

ASSAM State Surveillance of Antimicrobial Resistance (AARSNET)



Annual Report–2026
(Reporting Period-January 2025 to December 2025)

Messages

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Dr. Himanta Biswa Sarma



মুখ্যমন্ত্রী, অসম
Chief Minister, Assam



CMS.7/2023/8053
Dispur, 31 Bhado, 1433 Bhaskarabda
18 September 2026

MESSAGE

I am pleased to learn that the First Annual Report of the Assam State Antimicrobial Resistance Surveillance Network (AARSNET) is being released on the occasion of the Foundation Day of Gauhati Medical College and Hospital. The report, based on surveillance data collected from 12 medical colleges during 2025, marks an important milestone in Assam's efforts to strengthen antimicrobial resistance surveillance.

Antimicrobial Resistance is an emerging public health challenge that can undermine the effectiveness of life saving medicines. Addressing this challenge requires not only strengthened healthcare systems but also responsible antimicrobial use, effective infection prevention and control and coordinated action across the human, animal and environmental sectors.

The establishment of AARSNET, with Gauhati Medical College and Hospital as its nodal centre, will provide a stronger evidence base for informed policymaking and help Assam develop more effective strategies to combat AMR. I believe that this initiative will also contribute to the implementation of NAP-AMR 2.0 and strengthen the State's commitment to the One Health approach.

I appreciate the efforts of all the medical colleges, laboratories, healthcare professionals and other stakeholders associated with this important initiative. I extend my best wishes for the continued expansion and success of AARSNET and for its contribution towards safeguarding public health in Assam.

(Dr. Himanta Biswa Sarma)

অশোক সিংহল
মন্ত্রী
Ashok Singhal
Minister



স্বাস্থ্য আৰু পৰিয়াল কল্যাণ,
চিকিৎসা শিক্ষা আৰু গৱেষণা বিভাগ
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Health & Family Welfare,
Medical Education & Research Deptts.
Government of Assam
Dispur
17 September, 2026

MESSAGE

Antimicrobial Resistance (AMR) is emerging as one of the most significant public health challenges of our time. Its growing impact on the effectiveness of life-saving medicines calls for coordinated, evidence-based action across the human, animal and environmental sectors through a strong One Health approach.

Laboratory-based surveillance is a critical pillar in addressing AMR, as it generates essential evidence for appropriate clinical management, effective infection prevention and control, and informed public health policies. In this context, the release of the First Annual Report of the State Antimicrobial Resistance Surveillance Network marks an important milestone in Assam's efforts towards strengthening AMR surveillance and response.

With Gauhati Medical College and Hospital serving as the designated nodal centre, Assam has taken a significant step towards establishing a robust and coordinated surveillance system. The data and insights presented in this report will help strengthen evidence-based decision-making and support more effective strategies to combat antimicrobial resistance.

I place on record my sincere appreciation to the State AMR Surveillance Team, GMCH, participating laboratories, healthcare professionals and all stakeholders whose dedicated efforts have contributed to this important initiative. I am confident that this report will serve as a valuable reference for strengthening laboratory capacity, promoting rational antimicrobial use, improving infection prevention and control, and translating laboratory evidence into meaningful public health action.

I congratulate everyone associated with this significant achievement and extend my best wishes for the continued success of the State Antimicrobial Resistance Surveillance Network.


(Ashok Singhal)

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आयुक्त एवं सचिव
Dr. P. Ashok Babu, IAS
Commissioner & Secretary

असम सरकार
स्वास्थ्य एवं परिवार कल्याण विभाग
Government of Assam
Health & Family Welfare Department



MESSAGE

Antimicrobial resistance (AMR) has emerged as one of the most significant public health challenges of our time. Addressing this growing threat requires sustained commitment, coordinated efforts, robust surveillance, and evidence-based interventions.

It is a matter of great satisfaction that the first State AMR Surveillance Report of Assam is being published. This report marks an important milestone in strengthening the State's capacity to monitor antimicrobial resistance, understand local resistance patterns, and guide appropriate clinical and public health interventions.

The strengthening of the State AMR Surveillance Laboratory Network under the National Programme on AMR Containment (2021–2026), with Gauhati Medical College and Hospital (GMCH), Guwahati, as the nodal centre, is a significant step towards establishing a systematic and coordinated surveillance mechanism in Assam. The contribution of the State's surveillance data to the national AMR surveillance system and the Global Antimicrobial Resistance and Use Surveillance System (GLASS) further reflects Assam's commitment to addressing this important public health challenge.

I commend the dedicated efforts of the participating laboratories, healthcare professionals, programme teams, and all stakeholders associated with this initiative. The evidence generated through this surveillance will support rational antimicrobial use, strengthen Antimicrobial Stewardship and infection prevention and control practices, and inform future policies and strategies for AMR containment in the State.

I extend my sincere appreciation to all those involved in bringing out this important report and convey my best wishes for the continued success of the State AMR Surveillance Programme. With collective commitment and sustained action, we can work towards containing AMR and safeguarding the effectiveness of antimicrobials for future generations.

My best wishes for better health outcomes for the people of Assam.



(Dr. P. Ashok Babu, IAS)

ড° লক্ষ্মণন এছ, আই.এ.এছ.

অভিযান সঞ্চালক, ৰাষ্ট্ৰীয় স্বাস্থ্য অভিযান, অসম

Dr. Lakshmanan. S, IAS

Mission Director, National Health Mission, Assam

Keynote Address for the First Annual Report of AARSNET

I am honoured to be a part of the efforts of the state of Assam against Antimicrobial Resistance and the comprehensive efforts undertaken by the Assam State AMR Surveillance Network – AARSNET. It is indeed a moment of pride when the First Annual Report AARSNET is being released.

Antibiotics made modern medicine possible. A caesarean section, a chemotherapy, a kidney transplant - all depend on effective antibiotics. However, today that foundation is being challenged with the emergence of widespread resistance by microorganisms against established antibiotics. Globally, AMR causes 1.27 million direct deaths. In India, as per ICMR's latest multicentric study from 20 tertiary hospitals - 2022 to 2025, published in Lancet Regional Health: 61% of Gram-negative infections are now Carbapenem-Resistant - our last line of broad spectrum antibiotics.

Understanding the importance of AMR, in 2017, Gauhati Medical College was designated as Nodal Centre under National AMR Surveillance Network (NARS-Net) under NCDC. Today, I am proud to say - AARSNET is one of the largest state networks in India. Started with 12 Govt Medical Colleges - GMCH, AMCH, SMCH, JMCH, FAAMCH, Tezpur, Lakhimpur, Dhubri, Diphu, Nagaon, Kokrajhar, Nalbari. This year we added 2 more - Tinsukia and Pragjyotishpur Medical College. All labs follow uniform SOP - WHONET, ICMR data entry, EQAS with NCDC. With more than 32,000 culture isolates in the first year itself, - blood, urine, pus - AARSNET was able to generate Assam's first state antibiogram. It is observed that E. coli - 78% resistant to Fluoroquinolones, Klebsiella pneumoniae - 58% to 3rd gen Cephalosporins and Carbapenem resistance 48% in Assam vs National 61% and so on. But the positive learning is that we still have a window to act and that is now!

As administrators, we must talk about the money we spend on public health, especially for procurement of Antibiotics. As per ICMR BMJ Open study and the 2025 Lancet study, in Government hospitals, antibiotic cost alone for resistant infection is Rs. 40,000-62,000 per patient vs Rs. 20,000-41,000 for sensitive infection - 1.1 to 2 times higher. If we add ICU bed, diagnostics, manpower - total cost in private hospitals is about Rs 3 Lakh vs Rs 1.5 Lakh in Government Hospitals. Further, stay at Hospital also increases significantly up to 23 days for resistant vs 12 days for sensitive.

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অভিযান সঞ্চালক, ৰাষ্ট্ৰীয় স্বাস্থ্য অভিযান, অসম

Dr. Lakshmanan. S, IAS

Mission Director, National Health Mission, Assam

Let's imagine, what would be the saving if we reduce AMR by even 20% in Assam? Anticipating at least 10,000 culture-positive sepsis admissions per year in medical colleges. If 40% are resistant, and we save even Rs. 20,000 per case by preventing resistance, i.e, $1,00,00 \times 40\% \times \text{Rs. } 20,000 = \text{Rs. } 8 \text{ Crore}$ per year - only on antibiotics, only in medical colleges. Add private sector and community, saving is more than Rs. 50 crore annually for Assam. This is money that can be utilized for saving valuable lives through different procedures.

Hence the importance of AARSNET. AARSNET is not a lab report factory. It is an action network. Keeping vigil on emerging AMR and Strict Infection Prevention - Hand hygiene, bundle care as 85% HAI are preventable, are to be the twin pillars of fight against the challenge. An effective control over OTC sale of Watch/Reserve without prescription will also help significantly.

I take this opportunity to congratulate and thank GMCH Microbiology team for nodal work, all 12 colleges, NCDC, and NHM Assam for funding. I am sure, with our continuous and committed efforts, we can succeed in our fight against AMR.

Let us pledge - "Preserve antibiotics for next generation - Use when needed, not when wanted.

Warm regards,



Dr Lakshmanan. S, IAS
Mission Director, NHM, Assam



सत्यमेव जयते

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Date : 14/09/2026

Antimicrobial resistance (AMR) is a major public health threat that can lead to treatment failures, prolonged hospital stays, increased healthcare costs, morbidity, mortality, and limited treatment options. State-level AMR surveillance is therefore essential to generate reliable data on local resistance patterns and emerging trends. Such information helps clinicians select appropriate empirical antimicrobial therapy, strengthen Antimicrobial Stewardship Programmes, and improve infection prevention and control practices.

The effectiveness of surveillance depends on translating data into action. Regular dissemination of findings can promote rational antimicrobial use, strengthen infection-control measures, and enable early identification of emerging resistance. Combating AMR requires coordinated efforts among microbiologists, clinicians, pharmacists, laboratories, policymakers, public health authorities, academic institutions, and communities. Responsible use of antimicrobials—the right drug, at the right dose, for the right duration, and only when indicated—is equally important.

I hope that the findings of this first annual report of state AMR Surveillance emphasize the importance of sustained laboratory capacity, standardized data collection, timely reporting, and collaboration among healthcare institutions, public health authorities, policymakers, and communities. These data would also support policymakers and public health authorities in identifying priority threats, allocating resources, developing State AMR action plans, and implementing targeted interventions., and ultimately contributes to **safer healthcare, improved patient outcomes, and protection of public health.**

(Dr. Abhijit Sarma)

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Dated: 14-09-2026

MESSAGE

It gives me immense pleasure to present the first **State Antimicrobial Resistance (AMR) Surveillance Report** of Assam (AARSNET), a significant milestone reflecting our collective commitment to addressing one of the most pressing public health challenges of our time. Antimicrobial resistance poses a serious threat to the effective prevention and treatment of infectious diseases, with far-reaching consequences for patient outcomes, healthcare systems, and public health.

The **National Programme on AMR Containment**, Government of India, seeks to strengthen AMR surveillance and containment activities in State Government Medical Colleges and tertiary-care Government hospitals. Under the programme for 2021-2026, states are supported to establish and strengthen State AMR Surveillance Laboratory Networks.

In Assam, **Gauhati Medical College and Hospital, Guwahati**, has been designated as the **Nodal Centre for State AMR Surveillance**, entrusted with coordinating and strengthening the surveillance network across the State. The participating laboratories contribute to the generation of reliable and meaningful AMR surveillance data by adhering to standardized laboratory testing procedures, quality-assurance practices, and data-management protocols established under the National Programme on AMR Containment.

This report represents the **first State AMR Surveillance Report from Assam** and has been submitted to NCDC for inclusion in national AMR surveillance data and contribution to the Global AMR Surveillance System (GLASS). The findings will provide valuable evidence for understanding resistance trends, guiding appropriate antimicrobial therapy, strengthening antimicrobial stewardship, and supporting infection prevention and control.

I sincerely commend the dedicated efforts of all stakeholders involved and hope that these initiatives will translate into meaningful action, strengthen our response to AMR, and contribute significantly to safeguarding public health in Assam.

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Antimicrobial resistance continues to threaten the effective prevention and treatment of infectious diseases. Addressing AMR therefore requires sustained, coordinated, and evidence-driven action across healthcare institutions and public health systems.

India's National Programme on AMR Containment (2021–2026) supports States in strengthening AMR surveillance through State AMR Surveillance Laboratory Networks. In Assam, Gauhati Medical College and Hospital, Guwahati, serves as the nodal centre. Standardized laboratory testing, quality control, and data-management procedures ensure the quality, comparability, and reliability of AMR surveillance data, enabling evidence-based interventions at the State level.

I am particularly pleased to note that this is the first State AMR Surveillance Report generated for Assam. The data generated through this initiative have also been submitted to the National Centre for Disease Control (NCDC) for inclusion in the national AMR surveillance dataset and subsequent contribution to the Global Antimicrobial Resistance and Use Surveillance System (GLASS).

Robust AMR surveillance is essential for understanding resistance trends, guiding appropriate antibiotic therapy, strengthening antimicrobial stewardship, and supporting infection prevention and control. Effective AMR containment requires standardized laboratory practices, quality data, timely reporting, responsible antimicrobial use, and collaboration among healthcare professionals, laboratories, policymakers, and the community.

The contributions of all stakeholders in Assam are sincerely acknowledged. I hope this report will provide a valuable baseline for future surveillance, help identify emerging resistance patterns, guide targeted interventions, and strengthen the State's response to AMR, ultimately improving patient care, healthcare safety, and public health outcomes.


Prof. (Dr.) Babul Kr. Bezbaruah

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Acknowledgement

As the Nodal Officer and on behalf of State AMR Surveillance Network (AARSNET), I offer my sincere thanks to the Department of Health and Family Welfare, Ministry of Health and Family Welfare, Government of India for designating Gauhati Medical College and Hospital as the Nodal centre to coordinate the State AMR surveillance in the state of Assam.

We express our sincere gratitude to the Government of Assam, under the visionary leadership of the Hon'ble Chief Minister, for the continued support and commitment towards strengthening antimicrobial resistance (AMR) surveillance in the State. We gratefully acknowledge the Government's support in facilitating the release of the State Annual AMR Surveillance Report, and look forward to continued support in translating surveillance findings into meaningful actions for prevention and containment of AMR in Assam.

On behalf of the Department of Microbiology, Gauhati Medical College and Hospital, I sincerely acknowledge the institutional support extended by our Principal cum-Chief Superintendent. His constant support and leadership has been instrumental in facilitating the publication and release of this report on the 66th Foundation day of Gauhati Medical College and Hospital.

The State Nodal Site of AMR Surveillance, Assam, sincerely acknowledges the National Centre for Disease Control (NCDC) for its invaluable technical guidance, continuous support, encouragement and financial assistance in strengthening AMR surveillance activities. We express our heartfelt gratitude to the entire NCDC team for their unwavering commitment and collaboration, which have been pivotal in advancing the State AMR Surveillance Network and facilitating the successful compilation of this report.

I offer my heartfelt gratitude to all the participating network sites, their faculties, laboratory and data management staff for their commitments and sincere efforts for timely data reporting which has significantly contributed to the quality and credibility of this report.

I deeply appreciate the dedication and perseverance of every team member of AARSNET, whose collective efforts have transformed this surveillance data into a valuable resource for understanding AMR trends and guiding evidence based interventions in Assam.

This report is a testament to our shared commitment in combating AMR. I look forward to our continued collaboration and strengthen efforts towards advancing AMR Surveillance and containment in the State.

With sincere appreciation and gratitude.

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Acronyms

AMR	Antimicrobial resistance
AST	Antimicrobial susceptibility testing
BMD	Broth microdilution
CRE	Carbapenem resistant Enterobacteriaceae
CRAB	Carbapenem-resistant <i>Acinetobacter baumannii</i>
EQAS	External quality assessment scheme
GAP-AMR	Global Action Plan on Antimicrobial Resistance
GLASS	Global Antimicrobial Resistance Surveillance System
IPD	In-patient
ICU	Intensive care unit
IQC	Internal quality control
LIMS	Laboratory information management system
AARSNET	Assam State Antimicrobial Resistance Surveillance Network
MRSA	Methicillin resistant <i>Staphylococcus aureus</i>
MoHFW	Ministry of Health & Family Welfare
NAP-AMR	National Action Plan on Antimicrobial Resistance
NFGNB	Non-fermenting Gram-negative bacilli
NRL	National reference laboratory
OPD	Out-patient
OSBF	Other sterile body fluids
R	Resistant
S	Sensitive
RIS	Resistant Intermediate Sensitive
SOP	Standard Operating Procedure
VRE	Vancomycin Resistant <i>Enterococci</i>
WHO	World Health Organization

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1. Summary

The irrational and excessive use of antimicrobial agents has significantly accelerated the emergence and spread of drug-resistant pathogens. As a consequence, Antimicrobial Resistance (AMR) has become one of the most pressing public health challenges worldwide and in India, leading to increased healthcare costs, treatment failures, prolonged hospital stays, and higher mortality rates.

Recognizing the gravity of the problem, the Ministry of Health & Family Welfare (MoHFW) has identified AMR among the country's top ten public health priorities. The National Health Policy 2017 also highlights AMR as a critical health threat and calls for coordinated, multisectoral interventions to address it.

India's National Action Plan on Antimicrobial Resistance (NAP-AMR) is aligned with the World Health Organization Global Action Plan on Antimicrobial Resistance (GAP-AMR) while incorporating national priorities. In addition to the five strategic objectives of GAP-AMR, India has introduced a sixth strategic priority focused on strengthening leadership, governance, and collaborations at national, sub-national, and international levels to effectively contain AMR.

The Assam Antimicrobial Resistance Surveillance Network (AARSNET) was started in the year 2023 with inclusion of 12 medical colleges. The nodal centre of the state site being Gauhati Medical College Hospital, Guwahati. The network has played a pivotal role in strengthening AMR surveillance and containment efforts across the state. The first sensitisation workshop was conducted in January 2024 with the 11 included sites apart from Gauhati Medical College Hospital, Guwahati.

In 2025, encompassing these 12 participating laboratories, the state site carried out extensive surveillance activities. This activity has been accompanied by a steady increase in the number of clinical isolates processed and analysed over the years, generating valuable data on antimicrobial resistance trends. Concurrently, sustained efforts have been made to build laboratory capacity, standardize diagnostic practices, and ensure the delivery of high-quality microbiological services across all participating centres, thereby reinforcing the reliability and effectiveness of the surveillance system. At the same time, ongoing investments in laboratory strengthening, workforce training, and quality management systems have improved diagnostic performance and data quality across participating centres, thereby enhancing the overall effectiveness of the AMR surveillance program.

The AARSNET Report 2025 represents the first annual publication under the Assam Surveillance of Antimicrobial Resistance (AARSNET) network. This report presents AMR surveillance data for nine priority pathogens collected from 12 sentinel surveillance laboratories situated across various districts of Assam. The pathogens covered include *Escherichia coli*, *Klebsiella* species, *Pseudomonas* species, *Acinetobacter* species, *Salmonella enterica* serotype *Typhi* and *Paratyphi*, *Staphylococcus aureus*, and *Enterococcus*

species,

The data presented in this report covers the period from January 2025 to December 2025.

A total of 14179 priority pathogens isolated from 13369 patients were analyzed for antimicrobial susceptibility testing (AST) between 1st January 2025 and 31st December 2025. Among all isolates, *E. coli* species was the most frequently isolated organism, accounting for 36% of total isolates, followed by *Klebsiella* species (21.5%), *Staphylococcus aureus* (13%), *Enterococcus* species (12%), *Acinetobacter* species (9%) and *Pseudomonas* Species (8%). *Shigella flexneri*, *Shigella sonnei* and *Shigella* Species together accounted for 0.1% (17 isolates), and 0.01% (2 isolates) of *Salmonella typhi* was also reported. No *Vibrio cholerae* isolates were reported during this period. The majority of these priority pathogens were isolated from urine specimens, followed by pus aspirates, blood, and other sterile body fluids.

