

Original article

Blood Culture Yield, Organism Distribution, and Recorded Antimicrobial Susceptibility at a Pediatric Tertiary Referral Center in Benghazi, Libya: A Retrospective Register-based Study

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Blood culture services are expected to recover clinically meaningful bloodstream pathogens while limiting growth of organisms introduced during specimen collection, but where records are kept on paper, both quality indicators and resistance signals are difficult to aggregate and often go unexamined. We transcribed 914 unique blood culture records from the handwritten microbiology register of a pediatric tertiary referral center in Benghazi, Libya, covering 22 March 2025 through 30 March 2026, and classified growth descriptively as potentially clinically significant or potential contaminant based on organism identity alone, since the register did not document culture-set counts or clinical context. Proportions are reported with 95% Wilson confidence intervals, group comparisons used Monte Carlo exact tests, and monthly trends were assessed by Spearman rank correlation; susceptibility results were analyzed only as recorded test outcomes, because testing method and interpretive breakpoints were not documented. Of 914 cultures, 718 (78.6%) showed no growth, 189 (20.7%, 95% CI 18.2–23.4) yielded an organism, and 7 (0.8%) had no final result. Eighty-seven cultures (9.5%, 95% CI 7.8–11.6) contained potentially significant organisms, whereas 102 (11.2%, 95% CI 9.3–13.4) met the organism-based potential contaminant rule, 101 of which grew *Staphylococcus epidermidis* alone. Gram-negative organisms accounted for 49 of 87 (56.3%) potentially significant isolates, with *Staphylococcus aureus* (n=29), *Escherichia coli* (n=20), and *Klebsiella* spp. (n=12) were the most frequent named pathogens. Among Gram-negative test results with at least 10 observations, recorded susceptibility was 21 of 34 (61.8%) to imipenem, 5 of 24 (20.8%) to ceftazidime, and 1 of 12 (8.3%) to cefotaxime, and 8 of 16 *S. aureus* isolates tested with cefoxitin were recorded as resistant. Growth categories did not differ detectably across clinical areas or pediatric age bands, and neither showed a monthly trend. The register held two quality signals worth acting on: a high frequency of *S. epidermidis* among positive cultures and recorded resistance patterns that give cause for concern. Absent culture-set counts, clinical adjudication, and documented susceptibility methods, these data cannot establish a formal contamination rate or a cumulative antibiogram, so standardized prospective capture of collection and testing variables is the necessary next step.

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BY 4.0**Introduction**

Blood culture remains the reference microbiological method for detecting many bloodstream infections, and its usefulness rests on both sensitivity and specificity. A false-positive culture arising from skin flora can trigger unnecessary antimicrobial exposure, repeat sampling, further diagnostic work, prolonged admission, and avoidable cost [1–3]. In the other direction, inadequate blood volume or too few culture sets reduces pathogen recovery and allows genuine bacteremia to pass undetected [4].

Contamination of blood cultures is therefore treated as a core laboratory quality indicator. CLSI M47 sets a benchmark below 3%, with a 1% goal where best practice is followed [4]. Recent evidence-based guidance from the American Society for Microbiology observes that the 3% limit rests largely on expert opinion and survey data, and treats the supporting evidence as contested, with institutional rates reported from under 1% to above 10% [5,6]. That same guidance confirms that meaningful reductions are achievable through appropriate antisepsis, standardized collection practice, dedicated phlebotomy teams, education with feedback, and initial specimen diversion where feasible [5,7,8]. Any comparison of contamination rates requires compatible definitions and adequate information on culture sets, since organism identity by itself cannot separate contamination from true infection, particularly for coagulase-negative staphylococci in neonates and in patients with intravascular devices [1,2,6].

Antimicrobial resistance poses a second and connected challenge. Routine diagnostic microbiology supplies much of the data on which resistance surveillance depends, though data system constraints remain substantial in lower-resource settings [9]. The Global Burden of Disease 2021 analysis estimated 1.14 million deaths attributable to bacterial resistance in that year and documented a marked rise in burden linked to carbapenem resistance among Gram-negative organisms [10]. Libyan data are comparatively sparse, yet what exists points to a heavy burden. A multicenter Libyan study reported

healthcare-associated infection in 13.7% of 22,170 admissions, with the highest incidence at Benghazi Medical Center (17.9%) and a case fatality ratio of 10.3% among patients with bloodstream infection [11]. A national meta-analysis estimated 2,183 resistance-attributable deaths in Libya in 2024 and identified high pooled resistance in carbapenem-resistant *Acinetobacter baumannii* and third-generation cephalosporin-resistant Enterobacterales [12]. A prospective cohort from two Libyan hospitals subsequently reported multidrug-resistant Gram-negative organisms in 37.4% of 673 bloodstream infection episodes, with higher 30-day mortality among resistant than susceptible infections (32.1% versus 18.8%) [13].

Paper-based records are hard to aggregate, standardize, and deduplicate, so clinically useful information can sit unexamined for months [9]. We therefore analyzed roughly twelve months of consecutive entries from a handwritten microbiology register at a pediatric referral hospital in Benghazi. Our objectives were to quantify culture volume and overall growth, describe the organisms recovered, estimate an organism-based potential contaminant proportion, summarize recorded susceptibility results with appropriate caution, and test whether either growth category varied by clinical area, age group, or calendar month. A secondary objective was to specify which additional data fields a defensible prospective surveillance system would require.

