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Spectrum and Demographic Distribution of Organisms Recovered from Blood Cultures at a Public-Sector Tertiary Hospital in Karachi: A Retrospective Laboratory-Based Study

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Abstract

Background: Bloodstream infections (BSIs) are a major public health concern due to their high morbidity and mortality, particularly in low- and middle-income countries. Blood culture remains the gold standard for diagnosis. The distribution of BSI pathogens varies globally, with *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Candida albicans* commonly implicated, while in Southeast Asia, typhoidal Salmonella species remain the leading community-acquired pathogens. Despite this, large-scale organism-level data from routine blood culture testing in Pakistan remain limited. This study aimed to describe blood culture positivity, the spectrum of organisms recovered, and their distribution according to age and gender in a public-sector tertiary care hospital in Karachi, Pakistan.

Methods: This one-year retrospective study (1st June 2024 to 30 June 2025) analyzed 28,186 blood culture records from Dr. Ruth K. M. Pfau Civil Hospital, Karachi, Pakistan. Extracted variables included age, gender, culture result, and identified organism. Analyses were conducted at the blood-culture record level because patient-level de-duplication was not possible. Organisms were grouped as skin-associated, enteric/Enterobacterales-associated, or other isolates. Descriptive statistics were used to summarize the data, and chi-square tests were used to assess associations between culture results, demographic characteristics, and organism groups.

Results: Among 28,186 samples, 8,925 (31.7%) demonstrated microbial growth. Most isolates were of skin-associated (6,385; 22.7%), with gastrointestinal associated (1,975; 7.0%) and others (565; 2.0%). Pediatric blood culture records accounted for 52.1% of positive isolates, and culture positivity differed significantly across age groups and by gender (both $p<0.001$). Coagulase-negative staphylococci were the predominant skin-associated isolates, accounting for 5,980 (93.7%) of this category. Among enteric/Enterobacterales-associated isolates, Salmonella Typhi 519 (29.9%), *Klebsiella pneumoniae* 515 (26.1%), and Escherichia coli 489 (24.8%) were most frequently recovered. Among other isolates, Acinetobacter baumannii 204 (36.1%) and *Pseudomonas aeruginosa* 177 (31.3%) predominated. The distribution of organism categories also differed significantly by gender ($p=0.030$).

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Conclusion: This study demonstrates substantial variation in organisms recovered from blood cultures across age and gender groups in a large public-sector tertiary-care hospital in Karachi. The predominance of CoNS highlights the importance of strengthening blood-culture collection practices and laboratory quality assurance, while the recovery of *Salmonella Typhi*, *K. pneumoniae*, *E. coli*, *A. baumannii*, and *P. aeruginosa* supports continued institution-specific microbiological surveillance and antimicrobial stewardship.

Keywords: Blood Culture; Bacteremia; Bloodstream Isolates; Laboratory Surveillance; Pakistan

Abbreviations: BSIs: Bloodstream Infections; CoNS: Coagulase-Negative Staphylococci.

Introduction

Bloodstream Infections (BSIs) are a critical public health concern due to their high morbidity and mortality worldwide, particularly in low-and middle-income countries, including those in South and Southeast Asia. BSIs are defined as the presence of a viable infectious microorganism, such as a bacterial or fungal organism, in the bloodstream that causes illness. Microorganisms, when present in blood circulation, can damage any organ of the body. BSI can cause life-threatening conditions like sepsis and organ failure. Therefore, it is important to diagnose BSI early and start appropriate antimicrobial therapy [1]. Nearly 2.91 million deaths worldwide in 2019 were due to bloodstream infections [2].

BSI is considered a global health priority because it increases the burden of sepsis and antibiotic use in both hospitalized and community settings. The most reliable diagnostic tool for bloodstream infections is blood culture; however, its interpretation is often challenged by contamination with skin flora such as coagulase-negative staphylococci (CoNS) or false negatives [3]. Common causative organisms of BSIs include Escherichia coli, Staphylococcus aureus, Coagulase-negative staphylococci, *Klebsiella pneumoniae*, and Candida albicans, but their distribution varies across regions [4]. In Southeast Asia, typhoidal Salmonella species remain among the leading causes of community-acquired BSI, while Gram-positive skin flora, such as CoNS, are frequent isolates in hospital laboratories.

