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ANTIMICROBIAL RESISTANCE SURVEILLANCE AND RESEARCH NETWORK



Division of Descriptive Research
Indian Council of Medical Research, New Delhi

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ICMR - Antimicrobial Resistance Surveillance & Research Network (AMRSN)
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List of acronyms

AFST	Antifungal susceptibility testing
AMA	Antimicrobial agent
AMR	Antimicrobial resistance
AMRSN	Antimicrobial Resistance Research & Surveillance Network
AMS	Antimicrobial susceptibility
AST	Antimicrobial susceptibility testing
BAL	Bronchoalveolar lavage
BSI	Bloodstream infections
CLSI	Clinical & Laboratory Standards Institute
CoNS	Coagulase-negative *Staphylococci*
CRAB	Carbapenem-resistant *Acinetobacter baumannii*
CRE	Carbapenem-resistant *Enterobacterales*
CS	Carbapenem-susceptible
CSF	Cerebrospinal fluid
DEC	Diarrheagenic *Escherichia coli*
DI	Deep infections
ESBLs	Extended-spectrum beta-lactamases
GNB	Gram-negative bacteria
GPC	Gram-positive cocci
hVISA	Heteroresistant vancomycin-intermediate *Staphylococcus aureus*
ICMR	Indian Council of Medical Research
ICU	Intensive care unit
IPC	Infection prevention and control
LRT	Lower respiratory tract
MβL	Metallo-beta-lactamase
MDR	Multi drug resistance
MIC	Minimum inhibitory concentration
MRSA	Methicillin-resistant *Staphylococcus aureus*
MSSA	Methicillin-sensitive *Staphylococcus aureus*
NFGNB	Non-fermenting Gram-negative bacteria
NTS	Non Typhoidal Salmonella
OPD	Outpatient department
R	Resistant
RC	Regional centres
S%	Susceptibility% (Sensitive/Tested)
SDD	Susceptible-dose dependent
SOSA	Staphylococci other than *Staphylococcus aureus*
SI	Superficial infections
SS	Sterile sites
ST	Sequence types
TMP-SMX	Trimethoprim-Sulfamethoxazole
UTI	Urinary tract infections
VAP	Ventilator-associated Pneumonia
VRE	Vancomycin-resistant *Enterococci*
WGS	Whole genome sequencing
XDR	Extensively drug-resistant

Executive summary

ICMR- Antimicrobial Resistance Surveillance and Research Network (ICMR-AMRSN)

Antimicrobial resistance (AMR) remains a major public health challenge, requiring sustained surveillance to understand emerging resistance patterns and inform appropriate clinical and public health responses. Since 2013, the Indian Council of Medical Research (ICMR) has supported the Antimicrobial Resistance Research and Surveillance Network (AMRSN) to generate systematic laboratory-based evidence on AMR across India.

The **2025 annual report, the ninth detailed report of the ICMR-AMRSN**, presents surveillance findings on pathogen distribution, antimicrobial susceptibility patterns and resistance trends among major bacterial and fungal pathogens from participating hospitals across India. In 2025, the tertiary-care network expanded from 20 to 30 hospitals, strengthening its geographical and institutional representation.

A significant milestone in 2025 was the inclusion of the **secondary-care hospitals** in this network. 34 secondary hospitals, including 12 district hospitals, small private hospitals and other healthcare facilities have contributed data to this report. Participating hospitals were classified into three categories based on bed strength to facilitate the assessment of resistance patterns across hospitals with different capacities and patient volumes. **Category I comprising of** ≤200 beds, **category II:** 201–499 beds, and **category III:** ≥500 beds. Hospitals were inducted in the network based on the availability of microbiologists, functional microbiology laboratories having culture and antimicrobial susceptibility testing (AST) facilities by manual and/or automated systems.

To support this expansion, the number of Regional Centres was increased from 15 to 26 in 2025. Of these, 17 Regional Centres function as hubs, each supporting two to three hospitals as spokes by providing mentorship and oversight to secondary-care hospitals functioning as sub-regional centres for standardisation and uniformity.

The network is supported by six Nodal Centres providing reference laboratory services for major bacterial and fungal pathogen groups. These centres facilitate cross-verification of susceptibility status of isolates referred by Regional and Sub-regional Centres and undertake advanced characterisation of resistance mechanisms, including molecular and whole-genome sequencing (WGS) analyses.