Materials and methods

Study design and setting

This was a retrospective observational study of laboratory records, reported with reference to the STROBE recommendations for observational research [14]. The source was the handwritten Blood Culture and Sensitivity register of the Microbiology Department at Benghazi Children's Hospital, Benghazi, Libya, a pediatric tertiary referral center. The register receives specimens from the pediatric intensive care unit, two neonatal units, general pediatric medical wards, hematology, nephrology and dialysis, isolation areas, and other hospital services. All available consecutive entries between 22 March 2025 and 30 March 2026 were used, a span of 374 calendar days inclusive. No sample size calculation was performed, since the design was a census of the available register period.

Data source, transcription, and de-duplication

Three consecutive register volumes were available as photographic images. The volumes overlapped at accession numbers 478 to 491 and 779 to 806. Duplicate entries created by these overlaps were identified by accession number and removed. The laboratory numbering sequence restarted after accession 1000 in February 2026, and post-reset accession numbers were prefixed during processing to preserve uniqueness. After de-duplication, 914 unique records remained (Figure 1).

Patient names were not entered into the analytical dataset. Variables extracted were accession number, date, requesting clinical area, age where recorded, Gram stain result, named organism, and free-text susceptibility results. Original ward terminology was preserved and mapped to standardized analytic categories. Blank, illegible, or unresolved fields were coded as not recorded, and no missing value was imputed.

Age was not a dedicated register field. From approximately May 2025, laboratory staff began writing age into the vial identifier field using day, month, or year notation. Age was therefore available for 448 of 914 records (49.0%). All age-stratified analyses were restricted to that subset and should be read as analyses of a subset defined by calendar time rather than by patient characteristics.

Outcome definitions

A record was classified as no growth where the register explicitly documented no growth, and as growth-positive where any organism was named. Seven records without an interpretable final result were retained as a separate category. For descriptive analysis, growth-positive cultures were divided into potentially clinically significant growth and potential contaminant growth. The operational rule placed cultures containing *S. epidermidis* in the potential contaminant category, and grouped all other named bacterial organisms as potentially clinically significant. One record containing *S. epidermidis* together with fungal growth was retained in the potential contaminant category for consistency with the pre-specified rule, although it remains clinically indeterminate.

The classification is deliberately described as potential rather than confirmed contamination. The register did not document whether one or several culture sets were collected, whether the same organism was recovered from separate venipunctures, whether a specimen was drawn peripherally or through an indwelling line, or whether the patient carried a device or presented a compatible clinical syndrome. These variables are central to clinical adjudication of coagulase-negative staphylococci [1,2,4]. The 11.2% estimate is accordingly not equivalent to a formally measured CLSI contamination rate.

Antimicrobial susceptibility data

Identification and susceptibility testing were performed by the hospital laboratory as part of routine care. The register did not record the identification platform, testing method, quality control procedures, or interpretive breakpoints. Results

were transcribed exactly as written and mapped to susceptible or resistant categories, with the few intermediate results grouped with resistant for descriptive tabulation.

Local antibiotic abbreviations were retained as written and were not merged, even where two codes are conventionally synonymous. Thirty-eight distinct agent codes appeared across only 85 records, and several pairs conventionally denote the same agent: GEN and CN for gentamicin, AMC and AUG for amoxicillin-clavulanate, AK and AN for amikacin, CT and COL for colistin, C and CHL for chloramphenicol, and E and ERY for erythromycin. The decision not to merge followed an internal consistency check. Among Gram-negative organisms, GEN and CN returned markedly discordant susceptibilities, 22 of 27 (81.5%) against 5 of 15 (33.3%). A difference of that magnitude for a single agent is not biologically plausible, and indicates either that the codes were not used synonymously in this laboratory or that they were applied inconsistently. Pooling them would have produced a spurious composite estimate (Figure 3c). Several operational explanations are plausible, none of which the register can confirm or exclude. The two codes may correspond to different periods of the register, during which the laboratory used different automated panels, disk lots, or interpretive breakpoint versions; CLSI breakpoints for aminoglycosides have been revised across the window this register covers, and a shift from an older to a newer breakpoint table would lower the apparent susceptible proportion without any change in the organisms tested. The two codes may also reflect different technologists or shifts recording results from the same testing process in different conventions, which would represent a labeling inconsistency rather than a testing one. A further possibility is confounding by case mix: if cultures coded GEN disproportionately came from more susceptible organisms and cultures coded CN from a different, less susceptible mix, the discrepancy would reflect which isolates happened to carry each code rather than a difference in gentamicin susceptibility itself. The register lacks the identification method, testing date, and shift or technologist information needed to distinguish these explanations. The practical implication extends beyond this one agent. A register that can produce a 48-percentage-point split between two labels for the same drug cannot be assumed reliable for agents coded only once, since an undetected labeling or testing inconsistency there would leave no comparable internal check. This is the central reason the susceptibility results in this study are presented as register entries rather than as a cumulative antibiogram. Unresolved abbreviations, including a code recorded as CL, were not inferred.

Susceptibility findings are presented as recorded test results and must not be read as a formal antibiogram or as definitive resistance prevalence. CLSI M100 states that interpretive tables are valid only where standardized methodology is followed [15]. CLSI M39 further recommends patient-level de-duplication, first-isolate rules, final verified results, routine testing of reported agents, and adequate isolate numbers for cumulative reporting [16]. The register lacks the patient identifiers and testing metadata needed to demonstrate those conditions, so pooled results were used only to identify signals that justify prospective standardized surveillance.