The escalating burden of antimicrobial resistance (AMR) is largely driven by the inappropriate and excessive use of antibiotics, which promotes the selection and spread of resistant bacterial strains. Unless antibiotic prescribing and utilization practices are optimized, the effectiveness of both existing and newly introduced antimicrobial agents will continue to diminish due to the rapid emergence of resistance. This challenge is especially critical for infections caused by WHO priority pathogens, particularly carbapenem-resistant Gram-negative bacteria, which are associated with limited treatment options, increased healthcare costs, and poor clinical outcomes.

The surveillance data revealed a substantial burden of multidrug-resistant organisms (MDROs), including Methicillin-Resistant *Staphylococcus aureus* (MRSA), Vancomycin-Resistant *Enterococcus* (VRE), Carbapenem-Resistant Enterobacterales (CRE), and multidrug-resistant Gram-negative bacilli. The findings also raise concerns about the possibility of emergence of colistin resistance among Enterobacterales and non-fermenting Gram-negative bacteria, as well as linezolid resistance in VRE and *S. aureus*. The rising prevalence of resistance to key therapeutic agents, including third-generation cephalosporins, carbapenems, and last-resort antibiotics such as colistin, vancomycin, and linezolid, represents a significant challenge to patient management, infection control efforts, and public health systems.

2. Assam Surveillance of Antimicrobial Resistance (AARSNET)

The Assam Surveillance of Antimicrobial Resistance (AARSNET) network is working under the guidance of National Centre for Disease Control with oversight of the State Government of Assam. The network plays a crucial role in strengthening antimicrobial resistance (AMR) surveillance and supporting containment strategies across the state.

AARSNET objectives are:

- To provide baseline data for measuring the burden and distribution of antimicrobial resistance (AMR) across Assam.
- To generate evidence for benchmarking the prevalence and patterns of antimicrobial resistance throughout Assam.
- To assess and document the magnitude and geographic distribution of antimicrobial resistance across the state.
- To establish a comprehensive understanding of the AMR burden and its distribution across Assam.
- To create a state-wide reference framework for monitoring the burden and spread of antimicrobial resistance in Assam.

AARSNET network laboratories-strengthening and expansion

The AARSNET network has consistently contributed towards AMR containment efforts in Assam and remains an important component of the National Programme on AMR Containment since its inception. The network has been actively engaged in systematic collection, analysis, and sharing of AMR surveillance data. The AARSNET surveillance network comprised of 12 laboratories from government sectors (medical colleges), was started in 2023. All participating laboratories follow standardized methodologies for antimicrobial susceptibility testing (AST) along with uniform quality assurance practices. Few sites are NABL accredited whereas few others are in the road to initiate accreditation in their facilities.

WHONET software has been utilized for compilation, analysis, and monthly reporting of AMR surveillance data across the network. Capacity-building activities, including training programs on WHONET, antimicrobial susceptibility testing, and broth microdilution techniques, antibiogram preparation and sensitization on healthcare associated infection surveillance have been regularly conducted to enhance the technical competencies of network laboratories.

A major objective of the programme is to generate high-quality AMR surveillance data for monitoring resistance trends across different geographical regions of Assam through a robust sentinel surveillance system.

The seven priority pathogens currently monitored under AARSNET include *Staphylococcus aureus*, *Enterococcus* species, *Escherichia coli*, *Klebsiella* species, *Salmonella enterica* serotype Typhi and Paratyphi, *Pseudomonas* species, and *Acinetobacter* species. Clinical specimens processed for

surveillance include blood, urine, pus aspirates, other sterile body fluids, and stool samples (specifically for *Salmonella Typhi* and *Paratyphi*). In line with the updated NCDC surveillance Standard Operating Procedures (SOPs), *Shigella* species and *Vibrio cholerae* were incorporated into the AARSNET priority pathogen list in the 2024 and have been included in the surveillance framework over the past two years.

All sentinel surveillance laboratories have received structured training in AMR surveillance, quality assurance protocols, and AMR data management using WHONET software. The AARSNET network follows a standardized framework for AMR data collection, analysis, and reporting through the use of WHONET, an open-source microbiology data management platform. Continuous technical support and hand-holding are being provided to participating sites to strengthen specimen collection practices, bacterial culture and identification techniques, and antimicrobial susceptibility testing procedures. This support includes regular guidance, monitoring, and onsite visits aimed at improving the overall quality and consistency of AMR surveillance activities. At the institutional level, the analyzed AMR surveillance data is being utilized for the preparation of hospital antibiograms, which assist clinicians in selecting appropriate empiric antimicrobial therapy for patient management.

In addition, regular feedback on submitted surveillance data is being provided every month using a standardized feedback mechanism to enhance the completeness, accuracy, and quality of AMR data reporting across all network laboratories.

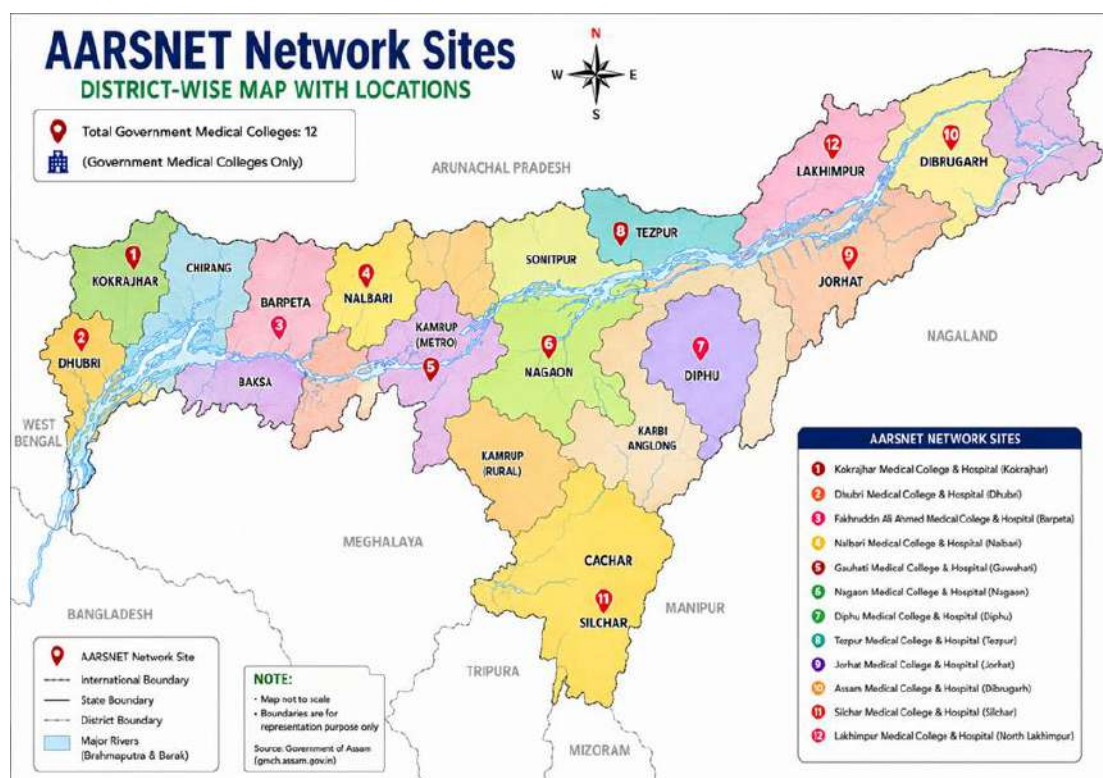


Figure 1: AARSNET Network Laboratories Strengthening and Expansion

Figure1 illustrates the 12 AARSNET network laboratories that participated in AMR surveillance activities since the year 2024. Continuous hand-holding support and extensive capacity-building initiatives significantly enhanced AMR data collection and reporting across the network sites during

2024, and 2025.

Sensitization programs on data management using WHONET software and hands on training on broth microdilution techniques, antibiogram preparation and sensitization training on Health care associated infection surveillance were conducted for participating laboratories, which contributed towards standardization and streamlining of antimicrobial susceptibility testing (AST) practices across the network. These trainings were implemented in accordance with standard operating procedures for antimicrobial susceptibility testing, internal quality control (IQC), data management, and other technical protocols developed by NCDC and AARSNET, based on internationally accepted standards and guidelines, including those of the Clinical and Laboratory Standards Institute (CLSI).

A review meeting with the participating sites was also conducted in January 2026 to take the necessary feedback, review the processes and form road maps for future activities

In addition, AARSNET continued to provide technical guidance and onsite support to participating laboratories for configuring laboratory systems to facilitate seamless data import from automated systems, hospital information systems, and Excel databases into WHONET software through the use of backlink.

3. Data Collection under AARSNET

Data on priority pathogens and their antimicrobial susceptibility patterns were reported by participating AARSNET laboratories for the period January–December 2025 following established data validation procedures. Laboratories utilizing automated antimicrobial susceptibility testing (AST) systems were trained in the use of Bac Link software to facilitate direct import of data into WHONET, thereby minimizing transcription errors and reducing duplication in data entry.

WHONET data files remained the preferred mode of data submission to AARSNET. To ensure data quality and standardization, regular monthly feedback was provided to participating laboratories based on the following indicators:

- i. Timeliness of reporting and compliance with the prescribed mode of data submission
- ii. Completeness of demographic and clinical information
- iii. Accuracy and standardization of isolate identification and nomenclature
- iv. Adherence to AARSNET AMR surveillance standard operating procedures (SOPs), including recommended pathogen–antimicrobial combinations
- v. Compliance with established reporting formats and data submission requirements

Participating laboratories received continuous feedback on the quality, consistency, and completeness of submitted datasets. Whenever discrepancies or data quality issues were identified, laboratories were advised to review, validate, and resubmit corrected datasets in a timely manner.

To further strengthen AMR surveillance and promote uniform data management practices across the network, regular online review meetings, along with virtual and onsite training sessions, were conducted to provide technical support and continuous capacity building for participating laboratories.

Following submission, validated WHONET datasets underwent centralized review, quality assurance checks, and detailed analysis for inclusion in the annual AARSNET surveillance report. Participating laboratories received periodic feedback on the quality, completeness, and consistency of the data submitted to the network. Where necessary, laboratories were requested to review, validate, and promptly resubmit corrected datasets to ensure data accuracy and integrity. To enhance AMR surveillance data management and promote compliance with standardized reporting practices, regular online review meetings, along with virtual and onsite training programs, were conducted to provide technical guidance and continuous capacity building for network laboratories.

Following submission, the WHONET datasets underwent comprehensive validation, quality assurance checks, and detailed analysis before being incorporated into the annual AARSNET surveillance report.

4. Data Analysis

Data de-duplication was performed on antimicrobial susceptibility testing (AST) data received from AARSNET network laboratories in WHONET format. The purpose of this process was to eliminate duplicate isolates from the same patient during a single episode of hospitalization and to retain only the first isolate per specimen type and pathogen for analysis.

Prior to de-duplication, all relevant variables containing patient information, location details, specimen type, and pathogen identification were reviewed to ensure completeness and consistency of records. For the purpose of this report, only one AST result corresponding to the first isolate obtained from the same patient during the hospital stay was included for each pathogen and specimen type.

In certain situations, repeated samples collected from the same patient during hospitalization may yield the same pathogen with varying AST profiles over time. For instance, if two blood culture samples from the same patient showed growth of *E. coli*, only the AST profile of the first isolate was considered for analysis. However, if one blood culture yielded *E. coli* and another yielded *Klebsiella pneumoniae*, both isolates were included in the dataset. Similarly, isolates from different specimen types were treated separately; therefore, if *E. coli* was isolated from both blood and urine samples of the same patient, both results were included in the analysis.

Priority pathogens under surveillance in AARSNET

The clinical specimens included under the AARSNET surveillance network were collected according to the criteria outlined in Table 1, while Table 2 presents the list of priority pathogens included for AMR surveillance.

Table 1: Clinical specimens included in AMR Surveillance

Clinical specimen	Laboratory case-definition
Blood	Isolation of pathogen from blood
Urine	Clinically significant bacteriuria
Pus aspirate (PA)	Significant growth from aspiration of purulent material from a closed infected site
Other sterile body fluids (OSBF)	Significant growth from CSF, pleural fluid, peritoneal fluid, synovial fluid, pericardial fluid
Stool	Isolation of pathogen from stool

Table 2: Priority pathogens for AMR surveillance

<i>Specimen</i>	<i>Enterococcus species</i>	<i>Staphylococcus aureus</i>	<i>Escherichia coli</i>	<i>Klebsiella species</i>	<i>Acinetobacter species</i>	<i>Pseudomonas species</i>	<i>Salmonella Typhi and Paratyphi</i>	<i>Shigella sp. Vibrio cholerae</i>
Blood	☒	☒	☒	☒	☒	☒	☒	
Urine	☒		☒	☒	☒	☒		
Pus aspirate	☒	☒	☒	☒	☒	☒		
OSBF	☒	☒	☒	☒	☒	☒		
Stool							☒	☒

As per the updated NCDC surveillance Standard Operating Procedures (SOPs), *Shigella* species and *Vibrio cholerae* isolated from stool specimens were incorporated into the AARSNET priority pathogen list since 2024 and have been consistently included in subsequent surveillance reports, including the current reporting cycle.

AMR surveillance data of **14179** priority pathogens collected by AARSNET surveillance sites was de-duplicated & analyzed for this report. After de-duplication, the number of isolates from unique patients was **13369** (see Figure 2).

Demography and Distribution of Priority pathogens under surveillance

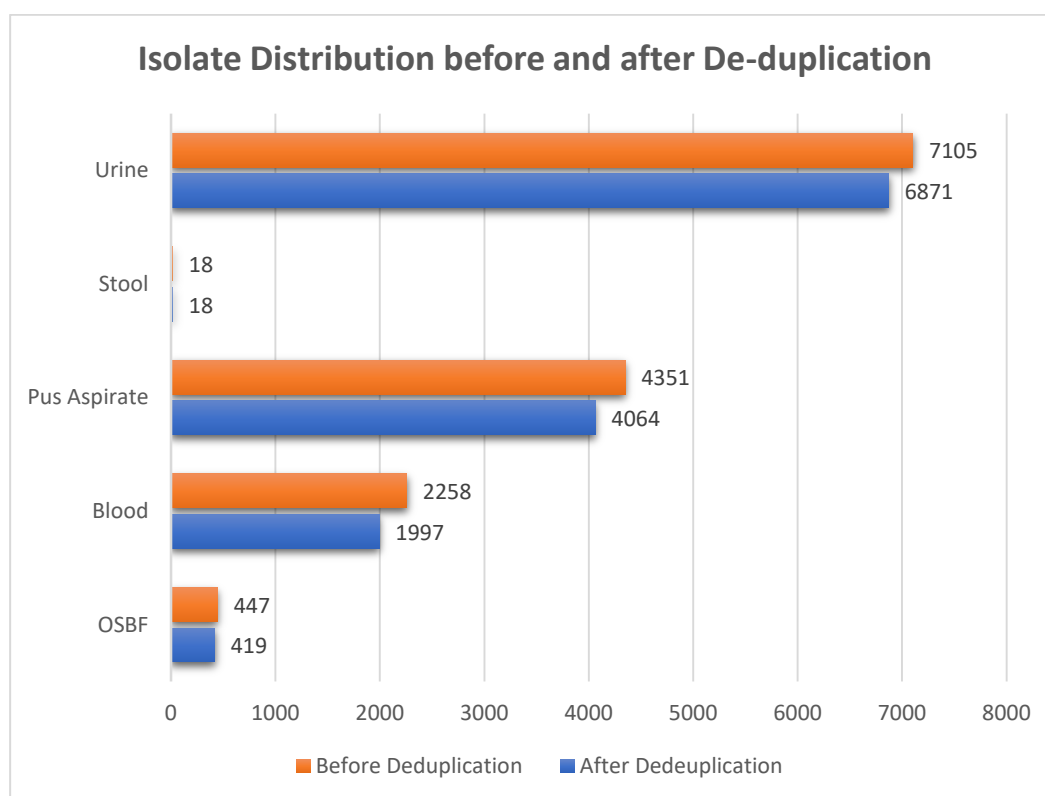


Figure 2: Distribution of isolates before and after de-duplication

Gram-negative bacteria are major causative agents of infections among patients attending tertiary care healthcare facilities, including bloodstream infections, wound infections, and meningitis. These organisms, particularly those belonging to the Enterobacteriaceae family and non-fermenting groups, often exhibit high levels of antimicrobial resistance, making treatment increasingly challenging. AARSNET surveillance data also indicate a predominance of Gram-negative organisms, including multidrug-resistant organisms (MDROs). Among Gram-positive pathogens, *Staphylococcus aureus* and *Enterococcus* species were the most commonly identified organisms.

For the year 2025, *Escherichia coli* was the most frequently isolated organism, accounting for 36% (4828) of total isolates, followed by *Klebsiella* species at 21.5% (2890 isolates), *Staphylococcus aureus* at 13% (1711 isolates), *Enterococcus* species at 12% (1653 isolates), *Acinetobacter* species at 9% (1204 isolates), and *Pseudomonas* species at 8% (1065 isolates). *Shigella* species accounted 17 isolates and *Salmonella* species accounted for 1 isolate respectively, as shown in Figure 3.

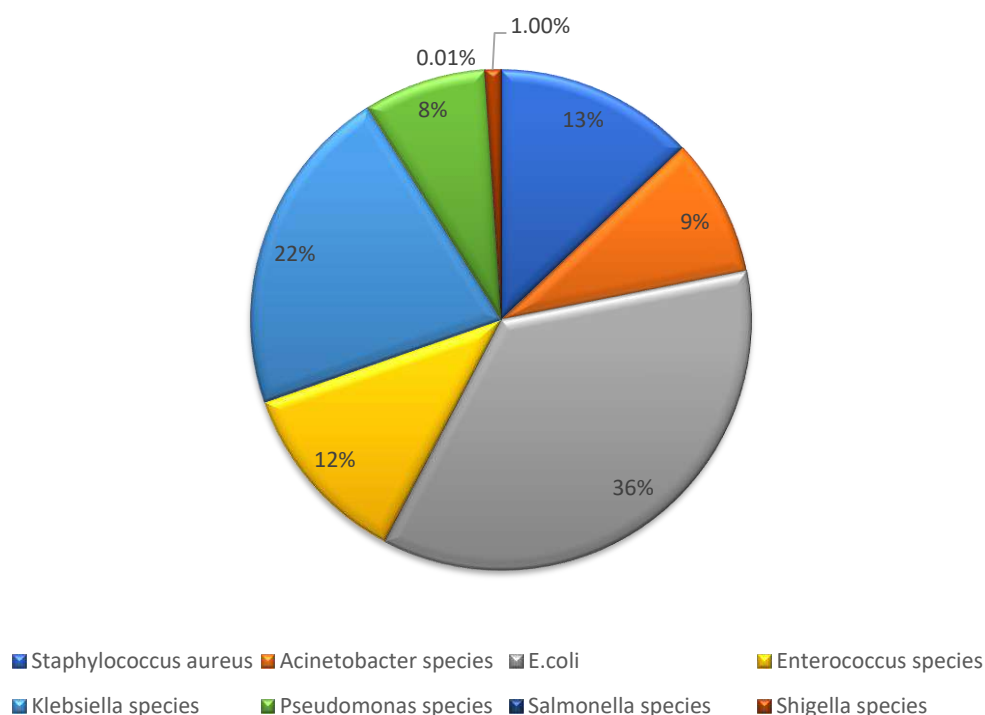


Figure 3: Distribution of isolates (2025)

Total number of isolates from unique patients (after de-duplication) was 13369. The specimen wise distribution is depicted in Figure 4. Pathogens included in this report were predominantly isolated from urine specimens (6871; 51%), followed by Pus Aspirate (4064; 30%), Blood (1997; 15%), other sterile body fluids (419; 3.1%) and stool (18 isolates).

