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Blood Culture Positivity, Etiology, and Antimicrobial Resistance in Hospitalized Children: A Retrospective Study from Eastern Romania

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Abstract

Pediatric blood culture data from Eastern Europe remain scarce. We describe the positivity rate, etiology, antimicrobial resistance, and predictors of positivity of blood cultures from hospitalized children in Eastern Romania. We retrospectively analyzed 1437 blood cultures from inpatients aged 0–18 years at a tertiary pediatric hospital in Galați, Romania (January 2023–July 2026). Any laboratory-reported organism was considered a positive result. Predictors of positivity were assessed by multivariable logistic regression with patient-clustered standard errors (2024–2026 subperiod). The overall positivity rate was 5.43% (78/1437) and remained stable during 2023–2025 (Cochran–Armitage $p = 0.767$). Among the few patient-level variables available, intensive care admission was the only independent predictor of positivity (adjusted odds ratio 2.12, 95% CI 1.13–3.95), a finding robust to sensitivity analyses, including reclassification of coagulase-negative staphylococci (CoNS) as negative. Gram-positive organisms accounted for 63% of positive cultures, mainly CoNS, many of which may represent contamination; Gram-negative organisms accounted for 31%, led by ESBL-producing *Klebsiella pneumoniae*, and fungi (6%). Resistance was low to vancomycin (2.7%; automated testing, not confirmed by a reference method), linezolid (0%), and meropenem (0%) but high to oxacillin (81.8%), penicillin G (63.3%), and macrolides (58.8–59.5%). Blood culture positivity was low and concentrated in intensive care wards. These laboratory-based data may inform the review of local empirical therapy protocols but cannot by themselves support treatment recommendations; structured criteria are needed to distinguish true CoNS bacteremia from contamination.

Keywords: blood culture; bloodstream infection; children; antimicrobial resistance; coagulase-negative staphylococci; *Klebsiella pneumoniae*; ESBL; intensive care unit; Romania

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1. Introduction

Bloodstream infections remain a leading cause of morbidity and mortality among hospitalized children worldwide, and blood culture continues to be the diagnostic reference standard for bacteremia and fungemia [1–3]. As the only test capable of directly identifying the causative organism together with its antimicrobial susceptibility profile, blood culture occupies a central place in clinical decision-making: a positive result allows clinicians to

de-escalate or target empirical antimicrobial therapy, while a properly interpreted negative result supports safe discontinuation of unnecessary antimicrobials. Its diagnostic value, however, is limited by reduced sensitivity in patients already receiving antimicrobials, by the turnaround time required for organism growth and identification, and by the risk of contamination with skin commensals, all of which complicate the distinction between true bacteremia and a false-positive result [1,3].

The clinical definitions of sepsis and septic shock in children have evolved substantially. The 2005 International Pediatric Sepsis Consensus Conference criteria [4] relied on systemic inflammatory response syndrome (SIRS)-based thresholds, later superseded in adults by the Sepsis-3 definition of sepsis as life-threatening organ dysfunction caused by a dysregulated host response to infection [5]. Because Sepsis-3 was not validated in children, the Society of Critical Care Medicine Pediatric Sepsis Definition Task Force developed the 2024 Phoenix Sepsis Score and its accompanying international consensus criteria, derived and validated in pediatric populations [6]. Under this definition, sepsis in children with suspected or confirmed infection is identified by a Phoenix score of at least 2 points, calculated from four organ-dysfunction domains (respiratory, cardiovascular, coagulation, and neurological), with septic shock denoting the subset of children who additionally meet the cardiovascular dysfunction criterion; this framework has replaced the SIRS-based approach and now underpins pediatric management guidelines [6,7]. In parallel, artificial intelligence-based early warning systems are being explored as adjuncts to conventional clinical and microbiological criteria, although their pediatric validation remains at an early stage [8].

Antimicrobial resistance (AMR) is a growing global threat, estimated to have been directly responsible for 1.27 million deaths worldwide in 2019, with a further 4.95 million deaths associated with antimicrobial-resistant infections [9]; recent forecasts project a continued rise in AMR-attributable mortality through 2050 [10]. European surveillance data indicate that Eastern and Southern European countries, including Romania, report some of the highest proportions of antimicrobial resistance among invasive bacterial isolates in the region [11], and Romanian pediatric cohorts have documented rising multidrug resistance among Gram-negative isolates in recent years [12]. Gaps in pediatric microbiological surveillance in Romania have also been highlighted for other bacterial infections, such as pneumococcal acute otitis media, before and after the COVID-19 pandemic [13]. The World Health Organization AWaRe classification of antibiotics was developed to support stewardship efforts and to monitor the appropriateness of antimicrobial use in this context [14].

Despite this regional burden, published pediatric blood culture data from Romanian hospitals remain limited, particularly regarding the interplay between hospital ward type, patient age, etiology, and antimicrobial susceptibility over a multi-year period. The aim of this study was to characterize the positivity rate, temporal trend, ward- and age-specific distribution, etiological spectrum, and antimicrobial resistance pattern of blood cultures collected from children hospitalized in a tertiary pediatric hospital in Galați, Romania, and to identify independent predictors of culture positivity.

2. Materials and Methods

2.1. Study Design, Setting, and Period

We conducted a retrospective, single-center, observational study of all blood cultures processed by the Microbiology Department of the "Sf. Ioan" Clinical Emergency Hospital for Children, a tertiary pediatric hospital in Galați, Romania, between 1 January 2023 and 7 July 2026. Data for 2026 are partial (1 January–7 July 2026, hereafter "January–July 2026") and are interpreted accordingly.

2.2. Study Population and Data Collection

Consecutive blood culture records from pediatric inpatients (0–18 years) were extracted from the laboratory information system, comprising 1439 records with 68 variables, including demographic data (age, sex, area of residence), clinical data (admission diagnosis, hospital ward, interval from admission to blood culture collection), and antimicrobial susceptibility results for 45 antimicrobials. Two records corresponding to patients older than 18 years (registered in the emergency department) were excluded, leaving 1437 blood cultures for the final analysis.

A blood culture was classified as positive when any bacterial or fungal organism was isolated and reported by the microbiology laboratory. All reported organisms, including coagulase-negative staphylococci (CoNS) and other common skin commensals (e.g., *Bacillus* spp. and viridans group streptococci), were counted as positive results irrespective of the number of positive bottles or sets, because the information required to adjudicate contamination (number of positive sets, time to positivity, clinical signs of infection, presence of a central venous catheter) was not available in the laboratory database. Consequently, no isolate was excluded as a contaminant; the term "positive blood culture" is therefore used throughout this manuscript in preference to "bacteremia", and the influence of CoNS on the main findings was explored in a sensitivity analysis (Section 3.7).

Blood cultures were counted at the level of each ordered sample rather than one per patient; patients could therefore contribute more than one blood culture. In the laboratory information system, aerobic, anaerobic, and fungal bottles belonging to the same blood culture request were registered as separate test records; the descriptive counts in Table 1 refer to these records (1118 records in 2024–2026). For the 2024–2026 subperiod, patient-level identifiers were available: these records corresponded to 1034 distinct blood culture requests (unique laboratory accession numbers) collected from 630 patients during 664 hospital admissions, and 268 patients (42.5%) contributed more than one request. All regression analyses of the 2024–2026 subperiod were performed at the level of the blood culture request. Three units of analysis were therefore used: the blood culture record (bottle-level laboratory entry), the only unit available for the whole study period and therefore used for the descriptive analyses, because request identifiers were not available for 2023; the blood culture request, used for all analyses of the 2024–2026 subperiod; and the patient, used for clustering and for the first-culture sensitivity analysis. The unit of analysis is stated in the title of each table.

Table 1. Number of blood culture records processed and number and proportion of positive records by calendar year (2023–2026; 2026 data partial, January–July).

Year	Blood Cultures (*n*)	Positive (*n*)	Positivity Rate (%)
2023	319	18	5.64%
2024	426	27	6.34%
2025	467	29	6.21%
2026	225	4	1.78%
Total	**1437**	**78**	**5.43%**

Patient origin was classified as local (residence in Galați municipality) or non-local (residence elsewhere, i.e., other localities of Galați County, including Tecuci, and neighboring counties, mainly Brăila). Patient origin is distinct from area of residence, a separate variable recorded in the laboratory information system that classifies the patient's place of residence as urban or rural; non-local patients could therefore have either urban or rural residence. Area of residence (urban vs. rural) was used in the bivariate and multivariable

analyses, whereas patient origin (local vs. non-local) was examined only descriptively and in the exploratory analysis of Section 3.8.3. The time variable available in the laboratory database was the interval, in calendar days, between hospital admission and blood culture collection (date of sampling minus date of admission); a value of 0 days indicates that the blood culture was collected on the day of admission. The total length of hospital stay was not recorded in this database and could not be analyzed.

