# MICROORGANISMS AND ANTIBIOTIC RESISTANCE IN PEDIATRIC ICU PATIENTS: A RETROSPECTIVE STUDY, MOGADISHU, SOMALIA

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**Abstract.** Antimicrobial resistance is a major public health issue, especially in developing countries. This study retrospectively assessed microorganisms and antibiotic resistance in patients from a pediatric intensive care unit (PICU) of a tertiary hospital in Mogadishu, Somalia, between January 2022 and December 2023. Cultures and antibiotic susceptibility tests were conducted on clinical samples collected. Standard bacteriological methods identified 24.5% of the samples ($n$ = 1,424) as positives, 85% from patients ≤1 year of age, with 66% being male. Cultures were predominantly from blood (73%), followed by urine (10%) and then wound (7%), with Gram-negative bacteria accounting for 58%, Gram-positive bacteria 27% and *Candida* spp 15% of the samples. The most frequent Gram-negative and -positive bacteria were *Escherichia coli* (26%) and coagulase-negative staphylococci (19%). Antibiogram profiling revealed that the Gram-negative bacteria isolates were resistant to amoxicillin/clavulanic acid (59%), ampicillin/sulbactam (60%), and trimethoprim/sulfamethoxazole (52%), while Gram-positive bacteria isolates were resistant to ciprofloxacin (69%), levofloxacin (72%) and methicillin (51%). Although the data were limited to a single hospital, the high prevalence of antibiotic resistance emphasizes the need for

maintaining an up-to-date antibiogram database for appropriate antibiotic use, especially among the very young PICU patients in Somalia and elsewhere.

**Keywords:** antibiogram, bacterium, pathogen, pediatric ICU, yeast

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## INTRODUCTION

Hospital infections remain a major issue in pediatric intensive care units (PICUs), causing significant morbidity and mortality (Avcu and Atikan, 2021). Weak immunity, presence of invasive devices and prolonged stay increase infection risks. Antibiotics have revolutionized infectious disease treatment, dramatically reducing morbidity and mortality (Ferraz, 2024). However, antibiotics misuse, use in animal growth promotion, poor sanitation, and increased travel have driven the rise and spread of antimicrobial resistance (AMR) (Moo *et al*, 2020). Common drug-resistant pathogens include methicillin-resistant *Staphylococcus aureus* (MRSA), multidrug-resistant Gram-negative bacteria and vancomycin-resistant enterococci (Edwardson and Cairns, 2019).

AMR, dubbed the "Silent Pandemic," causes preventable mortality, increases healthcare costs, hinders disease control, threatens health security, and harms the economy (Founou *et al*, 2021). AMR burden varies globally but disproportionately affects low- and middle-income countries, with Africa being the most severely impacted (Anyaegbunam *et al*, 2024). Weak health system, limited laboratory capacity and poor regulation of antibiotics use have worsened the problem in Somalia (Hassan *et al*, 2024).

Somalia reported 8,400 deaths directly attributed to AMR and 32,700 AMR-related deaths in 2019, making the country among the top 10 nations globally with the highest AMR-associated mortality (Hassan *et al*, 2024). Worldwide, drug-resistant infections caused 700,000 deaths annually, potentially rising to 10 million by 2050 without intervention (O'Neill, 2016).

Data on nosocomial infection and drug resistance in PICUs of low-income countries are limited (Rosenthal *et al*, 2012). In Somalia, such studies are scarce, hindering infection control and the development of policy on rational antibiotic use. We retrospectively assessed microorganisms isolated from PICU patients in a Somali tertiary hospital and their antibiogram profiles. The results of this study may guide the updating of empirical treatment protocols based on local resistance patterns, the implementation of antibiotic stewardship programs to combat antimicrobial resistance, and the strengthening of infection control measures.

## MATERIALS AND METHODS

### Study area and population

Data of clinical cultures from patients admitted to the PICU of a tertiary hospital, Mogadishu, Somalia, from January 2022 to December 2023, were retrieved and reviewed. This hospital serves over 2 million people and is among the largest in the country.

### Data collection

Microbial isolates ($n$ = 349) were successfully cultured from clinical samples (blood, cerebrospinal fluid (CSF), urine, wound, and other sources; $n$ = 1,434). Data on patients' age, sex and type of clinical sample were collected.

### Microbiological analysis

Microbiological analysis was carried out according to standard laboratory procedures (WHO SEARO, 2000). In brief, samples were cultured on blood, chocolate and eosin-methylene blue (EMB) agar plates (Laborlar, Istanbul, Türkiye) for 24 hours at 37 °C, and

another 24 hours if no colonies were observed during the first period. Isolates were identified by colony morphology, Gram staining and standard biochemical tests, *viz* hemolysis on blood agar, and catalase and coagulase tests for Gram-positive bacteria; and oxidase, triple sugar iron, motility, and urease tests for Gram-negative bacteria.