Statistical analysis

Categorical variables are reported as counts and percentages. Ninety-five percent confidence intervals for proportions were calculated by the Wilson score method [17], implemented as a matrix routine in IBM SPSS Statistics (version 26.0, IBM Corp., Armonk, NY, USA) [19]. Age is summarized as median and interquartile range. Comparisons of both growth categories across the seven clinical areas submitting at least 20 cultures, and across the five pediatric age bands with at least 10 observations, used the Monte Carlo approximation to the Freeman-Halton exact test in SPSS CROSSTABS, with 100,000 samples at 99% confidence [18]. Exact tests were chosen in preference to the Pearson chi-square statistic because several expected cell counts fell below five; both approaches were computed and gave concordant results, which are reported together. Monotonic trends in monthly proportions were assessed by Spearman rank correlation across 13 calendar-month strata, computed in SPSS NONPAR CORR. All tests were two-sided at an alpha of 0.05. No correction for multiple comparisons was applied, so subgroup analyses are exploratory.

Ethical considerations

This study analyzed pre-existing entries from the hospital's blood culture register, generated during routine clinical care. No patient names or other direct identifiers were transcribed, and the analytical dataset contains no personally identifying information, so no individual patient can be identified from the results reported here. As the study relied exclusively on retrospective review of routinely collected laboratory data, with no patient contact, additional sampling, or intervention of any kind, it was conducted in accordance with accepted ethical standards for biomedical research and the principles of the Declaration of Helsinki. Where fewer than five records fell within a single reporting category, results were aggregated to prevent deductive identification.

Results

Culture volume and overall yield

The 914 unique records covered 22 March 2025 through 30 March 2026. Of these, 718 (78.6%) documented no growth, 189 (20.7%, 95% CI 18.2–23.4) documented growth of an organism, and 7 (0.8%) lacked an interpretable final result. Under the organism-based classification, 87 cultures (9.5%, 95% CI 7.8–11.6) contained potentially significant organisms

and 102 (11.2%, 95% CI 9.3–13.4) met the potential contaminant rule (Table 1, Figure 1). A clinical area was recorded for 885 of 914 cultures (96.8%).

Table 1. Primary outcomes among 914 consecutive blood culture records.

Outcome	n	% of 914 (95% CI)
Blood cultures processed	914	–
No growth	718	78.6 (75.8–81.1)
Any organism recorded	189	20.7 (18.2–23.4)
Potentially clinically significant growth	87	9.5 (7.8–11.6)
Potential contaminant growth	102	11.2 (9.3–13.4)
No final interpretable result	7	0.8 (0.4–1.6)

Percentages use all 914 cultures as the denominator. Potential contaminant is an organism-based analytic category and not a clinically adjudicated contamination rate. CI, confidence interval.

Organisms recovered

S. epidermidis dominated the positive cultures. It was recovered alone from 101 of 189 (53.4%), and one further record documented *S. epidermidis* with fungal growth. Among the 87 potentially significant isolates, 49 (56.3%, 95% CI 45.9–66.3) were Gram-negative. *S. aureus* was the most frequently named potentially significant organism (n=29), followed by *E. coli* (n=20), Gram-negative bacilli identified no further than morphology (n=15), and *Klebsiella* spp. (n=12, taking the 11 records recorded as *Klebsiella* spp. together with one *K. pneumoniae*) (Figure 2).

Recorded antimicrobial susceptibility

Susceptibility information was present for 85 of 189 growth-positive cultures (45.0%) and for 80 of 87 cultures in the potentially significant category (92.0%). Five *S. epidermidis* isolates also carried recorded results. Because agents were not tested uniformly, denominators varied considerably, from 34 down to the 10-result threshold applied here. Figure 3 shows every agent code with at least 10 recorded results for Gram-negative organisms and for *S. aureus*. These percentages describe register entries rather than standardized isolate-level resistance estimates.

Among Gram-negative organisms, recorded susceptibility was low for the cephalosporins tested, at 1 of 12 (8.3%, 95% CI 1.5–35.4) for cefotaxime and 5 of 24 (20.8%, 95% CI 9.2–40.5) for ceftazidime. Carbapenem results were intermediate, with 21 of 34 (61.8%, 95% CI 45.0–76.1) recorded as susceptible to imipenem, and 13 of 20 (65.0%, 95% CI 43.3–81.9) to piperacillin-tazobactam. Aminoglycoside results could not be pooled because of the code discordance described in section 2.4. Cefoxitin results in Gram-negative organisms (0 of 19 susceptible) are shown for completeness and carry no interpretation as acquired resistance. For *S. aureus*, cefoxitin was recorded for 16 isolates, of which 8 were resistant and 8 susceptible (50.0% resistant; 95% CI 28.0–72.0). That proportion indicates that methicillin resistance warrants formal prospective surveillance, though the register cannot establish a prevalence while the testing method and breakpoints remain unknown.

Clinical area comparisons

Specimens were submitted from 23 recorded clinical areas. The neonatal ward (n=220), the intensive care unit (n=193), and the neonatal unit (n=117) together accounted for 530 of 914 cultures (58.0%). Among the seven areas submitting at least 20 cultures, the proportion with potentially significant growth ranged from 2.6% to 11.1%, and the potential contaminant proportion from 5.1% to 15.0% (Figure 4). Neither distribution differed detectably across these areas (exact p=0.354 for potentially significant growth, chi-square 6.66 with 6 degrees of freedom; exact p=0.295 for potential contaminant growth, chi-square 7.30 with 6 degrees of freedom). These null results do not demonstrate equivalence, since several strata were small.

