Research Square

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Epidemiological profile and antimicrobial resistance patterns of culture- confirmed early-onset neonatal sepsis in Kazakhstan: a three-year retrospective study

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Abstract

Background

Early-onset neonatal sepsis (ENS) remains an important cause of neonatal morbidity, and antimicrobial resistance complicates its management. This study aimed to characterize the bacterial etiology and antimicrobial resistance patterns of culture-confirmed ENS in a specialized perinatal center in Kazakhstan.

Methods

This retrospective observational study included 76 neonates with culture-confirmed ENS, selected from 162 neonates evaluated for suspected sepsis at the Center for Perinatology and Pediatric Cardiac Surgery in Almaty, Kazakhstan, between 2016 and 2018. Bacterial identification and antimicrobial susceptibility testing were performed using the VITEK 2 system. Pathogen distribution and resistance patterns were summarized using descriptive statistics, and differences in multidrug resistance (MDR) between bacterial species were assessed using Pearson's chi-square test.

Results

The predominant pathogens were *Staphylococcus aureus* (28/76, 36.8%), *Escherichia coli* (22/76, 28.9%), and *Klebsiella pneumoniae* (18/76, 23.7%). MDR was identified in 28.6%, 50.0%, and 61.1% of isolates, respectively, without a statistically significant difference between species ($p = 0.076$). Imipenem resistance was reported in 35.7% of *S. aureus*, 22.7% of *E. coli*, and 50.0% of *K. pneumoniae* isolates. Descriptive annual data indicated increasing macrolide resistance among *S. aureus* and β-lactam resistance among *E. coli* and *K. pneumoniae* during the study period. The reported overall blood culture contamination rate was 12.5%.

Conclusions

S. aureus, *E. coli*, and *K. pneumoniae* were the predominant pathogens in culture-confirmed ENS. Antimicrobial resistance was observed among all three species, highlighting the importance of local microbiological surveillance, diagnostic quality assurance, infection prevention, and antimicrobial stewardship. Further multicenter studies are needed to assess neonatal sepsis and antimicrobial resistance in Kazakhstan.

Background

Sepsis remains a major global public health challenge and is associated with substantial morbidity and mortality worldwide [1, 2]. Its considerable burden has led to increasing international attention to early

recognition, effective treatment, and the development of coordinated prevention strategies [3, 4]. Neonatal sepsis is a particularly important clinical problem because of the vulnerability of newborns to severe infections and the difficulties associated with their timely diagnosis and management [5–7].

Early-onset neonatal sepsis (ENS), generally defined as sepsis occurring within the first 72 hours of life, presents significant diagnostic and therapeutic challenges. Its clinical manifestations are frequently nonspecific and may overlap with those of noninfectious neonatal conditions, complicating early recognition and treatment decisions [5, 8, 9]. The distribution of causative microorganisms varies across geographical regions, patient populations, and healthcare settings. Gram-positive and Gram-negative bacteria, including *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella pneumoniae*, contribute to neonatal infections, although their relative frequencies may differ between institutions [6, 8, 10].

Antimicrobial resistance (AMR) represents an additional challenge in neonatal sepsis management. The emergence and spread of multidrug-resistant (MDR) pathogens can limit therapeutic options and complicate the selection of appropriate empirical antimicrobial regimens [11, 12]. MDR Gram-negative bacteria, particularly *K. pneumoniae* and *E. coli*, are of particular concern in neonatal healthcare settings because of their resistance mechanisms and potential implications for treatment [12]. Resistance among Gram-positive pathogens is also clinically relevant [13]. In *S. aureus*, macrolide resistance can involve resistance genes carried on mobile genetic elements [14].

Accurate microbiological diagnosis is essential for identifying causative pathogens and guiding antimicrobial therapy. Blood culture remains a key diagnostic method, although its sensitivity and clinical interpretation may be affected by specimen volume, previous antimicrobial exposure, sampling procedures, and contamination [5, 9, 10]. Clinical assessment and diagnostic scoring approaches may complement microbiological investigations, particularly when laboratory findings are inconclusive [15]. Improving diagnostic accuracy is important for reducing unnecessary antimicrobial exposure while ensuring timely treatment of neonates with suspected infection [8, 9].