**Antibiogram profiling**

An antibiogram profile of isolates was performed on Mueller-Hinton agar (Laborlar, Istanbul, Türkiye) using the Kirby-Bauer's disk diffusion method (Bauer *et al*, 1966). Commercially available antibiotic disks (Bioanalyse, Ankara, Türkiye) were incubated for 24 hours at 37 °C. Zones of inhibition were measured using a caliper and results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines to classify a microorganism as sensitive or resistant to the test drug (CLSI, 2020).

**Statistical analysis**

Microorganism types and antibiogram results were reported as percentages. Group differences were tested using the $\chi 2$ method, with significance set at $p$-value <0.05. Data were analyzed using state full term of SPSS (SPSS) version 22 (IBM Corp, Armonk, NY).

**Ethical considerations**

The research protocols were approved by the Ethics Committee of Mogadishu Somali Türkiye Recep Tayyip Erdoğan Training and Research Hospital (approval no. 05.02.2024/923, MSTH/17196). Prior informed consents were not obtained from the participants due to the nature of the study (retrospective review of anonymized records).

## RESULTS

Clinical specimens ($n$ = 1,424; 638 (44.8%) in 2022 and 786 (55.2%) in 2023) were submitted to the laboratory for microbiological analysis, from which a variety of microorganisms [$n$ = 349 (24.5%)]

were successfully isolated. From 2022 to 2023, the frequency of almost all microbial species isolated increased, the exceptions being coagulase-negative staphylococci (CoNS), which decreased and *Enterococcus* spp, which remained unchanged (Fig 1). Notable rises were observed for *Candida* spp, *E. coli* and *Klebsiella* spp.

The highest isolation rate (85%) occurred in the ≤1 year of age group, with *E. coli* being the most predominant (29%), followed by CoNS (20%) and *Klebsiella* spp (17%) (Table 1). In the 2-6 years of age group, *Candida* spp (25%) were predominant, followed by *Pseudomonas* spp (22%) and *Klebsiella* spp (12%). For the 7-16 years of age group, *Candida* spp (26%) remained predominant, followed by *Staphylococcus aureus* (20%). The relationship between age group

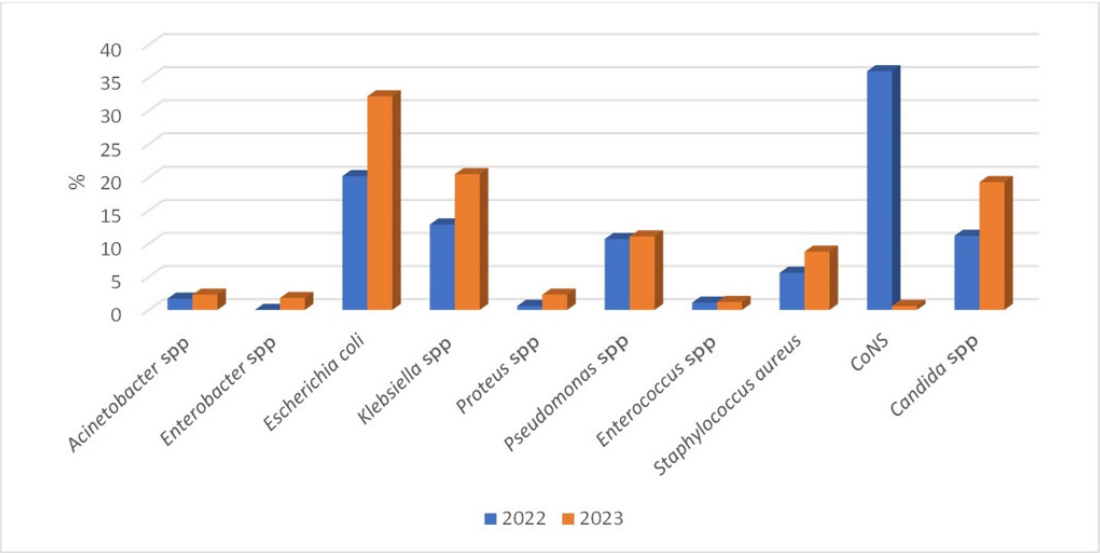


Fig 1 - Comparison of pathogens cultured from PICU patients in a tertiary hospital, Mogadishu, Somalia, between 2022 and 2023