AMR surveillance data from the participating secondary-care hospitals, providing an assessment of pathogen distribution and antimicrobial susceptibility profiles of only major

Gram-negative and Gram-positive bacterial pathogens is presented in this *report.* These include Enterobacterales, particularly *Escherichia coli* and *Klebsiella pneumoniae*; non-fermenting Gram-negative bacilli, including *Acinetobacter baumannii* and *Pseudomonas aeruginosa*; Gram-positive cocci, including *Staphylococcus aureus;* and *Enterococcus spp*.

Together, the tertiary-care and secondary-care surveillance components strengthen the scope and depth of national AMR surveillance by generating complementary evidence from different levels of healthcare. The findings provide an important evidence base for understanding resistance patterns, strengthening laboratory and surveillance capacity, guiding context-specific antimicrobial stewardship interventions and provide critical evidence for informing public health strategies to address AMR in India.

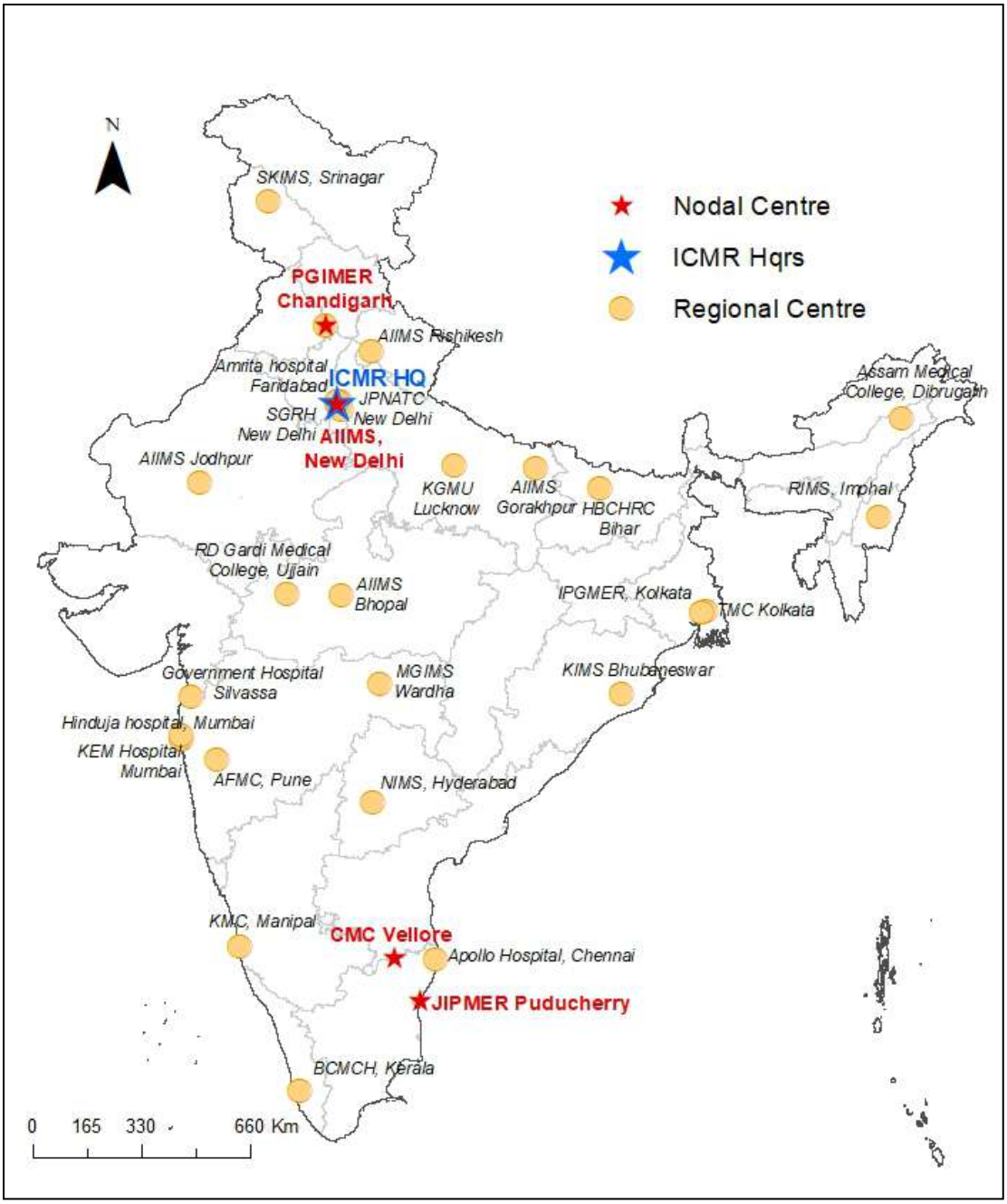


Figure I: Antimicrobial Resistance Research & Surveillance Network (AMRSN): Nodal and Regional Centres