Infection prevention and antimicrobial stewardship are essential components of neonatal care. Healthcare-associated infections contribute to the burden of sepsis, emphasizing the importance of effective infection prevention measures and appropriate clinical practices [16, 17]. Rational antimicrobial prescribing, regular evaluation of local susceptibility patterns, and coordinated stewardship programs can help optimize antibiotic use and address the spread of resistant microorganisms in neonatal intensive care settings [11, 18].

Although substantial international evidence is available on neonatal sepsis, diagnostic approaches, and antimicrobial resistance, local microbiological surveillance remains important because pathogen distribution and susceptibility patterns may vary between healthcare institutions. Institution-specific data can support the selection of empirical antimicrobial regimens, inform infection prevention strategies, and identify priorities for improving diagnostic and antimicrobial stewardship practices.

Therefore, this study aimed to characterize the epidemiological profile of culture-confirmed early-onset neonatal sepsis, describe the distribution of bacterial pathogens, and assess antimicrobial resistance patterns over a three-year period (2016–2018) in a specialized perinatal center in Almaty, Kazakhstan.

Methods

Study design and setting

This retrospective, single-center observational study was conducted at the State Public Health Institution “Center for Perinatology and Pediatric Cardiac Surgery” in Almaty, Kazakhstan.

Clinical medical records and microbiological laboratory data collected between 1 January 2016 and 31 December 2018 were retrospectively reviewed. The source population consisted of neonates evaluated for suspected early-onset neonatal sepsis (ENS) during the study period. All available records were screened according to the predefined eligibility criteria. No a priori sample size calculation was performed because the study included all eligible cases identified during the observation period.

Of the 162 neonatal medical records initially identified, 76 cases of culture-confirmed ENS were included in the final analysis.

The study was designed to characterize the distribution of bacterial pathogens, their antimicrobial resistance profiles, and the available descriptive changes in resistance during the observation period. Reporting was guided by the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) recommendations.

Study population and participant selection

The source population comprised neonates who underwent clinical evaluation for suspected ENS during the first 72 hours of life.

The analytical cohort was restricted to neonates with culture-confirmed ENS, defined as clinical findings compatible with neonatal infection together with the isolation of a clinically relevant bacterial pathogen from blood culture.

Definition of early-onset neonatal sepsis

Early-onset neonatal sepsis was defined as neonatal sepsis with clinical onset within the first 72 hours of life.

Clinical suspicion of ENS was established by the attending physicians based on documented clinical manifestations and available laboratory findings. Relevant manifestations included temperature

instability, poor feeding, respiratory distress, lethargy, irritability, and other signs compatible with systemic infection.

Clinical suspicion was distinguished from microbiological confirmation. For the present analysis, only culture-confirmed cases were included because the study focused on bacterial identification and antimicrobial resistance.

Inclusion and exclusion criteria

Neonates were eligible for inclusion if they met the following criteria:

1. 1. Age of 72 hours or less at the time of evaluation.
2. 2. Clinical and laboratory findings compatible with ENS.
3. 3. Blood culture obtained as part of the diagnostic evaluation.
4. 4. Isolation of a clinically relevant bacterial pathogen.
5. 5. Availability of interpretable microbiological data and antimicrobial susceptibility results.

The exclusion criteria were:

1. 1. Systemic antimicrobial therapy administered before blood culture collection.
2. 2. Unavailable or uninterpretable blood culture results.
3. 3. Isolation of a microorganism classified as a contaminant.
4. 4. Major congenital anomalies.
5. 5. Severe noninfectious conditions that could substantially interfere with the clinical assessment of sepsis.
6. 6. Missing essential clinical or microbiological information required for the analysis.

Clinical and microbiological data collection

Clinical and microbiological information was retrospectively extracted from hospital medical records and laboratory documentation.

The collected variables included neonatal age at evaluation, clinical diagnosis, relevant clinical manifestations, blood culture results, bacterial species, antimicrobial susceptibility results, antimicrobial resistance profiles, multidrug-resistant phenotype where applicable, and year of diagnosis.

Microbiological laboratory records were used as the primary source of bacterial identification and antimicrobial susceptibility data.

Blood culture collection and microbiological procedures

Blood specimens were collected by trained healthcare personnel using aseptic techniques and the institutional procedures applicable during the study period.

A minimum of 1 mL of venous blood was inoculated into pediatric blood culture bottles. Blood culture specimens were processed under routine laboratory conditions.

