

Antimicrobial resistance in bloodstream infections in a children's hospital, Myanmar

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Abstract

Background

Antimicrobial resistance (AMR) is a threat to human health. Children represent one of the most vulnerable populations affected by AMR. Sepsis causes substantial mortality in children worldwide. The incidence and mortality rates of sepsis in neonates are particularly high. This study aimed to determine the drug susceptibility of bacterial isolates causing bloodstream infections in children in Myanmar.

Methods

From August 2023 to July 2025, 4,263 blood samples were collected from children (aged birth–13 yrs old; median age: 228 days) at Yangon Children's Hospital. Among 765 culture-positive samples, 160 isolates of *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, and *Salmonella* spp. were identified using biochemical methods and matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS). Drug susceptibility was tested according to the Global Antimicrobial Resistance and Use Surveillance System (GLASS) protocols using the disk diffusion and broth microdilution methods. Gram-negative isolates were further tested for NDM metallo- β -lactamase (MBL) production using an immunochromatographic test (ICT).

Results

Of the 160 isolates, *K. pneumoniae* was the most prevalent (53.1%), followed by *S. aureus* (16.3%), *Salmonella* Typhi/Paratyphi A (15.6%), *E. coli* (8.1%), and *A. baumannii* (6.9%). Overall, 82.5% were resistant to at least one antibiotic included in the GLASS protocols: 96.5% of *K. pneumoniae* isolates, 96.0% of *S. Typhi/Paratyphi A*, 92.3% of *E. coli*, 45.5% of *A. baumannii*, and 38.5% of *S. aureus* were drug-resistant. Meropenem resistance was found in 72.9% of *K. pneumoniae* and 38.5% of *E. coli* isolates. The ICT kit revealed that 48.5% of 143 Gram-negative isolates and 92% of 71 meropenem-resistant Gram-negative isolates produced NDM-MBL.

Conclusions

This study highlights a high prevalence of antimicrobial resistance and NDM-MBL production among Gram-negative pathogens causing bloodstream infections in children in Myanmar, and demonstrates that rapid diagnostic tools such as ICT kits could be valuable for guiding treatment decisions and infection control.

Background

Antimicrobial resistance (AMR) is a major threat to human health worldwide [1]. Children, particularly neonates, represent one of the most vulnerable populations affected by AMR [2]. Among children younger than 5-yrs old, 193,000 deaths were caused by AMR and 840,000 deaths were associated with AMR in 2021 globally [2]. Sepsis causes substantial mortality in children worldwide [3]: an estimated 20.3 million cases of sepsis occurred in children younger than 5-yrs old, leading to 2.9 million deaths [4]. The incidence and mortality rates of sepsis in neonates are particularly high in low- and middle-income countries [3], which accounted for 78.9% of the world's total reported neonatal sepsis cases and 93.9% of global neonatal sepsis-related deaths in 2019 [5]. A review article published in 2019 [6] revealed that the majority of pathogens causing neonatal sepsis were antimicrobial-resistant in South Asia. Gram-negative bacteria of these pathogens were highly resistant to first line drugs recommended by the World Health Organization (WHO), including ampicillin, gentamicin, and third generation cephalosporins such as cefotaxime; however, most were susceptible to meropenem, and half of *Staphylococcus aureus* isolates were resistant to methicillin [6]. In the Global report on the epidemiology and burden of sepsis, WHO highlighted that very little data on sepsis epidemiology are available, particularly in low- and middle-income countries where the burden seems to be higher [4]. Reliable epidemiological data are therefore essential to understanding the true burden of neonatal sepsis.

