सत्यमेव जयते

Ministry of Health & Family Welfare
Government of India

Annual Report
National Antimicrobial Resistance Surveillance Network (NARS-Net)

Reporting period:
January – December 2024

National Programme on AMR Containment,
National Centre for Disease Control (NCDC)
Directorate General of Health services
Ministry of Health & Family Welfare
Government of India

Table of Contents

Acronyms

AMR	Antimicrobial Resistance
AFST	Antifungal susceptibility testing
Amox-Clav	Amoxicillin-Clavulanic acid
AST	Antimicrobial Susceptibility Testing
BMD	Broth Microdilution
CBDDR	Centre for Bacterial Diseases and Drug Resistance
CI	Confidence Interval
CLSI	Clinical and Laboratory Standards Institute
CRE	Carbapenem Resistant Enterobacterales
CSV	Comma Separated Value
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic Acid
E. coli	*Escherichia coli*
EME	Emergency
EQAS	External Quality Assessment Scheme
ESBL	Extended Spectrum β-lactamase
EUCAST	European Committee for Antimicrobial Susceptibility Testing
GBD	Global Burden of Disease
GLASS	Global Antimicrobial Resistance and Use Surveillance System
GNB	Gram-Negative bacilli
GPC	Gram-Positive cocci
ICU	Intensive Care Unit
IPD	Inpatient Department
IN	Inpatient
ID	Identification
IQC	Internal Quality Control
ITS	Internal Transcribed Spacer
LIMS	Laboratory Information Management System
MALDI-TOF	Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry
MIC	Minimum Inhibitory Concentration
MICU	Medical Intensive Care Unit
MOPS	3-(N-morpholino) propane sulfonic acid
MoHFW	Ministry of Health and Family Welfare
MRSA	Methicillin-Resistant Staphylococcus aureus
NARS-Net	National Antimicrobial Resistance Surveillance Network
NCC	National Coordinating Centre
NCDC	National Centre for Disease Control
NFGNB	Non-fermenting Gram-negative bacilli

NICU	Neonatal Intensive Care Unit
NRL	National Reference Laboratory
OPD	Outpatient Department
OSBF	Other Sterile Body Fluids
OUT	Outpatient
PA	Pus Aspirate
PICU	Pediatric Intensive Care Unit
Pip-Tazo	Piperacillin-Tazobactam
%R	Percentage Resistant
R I S	Resistant Intermediate Sensitive
RPMI	Roswell Park Memorial Institute medium
SICU	Surgical Intensive Care Unit;
SOP	Standard Operating Procedure
TICU	Trauma Intensive Care Unit
TMP-SMX	Trimethoprim-Sulfamethoxazole
UNK	Unknown
UT	Union Territory
VBA	Visual Basic Application
VISA	Vancomycin Intermediate resistant *S. aureus*
VRE	Vancomycin-Resistant *Enterococcus* species
VRSA	Vancomycin Resistant *S. aureus*
WHO	World Health Organization

List of Tables

List of Figures

Executive Summary

Antimicrobial Resistance (AMR) surveillance is crucial for tracking and combating the growing threat of AMR. This is the eighth report of National AMR Surveillance Network (NARS-Net) established under the National Programme on AMR Containment coordinated by the National Centre for Disease Control (NCDC). This report includes bacterial AMR surveillance data from 54 sentinel surveillance sites and Fungal AMR Surveillance data from 28 sites being strengthened under NARS-Net. NARS-Net which has been expanded in a phased manner currently includes 60 laboratories in 33 states/UTs (as of March 2025). This report provides insights into resistance patterns, trends and emerging resistance across the network sites.

The current report includes data of bacterial and fungal AMR Surveillance for the reporting period from 01 January 2024 to 31 December 2024. Standard operating procedures (SOPs) on antimicrobial susceptibility testing (AST), internal quality control (IQC), AMR data management developed under the programme are implemented at NARS-Net sites to ensure quality data. The panel of antimicrobials used for surveillance is standardized in alignment with the prescription practices of clinicians in the country. Trainings and workshops are conducted regularly for NARS-Net sites to ensure compliance to the SoPs under the programme. Wet-lab trainings on colistin agar dilution and broth microdilution (BMD) testing, both at the NRL at NCDC and onsite during site visits, have contributed to an increase in the number of sentinel sites performing MIC determination and submitting quality data. Furthermore, monthly feedbacks through data quality monitoring calls has played a crucial role in improving compliance to data standards defined under the programme. Also, External Quality Assessment Scheme (EQAS) conducted by AMR-NRL has played a significant role in improving data quality. The key findings of this report are:

- Over the years, with increasing number of sites, there has been a gradual increase in the number of reported isolates, rising from 25,833 in 2017 to 1,95,077 in the current data reporting period.
- The most commonly isolated priority bacterial pathogen was *E. coli* (33%), which is similar to the previous five years, followed by *Klebsiella* species (23%), *S. aureus* (12%), *Pseudomonas* species (11%), *Acinetobacter* species (10%) *Enterococcus* species (10%) and *Salmonella* enterica serovar Typhi and Paratyphi (0.5%).
- Among the specimen types, urine (45%) was the most frequently reported specimen followed by pus aspirate (31%) and blood (18%). From urine specimens, *E. coli* (51%) was the most frequently isolated pathogen, while *Klebsiella* species (23%) was the most commonly isolated pathogen from blood specimens and from pus specimens *S. aureus* (26%) was the predominant isolate.
- Most *Enterococcus* species were isolated from urine specimens (68%) and most *S. aureus* isolates were from pus aspirates (66%) consistent with the previous reports.

- Proportion of MRSA has declined this year in all location settings than last year's report, it has reduced from 69% to 63% in intensive care units, from 62% to 55% in inpatient wards and from 59% to 44% in outpatients.
- Trend analysis of MRSA isolated from blood showed slight decrease in MRSA proportion from 59% (2021) to 56% (2024).
- Proportion of VRE among blood isolates was observed to be 21% in ICU setting and 24% in inpatients. Trend analysis of VRE isolated from blood has shown consistent increase from 2021 (11%) to 2024 (22%).
- Trend analysis for ESBL producing *E. coli* from blood has shown an increase over the last 4 years from 2021 (76%) to 2024 (81%).
- Similar trend has been observed in blood isolates of ESBL producing *Klebsiella* spp. with consistently high levels of resistance with 81% in 2021 and 84% in 2024.
- Moreover, 3-year trend analysis has shown increase in carbapenem resistant *E. coli* (from 35% to 43%), *Klebsiella* species (47% to 59%) and *Acinetobacter* species (59% to 70%). This consistent increase in carbapenem resistance is of great concern and could be due to penems being the first line of antibiotics used for inpatients in many hospitals.
- *Candida tropicalis* was the most frequently isolated Candida species in invasive Candidemia infections, mostly occurring in ICU settings, predominantly isolated from NICU (41%).
- *C. auris*, a known multidrug-resistant species, was primarily found in ICUs (60%) and inpatient wards (18%). *Candida albicans* showed a strong presence in ICUs (45%) and also appeared notably in inpatients (35%).
- The antifungal susceptibility patterns revealed fluconazole resistance in several species, most notably *C. auris* (66%), *C. parapsilosis* (16%), *W. anomalus (15%), C. albicans* (8%), and *C. tropicalis* (7%). Although resistance to amphotericin B, itraconazole, and 5-fluorocytosine remained low, emerging resistance to echinocandins in some species is a matter of concern.

The above increase in resistance trends may be attributed to the increased use of antimicrobials during the COVID-19 pandemic and rise in data reporting due to increase in the number of sentinel sites in the NARS-Net. This report emphasizes on the pressing need for strengthening surveillance system, targeted interventions, development of evidence-based policies, sustained collaborations and investments to combat AMR. The AMR surveillance data in this report serves as a crucial resource for policy makers, healthcare professionals, and researchers working to address the growing threat of AMR.

The AMR surveillance data in the current report like previous years continues to have the limitation of samples for culture and sensitivity being referred only for patients requiring admission and often not responding to the first line of antibiotics. This limitation has the potential to skew the AMR trends to higher side than the actual trends.

1. Bacterial AMR Surveillance

1.1. Introduction

Antimicrobial resistance (AMR) is a rapidly escalating global health threat. As pathogens evolve to resist the existing antimicrobials, once-manageable diseases become increasingly difficult or impossible to cure. Global Burden of Disease 2021 report by Antimicrobial Resistance Collaborators published in *The Lancet* (2024) estimated that 4.71 million deaths were associated with bacterial AMR including 1.14 million deaths attributable to bacterial AMR.[1] The report also states that among Gram-negative bacteria, resistance to carbapenems increased more than any other antibiotic class, rising from 0.619 million deaths in 1990 to 1.03 million associated deaths in 2021. The report also forecasted that an estimated 1.91 million deaths attributable to AMR and 8.22 million deaths associated with AMR could occur globally in 2050. These figures highlight the immense burden of AMR on public health, particularly in low- and middle-income countries where access to quality healthcare and diagnostics is limited. Beyond mortality, AMR also leads to prolonged illness, increased healthcare costs, and greater risk of complications, posing a serious threat to modern medicine, including surgery, cancer therapy, and intensive care. Without urgent and coordinated action, AMR will continue to undermine modern medicine and threaten global health security. To monitor AMR, a robust surveillance system is needed in the global fight against drug-resistant infections, providing the critical data needed to track resistance patterns, update treatment guidelines, and guide public health interventions.

To address the problem of AMR, Government of India initiated the National Programme on AMR containment in 2013, during the 12th (2012-2017) five-year plan which is being coordinated by the National Centre for Disease Control (NCDC). Under the programme, the National AMR Surveillance Network (NARS-Net) has been established to monitor real time AMR trends and to generate annual reports on National AMR Surveillance data from tertiary healthcare facilities. The current report is the eighth annual report of AMR Surveillance data which includes data from 54 network sites. (Fig. 1)

NARS-Net is being expanded in a phased manner to have representation from all states and Union Territories in the country. Currently, NARS-Net includes 60 medical college laboratories from 27 states and 6 UTs (as of March 2025) with adequate geographical representation. The NARS-Net sentinel surveillance sites conduct laboratory-based AMR surveillance of nine priority bacterial pathogens namely *Staphylococcus aureus, Enterococcus* species, *Escherichia coli*, *Klebsiella* species, *Pseudomonas* species, *Acinetobacter* species, *Salmonella enterica* serotype Typhi and Paratyphi, *Shigella* species and *Vibrio cholerae.* (Table 1) The AMR surveillance data of these priority pathogens submitted by the NARS-Net

---

[1] Naghavi, Mohsen et al. Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050. The Lancet, Volume 404, Issue 10459, 1199 - 1226

sites to AMR programme unit at NCDC is being collated and analyzed at NCDC after validation using WHONET, a microbiology data management open-source offline software. After data validation, the annual National AMR surveillance report[2] and the semi-annual bulletins[3] are developed which are then made available on NCDC website for use by various stakeholders at national and state level. The network data is also submitted annually by NCDC to the World Health Organization's Global AMR Surveillance and Use System (WHO-GLASS) since 2018. MoHFW designated NCDC as the National Coordinating Centre for AMR Surveillance in India in the year 2017.

Table 1: Priority Pathogens and specimens included under Bacterial AMR Surveillance

Specimen	*S. aureus*	*Enterococcus* spp.	*Klebsiella* spp.	*Escherichia coli*	*Acinetobacter* spp.	*Pseudomonas* spp.	*Salmonella Typhi / Paratyphi*	*Shigella species*	*Vibrio cholerae*
Blood	✓	✓	✓	✓	✓	✓	✓		
Urine		✓	✓	✓	✓	✓			
Pus Aspirate	✓	✓	✓	✓	✓	✓			
Other Sterile body fluids*	✓	✓	✓	✓	✓	✓			
Stool							✓	✓	✓

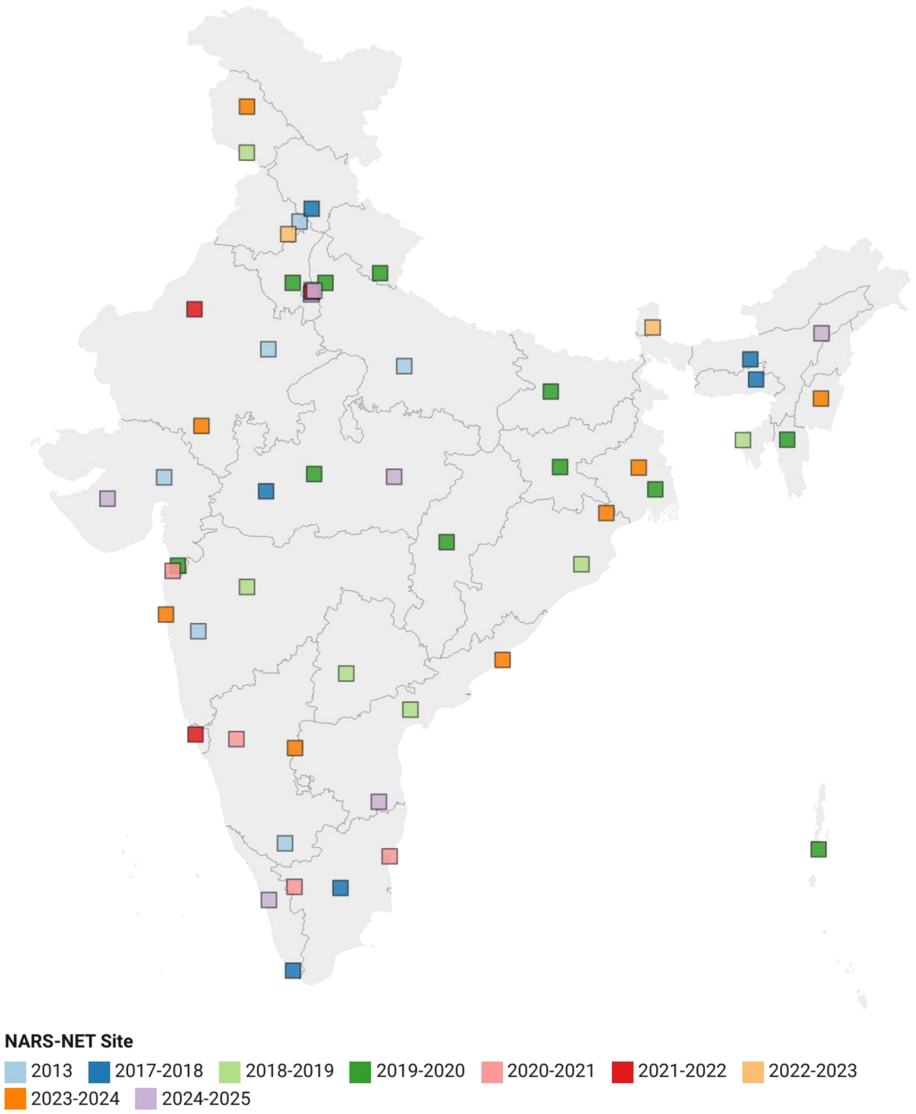
* Other sterile body fluids (OSBF)- Include abdominal fluid, amniotic fluid, bile, cerebrospinal fluid, cyst, endocardium, hip fluid, joint fluid, knee fluid, lymph node, semen, broncho-alveolar lavage, spleen, pleural fluid, pericardial fluid, bone marrow, Bartholin's cyst, fluid, gastric fluid, gallbladder, breast milk and prostatic fluid.

All NARS-Net sites submit AMR data of nine priority pathogens from the pre-defined specimen types to NCDC programme unit. Sites perform antimicrobial susceptibility testing by disk diffusion, broth microdilution, agar dilution, and automated antimicrobial susceptibility testing systems as per the programme SoPs. The programme unit at NCDC provides technical guidance and training support to the sentinel surveillance network laboratories towards accurate pathogen identification and antimicrobial susceptibility testing (AST), implementing quality management systems and standardized AMR surveillance data management.

---

[2] https://ncdc.mohfw.gov.in/reports/

[3] https://ncdc.mohfw.gov.in/amr-semi-annual-bulletin/



Source: CBDDR, NCDC, MOHFW, GOI • Map data: © OSM • Created with Datawrapper

Figure 1:Geographical Location of National AMR Surveillance Network laboratories which have submitted AMR data from January to December 2024

National Reference Laboratory (NRL) has been established at NCDC in 2018-19 to implement External Quality Assessment Scheme (EQAS) for the network labs so as to ensure quality AMR Surveillance data. Additionally, NRL also confirms all antibiotic-resistant alert strains, as defined under the programme, submitted by network sites and only the confirmed alerts are included in the annual report. Feedback on EQAS and Alert confirmation is shared with the respective sentinel sites.

The network sites are mandated to perform Internal quality control testing as per the programme SoPs.[4] In addition, onsite support visits and trainings on data management are conducted to strengthen bacteriology laboratory capacity, identify the challenges and improve the quality of culture, identification and AST practices. The programme unit at NCDC also frequently organizes workshops on use of WHONET AMR data management software to

---

[4] Standard Operating procedure for AMR Surveillance NARS-Net. January 2023. https://ncdc.mohfw.gov.in/wp-content/uploads/2024/03/58495493521681880873.pdf.

facilitate timely AMR surveillance data flow from network sites to NCDC. Annual meetings to review the performance of each site under NARS-Net are also conducted to discuss and resolve site-specific challenges. This process plays a crucial role in strengthening and standardizing antimicrobial resistance surveillance across the network.

The WHONET 2024, an open-source offline microbiology data management desktop application, has been used for collecting, collating and analyzing routine antimicrobial susceptibility data generated by manual testing methods and automated systems at the laboratories. In this report, M100 34th Ed. of Clinical & Laboratory Standards Institute (CLSI) guideline[5] is used for the classification of the isolates as susceptible (S), intermediate (I), or resistant (R). AMR data submitted monthly is reviewed during the monthly data quality monitoring virtual calls conducted by the designated AMR nodal officer at NCDC for the designated programme sites. The monthly data calls with the sites support them in validation of data with respect to the completeness of data fields and compliance with the AMR Surveillance panel of antibiotics. The errors observed in the data during data monitoring calls are notified to the sites in the feedback emails. The subsequently received revised corrected files are cleaned by NCDC nodal officers. A single file is generated from all the cumulative AMR data files from each site and data de-duplication is done before carrying out the analysis.

1.2. Findings

This annual AMR surveillance report includes data of 2,06,745 priority pathogen isolates submitted by 54 NARS-Net sites for the reporting period from 1st January 2024 to 31st December 2024 (List at Annexure-1.4). The data reported was cleaned and validated at NCDC before analysis and annual report preparation. All the colistin-resistant Gram-negative priority bacterial isolates were confirmed using broth microdilutionas per the programme SoP .

1.2.1. Data Deduplication

For data analysis, only the first antibiotic susceptibility result has been considered for each patient per specimen type and pathogen. For example, if two blood cultures from the same patient yielded growth of *E. coli*, only the first has been included in the data; if the growth of *E. coli* was detected in one culture and of *K. pneumoniae* in the other, both results have been considered. If there was growth of *E. coli* in one blood culture and in one urine culture from the same patient, both specimen types have been included. From each patient, only the first isolate of a given species isolated during the investigated time interval was included, regardless of its susceptibility profile.