Microbial identification and antimicrobial susceptibility testing were performed using the VITEK 2 automated system (bioMérieux, France). Bacterial species identified from positive blood cultures were recorded for subsequent analysis.

Only isolates considered clinically relevant on the basis of the available microbiological and clinical documentation were included in the analytical cohort.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed using the VITEK 2 automated system as part of routine microbiological diagnostics.

The antimicrobial agents tested were those included in the laboratory susceptibility panels applicable to the identified bacterial species during the study period.

The available laboratory results were used to describe antimicrobial resistance separately for each bacterial species and antimicrobial agent. Resistance proportions were reported according to the susceptibility classifications recorded in the microbiological documentation.

Definition of multidrug resistance

Multidrug resistance (MDR) was defined as acquired nonsusceptibility to at least one antimicrobial agent in three or more antimicrobial categories.

The proportion of isolates classified as MDR was summarized separately for each bacterial species using the available microbiological results.

Study outcomes

The primary outcomes were the distribution of bacterial pathogens isolated from blood cultures and the antimicrobial resistance profiles of the predominant bacterial species.

Secondary outcomes included the occurrence of multidrug-resistant phenotypes and descriptive changes in antimicrobial resistance during the study period.

Statistical analysis

Statistical analyses were performed using R statistical software. Categorical variables were summarized as absolute frequencies and percentages. The distribution of bacterial pathogens was calculated using the total number of culture-confirmed cases as the denominator. Exact binomial 95% confidence intervals (CIs) were calculated for pathogen proportions.

Antimicrobial resistance and multidrug resistance (MDR) were summarized as proportions for each bacterial species. Differences in MDR proportions among the predominant bacterial species were assessed using Pearson's chi-square test. Fisher's exact test was used for pairwise comparisons where appropriate.

Annual antimicrobial resistance rates were presented descriptively to characterize changes during the observation period. No inferential analysis of temporal trends was performed.

All statistical tests were two-sided, and a p-value < 0.05 was considered statistically significant.

Handling of missing data

The completeness of the available clinical and microbiological records was assessed before analysis. Records with missing information that prevented confirmation of eligibility or interpretation of microbiological findings were excluded.

No statistical imputation was performed for missing microbiological or antimicrobial susceptibility data.

Quality control and potential sources of bias

Predefined eligibility criteria were applied to the available medical records. Clinical information was obtained from hospital documentation, whereas bacterial identification and antimicrobial susceptibility results were obtained from microbiological laboratory records.

Potential sources of bias included the retrospective study design, incomplete documentation, selection of neonates who underwent blood culture testing, and the single-center setting.

The relatively small number of isolates limited the precision of resistance estimates and the statistical power of comparisons between bacterial species.

Ethical considerations

The study protocol was reviewed and approved by the Institutional Review Board of the State Public Health Institution "Center for Perinatology and Pediatric Cardiac Surgery" (02–04/2016).

Written informed consent was obtained from parents or legal guardians for clinical evaluation and blood sampling. The use of routinely collected clinical and microbiological data for research was conducted in accordance with the applicable institutional consent procedures.

All study procedures were conducted in accordance with the Declaration of Helsinki.

Manuscript preparation

ChatGPT (OpenAI) assisted with language editing, manuscript formatting, bibliographic checks, and preparation of tables and figures from the reported aggregate data.

Results

Study population and distribution of bacterial pathogens

A total of 162 neonates evaluated for suspected early-onset neonatal sepsis during the study period were initially identified. Following application of the predefined eligibility and exclusion criteria, 86 neonates were excluded, and 76 neonates with culture-confirmed ENS were included in the final analysis.

The distribution of bacterial pathogens isolated from blood cultures is presented in Table 1. *Staphylococcus aureus* was the most frequently identified pathogen, accounting for 36.8% (28/76) of isolates, followed by *Escherichia coli* (28.9%, 22/76) and *Klebsiella pneumoniae* (23.7%, 18/76). Other bacterial species, including *Enterobacter* spp. and *Pseudomonas aeruginosa*, collectively accounted for 10.5% (8/76) of isolates.

Overall, the three predominant pathogens—*S. aureus*, *E. coli*, and *K. pneumoniae*—accounted for 89.5% (68/76) of bacterial isolates identified among culture-confirmed ENS cases.