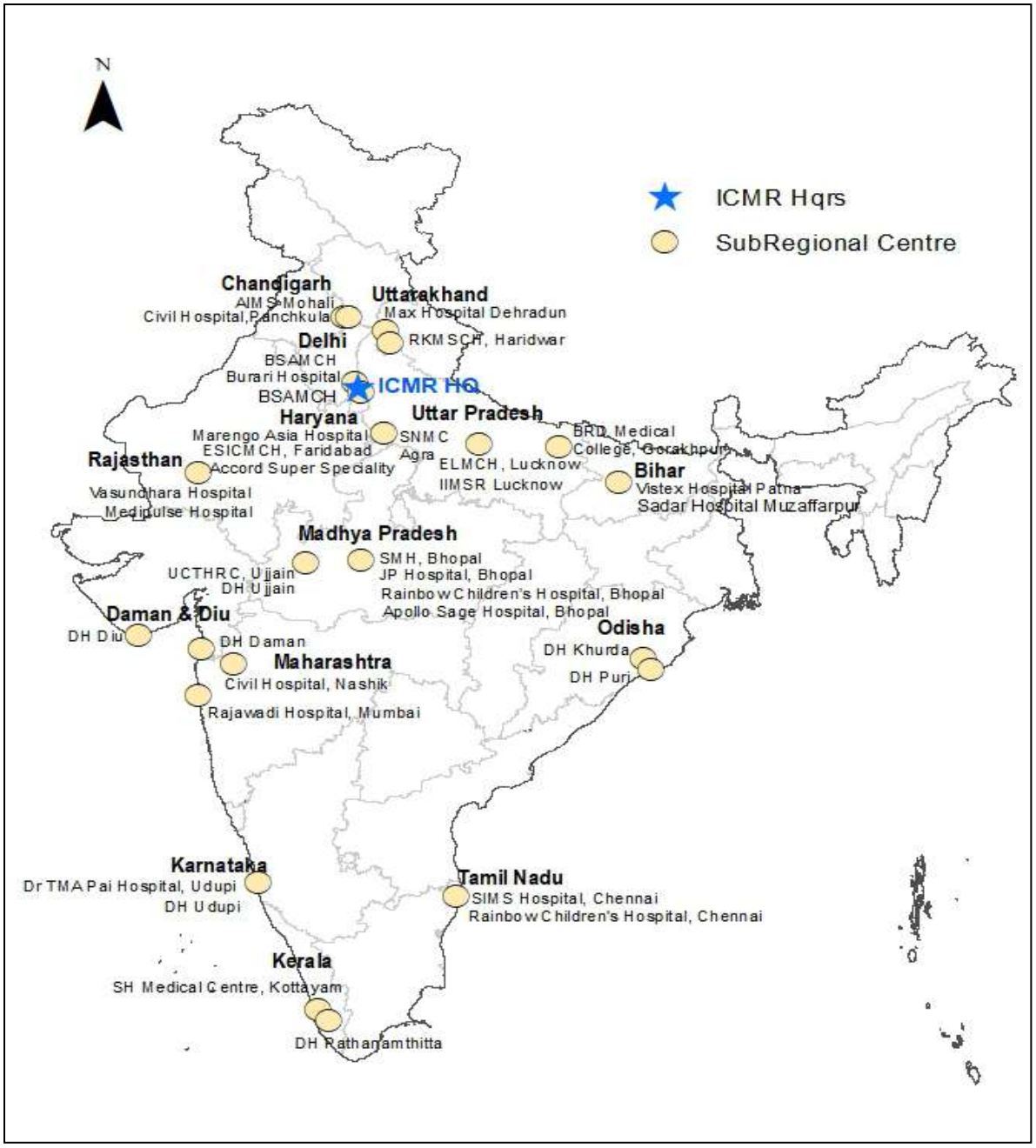


Figure II: Antimicrobial Resistance Research & Surveillance Network (AMRSN): Sub-Regional Centres

Highlights of surveillance data 2025:

- This report presents antimicrobial resistance surveillance data from 30 tertiary-care hospitals and from 34 secondary- care hospitals for the period **1 January 2025 to 31 December 2025**. During this period, 1,13,008 culture-positive isolates were reported by tertiary-care hospitals and 20,529 by secondary-care hospitals.
- In the tertiary–care hospitals, Gram-negative bacteria (GNB) remained the most commonly isolated pathogens (approximately 75%) from most clinically relevant samples, like blood, urine, CSF, and respiratory tract samples, except for pus/exudates samples.
- In the secondary-care hospitals, pathogen distribution varied across hospital bed-size categories. Urine was the predominant source of isolates, followed by blood, lower respiratory tract and skin/soft tissue specimens. *Escherichia coli* was the most commonly isolated pathogen, followed by *Klebsiella pneumoniae*, *Pseudomonas aeruginosa, Acinetobacter baumannii,* and *Staphylococcus aureus*. Among all specimens**,** *Escherichia coli* was the most frequently isolated organism in Categories 1 and 2, but its proportion decreased to 22.8% in Category III. In contrast, *Staphylococcus aureus, Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* were more common in Category III hospitals than in Categories I and II.
- Overall, *E. coli* dominated the community-type urinary infections in the smaller hospitals whereas samples from larger hospitals showed a diverse pathogen distribution, with higher proportions of *S. aureus* and non-fermenting Gram-negative bacilli, including *P. aeruginosa* and *A. baumannii.*
- The 2025 report also includes additional antimicrobial agents, broadening the scope of susceptibility profiling. These include β-lactam/β-lactamase inhibitor combinations like ceftazidime–avibactam and cefoperazone–sulbactam and tetracycline like tigecycline and minocycline for Enterobacterales.

Enterobacterales

Tertiary- Care Hospitals

- *Escherichia coli* and *Klebsiella pneumoniae* were the most commonly isolated pathogens.
- Susceptibility of *E. coli* isolates to third-generation cephalosporins was low, with only 18.4% and 24.7% susceptible to cefotaxime and ceftazidime, respectively. Low susceptibility was observed even among isolates from OPD patients, suggesting that resistance to third-generation cephalosporins is widespread in the community suggesting high prevalence of ESBL-producing isolates.

- Susceptibility to piperacillin-tazobactam was also low at 42.6%, while susceptibility to carbapenems ranged from 60% to 65%. Among the other antibiotics tested, susceptibility was 73% for amikacin, 93.0% for tigecycline and 51.5% for ceftazidime-avibactam.
- *K. pneumoniae* showed an alarmingly high resistance profile, with only 29.2% susceptible to piperacillin-tazobactam, 23–27% to third-generation cephalosporins, and only 35–40% to carbapenems. Amikacin susceptibility was limited to 44.5%, and for ceftazidime-avibactam was 37.7%, whereas 79.3% of isolates were susceptible to tigecycline.
- In *E. coli*, TEM (21.0%) was most common, followed by CTXM-1 (13.0%), OXA-1, OXA-48 and NDM-1 (12.0% each).
- In *K. pneumoniae* isolates, TEM gene was the most prevalent, present in 20% of the isolates, followed by SHV in 19.0%, OXA-48 in 17.0%, NDM in 13%, CTXM-1 in 12%.

Secondary-Care Hospitals

- The susceptibility data show a graded decline in the susceptibility of *E. coli* to various antibiotics across 3 categories.
- Ceftriaxone susceptibility declined from 39.8% in category I to 28.0% in category II and 11.5% in category III hospitals, indicating high prevalence of resistance to 3rd generation cephalosporins even in smaller hospitals. Meropenem susceptibility also decreased across the three categories, from 80.3% to 77.5% and 67.1%, respectively.
- Ciprofloxacin susceptibility was low across all the categories (21.0%, 16.5% and 6.2% in all categories), while amikacin retained comparatively higher activity, with susceptibility rates of 85.4%, 72.1% and 65.0% across the three categories, respectively.
- Among *Klebsiella pneumoniae*, susceptibility to cefotaxime declined from 38.3% in Category I to 29.0% in Category II and 10.9% in Category III and that of meropenem fell from 70.2% to 56.1% and 60.5%. Amikacin showed the highest susceptibility among the agents reported; however, this declined substantially from 73.6% in Category I to 49.9% in Category II and 47.4% in Category III
- From the data of these 2 top pathogens from *Enterobacterales*, it is quite clear that resistance to 3rd generation cephalosporins and fluoroquinolones is very common regardless of the healthcare setting, but carbapenem resistance is less common in smaller hospitals, similarly amikacin retains good susceptibility rates across different healthcare settings.

