), tigecycline (100%) and rifampicin (100%) (Table 4).

Table 4. Antimicrobial Susceptibility Profile of *Staphylococcus aureus* Isolates

Antibiotic	Tested (n)	Resistant, n (%)	Sensitive, n (%)
Oxacillin	8	3 (37.5)	5 (62.5)
Erythromycin	8	5 (62.5)	3 (37.5)
Clindamycin	8	6 (75.0)	2 (25.0)
Tetracycline	8	5 (62.5)	3 (37.5)
Gentamicin	4	3 (75.0)	1 (25.0)
Cefoxitin	6	3 (50.0)	3 (50.0)
Vancomycin	4	0 (0.0)	4 (100.0)
Linezolid	2	0 (0.0)	2 (100.0)
Tigecycline	2	0 (0.0)	2 (100.0)
Rifampicin	3	0 (0.0)	3 (100.0)

***Staphylococcus haemolyticus* Isolates.** Ten out of 12 *S. haemolyticus* isolates were available for AST results. High multidrug resistance levels were recorded among these CoNS isolates; erythromycin (70.0%), gentamicin (70.0%), tetracycline (60.0%), tobramycin (60.0%) and cefoxitin (40.0%) showed high levels of resistance. All of *S. haemolyticus* isolates tested (100%) were sensitive to vancomycin, linezolid and tigecycline. This is depicted in Table 5. However, due to very small numbers of isolates being tested for some of the antimicrobials used in this study (e.g., 2 to 4 isolates for Linezolid, Tigecycline, Rifampicin), the observed 100% susceptibility rates for these agents can only be viewed as indicative and require further validation with larger sample sizes

Table 5. Antimicrobial Susceptibility Profile of *Staphylococcus haemolyticus* Isolates

Antibiotic	Tested (n)	Resistant, n (%)	Sensitive, n (%)
Erythromycin	10	7 (70.0)	3 (30.0)
Gentamicin	10	7 (70.0)	3 (30.0)
Tetracycline	10	6 (60.0)	4 (40.0)
Tobramycin	10	6 (60.0)	4 (40.0)
Cefoxitin	10	4 (40.0)	6 (60.0)
Clindamycin	10	3 (30.0)	7 (70.0)
Levofloxacin	10	2 (20.0)	8 (80.0)
Rifampicin	5	3 (60.0)	2 (40.0)
Vancomycin	5	0 (0.0)	5 (100.0)
Linezolid	5	0 (0.0)	5 (100.0)
Tigecycline	4	0 (0.0)	4 (100.0)

Gram-Negative Isolates.
Out of the Gram-negative isolates, one of the E. coli isolates (Sample 68) had the XDR profile by exhibiting resistance to the gentamicin, tobramycin, ampicillin, ceftriaxone, cefoxitin, levofloxacin, and cefepime while susceptible only to imipenem and amikacin. The *A. baumannii* isolate (Sample 90) exhibited a pandrug-resistant phenotype by being resistant to gentamicin, cefuroxime, ceftriaxone, cefepime, imipenem, ciprofloxacin, and levofloxacin and remained susceptible only to tigecycline and trimethoprim/sulfamethoxazole. The *B. cepacia* isolate was resistant to ceftazidime while being susceptible to meropenem and levofloxacin. The *E. faecalis* isolate was resistant to many drugs while being susceptible only to chloramphenicol.

4-DISCUSSION

This retrospective study provides a comprehensive characterization of the bacterial isolates recovered from blood cultures of febrile patients, offering valuable insights into the local epidemiology of bloodstream infections and the antimicrobial resistance landscape. The overall blood culture positivity rate of 17.7% observed in this study falls within the range reported in previous investigations, which have documented positivity rates varying from approximately 5% to 30% depending on the patient population, clinical setting, and pre-analytic factors [3,4]. The relatively low positivity rate may reflect the inclusion of a broad spectrum of febrile patients, many of whom may have had non-bacteremic etiologies of fever.