We describe here the drug susceptibility profiles of five pathogens, *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*, *S. aureus*, and *Salmonella* species, isolated from blood samples from children suspected of bacteremia at a children's hospital in Myanmar. WHO launched the Global Antimicrobial Resistance and Use Surveillance System (GLASS) in 2015 to strengthen AMR surveillance in each country and region [1]. In August 2023, AMR laboratory-based surveillance was initiated in Myanmar, involving ten clinical microbiology laboratories across nine hospitals and a public health laboratory, including Yangon children's hospital and the National Health Laboratory, Yangon. The surveillance has been conducted in accordance with GLASS protocols and WHO laboratory procedures. In addition, matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) was used for accurate bacterial identification. Drug susceptibility testing was performed using both the disk diffusion and broth microdilution methods. An immunochromatographic kit was also used to detect the production of NDM metallo- β -lactamase (MBL), which confers resistance to almost all β -lactams, including carbapenems, cephalosporins, and penicillins [7]. Our previous study showed that > 90% of carbapenem-resistant *Enterobacteriaceae* produced NDM-MBL in Myanmar [8].

Yangon Children's Hospital joined the AMR surveillance to characterise the drug susceptibility profiles of bloodstream infection pathogens isolated from paediatric patients in Myanmar.

Methods

Bacterial isolates

A total of 4,263 blood samples were cultured as part of routine clinical care from children suspected of bacteremia, aged from birth to 13 years, at Yangon Children's Hospital between August 2023 and July

2025. Of these, 765 (17.9%) were culture-positive. From the culture-positive samples, 160 isolates were used in this study and identified as one of the following five target species: *A. baumannii*, *E. coli*, *K. pneumoniae*, *S. aureus*, and *Salmonella* species.

Bacterial identification and drug susceptibility tests

Bacterial isolates were first identified using conventional biochemical methods, then confirmed using MALDI-TOF MS (Shimadzu Corporation, Kyoto, Japan). Serotypes of *Salmonella* isolates were determined by agglutination tests using *Salmonella* antisera (Denka Seiken, Tokyo, Japan). Drug susceptibility testing was performed using the disk diffusion and broth microdilution methods in accordance with the Clinical and Laboratory Standards Institute (CLSI) [9] and European Committee on Antimicrobial Susceptibility Testing [10] guidelines, and zone diameters and minimum inhibitory concentrations (MICs) were determined, respectively. The susceptibility of the five species to the following antibiotics was determined according to GLASS protocols [11]: amikacin, colistin, gentamicin, meropenem, and tigecycline for *A. baumannii*; ampicillin, cefepime, cefotaxime, ceftazidime, ciprofloxacin, colistin, co-trimoxazole, and meropenem for *E. coli*; cefepime, cefotaxime, ceftazidime, ciprofloxacin, colistin, co-trimoxazole, and meropenem for *K. pneumoniae*; ceftazidime, ciprofloxacin, and meropenem for *S. aureus*; and cefotaxime, ceftazidime, ciprofloxacin, and meropenem for *Salmonella* species. A drug-resistant isolate was defined by GLASS as an isolate resistant to at least one of the antibiotics listed above [11].

Detection of NDM metallo- β -lactamase

A. baumannii, *E. coli*, *K. pneumoniae*, and *Salmonella* isolates were tested for NDM-MBL production using an immunochromatographic test (ICT) kit (KBM Line Check NDM™, Kohjin Bio Co., Ltd., Tokyo, Japan) [8].

Statistics

Statistical analyses were performed using IBM SPSS Statistics ver. 20 (IBM, NY, USA). The chi-square test was used to assess associations, and a two-tailed p-value < 0.01 was considered statistically significant.

Results

Bacterial isolates

Among the 4,263 cases that underwent blood culture testing, 1,846 (43%) were female and 2,417 (57%) were male, showing a significant male predominance ($p < 0.01$). Among the 765 blood culture-positive cases, 317 (41%) were female and 448 (59%) were male, again showing a significant male predominance ($p < 0.01$). Of these, 160 isolates were obtained from 160 children aged 1 day to 13 years with bloodstream infections, belonging to one of the following five species: *A. baumannii*, *E. coli*, *K. pneumoniae*, *S. aureus*, and *Salmonella* species. As shown in Table S1, the median age was 228 days

(interquartile range [IQR]: 9.5–2,190 days). Neonates (< 28 days) accounted for 40.0% (64/160) of cases, followed by children aged 6–12 years (28.8%, 46/160). Overall, males accounted for 63.1% (101/160) of cases and were significantly more common than females ($\chi^2 = 11.03, p < 0.01$) (Table S1).