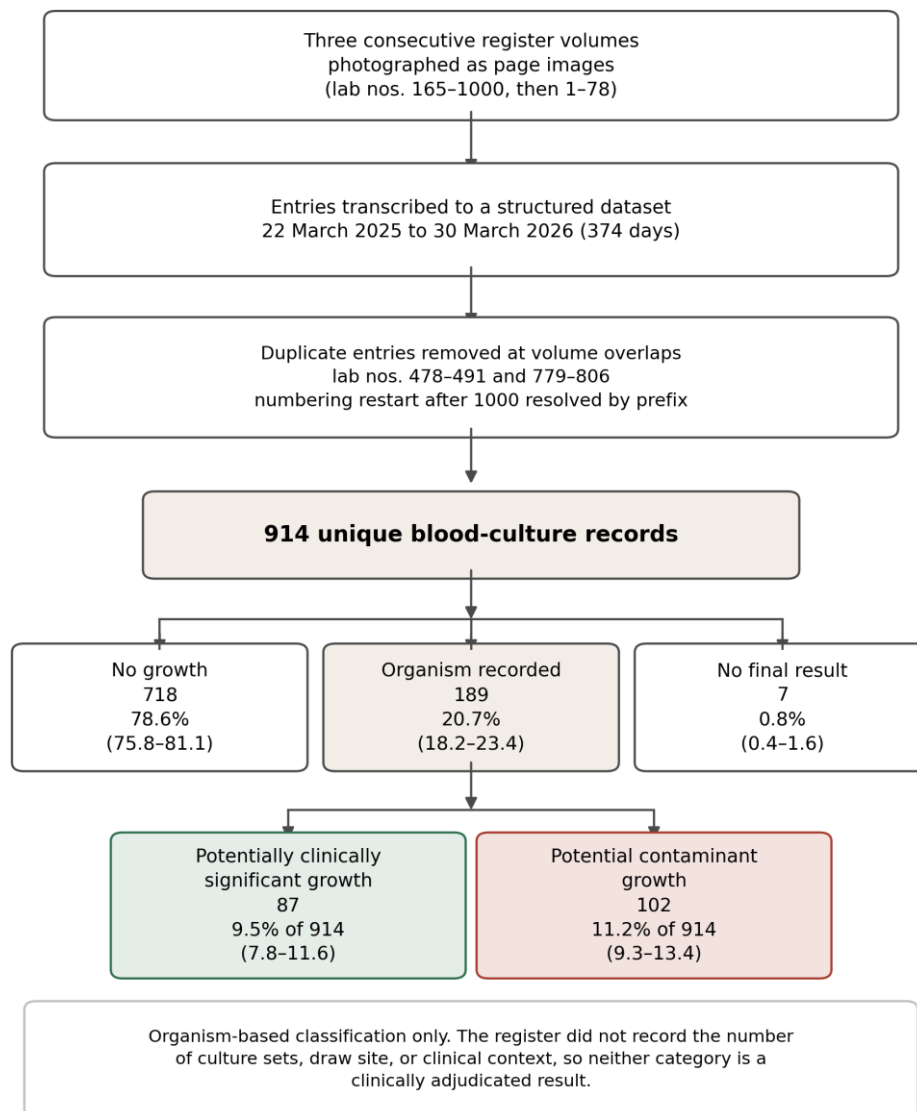


Figure 1. Flow of blood culture records from three handwritten register volumes to the final analytic categories. Counts are records, and percentages use all 914 unique records as the denominator, with 95% Wilson confidence intervals in parentheses.

Age distribution

Age was available for 448 of 914 records (49.0%). Of these 448 age-documented records, 447 were pediatric (0 to 17 years) and one was from a 57-year-old adult; the adult record is excluded from the pediatric age-band analyses and from Figure 5, which accordingly presents the 447 pediatric records. Median age among the 447 pediatric records was 122 days, with an interquartile range of 16 days to 3.0 years. Of these, 173 came from neonates aged 0 to 28 days and 364 from children under five years. Potentially significant growth did not differ detectably across the five pediatric age bands (exact $p=0.291$, chi-square 4.97 with 4 degrees of freedom), and neither did potential contaminant growth (exact $p=0.966$, chi-square 0.58 with 4 degrees of freedom) (Figure 5). Because age recording began partway through the study and was never systematic, these results should not be generalized to the full cohort.

Temporal pattern

Across 13 calendar-month strata, neither potentially significant growth nor potential contaminant growth showed a monotonic trend (Spearman $\rho = -0.03$, $p=0.93$, and $\rho = 0.08$, $p=0.79$, respectively). Monthly culture volume ranged from 15 to 104 (Figure 6). The first and last months were partial, and monthly denominators were modest, so the absence of a monotonic trend should not be read as evidence of process stability.