2.3. Microbiological Methods

Blood samples were collected into pediatric or standard aerobic/anaerobic blood culture bottles and incubated in the BacT/ALERT continuous-monitoring automated blood culture system (bioMérieux, Marcy-l'Étoile, France). The type of bottle used (pediatric or standard) and the volume of blood inoculated were not recorded in the laboratory database and could not be analyzed. Bacterial and fungal isolates recovered from bottles flagged positive were identified using the Vitek automated identification system (bioMérieux) and matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry. Antimicrobial susceptibility testing (AST) was performed by disk diffusion and by the automated Vitek AST system, which additionally provided minimum inhibitory concentration (MIC) estimates. Glycopeptide (vancomycin and teicoplanin) MICs for staphylococci were obtained with the Vitek AST system only and were not confirmed by a reference broth microdilution or gradient-diffusion method.

Susceptibility results for all agents, including cefoxitin screening for methicillin resistance in *Staphylococcus aureus*, were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) M100 performance standards [15], which were applied by the hospital laboratory throughout the study period. Susceptibility categories were analyzed as reported by the laboratory at the time of testing and were not re-interpreted retrospectively; changes in CLSI breakpoints between editions during 2023–2026 may therefore have slightly affected comparability across years. Resistance rates were calculated as the proportion of isolates categorized as resistant among those tested for each agent. Intermediate results were grouped with susceptible results, so that the reported rates reflect resistance in the strict sense rather than overall non-susceptibility; the rates may therefore underestimate non-susceptibility. Antimicrobial panels were organism-specific (e.g., oxacillin and glycopeptides for staphylococci, cephalosporins and carbapenems mainly for Gram-negative bacteria), not every agent was tested for every isolate, and fungal isolates were not included in the antibacterial susceptibility analysis; denominators therefore differ between agents and are reported for each agent (Tables 2–4).

Extended-spectrum beta-lactamase (ESBL) production in *Klebsiella pneumoniae* isolates was identified phenotypically, by screening on a selective chromogenic ESBL medium (CHROMID® ESBL, bioMérieux, Marcy-l'Étoile, France) followed by isolate identification and AST as described above; the ESBL phenotype was confirmed on the basis of the susceptibility profile together with a phenotypic synergy test with a beta-lactamase inhibitor. Molecular characterization of ESBL-encoding genes was not performed. Methicillin resistance in *S. aureus* was identified with an analogous approach, with screening on a selective chromogenic MRSA medium (CHROMID® MRSA, bioMérieux, Marcy-l'Étoile, France) followed by isolate identification and AST; isolates were classified as methicillin-resistant (MRSA) or methicillin-susceptible (MSSA) on the basis of cefoxitin susceptibility. Molecular detection of the *mecA*/*mecC* genes was not performed.

Table 2. Antimicrobial resistance rates by antimicrobial agent, pooled across all species (antimicrobials with at least 15 tests performed). Species-stratified resistance profiles are presented in Tables 3 and 4.

Antimicrobial	Tested (*n*)	Resistant (*n*)	Resistance (%)
Oxacillin	33	27	81.8%
Penicillin G	30	19	63.3%
Erythromycin	37	22	59.5%
Azithromycin	17	10	58.8%
Clarithromycin	17	10	58.8%
Gentamicin	44	22	50%
Clindamycin	45	22	48.9%
Ceftazidime	17	8	47.1%
Ceftriaxone	27	12	44.4%
Ampicillin	19	8	42.1%
Cefotaxime	19	8	42.1%
Moxifloxacin	24	7	29.2%
Ciprofloxacin	28	8	28.6%
Trimethoprim-sulfamethoxazole	41	11	26.8%
Levofloxacin	16	4	25%
Tetracycline	25	6	24%
Teicoplanin	32	4	12.5%
Amikacin	20	1	5%
Tigecycline	20	1	5%
Vancomycin	37	1	2.7%
Linezolid	39	0	0%
Meropenem	27	0	0%

2.4. Statistical Analysis

Categorical variables are reported as counts and percentages and continuous variables as medians with interquartile ranges (IQR) or means with standard deviations (SD), as appropriate. 95% confidence intervals for positivity rates were calculated with the Wilson score method. Associations between blood culture positivity and categorical variables (ward type, sex, area of residence, age group, calendar month) were assessed using Pearson's χ^2 test of independence, and Fisher's exact test was used for 2 × 2 tables with expected cell counts below 5. The annual trend in positivity across the years with complete data (2023–2025) was assessed using the Cochran–Armitage trend test [16,17]. The interval from admission to blood culture collection, a non-normally distributed variable, was compared between groups using the Mann–Whitney U test [18] or the Kruskal–Wallis test, as appropriate. Associations between continuous variables (age and the admission-to-sampling interval) were assessed using the Pearson correlation coefficient and, because the interval was strongly right-skewed, the Spearman rank correlation coefficient [19]; point-biserial correlation was used for the association between binary positivity and continuous variables. Bivariate tests treated blood cultures as independent observations. To describe factors associated with the timing of blood culture collection, exploratory univariate and multivariable linear regression models were fitted on the log-transformed admission-to-sampling interval (log[days + 1]); these models were descriptive and were not intended for prediction.

Table 3. Antimicrobial resistance rates (resistant/tested isolates, %) for the principal Gram-positive species, 2024–2026 subperiod.

Organism	Oxacillin	Penicillin G	Erythromycin	Clindamycin	Gentamicin	TMP-SMX	Teicoplanin	Vancomycin	Linezolid
***Staphylococcus epidermidis* (*n* = 11)**	10/11 (90.9%)	8/8 (100%)	6/11 (54.5%)	7/11 (63.6%)	5/10 (50%)	2/11 (18.2%)	3/5 (60%)	1/5 (20%)	0/10 (0%)
***Staphylococcus hominis* (*n* = 4)**	3/4 (75%)	2/2 (100%)	3/4 (75%)	2/4 (50%)	1/3 (33.3%)	1/4 (25%)	0/2 (0%)	0/2 (0%)	0/3 (0%)
***Staphylococcus aureus*—MSSA (*n* = 3)**	0/3 (0%)	1/3 (33.3%)	2/3 (66.7%)	2/3 (66.7%)	0/3 (0%)	0/3 (0%)	—	0/3 (0%)	0/3 (0%)
***Staphylococcus aureus*—MRSA (*n* = 2)**	1/1 (100%)	2/2 (100%)	0/2 (0%)	0/2 (0%)	1/2 (50%)	0/1 (0%)	0/1 (0%)	0/2 (0%)	0/2 (0%)

TMP-SMX, trimethoprim-sulfamethoxazole; MSSA, methicillin-susceptible *Staphylococcus aureus*; MRSA, methicillin-resistant *Staphylococcus aureus*.

Table 4. Antimicrobial resistance rates (resistant/tested isolates, %) for the principal Gram-negative species, 2024–2026 subperiod.

Organism	Ampicillin	Amox-clav	Ceftriaxone	Ceftazidime	Cefepime	Gentamicin	Ciprofloxacin	Meropenem	TMP-SMX
***Klebsiella pneumoniae*, ESBL-producing (*n* = 7)**	—	7/7 (100%)	7/7 (100%)	7/7 (100%)	2/2 (100%)	6/7 (85.7%)	1/2 (50%)	0/7 (0%)	5/7 (71.4%)
***Escherichia coli* (*n* = 4)**	2/4 (50%)	2/2 (100%)	0/4 (0%)	0/4 (0%)	—	0/4 (0%)	—	0/2 (0%)	0/3 (0%)
***Pseudomonas aeruginosa* (*n* = 3)**	—	—	—	0/3 (0%)	0/3 (0%)	—	0/2 (0%)	0/3 (0%)	—

Amox-clav, amoxicillin-clavulanate; TMP-SMX, trimethoprim-sulfamethoxazole. Denominators differ between antimicrobials because not every agent was tested for every isolate. For *E. coli*, amoxicillin-clavulanate results were available for only two of the four isolates; the 2/2 (100%) value should not be interpreted as a species-level resistance rate. Percentages based on denominators of four or fewer isolates are shown for completeness only and should be interpreted with caution.