Gram-positive organisms were most commonly isolated (72.7%) among positive blood culture findings and this is in agreement with data reported from numerous large-scale surveillance studies worldwide [5,6]. A high percentage (36.3%) of the isolates comprised of coagulase-negative *staphylococci*. CoNS are well-established as being the most common organism to contaminate blood cultures and reported contamination rates vary from 0.6% to>6%. As the data were derived from laboratory records, however, additional clinical data on the patient status, blood culture quantity, and time to positivity were absent and thus did not allow us to distinguish between blood contamination and the presence of true bacteremia; thus, the calculated incidence of *Staphylococcus haemolyticus* reflects either bacteremia or contamination. Therefore, the prevalence of true *S. haemolyticus* bacteremia in our series is possibly significantly less than 36.3%. Prospective studies correlating clinical presentation, time-to-positive of blood cultures, time-to-result of the blood culture, identification at genus and species level and quantitative bacterial burden at the time of draw of blood cultures will help in quantifying the true burden of CoNS BSI in our context. As has been found from previous studies, the percentage of CoNS-positive blood cultures that are true bacteremia is typically between 10-25% [15,16]. Multidrug resistance was found to be high in this species which is in agreement with data that *S. haemolyticus* tends to be prone to developing multi-resistance [13][22].

S. aureus was the second most frequently isolated bacteria (33.3%); this is not surprising since *S. aureus* is known to be one of the most common causes of blood stream infection in the world [12]. A considerable proportion of tested *S.aureus* isolates showed resistance to oxacillin (37.5). While this rate falls within the global estimated range of 20-40% it remains a significant concern for empirical therapy in our region. These findings are of great clinical importance, these findings suggest that empirical β-lactam therapy may be ineffective against *S. aureus* strains circulating in this area, and therefore vancomycin or any other glycopeptides must be considered in empiric therapy of staphylococcal bacteremia. These reassuring results of 100% vancomycin activity against S. aureus and *S. haemolyticus* isolates and linezolid activity against both *Staphylococcus* species ensures that there is continued support for the clinician in their treatment of severe *staphylococcal* infections as a last resort [8]. Tigecycline also maintained 100% activity against all *Staphylococcus* isolates. Preserving the efficacy of these last-line antimicrobial agents is therefore essential. to develop by selecting against these bugs with the very few antibiotics that we do have available to treat them [23,24]. A total of 24.2% of the cultures were positive for a Gram-negative-bacteria, *E. coli* being the most isolated Gram-negative. The isolation of an extremely drug-resistant *E. coli* and a pan-drug resistant *A. baumannii* isolate are of serious concern, these findings indicate the emergence of highly resistant bacterial pathogens with severely limited therapeutic options. The resistance of the *A. baumannii* to imipenem is also very troubling and a phenomenon also reported with increasing carbapenem resistance in *Acinetobacter spp*. [11]. Isolation of *B. cepacia* was of interest as it is one of the rare organisms isolated in BSI, normally in immunosuppressed patients [19,20]. The high blood culture positive rate in the pediatric population (age under one year: 16.6%) and elderly (age over sixty: 22.5%) was supportive of the widely known epidemiological fact that susceptibility to BSIs is maximal at the extremes of age [21]. Our findings reconfirm that high suspicion for BSIs is always warranted in febrile patients at both age extremes.

Our study is associated with some significant limitations. Firstly, due to its retrospective design, there are intrinsic flaws due to incompleteness of records. Secondly, our study could not discriminate between true CoNS bacteremia and mere contamination. Further prospective studies involving clinical correlation, collection of serial blood cultures, catheter data, and blood culture time-to-positivity need to be conducted to clarify the clinical significance of these coagulase-negative *staphylococci*.

Third, limited sample size of patients with positive blood cultures (n=33) does not allow for adequate statistical power for the purpose of subgroup analysis. Fourth, no studies about the identification of mechanisms of resistance and typing of isolates have been done.