Deduplication of reported data of 2,06,745 isolates using WHONET revealed 1,95,077 unique patients isolate data. For the surveillance period, only one result has been

---

[5] Clinical Laboratory Standard Institute. Performance Standard for Antimicrobial Susceptibility Testing. 34th Ed. CLSI Supplement M-100. Clinical and Laboratory Standard Institute. USA. 2024.

considered for each patient per specimen type and each pathogen. The unique patient isolate data file has been used for AST analysis. Fig 2 depicts the distribution of AMR surveillance priority pathogen isolates before and after deduplication.

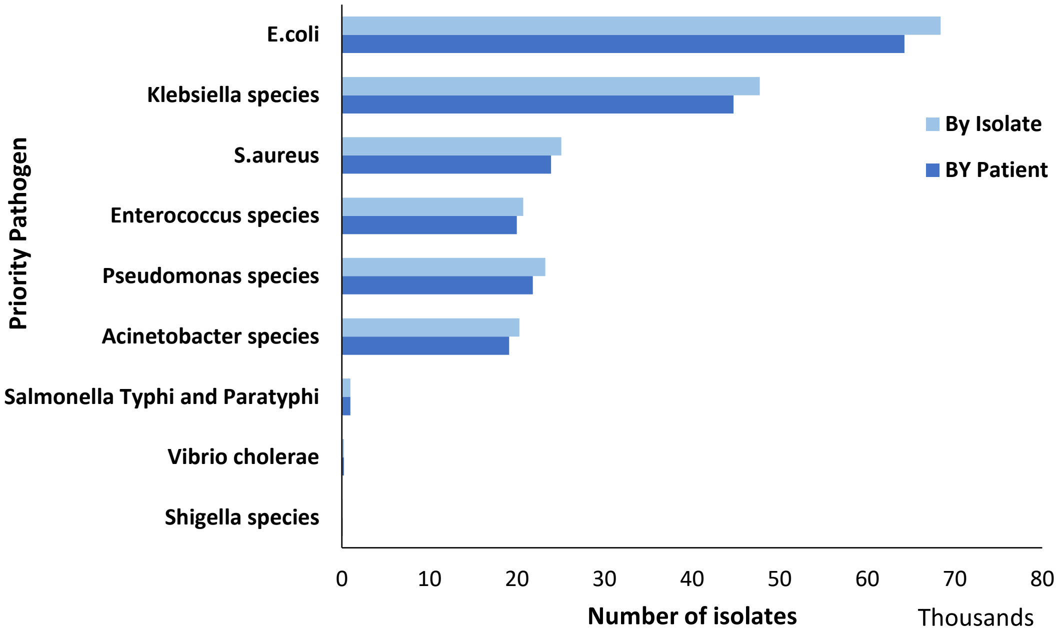
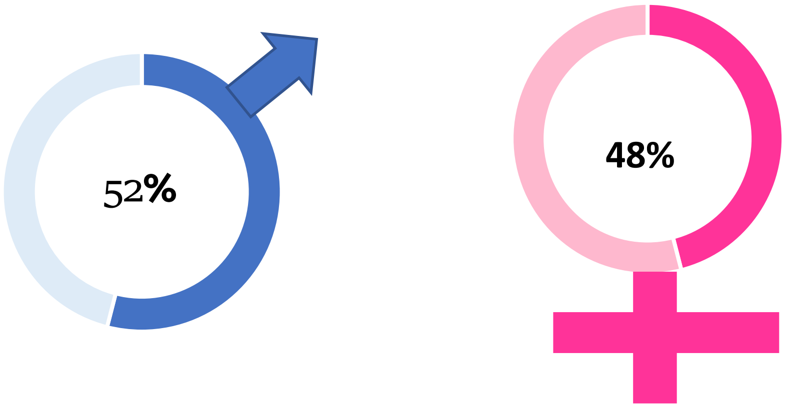


Figure 2: Distribution of priority pathogen isolates and unique patient isolates

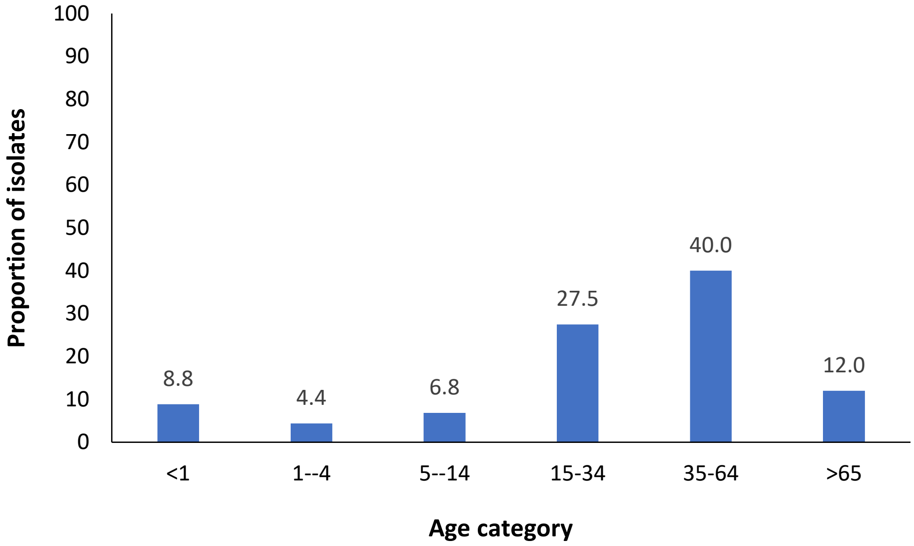
1.2.2. Age and Gender distribution of reported AMR data

Among 1,95,077 unique patients, AST data in this report is from 52% of male and 48% of female patients (Fig 3). Majority of patients were in the age category 35-64 (40%) and 4% patients were in the age category 1-4. About 67 % patients were from the productive age group of 15-64. Figure 4 represents the distribution of priority bacterial pathogen isolates by age category.



*Gender details were missing for 148 isolates

Figure 3: Distribution of priority pathogen isolates by gender (N=1,95,077)



*Age details were missing for 940 (0.5%) isolates

Figure 4: Distribution of all priority pathogen isolates by age category (N=1,95,077)

The analysis of 2024 AMR surveillance data revealed that the highest number of isolates were from urine specimens (45%) (Table 2). The most commonly isolated priority bacterial pathogen was *E. coli* (33%), which is similar to the previous five years, followed by *Klebsiella* species (23%), *S. aureus* (12%), *Pseudomonas* species (11%), *Acinetobacter* species (10%) *Enterococcus* species (10%) and *Salmonella* enterica serovar Typhi and Paratyphi (0.5%) (Table 3).

Table 2: Distribution of priority pathogen isolates based on specimen type (N=1,95,077)

Specimen Type	Number of isolates	(%)
Urine	88,374	(45 %)
Blood	34,229	(18 %)
Pus Aspirate	61,255	(31 %)
Other sterile body fluids	10,878	(6 %)
Stool	341	(0.17 %)
Total	**1,95,077**	

Amongst urine specimens, *E. coli* (51%) was the most commonly isolated pathogen, from blood specimens the most common isolated priority pathogen was *Klebsiella* species (23%); and among isolates from pus specimens, *S. aureus* (26%) was the most common isolate. Among stool specimens, most common pathogen reported was *Vibrio cholerae* (70%), followed by *Shigella* species (24%) and *Salmonella* Typhi and Paratyphi (6%). (Table 3) However, among non-lactose fermenting Gram-negative bacilli, *Pseudomonas* species was most commonly isolated from pus aspirates (48%) and *Acinetobacter* species from blood (39%). (Table 4) Amongst Gram-positive organisms, *Enterococcus* species was most commonly isolated from urine specimens (68%) and *S. aureus* from pus aspirates (66%). (Table 4)

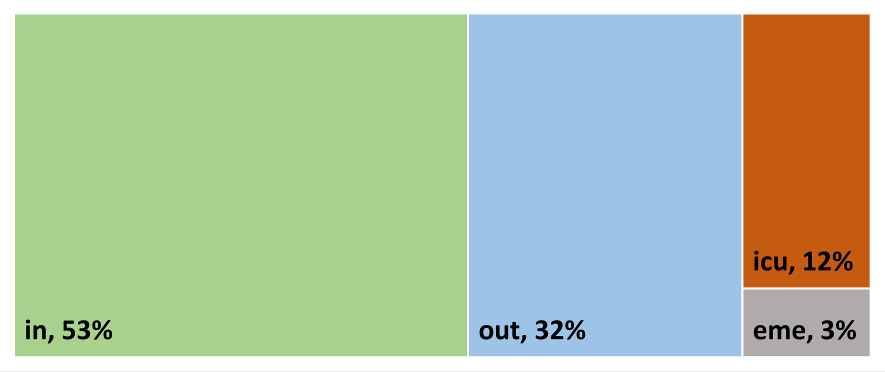
Table 3: Specimen type wise distribution of isolates (N= 1,95,077)

Priority Pathogen	Blood	Pus aspirate	OSBF	Urine	Stool	Total	
	N (%)	N (%)	N (%)	N (%)	N	N	(%)
S. aureus	6958 (20%)	15846 (26%)	1105 (10%)	x	X	23,909	(12)
Enterococcus spp.	3679 (11%)	1942 (3%)	822 (8%)	13533 (15%)	X	19,976	(10)
Escherichia Coli	3621 (11%)	13577 (22%)	2345 (22%)	44711 (51%)	X	64,254	(33)
Klebsiella spp.	8012 (23%)	13576 (22%)	2540 (23%)	20597 (23%)	X	44,725	(23)
Salmonella Typhi and *Paratyphi*	942 (2%)	x	x	x	20	962	(0.5)
Pseudomonas spp.	3530 (10%)	10513 (17%)	1695 (16%)	6070 (7%)	X	21,808	(11)
Acinetobacter spp.	7487 (22%)	5801 (9.5%)	2371 (22%)	3463 (4%)	X	19,122	(10)
Shigella species	x	x	x	x	81	81	(0.04)
Vibrio cholerae	x	x	x	x	240	240	(0.12)
Total	34,229 (100)	61,255 (100)	10,878 (100)	88,374 (100)	341	1,95,077	(100)

x - Specimen type not included under the program; *OBSF- Include abdominal fluid, amniotic fluid, bile, cerebrospinal fluid, cyst, endocardium, hip fluid, joint fluid, knee fluid, lymph node, semen, broncho-alveolar lavage, spleen, pleural fluid, pericardial fluid, bone marrow, bartholin's cyst, fluid, gastric fluid, gall bladder, breast milk and prostatic fluid

Table 4: Proportion of priority pathogens isolated from various specimen types (N= 1,95,077)

Priority	*S. aureus* N (%)	*Enterococcus* spp. N (%)	*Escherichia coli* N (%)	*Klebsiella* spp. N (%)	*Salmonella Typhi* and *Paratyphi* N (%)	*Pseudomonas* spp. N (%)	*Acinetobacter* spp. N (%)	*Shigella* species N	*Vibrio cholerae* N
Blood	6958 (29%)	3679 (18%)	3621 (6%)	8012 (18%)	942 (98%)	3530 (16%)	7487 (39%)	x	x
Pus aspirate	15846 (66%)	1942 (10%)	13577 (21%)	13576 (30%)	x	10513 (48%)	5801 (30%)	x	x
OSBF	1105 (4.6%)	822 (4%)	2345 (4%)	2540 (5.6%)	x	1695 (8%)	2371 (12%)	x	x
Urine	x	13533 (68%)	44711 (70%)	20597 (46%)	x	6070 (28%)	3463 (18%)	x	x
Stool	x	x	x	x	20 (2%)	X	x	81	240
Total	23,909 (100%)	19,976 (100%)	64,254 (100%)	44,725 (100%)	962 (100%)	21,808 (100%)	19,122 (100%)	81	240



IN – Inpatient; OUT–Outpatient; ICU –Intensive care; EME –Emergency; UNK – Unknown; *Location type field was missing in 34 isolates

Figure 5: Distribution of isolates by location type (N=1,95,077)

In the 2024 AMR surveillance data, the majority of isolates (53%) were from patients admitted in hospital wards whereas the least number of isolates (3%) belonged to patients from the Emergency department. Almost a third of the isolates (32%) were from patients visiting the outpatient clinics. About 12% of the priority pathogens were isolated from Intensive care units (ICU) (Fig. 5).

Table 5: Distribution of priority pathogen isolates by location type (N=1,95,077)

Priority Pathogen	Inpatient (N=104,050)		Outpatient (N=62,809)		I.C.U. (N=23,130)		Emergency (N=5,054)	
	N	(%)	N	(%)	N	(%)	N	(%)
Escherichia coli	32346	(31)	26244	(42)	3971	(17)	1680	(33)
Klebsiella species	24752	(24)	12734	(20)	6305	(27)	930	(18)
Salmonella Typhi and *Paratyphi*	498	(0.5)	369	(0.6)	57	(0.5)	37	(0.73)
Pseudomonas species	11699	(11)	7095	(11)	2584	(11)	426	(8.4)
Acinetobacter species	10452	(10)	3387	(5)	4710	(20)	573	(11)
S. aureus	12946	(12)	7513	(12)	2505	(11)	937	(18)
Enterococcus species	11137	(11)	5411	(9)	2981	(13)	445	(9)
Shigella species	52	(0.05)	25	(0.04)	2	(0.01)	1	(0.02)
Vibrio cholerae	168	(0.16)	31	(0.05)	15	(0.06)	25	(0.5)

*Location type field was missing in 34 isolates

Amongst the inpatients, the most commonly isolated priority pathogen was *Escherichia coli* (31%) followed by *Klebsiella* spp. (24%), whereas in Intensive care units *Klebsiella* spp. (27%) was the most commonly isolated pathogen followed by *Acinetobacter* spp. (20%) and *Escherichia coli* (17%) (Table 5). *Escherichia coli* was also the most commonly isolated pathogen from outpatient clinics (42%) and emergency departments (33%). (Table 5, Fig. 6).

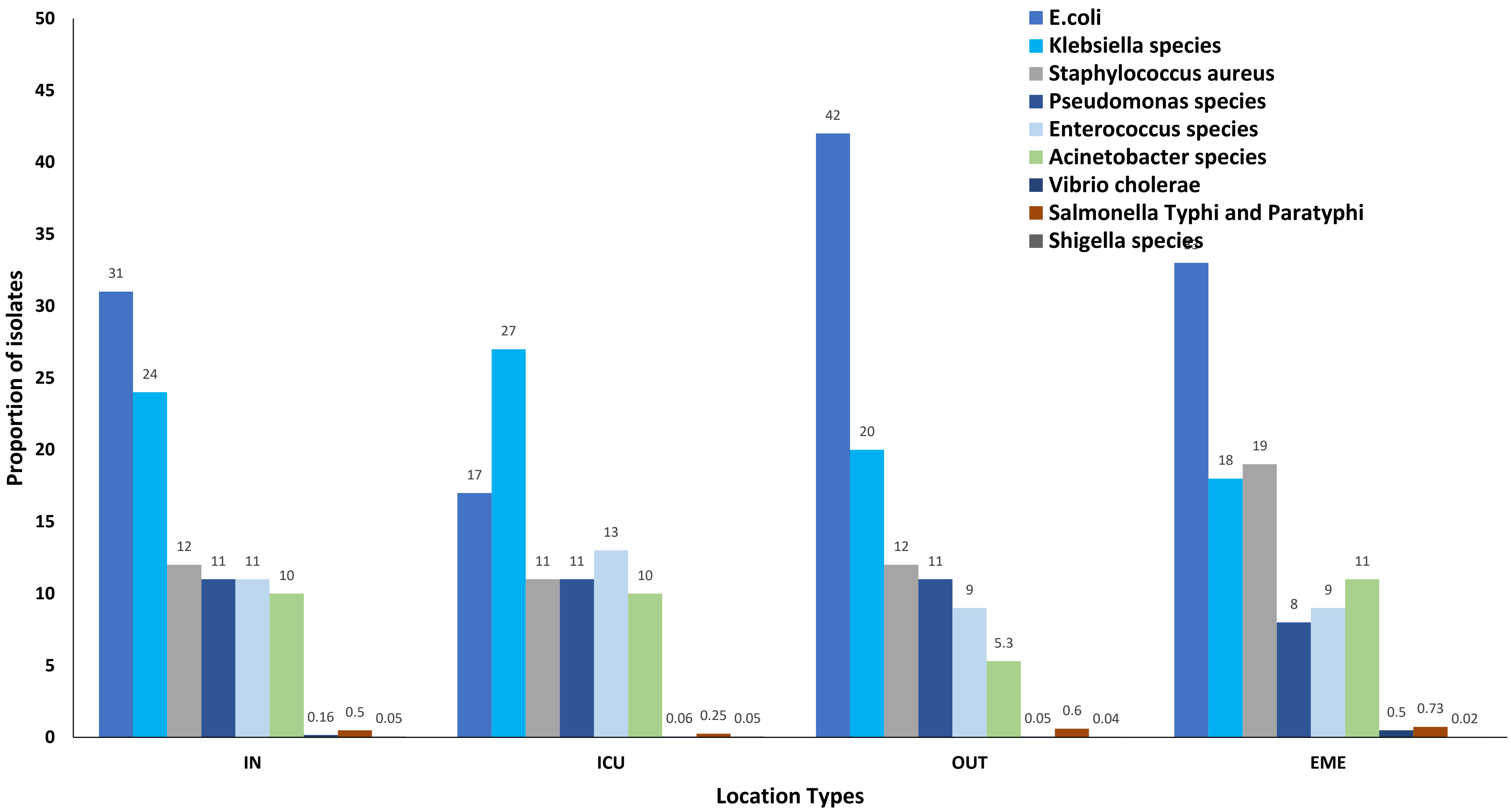


Figure 6: Distribution of priority pathogen isolates by location-type

1.2.3. AMR Surveillance of priority pathogens

1.2.3.1. Gram-Positive Cocci

The AMR surveillance under NARS-Net covers the two most prevalent Gram-positive bacterial human pathogens i.e., *Staphylococcus aureus* and *Enterococcus* species. The AST data of 45,789 Gram-positive cocci (GPC) were submitted to NCDC, of which 43,885 isolates were from unique patients.

Staphylococcus aureus

During the 2024 reporting period, a total of 25,070 *S. aureus* isolates data was submitted to NCDC of which 23,909 isolates were from unique patients (Fig. 2) constituting 12% of priority pathogens included in this annual report data. AST data analysis of 23,909 isolates reveals that majority of *S. aureus* were isolated from pus specimens (66%) and least from other sterile body fluids (5%). In this report, *S. aureus* is observed to be a significant cause of bacteremia (29%). (Table 4).