Clinical relevance

- *E. coli* was the predominant pathogen isolated from the urine samples. Fairly good susceptibility was observed for nitrofurantoin (79.1%) and fosfomycin (96.5%), and

therefore, nitrofurantoin or single-dose fosfomycin remains the drug of choice for treating cystitis.

- Ertapenem or amikacin can be used for the treatment of upper urinary tract infections (UTIs), febrile UTIs. The use of quinolones and third-generation cephalosporins should be avoided for these infections to prevent further resistance development.
- Resistance to carbapenems in *K. pneumoniae* (a very important pathogen causing bloodstream infection) and other *Enterobacterales* shows increasing trend. Since significant percentage of these isolates are only OXA-48 producers which can be treated with newer BL-BLI (ceftazidime-avibactam) alone, hence identification of the carbapenemase (by molecular or immunochromatography tests) is of great importance.
- MβLs alone or in combination with OXA-48-like carbapenemase require either aztreonam-avibactam (after demonstrating *in vitro* susceptibility) or polymyxin-based combination therapy.

Non-fermenting Gram-negative Bacteria

Tertiary- Care Hospitals

- Temporal analysis over the last nine years reveals relatively stable susceptibility for most agents. Ciprofloxacin showed the greatest year-on-year volatility and a partial recovery by 2025 (56.6% susceptible), while susceptibility to cefoperazone-sulbactam and ceftazidime-avibactam was 61.4% and 57.2% respectively.
- 419 isolates were tested for enzymatic mechanisms of resistance, comprising of 84 isolates (20.0%) that were carbapenem-resistant (CR) and 335 isolates (80.0%) that were carbapenem-susceptible (CS). Metallo-β-lactamases (MβLs) was the predominant carbapenemase (NDM in 22 isolates, and VIM in 10).
- Notably, 337 isolates (80.4%) were PCR-negative for all the screened resistance determinants. The high proportion of PCR-negative isolates indicates that carbapenem resistance in *P. aeruginosa* cannot be attributed solely to the carbapenemase genes and may involve other mechanisms.
- A high prevalence of carbapenem resistance was observed among *A. baumannii*, with 91.1% of revived isolates exhibiting carbapenem resistance, highlighting a substantial therapeutic and infection-control challenge. OXA-23 was the predominant carbapenemase determinant, with frequent detection of OXA-23 + NDM co-profiles.
- A total of 794 *Stenotrophomonas maltophilia* isolates were collected and levofloxacin (87%) and minocycline (85.6%) demonstrated the highest overall susceptibility, followed by trimethoprim-sulfamethoxazole (82.3%).

Secondary-Care Hospitals

- *P. aeruginosa* was mostly isolated from Category II and III hospitals. Susceptibility rates to various antibiotics remained fairly stable across the 3 categories, with very minimal variation. Most of the antibiotics retained good susceptibility rates (over 50%)
- *A. baumannii* was mostly isolated from Category II and III hospitals. A marked difference was observed between Category II and III hospitals, with meropenem susceptibility declining from 43.4% to 20.5% and imipenem susceptibility from 41.3% to 16.5%. Minocycline demonstrated the highest overall susceptibility against *A. baumannii* (56.1%).

Clinical relevance

- In the difficult-to-treat *P. aeruginosa*, newer β-lactams such as ceftolozane-tazobactam, ceftazidime-avibactam or aztreonam-avibactam and cefiderocol should be selected according to susceptibility testing and not on carbapenemase detection alone.
- Susceptibility of *A. baumannii* to minocycline was close to 50% making it the most effective antibiotic after colistin.
- For *A. baumannii*, combination regimens involving colistin or polymyxin B with tigecycline or minocycline or high-dose ampicillin–sulbactam may be considered as salvage approaches in most settings, though efficacy is inconsistent and toxicity is high, use of ceftazidime-avibactam should be avoided solely on the basis of carbapenemase detection because avibactam lacks activity against metallo-β-lactamases
- Cefiderocol (if available and susceptible *in vitro*) can be used for both OXA- and NDM-producing *A. baumannii*.

Gram-positive cocci

Tertiary- Care Hospitals

- The overall proportion of MRSA was 56.8%. The anti MRSA antibiotics such as vancomycin, teicoplanin and tigecycline showed excellent in vitro activity (100% against MRSA isolates). Linezolid resistance was reported in 5.4% of isolates; however, given its important role in the treatment of drug-resistant tuberculosis and the high TB burden in India, linezolid should be used judiciously.
- Staphylococci other than *Staphylococcus aureus* (SOSA) are being increasingly recognized as opportunistic pathogens. The rate of methicillin resistance among SOSA across all the years under study steadily increased from 67% in 2017 – nearly 79 %

during 2025. Susceptibility to vancomycin remained excellent through all the years of study, while linezolid resistance increased from 1.9% in 2024 to 5.4% in 2025.