Table 1
Distribution of bacterial pathogens in culture-confirmed early-onset neonatal sepsis

Bacterial pathogen	n	Proportion (%)	95% CI (%)
Staphylococcus aureus	28	36.8	26.1–48.7
Escherichia coli	22	28.9	19.1–40.5
Klebsiella pneumoniae	18	23.7	14.7–34.8
Other bacterial species	8	10.5	4.7–19.7
Total	76	100.0	—

CI, confidence interval. Proportions use 76 culture-confirmed cases as the denominator. Confidence intervals are exact binomial intervals. Other species included *Enterobacter* spp. and *Pseudomonas aeruginosa*. Percentages may not sum to 100.0 because of rounding.

Antimicrobial susceptibility and resistance patterns

The reported antimicrobial resistance profiles of the predominant bacterial pathogens are summarized in Table 2 and displayed in Fig. 1.

Among *S. aureus* isolates, the reported resistance rates were 78.6% for ampicillin, 67.9% for erythromycin, 57.1% for moxifloxacin, 42.9% for cefepime, and 35.7% for imipenem.

Among *E. coli* isolates, the highest reported resistance rate was observed for ampicillin (90.9%), followed by cefepime (54.5%), moxifloxacin (40.9%), imipenem (22.7%), and erythromycin (18.2%).

K. pneumoniae isolates demonstrated reported resistance rates of 94.4% for ampicillin, 50.0% for imipenem, 44.4% for cefepime, 38.9% for moxifloxacin, and 11.1% for erythromycin.

The reported antimicrobial resistance profiles varied across the three predominant bacterial species.

Table 2
Reported antimicrobial resistance and multidrug resistance among the predominant bacterial pathogens

Antimicrobial agent or phenotype	***S. aureus*** **(n = 28)**	***E. coli*** **(n = 22)**	***K. pneumoniae*** **(n = 18)**
Ampicillin	78.6	90.9	94.4
Erythromycin	67.9	18.2	11.1
Moxifloxacin	57.1	40.9	38.9
Cefepime	42.9	54.5	44.4
Imipenem	35.7	22.7	50.0
MDR, n/N (%)	8/28 (28.6)	11/22 (50.0)	11/18 (61.1)

Antimicrobial resistance values are reported percentages. Column n values denote the total number of isolates of each species, not verified antimicrobial-specific testing denominators. MDR, multidrug resistance; n/N, number of MDR isolates divided by the total number of isolates of that species. Percentages reproduce the recorded classifications; breakpoint criteria are not specified.

The plot displays the percentages summarized in Table 2. These values reflect the recorded laboratory classifications. Antimicrobial-specific testing denominators and breakpoint criteria are not specified; comparisons across species and agents require caution.

Temporal changes in antimicrobial resistance

Antimicrobial resistance patterns were assessed descriptively over the three-year observation period (Fig. 2). Macrolide resistance among *S. aureus* isolates increased from 0% in 2016 to 43.2% in 2017 and 82.7% in 2018. β-lactam resistance among *K. pneumoniae* isolates increased from 11% to 16% and 19%, respectively. A similar increase was observed among *E. coli* isolates, with resistance rates of 7% in 2016, 18% in 2017, and 26% in 2018.

A, macrolide resistance among *S. aureus*. B, β-lactam resistance among *K. pneumoniae* and *E. coli*. Annual isolate counts and testing denominators were unavailable in the aggregate data. The two panels represent different antimicrobial classes. Connecting lines show the reported sequence only; no inferential test of temporal trends was performed.

Multidrug resistance according to bacterial pathogen

The frequency of multidrug resistance (MDR) varied among the three predominant bacterial pathogens (Table 2). MDR was identified in 28.6% (8/28) of *S. aureus* isolates, 50.0% (11/22) of *E. coli* isolates, and 61.1% (11/18) of *K. pneumoniae* isolates.

Although the highest proportion of MDR was observed among *K. pneumoniae* isolates, the overall difference between the three bacterial species did not reach statistical significance (Pearson's χ^2 test, $p = 0.076$).

In an exploratory comparison, *K. pneumoniae* isolates had higher observed odds of MDR than *S. aureus* and *E. coli* isolates combined (crude odds ratio [OR] = 2.56). However, this difference was not statistically significant (Fisher's exact test, $p = 0.105$).

Blood culture contamination

Blood culture contamination was assessed separately from clinically relevant bacterial isolates.