Bacterial distribution and drug-resistant profiles

There was no significant association between bacterial species and sex ($\chi^2 = 6.44, df = 5, p = 0.27$). As shown in Fig. 1, among the 160 isolates, 11 were *A. baumannii* (6.9%), 13 were *E. coli* (8.1%), 85 were *K. pneumoniae* (53.1%), 26 were *S. aureus* (16.3%), and 25 were *Salmonella* species (15.6%). Of the *Salmonella* isolates, 24 were *Salmonella enterica* serovar Typhi and one was *Salmonella enterica* serovar Paratyphi A. Of the 160 isolates, 132 (82.5%) were resistant to at least one tested antibiotic (Fig. 1). Most *K. pneumoniae* (96.5%), *S. Typhi*/Paratyphi A (96.0%), and *E. coli* (92.3%) isolates were drug-resistant. In contrast, fewer than 50% of *A. baumannii* (45.5%) and *S. aureus* (38.5%) isolates were drug-resistant; in other words, the majority of *A. baumannii* and *S. aureus* isolates were susceptible to all antibiotics tested.

MICs and antimicrobial resistance rates for blood culture isolates are shown in Table 1. Of 11 *A. baumannii* isolates, three (27.3%) were resistant to amikacin, four (36.4%) to gentamicin, and four (36.4%) to meropenem, while no isolates were resistant to colistin. These isolates showed relatively low MIC values for tigecycline, although one isolate had a relatively high MIC of 4 µg/mL. Of 13 *E. coli* isolates, 12 (92.3%) were resistant to ampicillin, 10 (76.9%) to cefepime, 12 (92.3%) to cefotaxime, 9 (69.2%) to ceftazidime, 10 (76.9%) to ciprofloxacin, 1 (7.7%) to colistin, 11 (84.6%) to co-trimoxazole, and 5 (38.5%) to meropenem. Of 85 *K. pneumoniae* isolates, 81 (95.3%) were resistant to cefepime, 82 (96.5%) to cefotaxime, 80 (94.1%) to ceftazidime, 66 (74.1%) to ciprofloxacin, 3 (3.5%) to colistin, 72 (84.7%) to co-trimoxazole, and 62 (72.9%) to meropenem. Among 26 *S. aureus* isolates, 10 (38.5%) were resistant to ceftazidime, indicating methicillin resistance. Of 25 *S. Typhi*/Paratyphi A isolates, 24 (96.0%) were resistant to ciprofloxacin, whereas no isolates were resistant to cefotaxime, ceftazidime, or meropenem. Zone diameters and antimicrobial resistance rates are shown in Table S2 and were largely consistent with the MIC-based results. All bacterial isolates tested and their drug susceptibility profiles are shown in Table S3.

Immunochromatographic test for detecting NDM-MBL production

Of the 160 isolates, 134 were Gram-negative, comprising 11 *A. baumannii*, 13 *E. coli*, 85 *K. pneumoniae*, and 25 *S. Typhi*/Paratyphi A. All 134 isolates were tested for NDM-MBL production by ICT (Table 2 and Table S3). Of these, 66 (44.2%) were positive for NDM-MBL production: 2 of 11 (18.2%) *A. baumannii*, 5 of 13 (38.5%) *E. coli*, 59 of 85 (69.4%) *K. pneumoniae*, and none of 25 (0%) *S. Typhi*/Paratyphi A. Regarding meropenem resistance, 71 of the 134 Gram-negative isolates (53.0%) were resistant to meropenem: 4 of 11 (36.4%) *A. baumannii*, 5 of 13 (38.5%) *E. coli*, 62 of 85 (72.9%) *K. pneumoniae*, and none of 25 (0%) *S. Typhi*/Paratyphi A (Table 2). All NDM-MBL-producing isolates ($n = 65$) were resistant to meropenem (data not shown). Among the 71 meropenem-resistant isolates, 65 (91.5%) were positive for

NDM-MBL production: 2 of 4 (50.0%) *A. baumannii*, 5 of 5 (100%) *E. coli*, and 58 56 of 62 (93.5 90.3%) *K. pneumoniae*.