Approximately half of *S. aureus* isolated from blood (56%; 95% CI (confidence interval): 54.7-57.3) were resistant to cefoxitin (a surrogate for mecA-mediated oxacillin resistance) meanwhile, the resistance to cefoxitin in pus aspirates (54%; 95% CI: 53.2-54.9) and other sterile body fluids (49%; CI: 45.5-51.9) was slightly lower in comparison to the blood isolates (Table 6). For analysis of linezolid resistance in *S. aureus,* CLSI breakpoint for 2023-24 have been considered. Linezolid resistance in *S. aureus* isolated from blood was found to be less than 1% consistent with the observations over last three years. Out of 14,190 isolates tested on Vancomycin screen agar, single isolate showed growth on the vancomycin screen agar plate which was not confirmed as resistant by broth microdilution testing.

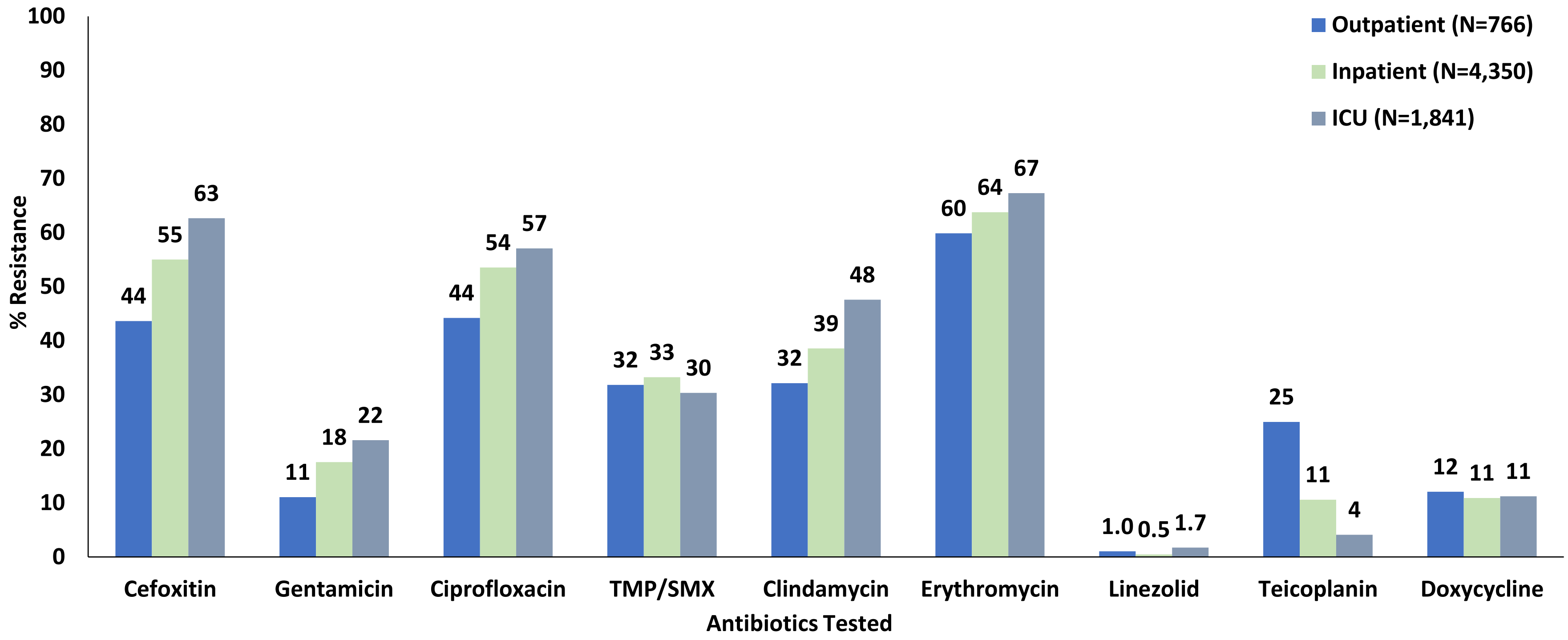
Among the AMR Surveillance priority pathogens isolated in the data reporting period, *S. aureus* was mainly isolated from inpatient wards followed by outpatient clinics and the intensive care settings (Table 5). Notably, proportion of MRSA has declined this year in all location settings in comparison to last year, it has reduced from 69% to 63% in intensive care units, from 62% to 55% in inpatient wards and from 59% to 44% in outpatients (Fig. 7). Resistance to all the surveillance panel antibiotics were proportionately higher among isolates from intensive care setting than those from outpatient clinics and the inpatient wards as seen in Fig. 7.

Table 6: Resistance profile of *Staphylococcus aureus* (N=23,909)

Antibiotic tested	Blood (N=6,958)			Pus Aspirate (N=15,846)			Other Sterile Body Fluids (N=1,105)		
	Number Tested	(%R)	95% CI	Number Tested	(%R)	95% CI	Number Tested	(%R)	95% CI
Cefoxitin	5967	(56)	54.7-57.3	13694	(54)	53.2-54.9	962	(49)	45.5-51.9
Ciprofloxacin	5801	(54)	52.5-55.0	13269	(69)	68.0-69.6	917	(57)	54.1-60.6
Clindamycin	6367	(40)	39.1-41.5	14596	(29)	28.2-29.6	923	(37)	34.1-40.4
Doxycycline	4954	(11)	10.3-12.1	10650	(6)	5.7-6.7	761	(10)	7.9-12.3
Erythromycin	6248	(64)	63.1-65.5	14354	(53)	52.6-54.3	937	(56)	53.1-59.5
Gentamicin	5055	(18)	17.1-19.2	11675	(18)	17.8-19.2	815	(19)	16.5-22
Linezolid*	6282	(0.06)	0.05-0.1	14109	(0.0)	0.0-0.0	990	(0.0)	0.0-0.0
TMP/SMX	5400	(32)	31-33.5	12004	(20)	19.5-20.9	835	(28)	24.6-30.7
Teicoplanin	1249	(9)	8.0-11.3	2250	(8)	6.7-9.0	231	(5)	2.5-8.6

*Alert pathogens confirmed at NRL have been included in the data

TMP-SMX: Trimethoprim-Sulfamethoxazole



*Data of the emergency department was clubbed with data from inpatient wards; Location type for 1 isolate data is unknown

TMP-SMX: Trimethoprim-Sulfamethoxazole

Figure 7: Resistance profile of *S. aureus* in blood (N=6,958) by location type

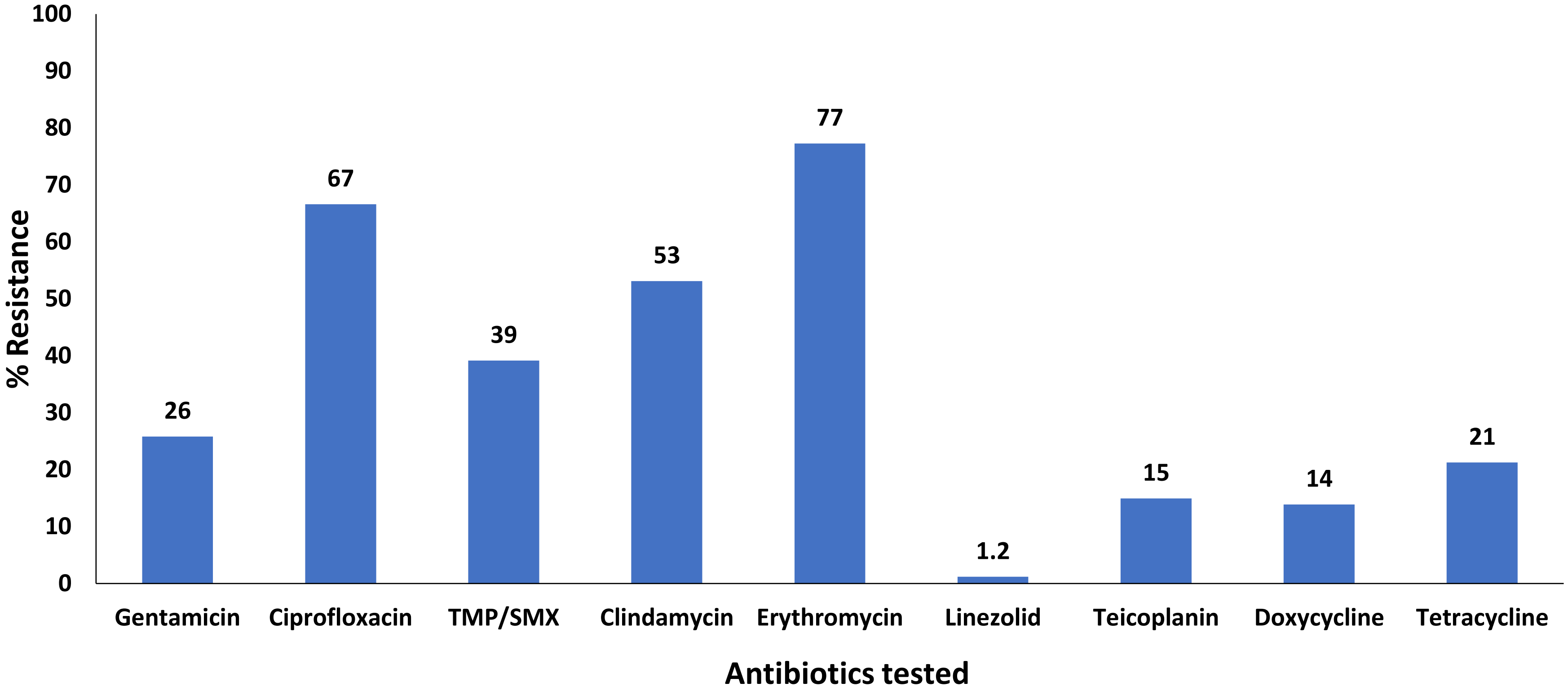


Figure 8: Resistance profile of Methicillin Resistant *S. aureus* (MRSA) in blood (N=3,342)

Enterococcus species

Enterococcus species isolates comprised of 10% of the annual AMR data and contributed to 46% of the Gram-positive cocci data reported during 2024 (Table 3). A total of 20,719 *Enterococcus* species isolates data was submitted by the NARS-Net sites of which 19,976 isolates were from unique patients (Fig. 2). Upon analysis of 19,976 unique patient isolates, isolation rates from specimen types like urine, blood, pus aspirates and other sterile body fluids were 68%, 18%, 10% and 4% respectively (Table 4). Among *Enterococcus* species isolated from blood, highest resistance was observed to erythromycin 79% (CI: 77.3- 80.2) and Ampicillin (71%, CI: 69.4-72.7) (Table 7). Notably resistance to vancomycin (22%, CI: 20.9-23.8) and teicoplanin (26%, CI: 24.4-27.9) is constantly increasing from last 3 years. Resistance to linezolid (1.7%, CI: 1.3-2.2) among blood isolates is similar to last year's report.

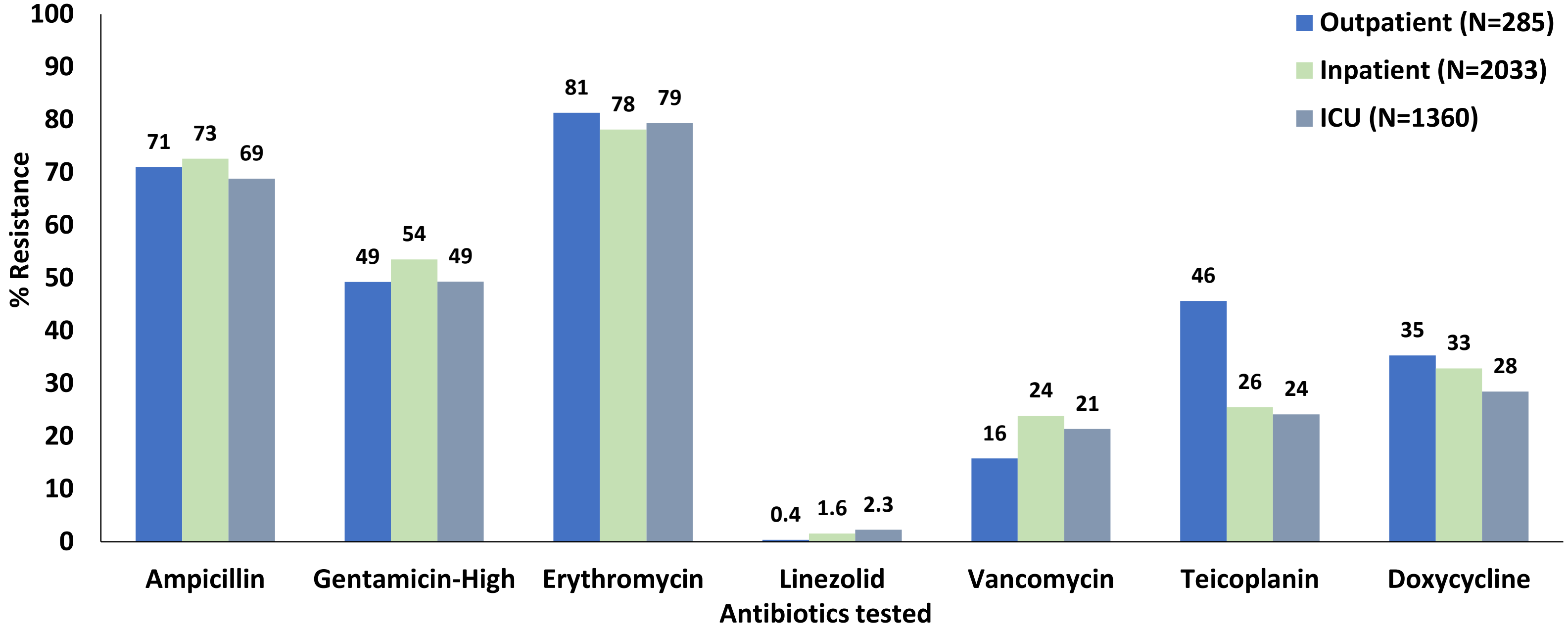
Among the urinary isolates, 58% were resistant to first-line antibiotic ampicillin (CI: 57.1 – 58.9) and 53% to gentamicin-high (CI: 52.2-54.1). Highest resistance was observed to ciprofloxacin (82%, CI: 81.1 - 82.8) and lowest was observed to linezolid 0.44 % (CI: 0.3-0.6). Resistance to vancomycin among urinary isolates was higher than that in last year's report (6% in 2023 to 12% in 2024) (Table 7).

Enterococcus spp. isolates from inpatient wards were almost double the outpatient patient isolates which were in turn nearly twice the isolates from ICU patients. (Table 5). AST analysis of blood isolates of *Enterococcus* spp. showed higher resistance to linezolid in isolates from patients in intensive care units in comparison to those from inpatient wards and outpatient clinics. (Fig. 9) Incidence of VRE among blood isolates is 24% in inpatients and 21% in ICU settings. (Fig. 9) Higher vancomycin resistance was observed in blood isolates than in urinary isolates (Fig. 9, 10). Among urinary isolates of *Enterococcus* species, 43% resistance was observed to nitrofurantoin in ICU settings.

Table 7: Resistance profile of *Enterococcus* species (N=19,976)

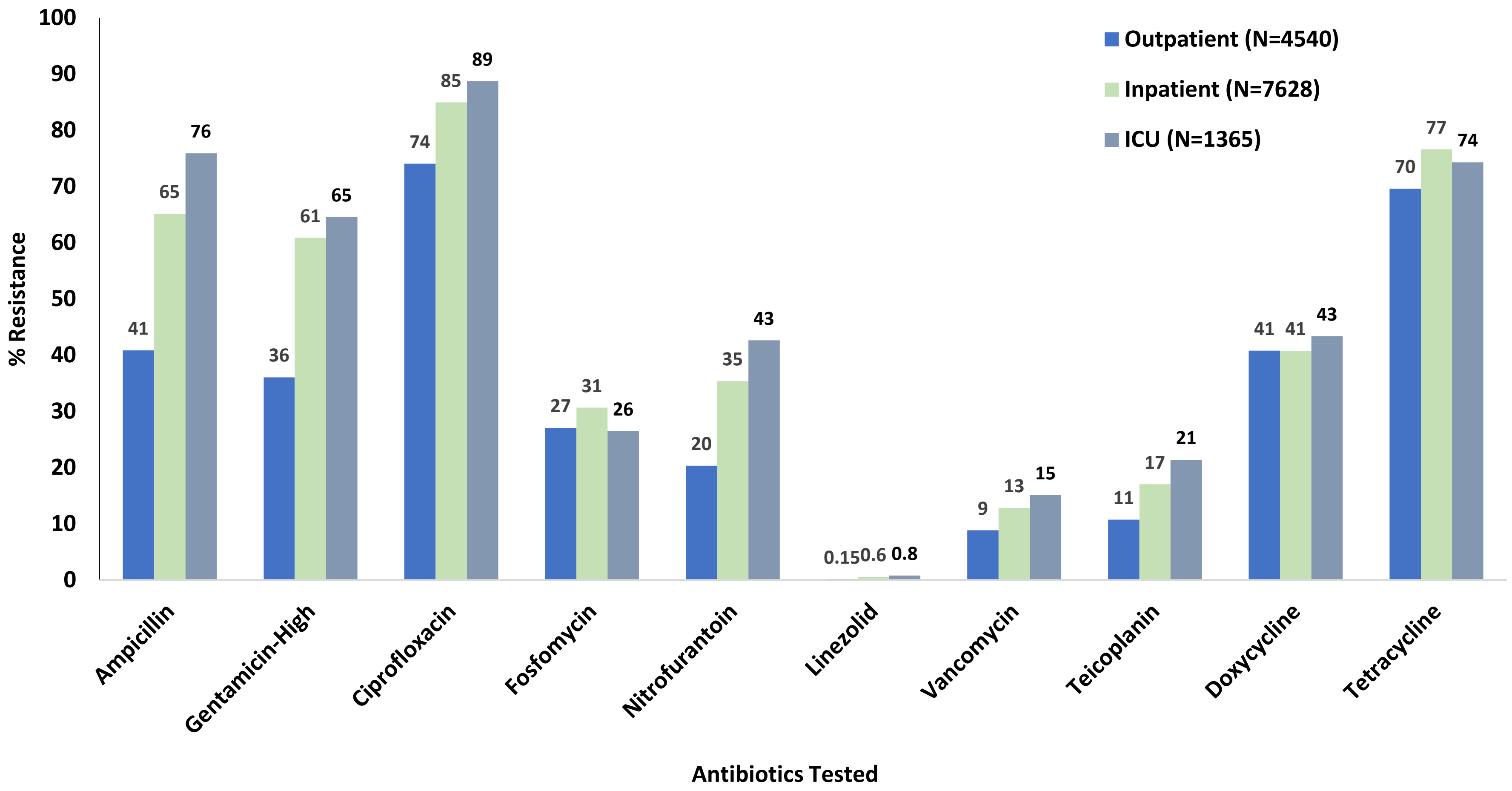
	Blood (N=3,679)			Pus Aspirate (N=1,942)			OSBF (N=822)			Urine (N=13,533)		
Antibiotic Tested	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**
Ampicillin	3061	(71)	69.4-72.7	1633	(47)	44.6-49.5	692	(63)	59.1-66.5	11348	(58)	57.1-58.9
Doxycycline	2349	(31)	29.6-33.3	1271	(26)	23.7-28.6	598	(34)	30.5-38.3	3919	(41)	39.6-42.7
Erythromycin	3164	(79)	77.3-80.2	1542	(69)	66.5-71.2	686	(76)	72.1-78.6		X	
Gentamicin-High	2990	(52)	49.8-53.4	1475	(39)	36.7-41.7	704	(47)	43.0-50.5	10631	(53)	52.2-54.1
Linezolid	3511	(1.7)	1.3-2.2	1768	(1)	0.6-1.6	778	(1.2)	0.6-2.3	12261	(0.44)	0.3-0.6
Teicoplanin	2487	(26)	24.4-27.9	1258	(18)	16.1-20.4	542	(16)	13.1-19.5	8401	(15)	14.6-16.2
Vancomycin	3273	(22)	20.9-23.8	1703	(6.8)	5.7-8.1	770	(17)	14.8-20.3	12296	(12)	11.2-12.3
Ciprofloxacin		x			x			x		7755	(82)	81.1-82.8
Fosfomycin		x			x			x		3434	(20)	18.8-21.5
Nitrofurantoin		x			x			x		7357	(27)	25.6-27.7
Tetracycline		x			x			x		6067	(73)	71.4-73.7

*Alert pathogens confirmed at NRL, NCDC only were included in the data



*Data from the emergency department was clubbed with data from inpatient wards; the Location type for 1 isolate was unknown

Figure 9: Resistance profile of *Enterococcus* species in blood (N=3,679) by location type



*Data from the emergency department was clubbed with data from inpatient wards

Figure 10: Resistance profile of *Enterococcus* species in urine (N=13,533) by location type

1.2.3.2. Gram-Negative Bacilli

Seven Gram-Negative bacteria of public health importance are included under AMR surveillance being coordinated at NARS-Net sites. These are *Escherichia coli, Klebsiella* species, *Pseudomonas* species, *Acinetobacter* species, *Salmonella* enterica serovar Typhi and Paratyphi, *Shigella* species and *Vibrio cholerae*. In the current report, 1,60,956 isolates of Gram-negative bacilli have been reported from 1,51,192 unique patients which account for 78% of total priority pathogens reported from 54 sentinel surveillance sites.