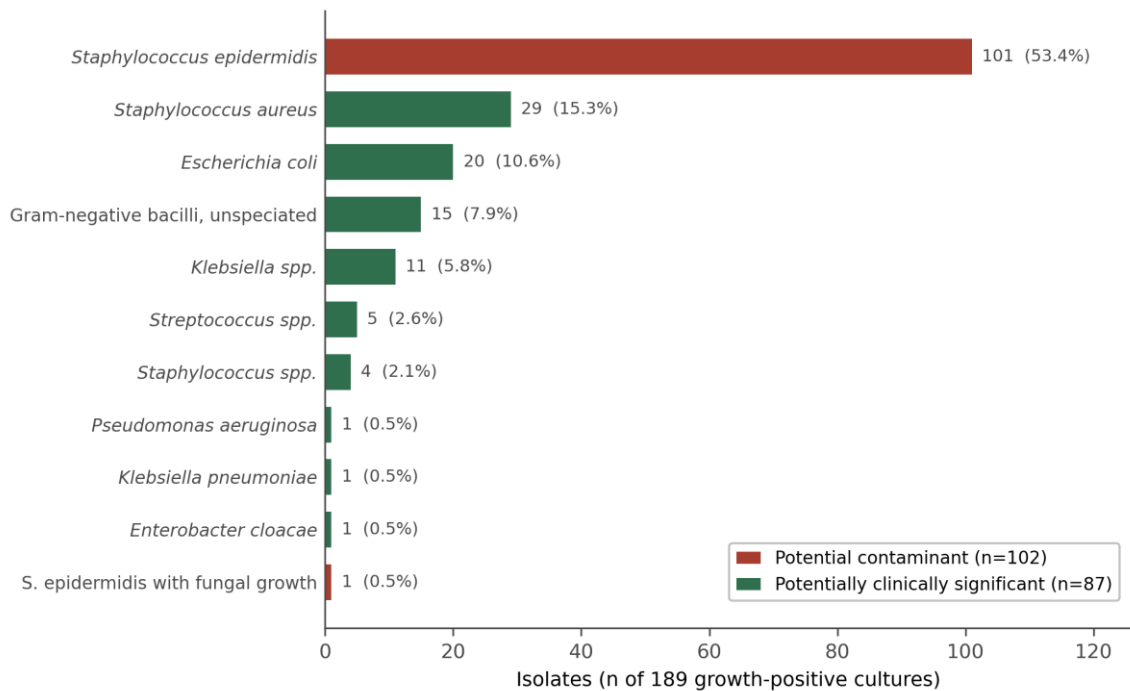


Figure 2. Organisms recorded among the 189 growth-positive blood cultures, with counts and the percentage of positives beside each bar.

Color marks the analytic category. Organism names reproduce the level of identification recorded in the register, which is why two labels appear at genus level alongside their speciated counterparts. The two register spellings for streptococci were combined, since both record a genus-level identification, whereas *Klebsiella spp.* and *K. pneumoniae* are kept apart because they sit at different levels of identification and merging them would conceal that only one isolate was speciated. Isolates recorded only as *Staphylococcus spp.* may include coagulase-negative species; reclassifying all four would move the potential contaminant proportion from 11.2% to 11.6% and alters no conclusion. The culture yielding *S. epidermidis* with fungal growth is retained in the pre-specified contaminant category but is clinically indeterminate.

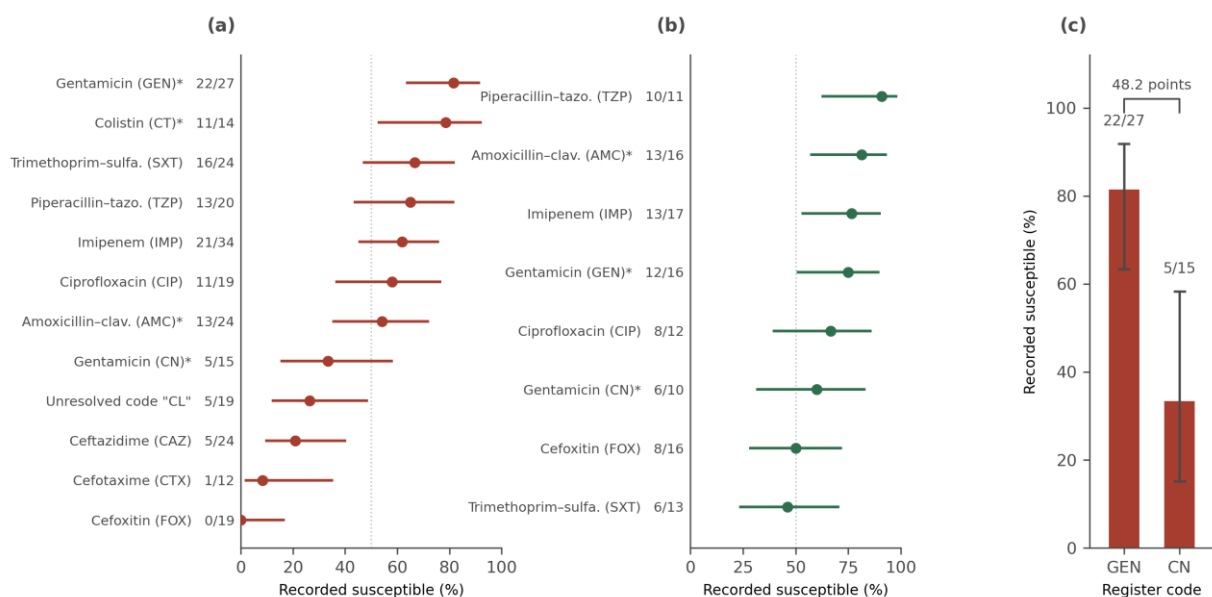


Figure 3. Recorded susceptibility for (a) Gram-negative isolates and (b) *Staphylococcus aureus*, restricted to agent codes with at least 10 recorded test results, and (c) the discordance between two conventionally synonymous register codes for gentamicin among Gram-negative organisms.

In (a) and (b), points show the percentage recorded susceptible and horizontal lines the 95% Wilson confidence interval; the number susceptible over the number tested follows each agent label, and the dotted line marks 50%. Asterisks mark codes belonging to a conventionally synonymous pair that was not merged. In (c), bars show the percentage recorded

susceptible with 95% Wilson confidence intervals; the 48.2-point gap between GEN and CN is not biologically plausible for a single agent and is the basis for the decision described in section 2.4. Denominators throughout are isolate-agent pairs, not isolates. Testing method, quality control, and breakpoints were not documented, so no formal antibiogram or treatment recommendation follows from these results.