CoNS: coagulase-negative staphylococci; PICU: pediatric intensive care unit

Table 1

Pathogens isolated from clinical samples of PICU patients in a tertiary hospital, Mogadishu, Somalia, January 2022 - December 2023

| Pathogen | Frequency according to age group, *n* (%) | | | *p*-value* | Frequency according to sex, *n* (%) | | *p*-value* |
|---|---|---|---|---|---|---|---|
| | ≤1 year (N = 298) | 2-6 years (N = 32) | 7-16 years (N = 19) | | Male (N = 229) | Female (N = 120) | |
| *Acinetobacter* spp | 5 (2) | 2 (7) | 0 (0) | 0.001 | 3 (1) | 4 (3) | 0.535 |
| *Enterobacter* spp | 3 (1) | 0 (0) | 0 (0) | | 2 (1) | 1 (1) | |
| *Escherichia coli* | 86 (29) | 2 (7) | 3 (16) | | 69 (30) | 22 (18) | |
| *Klebsiella* spp | 51 (17) | 4 (12) | 3 (16) | | 37 (16) | 21 (17) | |
| *Proteus* spp | 2 (1) | 3 (9) | 0 (0) | | 3 (1) | 2 (2) | |
| *Pseudomonas* spp | 29 (10) | 7 (22) | 2 (11) | | 22 (10) | 16 (13) | |
| *Enterococcus* spp | 4 (1) | 0 (0) | 0 (0) | | 2 (1) | 2 (2) | |
| *Staphylococcus aureus* | 18 (6) | 3 (9) | 4 (20) | | 17 (8) | 8 (7) | |
| CoNS | 60 (20) | 3 (9) | 2 (11) | | 40 (17) | 25 (21) | |
| *Candida* spp | 40 (13) | 8 (25) | 5 (26) | | 34 (15) | 19 (16) | |
| Total (N = 349) | 298 (85) | 32 (9) | 19 (6) | | 229 (66) | 120 (34) | |

*Statistically significant when *p*-value <0.05 using $\chi^2$-test for comparison of types of microorganisms among groups

CoNS: coagulase-negative staphylococci; PICU: pediatric intensive care unit

and microorganisms is significantly different ($p$-value = 0.001, $\chi$2-test). Both males and females were most frequently infected with *Candida* spp (15 and 16% respectively), CoNS (17 and 21% respectively), *E. coli* (30 and 18% respectively), and *Klebsiella* spp (16 and 17% respectively) (Table 1). Of the 349 isolates studied over the 2 years, 58% were Gram-negative bacteria, 27% Gram-positive bacteria and 15% *Candida* spp. The distribution was as follows (from highest to lowest): *E. coli* (26%), CoNS (19%), *Klebsiella* spp (17%), *Candida* spp (15%), *Pseudomonas* spp (11%), *S. aureus* (7%), *Acinetobacter* spp (2%), and *Enterobacter* spp, *Enterococcus* spp and *Proteus* spp (1% each) (Table 1).

The frequency of infectious agents isolated varied depending on their clinical source. The main source was blood (73%), followed by urine (10%) and then wound (7%) (Table 2). As expected, blood samples yielded predominantly *E. coli* (32%), followed by CoNS (22%), *Klebsiella* spp (16%), and then *Candida* spp and *Pseudomonas* spp (9% each). Of note, nearly equal numbers of *Candida* spp isolates were obtained from blood and urine ($n$ = 24 and 21 respectively), and of the *Proteus* spp isolates ($n$ = 5) with 3 isolates from wound while the remaining were from blood and urine. The differences in distributions of the infective microorganisms among the clinical sources are statistically significant ($p$-value <0.001, $\chi$2-test) (Table 2).

Of the Gram-positive bacteria isolates, the majority of CoNS isolates ($n$ = 65) were resistant to ciprofloxacin, clindamycin, erythromycin, fusidic acid, levofloxacin, and tetracycline, but sensitive to cefoxitin, daptomycin, gentamicin, linezolid, quinupristine/dalfopristin, and teicoplanin (Table 3). The majority of *S. aureus* isolates ($n$ = 25) were resistant to cefoxitin, but sensitive to ciprofloxacin, clindamycin, daptomycin, erythromycin, fusidic acid, gentamicin, levofloxacin, linezolid (all isolates), quinupristine/dalfopristin (all

Table 2

Distribution of pathogens according to source from PICU patients in a tertiary hospital, Mogadishu, Somalia, January 2022 - December 2023

| Pathogen | Frequency according to source of clinical samples, *n* (%) | | | | | | | | *p*-value* |
|---|---|---|---|---|---|---|---|---|---|
| | Blood (N = 256) | Urine (N = 34) | Wound (N = 24) | Sputum/ respiratory tract (N = 10) | Cerebro-spinal fluid (N = 6) | Throat/ ear (N = 4) | Peritoneal/ pleural fluid (N = 4) | Others (catheter, stool, etc) (N = 11) | |
| *Acinetobacter* spp | 7 (3) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | <0.001 |
| *Enterobacter* spp | 2 (1) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 1 (9) | |
| *Escherichia coli* | 82 (32) | 5 (15) | 1 (6) | 0 (0) | 0 (0) | 1 (25) | 0 (0) | 2 (18) | |
| *Klebsiella* spp | 40 (16) | 7 (21) | 7 (29) | 2 (20) | 0 (0) | 1 (25) | 1 (25) | 0 (0) | |
| *Proteus* spp | 1 (1) | 1 (2) | 3 (12) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | |
| *Pseudomonas* spp | 23 (9) | 0 (0) | 5 (21) | 5 (50) | 2 (33) | 2 (50) | 1 (25) | 0 (0) | |
| *Enterococcus* spp | 3 (1) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 1 (9) | |
| *Staphylococcus aureus* | 17 (6) | 0 (0) | 3 (12) | 1 (10) | 1 (17) | 0 (0) | 2 (50) | 1 (9) | |
| CoNS | 57 (22) | 0 (0) | 3 (12) | 0 (0) | 3 (50) | 0 (0) | 0 (0) | 2 (18) | |
| *Candida* spp | 24 (9) | 21 (62) | 2 (8) | 2 (20) | 0 (0) | 0 (0) | 0 (0) | 4 (36) | |
| Total (N = 349) | 256 (73) | 34 (10) | 24 (7) | 10 (3) | 6 (2) | 4 (1) | 4 (1) | 11 (3) | |