Distribution of isolate specimen wise

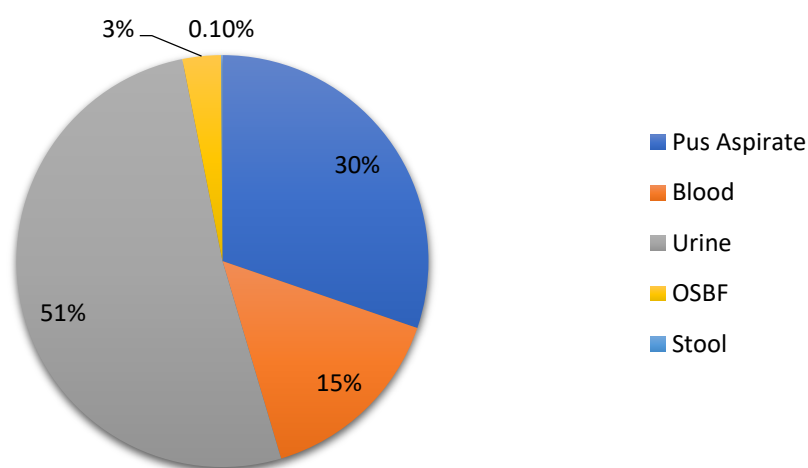


Figure 4: Specimens received in 2025 (n=13369)

Urine cultures were interpreted in conjunction with clinical symptoms suggestive of urinary tract infection (UTI), including dysuria, urinary frequency, supra pubic pain, flank pain, and fever. Reporting of mixed bacterial growth or samples collected from urine collection bags was excluded

from analysis. For clean-catch (or mid-stream) urine samples:

Bacterial growth of $>100,000(>10^5)$ organisms or colony forming units (CFU)/mL is suggestive of urinary tract infection (UTI) – clinically significant bacteriuria.

Growth of 1,000 – 100,000 CFUs/mL (10^3 – 10^5 CFU/mL) may indicate UTI in patients with pyelonephritis, prostatitis, epididymitis or fungal infections, or samples collected on cystoscopy or other invasive procedures.

Pus aspirates include aspiration of purulent material from a closed infected site only. Pus “swabs” and “wound swabs” were not included in AMR surveillance reporting. Other sterile body fluids include cerebrospinal fluid (CSF), pleural fluid, peritoneal fluid (ascites), synovial fluid, and pericardial fluid.

The specimen wise distribution of priority pathogens is shown in Table 2 and Figure 5. Urine being the most common specimen received, 6871 culture positive isolates were reported in the year 2025. *Escherichia coli* (53.8%) was the most common causative pathogen for urinary tract infections followed by *Enterococcus* spp. (20%), *Klebsiella* spp. (19.5%). Other bacteria isolated from urine included *Pseudomonas* spp. (4%) and *Acinetobacter* spp. (3%).

Among blood culture isolates, *Acinetobacter* species were most frequently reported (29.5%), followed by *Klebsiella* species (21%), *Staphylococcus aureus* (20.3%), *Escherichia coli* (11%), *Enterococcus* species (11%). and *Pseudomonas* species (6.3%),

In pus aspirates, *Staphylococcus aureus* (31%) and *Klebsiella* species (24.5%) were the most common pathogens, followed by *Escherichia coli* (20.5%), *Pseudomonas* species (14%), *Acinetobacter* species (7.5%), and *Enterococcus* species (0.02%).

For other sterile body fluids, the most frequently isolated organisms were *Klebsiella* sp. (29%), *Acinetobacter* species (25%) and followed by *Pseudomonas* species (19%), *Escherichia coli* (17%), *Staphylococcus aureus* (7.6%), and. *Enterococcus* species (3%).

Eighteen isolates were reported from the stool specimens viz. *Shigella* spp. (17), and *S. Typhi* (1).

Table 3: Specimen wise distribution of priority pathogens (n=13369)

Organism	Blood	OSBF	PA	Urine	Stool	Total
<i>Staphylococcus aureus</i>	406 (20.3%)	32 (7.6%)	1273 (31%)	-		1711(12.7%)
<i>Acinetobacter</i> sp.	591 (29.5%)	104 (25%)	308 (7.5%)	201 (3%)		1204 (9%)
<i>Escherichia coli</i>	226 (11.3%)	70 (17%)	834 (20.5%)	3698 (54%)		4828 (36%)
<i>Enterococcus</i> sp.	219 (11%)	13 (3%)	69 (0.02%)	1352 (20%)		1653 (12%)
<i>Klebsiella</i> sp.	429 (21.4%)	120 (29%)	996 (24.5%)	1345 (19.5%)		2890 (21.6%)
<i>Pseudomonas</i> sp.	126 (6.3%)	80 (19%)	584 (14%)	275 (4%)		1065 (8%)
<i>Salmonella</i> sp.					1 (5.5%)	1 (0.007%)
<i>Shigella</i> sp					17(94.4%)	17 (0.12%)
Total	1997 (15%)	419 (3.1%)	4064(30.3%)	6871(51.4%)	18(0.1%)	13369

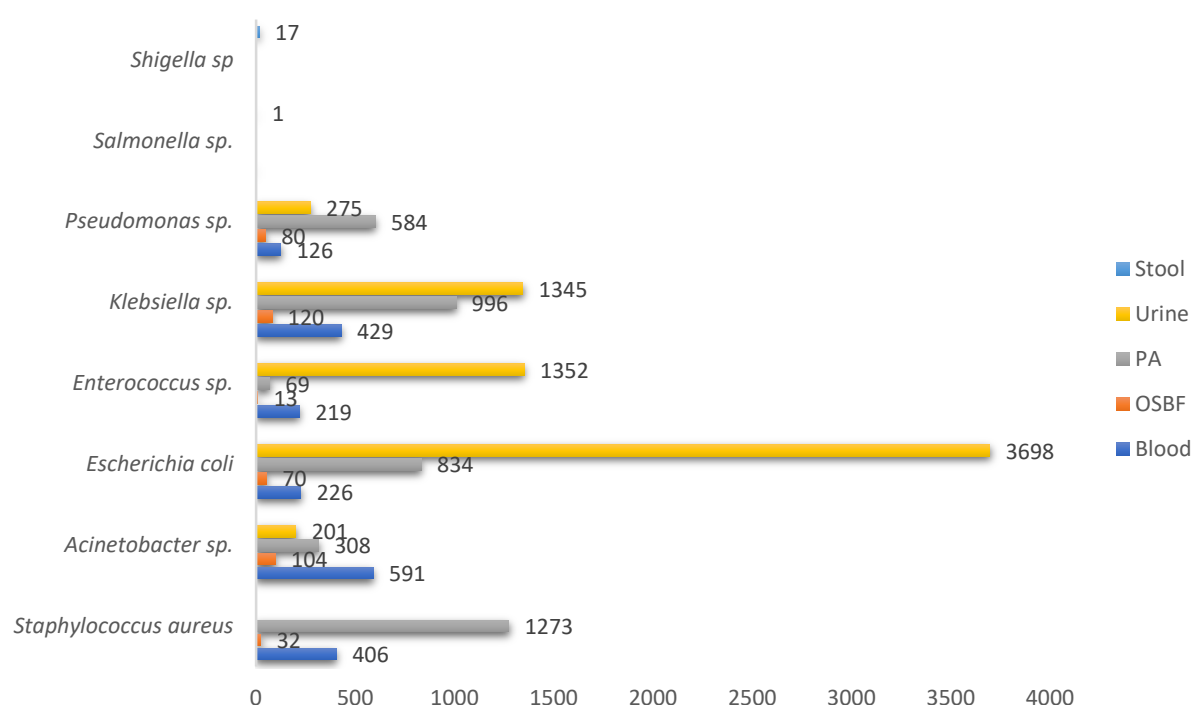


Figure 5: Specimen wise distribution of priority pathogens (n=13369)

The overall distribution of isolates by gender is presented in Figure 6. The proportion of isolates was slightly higher among female patients (54%) compared to male patients (45%).

Samples were received from multiple hospital settings, including outpatient departments (OPD), in patient wards (IPD), and intensive care units (ICU), as illustrated in Figure 7. In 2025, the majority of isolates were obtained from IPD patients (6107; 45.6%), followed by OPD patients (5715; 42.7%), and ICU patients (1547; 11.5%). Overall, the AARSNET dataset predominantly comprises isolates from hospitalized patients.

GENDER WISE DISTRIBUTION OF ISOLATES



Figure 6: Distribution of isolates on the basis of gender (2025)

Isolates from intensive care units

Overall, 57% of isolates in 2025 were obtained from hospitalized patients (including both IPD and ICU settings), reflecting a predominance of invasive and severe infections.

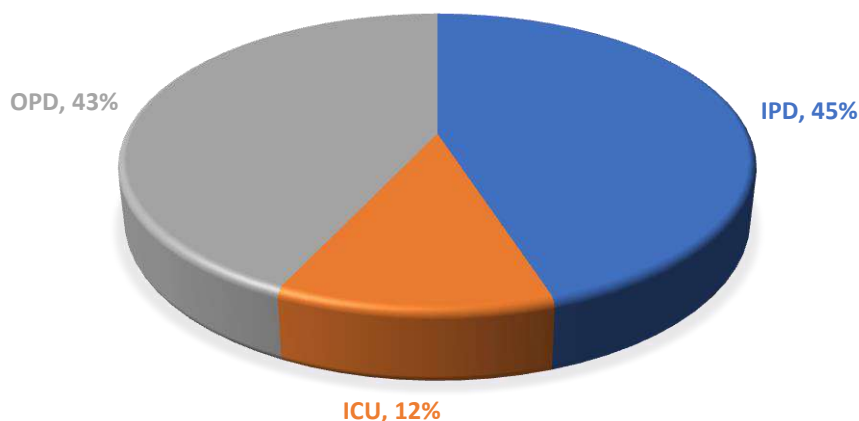


Figure 7: Location wise distribution of isolates

Table 4: Location wise distribution of priority pathogens

Priority Pathogens	ICU (%)	IPD (%)	OPD (%)
Acinetobacter sp.	448 (29%)	524 (8.5%)	232 (4%)
Escherichia coli	206 (13.3%)	1885 (31%)	2737 (48%)
Enterococcus sp.	242 (15.6%)	796 (13%)	615 (10.7%)
Klebsiella sp.	372 (24%)	1321 (21.6%)	1168 (20.4%)
Pseudomonas sp.	98 (6.3%)	578 (9.5%)	445 (8%)
Staphylococcus aureus	181 (11.7%)	987 (16%)	516 (9%)
Shigella sp.		15 (0.2%)	2 (0.03%)
Salmonella sp.			1 (0.01%)
Total	1547 (11.5%)	6107 (45.6%)	5715 (42.7%)

The highest numbers of isolates were reported from IPD patients (45.6%), with a clear predominance of Gram-negative organisms.

Overall, *Escherichia coli* was the most frequently isolated pathogen (36%), followed by *Klebsiella* species (21.6%), *Staphylococcus aureus* (12.7%), *Enterococcus* species (12%), *Acinetobacter* species (9%), *Pseudomonas* species (8%) and *Shigella* species (0.12%), and *Salmonella enterica* serotype Typhi and Paratyphi accounted for (0.007%) of isolates.

Among OPD patients, *Escherichia coli* was the predominant pathogen (48%), followed by *Klebsiella* species (20.4%), *Staphylococcus aureus* (9%), *Enterococcus* species (10.7%), *Pseudomonas* species (8%), and *Acinetobacter* species (4%). *Salmonella Typhi* and *Paratyphi* accounted for (0.01%) of isolates, while *Shigella* species (0.03%).

In IPD and OPD settings, *Escherichia coli* remained the leading pathogen (31% and 48%, respectively). In contrast, ICU settings showed a different distribution, with *Acinetobacter* species being the predominant organism (29%) followed by *Klebsiella* species (24%), *Escherichia coli* (12%), *Enterococcus* species (15.6%), *Staphylococcus aureus* (11.7%) and *Pseudomonas* species (6.3%)

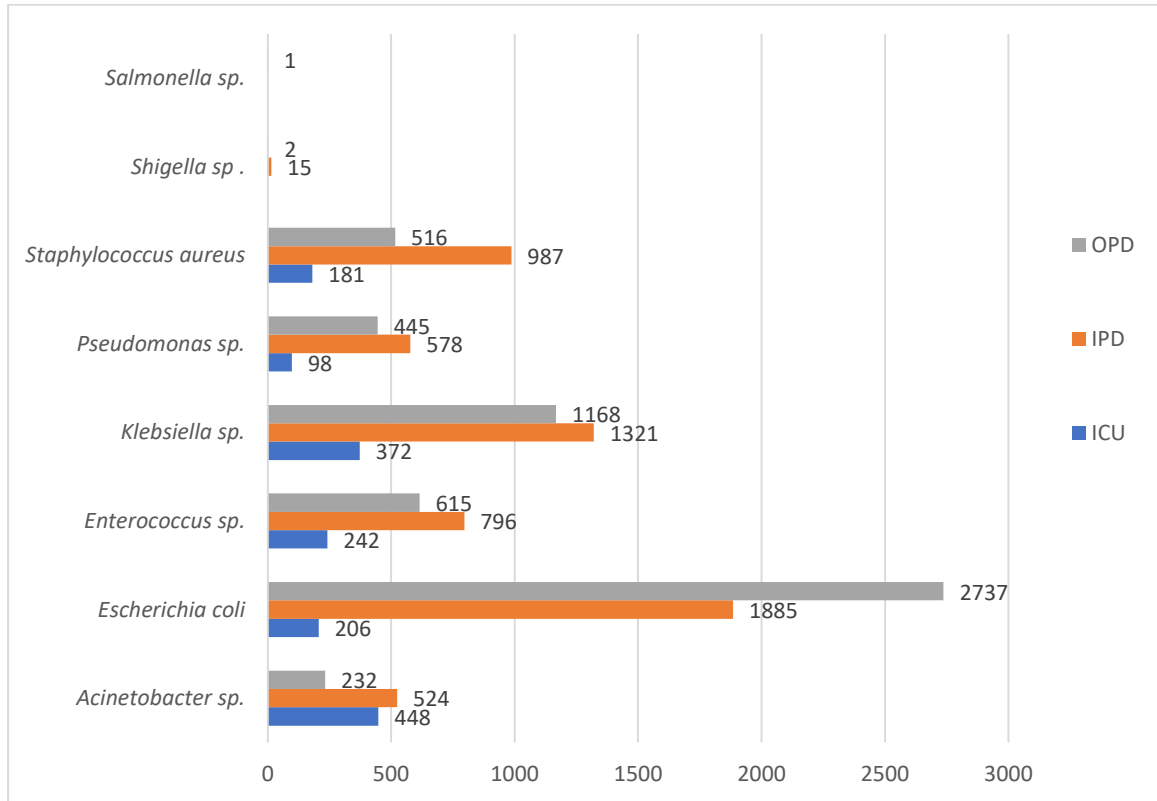


Figure 8: Location wise isolation of different priority pathogens

5. AMR profile of priority pathogens

This AMR dataset presents the resistance patterns of priority pathogens isolated from patients attending outpatient departments, inpatient wards, and intensive care units across AARSNET surveillance sites, thereby encompassing both community-acquired and healthcare-associated infections.

The data generated under the Assam Surveillance of Antimicrobial Resistance (AARSNET) network is restricted to a selected panel of antimicrobials, as defined in the Standard Operating Procedures (SOPs).

Gram-Positive Cocci

Staphylococcus aureus

Staphylococcus aureus is one of the most common Gram-positive human pathogens, responsible for a wide spectrum of infections ranging from minor skin and soft tissue infections such as boils, impetigo, wound infections, and cellulitis to more severe conditions including osteoarticular infections, pneumonia, endocarditis, and septicemia. It is also a leading cause of antibiotic-resistant healthcare-associated infections, primarily driven by methicillin-resistant *Staphylococcus aureus* (MRSA) and linezolid-resistant strains.

In the AARSNET surveillance data, *S. aureus* accounted for 12.7% of all reported isolates (Figure 3). During 2025, antimicrobial susceptibility testing (AST) data were available for 1711 *S. aureus* isolates obtained from 1711 unique patients (Figure 2). The organism was predominantly isolated from pus aspirates (1273 isolates), other sterile body fluids (32 isolates), and blood cultures (406 isolates).

Key findings: Resistance profile of *Staphylococcus aureus*

Figure 10 illustrates the overall resistance profile of *Staphylococcus aureus* isolates obtained from 1711 unique patients.

A total of 406 bloodstream isolates, 32 other sterile body fluid (OSBF) isolates, and 1,273 pus aspirate isolates of *Staphylococcus aureus* were analysed. Antimicrobial resistance patterns demonstrated notable differences between bloodstream and pus aspirate isolates, while the small number of OSBF isolates precluded meaningful interpretation.

Cefoxitin resistance, used as a surrogate marker for methicillin resistance (MRSA), was high in both specimen types, with 59% (163/275) resistance among blood isolates and 50% (366/728) among pus aspirate isolates. This indicates a substantial burden of MRSA, particularly in bloodstream infections.

Among non- β -lactam agents, ciprofloxacin resistance was also high, affecting 54% (143/265) of blood isolates and 60% (416/694) of pus aspirate isolates, suggesting limited utility of fluoroquinolones for empirical treatment.

Erythromycin resistance was observed in 47% of blood isolates compared with 30% of pus isolates, indicating greater macrolide resistance among invasive isolates.

Resistance to Gentamicin was moderate, at 31% (98/321) in blood isolates and 22% (172/796) in pus aspirates. Similarly, trimethoprim/sulfamethoxazole resistance was 28% (92/332) in blood isolates and 18% (148/836) in pus aspirates, demonstrating comparatively better activity in skin and soft tissue isolates than in bloodstream isolates.

Resistance to clindamycin was relatively low overall but differed markedly between specimen types, with 16% (58/355) resistance in blood isolates compared with only 2% (22/1,197) in pus aspirates. Likewise, Doxycycline and Tetracycline retained excellent activity, with resistance rates of only 28%, making these agents valuable therapeutic options, particularly for susceptible skin and soft tissue infections.

Importantly, Linezolid and Teicoplanin remained highly effective. Linezolid resistance was extremely rare, observed in only 1.0% (4/398) of blood isolates and 0.2% (3/1,151) of pus aspirates, while Teicoplanin resistance remained low at 2% in both specimen types. These findings indicate preserved susceptibility to key anti-MRSA agents and support their continued role in the management of severe MRSA infections.

These findings underscore the importance of continued antimicrobial resistance surveillance and support the use of local antibiograms to guide empirical therapy and antimicrobial stewardship interventions.