1.2.3.2.1. Enterobacteriaceae

Data of 1,17,184 isolates of *E. coli, Klebsiella* species, *Salmonella enterica* serovar Typhi and Paratyphi and *Shigella* species was submitted by network sites from 1,10,022 unique patients. Enterobacteriaceae accounted for 56% of all the priority pathogens.

Escherichia coli

A total of 68,384 *E. coli* isolates were reported from 64,254 unique patients. *E. coli* contributed to one-third of the unique patient AST data during the year 2024 (Fig. 2). *E coli* was most commonly isolated from the urine samples (70%) followed by pus aspirate (21%), blood (6%) and sterile body fluids (4%) respectively. (Table 4).

E. coli isolates showed more than 50% resistance to all the tested antibiotics except carbapenems, colistin and aminoglycosides. The highest resistance was observed to ampicillin as noted in previous years (Table 8). High proportion of resistance to ciprofloxacin was observed ranging between 73% to 78% in all specimen types. Resistance to nitrofurantoin in urinary isolates showed an increasing trend over last 3 years (increased from 9% in 2022 to 19% in 2024). (Table 8)

Amongst third generation cephalosporins tested, resistance ranging between 79% to 83% was observed in all specimen types. β-lactam inhibitor combination i.e. amoxicillin-clavulanate also had high resistance of 68% in blood isolates. Among carbapenems, ertapenem (49%) had higher resistance rate than imipenem (40%) and meropenem (36%) in *E. coli* blood isolates (Table 8). For colistin susceptibility testing, isolates tested using colistin agar screen and broth microdilution method as per CLSI-M100 Ed. 34 were only considered in this report. Two isolates from blood, one from OSBF, three from pus aspirate and seven from urine were confirmed as colistin resistant at AMR-NRL, NCDC.

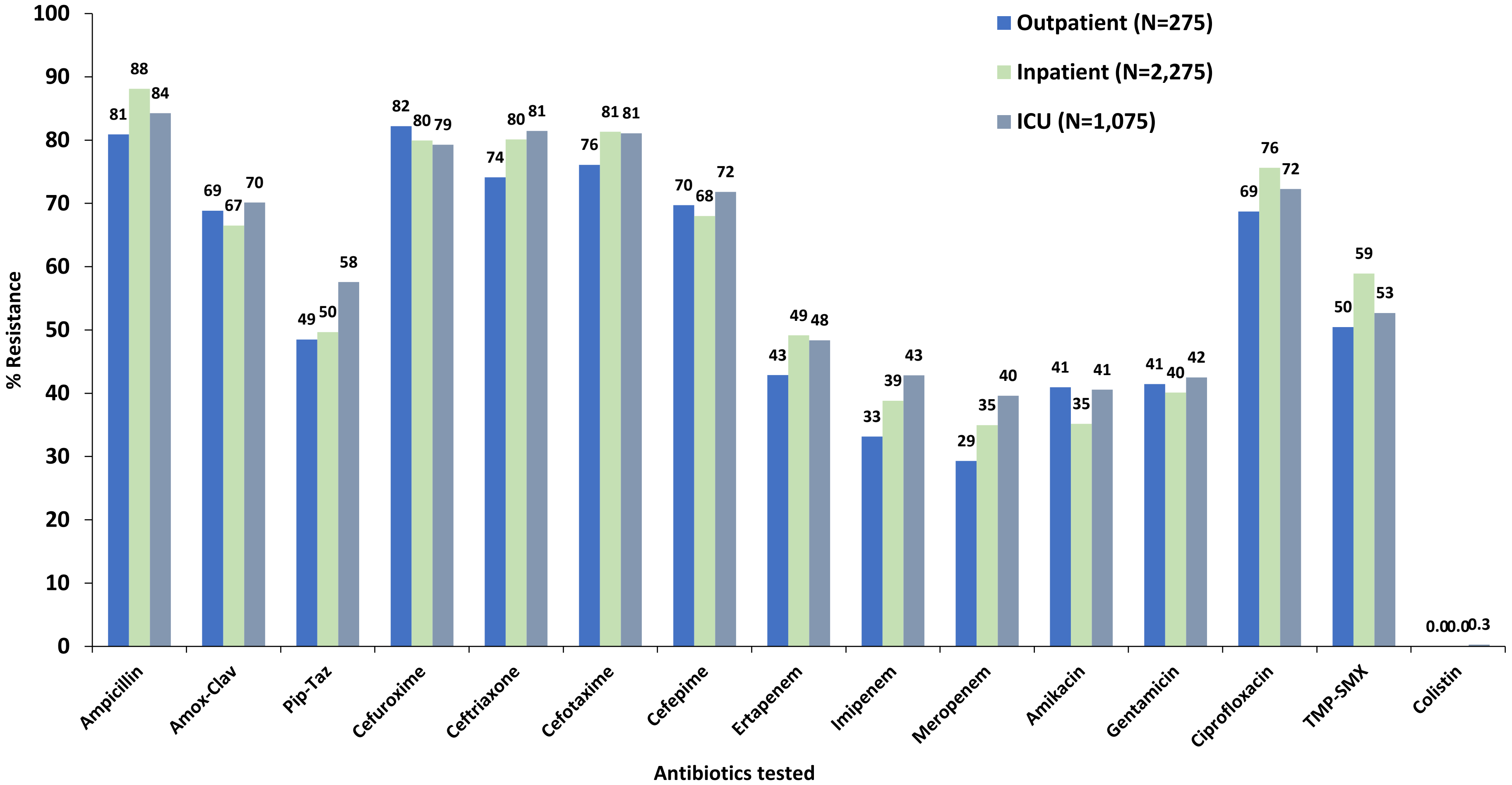
Among the blood isolates of *E. coli*, resistance profile based on the location type showed higher resistance to all the antibiotics in the surveillance panel in isolates from the intensive care units as compared to isolates from inpatient and outpatient departments (Fig. 11). Among urinary isolates of ICU patients, 23% resistance was observed to nitrofurantoin. (Fig. 12) Carbapenemase producing *E. coli* isolates were most frequently isolated from blood samples followed by pus and OSBF samples and least from urine samples of patients in all location types. (Fig 11; 12)

Table 8: Resistance profile of *Escherichia coli* (N=64,254)

	Blood (N=3,621)			PA (N=13,577)			OSBF (N=2,345)			Urine (N=44,711)		
Antibiotic Tested	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**
Ampicillin	2278	(86)	85.0-87.8	8491	(89)	87.2-89.9	1490	(89)	87.5-90.7	30771	(87)	84.7-89.3
Amox-Clav	2759	(68)	66.0-69.5	9744	(63)	61.3-65.4	1638	(71)	68.4-72.9	31408	(59)	57.2-63.4
Pip-Taz	3239	(52)	50.3-53.7	11220	(49)	48.1-50.9	2019	(55)	53.1-57.5	34001	(40)	37.3-43.8
Ceftriaxone	2420	(80)	78.6-81.8	8687	(80)	78.4-81	1383	(83)	80.9-84.9	22108	(74)	69.8-76.7
Cefotaxime	2078	(81)	79.0-82.5	9635	(81)	79.6-82.2	1637	(83)	80.9-84.6	34490	(76)	73.3-78
Cefepime	2714	(69)	67.5-71.0	9944	(60)	58.9-62	1818	(64)	61.4-65.8	28581	(54)	50.8-56.7
Ertapenem	1634	(49)	46.2-51.1	6225	(34)	31.6-36.3	1150	(45)	42.1-47.9	17191	(25)	22.2-29.9
Imipenem	3062	(40)	37.9-41.4	10316	(28)	26.3-30.1	1853	(38)	35.6-40.0	32038	(23)	21.6-25.9
Meropenem	2667	(36)	34.1-37.8	10297	(28)	26.1-29.2	1796	(34)	31.9-36.3	26633	(20)	16.7-22.6
Amikacin	3254	(37)	35.5-38.9	11405	(29)	27.9-30.8	2064	(27)	25.1-29.0	34617	(25)	23.6-29.1
Gentamicin	2797	(41)	39.1-42.8	9845	(34)	32.9-36.1	1737	(33)	30.7-35.1	30890	(32)	30-38.5
Ciprofloxacin	3129	(74)	72.6-75.7	11149	(77)	75-77.2	1988	(78)	76.4-80.1	36167	(73)	70.9-78.6
TMP-SMX	2748	(56)	54.6-58.3	10466	(58)	55.5-59.6	1920	(62)	59.8-64.2	37565	(55)	53-59.4
Colistin	2351	(0.09)	0-0.3	7605	(0.04)	0-0.2	1381	(0.07)	0-0.5	20173	(0.035)	0-0.5
Fosfomycin		X			X			X		21602	(4)	3.2-5.6
Nitrofurantoin		X			X			X		41460	(19)	16.9-20.3
Doxycycline		X		2080	(41)	37.5-42.8	813	(49)	45.1-52.1		X	

x- Drug bug combination for the specimen type not included in the NARS-Net surveillance panel

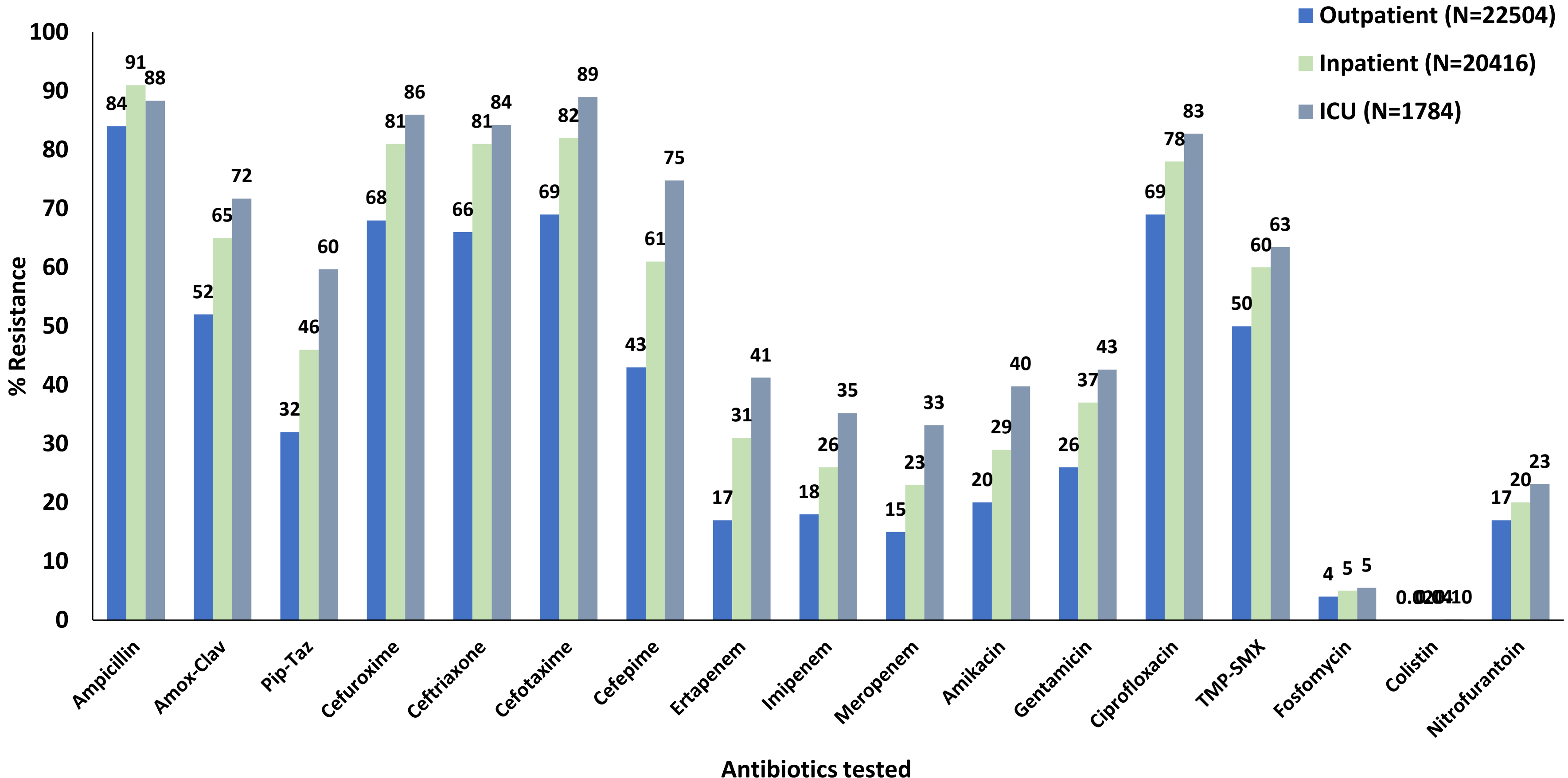
TMP/SMX - Trimethoprim/sulfamethoxazole
Amox-clav -Amoxicillin/Clavulanic acid



Pip-Taz: Piperacillin-Tazobactam
Amox-Clav: Amoxicillin-Clavulanic acid
TMP-SMX: Trimethoprim-Sulfamethoxazole

*Data from the emergency department was clubbed with data from inpatient wards; the Location type for 4 isolates is unknown

Figure 11: Resistance profile of *Escherichia coli* isolated from blood (N=3,625) by location type



Pip-Taz: Piperacillin-Tazobactam
Amox-Clav: Amoxicillin-Clavulanic acid
TMP-SMX: Trimethoprim-Sulfamethoxazole

**Data from the emergency department was clubbed with data from inpatient wards; the Location type for 7 isolates is unknown*

Figure 12: Resistance profile of *Escherichia coli* isolated from urine (N=44,711) by location type

Klebsiella species

In the current data reporting period, 47,744 *Klebsiella* species isolates were reported of which 44,725 were from unique patients. The isolation rate of *Klebsiella* spp. in data reported by the sentinel sites was highest from urine (46%) followed by pus aspirate (30%), blood (18%) and OSBF (6%) (Table 4).

Blood isolates showed more than 50% resistance to all the tested antibiotics except for colistin. Proportion of ESBL producing *Klebsiella* species from blood was higher (84%) than urinary isolates (70%). Majority of carbapenemase producing *Klebsiella* species were isolated from blood (55%-57%) followed by OSBF (46%-48%), pus aspirates (43%) and urine specimens (31% - 32%). Two-third of the urinary isolates tested showed resistance to aminoglycosides (amikacin and gentamycin,40%); whereas more than half of the blood isolates had resistance to aminoglycosides (amikacin;60% and gentamycin; 55%) (Table 9). Approx. 50% of urinary isolates showed resistance to nitrofurantoin.

Resistance to the reserve antibiotic, colistin, was found to be highest in *Klebsiella* spp. compared to other Gram-negative priority pathogens isolated from all the specimen types which is similar to observations in previous year's report. All colistin resistant isolates have been confirmed at the AMR NRL at NCDC.

Location type wise AST data revealed higher resistance to all the tested antibiotics except ertapenem and gentamicin in *Klebsiella* species isolated from blood of ICU patients compared to the *Klebsiella* species isolated from inpatients and outpatients (Fig. 13). Among carbapenems, ertapenem showed highest resistance (71%) followed by meropenem (61%) and imipenem (57%) in blood isolates from ICU patients. Similarly, high resistance was observed to third generation cephalosporins viz. cefotaxime (88%), cefuroxime (87%) and ceftriaxone (86%) among blood isolates from intensive care units. Moreover, more than 60% resistance was observed to the first line antibiotics. (Fig. 13). Fifty-five percent of *Klebsiella* spp. isolated from blood showed resistance to imipenem and 57% were resistant to meropenem (Table 9).