A systematic review of LMIC reports Salmonella enterica serovars typhi and paratyphi as leading causes of bloodstream infection, followed by Staphylococcus aureus, in Asia [5]. Literature from Southeast Asia continues to report enteric organisms Escherichia coli and S. aureus among blood cultures [6]. Previous studies have largely focused on antimicrobial resistance trends; However, relatively few studies have comprehensively described the spectrum and demographic distribution of organisms recovered through routine blood-culture testing in large public-sector hospitals in Pakistan. To address this gap, we conducted a retrospective laboratory-based study of blood cultures in a public-sector tertiary-care, teaching hospital in Karachi, aiming to describe blood culture positivity, the spectrum of organisms recovered, and their distribution according to age and gender.

Material and Methods

This retrospective, descriptive, laboratory-based study analysed blood culture records from the Department of Microbiology, Dr. Ruth KM. Pfau Civil Hospital, a public-sector tertiary care teaching hospital in Karachi, Pakistan. It comprises approximately 1900 beds and provides comprehensive inpatient, outpatient, emergency, surgical, diagnostic, and specialized clinical services to a diverse patient population. The central laboratory provides diagnostic services across major disciplines, processing specimens of patients from various medical, surgical, and allied departments of the hospital as well as outpatient services. A total of 28,186 blood culture records processed were included in our study. Laboratory records of blood cultures processed between 1st June 2024 and 30 June 2025 (one year) were reviewed. Since this was a retrospective study, no formal sample size calculation was performed because all eligible blood culture records from the predefined one-year study period were included.

Laboratory data were retrieved from the departmental blood culture register/Excel database maintained by the Microbiology laboratory. Variables extracted included patient age, gender, culture positivity status, and identified organism. All blood culture records were included irrespective of repeat sampling, as the dataset did not allow for episode-based de-duplication. No additional sampling or patient contact occurred, as the study relied solely on anonymized laboratory data. Consequently, analyses were conducted at

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the blood culture record level rather than the unique patient level.

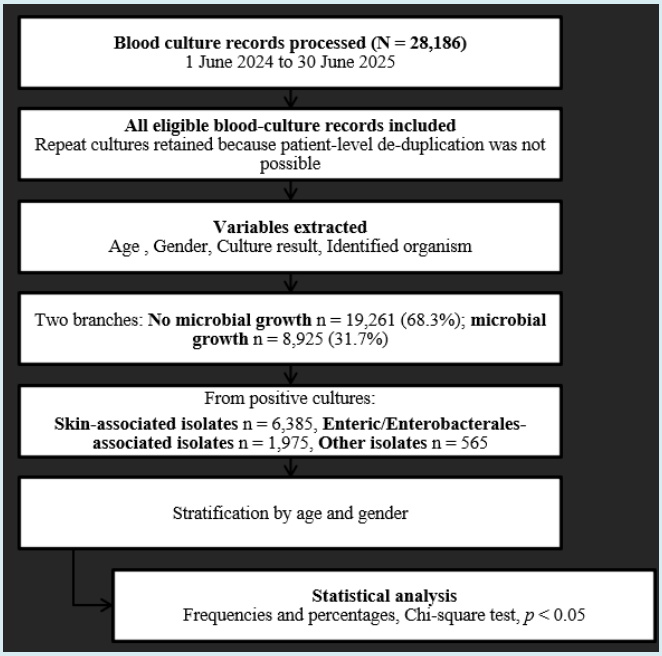


Figure 1: Schematic flow of blood-culture record selection, classification, and analysis.

Blood samples were collected aseptically and transferred into BD BACTEC blood culture bottle which were placed in BD BACTEC 9240 automated blood culture system. Bottles flagged positive were Gram-stained and subcultured on blood agar and MacConkey's agar for organism isolation. Organisms were identified based on colony morphology, Gram-stain characteristics, and standard biochemical identification tests using CLSI guidelines.