Table 5: Specimen wise resistance profile of Staphylococcus aureus (n=1711)

Antibiotic Tested	Blood (N=406)			OSBF (N=32)			Pus Aspirate (N=1273)		
	Number Tested	Number Resistant	%Resistant	Number Tested	Number Resistant	%Resistant	Number Tested	Number Resistant	%Resistant
Cefoxitin	275	163	59%				728	366	50%
Ciprofloxacin	265	143	54%				694	416	60%
Clindamycin	355	58	16%				1197	22	2%
Doxycycline	313	9	3%				937	22	2%
Erythromycin	337	158	47%				1128	333	30%
Gentamicin	321	98	31%				796	172	22%
Linezolid	398	4	1.00 %				1151	3	0.20 %
Teicoplanin	83	2	2%				218	5	2%
Tetracycline	97	8	8%				447	33	7%
Trimethoprim/Sulfamethoxazole	332	92	28%				836	148	18%

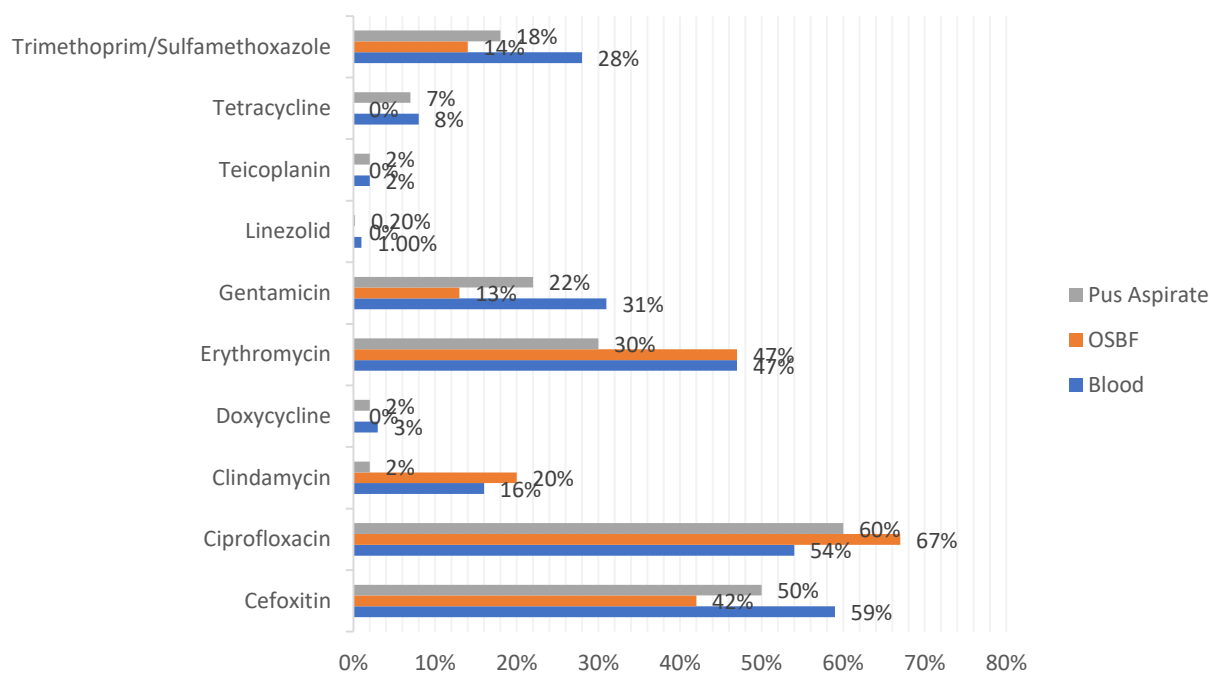


Figure 9: Specimen wise distribution of Resistance profile of *Staphylococcus aureus* (n=1711)

OVERALL RESISTANCE PROFILE OF STAPHYLOCOCCUS AUREUS

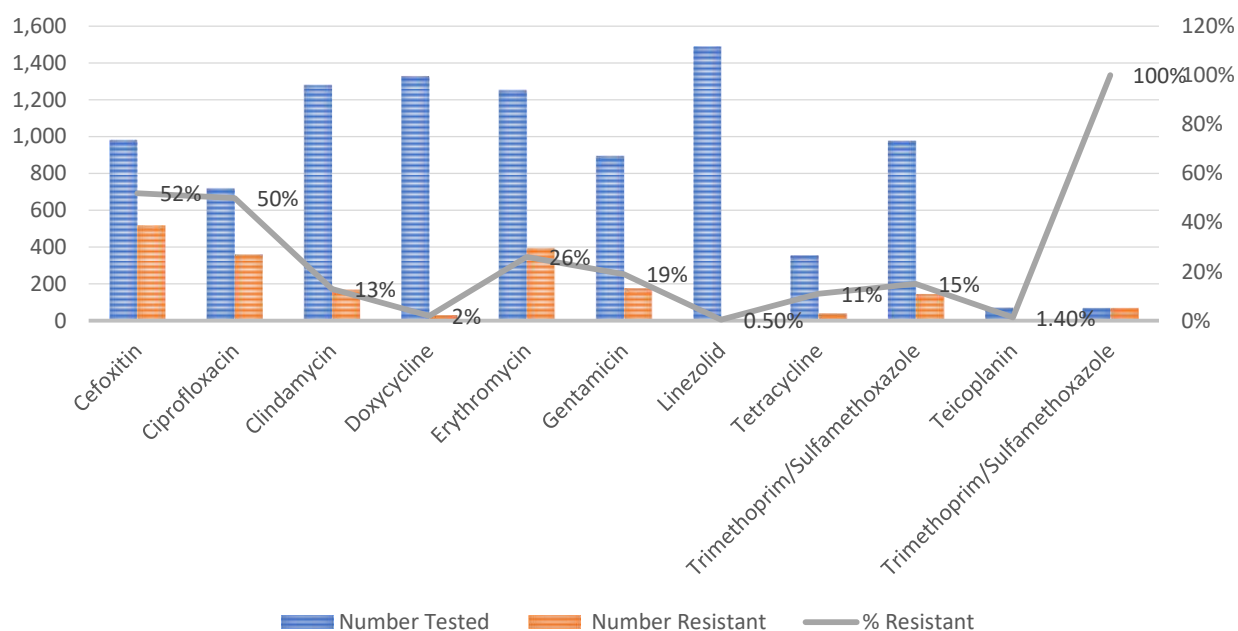


Figure 10: Overall Resistance profile of *Staph. aureus*

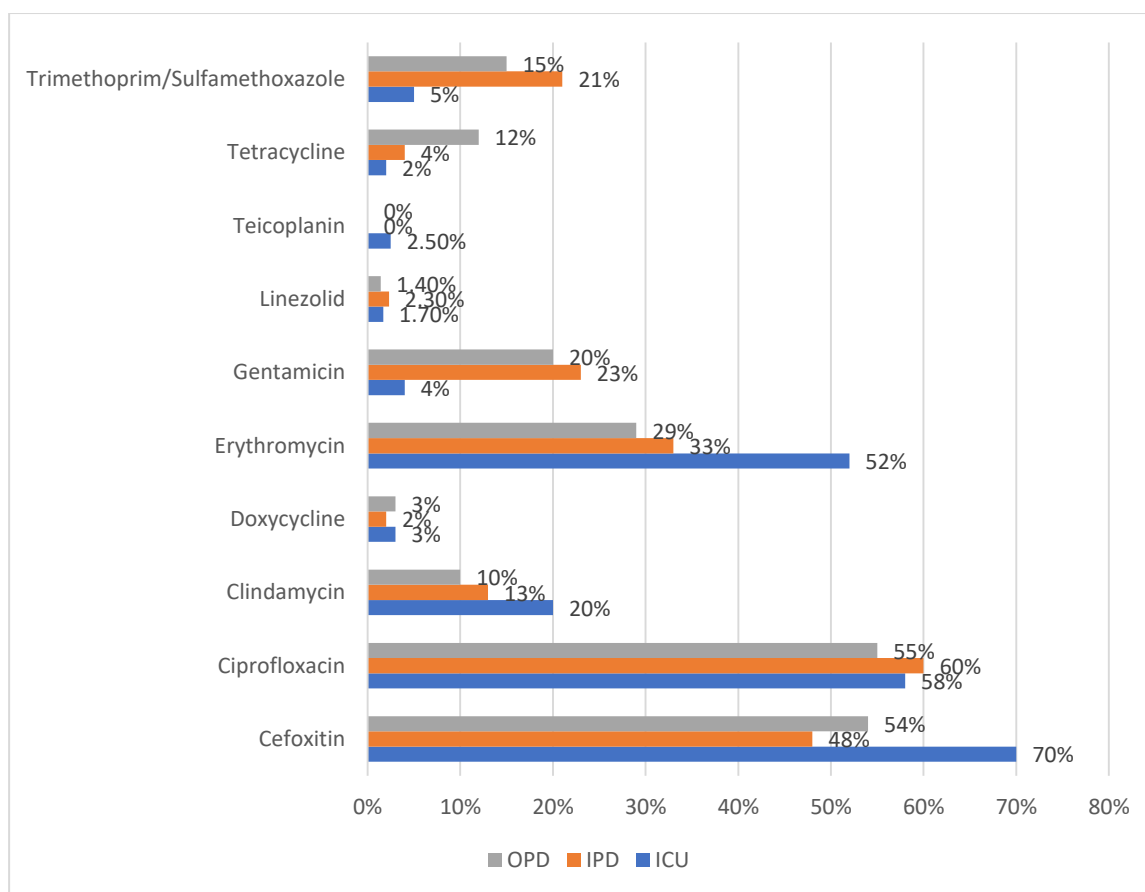


Figure 11: Location wise resistance profile of *Staphylococcus aureus* isolates (n=1711)

Figure 11 presents the resistance profile of *Staphylococcus aureus* according to patient location (Inpatient, Outpatient, and ICU). It provides valuable epidemiological information because it demonstrates how antimicrobial resistance increases with healthcare exposure. A clear gradient is visible. Cefoxitin resistance (marker for MRSA) was highest in the ICU (70%), followed by OPD (54%), and lowest in the IPD (48%), indicating a greater burden of MRSA among ICU isolates. Ciprofloxacin resistance was consistently high across all settings, ranging from 55–60% (OPD 55%, IPD 60%, ICU 58%), suggesting limited utility of fluoroquinolones for empirical therapy. Erythromycin resistance showed marked variation, with the highest resistance in ICU isolates (52%), compared with 33% in IPD and 29% in OPD, reflecting increased macrolide resistance in critically ill patients. Clindamycin resistance was also highest in the ICU (20%), compared with 13% in IPD and 10% in OPD, indicating the need for D-test confirmation before reporting clindamycin susceptibility. Gentamicin resistance remained relatively low in ICU isolates (4%) but was higher in IPD (23%) and OPD (20%). Trimethoprim/Sulfamethoxazole resistance was greatest in IPD isolates (21%), followed by OPD (15%), while ICU isolates showed only 5% resistance.

In contrast, linezolid, teicoplanin, doxycycline, and tetracycline retained excellent in vitro activity suggesting excellent glycopeptide activity, making them valuable therapeutic options where clinically appropriate. The higher resistance observed in ICU isolates likely reflects greater antibiotic selection pressure and the predominance of healthcare-associated strains. These findings support the need for unit-specific antibiograms and strengthened antimicrobial stewardship, particularly in critical care settings.

VRSA (Vancomycin Resistant *Staphylococcus aureus*)

Serious infections caused by Methicillin-Resistant *Staphylococcus aureus* (MRSA) require timely initiation of effective antimicrobial therapy. Vancomycin remains one of the cornerstone agents for the treatment of MRSA infections, as resistance to vancomycin among *S. aureus* isolates continues to be rare. It is also commonly used for empirical treatment when MRSA is suspected, particularly in healthcare-associated and nosocomial infections. In addition, vancomycin serves as an important therapeutic option for severe Gram-positive infections in patients with significant β -lactam allergy.

Although vancomycin-resistant *S. aureus* (VRSA) has been reported sporadically, often through acquisition of vancomycin resistance determinants from enterococci, such isolates remain exceedingly uncommon. Nevertheless, the emergence of reduced susceptibility or resistance to vancomycin underscores the importance of continued surveillance, antimicrobial stewardship, and stringent infection prevention measures. Given the limited number of alternative agents available for treating resistant Gram-positive infections, preservation of vancomycin efficacy remains a critical public health priority.

Detection of vancomycin resistance in the AARSNET network was performed using vancomycin screen agar. In addition, as per the latest Clinical and Laboratory Standards Institute (CLSI) recommendations, the broth microdilution method was employed for the quantitative determination of in vitro vancomycin activity against aerobic Gram-positive cocci, including both *Staphylococcus aureus* and *Enterococcus* species.

None of the *Staphylococcus aureus* isolates were resistant to Vancomycin.

Linezolid resistance in *Staphylococcus aureus*

Among isolates from 1711 unique patients tested for linezolid susceptibility, 4 isolates were found to be resistant, corresponding to an overall resistance rate of 0.23% (confirmed at NRL) indicating the emergence of linezolid resistance.

***Enterococcus* Species**

Enterococcus species are important Gram-positive cocci responsible for a wide range of opportunistic infections, particularly in immunocompromised patients. The most commonly associated clinical syndromes include enterococcal septicemia, intra-abdominal infections, and urinary tract infections (UTIs). They are frequently implicated in catheter-associated UTIs, infections in patients with structural urinary tract abnormalities, and immunosuppressed individuals. In intra-abdominal infections—especially those involving the biliary tract—*Enterococcus* species often occur in association with other intestinal flora, particularly *Enterococcus faecium*. These infections may progress to bacteremia and septicemia. Additionally, *Enterococcus faecalis* is an important, though less common, cause of infective endocarditis.

The two most clinically significant species are *Enterococcus faecalis* and *Enterococcus faecium*, both of which contribute substantially to healthcare-associated infections.

In the AARSNET surveillance data for 2025, *Enterococcus* species accounted for 9% of all reported isolates. A total of 1653 isolates were recorded, of which 1653 unique patient isolates were included in the WHONET analysis. As shown in Table 6, the majority of isolates were obtained from urine samples (1352), followed by blood (219), pus (69), and other sterile body fluids (9). Most isolates were reported from inpatient departments and intensive care units, reflecting a predominance of healthcare-associated infections.

Key findings: Resistance profile of *Enterococcus* species

Table 6 illustrates the overall resistance profile of *Enterococcus* species isolates obtained from 1653 unique patients.

Ampicillin resistance was highest among blood isolates (86%), followed by pus aspirates (66%) and urine isolates (64%), indicating widespread resistance to this first-line agent. Ciprofloxacin resistance was also substantial, with 87% resistance in blood isolates and 49% in urine isolates, suggesting poor utility of fluoroquinolones for empirical treatment of enterococcal infections. Erythromycin resistance remained high across all specimen types, reaching 86% in blood, 71% in urine, and 56% in pus aspirates, reflecting extensive macrolide resistance. Tetracycline resistance was similarly elevated in both blood (65%) and urine (66%) isolates. Penicillin G resistance exceeded 70% in both blood (75%) and urine (73%) isolates, further limiting the effectiveness of β -lactam therapy. High-level gentamicin resistance (HLGR), an important predictor of failure of synergistic aminoglycoside therapy, was observed in 42% of urine isolates, 33% of blood isolates, and 23% of pus aspirates. Nitrofurantoin resistance remained relatively low to moderate, with 39–40% resistance among urinary and blood isolates, indicating that approximately 60% of urinary isolates remained susceptible. Doxycycline resistance was comparatively lower, ranging from 11% in pus aspirates to 29% in blood and 34% in urine isolates. Resistance to the anti-enterococcal agents Linezolid, Vancomycin, and Teicoplanin remained relatively low. Linezolid resistance was observed in only 1 isolate which was confirmed at the NRL, while Vancomycin resistance ranged 15 isolates. Teicoplanin resistance was also low, ranging from 12–15% across specimen types.

Antibiotic name	Blood (n=219)			Urine (n=1352)			Pus Aspirate(n=69)		
	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R
Ampicillin	86	74	86%	1110	709	64%	35	23	66%
Ciprofloxacin	151	131	87%	361	730	49%			
Doxycycline	90	26	29%	604	203	34%	35	4	11%
Erythromycin	154	132	86%	45	32	71%	32	18	56%
Gentamicin-High	179	59	33%	1279	532	42%	53	12	23%
Linezolid	216	8	4%	1268	27	2%	60	1	2.00%
Teicoplanin	169	21	12%	723	85	12%	34	5	15%
Tetracycline	133	86	65%	516	342	66%			
Vancomycin	211	32	15%	1297	66	5%	62	3	5%
Penicillin G	117	88	75%	22	16	73%			
Nitrofurantoin	104	42	40%	1303	511	39%			

Table 6: Specimen wise resistance profile of *Enterococcus* species (n=1653)

To summarise, the data demonstrates high levels of resistance to commonly used antibiotics, including Ampicillin, Ciprofloxacin, Erythromycin, Penicillin G, and Tetracycline, particularly among bloodstream isolates. The presence of high-level Gentamicin resistance in one-third to nearly half of isolates is clinically significant because it compromises synergistic therapy with cell wall-active agents. Encouragingly, Linezolid and Glycopeptides (Vancomycin and Teicoplanin) retained good in vitro activity, although the detection of 15 isolates resistant to Vancomycin indicates the emergence of Vancomycin-resistant Enterococci (VRE) and highlights the need for continued antimicrobial stewardship and ongoing AMR surveillance.

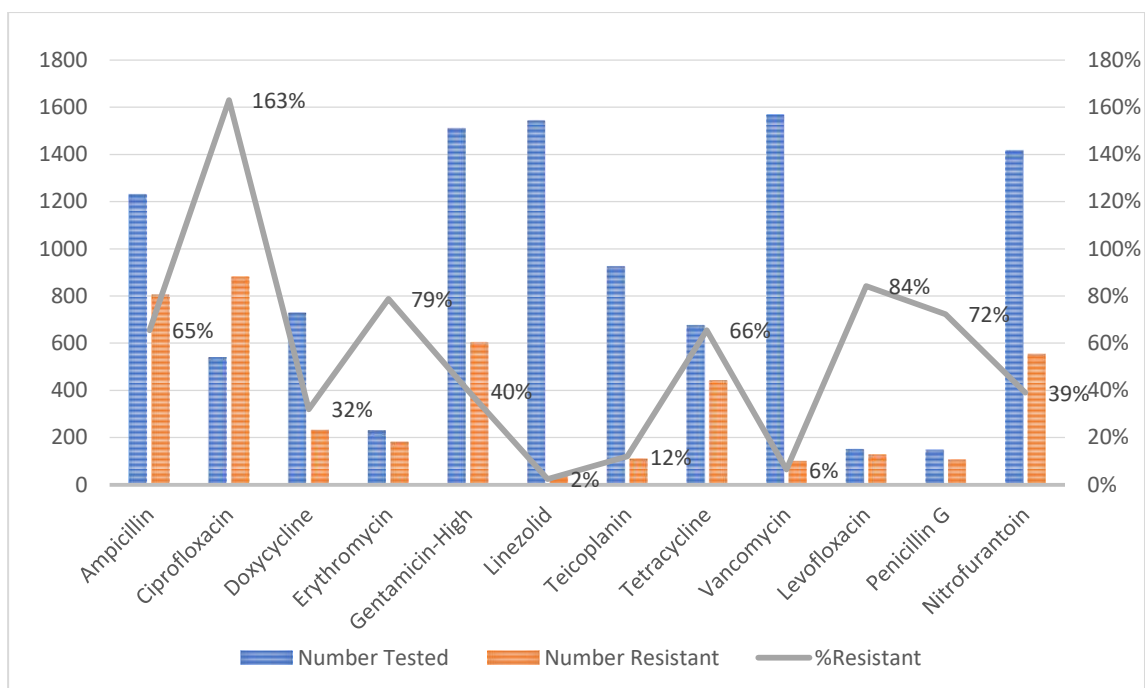


Figure 12: Resistance profile of *Enterococcus* species (n=1649)

The specimen-wise resistance pattern among isolates from urine, blood, pus, and other sterile body fluids (OSBF) is presented in Figure 12. The resistance profile demonstrates that blood isolates exhibited the highest levels of multidrug resistance, particularly to ampicillin, ciprofloxacin, erythromycin, and penicillin G, suggesting greater antimicrobial selection pressure among invasive hospital-acquired infections. The detection of high-level gentamicin resistance in one-third to nearly half of isolates further limits the use of synergistic aminoglycoside-based therapy. Despite these concerns, linezolid, vancomycin, and teicoplanin retained good in vitro activity, although the emergence of 15 isolates of VRE warrants continued surveillance, strict infection prevention measures, and antimicrobial stewardship to prevent further dissemination of resistant *Enterococcus* strains.