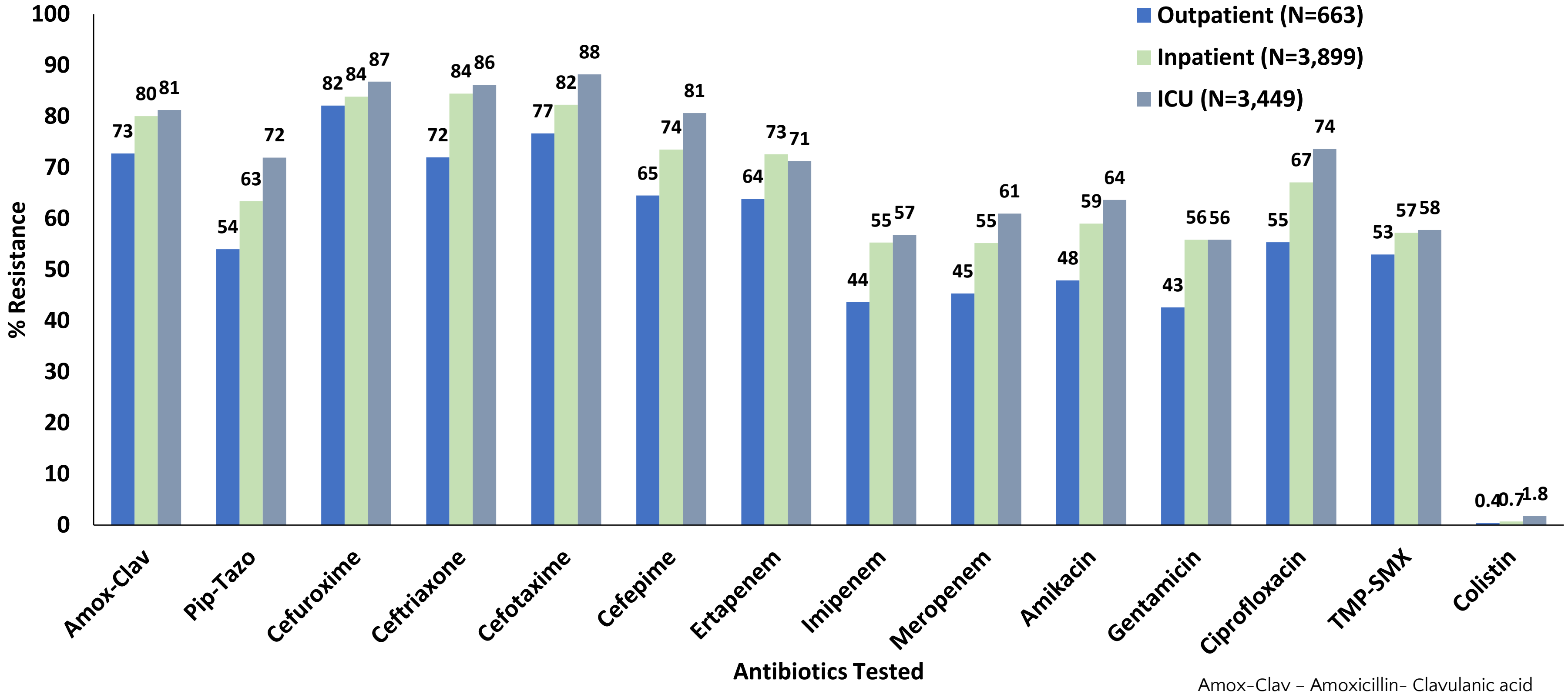
Table 9: Resistance profile of *Klebsiella* species (N=44,725)

	Blood (N=8,012)			PA (N=13,576)			OSBF (N=2,540)			Urine (N=20,597)		
Antibiotic Tested	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**	**Number Tested**	**(%R)**	**95% CI**
Amox-Clav	6020	(80)	79.0-81.0	10480	(72)	71.1-72.8	1924	(72)	69.6-73.7	15375	(64)	63.7-65.2
Pip-Taz	6819	(67)	65.4-67.7	11450	(58)	57.0-58.9	2193	(58)	55.9-60.0	16141	(48)	47.5-49.1
Ceftriaxone	5397	(85)	83.6-85.5	8840	(77)	77.1-78.8	1522	(77)	75.1-79.3	10801	(68)	67.6-69.4
Cefotaxime	4170	(84)	83.3-85.6	9532	(78)	65.3-67.1	1629	(76)	74.3-78.5	15466	(70)	69.5-70.9
Cefepime	5840	(76)	75.0-77.2	10374	(66)	47.6-50.2	1938	(67)	65.2-69.5	13777	(56)	54.7-56.3
Ertapenem	3293	(72)	70.1-73.2	5807	(49)	42.3-44.2	1276	(58)	54.9-60.4	8119	(41)	39.5-41.7
Imipenem	6569	(55)	54.0-56.4	10540	(43)	41.7-43.6	1942	(48)	46.1-50.6	15212	(32)	30.8-32.2
Meropenem	5660	(57)	55.9-58.5	10517	(43)	48.5-50.4	1985	(46)	44.1-48.5	13196	(31)	30.1-31.7
Amikacin	6931	(60)	59.1-61.4	11477	(49)	48.5-50.4	2229	(48)	46.1-50.3	16377	(40)	39.2-40.7
Gentamicin	6227	(55)	53.7-56.2	9904	(49)	69.1-70.9	1891	(50)	47.4-52.0	15092	(40)	39.0-40.5
Ciprofloxacin	6703	(69)	68.1-70.4	11002	(70)	56.4-58.3	2027	(68)	66.1-70.2	17245	(61)	60.6-62.0
TMP-SMX	5983	(57)	55.9-58.4	10657	(57)	0.3-0.6	2020	(57)	54.7-59.1	17110	(52)	51.4-52.9
Colistin	5150	(1.12)	0.9-1.5	7824	(0.40)	33.2-36.2	1574	(1.46)	1.0-2.2	10984	(0.30)	0.2-0.4
Doxycycline	X			3771	(35)	33.2-36.2	790	(38)	34.7-41.6	X		
Nitrofurantoin	X			X			X			18814	(49)	48.7-50.1

*Alert pathogens confirmed at NRL, NCDC only were included in the data

x- Drug bug combination for the specimen type not included in NARS-Net surveillance panel

TMP-SMX – Trimethoprim-Sulfamethoxazole
Amox-Clav -Amoxicillin-Clavulanic acid
Pip-Taz- Piperacillin-Tazobactam



Amox-Clav – Amoxicillin- Clavulanic acid
PipTaz – Piperacillin-Tazobactam
TMP-SMX – Trimethoprim-Sulfamethoxazole

*Data from the emergency department was clubbed with data from inpatient wards; the Location type for 1 isolate is unknown

Figure 13: Resistance profile of *Klebsiella* species isolated from blood (N=8,012) by location type

Salmonella enterica serovar Typhi and Paratyphi

In the current reporting period, data of 975 *Salmonella enterica* serovar Typhi and Paratyphi isolates was submitted to NCDC, of which 962 isolates were from unique patients. Twenty of these isolates were from stool specimens. Data of 834 unique isolates of *S. enterica* Typhi and 108 isolates of *S. enterica* Paratyphi from blood has been analyzed . Among the first line antibiotics, highest resistance was to ciprofloxacin (35%). Low resistance to other first-line antibiotics like ampicillin (5%), chloramphenicol (2%) and trimethoprim-sulfamethoxazole (5.3%) was observed. (Table 10) Ten isolates of *S. enterica* sero. Typhi were found to be resistant to ceftriaxone, two isolates were resistant to azithromycin. Four isolates of ceftriaxone resistant *S. enterica* serovar Paratyphi were observed during 2024. All the ceftriaxone resistant, azithromycin resistant and imipenem resistant *S. Typhi* isolates included in this report were confirmed at the AMR-NRL at NCDC.

Table 10: Resistance profile of *Salmonella enterica* Typhi and Paratyphi (N=942) from blood

Antibiotic tested	***S. Typhi* (N=834)**			***S. Paratyphi* (N=108)**		
	Number tested	**Resistance (%)**	**95% CI**	**Number tested**	**Resistance (%)**	**95% CI**
Ampicillin	713	(5)	4.0-7.5	86	(5)	1.5-12.1
Azithromycin	719	(0.27)	0.1-1.1		x	
Ceftriaxone	795	(1.4)	0.8-2.7	105	(4)	1.8-10.3
Chloramphenicol	707	(2)	1.2-3.6	85	(0)	0-5.4
Ciprofloxacin	807	(35)	32.0-38.7	101	(23)	15.3-32.4
Pefloxacin	539	(84)	80.8-87.1	65	(92)	82.2-97.1
Imipenem	804	(0)	0.0-0.0	103	(0)	0.0-0.0
TMP-SMX	805	(5.3)	3.9-7.2	92	(1.1)	0.1-6.8

*Alert pathogens confirmed at NRL, NCDC were included in the data for analysis; TMP-SMX: Trimethoprim-Sulfamethoxazole

Shigella species

In this reporting period, data of 81 isolates of *Shigella* species was submitted from stool specimens. Resistance in *Shigella* species was found to be highest to ciprofloxacin (85%) and ampicillin (74%) and lowest resistance was observed to chloramphenicol (10%) (Table 11).

Table 11: Resistance profile of *Shigella* species (N=81) from stool specimen

Antibiotics tested	Number tested	Resistance (%)	95% CI
Ampicillin	73	(74)	62.2-83.2
Azithromycin	67	(33)	22.1-45.5
Ceftriaxone	77	(40)	29.4-52.1
Chloramphenicol	70	(10)	4.5-20.1
Ciprofloxacin	78	(85)	74.3-91.5
Trimethoprim/ Sulfamethoxazole	78	(49)	37.3-60.2

1.2.3.2.2. Non-Fermenting Gram-Negative Bacilli

Among the non-fermenting Gram-Negative bacilli (NF GNB) included in the data submitted during January-December 2024 from the NARS-Net sentinel surveillance sites, *Pseudomonas* species was the most frequently isolated pathogen from 21,808 unique patients followed by *Acinetobacter* species (19,122) (Fig 2). Among the NF GNB, *Pseudomonas* species was the predominant isolate from inpatients, while *Acinetobacter* species was the predominant isolate from patients in ICU settings (Table 5).

***Pseudomonas* species**

In the current reporting year, surveillance sites submitted data of 23,255 isolates of *Pseudomonas* spp. from 21,808 unique patients (Fig 2). *Pseudomonas* spp. isolates included in the data during current reporting period were most commonly isolated from pus aspirate (48%), urine (28%), blood (16%), and other sterile body fluids (8%) (Table 4).

Blood isolates of Pseudomonas species showed highest resistance (42%; CI: 39.8-43.4) to third-generation cephalosporin (ceftazidime) followed by ciprofloxacin (29%; CI: 0.1-0.6) and piperacillin-tazobactam (21%; CI: 20-23) among first line treatment agents for *Pseudomonas* species. Similar resistance pattern was seen for pus aspirates and other sterile body fluids. Among second line agents, resistance to imipenem was 36% (CI: 33.7-37.3) and aztreonam was 40% (CI: 37.9-42.2) (Table 12).

Among urinary isolates, 58% *Pseudomonas* spp. isolates were resistant to ciprofloxacin, 41% to amikacin, and 32% to piperacillin-tazobactam. Approximately 40% of urinary isolates were resistant to aztreonam (Table 12).

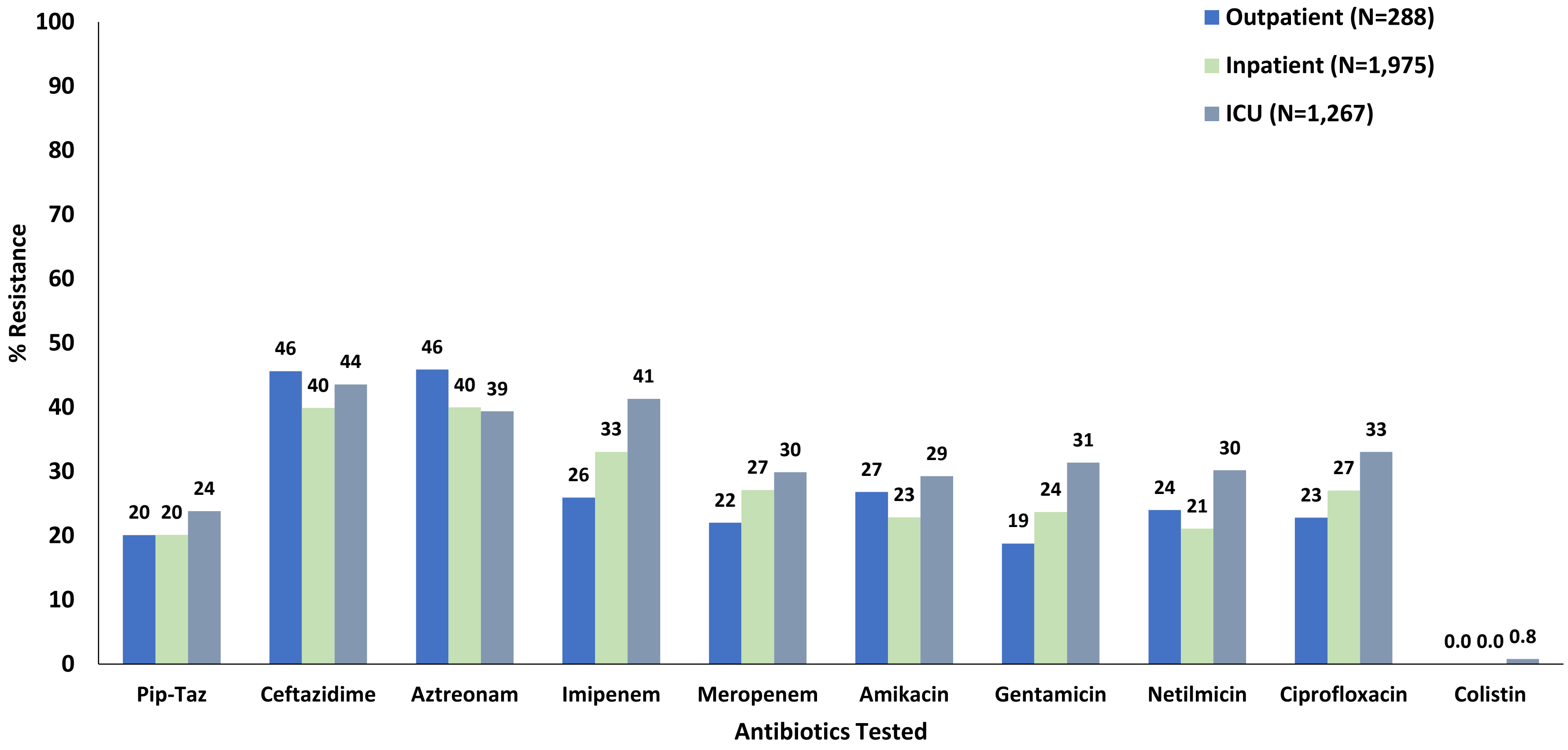
Among the reserve group of antibiotics namely colistin, five blood isolates (0.26%), two from pus aspirate (0.038%), and four from urine (0.13%) were found to be resistant (Table 12).

Isolates of *Pseudomonas* spp. from blood cultures of patients in Intensive care units, Inpatient and outpatient departments showed highest resistance to ceftazidime and aztreonam among the tested antibiotics (Fig.14). Among blood isolates from ICU patients, least resistance was observed to piperacillin-tazobactam (24%) followed by amikacin (29%) and meropenem (30%) (Fig. 14).

Table 12: Resistance profile of *Pseudomonas* species (N=21,808)

Antibiotic Tested	Blood (N=3,530)			Pus Aspirate (N=10,513)			OSBF (N=1,695)			Urine (N=6,070)		
	Number Tested	(%R)	95 % CI	Number Tested	(%R)	95 % CI	Number Tested	(%R)	95 % CI	Number Tested	(%R)	95 % CI
Amikacin	2760	(25)	23.9-27.1	7980	(32)	31.4-33.5	1376	(27)	25.0-29.8	5184	(41)	40.1-42.8
Aztreonam	2036	(40)	37.9-42.2	6795	(29)	28.0-30.1	1132	(34)	31.4-37.0	3947	(38)	36.3-39.3
Ceftazidime	2884	(42)	39.8-43.4	9062	(47)	45.9-48.0	1577	(45)	42.1-47.1	5304	(55)	53.5-56.2
Ciprofloxacin	2800	(29)	27.3-30.7	8604	(44)	43.0-45.1	1466	(33)	30.6-35.4	4945	(58)	56.2-59.0
Colistin	1958	(0.26)	0.1-0.6	5284	(0.038)	0-0.2	863	(0.0)	0.0-0.6	3149	(0.13)	0-0.3
Gentamicin	1958	(26)	24.1-28.0	5712	(35)	33.8-36.3	891	(22)	19.0-24.5	3411	(41)	39.3-42.6
Imipenem	2707	(36)	33.7-37.3	8574	(29)	27.7-29.7	1409	(33)	30.8-35.8	4949	(41)	39.2-42.0
Meropenem	2503	(28)	26.0-29.5	8368	(25)	24.2-26.1	1272	(28)	25.2-30.2	3939	(38)	36.8-39.9
Netilmicin	1382	(24)	22.0-26.6	4048	(34)	32.1-35.0	728	(23)	20.2-26.5	3057	(45)	42.8-46.3
Piperacillin/ Tazobactam	2985	(21)	20.0-23.0	9116	(27)	25.7-27.5	1506	(22)	20.2-24.4	5068	(32)	31.1-33.7

*Alert pathogens confirmed at NRL, NCDC only were included in the data



PipTaz – Piperacillin-Tazobactam

*Data from the emergency department was clubbed with data from inpatient wards

Figure 14: Resistance profile of *Pseudomonas* species isolated from blood (N=3,530) by location type

Acinetobacter spp.