*Statistically significant when *p*-value <0.05 using $\chi^2$-test for comparison of distribution of infective microorganisms among clinical sources

CoNS: coagulase-negative staphylococci; PICU: pediatric intensive care unit

isolates), teicoplanin (all isolates), and tetracycline. The majority of *Enterococcus* spp isolates (*n* = 4) were resistant to gentamicin (50% of the isolates) and penicillin G, but sensitive to daptomycin, gentamicin (50% of the isolates), linezolid (all isolates), quinupristine/dalfopristin (all isolates), teicoplanin (all isolates), and vancomycin (Table 3). The most effective antibiotics were daptomycin, linezolid, quinupristine/dalfopristin, and teicoplanin. The differences between antibiotic susceptibility and resistance of CoNS, *Enterococcus* spp and *S. aureus* are statistically significant (*p*-value <0.05) for cefoxitin, ciprofloxacin, clindamycin, erythromycin, fusidic acid, gentamicin, and levofloxacin.

Of the Gram-negative bacteria isolates, the majority of *E. coli* isolates (*n* = 73) were resistant to amoxicillin/clavulanic acid, ampicillin/sulbactam, cefepime, cefuroxime, tetracycline, and trimethoprim/sulfamethoxazole, but sensitive to amikacin, ceftazidime, ciprofloxacin, gentamicin, meropenem, and tazobactam/piperacillin (Table 4). The majority of *Klebsiella* spp isolates (*n* = 49) were resistant to amoxicillin/clavulanic acid, ampicillin/sulbactam, cefepime, ceftazidime, ciprofloxacin (50% of the isolates), gentamicin, tazobactam/piperacillin, and trimethoprim/sulfamethoxazole, but sensitive to amikacin, ciprofloxacin (50% of the isolates), imipenem, and meropenem. The majority of *Pseudomonas* spp isolates (*n* = 37) were resistant to ampicillin/sulbactam, but sensitive to amikacin, cefepime, ceftazidime, ciprofloxacin, imipenem, meropenem, and tazobactam/piperacillin. The majority of *Acinetobacter* spp isolates (*n* = 7) were resistant to amikacin, cefepime, ceftazidime, ciprofloxacin, gentamicin, imipenem, meropenem, tazobactam/piperacillin, and trimethoprim/sulfamethoxazole, but none were sensitive to the antibiotics tested. The majority of *Proteus* spp isolates (*n* = 5) were resistant to amoxicillin/clavulanic

Table 3

Antibiogram profile of Gram-positive bacteria cultured from PICU patients in a tertiary hospital, Mogadishu, Somalia, January 2022 - December 2023

| Antibiotic and test result | Frequency, *n* (%) | | | *p*-value* |
|---|---|---|---|---|
| | CoNS (N = 65) | *Staphylococcus aureus* (N = 25) | *Enterococcus* spp (N = 4) | |
| Cefoxitin† | | | | 0.003 |
| Sensitive | 38 (58) | 6 (24) | N/A | |
| Resistant | 27 (42) | 19 (76) | N/A | |
| Gentamicin | | | | 0.003 |
| Sensitive | 36 (55) | 23 (92) | 2 (50) | |
| Resistant | 29 (45) | 2 (8) | 2 (50) | |
| Ciprofloxacin | | | | < 0.001 |
| Sensitive | 20 (31) | 18 (72) | N/A | |
| Resistant | 45 (69) | 7 (28) | N/A | |
| Linezolid | | | | 0.628 |
| Sensitive | 63 (97) | 25 (100) | 4 (100) | |
| Resistant | 2 (3) | 0 (0) | 0 (0) | |
| Quinupristine/dalfopristin | | | | 0.612 |
| Sensitive | 62 (95) | 25 (100) | 4 (100) | |
| Resistant | 3 (5) | 0 (0) | 0 (0) | |
| Teicoplanin | | | | 0.453 |
| Sensitive | 60 (92.3) | 25 (100) | 4 (100) | |
| Resistant | 5 (7.7) | 0 (0) | 0 (0) | |
| Penicillin G | | | | N/A |
| Sensitive | N/A | N/A | 1 (25) | |
| Resistant | N/A | N/A | 3 (75) | |