A multivariable logistic regression model including age, sex, area of residence, ward type (intensive care vs. general ward), and calendar year (categorical, 2024 as reference) was fitted on the 2024–2026 subperiod, for which patient identifiers were available, to identify independent predictors of positivity; results are reported as adjusted odds ratios (aOR) with 95% confidence intervals (CI) [20]. Because individual patients could contribute more than one blood culture, standard errors were estimated with a cluster-robust (sandwich) variance estimator, with clustering on patient. Three sensitivity analyses were performed: (i) a generalized estimating equation (GEE) model with an exchangeable within-patient working correlation structure; (ii) a model restricted to the first blood culture of each patient; and (iii) a model in which cultures yielding only CoNS were classified as negative.

To characterize the possible origin of positive cultures in the absence of data on central venous catheters, positive blood cultures of the 2024–2026 subperiod were classified by the timing of collection, following the CDC/NHSN surveillance convention in which the day of admission is hospital day 1 [21]: cultures collected on hospital day 1 or 2 were considered present on admission and, by definition, could not meet the surveillance criteria for central line-associated bloodstream infection (CLABSI), whereas cultures collected on hospital day 3 or later were considered potentially hospital-onset. The analyses in Section 3.8 were prespecified as exploratory and were not adjusted for multiple comparisons. Statistical significance was set at $\alpha = 0.05$. All analyses were performed in Python 3 (pandas, SciPy, scikit-learn, statsmodels).

3. Results

3.1. General Characteristics of the Study Population

Of the 1437 blood cultures analyzed, patients had a median age of 2 years (range 0–17 years), and 54.1% were male. Blood cultures originated predominantly from the two intensive care wards (40.5% of all cultures), namely the pediatric anesthesia and intensive care unit (ICU1; "ATI") and the pediatric intensive/high-dependency care unit (ICU2; "Terapie Intensivă"), followed by general pediatric and neonatology wards. Most cultures (71.7%; 1030/1437) were collected from non-local children, i.e., children residing outside Galați municipality (other localities of Galați County, including Tecuci, and neighboring counties, mainly Brăila), and 28.3% (407/1437) from local children.

3.2. Overall and Annual Positivity Rate

The overall blood culture positivity rate was 5.43% (78/1437 blood culture records). At the level of the blood culture request, which avoids counting several bottles of the same request separately, positivity in the 2024–2026 subperiod was 5.03% (52/1034; 95% CI 3.86–6.54%), compared with 5.37% (60/1118) at the record level for the same subperiod. Annual numbers of blood cultures and positivity rates are shown in Figure 1 and Table 1. Annual positivity rates (95% CI) were 5.64% (3.60–8.74%) in 2023, 6.34% (4.39–9.06%) in 2024, 6.21% (4.36–8.78%) in 2025, and 1.78% (0.69–4.48%) in January–July 2026.

The Cochran–Armitage trend test applied to the years with complete data (2023–2025) showed no statistically significant trend ($z = 0.296$, $p = 0.767$), indicating a stable positivity rate over this period. The lower rate observed in 2026 (1.78%) should be interpreted in light of the partial coverage of that year. Although a proportion is not inherently biased by the length of the observation period, the 2026 estimate is based on only 225 blood cultures with four positive results, and the months not yet covered (August–December) include two of the months with the highest positivity in the pooled data (September and November; Table 5). The partial-year estimate is therefore subject to substantial sampling error and possible seasonal imbalance, which is why 2026 was excluded from the trend test. The annual rates in Table 1 are calculated at the level of blood culture records (bottle-level entries), whereas

the same-month comparison below uses blood culture requests; in January–July 2026, the 225 records corresponded to 209 requests and the four positive records to three positive requests, which explains the difference between the two estimates (1.78% vs. 1.44%). When the same calendar months were compared, positivity at the level of blood culture requests was 1.4% (3/209) in January–July 2026 versus 5.0% (24/479) in January–July 2024–2025 (Fisher's exact test, $p = 0.031$), and the difference persisted after multivariable adjustment (Table 6). Given the very small number of positive cultures in 2026, this finding should be interpreted with caution; possible explanations include random variation, changes in sampling practices or in the case mix of sampled patients, and a genuine decrease in bloodstream infections, which cannot be distinguished with the available data.

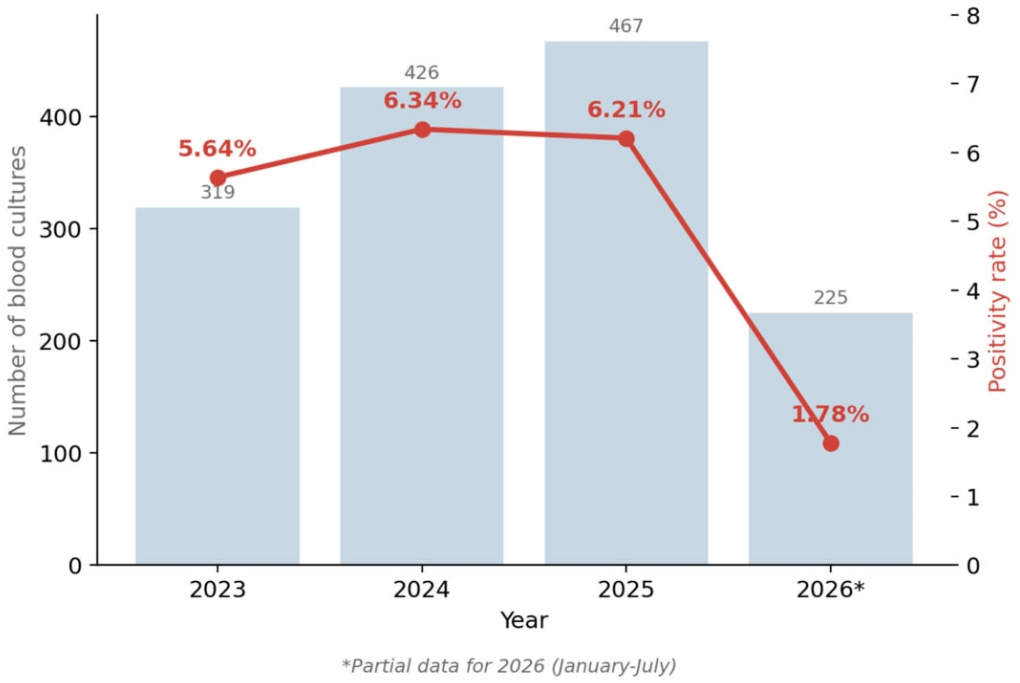


Figure 1. Annual number of blood cultures and positivity rate, 2023 2026 (2026 data partial, January July).

Table 5. Blood culture positivity rate by calendar month, pooled across the study period (blood culture records, 2023–2026).

Month	Cultures (*n*)	Positive (*n*)	Positivity Rate (%)
January	141	5	3.55%
February	112	3	2.68%
March	144	6	4.17%
April	115	2	1.74%
May	138	5	3.62%
June	183	17	9.29%
July	125	8	6.40%
August	86	6	6.98%
September	69	6	8.70%
October	114	3	2.63%
November	109	13	11.93%
December	101	4	3.96%

Table 6. Independent predictors of blood culture positivity in the multivariable logistic regression model (2024–2026 subperiod; $n = 1033$ blood culture requests from 629 patients; 52 positive). Standard errors were clustered by patient.

Variable	Adjusted OR	95% CI	*p*-Value
Age (per year)	0.94	0.87–1.02	0.140
Male sex (vs. female)	0.83	0.44–1.54	0.551
Urban residence (vs. rural)	0.94	0.50–1.77	0.856
ICU/high-dependency ward (vs. general ward)	2.12	1.13–3.95	0.019
Year 2025 (vs. 2024)	0.88	0.46–1.69	0.694
Year 2026, January–July (vs. 2024)	0.22	0.05–0.98	0.047

OR, odds ratio; CI, confidence interval; ICU, intensive care unit.

3.3. Positivity by Ward, Age Group, Sex, and Area of Residence

Positivity was significantly associated with ward type: the intensive care wards (ICU1 and ICU2) showed higher positivity rates (9.6% and 7.7%, respectively) than the general pediatric wards (1.1–2.5%; $\chi^2 = 10.884$, $p < 0.001$) (Figure 2).