5-CONCLUSIONS

This retrospective investigation shows the most commonly recovered bacterial isolates from blood cultures in patients with fever, an overall blood culture positivity rate of 17.7% was observed. Gram-positive organisms were most prevalent among the blood cultures. Among the Gram-positive organisms the *staphylococci*, with emphasis on *Staphylococcus haemolyticus* and *Staphylococcus aureus*, were the most frequently isolated. In *S. aureus* isolates we found presence of resistance to oxacillin thus MRSA was identified to exist among the population tested, as such, ongoing surveillance is advocated. It will be prudent to continue ongoing resistance surveillance for adjustment of empirical antimicrobial Therapy. Vancomycin, linezolid and tigecycline demonstrated complete activity against the tested *staphylococcal* isolates strains investigated, this would imply that these drugs can still be utilized empirically or for targeted treatment of MDR *staphylococcal* infections. The emergence of extensively drug-resistant organisms represents a major clinical challenge extensively drug-resistant Gram-negative organisms like carbapenem resistant *A. baumannii* are being detected. Future studies should focus on the characterization of resistance mechanisms using molecular methods and clinical outcome data collection, as well as multi-centric investigations.

Declarations

Availability of Data and Materials

The datasets generated and analyzed during the current study are available from the corresponding author upon reasonable request.

Conflicts of Interest:

The authors declare that they have no competing interests.

Funding

This research received no external funding.

REFERENCES

1] Vincent, J. L., Rello, J., Marshall, J., Silva, E., Anzueto, A., Martin, C. D., ... & EPIC II Group of Investigators, X. (2009). International study of the prevalence and outcomes of infection in intensive care units. Jama, 302(21), 2323-2329.

[2] Weinstein, M. P., Towns, M. L., Quartey, S. M., Mirrett, S., Reimer, L. G., Parmigiani, G., & Barth Reller, L. (1997). The clinical significance of positive blood cultures in the 1990s: a prospective comprehensive evaluation of the microbiology, epidemiology, and outcome of bacteremia and fungemia in adults. Clinical infectious diseases, 24(4), 584-602..

[3] Fabre, V., Carroll, K. C., & Cosgrove, S. E. (2022). Blood culture utilization in the hospital setting: a call for diagnostic stewardship. Journal of clinical microbiology, 60(3), e01005-21.

[4] Warhurst, G., Dunn, G., Chadwick, P., Blackwood, B., McAuley, D., Perkins, G. D., ... & Dark, P. (2015). Rapid detection of health-care-associated bloodstream infection in critical care using multipathogen real-time polymerase chain reaction technology: a diagnostic accuracy study and systematic review. Health technology assessment (Winchester, England), 19(35), 1.

[5] Musicha, P., Cornick, J. E., Bar-Zeev, N., French, N., Masesa, C., Denis, B., ... & Feasey, N. A. (2017). Trends in antimicrobial resistance in bloodstream infection isolates at a large urban hospital in Malawi (1998–2016): a surveillance study. The Lancet infectious diseases, 17(10), 1042-1052.

[6] Ince, D., Fiawoo, S., Choudhury, R., Cosgrove, S. E., Dobrzynski, D., Gold, H., ... & Nori, P. (2023, July). Epidemiology of gram-negative bloodstream infections in the United States: results from a cohort of 24 hospitals. In Open forum infectious diseases (Vol. 10, No. 7, p. ofad265). US: Oxford University Press.

[7] Abed, A. N., Ahmed, O., Abdulmajeed, M., & Khazaal, Y. M. (2021). Evaluate Multi-Drug Resistance Pattern of Microbial Flora from Hospital Premises of Baghdad Hospitals. Teikyo Med. J, 44, 2461-2466.

[8] Leal, H. F., Azevedo, J., Silva, G. E. O., Amorim, A. M. L., de Roma, L. R. C., Arraes, A. C. P., ... & Reis, J. N. (2019). Bloodstream infections caused by multidrug-resistant gram-negative bacteria: epidemiological, clinical and microbiological features. BMC infectious diseases, 19(1), 609.

[9] CLSI. (2023). M100: Performance standards for antimicrobial susceptibility testing (33rd ed.). Clinical and Laboratory Standards Institute.

[10] Magiorakos, A. P., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G., ... & Monnet, D. L. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clinical microbiology and infection, 18(3), 268-281.