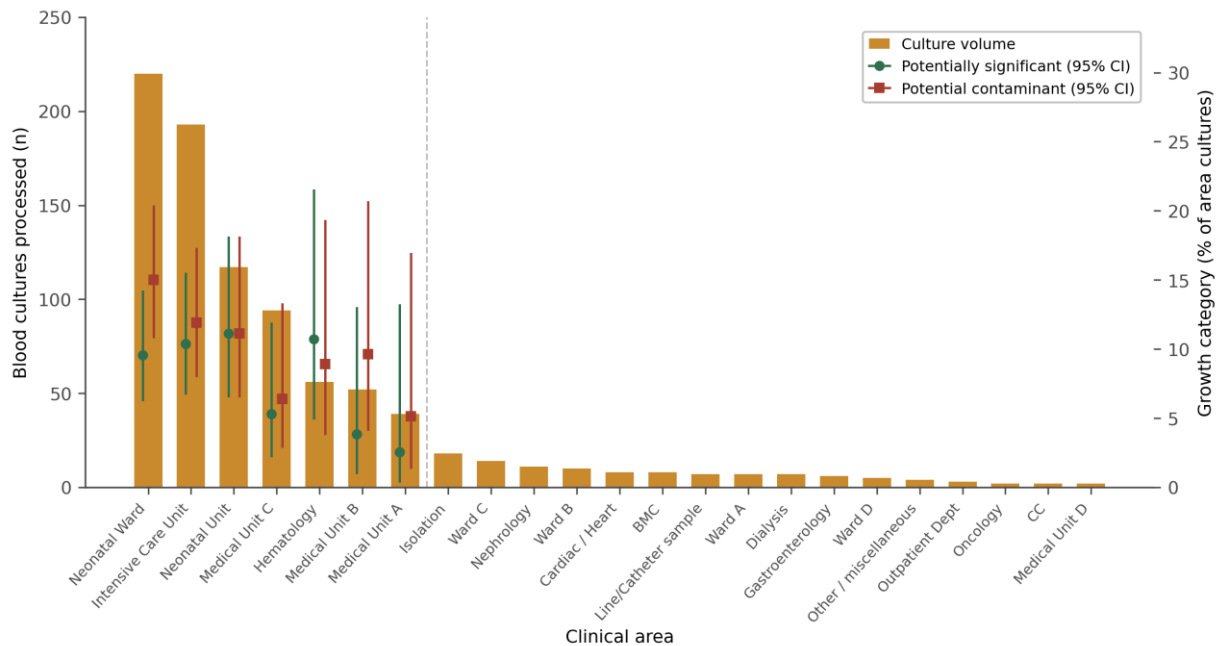


Figure 4. Blood culture volume across all 23 recorded clinical areas, with the two growth categories shown for the seven areas submitting at least 20 cultures.

Bars give the number of cultures processed against the left axis. Points give each growth category as a percentage of that area's cultures against the right axis, with 95% Wilson confidence intervals. The dashed line separates the seven areas entered into the comparison from the 16 smaller areas, which together submitted 114 cultures and were omitted because their proportions cannot be estimated with useful precision. Clinical area was not recorded for 29 cultures. Comparisons are exploratory and unadjusted for multiple testing.

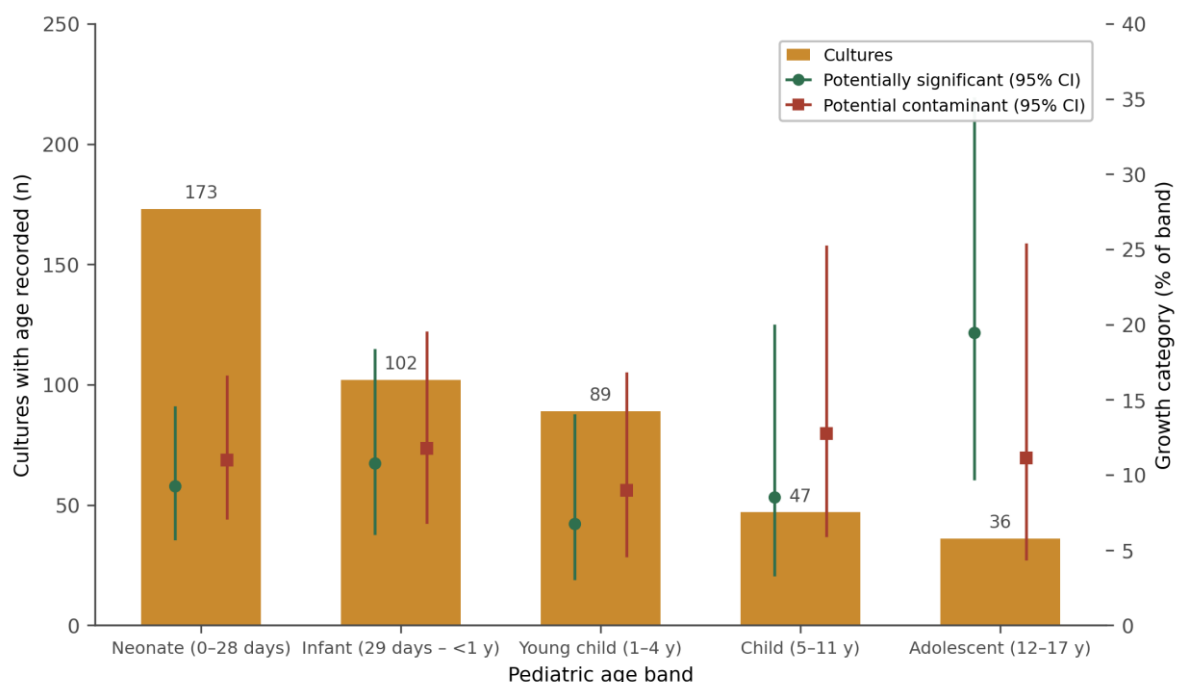


Figure 5. Distribution of the 447 pediatric records among the 448 records with age documented, and the two growth categories within each band. Bars give the number of cultures against the left axis, with counts printed above.