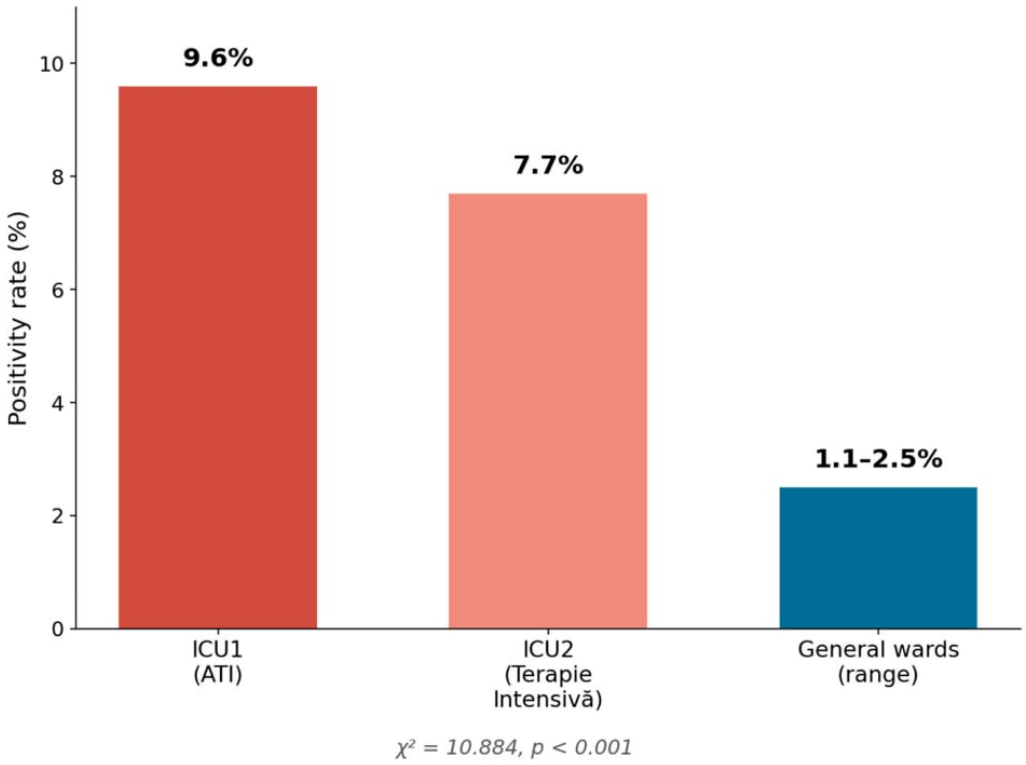


Figure 2. Blood culture positivity rate in the two intensive care wards (ICU1, pediatric anesthesia and intensive care unit; ICU2, pediatric intensive/high-dependency care unit) versus general wards (ranging across the six general pediatric wards with the highest culture volume).

The age distribution was strongly skewed toward infants under one year ($n = 507$), consistent with the concentration of neonatal and infant admissions in intensive care and neonatology wards (Figure 3). Although a numerically higher positivity rate was observed among infants under one year, the association between positivity and age group did not reach statistical significance ($\chi^2 = 7.879$, $p = 0.096$). No significant association was found between positivity and area of residence (rural vs. urban; $p = 1.00$) or sex ($p = 1.00$).

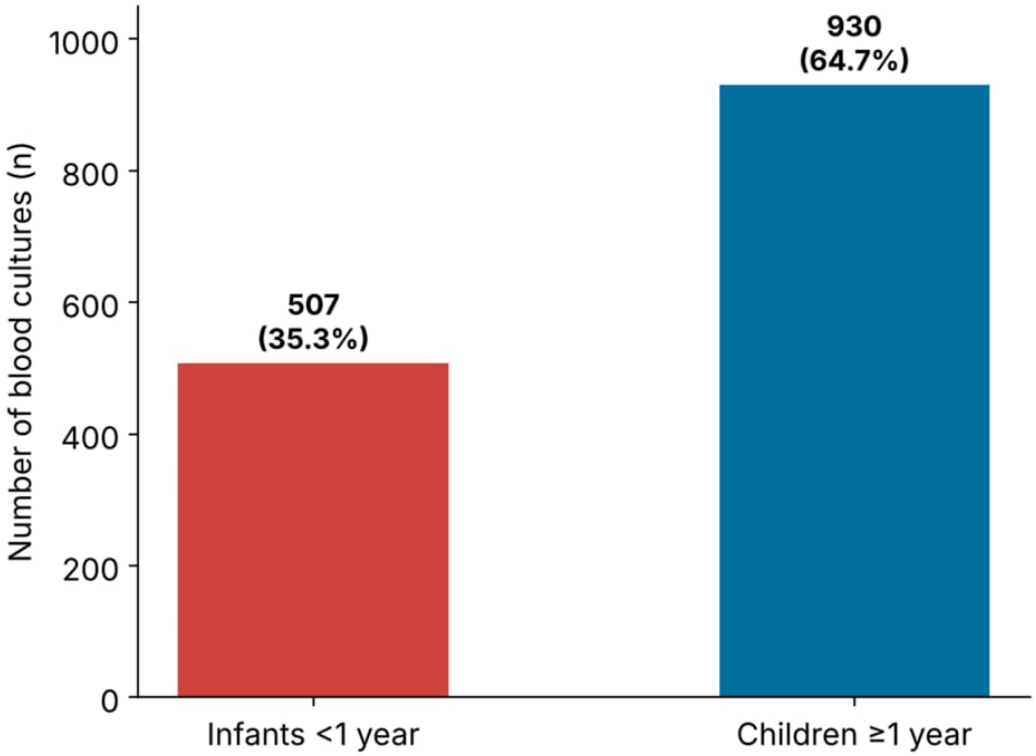


Figure 3. Age distribution of blood cultures collected during the study period (infants < 1 year vs. children ≥ 1 year).

3.4. Etiological Distribution

Gram-positive organisms accounted for 63% of positive cultures (Figure 4), predominantly CoNS (*Staphylococcus epidermidis*, $n = 15$; *S. hominis*, $n = 8$). *S. aureus* accounted for a smaller proportion of isolates, including both methicillin-susceptible ($n = 3$) and methicillin-resistant ($n = 2$) strains. Gram-negative organisms represented 31% of positive cultures, including seven isolates of ESBL-producing *K. pneumoniae* and four of *Escherichia coli*. Fungal isolates (*Candida* spp.) accounted for 6% of positive cultures. Two isolates of *Neisseria meningitidis* and two of *Salmonella* spp. (polyvalent I) were also identified (Table 7). Because CoNS (at least 25 isolates; Table 7) could not be adjudicated as true pathogens or contaminants, the predominance of Gram-positive organisms depends largely on their inclusion: when CoNS were excluded, non-CoNS Gram-positive organisms (at most 24 isolates) were no more frequent than Gram-negative organisms (24 isolates). The proportion of Gram-positive organisms should therefore be regarded as an upper estimate.

3.5. Antimicrobial Resistance Patterns

Resistance rates varied widely by antimicrobial class (Figure 5; Table 2). Because these pooled estimates combine different bacterial species and are based on 16–45 tested isolates per agent, they do not represent species-specific susceptibility patterns and should be interpreted with caution. Reserve and last-resort agents retained high activity: resistance was low for vancomycin (2.7%), amikacin (5.0%), and tigecycline (5.0%) and absent for linezolid and meropenem. In contrast, resistance was high for oxacillin (81.8%, reflecting a substantial proportion of methicillin-resistant staphylococci among the isolates tested), penicillin G (63.3%), and macrolides (erythromycin 59.5%, azithromycin 58.8%, clarithromycin 58.8%). These findings are broadly consistent with Romanian and European data showing high resistance in this region alongside preserved glycopeptide and carbapenem susceptibility [11,12]. Teicoplanin non-susceptibility (12.5% pooled) was also

reported; in the species-stratified analysis (Table 3), the single vancomycin-resistant isolate and most teicoplanin-resistant isolates were CoNS (*S. epidermidis*) rather than *S. aureus*, for which vancomycin and teicoplanin susceptibility was preserved in all isolates tested. Both the vancomycin and the teicoplanin results were obtained with the automated Vitek AST system and were not confirmed by a reference MIC method (broth microdilution or gradient diffusion). Because automated systems may occasionally report false glycopeptide resistance in staphylococci, because vancomycin resistance is rare in CoNS, and because the stratified denominators were very small (Table 3), these results should be regarded as unconfirmed and potentially false-resistant, and should not be interpreted as evidence of glycopeptide resistance in this setting.