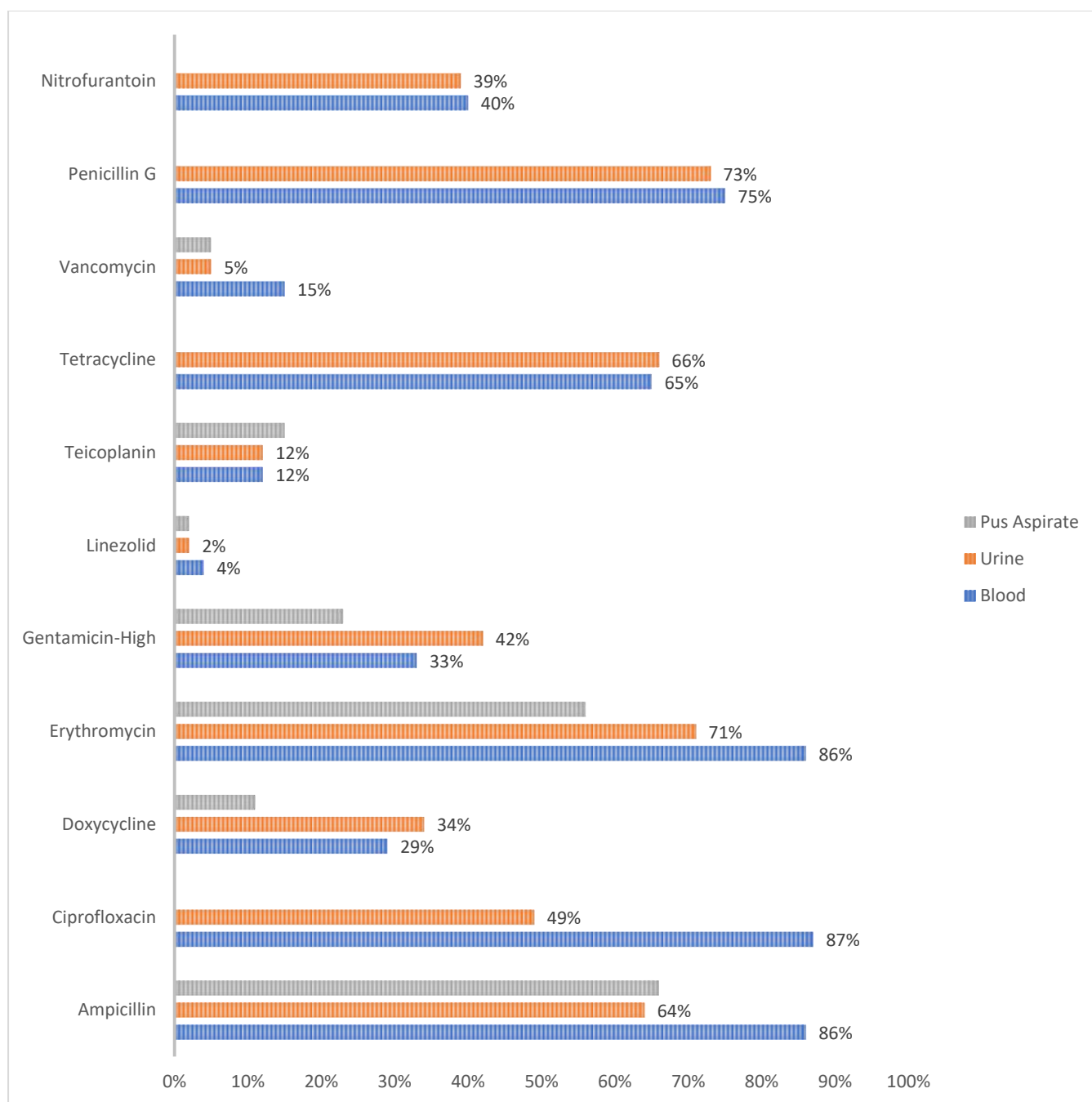


Figure 13: Specimen wise resistance profile of *Enterococcus* species(n=1653)

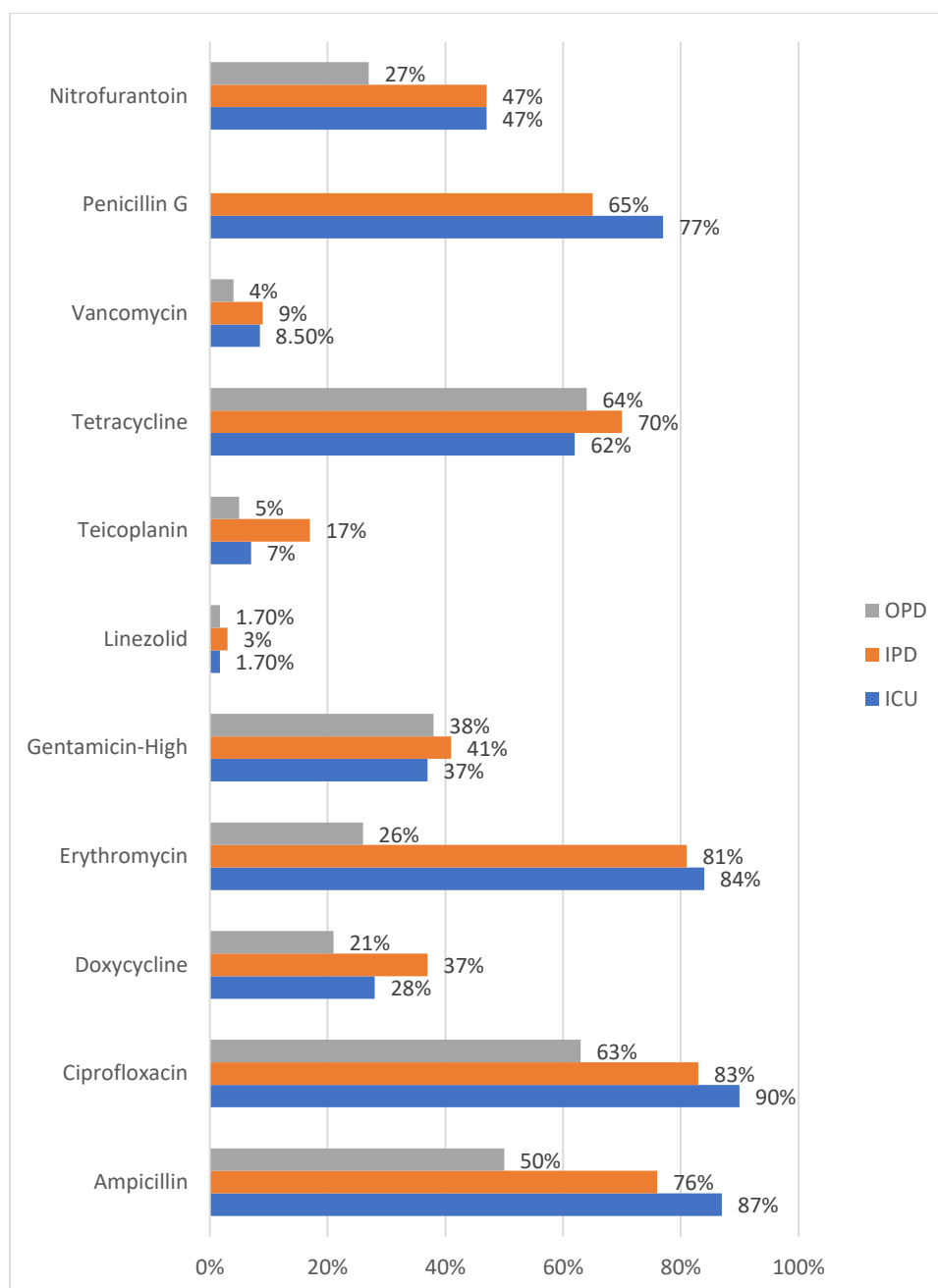


Figure 14: Location wise resistance profile of *Enterococcus* species

Figure 14 compares the antimicrobial resistance profile of *Enterococcus* isolates obtained from the Outpatient Department (OPD), Inpatient Department (IPD), and Intensive Care Unit (ICU). Overall, resistance was highest among ICU isolates, followed by IPD, while OPD isolates generally exhibited lower resistance, indicating increasing antimicrobial selection pressure with higher levels of patient care. The resistance profile demonstrates a clear trend of higher antimicrobial resistance among hospitalized patients, particularly those admitted to the ICU, where resistance to ampicillin, ciprofloxacin, erythromycin, and penicillin G exceeded 75–90%. The prevalence of high-level gentamicin resistance (~37–41%) further limits the effectiveness of synergistic therapy. In contrast, linezolid retained excellent activity across all healthcare settings, while vancomycin and teicoplanin also remained effective against the majority of isolates, despite the detection of low-level glycopeptide resistance. These findings underscore the importance of unit-specific antibiograms,

antimicrobial stewardship, and continuous surveillance to optimize empirical therapy and curb the emergence and spread of multidrug-resistant *Enterococcus* species.

VRE (Vancomycin Resistant *Enterococcus* species)

Vancomycin resistance among *Enterococcus* isolates was reported among 15 isolates in 2025 (confirmed at NRL), with higher resistance observed in blood isolates compared to other specimen types.

Vancomycin-resistant enterococci (VRE) were identified in both *E. faecium* and *E. faecalis*. The genus *Enterococcus* represents the first clinically significant group of Gram-positive cocci to acquire and disseminate resistance to vancomycin, which is a key cell wall-active agent used against Gram-positive organisms resistant to β -lactams, including methicillin-resistant staphylococci. The emergence and potential transfer of vancomycin resistance determinants to other clinically important pathogens, including the reported emergence of vancomycin-resistant *Staphylococcus aureus*, remains a serious public health concern.

The primary genetic determinants of resistance are the *vanA* and *vanB* gene clusters, highlighting the role of enterococci as reservoirs of transferable resistance genes.

Treatment options for VRE infections are limited and typically include agents reserved for resistant infections, such as teicoplanin or daptomycin.

Linezolid resistance in *Enterococcus* species

Linezolid resistance among vancomycin-resistant enterococci (VRE) strains was observed in 1 isolate only (confirmed at NRL).

High level aminoglycoside resistance in *Enterococcus* species

Combination therapy using high-dose parenteral cell wall-active agents such as ampicillin, amoxicillin, or vancomycin in combination with an aminoglycoside is generally recommended for the treatment of severe enterococcal infections, including endocarditis. In this context, high-level gentamicin resistance serves as an important predictor of the loss of synergistic activity between these agents against *Enterococcus* species. High-level gentamicin resistance was observed to be 33% of among a total of 1649 isolates tested.

Gram negative bacilli

Gram-negative bacteria (GNB) are among the most frequently isolated pathogens in clinical practice and are a leading cause of morbidity and mortality worldwide, particularly among critically ill patients. Within the AARSNET surveillance network, Gram-negative organisms account for the majority of priority pathogens reported from participating healthcare facilities. These organisms are responsible for a wide spectrum of infections, including bloodstream infections, pneumonia, urinary tract infections, surgical site infections, and other healthcare-associated infections (HAIs).

The emergence and spread of multidrug-resistant Gram-negative bacilli (MDR-GNB) have further complicated the management of these infections. MDR-GNB are increasingly implicated in infections occurring in intensive care units (ICUs), other hospital settings, and the community, posing significant therapeutic and public health challenges. Continuous surveillance of antimicrobial resistance among Gram-negative pathogens is therefore essential for guiding empirical therapy, informing infection prevention and control strategies, and supporting antimicrobial stewardship interventions.

A total of 9945 Gram-negative isolates were reported from 9896 unique patients across 12 network laboratories. The major Gram-negative pathogens reported under the AARSNET network included *Escherichia coli* 4809 (48.3%), *Klebsiella* species 2863 (29%), and non-fermenting Gram-negative bacilli such as *Pseudomonas* species 1049 (10.5%) and *Acinetobacter* species 1205 (12.1%). In addition, *Shigella* species (17 isolates) were also reported while only 1 isolate of *Salmonella typhi* was reported.

Enterobacteriaceae

Enterobacteriaceae constituted the majority 7691 (58%) of the overall priority pathogens in 2025. Therefore, Enterobacteriaceae represent the predominant group of pathogens associated with infections seen in healthcare facilities and contribute to the increasing multidrug resistant strains.

Escherichia coli

Escherichia coli was the predominant pathogen, accounting for 36% of all priority isolates, with 4828 isolates reported from 4828 unique patients. It was also identified as the leading causative agent of urinary tract infections (UTIs), with 3698 urine culture-positive specimen reported. This was followed by isolates from pus (834), blood (226), and other sterile body fluids (70). Antimicrobial susceptibility patterns for all culture-positive isolates were analyzed using WHONET software.

Key Findings: Resistance Profile of *Escherichia coli*

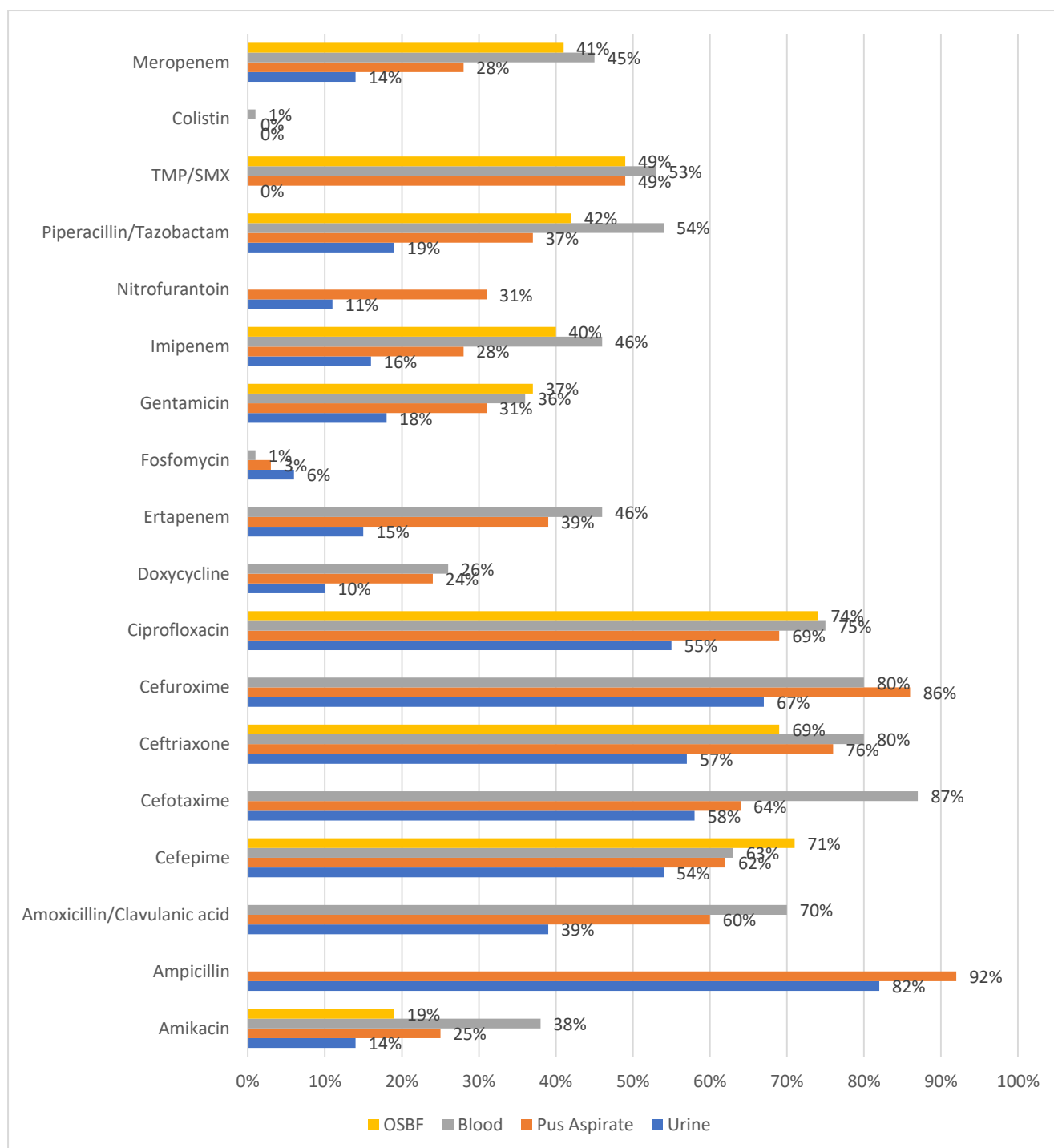
The antimicrobial resistance profile of *Escherichia coli* varied across specimen types, with the highest number of isolates recovered from urine (n = 3,698), followed by pus aspirates (n = 834), blood (n = 226), and other sterile body fluids (OSBF; n = 70). Overall, bloodstream and sterile site isolates demonstrated higher resistance than urinary isolates.

The data demonstrate high levels of multidrug resistance among *E. coli*, particularly to ampicillin, cephalosporins, ciprofloxacin, and amoxicillin/clavulanic acid, with resistance being consistently higher in bloodstream and sterile-site isolates than in urinary isolates. The substantial resistance to third-generation cephalosporins strongly suggests a high prevalence of extended-spectrum β -lactamase (ESBL)-producing *E. coli*. Furthermore, the increasing resistance to carbapenems, especially among bloodstream isolates (45–46%), is concerning and indicates the emergence of carbapenem-resistant *E. coli* (CRE). In contrast, fosfomycin, nitrofurantoin (for urinary isolates), colistin, amikacin, and piperacillin/tazobactam retained relatively good activity, although susceptibility to the latter declined in invasive infections. These findings underscore the importance of routine antimicrobial resistance surveillance, unit-specific antibiograms, and robust antimicrobial

stewardship programs to guide empirical therapy and limit further dissemination of multidrug-resistant *E. coli*.

Table 7: Specimen wise resistance profile of *E. coli* (n=4828)

	Urine (n=3698)			Pus Aspirate (n=834)			Blood (n=226)			OSBF (n=70)		
Antibiotic name	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R
Amikacin	3,134	446	14%	692	171	25%	211	80	38%	48	9	19%
Ampicillin	633	520	82%	122	112	92%						
Amoxicillin/Clavulanic acid	1,200	473	39%	384	230	60%	153	107	70%			
Cefepime	704	379	54%	510	315	62%	185	117	63%	34	24	71%
Cefotaxime	2,371	1382	58%	382	244	64%	114	99	87%			
Ceftriaxone	2,249	1278	57%	470	357	76%	95	76	80%	35	24	69%
Cefuroxime	350	236	67%	273	224	86%	66	53	80%			
Ciprofloxacin	2,780	1538	55%	507	345	69%	147	110	75%	35	26	74%
Doxycycline	337	35	10%	501	118	24%	34	9	26%			
Ertapenem	1699	261	15%	271	105	39%	70	32	46%			
Fosfomycin	2121	133	6%	169	5	3%	88	1	1%			
Gentamicin	2,262	400	18%	489	153	31%	166	59	36%	35	13	37%
Imipenem	1,508	246	16%	535	152	28%	191	88	46%	35	14	40%
Nitrofurantoin	3,518	393	11%	32	10	31%						
Piperacillin/Tazobactam	3,291	640	19%	776	284	37%	213	114	54%	50	21	42%
TMP/SMX	2,979	1	0%	622	306	49%	209	111	53%	43	21	49%
Colistin	1407	1	0%	329	0	0%	96	1	1%			
Meropenem	2460	345	14%	651	183	28%	208	94	45%	44	18	41%

Figure 15: Specimen wise resistance profile of *E. coli* (n=4828)

The data in Figure 15 highlights a high prevalence of multidrug-resistant *Escherichia coli*, with particularly high resistance to ampicillin, cephalosporins, ciprofloxacin, and amoxicillin/clavulanic acid. Resistance was consistently higher among bloodstream and other sterile-site isolates, reflecting greater antimicrobial selection pressure in severe healthcare-associated infections. The marked resistance to third-generation cephalosporins suggests widespread ESBL production, while the higher resistance to carbapenems (41–46% in invasive isolates) raises concern for the emergence of carbapenem-resistant *E. coli*. In contrast, fosfomycin, nitrofurantoin (for urinary isolates), colistin, and amikacin retained the greatest in vitro activity, although susceptibility to piperacillin/tazobactam

and carbapenems declined substantially in invasive infections. These findings emphasize the need for specimen-specific antibiograms, continuous antimicrobial resistance surveillance, and robust antimicrobial stewardship.