Points give each growth category as a percentage of the band against the right axis, with 95% Wilson confidence intervals. Of the 448 records with age documented, 447 were pediatric and are shown here; the remaining record, from a 57-year-old adult, is excluded. Age was unavailable for 466 of 914 cultures, and recording began partway through the study, so this subset is defined by calendar time rather than by patient characteristics.

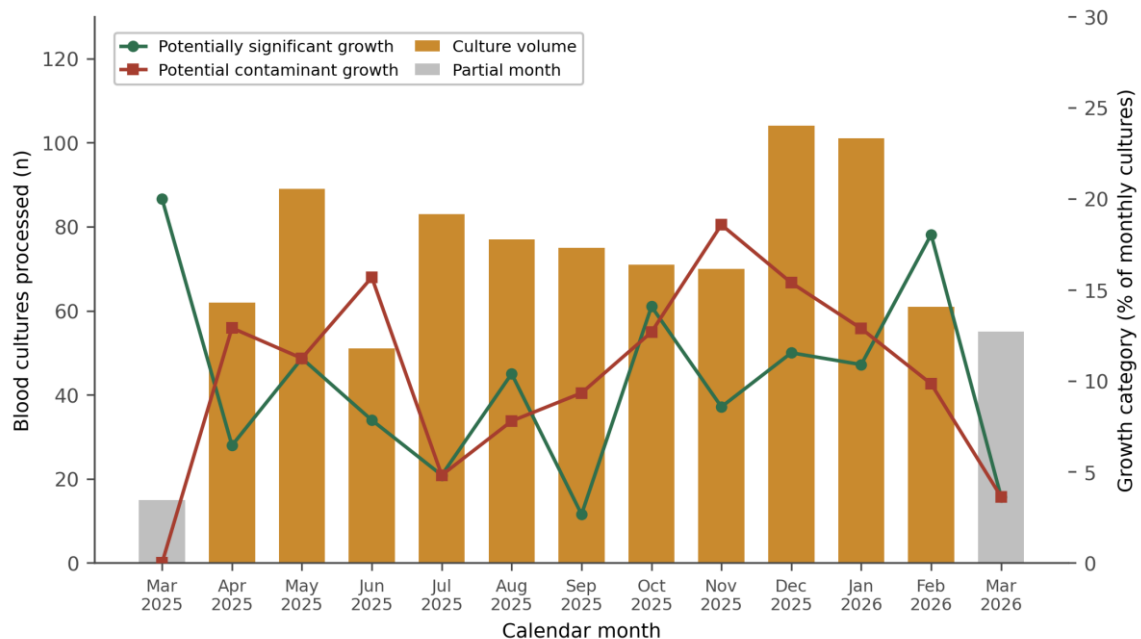


Figure 6. Monthly blood culture volume and the two growth categories across 13 calendar-month strata.

Bars show the number of cultures processed against the left axis, and lines show each growth category as a percentage of that month's cultures against the right axis. March 2025 and March 2026 were partial months and are shaded accordingly. Neither category showed a monotonic trend (Spearman rho -0.03 , $p=0.93$ for potentially significant growth; rho 0.08 , $p=0.79$ for potential contaminant growth).

Discussion

This analysis shows both the value and the limits of a handwritten microbiology register. One culture in five yielded an organism, yet more than half of all positive cultures contained *S. epidermidis*. Under the organism-based rule applied here, 102 of 914 cultures (11.2%) fell into the potential contaminant category, against 87 of 914 (9.5%) containing organisms considered potentially significant. The signal matters operationally because the commonly cited quality target for blood culture contamination sits below 3% [4], although recent evidence-based guidance regards the empirical basis for that specific threshold as contested and notes wide variation between institutions [5]. The 11.2% figure should nonetheless not be presented as a formal contamination rate. The register documented neither culture sets, repeated recovery, draw site, nor clinical context, and some *S. epidermidis* isolates, particularly in neonates and in patients with intravascular devices, may represent true bloodstream infection [1,2,20].

That distinction changes the reading of these data. The defensible conclusion is that cultures containing *S. epidermidis* were frequent enough to justify prospective contamination surveillance, rather than those contaminants outnumbered pathogens. A quality improvement program would need to capture the number of culture sets, bottle fill volume where feasible, peripheral versus line collection, the collecting ward or individual, antiseptic technique, and repeat isolation. Evidence-based interventions could then be selected and evaluated against a defined baseline [4,5,7,8]. These data are best understood as a case-finding signal that identifies a measurement gap, and not as proof of a particular collection failure or of responsibility attaching to any ward or staff group.

The organism distribution also merits attention. Gram-negative organisms made up 56.3% of the potentially significant category. *E. coli* and *Klebsiella* were prominent, while *S. aureus* was the single most frequent named organism. This pattern is compatible with earlier reports from Libyan hospitals and with the established importance of Gram-negative pathogens in hospital-acquired neonatal infection in resource-constrained settings [11,20]. Whether these infections were community-acquired or healthcare-associated cannot be determined here, since admission timing, diagnoses, devices, prior antimicrobial therapy, and outcomes were unavailable.