Data of a total of 20,276 *Acinetobacter* species isolates was submitted by network sites during this reporting period of Jan – Dec 2024, of which 19,122 were from unique patients. Among all specimen types under the programme, *Acinetobacter* species was most commonly isolated from blood (39%) followed by pus aspirate (30%), urine (18%) and other sterile body fluids (12%). (Table 4)

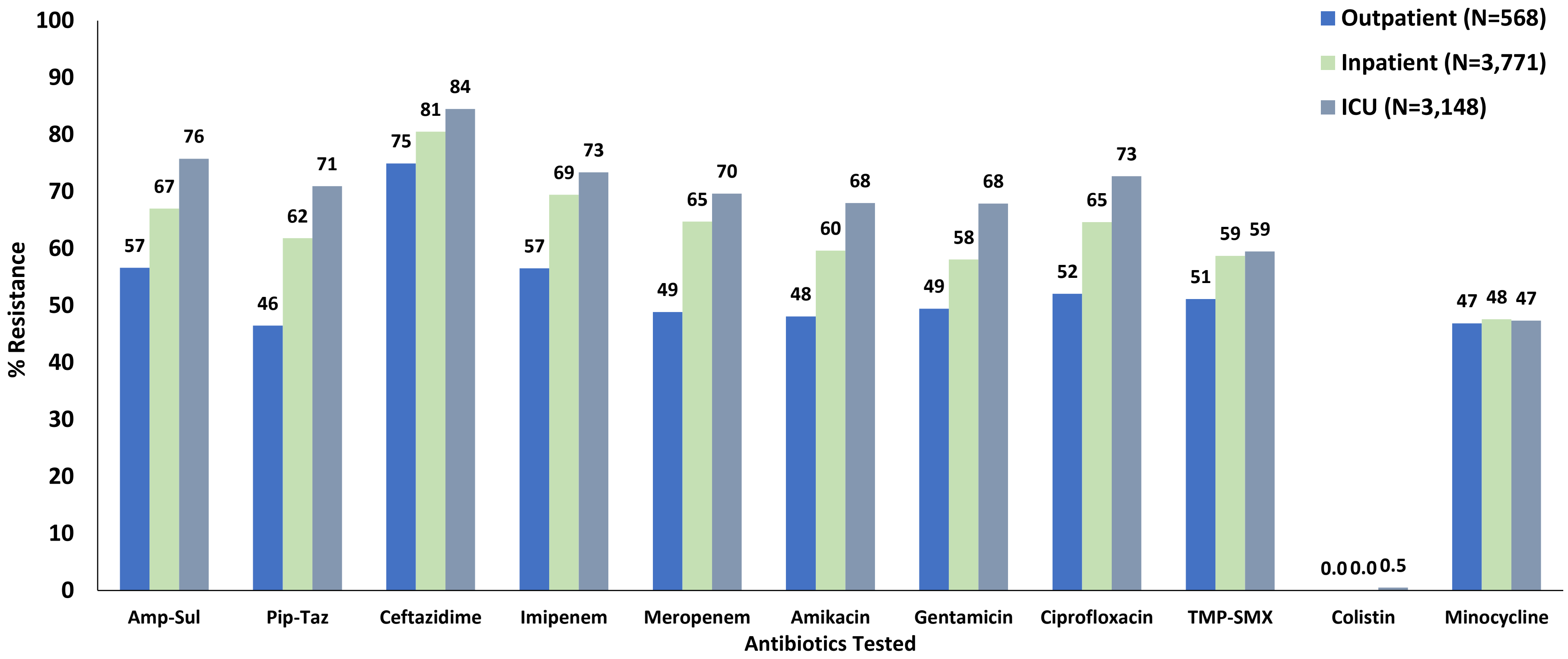
High level of resistance was observed to all the tested antibiotics including Minocycline in isolates from blood, pus samples and other sterile body fluids. (Fig. 15) Blood isolates showed the highest resistance to ceftazidime (82%; CI: 80.8- 82.8) followed by ampicillin-sulbactam (71%; CI: 68.7-72.3). Alarmingly high level of resistance to second line antimicrobial agents viz. imipenem (70%) and meropenem (66%) was observed among blood isolates. (Table 13) Sixty-nine percent of isolates from pus samples and 68% from other sterile body fluids were resistant to imipenem. Ten isolates from blood, one from OSBF, 4 each from pus aspirates and urine were resistant to colistin. (Table 13)

Table 13: Resistance profile of *Acinetobacter* species (N=19,122)

	Blood (N=7,487)			OSBF (N=2,371)			PA (N=5,801)			Urine (N=3,463)		
Antibiotic Tested	Number Tested	(%R)	95% CI	Number Tested	(%R)	95% CI	Number Tested	(%R)	95% CI	Number Tested	(%R)	95% CI
Amp-Sul	2614	(71)	68.7-72.3	1086	(64)	61.0-66.8	2825	(74)	72.7-76.0	1327	(59)	56.6-62.0
Pip-Taz	6144	(65)	63.5-65.9	1986	(61)	58.5-62.8	4730	(68)	66.7-69.4	2634	(44)	42.0-45.8
Ceftazidime	5524	(82)	80.8-82.8	1809	(76)	73.5-77.5	4021	(82)	80.4-82.8	2367	(65)	63.1-67.0
Imipenem	6179	(70)	69.1-71.4	1659	(68)	65.6-70.1	4446	(69)	67.8-70.6	2624	(44)	42.0-45.8
Meropenem	4935	(66)	64.8-67.4	1678	(64)	61.3-66.0	4383	(66)	64.9-67.7	2148	(39)	36.9-41.1
Amikacin	6258	(62)	61.2-63.6	2072	(58)	56.2-60.5	4695	(68)	67.1-69.8	2680	(46)	43.7-47.5
Gentamicin	5750	(62)	60.5-63.0	1865	(58)	55.4-59.9	4094	(68)	66.1-69.0	2349	(44)	41.6-45.7
Ciprofloxacin	6188	(67)	66.0-68.3	1757	(67)	64.7-69.1	4590	(77)	75.9-78.4	2748	(54)	51.9-55.6
TMP-SMX	5137	(59)	57.2-59.9	1765	(59)	56.7-61.3	3987	(68)	66.6-69.5	2732	(48)	46.0-49.7
Colistin	4386	(0.23)	0.1-0.4	1425	(0.07)	0-0.5	3004	(0.13)	0-0.4	1454	(0.28)	0.1-0.8
Minocycline	4776	(47)	46.0-48.9	1580	(43)	40.2-45.1	2985	(47)	44.7-48.3	2044	(45)	43.0-47.3
Tetracycline	X			x			x			1370	(50)	47.2-52.5

*Alert pathogens confirmed at NRL, NCDC only were included in the data

TMP-SMX: Trimethoprim-Sulfamethoxazole
Amp-Sul: Ampicillin-Sulbactam
Pip-Taz: Piperacillin-Tazobactam



**Data from the emergency department was clubbed with data from inpatient wards*

TMP-SMX: Trimethoprim-Sulfamethoxazole
Pip-Taz: Piperacillin-Tazobactam

Figure 15: Resistance profile of *Acinetobacter* species isolated from blood (N=7,487) by location type

1.2.3.2.3. Vibrionaceae

Vibrio cholerae

In the current reporting period (Jan – Dec 2024), data of 240 isolates of *Vibrio cholerae* confirmed at AMR-NRL has been analyzed. The highest resistance was observed to trimethoprim/sulfamethoxazole (73%)and lowest resistance to chloramphenicol (0.95). (Table 14)

Table 14: Resistance profile of *Vibrio cholerae* (N=240)

Antibiotic Tested	Number Tested	Resistant (%)	95% CI
Ampicillin	237	(21)	16.2-27.0
Trimethoprim/ Sulfamethoxazole	229	(73)	66.6-78.5
Azithromycin	221	(3)	1.4-6.7
Chloramphenicol	229	(0.9)	0.2-3.5
Doxycycline	210	(3)	1.5-7.0
Tetracycline	235	(2)	0.8-5.2

1.2.4.AMR Trends

AMR Surveillance Data from NARSNET sites has been analyzed over last 7 years from 2017 to 2024. During 2020 data reported was small in volume due to the COVID pandemic. Trend analysis of MRSA isolated from blood showed slight decrease in MRSA proportion from 59% (2021) to 56% (2024). (Fig. 16) This decrease in proportion of MRSA may be attributed to the increase in data submitted by the network sites. Trend analysis of VRE isolated from blood showed continuous increase from 2021 (11%) to 2024 (22%). (Fig. 18) Trend analysis for ESBL producing *E. coli* from blood showed an increase over the last 4 years from 2021 (76%) to 2024 (81%). (Fig. 19) Similar trend was observed in blood isolates of ESBL producing *Klebsiella* spp. which have shown consistently high level of resistance from 81% in 2021 to 84% in 2024. (Fig. 19) Moreover, 3-year trend analysis of carbapenemase producing *E. coli*, *Klebsiella* species and *Acinetobacter* species has shown consistent increase. (Fig 21,22)

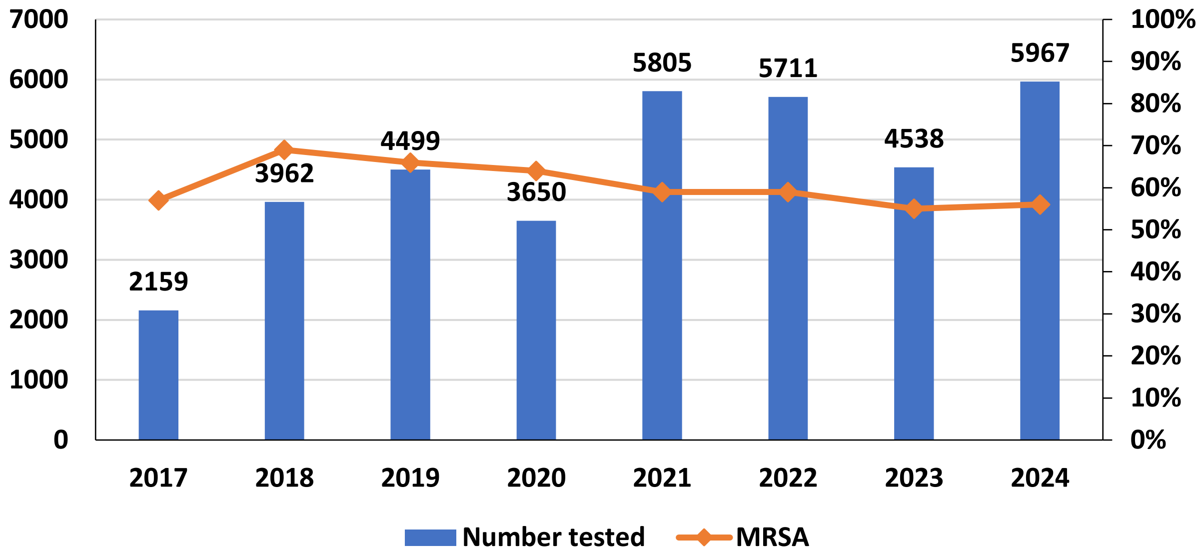
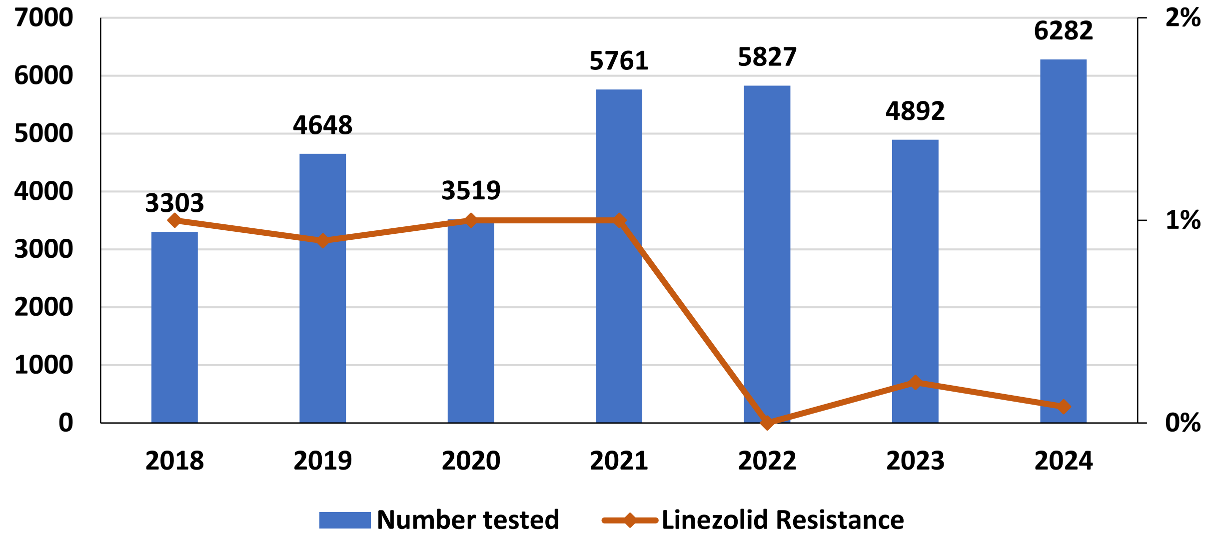
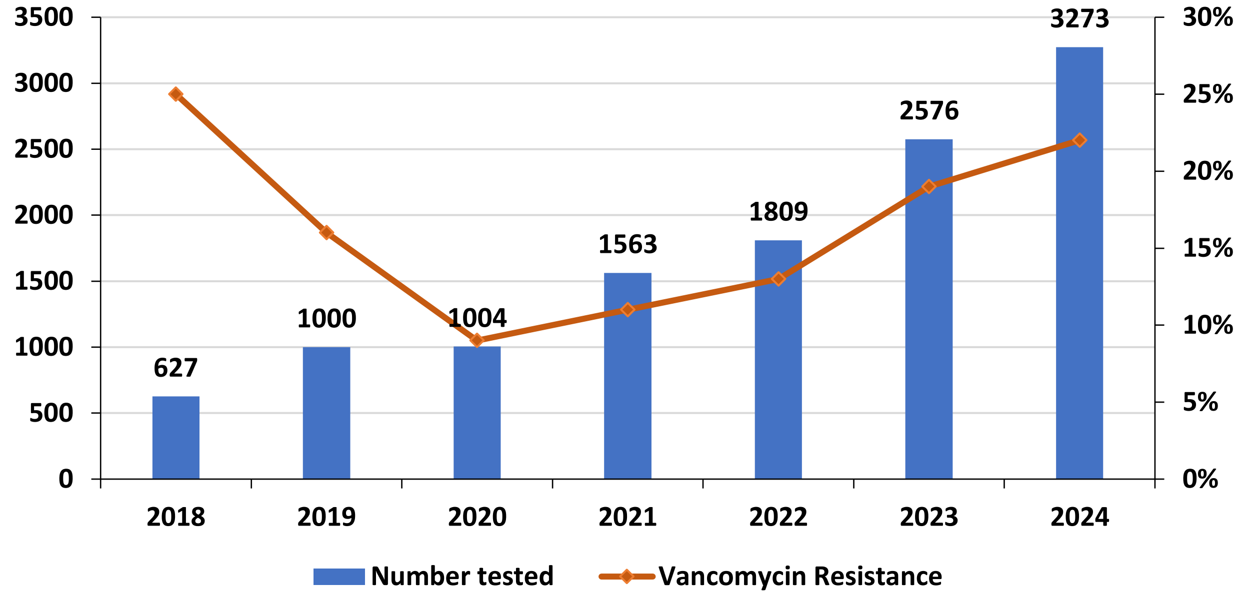


Figure 16: Trends of Methicillin-resistant *S. aureus* (MRSA) isolated from blood (2017-2024)



**Alert pathogens confirmed at NRL, NCDC only were included in the data; CLSI breakpoint for 2023-24 were considered for analysis of linezolid resistance in S.aureus*

Figure 17: Trends of Linezolid resistant *Staphylococcus aureus* isolated from blood (2018 to 2024)



*Alert pathogens confirmed at NRL, NCDC only were included in the data

Figure 18: Trends of Vancomycin resistant *Enterococcus* sp. (VRE) isolated from blood (2018-2024)

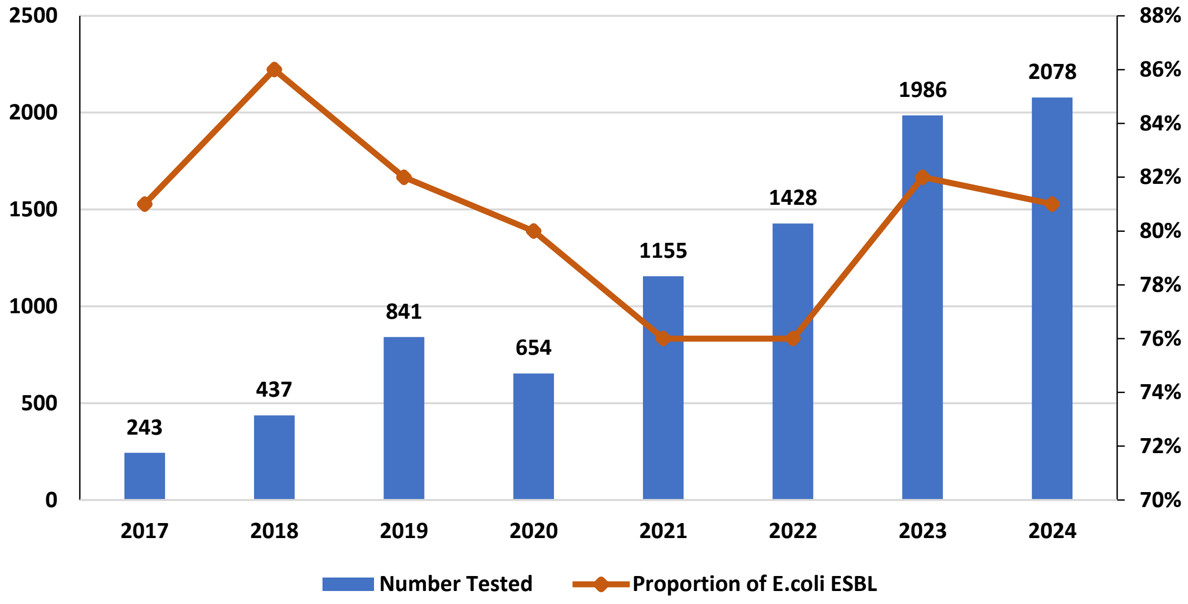


Figure 19: Trends of Extended spectrum beta-lactamase (ESBL) producing E. coli isolated from blood (2017-2024)

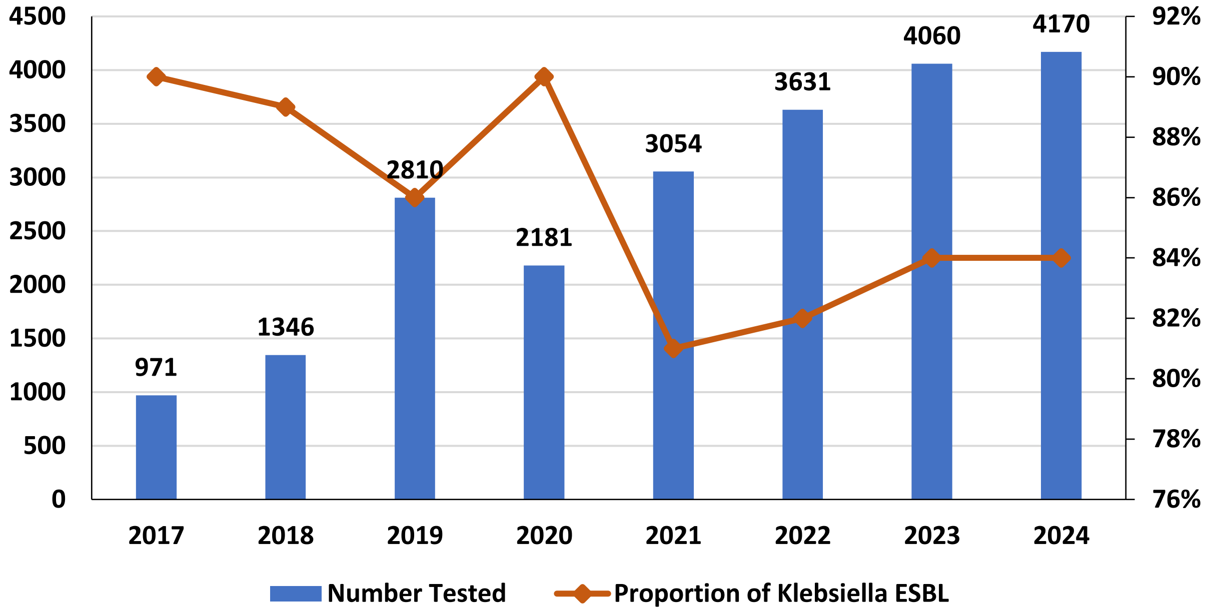


Figure 20: Trends of Extended-Spectrum Beta-Lactamase (ESBL) producing *Klebsiella* sp. in blood (2017-2024)