Data retrieved in Excel sheets were entered and analyzed using SPSS version 27. Descriptive statistics were used to summarize outcomes. The data were stratified by age group and gender. Age was categorized into five brackets: children (≤12 years), adolescents (13–18 years), young adults (19-35 years), adults (36–60 years), and older adults (>60 years). Based on microbiological characteristics, organisms were further classified into three major categories: skin-associated organisms, gastrointestinal-associated organisms, and others (organisms not fitting the above groups), such as respiratory, environmental, nosocomial etc. Results are presented as frequencies and percentages with tables and figures illustrating culture positivity rates and organism distribution. Associations between categorical variables (age group, gender, organism distribution) were tested using the Chi-square test. A p-value <0.05 was considered statistically significant. Because de- duplication was not possible, inferential findings were interpreted cautiously.

Results

Out of the total 28,186 blood culture samples processed, the majority yielded no growth (n=19,261, 68.3%), while n=8,925 (31.7%) demonstrated microbial growth.

Variable	Subgroup	N (%)
AGE (Mean ± SD: 21.44 ± 20.69)	Children / Pediatric	13157 (46.7%)
	Adolescents / Teenagers	1801 (6.4%)
	Young Adults	5199 (18.4%)
	Adults (Middle-aged)	6554 (23.3%)
	Older Adults / Elderly	1475 (5.2%)
GENDER	Male	15207 (54.0%)
	Female	12979 (46.0%)

Table 1: Age and gender distribution of blood culture record.

Table 1 shows the age and gender distribution of patients undergoing blood culture. For a total of 28,186 blood culture records included in the analysis, the mean age of the study population was 21.44 years (SD ± 20.69), with the largest proportion belonging to the pediatric age group (n = 13,157; 46.7%). This was followed by middle-aged adults (n = 6,554; 23.3%) and young adults (n = 5,199; 18.4%). Adolescents (n = 1,801; 6.4%) and older adults/elderly (n = 1,475; 5.2%) constituted smaller subgroups. With respect to gender, males accounted for 54.0% (n = 15,207) of cases, while females comprised 46.0% (n = 12,979).

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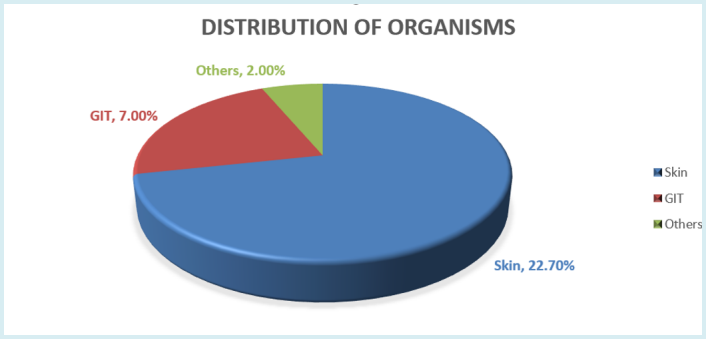


Figure 2: Distribution of blood culture isolates by organism group.

Figure 2 illustrates the distribution of blood culture isolates by organism groups. Out of 8,925 positive blood cultures, the majority of isolates were derived from skin-associated, n=6385 (22.7%) of total samples, followed by Organisms of gastrointestinal associated, which accounted for n=1,975 (7.0%) isolates, while other sources categorized as "others" represented 565 isolates (2.0%), which were from respiratory associated, environmental associated, nosocomial, etc.

Variable	Group	Results			P-Value
		Negative	Positive	Total	
AGE	Children / Pediatric	8508 (44.2%)	4649 (52.1%)	13157 (46.7%)	<0.001*
	Adolescents / Teenagers	1299 (6.7%)	502 (5.6%)	1801 (6.4%)	
	Young Adults	3595 (18.7%)	1604 (18.0%)	5199 (18.4%)	
	Adults (Middle-aged)	4718 (24.5%)	1836 (20.6%)	6554 (23.3%)	
	Older Adults / Elderly	1141 (5.9%)	334 (3.7%)	1475 (5.2%)	
GENDER	Male	10558 (54.8%)	4649 (52.1%)	15207 (54.0%)	<0.001*
	Female	8703 (45.2%)	4276 (47.9%)	12979 (46.0%)	

Table 2: Association of blood culture results by age and gender (Chi-square test).

Table 2 presents the association of blood culture results by age and gender. Culture positivity differed significantly across age groups (p<0.001), with the pediatric age group contributing the largest share of both negative (n = 8,508; 44.2%) and positive cultures (n = 4,649; 52.1%). Positivity declined progressively with increasing age. Older adults accounted for 3.7% of all positive cultures, representing 5.2% of the total blood-culture records. A statistically significant association was observed between gender and culture result (p<0.001).