Recorded susceptibility results carry concerning signals that require conservative interpretation. Among Gram-negative organisms, only 1 of 12 cefotaxime and 5 of 24 ceftazidime results were recorded as susceptible, while 21 of 34 imipenem results were. In *S. aureus*, 8 of 16 cefoxitin tests were recorded as resistant. These observations run in the same direction

as the substantial resistance burden reported for Libya [12,13] and as long-term African surveillance showing rising resistance among Gram-negative bloodstream isolates [21]. The data cannot, however, establish treatment-level susceptibility rates. Method, breakpoints, and quality control are unknown; testing was selective rather than uniform; patient-level duplicate removal is impossible; and most species-specific isolate counts fall below the thresholds recommended for a stable cumulative antibiogram [15,16]. The coding problem makes this concrete. Six pairs of conventionally synonymous abbreviations appear in the register, and for one of them the two codes produced susceptibility estimates 48 percentage points apart among Gram-negative organisms. That discrepancy cannot be resolved retrospectively and would on its own invalidate an aminoglycoside estimate. These results should therefore not be used to declare any agent unsuitable for empirical therapy or to issue a hospital antibiogram.

The pediatric setting bears directly on how the contaminant signal should be read. Obtaining blood from neonates and small infants is technically demanding, venous access is often poor, and the volume that can be drawn is small. Low inoculum volume reduces pathogen recovery, while difficult and prolonged draws raise the chance that skin flora enter the bottle. A population in which 173 of the age-documented cultures came from neonates, and 364 from children under five, is therefore exposed to both failure modes at once, which may depress the apparent yield of 9.5% and inflate the apparent contaminant proportion of 11.2% in the same dataset. Neither effect can be quantified here, since neither blood volume nor the number of attempts was recorded, and that is itself an argument for capturing both prospectively.

The main strength of the dataset is completeness at register level. All available consecutive entries across roughly twelve months were transcribed, overlapping volumes were de-duplicated by accession number, uncertain fields were left missing rather than guessed, and every principal denominator can be reproduced from the source dataset. An otherwise inaccessible paper archive has thereby been converted into a defensible baseline for laboratory quality improvement. Comparable difficulties in turning routine diagnostic data into resistance surveillance information are well recognized in low-resource settings [9].

The most actionable finding concerns the design of the record itself. A modest redesign of the register would materially raise its clinical and surveillance value. Dedicated fields should capture a patient identifier for secure de-duplication, age, date and time of collection, specimen source and draw site, the number of culture sets and bottles, blood volume where relevant, the collecting ward, the identification method, the susceptibility testing method and standard version, and final verified results. With those elements in place, the laboratory could calculate a defensible contamination indicator, evaluate interventions over time, and in due course construct a cumulative susceptibility report conforming to CLSI M39 principles [16].

The immediate priority is prospective measurement rather than retrospective attribution. Laboratory and clinical teams should agree on a standardized collection protocol and a contamination definition, then report to the indicator monthly using the number of cultures sets as the denominator where appropriate. Education, feedback, collection kits, optimized antisepsis, and trained collectors can then be evaluated locally against that baseline [4,5,7,8].

In parallel, susceptibility documentation should be standardized to a named method and a current interpretive standard, and the antibiotic abbreviations in use should be replaced by a controlled vocabulary. A future cumulative antibiogram should follow CLSI M39 requirements, including patient-level de-duplication, first-isolate rules, routinely tested agents, and adequate species-specific isolate numbers [16]. A prospective follow-up study after register redesign would permit before-and-after evaluation of contamination, diagnostic yield, and resistance trends with considerably stronger validity than the present record review allows. These findings carry several limitations. The source was a handwritten register transcribed from photographic images, and transcription error cannot be excluded despite coding uncertain fields missing rather than inferred. The potential contaminant classification rests on organism identity alone; without culture-set data, it may simultaneously overestimate contamination and underestimate true coagulase-negative staphylococcal bacteremia. Susceptibility denominators vary by agent, testing method, and breakpoints are undocumented; duplicate isolates cannot be removed, and the antibiotic coding problem described above undermines confidence in any single agent-level estimate. Age was available for only 49% of records, captured in a field not designed for it, so ward and age comparisons are exploratory, unadjusted, and likely underpowered. No clinical variables or outcomes were available, so sepsis incidence, attributable mortality, and risk factors for resistant infection cannot be estimated from this dataset.

Conclusion

Analysis of 914 consecutive blood culture records from a pediatric tertiary referral center in Benghazi identified a high frequency of positive cultures containing *S. epidermidis* together with recorded resistance signals that give cause for concern. The interpretation these data support is an organism-based potential contaminant proportion rather than a confirmed contamination rate, and descriptive susceptibility signals rather than a formal antibiogram. The study nonetheless establishes a reproducible baseline and identifies precisely which data elements are absent. Standardized prospective recording of culture sets, collection variables, patient-level identifiers, controlled antimicrobial coding, and testing methods with breakpoints would convert the existing paper workflow into a substantially stronger quality and surveillance system.

Conflict of interest

The authors declare that they have no competing interests.

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Author Contributions

AOB: conceptualization, methodology, data curation, formal analysis. AMA: methodology, validation, investigation, writing of the original draft. MNA: investigation, data curation, visualization, writing through review and editing. All authors read and approved the final manuscript and agree to be accountable for all aspects of the work.

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