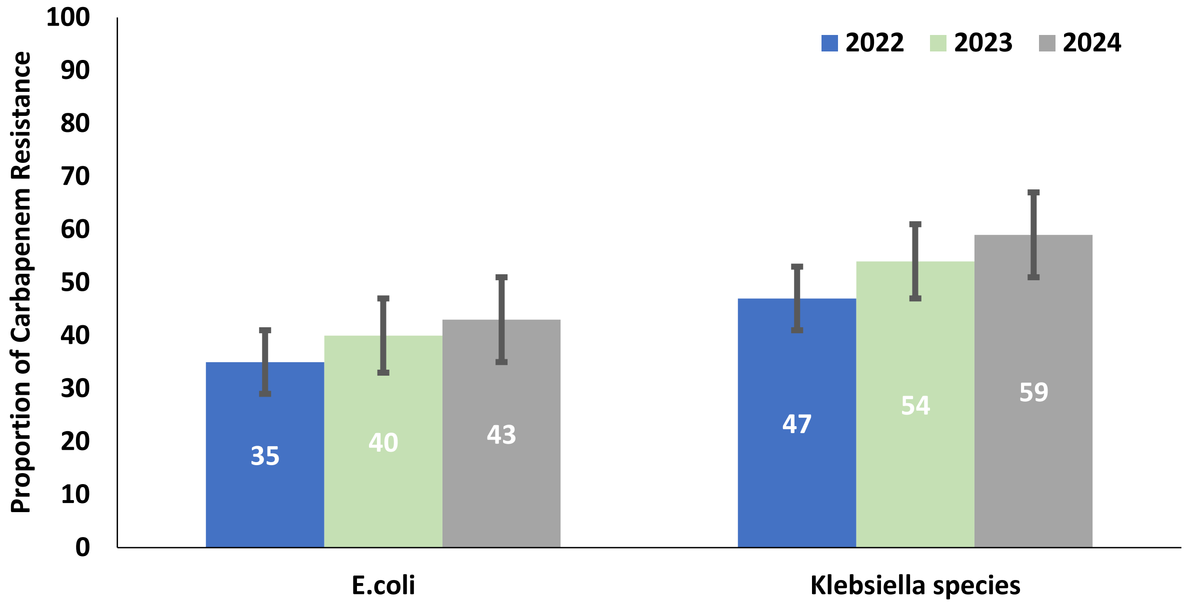


Figure 21: Three-year trend analysis (2022-2024) of Carbapenemase producing *E. coli* and *Klebsiella* species isolated from blood

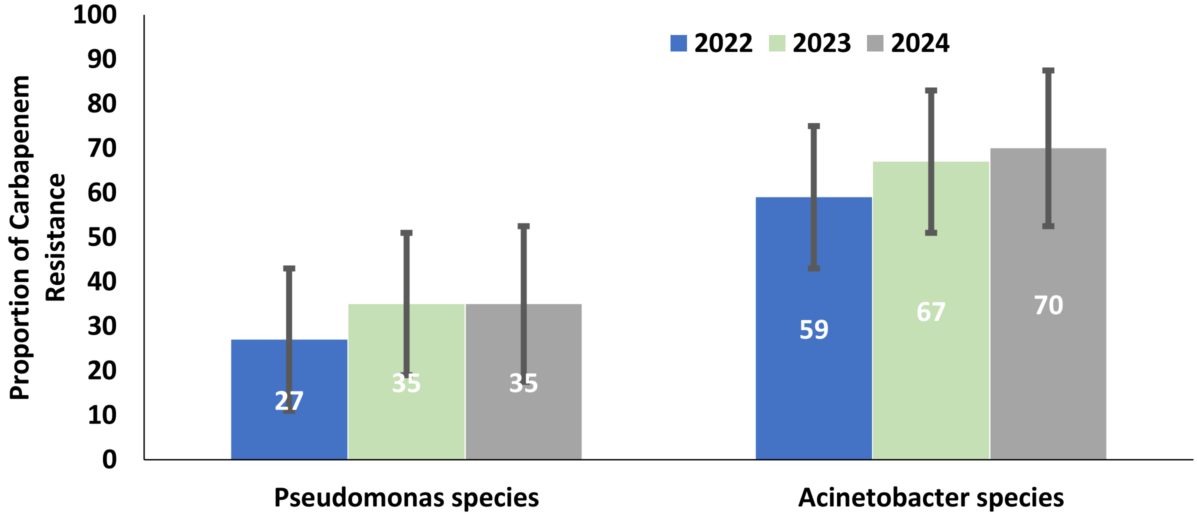


Figure 22: Three-year trend analysis (2022-2024) of Carbapenemase producing *Pseudomonas* species and *Acinetobacter* species isolated from blood

2. AMR Surveillance in Fungal pathogens

2.1. Background of National Reference Laboratory for AMR in fungal pathogens.

Under the National Programme on AMR Containment, the National Reference Laboratory (NRL) for antimicrobial resistance (AMR) in fungal pathogens has been established at Vallabhbhai Patel Chest Institute (VPCI), New Delhi.

2.2. AMR surveillance of *Candida* species from bloodstream infections

The National Reference Laboratory at VPCI during January 2024-December 2024 received a total of 1074 *Candida* strains from blood stream infections from 28 NARS-Net laboratories (Annexure-1) for phenotypic and molecular characterization and generating the antifungal susceptibility profile under "National Programme on AMR Containment".

2.2.1. Methodology:

a) Phenotypic characterization of *Candida* isolates: All the stains received at NRL were first screened on differential selective media CHROMagar *Candida* Medium.

b) Molecular characterization: All strains were identified by Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF**)** and by sequencing of internal transcribed spacer region (ITS) of ribosomal deoxyribonucleic acid (DNA) and of the D1/D2 domain of the large subunit ribosomal DNA in case a low or no identification was obtained by MALDI.

c) Antifungal susceptibility testing (AFST): AFST was performed using the Clinical and Laboratory Standards Institute (CLSI) broth microdilution method (BMD), following M27-A3/S4.31,32.[6] The antifungals tested were amphotericin B, itraconazole, voriconazole, posaconazole, 5-flucytosine, caspofungin, micafungin and anidulafungin. All antifungals were dissolved in Dimethyl sulfoxide (DMSO). Roswell Park Memorial Institute medium (RPMI) 1640 medium with glutamine without bicarbonate buffered to pH 7 with 0.165 M 3-(N-morpholino) propane sulfonic acid (MOPS) was used. Drug- and yeast-free controls were included, and microtitre plates were incubated at 35°C and read visually after 24 h. CLSI-recommended *Candida krusei* ATCC 6258 and *Candida parapsilosis* ATCC 22019 were used as quality control strains. The minimum inhibitory concentration (MIC) endpoints for all the drugs except amphotericin B were defined as the lowest drug concentration that caused a prominent

---

[6] Clinical Laboratory Standard Institute (CLSI). 2008. M27-A3. Reference method for broth dilution antifungal susceptibility testing of yeasts. 3rd ed. CLSI, Wayne, PA.

decrease in growth (50%) in relation to the controls and for amphotericin B, the MIC was defined as the lowest concentration at which there was 100% inhibition of growth compared with the drug-free control wells.

2.3. Significant Findings

The NRL for AMR in fungal pathogens was operational since January 2022. Over the years the number of isolates received at the NRL have increased due to more number of NARS-Net sites submitting the isolates. Total of 1074 Candida isolates from blood cultures were received during 2024 (Fig 23).

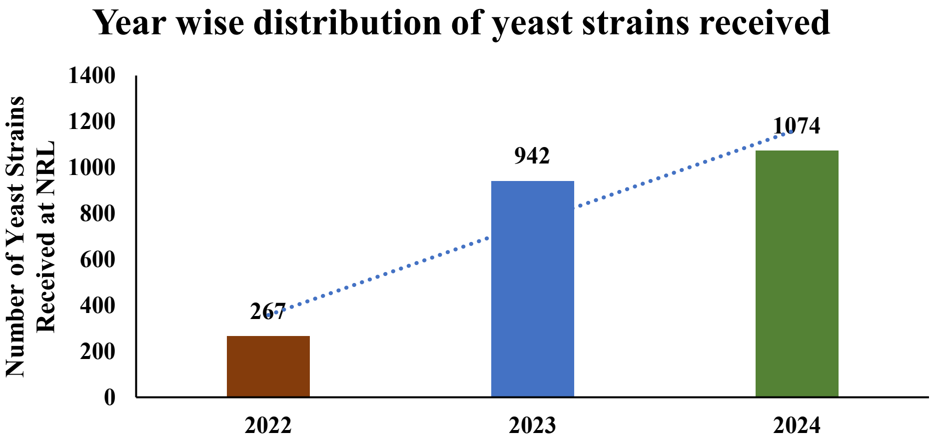


Figure 23: Data represent annual totals of clinical isolates submitted at Fungal NRL for identification and AFST. Error bars indicate standard deviations from monthly averages

2.3.1. Details of yeast isolates characterized at NRL during 2024:

Most common *Candida* species isolated from bloodstream infection was *Candida tropicalis* (34%) followed by *Pichia kudriavzevii* (14%), *Candida albicans* (9%), *Candida parapsilosis* (8%), *Candida auris* (8%) and *Cyberlindnera jadanii* (7%) (Fig 24). Non-albicans *Candida* (NAC) species dominate the distribution, highlighting the epidemiological shift from *C. albicans* (Table 15).

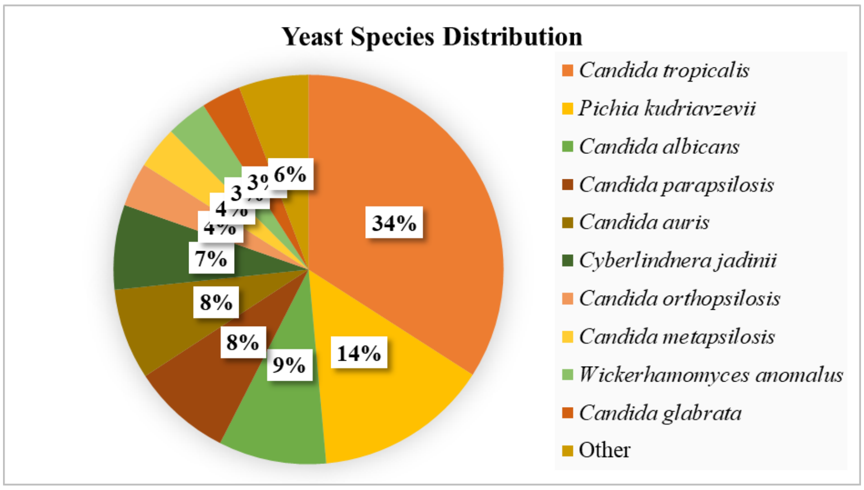


Figure 24: The pie chart illustrating the percentage distribution of various yeast species identified by MALDI-TOF MS and ITS sequencing at NRL, VPCI

Table 15: Distribution of other 6% yeast species characterized at NRL

Other Yeast Species Identified	Number of Isolates
Pichia ohmeri	12
Clavispora lusitaniae	10
Cyberlindnera fabianii	5
Cryptococcus gattii	4
Meyerozyma guilliermondii	4
Kluyveromyces marxianus	3
Candida viswanathii	2
Candida haemulonii	1
Diutina rugosa	1
Trichosporon asahii	1
Trichosporon mucoides	1
Yarrowia lipolytica	1

2.3.2. Age and Gender distribution of isolates:

Out of all the patients from whom yeast strains were isolated**,** 59% were male and 41% were female**.** Neonates and infants (<1 year) accounted for the majority of isolates (54%) (Fig 25). The remaining age groups each contribute 4–6% of total isolates.

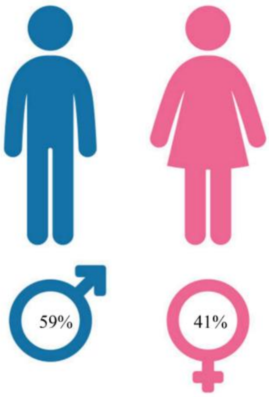


Figure 25: Gender-wise distribution of patients from whom yeast isolates (n=1074) were obtained

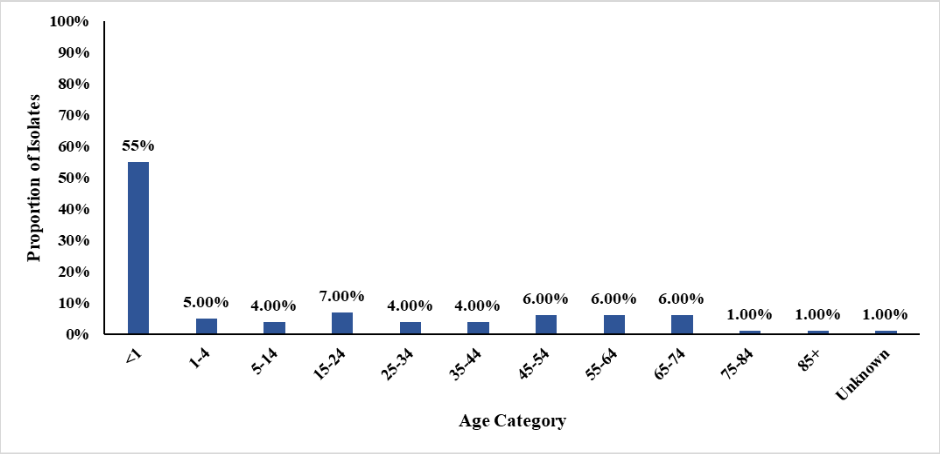


Figure 26: Age distribution of patients from whom yeast isolates were recovered

2.3.3. Location wise distribution of isolates:

The distribution of fungal isolates across healthcare settings showed distinct patterns among different yeast species (Table 16). Majority of the candidemia cases were from the neonatal intensive care unit (NICU) (29%) and 7% were from the pediatric intensive care unit (PICU). *Candida tropicalis* and *P. kudriavzevii* were the most commonly isolated species, with *C. tropicalis* being particularly prevalent in intensive care unit (ICU; 55%) and inpatient departments (27%) settings, while *P. kudriavzevii* was most common in ICUs (71%), indicating its growing clinical importance in critical care (Table 16). *C. auris*, a known multidrug-resistant species, was primarily found in ICU (60%) and inpatient wards (18%). *Candida albicans* showed a strong presence in ICU (45%) and was also isolated notably from inpatients (35%). Other species like *C. parapsilosis* and *C. glabrata* were also found mainly in ICU. Interestingly, less common species like *Cyberlindnera jadinii* and *Wickerhamomyces anomalus* were predominantly isolated from patients in ICUs. Overall, the ICUs accounted for the highest proportion of isolates for most species, highlighting critical care units as a major hub for opportunistic fungal infections (Table 16).

Table 16: Distribution of different yeast species by location type

Species (n=number of isolates)	Intensive Care Unit n (%)	Emergency n (%)	Inpatient - Medical & Pediatrics n (%)	Outpatient n (%)
***Candida tropicalis* (n=271)**	148 (55%)	32 (12%)	75 (27%)	16 (6%)
***Pichia kudriavzevii* (n=115)**	81 (71%)	5 (4%)	29 (25%)	–
***Candida albicans* (n=71)**	32 (45%)	12 (17%)	25 (35%)	2 (3%)
***Candida parapsilosis* (n=66)**	31 (47%)	13 (20%)	19 (28%)	3 (5%)
***Candida auris* (n=60)**	36 (60%)	10 (16%)	11 (18%)	3 (5%)
***Cyberlindnera jadinii* (n=56)**	44 (78%)	1 (2%)	10 (18%)	1 (2%)
***Wickerhamomyces anomalus* (n=27)**	10 (37%)	3 (11%)	13 (48%)	1 (4%)
***Candida glabrata* (n=26)**	15 (58%)	8 (31%)	–	3 (11%)
Others (n=382)	225 (60%)	30 (7%)	112 (29%)	15 (4%)
Total (n=1074)	622 (58%)	114 (11%)	294 (27%)	44 (4%)

Distribution of isolates across different ICU types:

Analysis of distribution of yeast isolates across ICU types highlights *C. tropicalis* as the most widespread species, with notable presence in NICU (41%), MICU (29%) followed by PICU (22%). *Pichia kudriavzevii* was predominantly isolated from NICU (81%%) and PICU (17%), suggesting its strong association with neonatal care units. *Cyberlindnera jadinii* and *W. anomalus* were strikingly predominant in NICU i.e., 95% and 90% respectively (Table 17).

Table 17: Distribution of different *Candida* species in different types of Intensive Care Units (ICUs)

Type of ICU*	NICU (n)	PICU (n)	MICU (n)	SICU (n)	TICU (n)
***Candida tropicalis* (n=148)**	61	32	43	7	5
***Pichia kudriavzevii* (n=81)**	66	14	1	-	-
***Candida albicans* (n=32)**	11	4	7	7	3
***Candida parapsilosis* (n=31)**	10	7	11	2	1
***Candida auris* (n=36)**	2	2	16	14	2
***Cyberlindnera jadinii* (n=44)**	42	2	-	-	-
***Wickerhamomyces anomalus* (n=10)**	9	1	-	-	-
***Candida glabrata* (n=15)**	2	4	4	4	1

*NICU, Neonatal Intensive Care Unit; PICU, Pediatric Intensive Care Unit; MICU, Medical Intensive Care Unit; SICU, Surgical Intensive Care Unit; TICU, Trauma Intensive Care Unit

2.3.4. Antifungal Susceptibility testing

Candida tropicalis:

The resistance pattern of 271 *C. tropicalis* to nine antifungal agents was assessed and is presented in the Figure 5. Among the antifungals tested, fluconazole exhibited the highest resistance (approx. 7% had MIC of ≥8 mg/L)**,** followed by voriconazole with a resistance of about 5% (MIC, ≥1 mg/L). Moreover, 2.5% of the fluconazole resistant isolates were cross-resistant to voriconazole. A low level of resistance was observed for micafungin (0.7%; MIC, ≥1 mg/L), and anidulafungin (0.3%; MIC, ≥1 mg/L). Other antifungals like amphotericin B, 5-flucytosine, itraconazole, and posaconazole demonstrated good activity against all *C. tropicalis* isolates (Fig 27).

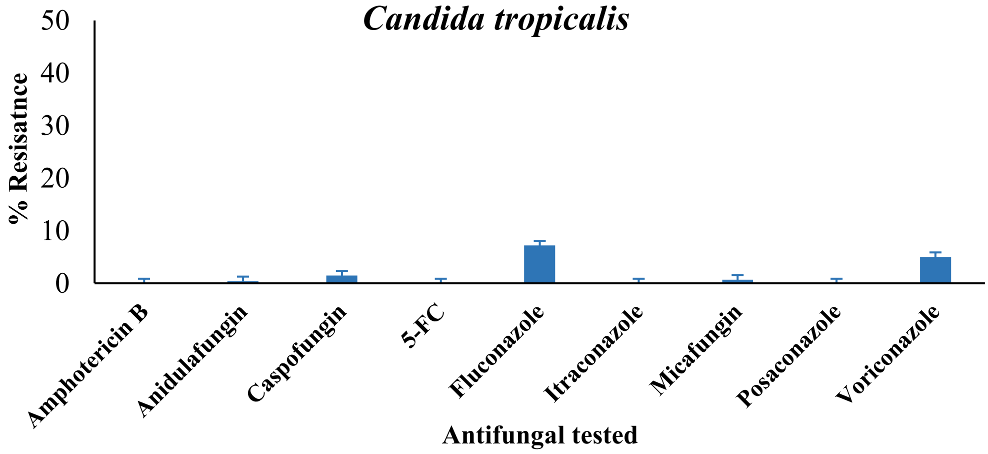


Figure 27: Resistance profile of *Candida tropicalis* isolates against nine antifungals, with error bars indicating standard deviation

Pichia kudriavzevii:

The antifungal susceptibility pattern of *P. kudriavzevii* (n=115) reveals a low resistance to anidulafungin and micafungin, with resistance of approximately 2%. *P. kudriavzevii* is intrinsically resistant to fluconazole. All other antifungal agents, including amphotericin B, 5-fluorocytosine, itraconazole, posaconazole, and voriconazole showed negligible or no resistance.