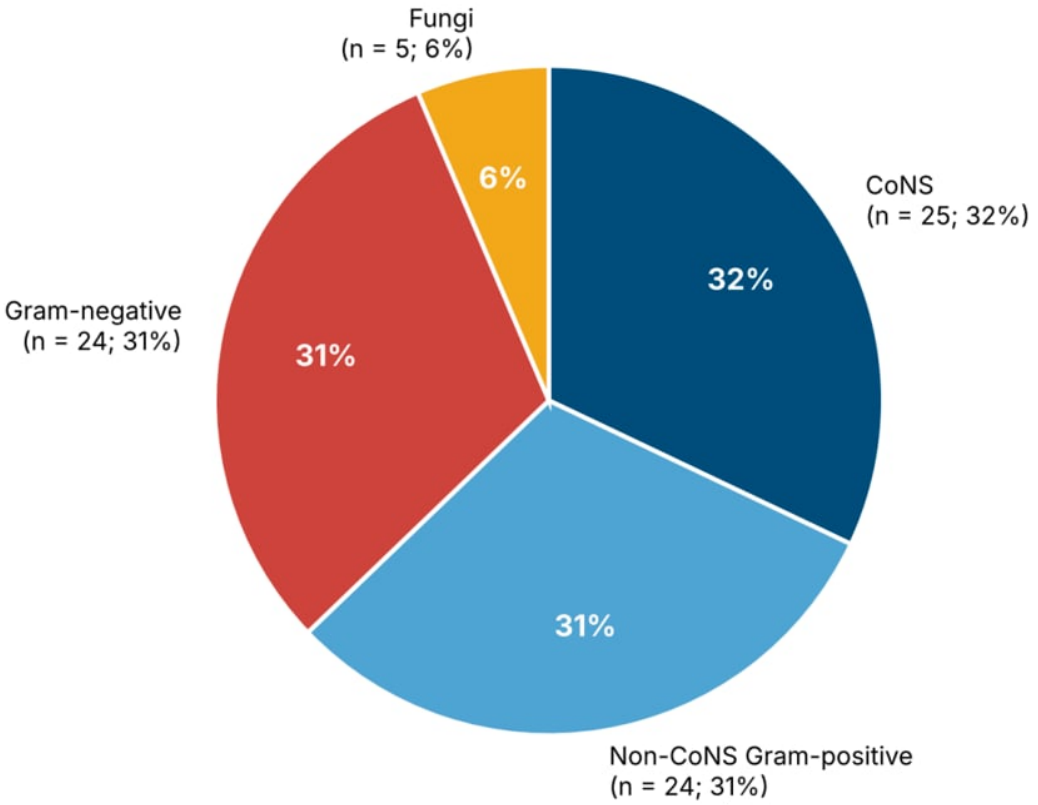


Figure 4. Etiological distribution of positive blood cultures ($n = 78$): coagulase-negative staphylococci (CoNS; $n = 25$, 32%), non-CoNS Gram-positive organisms ($n = 24$, 31%), Gram-negative organisms ($n = 24$, 31%), and fungi ($n = 5$, 6%). CoNS (*S. epidermidis*, $n = 15$; *S. hominis*, $n = 8$; *S. cohnii*, $n = 2$) could not be adjudicated as true pathogens or contaminants; the combined Gram-positive proportion (63%) should therefore be regarded as an upper estimate.

Table 7. Organisms isolated from the 78 positive blood culture records, 2023–2026. Organisms recovered from at least two positive blood cultures are shown.

Organism	Isolates (*n*)
Staphylococcus epidermidis	15
Staphylococcus hominis	8
***Klebsiella pneumoniae* ESBL-producing**	7
Escherichia coli	4
Streptococcus intermedius	4
Pseudomonas aeruginosa	3

Table 7. *Cont.*

Organism	Isolates (*n*)
Candida albicans	3
***Staphylococcus aureus* MSSA**	3
***Staphylococcus aureus* MRSA**	2
Streptococcus salivarius	2
Staphylococcus cohnii	2
Enterococcus faecalis	2
***Salmonella* spp. polyvalent I**	2
Neisseria meningitidis	2

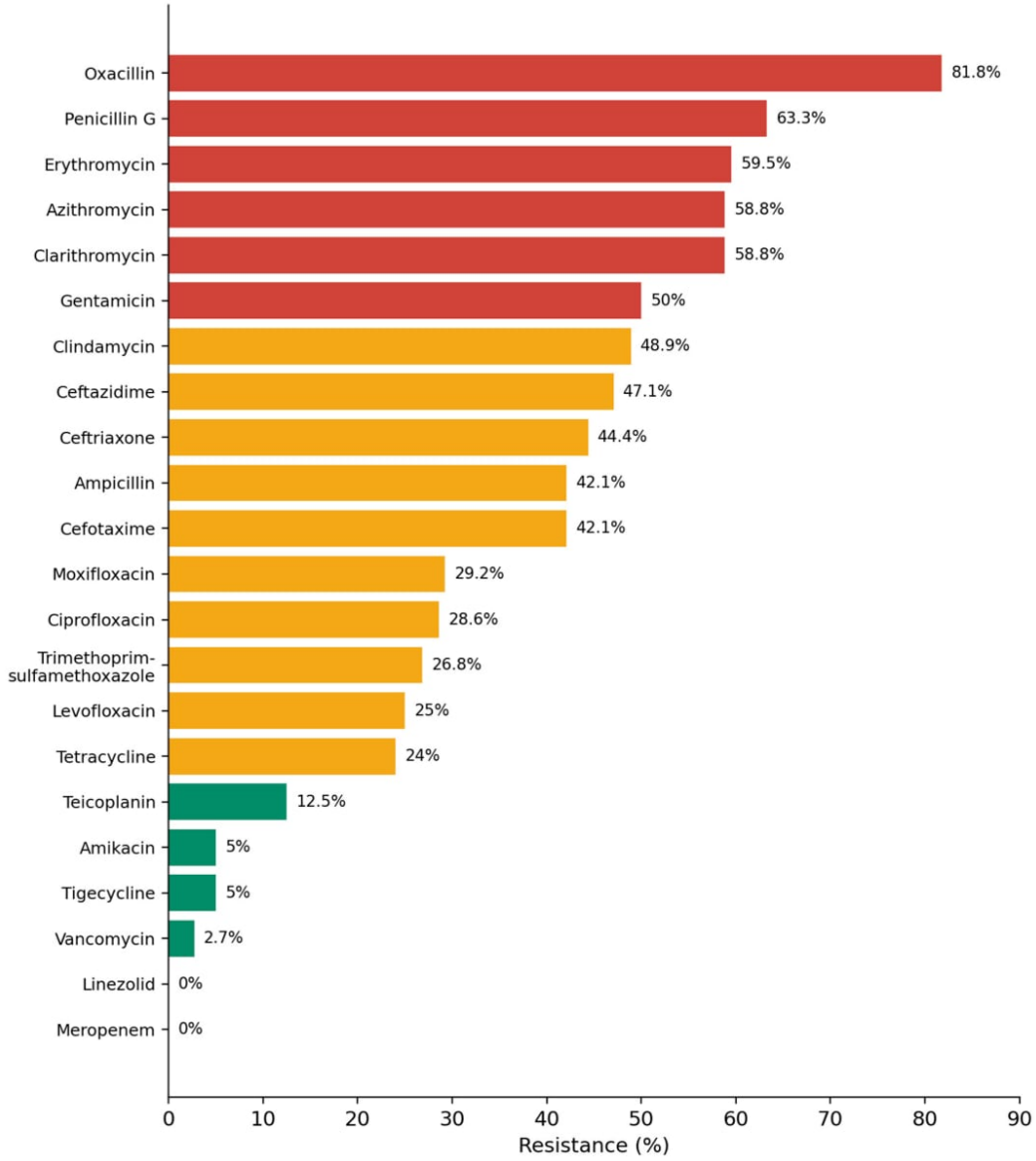


Figure 5. Antimicrobial resistance rates for antimicrobials with at least 15 susceptibility tests performed.

To address the heterogeneity of resistance mechanisms across taxa, resistance rates were additionally stratified by species for isolates with complete electronically archived susceptibility data (2024–2026 subperiod; 52 positive blood culture requests; these corre-

spond to the 60 positive records of this subperiod in Table 1, because bottles of the same request were registered as separate records and more than one bottle was positive in some requests). The 18 positive cultures from 2023 were not available in electronic format and could not be included in this stratified analysis (Tables 3 and 4). Species with fewer than two tested isolates for a given antimicrobial are omitted from the corresponding cell (—). Many species-specific estimates are based on two to five tested isolates; they are presented descriptively and should not be interpreted as reliable species-level resistance rates.