The reported overall blood culture contamination rate was 12.5% during the study period. Annual contamination rates were 9.8% in 2016, 15.2% in 2017, and 11.4% in 2018.

The highest reported contamination rate was observed in 2017, followed by a decrease in 2018.

Discussion

This study provides facility-level evidence on the distribution of bacterial pathogens and antimicrobial resistance patterns among neonates with culture-confirmed early-onset neonatal sepsis (ENS) in a specialized perinatal center in Kazakhstan. *Staphylococcus aureus* (36.8%), *Escherichia coli* (28.9%), and *Klebsiella pneumoniae* (23.7%) were the predominant pathogens, collectively accounting for 89.5% of the identified bacterial isolates. These findings indicate that both Gram-positive and Gram-negative organisms contribute substantially to the microbiological burden of ENS in this setting. Previous studies have documented considerable variation in the distribution of neonatal sepsis pathogens across geographical regions and healthcare settings, emphasizing the importance of local microbiological surveillance [5–8].

The observed antimicrobial resistance patterns are relevant to the selection of empirical antimicrobial therapy and the organization of neonatal infection management. Resistance to several antimicrobial agents was reported among the predominant pathogens, including resistance to ampicillin among *E. coli* and to cefepime and imipenem among the Gram-negative isolates. These findings are consistent with

broader concerns regarding antimicrobial resistance in neonatal intensive care units, particularly among Gram-negative organisms [11, 12]. However, the present study did not include molecular characterization or specific phenotypic confirmation of extended-spectrum β-lactamase (ESBL) production or carbapenemase activity. Consequently, the observed susceptibility profiles cannot be used to establish the prevalence of particular resistance mechanisms.

Multidrug resistance was identified in 28.6% of *S. aureus*, 50.0% of *E. coli*, and 61.1% of *K. pneumoniae* isolates. Although the highest observed MDR proportion was found among *K. pneumoniae*, the overall difference between the three predominant pathogens did not reach statistical significance (Pearson's χ^2 test, $p = 0.076$). In an exploratory comparison, *K. pneumoniae* had higher observed odds of MDR than *S. aureus* and *E. coli* combined (crude OR = 2.56), but this difference was also not statistically significant (Fisher's exact test, $p = 0.105$). These findings should therefore be interpreted as descriptive differences within the study cohort rather than evidence of an established association between bacterial species and MDR. Nevertheless, the observed MDR proportions highlight the importance of pathogen-specific resistance surveillance, particularly in neonatal settings where treatment options may be limited [11, 12].

The three-year observation period also revealed changes in antimicrobial resistance patterns. The reported macrolide resistance rate among *S. aureus* isolates increased from 0% in 2016 to 43.2% in 2017 and 82.7% in 2018. An increase in β-lactam resistance was also reported among *K. pneumoniae* (11%, 16%, and 19%, respectively) and *E. coli* (7%, 18%, and 26%, respectively). These changes were assessed descriptively, and no conclusions regarding their statistical significance can be drawn from the available annual data. The relatively small number of isolates and the absence of year-specific testing denominators further limit the interpretation of these trends.

Mobile genetic elements carrying macrolide resistance genes have been described in methicillin-resistant *S. aureus* [14]. However, these mechanisms were not investigated in the present study. The observed temporal changes therefore cannot be attributed to specific genetic mechanisms, antimicrobial prescribing practices, or selection pressure. Similarly, the reported changes in β-lactam resistance among the Gram-negative pathogens should be interpreted as descriptive observations rather than evidence of a particular mechanism of resistance.

Blood culture contamination represents another important finding from the perspective of diagnostic quality. The reported overall contamination rate was 12.5%, with annual rates of 9.8% in 2016, 15.2% in 2017, and 11.4% in 2018. Contamination may complicate the interpretation of microbiological results, particularly in neonates whose clinical manifestations of infection are often nonspecific. Previous research has emphasized the importance of reliable microbiological diagnosis in neonatal sepsis management [9, 10, 15]. However, the present study did not assess whether contaminated cultures resulted in additional antimicrobial treatment, prolonged hospitalization, or other adverse clinical consequences. Such outcomes should therefore be regarded as potential implications rather than demonstrated effects of contamination in this cohort.

The contamination findings highlight the importance of standardized blood culture collection procedures, consistent aseptic technique, staff training, and routine monitoring of microbiological quality. Infection prevention and control practices are particularly important in neonatal intensive care units because of the vulnerability of hospitalized neonates and the potential for healthcare-associated transmission of resistant microorganisms [16, 17].