Table 3 (cont)

| Antibiotic and test result | Frequency, *n* (%) | | | *p*-value* |
|---|---|---|---|---|
| | CoNS (N = 65) | *Staphylococcus aureus* (N = 25) | *Enterococcus* spp (N = 4) | |
| Daptomycin | | | | 0.141 |
| Sensitive | 64 (98) | 24 (96) | 3 (75) | |
| Resistant | 1 (2) | 1 (4) | 1 (25) | |
| Fusidic acid | | | | <0.001 |
| Sensitive | 30 (46) | 23 (92) | N/A | |
| Resistant | 35 (54) | 2 (8) | N/A | |
| Erythromycin | | | | 0.004 |
| Sensitive | 21 (32) | 17 (68) | N/A | |
| Resistant | 44 (68) | 8 (32) | N/A | |
| Clindamycin | | | | 0.009 |
| Sensitive | 29 (45) | 19 (76) | N/A | |
| Resistant | 36 (55) | 6 (24) | N/A | |
| Tetracycline | | | | 0.009 |
| Sensitive | 28 (43) | 19 (76) | N/A | |
| Resistant | 37 (57) | 6 (24) | N/A | |
| Levofloxacin | | | | <0.001 |
| Sensitive | 18 (28) | 19 (76) | N/A | |
| Resistant | 47 (72) | 6 (24) | N/A | |
| Vancomycin | | | | N/A |
| Sensitive | N/A | N/A | 3 (75) | |
| Resistant | N/A | N/A | 1 (25) | |

*Statistically significant when *p*-value <0.05 using the $\chi^2$ test for comparison of the distribution of infective Gram-positive microorganisms among different antibiotic susceptibility and resistance rates

†Cefoxitin disk was used to detect methicillin resistance.

CoNS: coagulase-negative staphylococci; N/A: not available; PICU: pediatric intensive care unit

Table 4

Antibiogram profile of Gram-negative bacteria cultured from PICU patients in a tertiary hospital, Mogadishu, Somalia, January 2022 - December 2023

| Antibiotics and test results | Frequency, *n* (%) | | | | | | *p*-value* |
|---|---|---|---|---|---|---|---|
| | *Escherichia coli* (N = 73) | *Klebsiella* spp (N = 49) | *Pseudomonas* spp (N = 37) | *Acinetobacter* spp (N = 7) | *Proteus* spp (N = 5) | *Enterobacter* spp (N = 3) | |
| Amoxicillin/ clavulanic acid | | | | | | | 0.390 |
| Sensitive | 12 (16) | 14 (29) | N/A | N/A | 1 (20) | 0 (0) | |
| Resistant | 61 (84) | 35 (71) | N/A | N/A | 4 (80) | 3 (100) | |
| Cefepime | | | | | | | <0.001 |
| Sensitive | 26 (36) | 12 (25) | 27 (73) | 1 (14) | 1 (20) | 2 (67) | |
| Resistant | 47 (64) | 37 (75) | 10 (27) | 6 (86) | 4 (80) | 1 (33) | |
| Ceftazidime | | | | | | | <0.001 |
| Sensitive | 47 (64) | 19 (39) | 32 (86) | 1 (14) | 4 (80) | 1 (33) | |
| Resistant | 26 (36) | 30 (61) | 5 (14) | 6 (86) | 1 (20) | 2 (66) | |
| Cefuroxime | | | | | | | 1.00 |
| Sensitive | 7 (10) | N/A | N/A | N/A | 0 (0) | 0 (0) | |
| Resistant | 66 (90) | N/A | N/A | N/A | 5 (100) | 3 (100) | |

Table 4 (cont)

| Antibiotics and test results | Frequency, *n* (%) | | | | | | *p*-value* |
|---|---|---|---|---|---|---|---|
| | *Escherichia coli* (N = 73) | *Klebsiella* spp (N = 49) | *Pseudomonas* spp (N = 37) | *Acinetobacter* spp (N = 7) | *Proteus* spp (N = 5) | *Enterobacter* spp (N = 3) | |
| Ampicillin/ sulbactam | | | | | | | 0.448 |
| Sensitive | 32 (44) | 16 (33) | 11 (30) | N/A | 2 (40) | 2 (67) | |
| Resistant | 41 (56) | 33 (67) | 26 (70) | N/A | 3 (60) | 1 (33) | |
| Tazobactam/ piperacillin | | | | | | | 0.091 |
| Sensitive | 38 (52) | 19 (39) | 24 (65) | 2 (29) | 4 (80) | 1 (33) | |
| Resistant | 35 (48) | 30 (61) | 13 (35) | 5 (71) | 1 (20) | 2 (67) | |
| Gentamicin | | | | | | | <0.001 |
| Sensitive | 59 (81) | 21 (43) | N/A | 3 (43) | 4 (80) | 3 (100) | |
| Resistant | 14 (19) | 28 (57) | N/A | 4 (57) | 1 (20) | 0 (0) | |
| Amikacin | | | | | | | <0.001 |
| Sensitive | 64 (88) | 26 (53) | 32 (86) | 3 (43) | 4 (80) | 3 (100) | |
| Resistant | 9 (12) | 23 (47) | 5 (14) | 4 (57) | 1 (20) | 0 (0) | |
| Imipenem | | | | | | | 0.052 |
| Sensitive | N/A | 36 (73) | 25 (68) | 2 (29) | N/A | N/A | |
| Resistant | N/A | 13 (27) | 12 (32) | 5 (71) | N/A | N/A | |