Variable	Group	Organisims				P-Value
		Skin-associated Isolates	Enteric/ Enterobacterales associated Isolates	Other Isolates	TOTAL	
AGE	Children	3404 (53.3%)	963 (48.8%)	282 (49.9%)	4649 (52.1%)	<0.001*
	Adolescents	337 (5.3%)	135 (6.8%)	30 (5.3%)	502 (5.6%)	
	Young Adults	1085 (17.0%)	406 (20.6%)	113 (20.0%)	1604 (18.0%)	
	Adults	1333 (20.9%)	382 (19.3%)	121 (21.4%)	1836 (20.6%)	
	Older Adults	226 (3.5%)	89 (4.5%)	19 (3.4%)	334 (3.7%)	
GENDER	Male	3292 (51.6%)	1033 (52.3%)	324 (57.3%)	4649 (52.1%)	0.030*
	Female	3093 (48.4%)	942 (47.7%)	241 (42.7%)	4276 (47.9%)	

Table 3: Comparison of the origin of blood culture organisms by age and gender.

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Table 3 shows a comparison of the origin of blood cultures by age and gender. Among the 8,925 positive blood cultures, skin-associated organisms predominated across all age groups, particularly in children (n = 3,404; 53.3%), followed by gastrointestinal associated isolates (n = 963; 48.8%) and other organism isolates (n = 282; 49.9%). Pediatric patients thus contributed more than half of all positive isolates (52.1%), which is statistically significant ($p < 0.001$). In comparison, young adults and middle-aged adults contributed 18.0% (n = 1,604) and 20.6% (n = 1,836) of isolates, respectively, with both groups showing a balanced spread across skin, gastrointestinal, and other organisms. The elderly subgroup accounted for the smallest proportion of isolates (n = 334; 3.7%) across all categories.

When stratified by gender, positive blood cultures were slightly more frequent in males (52.1%) than in females (47.9%). The distribution of organism categories differed significantly between genders ($p = 0.030$). Organisms classified as other isolates were relatively more common among males (57.3%) than females (42.7%).

Source	RANK	Organism	n (%)	Age					Gender	
				Child	Adolescent	Young Adult	Adults	Older	Male	Female
Skin Associated Isolates	1	*Coagulase-Negative Staphylococci*	5980 (93.7%)	3204 (94.1%)	308 (91.4%)	1026 (94.6%)	1230 (92.3%)	212 (93.8%)	3069 (93.2%)	2911 (94.1%)
	2	*Staphylococcus aureus (MRSA)*	289 (4.5%)	137 (4.0%)	21 (6.2%)	44 (4.1%)	75 (5.6%)	12 (5.3%)	166 (5.0%)	123 (4.0%)
	3	*Staphylococcus aureus (MSSA)*	53 (0.8%)	28 (0.8%)	4 (1.2%)	7 (0.6%)	13 (1.0%)	1 (0.4%)	27 (0.8%)	26 (0.8%)
Enteric/ Enterobacterales Associated Isolates	1	*Salmonella typhi*	591 (29.9%)	447 (46.4%)	41 (30.4%)	75 (18.5%)	28 (7.3%)	0 (0.0%)	347 (33.6%)	244 (25.9%)
	2	*Klebsiella pneumoniae*	515 (26.1%)	160 (16.6%)	44 (32. 6%)	137 (33.7%)	147 (38.5%)	27(30.3%)	264 (25.6%)	251 (26.6%)
	3	*E. coli*	489 (24.8%)	195 (20.2%)	27 (20.0%)	111 (27.3%)	115 (30.1%)	41 (46.1%)	237 (22.9%)	252 (26.8%)
Other Isolates	1	*Acinetobacter baumannii*	204 (36.1%)	65 (23.0%)	12 (40.0%)	54 (47.8%)	60 (49.6%)	13 (68.4%)	110 (34.0%)	94 (39.0%)
	2	*Pseudomonas aeruginosa*	177 (31.3%)	74 (26.2%)	16 (53.3%)	46 (40.7%)	37 (30.6%)	4 (21.1%)	101 (31.2%)	76 (31.5%)
	3	*Burkholderia cepacia*	108 (19.1%)	103 (36.5%)	1 (3.3%)	1 (0.9%)	2 (1.7%)	1 (5.3%)	72 (22.2%)	36 (14.9%)

Table 4: Distribution of the most frequently isolated organisms by source with age and gender.