Discussion

Carbapenem-resistant *K. pneumoniae* appears to be a major causative pathogen in children's bloodstream infections in Myanmar (Table 2). The present study identified 85 *K. pneumoniae* isolates from blood samples, of which 62 (72.9%) were resistant to meropenem. According to the GLASS report of 2025 [12], in neighbouring countries, 51.1% of *K. pneumoniae* from blood samples were resistant to imipenem in Bangladesh, 61.2% in India, and 18.5% in Thailand, although none of these data were specific to children's bloodstream infections. *K. pneumoniae* bloodstream infections in children appear to be a serious problem across Bangladesh, India, and Myanmar. Regarding neonates, 39 samples (47.6% of *K. pneumoniae* isolates) were obtained from this age group in the present study (data not shown). Comprehensive infection control programmes should be implemented in children's wards, including neonatal care units and surgical wards, in Myanmar. Further epidemiological studies focusing on bloodstream infections in children are needed in Myanmar.

The present study showed that *S. Typhi*/Paratyphi A remain critical pathogens associated with bloodstream infections in children in Myanmar (Fig. 1). Most of these isolates (96.0%) were resistant to ciprofloxacin, which is one of the primary recommended antimicrobials for the treatment of enteric fever [13], encompassing both typhoid and paratyphoid fevers, which are clinically indistinguishable [14]. *S. Typhi* resistant to fluoroquinolones and third-generation cephalosporins has emerged and spread globally [15]. In neighbouring countries, the GLASS report of 2025 [12] records ciprofloxacin resistance rates among *Salmonella* spp. from blood samples of 16.4% in Bangladesh and 4.6% in Thailand. Ciprofloxacin-resistant *S. Typhi* emerged and spread rapidly in the 1990s [16], since when third-generation cephalosporins, macrolides, and carbapenems have been increasingly used [13]. Ceftriaxone-resistant *S. Typhi* producing the extended-spectrum β -lactamase (ESBL) CTX-M-15 emerged in Pakistan in 2016 [17].

Carbapenem-resistant *S. Typhi* producing NDM-5 MBL was isolated from a seven-year-old girl in Pakistan in 2022 [18] and from an 11-year-old boy in India in 2025 [19]. Drug-resistant *S. Typhi* producing ESBL and NDM-MBL should therefore be carefully monitored in Myanmar. This study has two limitations in relation to *Salmonella*: first, all *S. Typhi*/Paratyphi A isolates were from the Yangon region and not from other regions of Myanmar, as no *Salmonella* spp. isolates from blood samples have yet been detected in Mandalay or Nay Pyi Taw through the current AMR surveillance; second, molecular genetic analysis was not conducted. Further epidemiological studies of *Salmonella* spp. are therefore necessary, extending to other regions of Myanmar, and molecular epidemiology of *S. Typhi* isolates based on whole genome sequencing will be reported in due course.

The ICT kit for detecting NDM-MBL production could be a valuable tool when Gram-negative pathogens are detected from blood samples of children at children's hospitals in Myanmar.

Tada *et al.* [8] reported that, of 350 Gram-negative isolates obtained from patients of all ages across 10 hospitals in Myanmar between 2016 and 2018, 164 (46.9%) produced NDM-MBL as detected by the ICT kit, and that more than 90% of carbapenem-resistant *Enterobacteriaceae* isolates produced NDM-MBL. These findings are consistent with the present data for children: 48.5% of Gram-negative isolates were positive for NDM-MBL production, and 91.5% of meropenem-resistant Gram-negative isolates were positive for NDM-MBL production (Table 2). Of particular note, 68.2% of *K. pneumoniae* isolates from blood samples of children produced NDM-MBL (Table 2). Further studies across diverse hospital settings are needed to standardise the timing and application of the ICT kit. Nonetheless, the current evidence supports the utility of the ICT kit for detecting NDM-MBL production, thereby guiding antibiotic selection and potentially improving clinical outcomes for children with bloodstream infections in Myanmar.