The species-stratified profile shows that pooled resistance rates (Table 2) partly obscure clinically important species-level differences: methicillin (oxacillin) resistance was substantially more frequent among CoNS (*S. epidermidis*, 90.9%; *S. hominis*, 75%) than among *S. aureus*, while among Gram-negative isolates, resistance to third- and fourth-generation cephalosporins and to aminoglycosides was concentrated almost entirely in ESBL-producing *K. pneumoniae*, contrasting with the lower resistance observed in *E. coli* and *Pseudomonas aeruginosa*. Given the very small number of *E. coli* and *P. aeruginosa* isolates and the incomplete testing of some agents, these species-level estimates are descriptive only.

3.6. Interval from Admission to Blood Culture Collection

The interval from admission to blood culture collection did not differ significantly between positive and negative cultures (median 0 days, mean 4.63 days vs. median 1 day, mean 2.53 days; Mann–Whitney U = 50,346, $p = 0.432$). A median of 0 days indicates that more than half of the positive blood cultures were collected on the day of admission (53.8% of positive and 46.7% of negative blood culture requests in the 2024–2026 subperiod), i.e., in children in whom infection was present or suspected at presentation. The interval differed significantly across hospital wards (Kruskal–Wallis H = 132.495, $p < 0.001$), reflecting differences between wards in the timing of blood culture sampling.

Factors Associated with the Admission-to-Sampling Interval

Because the admission-to-sampling interval was strongly right-skewed, univariate and multivariable linear regression models were fitted on the log-transformed interval (log[days + 1]) for the 2024–2026 subperiod ($n = 1034$ blood culture requests from 630 patients). Candidate predictors were age, sex, area of residence (urban vs. rural), admission to an intensive care ward, and blood culture positivity (Tables 8 and 9).

Table 8. Univariate linear regression of factors associated with the log-transformed interval from admission to blood culture collection, 2024–2026 subperiod ($n = 1034$ blood culture requests).

Predictor	Coefficient (Log-Days)	95% CI	*p*-Value
Age (per year)	0.017	0.007 to 0.028	0.001
Male sex (vs. female)	0.000	−0.109 to 0.109	0.999
Urban residence (vs. rural)	−0.057	−0.166 to 0.052	0.303
Intensive care ward admission (vs. general ward)	−0.207	−0.317 to −0.097	<0.001
Positive blood culture (vs. negative)	0.161	−0.088 to 0.409	0.205

In both models, older age was associated with a modestly longer interval between admission and blood culture collection, while admission to an intensive care ward was associated with a significantly shorter interval. This is consistent with earlier sampling of critically ill children, in whom blood cultures are typically obtained at or shortly after admission, whereas in general wards cultures are more often collected later, when infection

is suspected during the hospital course. Blood culture positivity was associated with a longer interval in both models, but the association did not reach statistical significance. However, overall model fit was very low ($R^2 = 0.033$): the included variables explained only 3.3% of the variance in sampling timing, and most of the variability is attributable to factors not captured in the dataset (e.g., diagnosis, severity of illness, and treatment course). These models therefore have no predictive value and minimal clinical relevance; they are reported only to describe the direction of the associations, which should be regarded as exploratory.

Table 9. Multivariable linear regression of factors associated with the log-transformed interval from admission to blood culture collection, adjusted for all listed covariates (2024–2026 subperiod, $n = 1034$ blood culture requests; model $R^2 = 0.033$).

Predictor	Adjusted Coefficient (Log-Days)	95% CI	*p*-Value
Age (per year)	0.022	0.011 to 0.032	<0.001
Male sex (vs. female)	−0.011	−0.119 to 0.096	0.835
Urban residence (vs. rural)	−0.070	−0.178 to 0.037	0.200
Intensive care ward admission (vs. general ward)	−0.261	−0.373 to −0.150	<0.001
Positive blood culture (vs. negative)	0.223	−0.023 to 0.469	0.076

3.7. Multivariable Analysis

The multivariable logistic regression model was fitted on the 2024–2026 subperiod ($n = 1033$ blood culture requests from 629 patients, 52 positive; one request from an adult patient was excluded), with standard errors clustered on patient. Admission to an intensive care ward was the only patient-level characteristic independently associated with blood culture positivity (aOR 2.12, 95% CI 1.13–3.95, $p = 0.019$); age, sex, and area of residence were not significantly associated with positivity. Compared with 2024, positivity was similar in 2025 but lower in January–July 2026 (aOR 0.22, 95% CI 0.05–0.98, $p = 0.047$) (Table 6).

The association between intensive care ward admission and positivity was consistent across all sensitivity analyses: in the GEE model (estimated within-patient correlation 0.21; aOR 2.71, 95% CI 1.44–5.13, $p = 0.002$); in the analysis restricted to the first blood culture of each patient ($n = 629$, 34 positive; calendar year entered as a continuous term because no first culture was positive in 2026; aOR 3.60, 95% CI 1.72–7.51, $p < 0.001$); and when the 16 requests yielding only CoNS were classified as negative (positivity in this subperiod 3.48% instead of 5.03%; aOR 2.49, 95% CI 1.23–5.05, $p = 0.011$). Thus, neither repeated sampling of the same patients nor the inclusion of potential CoNS contaminants explained the higher positivity observed in intensive care wards.

3.8. Exploratory Correlation and Subgroup Analyses

A set of exploratory analyses, not adjusted for multiple comparisons, is summarized in Table 10 and should be regarded as hypothesis-generating. Because many comparisons were made with a small number of positive cultures, nominally significant results may be chance findings; effect sizes with 95% CIs are reported where they could be calculated, and none of these associations should be regarded as confirmed.

Table 10. Summary of exploratory correlation and subgroup analyses.

Analysis	Test	Statistic	*p*-Value	Result
Month vs. positivity	Pearson χ^2	25.50	0.008	Significant
Age vs. admission-to-sampling interval	Pearson r	0.041	0.124	Not significant
Age vs. admission-to-sampling interval	Spearman ρ	0.155	<0.001	Significant
Positivity vs. admission-to-sampling interval	Point-biserial r	0.083	0.002	Significant
Origin (local/non-local) vs. positivity	Pearson χ^2	0.011	0.916	Not significant
Origin vs. ICU admission	Pearson χ^2	19.83	<0.001	Significant
Admission-to-sampling interval by etiological group	Kruskal–Wallis H	8.30	0.016	Significant
ESBL *Klebsiella* vs. ward	Fisher's exact	OR = 1.09	1.00	Not significant
MRSA vs. ward	Fisher's exact	OR = 0.00	0.51	Not significant

3.8.1. Seasonal Variation in Positivity

Blood culture positivity varied by calendar month (Pearson $\chi^2 = 25.50$, $p = 0.008$), with peaks in June (9.3%), September (8.7%), and November (11.9%) and troughs in April (1.7%) and October (2.6%) (Table 5). Given the modest number of cultures per month, this pattern should be interpreted cautiously.

3.8.2. Age and the Admission-to-Sampling Interval

The Pearson correlation between age and the admission-to-sampling interval was weak and non-significant (r = 0.041, $p = 0.124$, $n = 1437$), whereas the Spearman rank correlation showed a significant positive monotonic association ($\rho = 0.155$, $p < 0.001$). This divergence indicates a monotonic but non-linear relationship, reflecting the strongly right-skewed distribution of the interval. Point-biserial correlation showed a small positive association between positivity and the admission-to-sampling interval (r = 0.083, $p = 0.002$), although the Mann–Whitney U test was not significant (Section 3.6).

3.8.3. Patient Origin: Local Versus Non-Local Patients

Local and non-local patients did not differ in blood culture positivity (5.65% vs. 5.34%; $\chi^2 = 0.011$, $p = 0.916$) or in the interval from admission to blood culture collection (median 1 day in both groups; Mann–Whitney $p = 0.759$). However, non-local patients were significantly more likely to be admitted to an intensive care ward (44.2% vs. 31.2%; $\chi^2 = 19.83$, $p < 0.001$) (Table 11). Expressed as odds ratios, non-local origin was not associated with positivity (OR 0.94, 95% CI 0.57–1.56) but was associated with intensive care admission (OR 1.74, 95% CI 1.37–2.22). This pattern is compatible with the hospital's role as a tertiary referral center, although clinical severity could not be assessed.