Table 4 shows the distribution of the most frequently isolated organisms recovered, i.e., categorized into skin-associated, gastrointestinal associated, and others isolates. Among skin flora, Coagulase-negative staphylococci accounted for almost all major isolates (93.7%) and were consistently frequent across age groups, ranging from 91.4% in adolescents to 94.6% in young adults, with comparable proportions in males (93.2%) and females (94.1%). Staphylococcus aureus was less common overall, though MRSA (4.5%) was more frequent than MSSA (0.8%), with slightly higher proportions in adolescents (6.2%) and in males (5.0%). Gastrointestinal organisms showed marked demographic variation: Salmonella typhi predominated in children (46.4%) and declined sharply in older groups, whereas *E. coli* was more frequent in adults (30.1%) and females (26.8%). *Klebsiella pneumoniae* was common across all age groups but showed no strong gender difference. Among opportunistic pathogens, Acinetobacter baumannii accounted for 36.1% of other isolates overall, with relatively high proportions among adults (49.6%) and older adults (68.4%); the corresponding proportions were 34.0% among males and 39.0% among females, while Pseudomonas aeruginosa accounted for 31.3% of other isolates overall, with proportions of 53.3% among adolescents and 40.7% among young adults. Burkholderia cepacia (19.1%) was relatively uncommon overall, but disproportionately isolated in

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children (36.5%) and more frequent in males (22.2%). These findings highlight clear age- and gender-specific patterns in bloodstream pathogen distribution, underscoring the need to consider demographic factors when interpreting culture results and guiding empiric therapy.

Supplementary Tables S1-S3 present the detailed distributions of skin-associated, gastrointestinal associated, and other organisms stratified by age and gender. In addition, Supplementary Figure SI illustrates the month-wise distribution of skin-associated, gastrointestinal-associated, and other-isolates organisms throughout the one-year study period.

Discussion

This one-year retrospective laboratory-based study included 28,186 blood culture samples, aimed at describing blood culture positivity and the spectrum and demographic distribution of organisms recovered from blood cultures. The overall positivity rate of blood culture was 31.7%, which is comparable to 36% positivity reported in a similar study conducted in Karachi, Pakistan [7]. The most reported organism among the positive samples was coagulase-negative staphylococci (CoNS), followed by Staphylococcus aureus (MRSA) and Staphylococcus aureus (MSSA). CoNS were the most frequent isolates, which is aligned with global findings identifying CoNS as the leading blood culture contaminant [8]. Yet occasionally it is a true pathogen in immunocompromised hosts [9]. A previous study from Pakistan reported CoNS in 74.1% of positive blood cultures; in contrast, our study found a markedly higher proportion, 93.7% [10]. Although frequently written off as contaminants, recent evidence indicates that CoNS can form biofilms and harbor transferable resistance determinants capable of spreading to Staphylococcus aureus and Escherichia coli, thus playing a crucial role in antimicrobial resistance [11]. Recent multicenter analyses have also reported a post-COVID rise in blood contamination rates, a plausible factor behind elevated CoNS yields in our study [12]. In this context, a local study reported a measurable reduction in blood culture contamination rates following structured interventions, emphasizing the importance of maintaining aseptic collection techniques and regular staff training in Pakistani hospitals [13].

Staphylococcus aureus (MRSA and MSSA) was also among the leading skin-associated isolates, in line with its worldwide status as a leading cause of BSIs. In our study, MRSA and MSSA constituted a small proportion of isolates (4.5% and 0.8%, respectively). By contrast, a regional study that focused exclusively on S. aureus isolates reported 36.1% MRSA and 63.9% MSSA, a difference likely reflecting variation in denominators and study scope, as the present analysis included all skin-derived organisms rather than S. aureus isolates alone [14].