[11] Mukhopadhyay, H., Bairagi, A., Mukherjee, A., Prasad, A. K., Roy, A. D., & Nayak, A. (2025). Multidrug resistant Acinetobacter baumannii: A study on its pathogenesis and therapeutics. Current Research in Microbial Sciences, 8, 100331.
[12] Abdollahi, A., Nojomi, M., Karimi, Y., & Ranjbar, M. (2024). Mortality patterns in patients with Staphylococcus aureus bacteremia during the COVID-19 pandemic: Predictors and insights. Heliyon, 10(2).
[13] Asai, N., Sakanashi, D., Suematsu, H., Kato, H., Hagihara, M., Watanabe, H., ... & Mikamo, H. (2021). Clinical characteristics and relevance of coagulase-negative Staphylococci other than S. epidermidis by positive blood culture. Journal of Microbiology, Immunology and Infection, 54(4), 632-638.
[14] Karlath, F. A., Rehan, M. A., Geiger, A., Mitchell, M. J., Arnaout, S., Greenough, T. C., & Ellison III, R. T. (2025, July). Retrospective Analysis of the Clinical Significance of Positive Blood Cultures in the Emergency Department: A Single-Center Study. In Open Forum Infectious Diseases (Vol. 12, No. 7, p. ofaf352). US: Oxford University Press.
[15] Hnaineh, Z., & Sokhn, E. S. (2025). Prevalence of bacteremia and antimicrobial resistance pattern among patients in South Lebanon. American Journal of Infection Control, 53(1), 139-143.
[16] Sautter, R. L., Parrott, J. S., Nachamkin, I., Diel, C., Tom, R. J., Bobenchik, A. M., ... & Baselski, V. (2024). American Society for Microbiology evidence-based laboratory medicine practice guidelines to reduce blood culture contamination rates: a systematic review and meta-analysis. Clinical microbiology reviews, 37(4), e00087-24.
[17] Belew, H., Tamir, W., Dilnessa, T., & Mengist, A. (2023). Phenotypic bacterial isolates, antimicrobial susceptibility pattern and associated factors among septicemia suspected patients at a hospital, in northwest Ethiopia: Prospective cross-sectional study. Annals of Clinical Microbiology and Antimicrobials, 22(1), 47.
[18] Hughes, J. A., Cabilan, C. J., Williams, J., Ray, M., & Coyer, F. (2023). Interventions to reduce peripheral blood culture contamination in acute care settings: A systematic review and meta-analysis. medRxiv, 2023-07.
[19] Siddiqui, T., Sahu, C., Patel, S. S., & Ghoshal, U. (2022). Clinical and microbiological profile of patients with bloodstream infections caused by Burkholderia cepacia complex. Journal of Laboratory Physicians, 14(03), 312-316.
[20] Ibrahim, T., Abdallah, T. A., Abdallah, A., Qazi, R., Alimam, A., Mohammad, H., ... & Hadi, H. A. (2024). Epidemiology, microbiological, clinical characteristics, and outcome of Burkholderia cepacia complex infections in non-cystic fibrosis adult patients from Qatar. IJID regions, 11, 100355.
[21] Wu, H. N., Yuan, E. Y., Li, W. B., Peng, M., Zhang, Q. Y., & Xie, K. L. (2022). Microbiological and clinical characteristics of bloodstream infections in general intensive care unit: a retrospective study. Frontiers in Medicine, 9, 876207.
[22] Abed, A. N., & Mnif, B. (2025). Emerging Resistance in Klebsiella pneumoniae: CTX-M Prevalence, Biofilm Formation, and Efficacy of Platanus orientalis Extract. Microbiology Research, 16(9), 203. https://doi.org/10.3390/microbiolres16090203
[23] Ton, S. Y., Fowler Jr, V. G., Skalla, L., & Holland, T. L. (2025). Management of Staphylococcus aureus bacteremia: a review. Jama, 334(9), 798-808.
[24] Ali, G. A., Goravey, W., Najim, M. S., Shunnar, K. M., Ibrahim, S. I., Daghfal, J., ... & Hadi, H. A. (2022). Epidemiology, microbiological and clinical characteristics of Enterococcus species bloodstream infections: a 10-year retrospective cohort study from Qatar. Annals of Medicine and Surgery, 80, 104258.