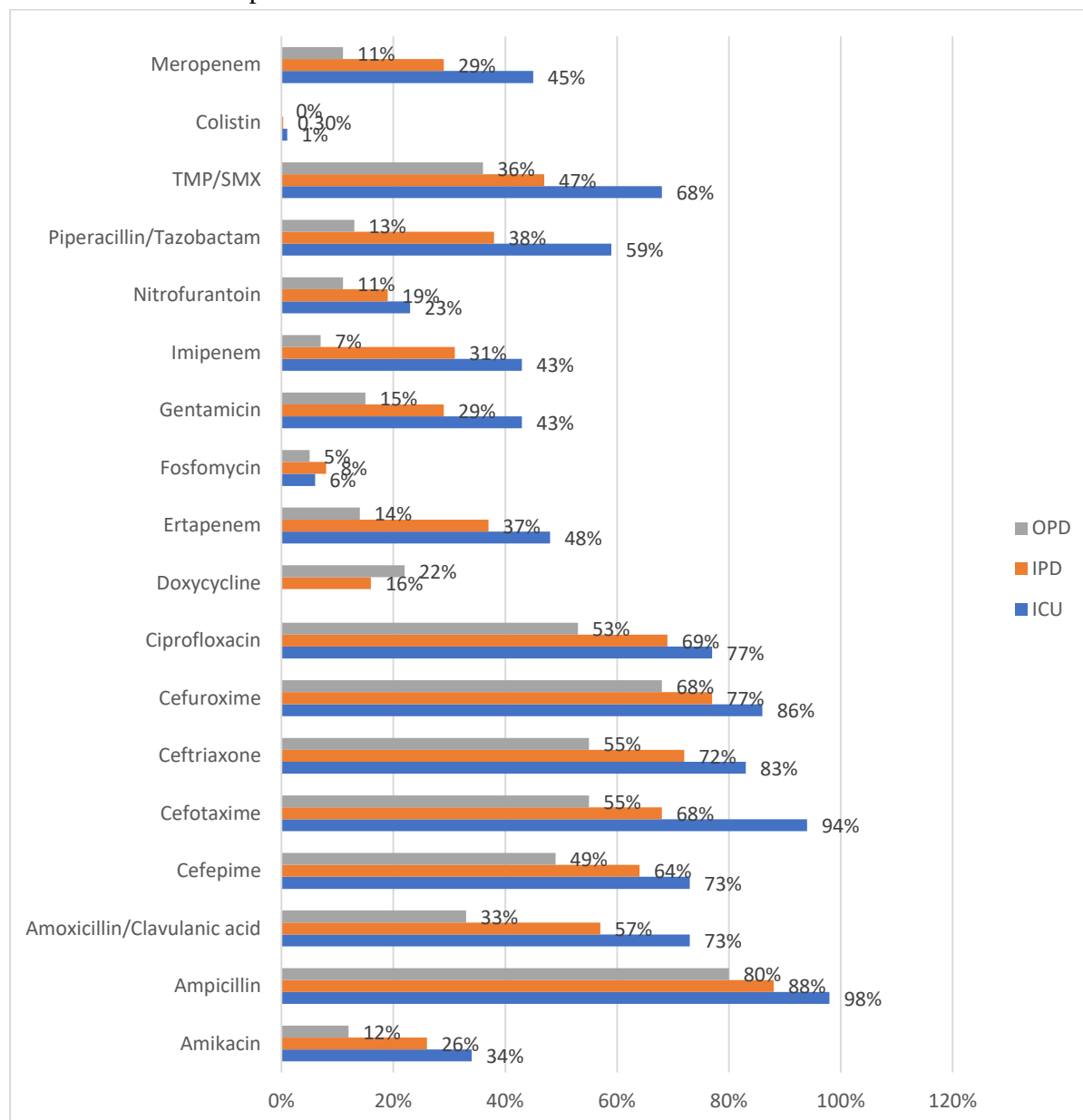


Figure 16: Location wise Resistance profile of *E. coli* species(n=4828)

The antibiogram in figure 16 demonstrates a progressive increase in antimicrobial resistance from OPD to ICU, reflecting the greater antimicrobial selection pressure and predominance of healthcare-associated *E. coli* strains in hospitalized patients. ICU isolates exhibited the highest resistance to β -lactams, fluoroquinolones, aminoglycosides, and carbapenems, with ampicillin (98%), cefotaxime (94%), cefuroxime (86%), ceftriaxone (83%), and ciprofloxacin (77%) showing particularly high resistance. The substantial resistance to third-generation cephalosporins is highly suggestive of widespread ESBL-producing *E. coli*, while the increasing resistance to carbapenems (43–48% in ICU isolates) indicates the emergence of carbapenem-resistant Enterobacterales (CRE), posing a significant therapeutic challenge. Despite these concerns, fosfomycin, nitrofurantoin (particularly for urinary infections), colistin, and amikacin retained relatively good activity, although even these

agents showed declining susceptibility in hospitalized patients. These findings underscore the importance of hospital unit-specific antibiograms, rigorous antimicrobial stewardship, infection prevention measures, and continuous surveillance to optimize empirical therapy and contain the spread of multidrug-resistant *E. coli*.

***Klebsiella* species**

For the year 2025, the AARSNET network sites reported 2890 *Klebsiella* species isolates from 2,890 unique patients. Similar to *Escherichia coli*, the highest number of *Klebsiella* spp. isolates were obtained from urine samples (1345), followed by pus (996), blood (429), and other sterile body fluids (120), as shown in Table 8.

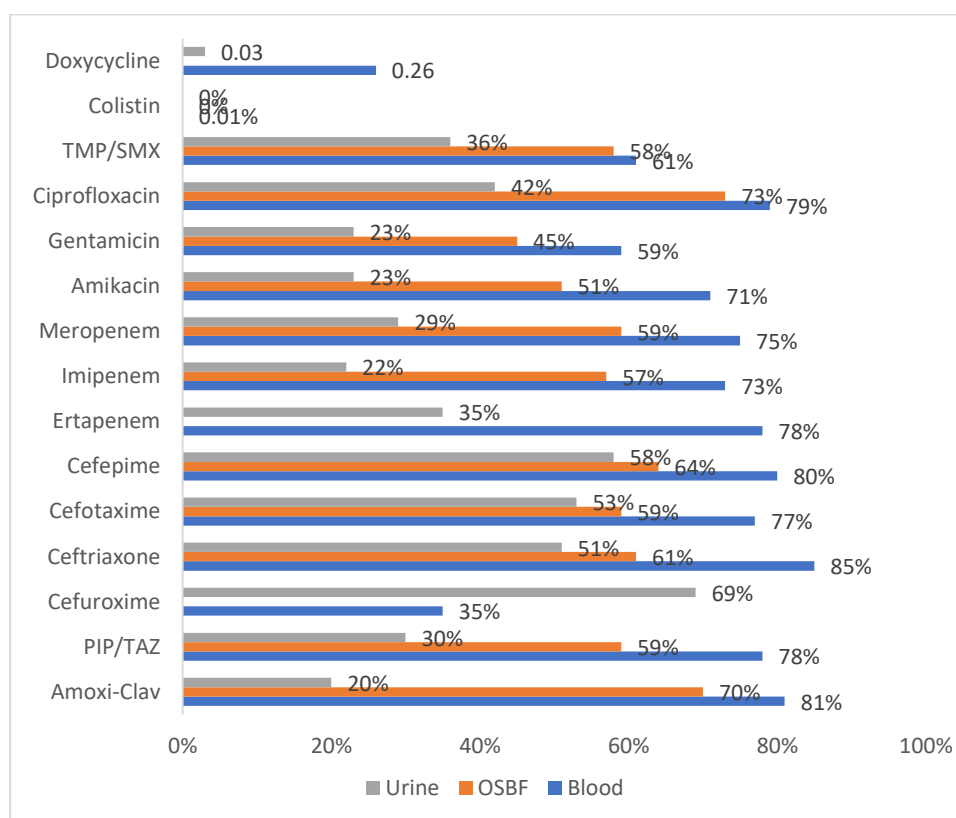
Klebsiella species are important opportunistic pathogens and a common cause of nosocomial infections involving the respiratory tract, urinary tract, bloodstream, and other normally sterile body sites. These infections are predominantly seen in hospitalized and severely ill patients.

Key findings—resistance profile of *Klebsiella* species

Table 8 demonstrates the antimicrobial resistance profile of *Klebsiella* species which varied across specimen types, with the highest number of isolates recovered from urine (n = 1,345), followed by pus aspirates (n = 996), blood (n = 429), and other sterile body fluids (OSBF; n = 120). Overall, bloodstream isolates exhibited the highest resistance, followed by OSBF isolates, whereas urinary isolates showed comparatively lower resistance to most antimicrobial agents. The data also demonstrates a marked difference between invasive and urinary isolates, with bloodstream isolates exhibiting the highest levels of multidrug resistance. Resistance to third-generation cephalosporins, piperacillin/tazobactam, fluoroquinolones, aminoglycosides, and carbapenems was particularly high among blood isolates, strongly suggesting widespread ESBL-producing and carbapenem-resistant *Klebsiella* spp. (CRKP). The exceptionally high carbapenem resistance in bloodstream isolates (73–78%) is of major clinical concern, as it substantially limits treatment options for severe infections. In contrast, urinary isolates retained comparatively better susceptibility to piperacillin/tazobactam, carbapenems, aminoglycosides, and amoxicillin/clavulanic acid. Colistin remained the most active antimicrobial agent, with virtually no resistance detected across specimen types, while nitrofurantoin showed only moderate activity against urinary isolates. These findings highlight the need for specimen-specific antibiograms, stringent antimicrobial stewardship, rapid detection of ESBL- and carbapenemase-producing strains, and robust infection prevention measures to curb the spread of multidrug-resistant *Klebsiella* species.

Table 8: Specimen wise resistance profile of *Klebsiella* species(n=2890)

Antibiotics Tested	Blood (n=429)			OSBF (n=120)			Pus Aspirate (n=996)			Urine (n=1345)		
	Number Tested	Number Resistant	% R	Number Tested	Number Resistant	% R	Number Tested	Number Resistant	% R	Number Tested	Number Resistant	% R
Amoxi-Clav	226	184	81%	33	23	70%				410	83	20%
PIP/TAZ	411	322	78%	76	45	59%				1209	358	30%
Cefuroxime	86	30	35%							143	98	69%
Ceftriaxone	131	112	85%	34	21	61%				853	439	51%
Cefotaxime	158	122	77%	34	20	59%				868	463	53%
Cefepime	350	279	80%	67	43	64%				268	155	58%
Ertapenem	100	78	78%							616	218	35%
Imipenem	366	268	73%	60	34	57%				571	127	22%
Meropenem	394	297	75%	75	44	59%				864	247	29%
Amikacin	410	293	71%	70	36	51%				1162	265	23%
Gentamicin	350	206	59%	56	25	45%				826	193	23%
Ciprofloxacin	345	274	79%	44	32	73%				1003	426	42%
TMP/SMX	398	244	61%	71	41	58%				1022	365	36%
Colistin	207	2	0.009%	47	0	0%				538	0	0%
Doxycycline	50	13	0.26							116	4	0.03
Nitrofurantoin										1238	557	45%

Figure 17: Specimen wise resistance profile of *Klebsiella* species (n=2890)

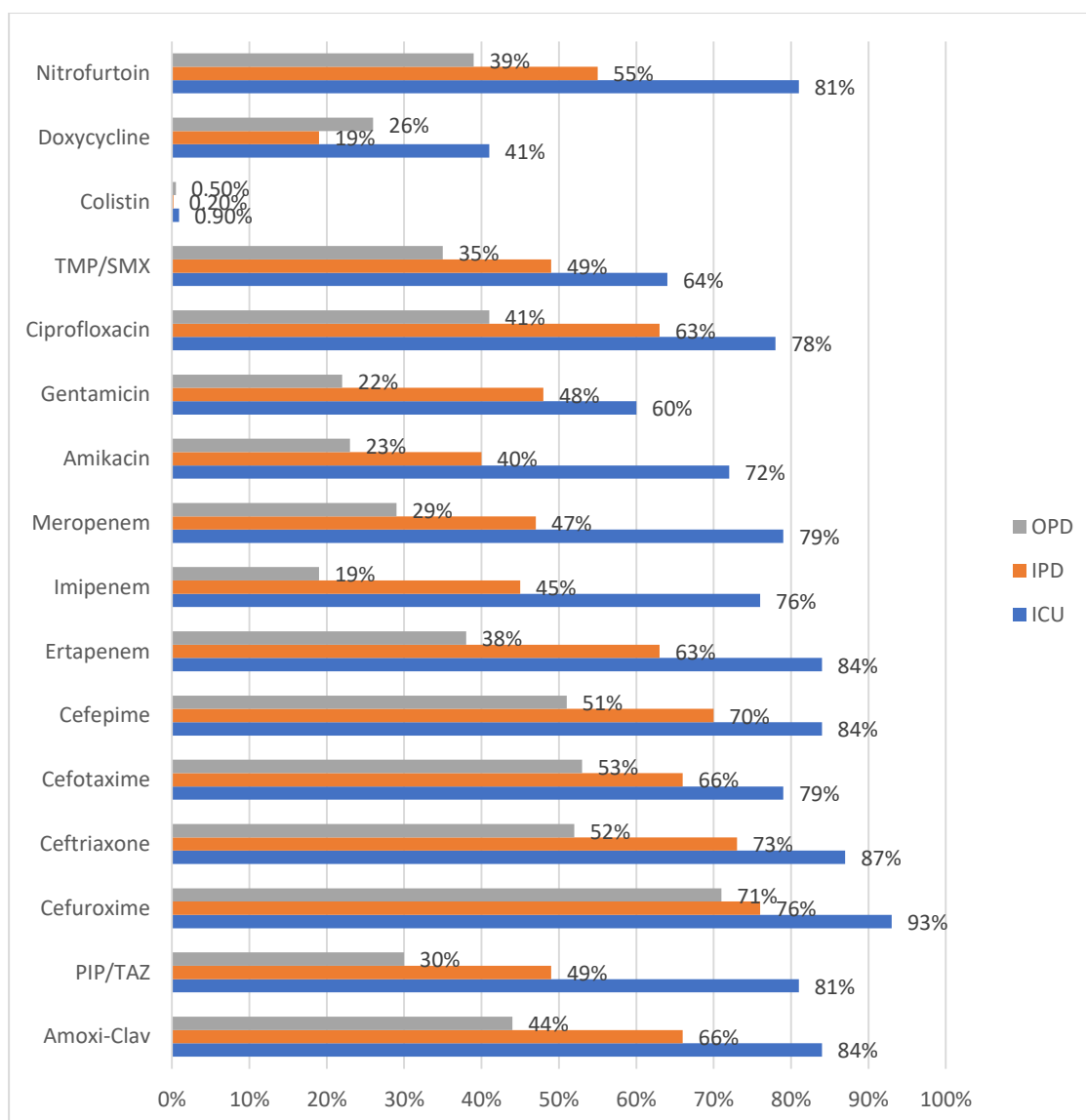


Figure 18: Location wise Resistance Profile of *Klebsiella* species in percentage (n=2890)

Analysis of the resistance profile according to location demonstrates a progressive increase in antimicrobial resistance from OPD to ICU, with ICU isolates showing the highest resistance to nearly all antibiotic classes. Particularly concerning are the very high resistance rates to third- and fourth-generation cephalosporins (79–93%), piperacillin/tazobactam (81%), and carbapenems (76–84%), indicating widespread circulation of ESBL-producing and carbapenem-resistant *Klebsiella* spp. in critical care settings. Aminoglycosides and fluoroquinolones also showed markedly reduced activity in ICU isolates, further limiting therapeutic options. In contrast, colistin retained excellent in vitro activity, with no resistance reported across all hospital locations. These findings underscore the urgent need for unit-specific antibiograms, robust antimicrobial stewardship, routine surveillance for ESBL and carbapenems-producing isolates, and stringent infection prevention and control practices to curb the spread of multidrug-resistant *Klebsiella* species and optimize empirical antimicrobial therapy.

The resistance profile highlights the serious challenge posed by multidrug-resistant Gram-negative pathogens in bloodstream infections. While most organisms exhibit extensive resistance to commonly used antibiotics, *Klebsiella* spp. show a distinctly higher level of resistance, particularly to carbapenems and broad-spectrum β -lactams, suggesting a greater burden of carbapenems-producing strains.

***Salmonella enterica* serotype Typhi and Paratyphi**

Salmonella enterica serovars Typhi and Paratyphi (collectively referred to as typhoidal *Salmonella*) are responsible for enteric fever, a distinct clinical syndrome that can result in significant morbidity and mortality if left untreated.

In contrast, non-typhoidal *Salmonella* gastroenteritis is typically self-limiting, and routine antimicrobial therapy is generally not recommended, as it does not alter the clinical course and may prolong intestinal carriage following resolution of symptoms, thereby increasing the risk of transmission. Antimicrobial treatment is reserved for patients with severe disease or septicemia, particularly in cases of typhoidal *Salmonella* infection, as well as in individuals with prosthetic vascular grafts. The standard therapeutic agents include ciprofloxacin, azithromycin, and ceftriaxone.

For the year 2025, AARSNET network sites submitted antimicrobial resistance (AMR) surveillance data for 1 *Salmonella* species isolate. This isolate was obtained from stool specimen.

Non-fermenting Gram-negative bacilli

The non-fermenting gram-negative bacilli (NFGNB) included in the priority pathogen list for AARSNET are *Pseudomonas* spp. and *Acinetobacter* spp. Among these, *Acinetobacter* spp. (1205; 9%) was the most common isolate followed by *Pseudomonas* spp. (1065; 8%).

***Pseudomonas* species**

Pseudomonas aeruginosa is an important opportunistic pathogen and a leading cause of healthcare-associated infections, particularly among critically ill and immunocompromised patients. It is commonly implicated in hospital-acquired and ventilator-associated pneumonia, bloodstream infections, urinary tract infections, surgical site infections, and other device-associated infections. The organism possesses multiple intrinsic and acquired resistance mechanisms, enabling it to survive in healthcare environments and develop resistance to several classes of antimicrobial agents. The increasing prevalence of multidrug-resistant (MDR) and carbapenem-resistant *P. aeruginosa* has emerged as a major public health concern, significantly limiting treatment options and contributing to increased morbidity, mortality, length of hospital stay, and healthcare costs.

For the year 2025, a total of 1065 *Pseudomonas* species isolates were reported from 1065 unique patients across AARSNET network sites, accounting for 8% of the total isolates.

Key findings—resistance profile of *Pseudomonas* species

1065 *Pseudomonas* spp. unique patient isolates were analyzed using WHONET software. The majority of isolates were obtained from pus (584), followed by urine (275), blood (126), and other sterile body fluids (80).

Analysis of antimicrobial resistance among *Pseudomonas aeruginosa* isolates revealed considerable variation across specimen types, with bloodstream and urine isolates generally demonstrating higher resistance rates than isolates from pus aspirates, and other sterile body fluids (OSBF). Resistance was observed across multiple antimicrobial classes, highlighting the therapeutic challenges associated with infections caused by this organism.

A total of 126 bloodstream, 275 urine, 584 pus aspirate, and 80 other sterile body fluid (OSBF) isolates of *Pseudomonas aeruginosa* were analyzed. The resistance profile demonstrated considerable variation across specimen types, with carbapenem and cephalosporin resistance remaining substantial, while colistin retained excellent activity.

High resistance to ceftazidime, fluoroquinolones, aminoglycosides, and carbapenems, particularly among bloodstream and pus aspirate isolates was observed. Piperacillin/tazobactam retained comparatively good activity, while colistin remained the most effective antimicrobial, with near-universal susceptibility across tested isolates. These findings indicate that colistin remains highly effective against multidrug-resistant *P. aeruginosa* and also highlight the ongoing challenge of multidrug-resistant *P. aeruginosa* and emphasize the importance of antimicrobial stewardship and continuous local resistance surveillance to guide empirical and targeted therapy.