Improving specimen collection and laboratory quality may also support more reliable antimicrobial treatment decisions.

From a public health perspective, antimicrobial resistance surveillance and diagnostic quality should be considered complementary components of neonatal infection management. Reliable microbiological results are necessary for interpreting local resistance patterns, selecting appropriate antimicrobial therapy, and supporting antimicrobial stewardship. Previous studies have emphasized the importance of rational antibiotic use and coordinated antimicrobial stewardship interventions in neonatal intensive care settings [11, 18]. The findings of the present study support the value of integrating routine pathogen-specific resistance monitoring with diagnostic quality assurance and infection prevention activities.

The results also demonstrate the potential value of institution-level surveillance in Kazakhstan. Although findings from a single specialized perinatal center cannot be considered nationally representative, they provide a baseline for monitoring local microbiological patterns and identifying areas that require further investigation. Periodic assessment of pathogen distribution, antimicrobial susceptibility, and blood culture contamination may help inform institutional protocols when interpreted alongside clinical guidelines and laboratory data. Future surveillance would benefit from standardized testing methods, clearly defined denominators, and the integration of microbiological findings with maternal and neonatal clinical characteristics.

Overall, this study highlights the importance of combining microbiological surveillance, diagnostic stewardship, antimicrobial stewardship, and infection prevention and control in neonatal care. The findings provide preliminary institution-level evidence and support the need for larger multicenter studies to characterize neonatal sepsis pathogens and antimicrobial resistance across different healthcare settings in Kazakhstan.

Strengths and limitations

The principal strength of this study is its focus on culture-confirmed ENS, allowing the analysis of pathogen distribution and antimicrobial resistance using microbiological findings rather than clinical suspicion alone. The simultaneous assessment of bacterial species, antimicrobial susceptibility, MDR, and blood culture contamination provides complementary information relevant to neonatal infection surveillance. The three-year observation period also allowed descriptive assessment of changes in resistance patterns within the study institution.

Several limitations should be considered when interpreting the findings. First, the relatively small sample size (n = 76) and the limited number of isolates within individual pathogen groups reduced the statistical power of comparisons and increased uncertainty in resistance estimates. In particular, the observed differences in MDR proportions did not reach statistical significance, and the exploratory odds ratio should be interpreted cautiously.

Second, the single-center retrospective design limits the generalizability of the findings. The study was conducted in a specialized perinatal facility, and its patient population, referral patterns, laboratory practices, and antimicrobial prescribing policies may differ from those of other hospitals in Kazakhstan. Consequently, the observed pathogen distribution and resistance rates should not be interpreted as national estimates.

Third, retrospective data collection depended on the completeness and accuracy of existing clinical and laboratory records. Selection bias cannot be excluded because the study included neonates who underwent clinical evaluation and blood culture testing rather than all neonates treated at the institution. The findings therefore describe the microbiological profile of culture-confirmed cases and do not provide an estimate of ENS prevalence among all neonates.

Fourth, the available aggregated data did not include the number of isolates tested against each antimicrobial agent in each study year. This limits the ability to independently verify annual resistance percentages and perform reliable inferential analyses of temporal changes. Potential variation in antimicrobial susceptibility testing panels, interpretive criteria, or laboratory procedures during the observation period may also have influenced the comparability of results.

Fifth, the study relied on routine phenotypic antimicrobial susceptibility testing without molecular characterization of resistance determinants. Therefore, specific resistance mechanisms, including ESBL production, carbapenemase activity, and macrolide resistance genes, could not be established.

Sixth, antimicrobial exposure and several potentially relevant maternal and neonatal characteristics were not systematically assessed. These included gestational age, birth weight, maternal infection status, delivery characteristics, invasive device exposure, antimicrobial treatment, and clinical outcomes. Consequently, the study could not determine the contribution of these factors to pathogen distribution, resistance patterns, or clinical prognosis.

Finally, although blood culture contamination was assessed, the available data did not permit an investigation of its underlying causes or its consequences for treatment decisions and clinical outcomes. The observational design also precludes causal interpretation of the reported temporal changes in antimicrobial resistance.