As shown in Table S1, male patients predominated in our study. A possible explanation is that male children in South Asian countries such as Myanmar may be more susceptible to infections with AMR pathogens than female children, potentially reflecting both sex-based differences in immune responses to AMR pathogens [20] and differences in healthcare-seeking behaviour between male and female children [21].

Conclusions

This study demonstrated that the majority of pathogens causing bloodstream infections in children in Myanmar were highly drug-resistant Gram-negative bacteria. NDM-MBL production was identified using the ICT kit, demonstrating the potential utility of this rapid and simple diagnostic tool in supporting treatment decisions and infection control measures. These findings may contribute to improved clinical management of bloodstream infections in children and to a better understanding of the burden of AMR in Myanmar.

Abbreviations

AMR Antimicrobial resistance

CLSI Clinical and Laboratory Standards Institute

GLASS Global Antimicrobial Resistance and Use Surveillance System

ICT Immunochromatographic test

MALDI -TOF MS matrix-assisted laser desorption ionization–time of flight mass spectrometry

MBL Metallo- β -lactamase

MIC Minimum inhibitory concentrations

Declarations

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Author contributions

TS and MK analyzed and summarized research data and drafted the manuscript, contributing equally and share first authorship. NSH and PES collected samples. ST performed bacterial identification. TTH, YU, TT, MMA supervised the study. TK and HHT designed and supervised the study.

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Ethical considerations

This study was conducted in accordance with the Declaration of Helsinki, and the protocol was approved by: Institutional Review Board (IRB), Ministry of Health, The Government of the Republic of the Union of Myanmar (Approval number IRB/2023-16, IRB number: 2023-20); the ethics committee of Juntendo University (number 809); and Biosafety Committee, Juntendo University (approval nos. BSL2/29-1). The need for individual written informed consent was waived by the IRB because this study collected clinical bacterial isolates from a microbiology laboratory from Yangon Children’s hospital, confidentially will be ensuring in data management, and the blood samples were not used in this study. Only anonymized data (age, sex, date of specimen collection, and specimen type) were collected and analyzed.

Data Availability Statement

The raw data for all bacterial isolates are provided in the Supplementary Material (Table S3).

Consent for publication

Not applicable.

Competing interests

The authors declare there are no conflicts of interest.

Consent to Participate declaration

Not applicable.

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Figures

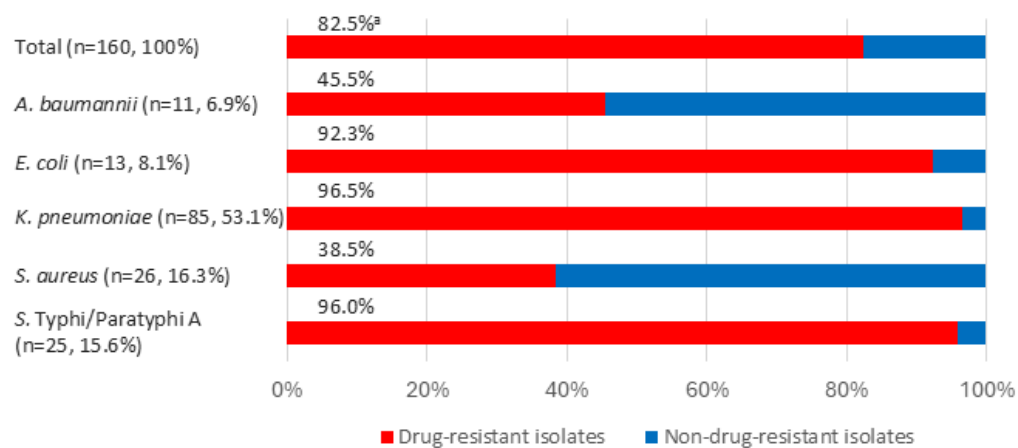


Figure 1

Percentage of drug-resistant isolates from blood samples of children

^aPercentage of drug-resistant isolates

Supplementary Files

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- [SupplementalTable1.pdf](#)
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