Table 4 (cont)

| Antibiotics and test results | Frequency, *n* (%) | | | | | | *p*-value* |
|---|---|---|---|---|---|---|---|
| | *Escherichia coli* (N = 73) | *Klebsiella* spp (N = 49) | *Pseudomonas* spp (N = 37) | *Acinetobacter* spp (N = 7) | *Proteus* spp (N = 5) | *Enterobacter* spp (N = 3) | |
| Meropenem | | | | | | | 0.052 |
| Sensitive | 61 (84) | 34 (69) | 30 (81) | 3 (43) | 5 (100) | 3 (100) | |
| Resistant | 12 (16) | 15 (31) | 7 (19) | 4 (57) | 0 (0) | 0 (0) | |
| Ciprofloxacin | | | | | | | <0.001 |
| Sensitive | 56 (78) | 24 (49) | 31 (84) | 2 (29) | 4 (80) | 3 (100) | |
| Resistant | 16 (22) | 25 (51) | 6 (16) | 5 (71) | 1 (20) | 0 (0) | |
| Trimethoprim/ sulfamethoxazole | | | | | | | <0.001 |
| Sensitive | 29 (43) | 8 (16) | N/A | 1 (14) | 1 (20) | 3 (100) | |
| Resistant | 39 (57) | 41 (84) | N/A | 6 (86) | 4 (80) | 0 (0) | |
| Tetracycline | | | | | | | 1.00 |
| Sensitive | 9 (16) | N/A | N/A | N/A | 1 (20) | 0 (0) | |
| Resistant | 48 (84) | N/A | N/A | N/A | 4 (80) | 3 (100) | |

*Statistically significant when $p$-value <0.05 using the $\chi^2$ test for comparison of the distribution of infective Gram-negative microorganisms among different antibiotic susceptibility and resistance rates

CoNS: coagulase-negative staphylococci; N/A: not available; PICU: pediatric intensive care unit

acid, ampicillin/sulbactam, cefepime, cefuroxime (all isolates), tetracycline, and trimethoprim/sulfamethoxazole, but sensitive to amikacin, ceftazidime, ciprofloxacin, gentamicin, meropenem (all isolates), and tazobactam/piperacillin. The majority of *Enterobacter* spp isolates ($n$ = 3) were resistant to amoxicillin/clavulanic acid (all isolates), ceftazidime, cefuroxime (all isolates), tazobactam/piperacillin, and tetracycline (all isolates), but were sensitive to amikacin (all isolates), ampicillin/sulbactam, cefepime, ciprofloxacin (all isolates), gentamicin (all isolates), meropenem (all isolates), and trimethoprim/sulfamethoxazole (all isolates). The most effective drugs were amikacin, gentamicin, and meropenem (Table 4). The differences between antibiotic susceptibility and resistance of the Gram-negative bacteria isolates are statistically significant ($p$-value <0.05) for amikacin, cefepime, ceftazidime, ciprofloxacin, gentamicin, and trimethoprim/sulfamethoxazole (Table 4).

The antibiotic susceptibility testing has revealed that out of 268 bacterial isolates, 202 (75.4%) were found to be MDR strains and 65 (69.1%) out of 94 Gram-positive isolates were MDR while out of 174 Gram-negative isolates, 137 (78.7%) were MDR.

## DISCUSSION

We retrospectively examined records of bacterial isolates from clinical samples of PICU patients in a tertiary hospital, Mogadishu, from 2022 to 2023. Of the 1,424 culture samples analyzed, 349 (24.5%) yielded positive results. Our findings are close to the 21.6% culture positivity rate reported in a similar study conducted in Ethiopia (Amsalu *et al*, 2024), but lower than in Bangladesh (13.6%), and India (19%) (Chowdhury *et al*, 2022; Mogasale *et al*, 2021). These differences may result from variations in patient characteristics, sampling methods, geography, epidemiology, and antibiotic usage policies.