Despite these limitations, the study provides institution-level baseline data on the microbiological profile and antimicrobial resistance patterns of culture-confirmed ENS in Kazakhstan. Larger prospective

multicenter studies incorporating standardized microbiological methods, detailed antimicrobial exposure data, and clinically relevant outcomes are needed to validate and extend these findings.

Conclusions

This study identified *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella pneumoniae* as the predominant pathogens in culture-confirmed early-onset neonatal sepsis in a specialized perinatal center in Kazakhstan. Antimicrobial resistance was observed among all three pathogens, with the highest proportion of multidrug resistance recorded in *K. pneumoniae*, although differences between bacterial species were not statistically significant. Descriptive changes in antimicrobial resistance were also observed during 2016–2018. The findings highlight the importance of local microbiological surveillance, reliable laboratory diagnosis, infection prevention and control, and antimicrobial stewardship in neonatal care. These institution-level data provide a baseline for continued surveillance and future multicenter studies in Kazakhstan.

Abbreviations

AMR
antimicrobial resistance
CI
confidence interval
ENS
early-onset neonatal sepsis
ESBL
extended-spectrum β-lactamase
MDR
multidrug resistance
OR
odds ratio
STROBE
Strengthening the Reporting of Observational Studies in Epidemiology.

Declarations

Ethics approval and consent to participate

The study was approved by the Institutional Review Board of the State Public Health Institution “Center for Perinatology and Pediatric Cardiac Surgery” (approval No. 02–04/2016). All procedures were conducted in accordance with the Declaration of Helsinki.

Written informed consent was obtained from parents or legal guardians for clinical evaluation and blood sampling. The use of routinely collected clinical and microbiological data for research was conducted in

accordance with the applicable institutional consent procedures.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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Author Contribution

Mairash Baimuratova: Conceptualization, methodology, validation, and formal analysis.Marzhan Kassenova: Conceptualization, methodology, software, resources, writing—original draft, and writing—review and editing.Bayan Imasheva: Investigation and editing.Mariya Laktionova: Writing—review and editing.Zaure Tobylbayeva: Visualization and project administration.All authors read and approved the final manuscript

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Availability of data and materials

The datasets supporting the findings of this study are available from the corresponding author upon reasonable request.