Candida albicans:

The resistance analysis of *C. albicans* (n=71) shows notable resistance to fluconazole (8%; MIC, ≥8 mg/L). A low rate of resistance (2%) was observed for micafungin (MIC, ≥1 mg/L), while all other antifungal agents including amphotericin B, anidulafungin, 5-fluorocytosine, itraconazole, posaconazole, and voriconazole exhibited good activity against all *C. albicans* isolates (Fig 28).

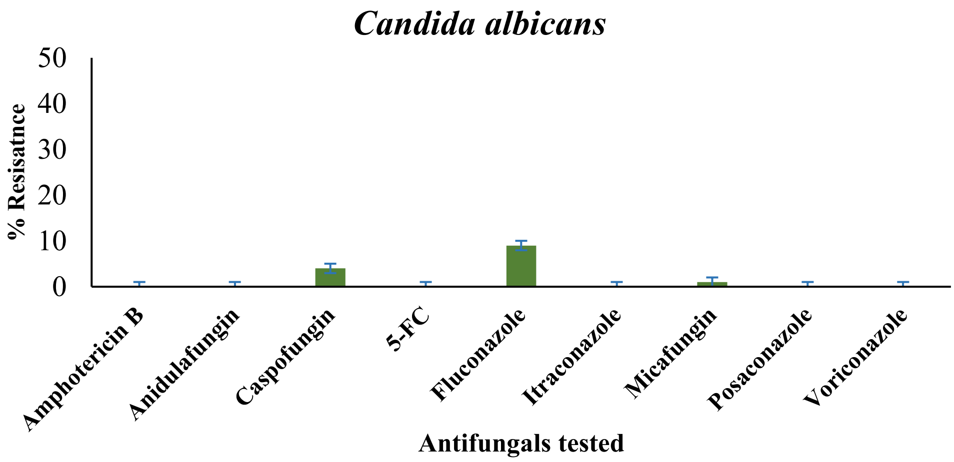


Figure 28: Resistance profile of *Candida albicans* isolates against nine antifungals, with error bars indicating standard deviation

Candida parapsilosis:

The antifungal susceptibility analysis of *C. parapsilosis* (n=66) revealed high resistance to fluconazole (MIC, ≥8 mg/L)**,** approximately 16%**,** highest among all antifungals tested for this species (Figure 29). Further, resistance was also observed for anidulafungin (3%; MIC, ≥8 mg/L)**,** and voriconazole (3%; MIC, ≥1 mg/L). Whereas, no significant resistance was detected against amphotericin B**,** 5-fluorocytosine**,** itraconazole**,** micafungin**,** or posaconazole**.**

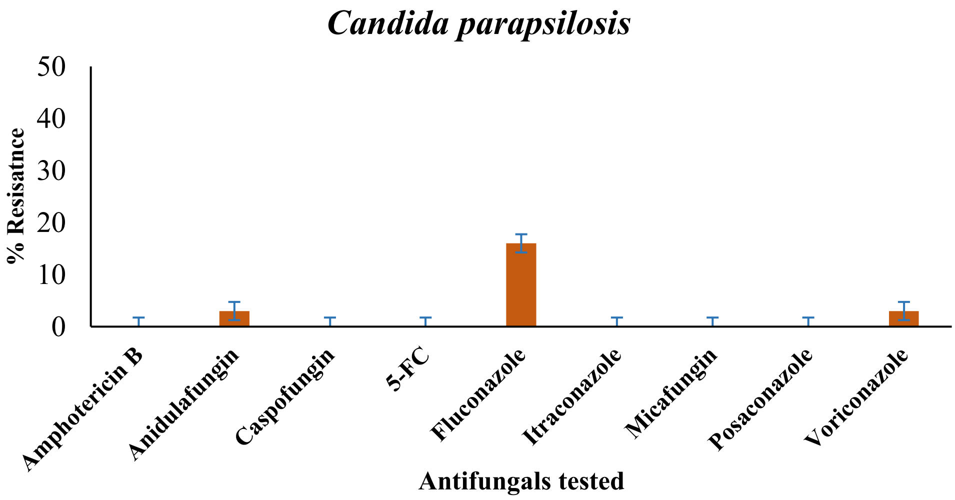


Figure 29: Resistance profile of *Candida parapsilosis* isolates against nine antifungals, with error bars indicating standard deviation

Candida auris:

There are currently no established *C. auris*-specific susceptibility breakpoints in CLSI-guidelines. Therefore, tentative breakpoints for *C. auris* were used against different antifungals as recommended by CDC 2024[7]. The antifungal susceptibility analysis of *C. auris*

---

[7] CDC, 2024. Antifungal Susceptibility Testing for C. auris. US https://www.cdc.gov/candida-auris/hcp/laboratories/antifungal-susceptibility-testing.html.

(n=60) showed that 66% of the isolates were resistant to fluconazole (MIC, ≥32mg/L). Notably, a small ratio of the isolates (6.7%) showed high MIC value for amphotericin B (MIC, 4 mg/L) (Fig 30).

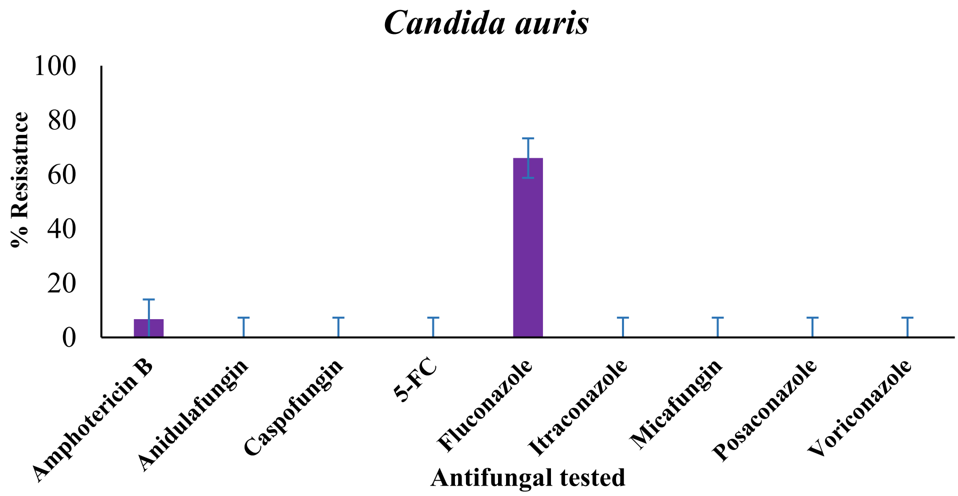


Figure 30: Resistance profile of *Candida auris* isolates against nine antifungals, with error bars indicating standard deviation

Wickerhamomyces anomalus:

Breakpoints for antifungal susceptibility testing of *W. anomalus* are not available, however epidemiological cut-off values (ECV) are given in CLSI M57SEd.4[8] which were used to categorise the isolates into wild type and non-wild type. All strains (n=27) exhibited low MICs for all the tested antifungals except fluconazole (Fig 31). Out of 27, 4 isolates (15%) were non-wild type as they exhibited MIC value of >8 mg/L for fluconazole.

---

[8] CLSI . 2022. M57SEd.4. Epidemiological cutoff values for antifungal susceptibility testing. CLSI, Wayne, PA.

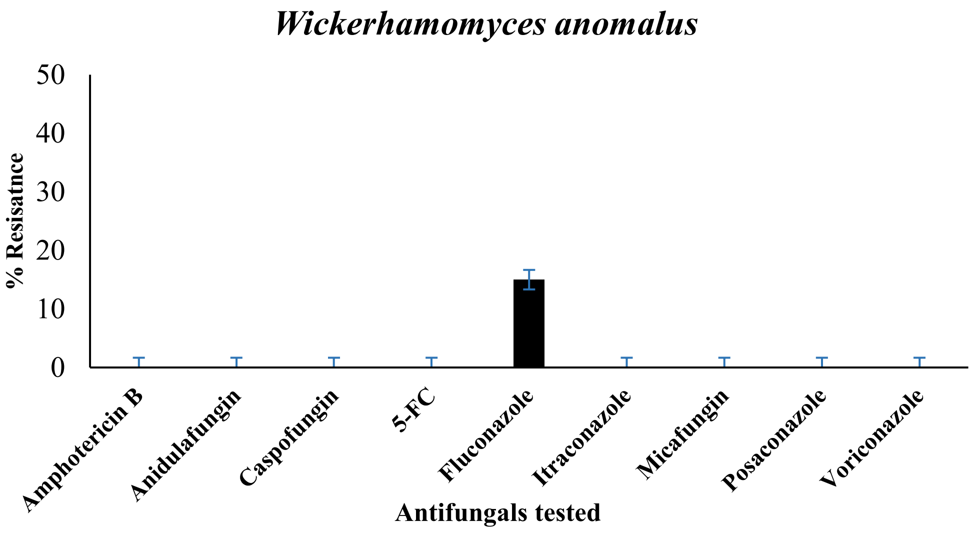


Figure 31: Resistance profile of *Wickerhamomyces anomalus* isolates against nine antifungals, with error bars indicating standard deviation

3. Discussion

This report is the eighth annual report of the National AMR Surveillance Network (NARS-Net). This report includes 2,06,745 isolates AST data submitted by 54 sites. Like the previous year's findings, one-third of the pathogens in the AMR Surveillance data for 2024 were *Escherichia coli* (33%). Amongst the urinary isolates, *E. coli* (51%) was the most commonly isolated priority pathogen, and urine was the most common specimen type (45%). As consistent with previous reports, *S. aureus* was most commonly isolated from pus aspirates (66%). *Klebsiella* species was most commonly isolated pathogen from urine (46%) and pus samples (30%).

Quality of AMR surveillance data submitted by the NARSNET sites has been ensured by continuous hands-on laboratory and data management trainings, site support visits, monthly data quality monitoring and feedback calls, and annual review meetings. EQAS program and confirmation of Alert isolates at AMR-NRL, CBDDR, NCDC also played an essential role in improving data quality of NARS-Net sites. Moreover, many of the sites are strictly performing internal quality control of media, antibiotic discs as per recommendations under the programme.

Compared to the previous year, the number of sites submitting data has increased from 41 to 54 sites situated in 33 states/UTs. Quality of colistin susceptibility testing has improved over the years, as 44 of 54 sentinel sites have standardized and started performing colistin agar dilution and colistin broth microdilution (BMD) tests. The wet lab trainings on broth microdilution for the remaining 10 labs has been done by AMR-NRL at NCDC.

The AMR surveillance data in the current report like previous years continues to have the limitation of samples for culture and sensitivity being referred only for patients requiring admission and often not responding to the first line of antibiotics. This limitation has the potential to skew the AMR trends to higher side than the actual trends.

Trend analysis for ESBL producing *E. coli* from blood showed an increase (2024; 81%) over the last 3 years (2021; 76%) (Fig. 21). This may be attributed to higher usage of third generation cephalosporins for all the Gram-negative priority surveillance pathogens. High percentage of resistance to third-generation cephalosporins and carbapenems in *E. coli* and *Klebsiella* species and *Acinetobacter* species in India is a matter of concern. These findings highlight serious challenges in treatment options for patients with infections caused by these priority bacterial pathogens.

There has been a gradual increase in the proportion of Vancomycin-resistant Enterococcus (VRE) from blood specimens (from 11% in 2021 to 21% in 2024). (Fig. 18) Linezolid resistance (1%) in blood isolates of *Enterococcus* species is almost similar to that reported last year. No Vancomycin-intermediate *Staphylococcus aureus* (VISA) or Vancomycin-resistant *Staphylococcus aureus* (VRSA) has been reported over last 8 years. Trend analysis of MRSA isolated from blood over the past 5 years showed a slight decrease from 59% (2021) to 56% (2024). (Fig 16). Among MRSA from blood specimens, highest resistance was observed to erythromycin (77%) followed by ciprofloxacin (67%) and clindamycin (53%).

A major observation of AMR surveillance for fungal pathogens is the predominance of NAC species in bloodstream infections, with *C. tropicalis* being the most frequently isolated (34%), followed by *P. kudriavzevii* (14%). *C. albicans* occurrence was found to be 9% followed by *C. parapsilosis* (8%). This shift from *C. albicans*, which historically dominated invasive candidiasis, reflects a broader global trend likely influenced by antifungal exposure and changing host demographics. High proportion of isolates from neonates (29%) is particularly noteworthy and points to their increased susceptibility to Candida infections due to underdeveloped immunity, frequent use of invasive devices, and prolonged stays in NICUs. Overall, most isolates across species were recovered from ICUs especially from NICU settings, underlining critical care environments as high-risk reservoirs for opportunistic yeast infections. The antifungal susceptibility patterns revealed fluconazole resistance in several species, most notably *C. auris* (66%), *C. parapsilosis* (16%), *W. anomalus (15%), C. albicans* (8%), and *C. tropicalis* (7%). Although resistance to amphotericin B, itraconazole and 5-fluorocytosine remained low, emerging resistance to echinocandins in some species is concerning. These findings underscore the necessity for routine species-level identification and susceptibility testing to guide appropriate therapy. The presence of rare yeasts such as *C. jadanii*, *Clavispora lusitaniae* and *Trichosporon* spp. further highlights the value of advanced diagnostic techniques in uncovering uncommon pathogens. Overall, this data emphasizes the importance of continued antifungal resistance monitoring, improved infection control practices in neonatal and ICU settings, and the need to update empirical treatment protocols in light of evolving resistance patterns.

The AMR surveillance data presented in this report provides critical insights into resistance trends and highlights areas needing focused attention. Strengthening surveillance systems, addressing site-specific challenges and fostering inter-sectoral collaboration will be essential to enhance data quality and support effective policy-making. The findings in this report reinforce the value of strengthening surveillance system and a unified national AMR network. Continued investment in laboratory capacity, data quality, and site-level support is essential to build a resilient national response to antimicrobial resistance. AMR Surveillance data are critical to the development of AMR action plans and treatment guidelines to contain AMR.

4. Annexure I

List of NARS-Net sites that contributed AMR surveillance data for priority bacterial pathogens for the period Jan 2024 to Dec 2024. AMR Surveillance Data for fungal pathogens is from the sites with star in the list below.

1. **BJ Medical College, Ahmedabad, Gujarat***
2. BJ Medical college, Pune, Maharashtra
3. **Government Medical College and Hospital, Chandigarh***
4. **GSVM Medical College, Kanpur, Uttar Pradesh***
5. **Lady Hardinge Medical College and Associated hospitals, Delhi***
6. Mysore Medical college, Mysuru, Karnataka
7. **SMS Medical College, Jaipur, Rajasthan***
8. Vardhman Mahavir Medical college and SJ Hospital, Delhi
9. **Government Medical College, Thiruvananthapuram, Kerala***
10. **KAPV. Government Medical College, Tiruchirappalli, Tamil Nadu***
11. **Gauhati Medical College and Hospital, Guwahati, Assam***
12. **NEIGRIHMS, Shillong, Meghalaya***
13. MGM College and Hospital, Indore, Madhya Pradesh
14. **Indira Gandhi Medical College, Shimla, Himachal Pradesh***
15. **Govt. Medical College and Hospital, Aurangabad, Maharashtra***
16. **Osmania Medical College, Hyderabad, Telangana***
17. Guntur Medical College, Guntur, Andhra Pradesh
18. Agartala Govt. Medical College, Agartala, Tripura
19. SCB Medical College & Hospital, Cuttack, Odisha
20. **Government Medical College & Hospital, Jammu, Jammu and Kashmir***
21. **Pandit Bhagwat Dayal Sharma, Post Graduate Institute of Medical Sciences (PGIMS) Rohtak, Haryana***
22. **Rajendra Institute of Medical Sciences, Ranchi, Jharkhand***
23. **Indira Gandhi Institute of Medical Sciences, Sheikpura, Patna, Bihar***
24. **Government Medical College, Haldwani, Uttarakhand***
25. **Pt. Jawaharlal Nehru Memorial Medical College, Raipur, Chhattisgarh***
26. **Gandhi Medical College, Bhopal, Madhya Pradesh***
27. **Calcutta School of Tropical Medicine, Kolkata, West Bengal***
28. GMERS Medical College and Civil Hospital, Valsad, Gujarat
29. Lala Lajpat Rai Memorial (LLRM) Medical College, Meerut, Uttar Pradesh
30. Coimbatore Medical College & Hospital, Coimbatore, Tamil Nadu
31. **Maulana Azad Medical College (MAMC) and Associated Hospitals, Delhi***
32. **Sardar Patel Medical College (SPMC) and Hospital, Bikaner, Rajasthan***
33. **Karnataka Institute of Medical Sciences (KIMS), Hubli, Karnataka***
34. Indira Gandhi Medical College & Research Institute (IGMC & RI) Puducherry
35. **NAMO Medical Education and Research Institute (MERI), Silvassa, Dadra & Nagar Haveli***
36. Goa Medical College & Hospital, Bambolim, Goa

37. **STNM Medical College & Hospital, Gangtok, Sikkim***
38. Government Medical College, Patiala, Punjab
39. **Zoram Medical College, Falkawn, Mizoram***
40. Andaman & Nicobar Islands Institute of Medical Sciences (ANIIMS), Andaman & Nicobar Islands
41. Jawahar Lal Nehru Institute of Medical Sciences (JNIMS), Manipur
42. Govt. Medical College Srinagar, Jammu and Kashmir
43. Rabindranath Tagore Medical College, Udaipur, Rajasthan
44. Andhra Medical College, Vishakhapatnam, Andhra Pradesh
45. **Vijayanagar Institute of Medical Sciences Ballari, Karnataka***
46. **Burdwan Medical College & Hospital Burdwan, West Bengal***
47. Grant Govt Medical College & Sir JJ Group of Hospitals, Byculla, Mumbai
48. Pt. Raghunath Murmu Medical College & Hospital Baripada, Odisha
49. Government Medical College, Thrissur, Kerala
50. S.V medical College, Tirupati, Andhra Pradesh
51. Jorhat Medical College and Hospital, Jorhat, Assam
52. University College of Medical Sciences & GTB Hospital, Delhi
53. Pandit Dindayal Upadhyay Medical College, Rajkot, Gujarat
54. Netaji Subash Chandra Bose Medical College, Jabalpur, Madhya Pradesh