The most frequently isolated

organisms were Gram-negative bacteria (58%), followed by Gram-positive bacteria (27%) and then fungi (15%). This result is concurring with other reports from India, Saudi Arabia, Romania, and China (Sharma *et al*, 2020; Bazaid *et al*, 2023; Prajescu *et al*, 2023; Li *et al*, 2024). We observed that the isolation rate for the microbiological species in 2023 is significantly higher (or remained unchanged) compared to 2022, except for CoNS. Similar trends have been reported in Türkiye and China (Atici *et al*, 2016; Li *et al*, 2024). The observed decrease in CoNS isolation may be attributed to several factors. CoNS are common skin commensals and frequently considered contaminants in blood cultures, particularly when aseptic techniques are suboptimal. Improved blood culture collection procedures and stricter adherence to infection control practices may have reduced contamination rates, thereby lowering the number of CoNS isolates reported. Additionally, increased awareness among clinicians about distinguishing true bloodstream infections from contaminants may have led to more selective reporting of CoNS findings.

We observed that the highest infection prevalence occurred in the ≤1 year of age group, consistent with previous findings from Bangladesh, Syria, and China (Chowdhury *et al*, 2022; Kahal *et al*, 2023; Li *et al*, 2024). This may be explained by immature immunity and a phenomenon called "disease tolerance" (Harbeson *et al*, 2018). Positive cultures were 2-fold more common in males than females, in agreement with other studies in India, Southern Ethiopia, Türkiye, and China (Sharma *et al*, 2020; Hailemariam *et al*, 2021; Ciğerci Günaydin *et al*, 2022; Li *et al*, 2024), but the converse in Syria (Kahal *et al*, 2023). The higher rate of positive cultures in boys compared to girls may be due to various biological and environmental factors. These include: biologically, men are known to have weaker innate and adaptive immune responses than women. This is related to

the presence of X-chromosome-linked immunity-related genes and immune-boosting hormones such as estrogen in women (Klein and Flanagan, 2016; Forsyth *et al*, 2024). These immune differences may make men more susceptible to infections and cause them to progress more easily. Furthermore, the higher rate of hospitalizations, more frequent invasive procedures, or earlier referral to healthcare by their families in boys may contribute to the higher rate of positive cultures in men compared to girls.

CoNS was the most frequent of the Gram-positive bacteria isolates, followed by *S. aureus* and then *Enterococcus* spp, as reported in Bangladesh, and India (Chowdhury *et al*, 2022; Sharma *et al* (2024). CoNS, a common skin flora, was long considered a contaminant (Hall and Lyman, 2006); however, it is now increasingly accepted as a major cause of nosocomial infections in immunocompromised children and patients with invasive procedures like mechanical ventilation and catheterization (Amsalu *et al*, 2024). Sharma *et al* (2024) from India noted that the increasing use of invasive devices in ICUs likely contributes to the pathogenic shift of CoNS, elevating antimicrobial resistance prevalence, raising healthcare costs, and adverse outcomes.

*E. coli* the most frequent of the Gram-negative bacteria isolates, followed by *Klebsiella* spp and then *Pseudomonas* spp, with *Acinetobacter* spp, *Enterobacter* spp and *Proteus* spp at much lower frequencies. These findings were consistent with studies from India and Romania (Mogasale *et al*, 2021; Prajescu *et al*, 2023); however, Bazaid *et al* (2023) (in Saudi Arabia) reported MRSA as the most frequent, Elghanam *et al* (2024) (in Egypt) *Klebsiella* spp and Sharma *et al* (2024) (in India) *Acinetobacter* spp. These variations may result from differences in study design, bacterial identification methods, geographic regions, and population dynamics.

We observed that most microbial isolates (73%) were cultured from blood specimens, in agreement

with reports from India (41.4%) and Türkiye (50%) (Sharma *et al*, 2024; Avcı and Atıkan, 2021). *E. coli* was the most frequent pathogen in blood samples. de la Torre *et al* (2017) reported a similar result from Spain.

We noted methicillin resistance (MR) was present in 41 and 76% of CoNS and *S. aureus* isolates. Duman *et al* (2011) in Türkiye reported 64.4% MRCoNS and 30.8% MRSA, Rutare (2013) in Kenya 64.1 and 46.5%, Sharma *et al* (2020) in India 75 and 33%, and Sharma *et al* (2024) in India 60 and 70% respectively. These differences may stem from antibiotic misuse, over-the-counter access and weak infection control policy.

In our study, the majority of Gram-positive bacteria isolates were sensitive to daptomycin, linezolid, quinupristin-dalfopristin, and teicoplanin, concordant with previous findings in Türkiye, Romania, Egypt, India (Ergül *et al*, 2017; Prajescu *et al*, 2023; Elghanam *et al*, 2024; Sharma *et al*, 2024), while the majority of Gram-negative bacteria isolates were sensitive to amikacin, gentamicin and meropenem, similar to the report of Ergül *et al* (2017) in Türkiye.

We observed that most *E. coli* isolates were resistant to amoxicillin/clavulanic acid (84%), ampicillin (89%), cefuroxime (90%), and tetracycline (84.2%), but sensitive to amikacin (88%), gentamicin (81%), and meropenem (85%). These findings are consistent (in part) with the findings of Ergül *et al*. (2017) in Türkiye, while Prajescu *et al* (2023) in Romania observed *E. coli* isolates (67.63%) are ampicillin-resistant.