Table 9: Specimen wise resistance profile of *Pseudomonas* species (n=1065)

Antibiotic name	Blood (n=126)			Urine (n=275)			Pus Aspirate (n=584)			OSBF (n=80)		
	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R
Amikacin	61	27	44%	241	110	45%	495	176	35%	30	9	30%
Aztreonam	110	52	47%	227	59	26%	435	150	34%	44	16	36%
Ceftazidime	119	66	55%	214	113	52%	531	307	57%	46	22	47%
Ciprofloxacin	84	33	39%	218	118	54%	371	158	42%	30	12	40%
Gentamicin	20	8	40%	165	78	47%	208	100	48%			
Imipenem	110	51	46%	224	95	42%	542	193	35%	38	13	34%
Meropenem	119	54	45%	236	92	39%	491	172	35%	46	18	39%
Netilmicin	10	4	40%	137	88	64%	173	110	63%			
Piperacillin/Tazobactam	123	37	30%	260	27	10%	574	115	20%	47	10	21%
Colistin	35	0	0%	159	0	0%	300	4	1%			

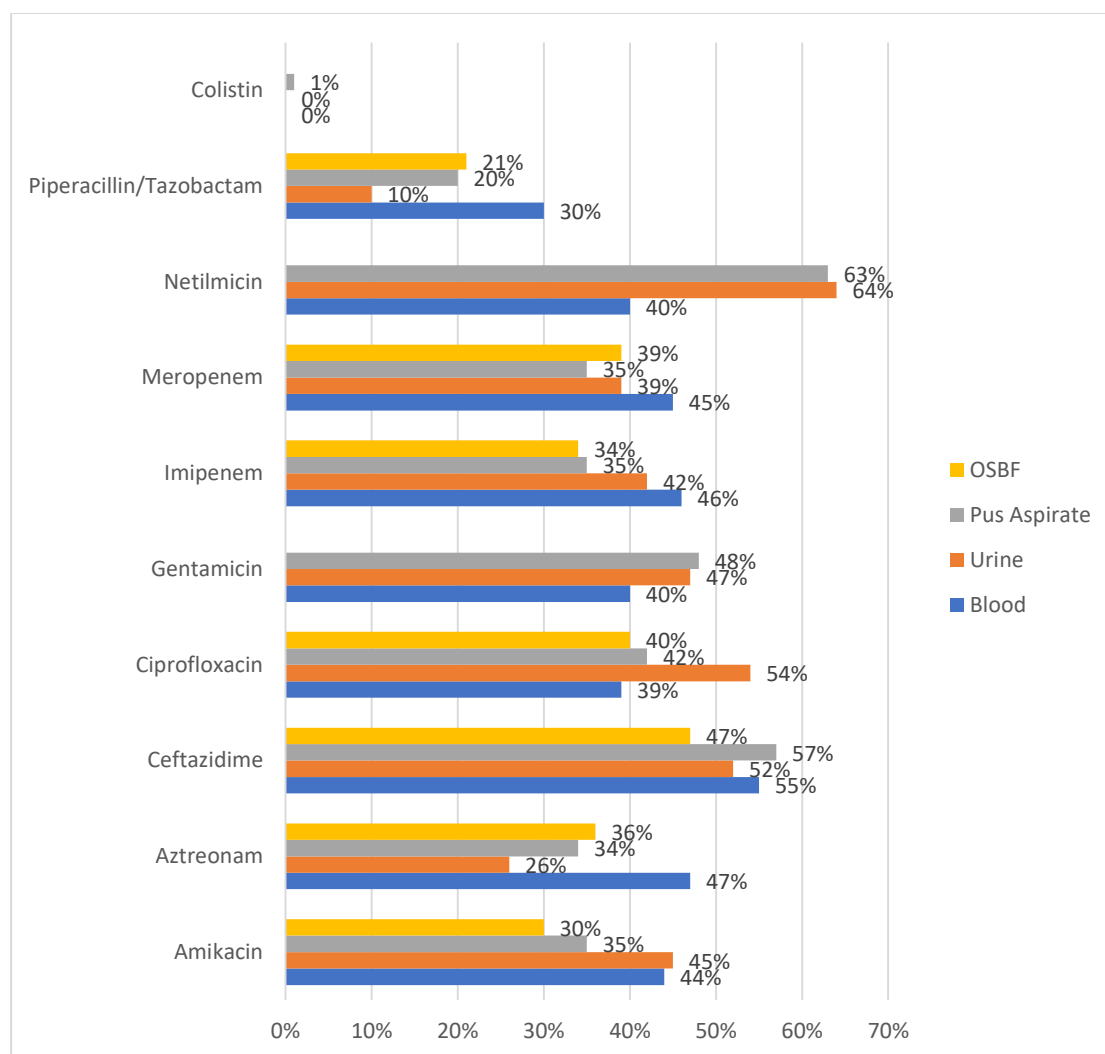


Figure 19: Specimen wise Resistance profile of *Pseudomonas* species (n=1065)

Figure 19 compares the antimicrobial resistance profile of *Pseudomonas aeruginosa* isolates recovered from blood, urine, pus aspirates, and other sterile body fluids (OSBF). Overall, resistance varied by specimen type, with blood and pus aspirate isolates generally exhibiting higher resistance than urinary and OSBF isolates. Moderate to high resistance was observed against several antipseudomonal β -lactams, aminoglycosides, and carbapenems, whereas colistin retained excellent activity across all specimen types. The antimicrobial resistance profile indicates moderate to high resistance among *Pseudomonas aeruginosa* isolates, particularly to ceftazidime, ciprofloxacin, aminoglycosides, and carbapenems. Blood isolates exhibited the highest resistance to carbapenems (45–46%) and piperacillin/tazobactam (30%), suggesting a greater burden of multidrug-resistant strains in invasive infections. Resistance to imipenem and meropenem approaching 40–46% is concerning and reflects the increasing prevalence of carbapenem-resistant *P. aeruginosa* (CRPA). Despite these challenges, piperacillin/tazobactam retained relatively good activity (70–90% susceptibility) across most specimen types, while colistin remained highly effective, with virtually no resistance detected. These findings emphasize the importance of ongoing antimicrobial resistance surveillance, specimen-specific antibiograms, antimicrobial stewardship, and strict infection prevention measures to optimize empirical therapy and limit the spread of multidrug-resistant *P. aeruginosa*.

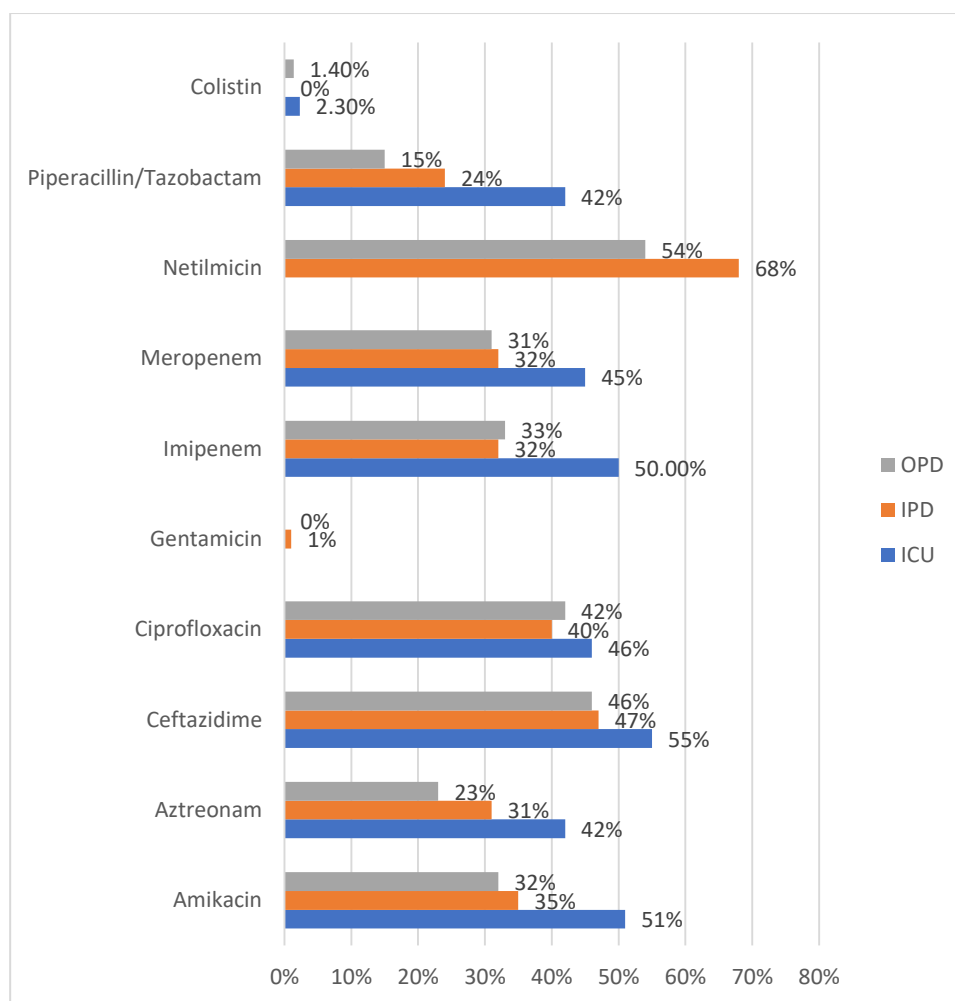


Figure 20: Location wise Resistance profile of *Pseudomonas* species in percentage (n=1065)

The figure 20 compares antimicrobial resistance among *Pseudomonas* isolates obtained from ICU, IPD, and OPD settings. Overall, resistance was consistently higher among isolates from the ICU, indicating greater antimicrobial selection pressure and circulation of multidrug-resistant strains in critical care areas. It demonstrates a clear increase in antimicrobial resistance from OPD to ICU, reflecting greater antibiotic selection pressure and the predominance of healthcare-associated *Pseudomonas aeruginosa* strains in hospitalized patients. ICU isolates exhibited the highest resistance to most antibiotic classes, particularly amikacin (51%), ceftazidime (55%), imipenem (50%), meropenem (45%), piperacillin/tazobactam (42%), and aztreonam (42%). The high resistance to carbapenems is indicative of an increasing burden of carbapenem-resistant *P. aeruginosa* (CRPA), which poses a significant therapeutic challenge in critical care settings. Despite these concerns, gentamicin and colistin retained excellent in vitro activity, while piperacillin/tazobactam remained more active than carbapenems, particularly in OPD and IPD isolates. These findings emphasize the importance of unit-specific antibiograms, continuous antimicrobial resistance surveillance, antimicrobial stewardship, and stringent infection prevention and control measures to optimize empirical therapy and limit the spread of multidrug-resistant *P. aeruginosa*.

Acinetobacter species are among the most common pathogens responsible for ventilator-associated pneumonia and other severe healthcare-associated infections, and they are known to cause outbreak in intensive care units. These organisms have a strong propensity to develop resistance to multiple

classes of antimicrobial agents. The presence of hetero resistance, wherein bacterial populations naturally contain subpopulations with reduced susceptibility, often necessitates the use of combination antimicrobial therapy.

Acinetobacter species accounted for 9% of the total isolates reported in 2025 (Figure 3). A total of 1204 *Acinetobacter* spp. isolates were obtained from 1200 unique patients. These isolates were recovered from blood (591), pus aspirates (308), other sterile body fluids (104), and urine (201), as shown in Table 10.

Table 10: Specimen wise resistant profile of *Acinetobacter* species

Antibiotic name	Pus Aspirate (n=308)			Blood (n=591)			Urine (n=201)			OSBF (n=104)		
	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R	Number Tested	Number Resistant	%R
Amikacin	264	204	77%	496	332	67%	141	36	25%	77	33	43%
Ampicillin/Sulbactam	104	78	75%	183	99	54%	95	42	44%	32	19	59%
Ceftazidime	285	246	86%	474	397	84%	102	51	50%	87	62	71%
Ciprofloxacin	235	180	76%	514	356	69%	142	43	30%	57	30	53%
Gentamicin	284	190	67%	552	352	64%	169	40	24%	84	39	46%
Imipenem	236	184	78%	545	426	78%	84	26	31%	63	37	59%
Meropenem	293	227	77%	548	406	74%	154	36	23%	90	53	59%
Minocycline	226	83	37%	506	93	18%	101	20	20%	75	7	9%
Piperacillin/Tazobactam	269	211	78%	539	401	74%	136	29	21%	84	47	56%
Tetracycline							57	17	30%			
TMP/SMX	257	189	73%	472	343	73%	158	48	30%	80	44	55%
Colistin	205	0	0%	287	8	3%	60	0	0%	59	0	0%

Key findings—resistance profile of *Acinetobacter* species

Table 10 demonstrates a very high resistance to ceftazidime, ampicillin/sulbactam, carbapenems, ciprofloxacin, and piperacillin/tazobactam, particularly in blood and pus aspirate isolates. Pus aspirate isolates consistently exhibited the highest resistance for most antibiotics, indicating a greater prevalence of multidrug-resistant organisms in wound infections. Urine isolates generally showed lower resistance, especially to carbapenems, aminoglycosides, and piperacillin/tazobactam. Minocycline demonstrated relatively good activity, while colistin remained the most effective antimicrobial, with virtually no resistance across specimen types.

Overall, the antibiogram indicates a high prevalence of multidrug-resistant isolates, with resistance particularly pronounced in bloodstream and wound infections. These findings emphasize the need for culture-guided therapy, antimicrobial stewardship, and ongoing local surveillance to preserve the efficacy of last-line agents such as colistin.

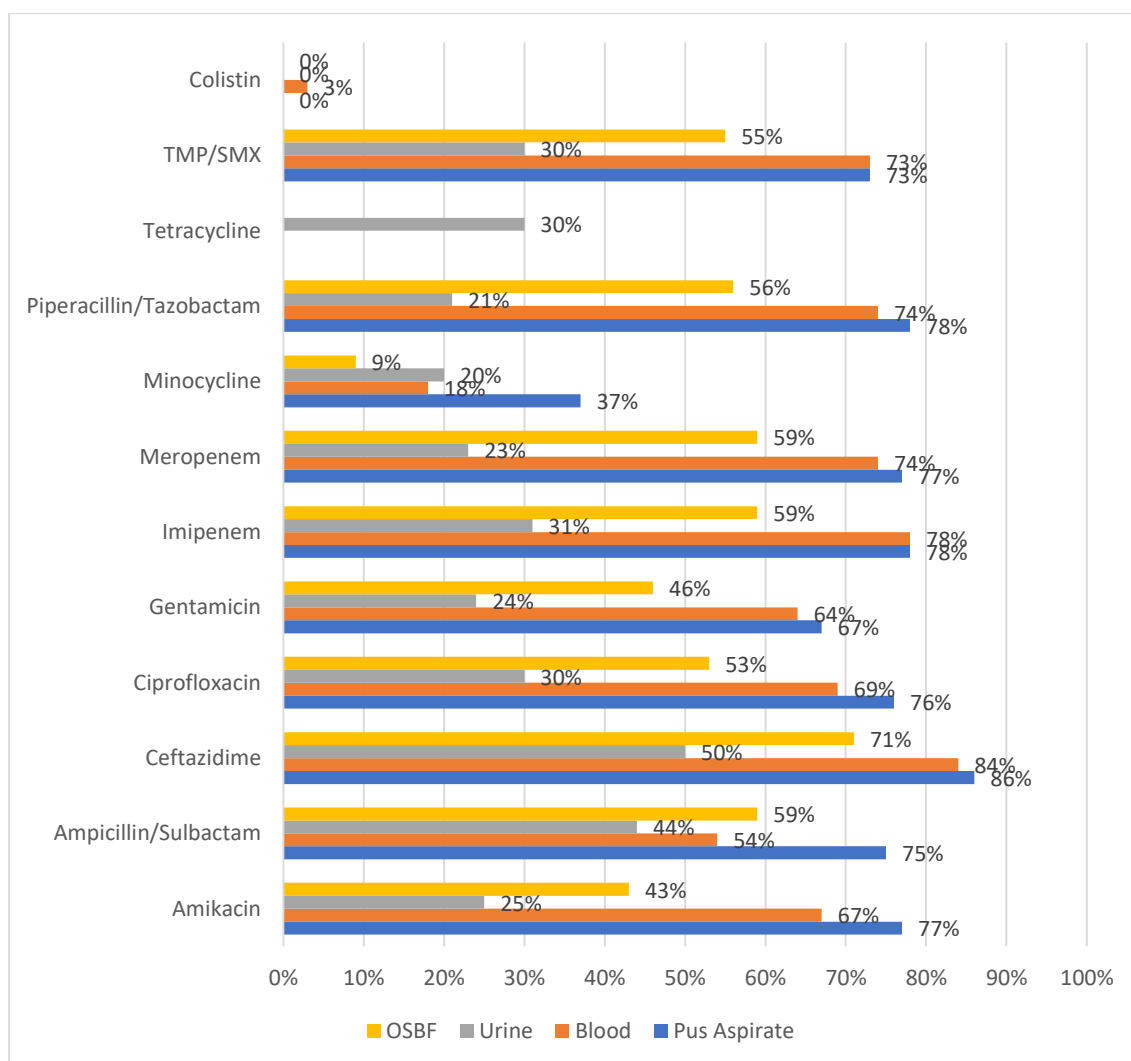


Figure 21: Specimen wise resistance profile of *Acinetobacter* species

Figure 21 demonstrates extensive multidrug resistance among *Acinetobacter baumannii*, with particularly high resistance to ceftazidime, ciprofloxacin, aminoglycosides, piperacillin/tazobactam, and carbapenems, especially in blood and pus aspirate isolates. The very high resistance to imipenem (78%) and meropenem (74–77%) confirms the widespread presence of carbapenem-resistant *Acinetobacter baumannii* (CRAB), which poses a major therapeutic challenge in invasive and healthcare-associated infections. Among the agents tested, colistin retained near-complete activity, while minocycline showed comparatively good in vitro efficacy, particularly in urine, blood, and OSBF isolates. These findings highlight the urgent need for strict antimicrobial stewardship, enhanced infection prevention and control practices, routine surveillance for CRAB, and specimen-specific antibiograms to optimize empirical therapy and limit the spread of multidrug-resistant *A. baumannii*.