Table 11. Ward distribution and positivity rate by patient origin (local vs. non-local; blood culture records, 2023–2026).

Origin	ICU/High-Dependency Ward	General Ward	% in ICU	Positive (*n*)	Positivity Rate
Local	127	280	31.2%	23	5.65%
Non-local	455	575	44.2%	55	5.34%

ICU, intensive care unit.

3.8.4. Admission-to-Sampling Interval by Etiological Group

Among positive cultures, the interval from admission to blood culture collection differed by etiological group (Kruskal–Wallis H = 8.30, $p = 0.016$; Figure 6; Table 12). Gram-positive isolates ($n = 49$) were recovered almost exclusively from cultures collected on or shortly after the day of admission (median 0 days, IQR 0–2). Gram-negative isolates ($n = 24$) also had a median interval of 0 days but a markedly wider distribution (IQR 0–9.25 days; mean 7.88 days), with about one quarter recovered after more than nine days of hospitalization, and fungal isolates ($n = 5$) were recovered after a median of 8 days (IQR 6–8). This pattern is compatible with a larger proportion of hospital-acquired infections among Gram-negative and fungal isolates; because the clinical context of sampling was not available, this interpretation remains hypothesis-generating.

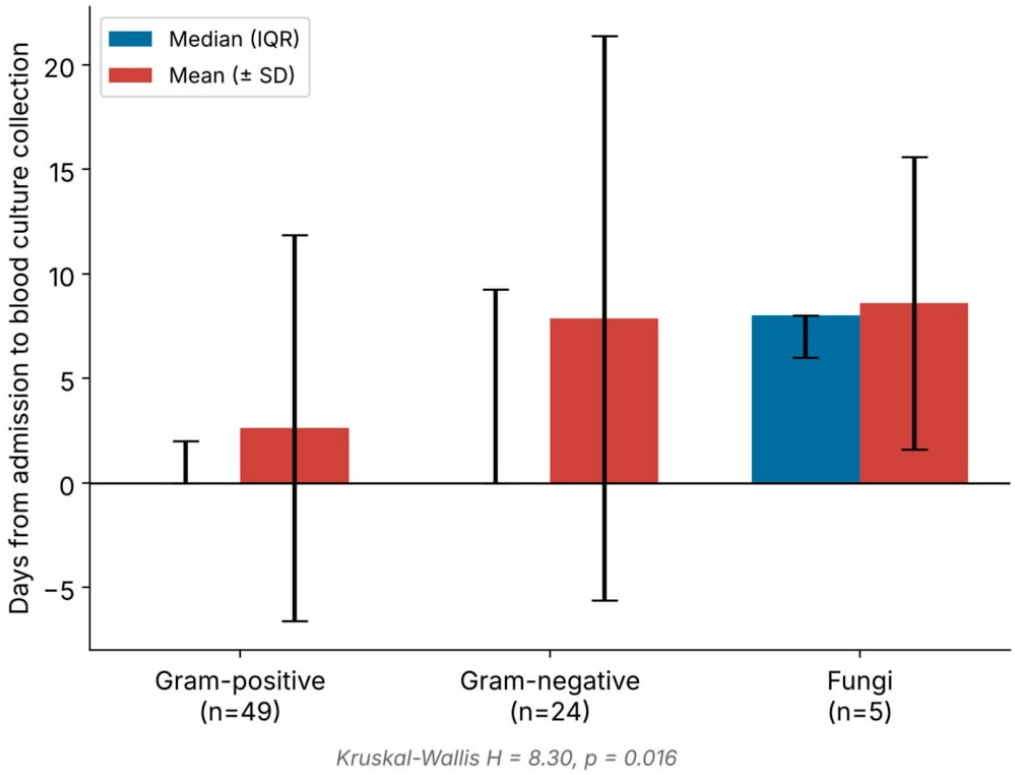


Figure 6. Interval from admission to blood culture collection by etiological group among positive cultures (Kruskal–Wallis H = 8.30, $p = 0.016$).

Table 12. Interval from admission to blood culture collection by etiological group among positive blood culture records ($n = 78$).

Etiological Group	*n*	Median (Days)	IQR (Days)	Mean ± SD (Days)	Range (Days)
Gram-positive	49	0	0–2	2.63 ± 9.22	0–62
Gram-negative	24	0	0–9.25	7.88 ± 13.50	0–48
Fungi	5	8	6–8	8.60 ± 6.99	1–20

IQR, interquartile range; SD, standard deviation.

3.8.5. Rare Resistant Phenotypes by Ward

Fisher's exact test showed no association between ward type and the presence of ESBL-producing *K. pneumoniae* (OR = 1.09, $p = 1.00$), MRSA ($p = 0.51$), or CoNS (OR = 1.02, $p = 1.00$) among positive cultures, most likely reflecting insufficient statistical power given the small number of these isolates ($n = 2$–17 per subgroup).

3.8.6. Timing of Positive Blood Cultures Relative to Admission

Of the 52 positive blood culture requests of the 2024–2026 subperiod, 35 (67.3%) were collected on hospital day 1 or 2 and were therefore present on admission, and 17 (32.7%) were collected on hospital day 3 or later and were potentially hospital-onset. The proportion collected on day 1–2 was higher in intensive care wards (23/30, 76.7%) than in general wards (12/22, 54.5%) and was similar for cultures yielding CoNS (11/16, 68.8%) and those yielding other organisms (24/36, 66.7%; Fisher's exact test, $p = 1.00$). Potentially hospital-onset cultures were more frequent among Gram-negative and fungal isolates (11/24, 45.8%) than among Gram-positive isolates (6/28, 21.4%; OR 3.10, 95% CI 0.93–10.39), although this difference did not reach statistical significance ($p = 0.080$). Thus, at least two-thirds of the positive cultures, including most of those from intensive care wards, could not have represented CLABSI as defined for surveillance purposes.

4. Discussion

This retrospective analysis of 1437 pediatric blood cultures from a tertiary hospital in Galați, Romania, found an overall positivity rate of 5.43%, within the range (1–8%) reported in pediatric blood culture studies internationally [1,3,22,23]. The stability of this rate across the years with complete data suggests a consistent baseline frequency of positive blood cultures in this setting, without a major disruptive event comparable to the COVID-19 pandemic, which influenced contamination and positivity rates elsewhere [24].

The independent association between intensive care ward admission and blood culture positivity (aOR 2.12, 95% CI 1.13–3.95), robust to accounting for repeated cultures from the same patient and to the reclassification of CoNS, is consistent with the literature identifying critical illness, invasive devices, and prolonged hospitalization as major risk factors for bloodstream infection in children [1,2,25–27]. However, our data do not allow these mechanisms to be confirmed: comorbidities, illness severity, prior antimicrobial exposure, central venous catheter status, and length of stay were not available, and because potential contaminants were included, the association with intensive care admission does not necessarily indicate a higher risk of true bloodstream infection; it may also reflect differences in case mix, sampling practices, or contamination between wards. Central-line care bundles have been shown to reduce catheter-associated bloodstream infection rates in pediatric and neonatal intensive care units [25–27]. However, because three-quarters of the positive cultures from intensive care wards in the 2024–2026 subperiod were collected on hospital day 1 or 2 (Section 3.8.6), the higher positivity in these wards appears to reflect mainly the admission of children with infection already present at presentation, including referrals from the surrounding area, rather than device-associated hospital-onset infection. The role of central venous catheters could not be assessed directly and should be addressed in prospective studies that record the vascular access device and the site of blood culture sampling.

The predominance of Gram-positive organisms, primarily CoNS, mirrors findings from numerous pediatric and neonatal cohorts and highlights a well-recognized diagnostic challenge: distinguishing true bacteremia from contamination when these skin commensals are isolated from a single blood culture set [22,23,28–33]. In our cohort, this predominance was driven by CoNS: in the 2024–2026 subperiod, reclassifying the 16 requests that yielded only CoNS as negative reduced positivity from 5.03% to 3.48%, and with CoNS excluded, Gram-positive organisms no longer outnumbered Gram-negative organisms. The Gram-positive predominance reported here should therefore be interpreted as an upper bound rather than as an estimate of true Gram-positive bloodstream infection. Other common skin commensals, such as viridans group streptococci, were also counted as positive and were not reclassified in the sensitivity analysis. The overall positivity rate of 5.43% should therefore be interpreted as the proportion of microbiologically positive blood cultures, an upper limit of the true

frequency of bloodstream infection, and the organism proportions as proportions of all reported isolates rather than of confirmed pathogens. The absence of systematic paired blood culture sampling at our center limited the application of validated contamination-adjudication criteria, and future prospective work should incorporate standardized definitions, such as those of the CDC/NHSN [21]. The relatively small proportion of MRSA (2 of 5 *S. aureus* isolates) is in line with international data describing MRSA bacteremia as a less frequent, though clinically significant, cause of pediatric bloodstream infection [34].