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Figures

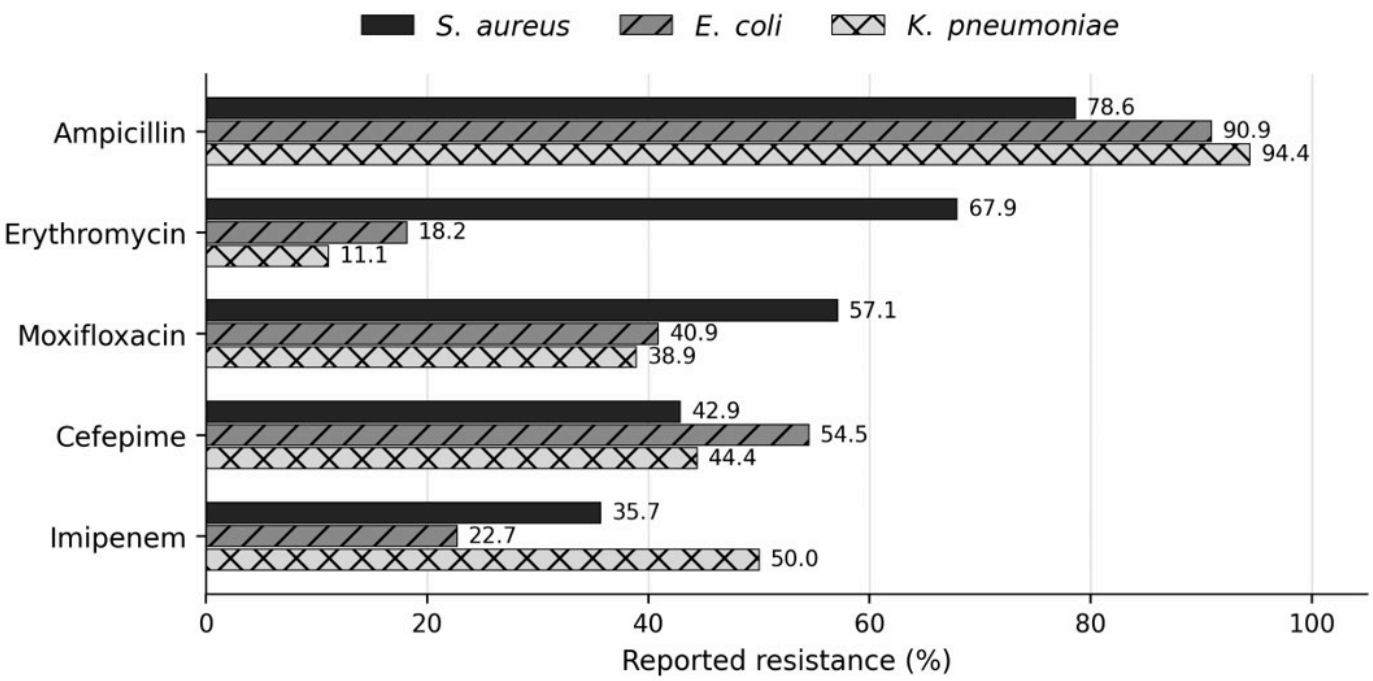


Figure 1

Reported resistance percentages by bacterial species and antimicrobial agent

The plot displays the percentages summarized in Table 2. These values reflect the recorded laboratory classifications. Antimicrobial-specific testing denominators and breakpoint criteria are not specified; comparisons across species and agents require caution.

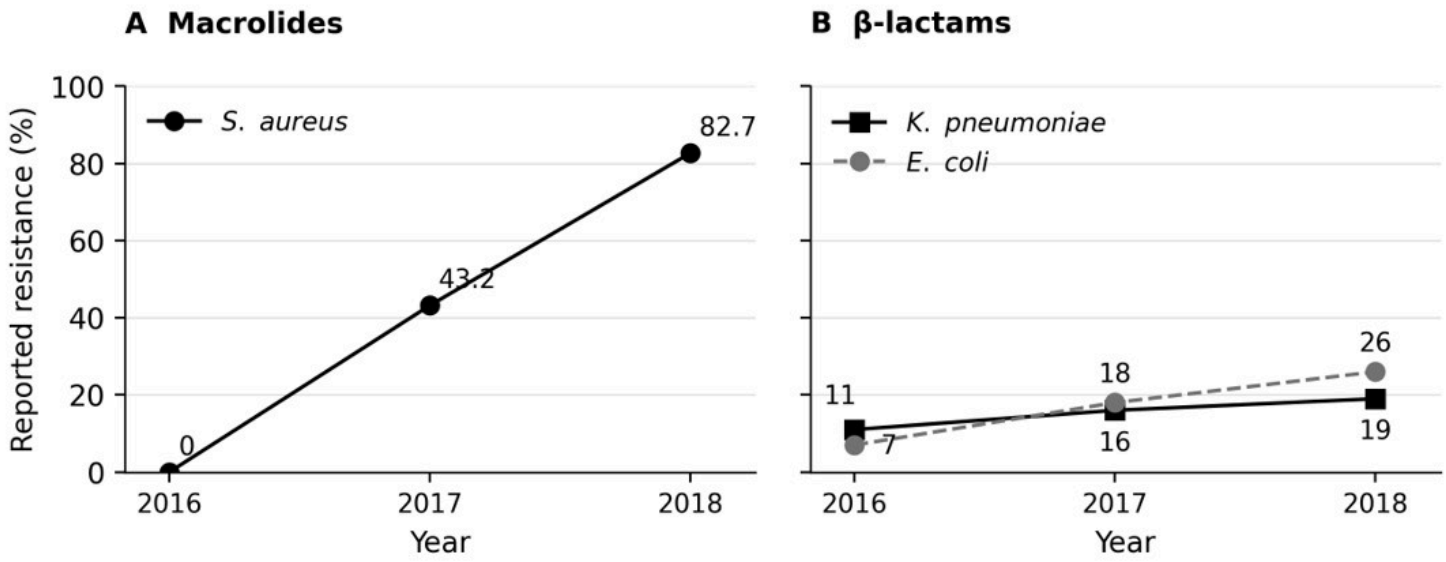


Figure 2

Reported annual antimicrobial resistance percentages during 2016–2018

A, macrolide resistance among *S. aureus*. B, β-lactam resistance among *K. pneumoniae* and *E. coli*. Annual isolate counts and testing denominators were unavailable in the aggregate data. The two panels represent different antimicrobial classes. Connecting lines show the reported sequence only; no inferential test of temporal trends was performed.