Salmonella typhi, *Klebsiella pneumoniae*, and Escherichia coli were the dominant organisms, respectively. Our findings are similar to the literature reporting S. typhi as the leading pediatric BSI pathogen in South Asia [15]. This is also consistent with national data indicating the continued burden of enteric fever in Pakistan [16]. An increasing burden of ESBL-producing Enterobacterales in adult bloodstream infections has been reported in studies from India, including those conducted among cancer patient cohorts [17]. Among the organisms categorized as others, non-fermenting Gram-negative bacilli, Acinetobacter baumannii (36.1%) and Pseudomonas aeruginosa (31.3%), were predominant in our study, consistent with reports from Morocco [18], Ethiopia [19] and Nepal [20] that identify these organisms as major healthcare-associated pathogens.

Our findings highlight the need for stricter aseptic techniques, particularly in pediatric blood culture collection, as children showed the highest positivity and a large proportion of likely contaminants. The predominance of Salmonella Typhi isolates underscores ongoing enteric fever transmission and supports the need for sustained typhoid vaccination and antimicrobial stewardship. Strengthening laboratory quality assurance and data linkage with clinical records could improve diagnostic accuracy and guide empiric therapy policies in similar tertiary-care settings. Future prospective laboratory-based studies are recommended to distinguish contamination from bloodstream infection and to provide a more comprehensive understanding of bloodstream pathogens, patterns, and antimicrobial susceptibility.

Strengths of the Study

This study analyzed a large sample size, provided details at the organism-level, and included grouping by age and gender, which offered a broad overview of bloodstream isolates in a tertiary-care setting. Being laboratory-based, this study reflects the actual testing practices used in routine diagnosis and helps support better use of antibiotics and infection control measures. The study provides an overview of the spectrum and distribution of bloodstream isolates in Karachi, Pakistan, and highlights key areas for diagnostic stewardship, laboratory quality improvement, and local guideline development, along with their implementation.

Limitations of the Study

As a retrospective, laboratory-based analysis, several potential confounders could not be controlled, including patient clinical severity, comorbidities, and inpatient versus

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outpatient status, all of which may influence both culture positivity rates and organism profiles. Accordingly, the number of blood-culture records should not be interpreted as the number of unique patients, and all analyses were conducted at the record level. Hence, some statistically significant associations may represent spurious or non-causal relationships. In addition, procedural factors such as variability in sampling technique, blood volume collected, and number of culture sets may also have contributed to differences in yield or contamination. Furthermore, antimicrobial susceptibility patterns were not included in the present analysis. As a single-center study, findings may not be fully generalizable to other settings. The classification used in this study reflects microbiological grouping rather than a confirmed anatomical focus of infection, as clinical source data were not available.

Conclusion

This study describes the spectrum of organisms recovered from blood cultures at a public-sector tertiary-care hospital in Karachi. CoNS, constituted the largest category, although the available laboratory data did not permit differentiation between contamination and true bloodstream infection. Among the enteric and Enterobacterales category, Salmonella Typhi, K. pneumoniae, and *E. coli* were commonly recovered, while A. baumannii and P. aeruginosa predominated among other organisms. The observed differences across age and gender groups highlight the need for improved blood-culture collection practices, laboratory quality assurance, patient-level data linkage, and institution-specific microbiological surveillance. In the Pakistani public health context these findings may help inform preventive measures at the tertiary care level, including strengthen infection prevention and control practices, improve diagnostic stewardship and targeted surveillance of clinically important blood stream pathogens.

Statements and Declarations

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The authors did not receive support from any organization for the submitted work.

Conflicts of Interest/Competing Interests

The authors have no conflicts of interest to declare that are relevant to the content of this article.

Ethics Approval, Consent

As this was a retrospective, anonymized, record-based study involving no direct patient contact and no additional sampling. Permission to access and utilize the departmental blood culture laboratory records was obtained from the Head of the Department of Microbiology, Dr. Ruth K. M. Pfau Civil Hospital, Karachi. After approval from hospital administration, all data were anonymized before analysis, and patient confidentiality was maintained throughout.

Data and/or Code Availability

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

Authors Contribution Statements

Conceptualization: SJ and SJAB, GF; Data curation: SJ, SJAB and SS; Investigation: SJ, SJAB, SS and GF; Writing–original draft: SJ, SJAB, SS, EAK and GF; Writing–review & editing: SJ, SJAB, SS, EAK and GF. All authors have read and agreed to the published version of the manuscript.

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