The identification of ESBL-producing *K. pneumoniae* as the leading Gram-negative pathogen is consistent with European and global trends documenting rising extended-spectrum beta-lactamase and carbapenemase production among Enterobacterales causing pediatric and neonatal bloodstream infections, particularly in regions with higher baseline resistance such as Eastern and Southern Europe [9–12,35–38]. The resistance profile observed, with high resistance to penicillins and macrolides but preserved susceptibility to vancomycin, linezolid, and carbapenems, indicates that these agents retained in vitro activity against the isolates tested in this setting; given the small number of isolates per species, the unconfirmed glycopeptide results, and the absence of clinical outcome data, this observation cannot by itself establish their clinical effectiveness. In line with WHO AWaRe principles, however, they should be reserved for patients with risk factors for resistant pathogens, critical illness, or documented resistance, with prompt de-escalation guided by culture results, rather than used as routine empirical therapy; local antibiograms such as the one reported here may contribute to, but cannot by themselves determine, institution-specific empirical protocols, which also require data on illness severity and clinical outcomes [14,39–42]. The low proportion of *Candida* isolates (6%) is consistent with the lower incidence of pediatric candidemia relative to bacterial bloodstream infections reported elsewhere [43–45], and the two *N. meningitidis* isolates are consistent with the continued, low-frequency occurrence of invasive meningococcal disease reported in the region [46–48], although our data do not allow conclusions about its epidemiology.

The exploratory analyses add nuance to these findings. The longer interval from admission to blood culture collection for fungal isolates and for a subset of Gram-negative isolates is compatible with a larger share of infections arising during hospitalization; however, this interpretation is derived from the published literature on the role of Enterobacterales and *Candida* spp. in healthcare-associated bloodstream infections in children [35–38,43–45], rather than from clinical data in our cohort, and the corresponding difference in the timing analysis did not reach statistical significance (Section 3.8.6). The divergence between the Pearson and Spearman correlations for age and the admission-to-sampling interval illustrates that skewed clinical time variables are better analyzed with rank-based methods [19]. Finally, the higher proportion of intensive care admissions among non-local patients, despite similar positivity rates, is compatible with the hospital's role as a referral center for the surrounding area, although this could not be linked to clinical severity in this dataset.

4.1. Comparison with Regional and International Data

Our positivity rate and etiological distribution are broadly comparable to those reported by Golli et al. in a pediatric cohort from Craiova, Romania, which documented substantial multidrug resistance among Enterobacterales during and after the COVID-19 pandemic [12]. Compared with Western European pediatric data, our resistance rates for oxacillin and penicillin appear elevated, consistent with the higher antimicrobial resistance reported across Eastern and Southern Europe by EARS-Net, although differences in laboratory reporting practices limit direct comparisons [11,49].

4.2. Limitations

This study has several limitations. First, it was a retrospective, single-center study, which limits the generalizability of the findings. Second, descriptive and bivariate analyses treated each blood culture record as an independent observation, although individual patients could contribute several blood cultures and the bottles of the same request were registered as separate records; this may have overstated the precision of the bivariate tests. The multivariable analysis was therefore restricted to the 2024–2026 subperiod, for which patient identifiers were available, and accounted for within-patient clustering; this correction could not be applied to the 2023 data. Request-level positivity in 2024–2026 (5.03%) was close to record-level positivity (5.37%), suggesting that counting bottles separately had only a small effect on the overall rate; however, repeated sampling of the same patients (42.5% of patients in 2024–2026 contributed more than one request) may have led to over-representation of some patients and episodes in the descriptive and bivariate analyses.

Third, data on the number of positive sets per episode, time to positivity, presence of an intravascular catheter, clinical signs of infection, inflammatory markers, antimicrobial therapy, and clinical course were not available in the laboratory database. This precluded the application of a comprehensive algorithm, such as those described by Healy et al. [30], Marchant et al. [31], and Chuang and Huang [33], to classify each CoNS isolate as a true pathogen or a contaminant. As a partial check, we assessed repeated isolation of the same organism from the same patient in the 2024–2026 subperiod: among the 44 patients with a positive culture, the same organism was isolated on more than one occasion in 3 patients, including one with *S. epidermidis* recovered twice. The remaining CoNS isolates were recovered from a single blood culture and cannot be confidently distinguished from contamination. Consequently, the reported positivity rate, etiological distribution, and resistance profile, particularly for CoNS, reflect all microbiologically positive results rather than confirmed bacteremia and may overestimate the true incidence of Gram-positive bloodstream infection. This also applies to other potential contaminants, such as viridans group streptococci, which were not addressed by the CoNS sensitivity analysis.

Fourth, the laboratory database did not record whether a central venous catheter was in place or whether blood cultures were drawn by peripheral venipuncture or through a catheter; therefore, CLABSI and catheter-related bloodstream infections could not be identified, and catheter-drawn samples, which are associated with higher contamination rates, could not be distinguished from peripheral samples. The timing analysis (Section 3.8.6) only partly mitigates this limitation. Immunosuppression and antimicrobial therapy administered before blood culture collection were also not recorded; prior antimicrobial exposure can reduce blood culture sensitivity and alter the recovered organism spectrum.

Fifth, data for 2026 were incomplete (January–July only); the small number of cultures and the absence of the August–December months, which included seasonal peaks in positivity in previous years, may have introduced substantial sampling error, and the lower positivity observed in this period requires confirmation with full-year data. Sixth, the relatively small number of positive cultures ($n = 78$) limited statistical power for subgroup analyses by species, and susceptibility data for the 2023 isolates were not available for species-stratified analysis. Seventh, glycopeptide susceptibility of staphylococci was determined only with an automated system and was not confirmed by a reference MIC method; the reported vancomycin and teicoplanin non-susceptibility may therefore include false-resistant results. Finally, clinical severity scores (e.g., Phoenix Sepsis Score, PRISM, PELOD), comorbidities, length of hospital stay, and mortality were not available, limiting the assessment of the clinical impact of positive blood cultures and precluding conclusions about the effectiveness or appropriateness of specific empirical treatment regimens.

5. Conclusions

In this retrospective cohort of pediatric blood cultures from a tertiary hospital in Galați, Romania, the overall positivity rate (5.43%) was stable during 2023–2025 and concentrated among children admitted to intensive care wards, and intensive care admission was, among the limited variables available, the only patient-level characteristic independently associated with positivity; given the missing clinical data and the inclusion of potential contaminants, this association should not be interpreted as evidence of a higher risk of true bloodstream infection. CoNS and ESBL-producing *K. pneumoniae* were the leading Gram-positive and Gram-negative organisms, respectively, while vancomycin, linezolid, and meropenem retained near-complete in vitro activity, although glycopeptide results were not confirmed by a reference method. Because CoNS could not be distinguished from contaminants and clinical severity and outcome data were not available, these findings should be regarded as descriptive laboratory surveillance data: they may inform the periodic review of local, stewardship-based empirical protocols but do not by themselves support specific treatment recommendations. They also underline the need for standardized criteria for adjudicating CoNS bacteremia, and continued prospective, multi-center surveillance of pediatric bloodstream infections in Romania.

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Informed Consent Statement: Patient consent was waived due to the retrospective design and the use of anonymized data.

Data Availability Statement: The data presented in this study are available on reasonable request from the corresponding authors. The data are not publicly available due to privacy restrictions.

Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

The following abbreviations are used in this manuscript:

AMR	Antimicrobial resistance
aOR	Adjusted odds ratio
AST	Antimicrobial susceptibility testing
CI	Confidence interval
CLABSI	Central line-associated bloodstream infection
CLSI	Clinical and Laboratory Standards Institute
CoNS	Coagulase-negative staphylococci
ESBL	Extended-spectrum beta-lactamase
GEE	Generalized estimating equation
ICU	Intensive care unit
IQR	Interquartile range
MIC	Minimum inhibitory concentration
MRSA	Methicillin-resistant *Staphylococcus aureus*
MSSA	Methicillin-susceptible *Staphylococcus aureus*
NHSN	National Healthcare Safety Network

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