We observed that most *Klebsiella* spp isolates were resistant to ampicillin (90%) and trimethoprim-sulfamethoxazole (84%), but susceptible to imipenem (73%) and meropenem (69%). These results align with those of Ergül *et al* (2017) (Türkiye). On the other hand, Khan *et al* (2021) (Pakistan) found *Klebsiella* spp isolates are 100% resistant to imipenem and 25% to meropenem. Sharma *et al* (2024) (India) noted 71.42 and 78.57% of

isolates are resistant to ceftriaxone and cefepime respectively, but only 0, 14.28, 21.42, and 28.57% resistant to colistin, tigecycline, imipenem, and meropenem. Elghanam *et al* (2024) (Egypt) reported isolates' resistance ranging 32 (tigecycline)-99% (cefazolin).

*P. aeruginosa* eradication is increasingly challenging due to its strong intrinsic and acquired antibiotic resistance mechanisms (Kahal *et al*, 2023). We noted *Pseudomonas* spp isolates were 70% resistant to ampicillin/sulbactam but mostly sensitive to amikacin (86%), ceftazidime (86%), ciprofloxacin (84%), and meropenem (81%). These results align with those of Prajescu *et al* (2023) in Romania. Khan *et al* (2021) in Pakistan reported over 75% of isolates are resistant to most tested antibiotics, but not meropenem. Kahal *et al* (2023) in Syria observed above 80% of isolates resistant to most tested antibiotics except cefpodoxime and colistin. On the other hand, Chowdhury *et al* (2022) in Bangladesh found much lower resistance, ranging from 0 to 50% of the *Pseudomonas* spp isolates.

*A. baumannii* is a multidrug-resistant pathogen that poses serious risks, especially to immunocompromised patients (Ergül *et al*, 2017). We observed *Acinetobacter* spp isolates showing high resistance to ceftazidime and trimethoprim-sulfamethoxazole (86% each), but half as much to amikacin, gentamicin and meropenem (43% each). Ergül *et al* (2017) (Türkiye) found no resistance of *Acinetobacter* spp isolates to colistin but over 90% resistance to other antibiotics. Sharma *et al* (2024) (India) reported similar phenomena, with colistin, imipenem, meropenem, minocycline, and tigecycline being the most effective antibiotics.

We observed that *Proteus* spp isolates showed 100% resistance to cefuroxime, and 80% to aminoglycosides and beta-lactams, but 100% susceptibility to meropenem. Chakraborty *et al* (2023) reported 100% resistance of *Proteus* spp isolates from pediatric

patients to aminoglycosides, beta-lactams, carbapenems, and second-generation cephalosporins. Kahal *et al* (2023) (Syria) reported 100% resistance of isolates to cephalosporin cefuroxime.

MDR organisms pose a significant global threat to pediatric patients in intensive care units. These pathogens complicate infection control and are associated with high mortality rates. Furthermore, the prevalence of resistant pathogens increases the need for more costly treatment options, placing an additional economic burden on the healthcare system (Ibrahim *et al*, 2019). In our study, 202 of the 268 bacterial isolates (75.4%) were identified as multidrug-resistant (MDR), with MDR observed in 69.1% of Gram-positive and 78.7% of Gram-negative strains. When compared to findings from other regions, our overall MDR rate was lower than that reported by Elghanam *et al* (2024) in Egypt, where 91% of 318 isolates were classified as MDR, including 92% of Gram-positive and 90% of Gram-negative strains. However, our MDR rate was notably higher than the 52% reported at King Chulalongkorn Memorial Hospital in Thailand (Sritippayawan *et al*, 2009). Such disparities across studies may be attributed to several factors, including differences in patient populations, geographic and demographic contexts, sample sizes, antimicrobial usage patterns, and the extent to which infection prevention and control strategies are effectively implemented.

In conclusion, we reported that in a pediatric intensive care unit (PICU) of a tertiary hospital, Mogadishu, as in other hospitals in Somalia and worldwide, Gram-negative bacteria were the most common nosocomial pathogens. Coagulase-negative staphylococci and *E. coli* was the predominant Gram-positive and -negative species respectively, as well as *Candida* spp. The frequency of resistance among the bacteria isolates was alarmingly high, especially against amoxicillin/clavulanic acid, ampicillin/sulbactam, cefuroxime,

tetracycline, and trimethoprim/sulfamethoxazole. Such resistance limits the effectiveness of empirical antibiotic therapy. Therefore, preserving potent antibiotics is crucial. Having up-to-date antibiogram profiles will help prevent unnecessary antibiotic use, and implementing stewardship programs, strengthening infection control and increasing public awareness of appropriate drug use are vital programs to combat multidrug resistance in PICUs in Somalia and elsewhere.

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## CONFLICT OF INTEREST DISCLOSURE

The authors declare no conflict of interest.

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