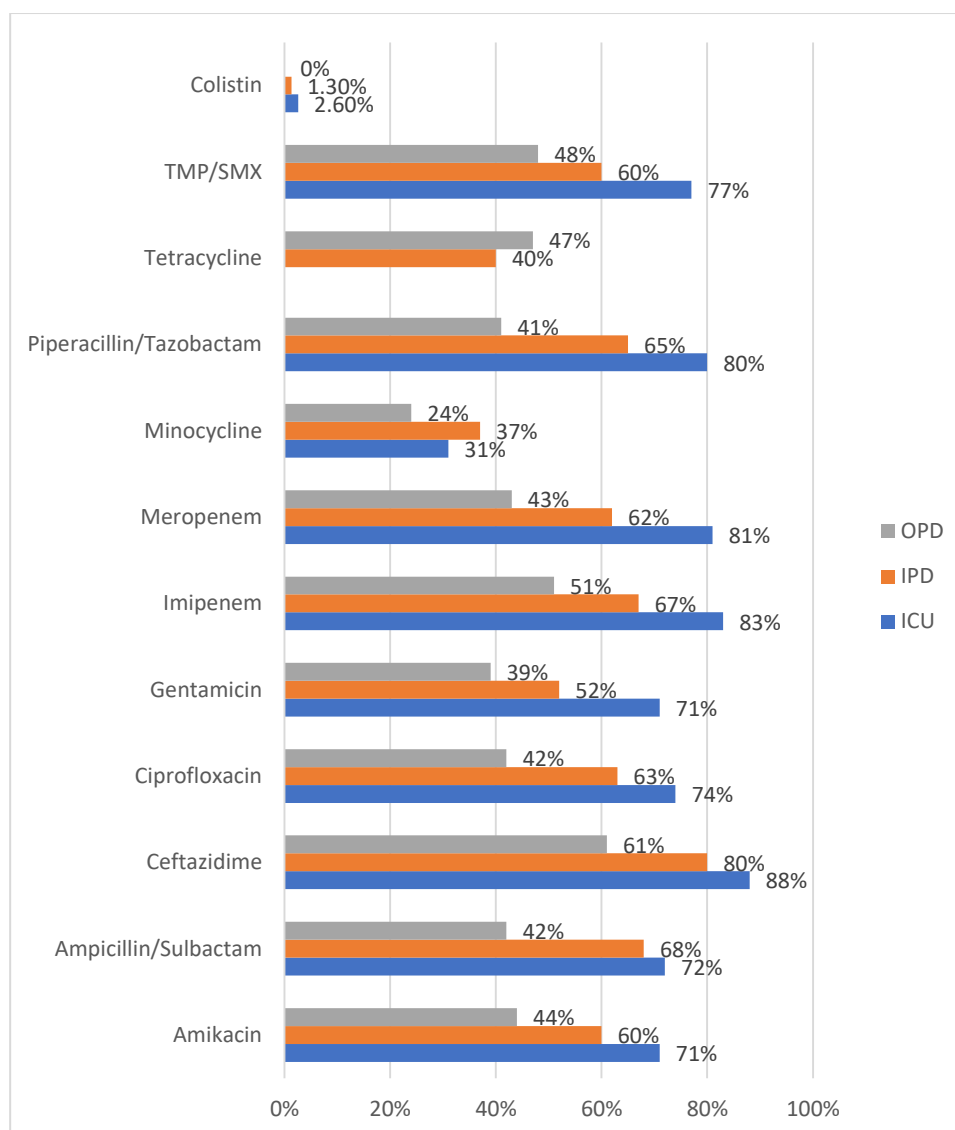


Figure22:Location wise Resistance profile of *Acinetobacter* species in percentage(n=1204)

The figure compares the antimicrobial resistance profile of *Acinetobacter baumannii* isolates recovered from the Outpatient Department (OPD), Inpatient Department (IPD), and Intensive Care Unit (ICU). A clear increase in resistance is observed from OPD to ICU, reflecting increasing antimicrobial selection pressure and a higher burden of multidrug-resistant (MDR) and carbapenem-resistant *A. baumannii* (CRAB) among critically ill patients.

Particularly concerning are the very high resistance rates to ceftazidime (88%), imipenem (83%), meropenem (81%), piperacillin/tazobactam (80%), TMP/SMX (77%), and ciprofloxacin (74%), confirming the widespread presence of multidrug-resistant and carbapenem-resistant *Acinetobacter baumannii* (CRAB) in hospitalized patients, especially in intensive care units. In contrast, colistin retained excellent in vitro activity, with resistance remaining below 3%, while minocycline showed the best activity among the non-polymyxin agents, particularly in OPD and ICU isolates. These findings highlight the critical need for unit-specific antibiograms, antimicrobial stewardship, active surveillance for CRAB, and stringent infection prevention and control measures to limit the spread of multidrug-resistant *A. baumannii* and guide appropriate empirical therapy.

6. Discussion

This data is crucial for understanding the current antimicrobial resistance (AMR) situation in Assam. Systematic collection and analysis of surveillance data under the AARSNET network supports the development of evidence-based strategies to mitigate the impact of AMR. Annual AMR surveillance has been conducted for the first time in 2025, enabling the assessment of resistance trends over time. The AMR patterns observed in 2025 would be taken as the baseline data for comparing the resistance patterns subsequently in future.

The AARSNET network has played a pivotal role in strengthening antimicrobial resistance (AMR) surveillance by facilitating the implementation of standardized protocols for specimen collection, laboratory testing, data management, analysis, and reporting across participating laboratories. The surveillance data generated through the network are compiled and analyzed to produce annual reports, which are disseminated to relevant stakeholders at both state and national levels for informed decision-making and policy development.

Participation in the network has significantly enhanced the quality assurance systems of member laboratories and strengthened their capacity for accurate and reliable AMR detection. To improve laboratory performance and ensure high-quality surveillance data, several capacity-building initiatives have been undertaken, including the implementation of internal quality control (IQC) measures, participation in external quality assessment (EQAS) programs, adoption of standardized data management standard operating procedures (SOPs), virtual and onsite training programs, supportive supervisory visits, and regular feedback on data quality and reporting practices.

Furthermore, targeted training workshops on broth microdilution (BMD) methods for colistin and vancomycin susceptibility testing have facilitated the adoption of BMD-based testing in several network laboratories. This has improved the accuracy and reliability of susceptibility testing for these critical last-resort antimicrobials, thereby strengthening the overall quality and credibility of AMR surveillance data generated through the network.

The total number of isolates reported to the AARSNET network in 2025 was 13299 after deduplication. The 12 participating laboratories collectively demonstrated strong state-level representativeness in terms of geographical coverage, inclusion of tertiary care hospitals, and representation of pathogens responsible for invasive infections. A total of 14346 priority pathogen isolates were initially reported and subsequently de-duplicated, resulting in 11834 unique patient isolates analyzed for this report. This robust dataset enhances the representativeness and reliability of AMR trends observed across the state.

Although accurately quantifying the overall burden of antimicrobial resistance (AMR) remains challenging, the surveillance data generated through the AARSNET network clearly demonstrate the widespread and sustained presence of AMR across diverse clinical settings. The findings indicate that resistance is well established throughout the network regions, with consistent resistance patterns observed over successive years of surveillance.

Escherichia coli continued to be the most frequently isolated pathogen in both inpatient (IPD) and

outpatient (OPD) settings, while *Klebsiella* species predominated among isolates recovered from intensive care units (ICUs). This distribution highlights the significant role of multidrug-resistant Gram-negative bacilli (MDR-GNB), particularly in severe, invasive, and healthcare-associated infections. The increasing proportion of isolates originating from ICUs further reflects the growing burden of critically ill patients and healthcare-associated infections within tertiary care facilities.

Of particular concern is the persistently high resistance to third-generation cephalosporins and carbapenems among Gram-negative pathogens, especially *Klebsiella pneumoniae*, which substantially limits available therapeutic options. Similarly, the high prevalence of carbapenem resistance among *Acinetobacter* species remains a major public health challenge, given the organism's propensity to cause outbreaks and the limited efficacy of currently available antimicrobial agents against resistant strains.

These findings underscore the urgent need for sustained antimicrobial stewardship interventions, strengthened infection prevention and control measures, enhanced diagnostic capacity, and continued expansion of AMR surveillance activities. A coordinated and evidence-based approach will be essential to contain the spread of resistant pathogens, preserve the effectiveness of existing antimicrobials, and mitigate the growing impact of AMR on patient outcomes and healthcare systems across the state.

Resistance to beta-lactam and beta-lactamase inhibitor, third generation Cephalosporins, ESBLs, AmpC and CPE

A significant resistance to third-generation cephalosporins has been observed among Gram-negative bacilli across AARSNET network laboratories. As a consequence, β -lactam/ β -lactamase inhibitor (BL-BLI) combinations, including co-amoxiclav and piperacillin–tazobactam, have increasingly been utilized as empirical treatment options for infections caused by multidrug-resistant Gram-negative bacilli (MDR-GNB). However, the current surveillance data indicate a rising trend in resistance to these agents among both *Escherichia coli* and *Klebsiella* species, raising concerns regarding their continued effectiveness as empirical therapeutic options.

The principal acquired β -lactamase mechanisms contributing to resistance among clinically important Gram-negative pathogens include extended-spectrum β -lactamases (ESBLs), plasmid-mediated AmpC (pAmpC) β -lactamases, and carbapenems. ESBL- and AmpC-producing organisms exhibit resistance to third-generation cephalosporins and are increasingly encountered among Enterobacterales and non-fermenting Gram-negative bacilli. The emergence and dissemination of carbapenemase-producing Enterobacterales (CPE) and carbapenem-resistant non-fermenters represent a more serious challenge, as these organisms are frequently associated with extensive multidrug resistance and limited therapeutic option. Carbapenem resistance continues to be a major concern within the AARSNET network. In 2025, the highest resistance was observed among *Acinetobacter* species (73%), followed by *Klebsiella* species (70%), *Pseudomonas* species (50%), and *Escherichia coli* (31%). These findings highlight the sustained burden of carbapenem-resistant Gram-negative pathogens in both healthcare-associated and invasive infections.

Resistance to Fosfomycin, which remains an important therapeutic option, particularly for urinary

tract infections caused by multidrug-resistant Enterobacterales was found to be 10% .Nevertheless, resistance may emerge through multiple mechanisms, including mutations affecting the GlpT and UhpT transport systems, alterations in the target enzyme encoded by the *murA* gene, and acquisition of plasmid-mediated *fos* genes that enzymatically inactivate the drug.

The dissemination of antimicrobial resistance among Enterobacterales, *Pseudomonas* species, and *Acinetobacter* species is largely driven by horizontal gene transfer mediated through plasmids, transposons, and other mobile genetic elements. These mechanisms facilitate the rapid acquisition and spread of resistance determinants across bacterial populations and species, contributing to the emergence, persistence, and transmission of multidrug-resistant Gram-negative organisms within healthcare settings.

Taken together, these findings underscore the urgent need for continuous AMR surveillance, strengthened antimicrobial stewardship programs, robust infection prevention and control measures, enhanced laboratory capacity for detection of resistance mechanisms, and sustained AMR surveillance to monitor emerging resistance trends and guide evidence-based therapeutic strategies.

Key messages and conclusions

Limited access to safe water, adequate sanitation, and effective infection prevention and control (IPC) measures continues to be a major driver of the transmission of infectious agents, including antimicrobial-resistant (AMR) microorganisms. Deficiencies in water, sanitation, and hygiene (WASH) infrastructure, coupled with inconsistent implementation of IPC practices, facilitate the spread of resistant pathogens within healthcare facilities and community settings, thereby exacerbating the burden of AMR.

In addition, the widespread and frequently inappropriate use of antibiotics during the COVID-19 pandemic is believed to have intensified the selective pressure on microorganisms, accelerating the emergence, persistence, and dissemination of antimicrobial resistance. These challenges highlight the critical need to strengthen WASH infrastructure, ensure strict adherence to evidence-based IPC practices, and promote antimicrobial stewardship through the rational and judicious use of antibiotics. A coordinated, multisectoral approach integrating these interventions is essential to mitigate the spread of AMR and safeguard the effectiveness of existing antimicrobial agents.

At the global level, the antimicrobial development pipeline remains critically limited and has been described by the World Health Organization (WHO) as “dry,” reflecting the scarcity of novel antibacterial agents capable of addressing the rapidly escalating challenge of antimicrobial resistance (AMR). In the absence of substantial improvements in antibiotic prescribing practices and antimicrobial stewardship, even newly introduced agents are likely to face declining effectiveness over time due to continued selection pressure and the emergence of resistant organisms. This concern is particularly acute for infections caused by WHO priority pathogens, including carbapenem-resistant Gram-negative bacteria. The increasing burden of AMR poses a significant threat to public health by progressively undermining the effectiveness of commonly used antibiotics for the treatment of bacterial infections. Of particular concern is the emergence of resistance to last-resort antimicrobial agents, including linezolid and vancomycin among *Staphylococcus aureus* and

Enterococcus species, as well as the detection of colistin resistance in Gram-negative pathogens. The loss of efficacy of these critical therapeutic options would severely limit treatment choices for serious and life-threatening infections. These trends highlight the urgent need to strengthen infection prevention and control (IPC) measures, optimize antimicrobial use through robust antimicrobial stewardship (AMS) programs, and enhance laboratory capacity for timely detection of resistant pathogens.

Surveillance data generated through the AARSNET network continue to demonstrate a substantial burden of multidrug-resistant organisms across healthcare facilities in Assam. These findings reinforce the need for a comprehensive, multisectoral, and coordinated Assam State Action Plan for AMR containment. While important progress has been made in strengthening surveillance and laboratory capacity, effective implementation of AMR control strategies continues to be constrained by limited prioritization, inadequate resource allocation, and challenges in scaling up IPC, AMS, and surveillance activities across the state.

Addressing the growing AMR threat will require sustained political commitment, increased investment, strengthened intersectoral collaboration under a One Health framework, and the integration of AMR containment strategies into routine healthcare delivery. Continued expansion of surveillance activities, improved access to quality diagnostics, enhanced stewardship interventions, and robust infection prevention measures will be essential to preserve the effectiveness of existing antimicrobials and mitigate the long-term impact of AMR on public health in Assam.

IMAGE GALLERY



राजेश भूषण, आईएएस
सचिव
RAJESH BHUSHAN, IAS
SECRETARY



भारत सरकार
स्वास्थ्य एवं परिवार कल्याण विभाग
स्वास्थ्य एवं परिवार कल्याण मंत्रालय
Government of India
Department of Health and Family Welfare
Ministry of Health and Family Welfare
D.O. No. Z-18025/8/12/1/2021-AMR
25.07.2023

Dear Arinash,

Antimicrobial Resistance (AMR) is a global public health threat that poses serious health and economic implications to all Countries. It threatens the effective prevention and treatment of an ever-increasing range of infections and threatens the safety and effectiveness of procedures such as surgical interventions, cancer treatment, organ transplants, etc.

India's National programme on AMR Containment aims to strengthen AMR surveillance and containment activities in State govt. medical colleges/tertiary care govt. hospitals. One of the activities approved under the programme for 2021-26 is to support States to establish/strengthen State AMR surveillance laboratory networks.

State AMR Surveillance networks would generate State level AMR surveillance data which would act as evidence to guide State level action to contain the problem of AMR. Gauhati Medical College and Hospital, Guwahati which is part of the National Programme on AMR Containment will be the nodal centre to coordinate the State AMR Surveillance in the state of Assam. The network sites would use standardized lab testing, quality control and data management SoPs already developed under the National Programme.

It is requested that all State medical colleges in Assam be directed to submit the AMR Surveillance data every month, starting from 1st August 2023, to Head, Department of Microbiology, Gauhati Medical College and Hospital, Guwahati in the designated software. Training for the same will be coordinated by Gauhati Medical College and Hospital, Guwahati and will be supported by National Centre for Disease Control (NCDC), Delhi. The annual State AMR surveillance data will be used to generate state AMR Surveillance reports which will be shared with various stakeholders in the

state. This data is also to be submitted to NCDC for inclusion in the National AMR surveillance data and submission to Global AMR Surveillance system.

Looking forward to your support in this important activity.

Warm Regards.

Yours sincerely,



(Rajesh Bhushan)

Shri Avinash P. Joshi

Principal Secretary,
Health & Family Welfare Department,
3rd Floor, "CM" Block, Assam Secretariat, Dispur,
Guwahati- 781006, Assam

Copy to:

1. Prof. (Dr.) Achyut Chandra Baishya, Principal cum Chief Superintendent
Gauhati Medical College and Hospital, Guwahati
2. Prof (Dr.) Ajanta Sharma, Head of Department
Department of Microbiology, Gauhati Medical College and Hospital, Guwahati

Letter from Secretary, Department of Health and Family Welfare, Government of India, designating Gauhati Medical College and Hospital, Guwahati, Assam as nodal centre for State AMR Surveillance Network.



State Level Sensitization on Antimicrobial Resistance Surveillance and training Workshop on AMR Data Management – 8th Jan 2024- 9th Jan 2024



State level training on Data Management and preparation of Anti-biogram using WHONET and Sensitization on HAI Surveillance - 7th and 8th November, 2025



Hands on Training Workshop for determination of Minimum Inhibitory Concentration for Colistin and Vancomycin by Microbroth dilution (MBD) training, 4th and 5th November, 2024



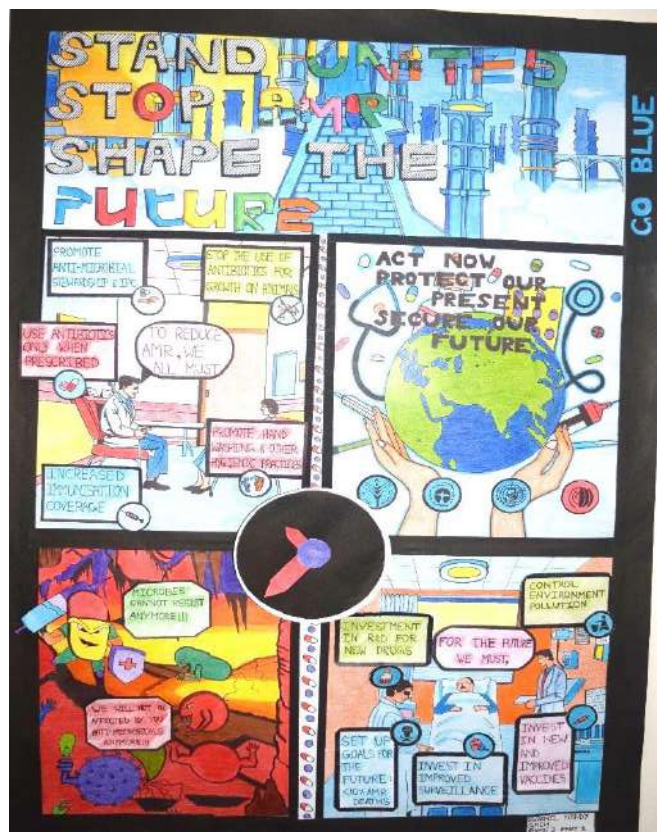
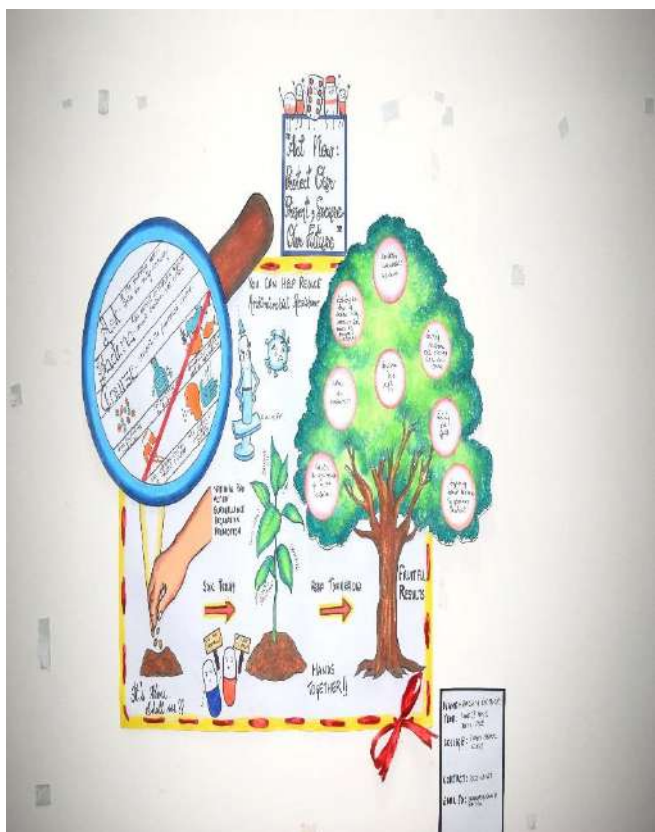
Annual Review Meeting 2025, for AARSNET sites, 8th and 9th January, 2026



Hand Hygiene Day, 5th May 2025



Awareness and demonstration of hand hygiene among patient attendants on Hand hygiene Day



Poster Competition under 'Go Blue Campaign' held on the occasion of WAAW (World Anti-microbial Resistance Awareness Week, 2025)



GO BLUE Campaign as a part of Celebration of World Anti-Microbial Resistance Awareness Week

(18th Nov- 24th Nov 2025)



Assam State AMR Surveillance team with Dr. Lata Kapoor, Additional Director, CBDDR, NCDC, New Delhi, at the Annual Review Meeting, 2026.