- Among *Enterococcus* spp, *E. faecalis* showing a slightly higher number of isolates.
- Overall vancomycin resistance in enterococci was 20%, slightly lower than 22% in 2024. However, the rate was 7.5 times higher in *E. faecium* compared to *E. faecalis* (33% vs 4.4%).

Secondary-Care Hospitals

- The MRSA rates differed significantly across the different categories of secondary hospitals. It ranged from 46.4% in Category I increasing to 54.1% in category II and rising 86% among the category III hospitals**.**
- Antibiotics like vancomycin, tigecycline and teicoplanin showed 100% susceptibility across all the categories.
- Enterococci were mainly isolated from category II hospitals, so comparative report is not very meaningful. Susceptibility rates of *E. faecalis* to ampicillin was high (~87%), while vancomycin resistance in *E. faecium* was ~25%.

Clinical relevance

- Among MRSA isolates*,* vancomycin susceptibility remains generally high; however, the emergence of hVISA (heteroresistant vancomycin-intermediate *Staphylococcus aureus*), which often goes undetected in routine clinical laboratories, is worrisome, as it may lead to therapeutic failure. While vancomycin may continue to be used for serious MRSA infections, alternative drugs should be considered if the MIC value is close to the susceptibility breakpoint.
- For serious infections such as meningitis or bacteremia caused by *Enterococcus* spp., vancomycin may be used as empirical therapy, with de-escalation based on susceptibility results. In cases where linezolid resistance is detected, daptomycin can be considered as an alternative treatment options.

Enteric fever pathogens

Highlights of AMR trends

- S. Typhi showed highest susceptibility to azithromycin (99.4%), ceftriaxone (96.6%), trimethoprim-sulfamethoxazole (97.1%), chloramphenicol (96.4%), and ampicillin (93.6%).

- Ceftriaxone susceptibility in S. Typhi was high in the North (98.4%) and South (96.7%) but was comparatively lower in the West (83.3%) and Central regions (15/18).
- S. Paratyphi A showed high susceptibility to ceftriaxone (98.6%), chloramphenicol (99.3%), trimethoprim-sulfamethoxazole (100%), and ampicillin (97.1%).
- Fluoroquinolone susceptibility against both was observed to be lowest. Ciprofloxacin susceptibility was observed in 2.0% of S. Typhi and 0.4% S. Paratyphi A isolates.

Clinical relevance

- Trimethoprim-sulfamethoxazole (TMP-SMX) and azithromycin remain effective oral treatment options for uncomplicated enteric fever.
- IV ceftriaxone is recommended for patients with complicated enteric fever requiring hospitalisation.
- Routine empirical use of carbapenems for enteric fever is not recommended. Their use should be restricted to selected cases, such as confirmed or strongly suspected XDR enteric fever.

Diarrheal pathogens

Highlights of AMR trends

- Only 0.9% of the total isolates were from stool samples, indicating poor representation of the true picture of bacterial diarrhoea. Other causes of diarrhoea, like viruses, *Entamoeba* and parasites, were not studied for this report.
- The predominant species from these samples were *Aeromonas* spp., *Shigella* spp. (*Shigella flexneri* and *Shigella sonnei*), *Vibrio cholerae*, and diarrhoeagenic *Escherichia coli* (DEC).
- Among *Aeromonas* spp., trimethoprim-sulfamethoxazole, meropenem, cefixime, ceftriaxone and tetracycline retained high in vitro activity, whereas ciprofloxacin continued to exhibit poor susceptibility. Similarly, *Shigella flexneri* and *Shigella sonnei* exhibited persistent resistance to fluoroquinolones.
- Among *Vibrio cholerae*, tetracycline maintained excellent activity. DEC continued to demonstrate extensive multidrug resistance, with extremely poor susceptibility to ampicillin, cefixime, ciprofloxacin and nalidixic acid.

Clinical relevance

- Among faecal isolates, AST results demonstrate high resistance to fluoroquinolones (like norfloxacin and ofloxacin) and cephalosporins (like cefixime), indicating that empirical use of these drugs should be avoided to treat diarrhoea in India.
- *Vibrio cholerae* and *Shigella* spp. isolates demonstrated good susceptibility to tetracycline (or doxycycline) and azithromycin, respectively.

Streptococcus pneumoniae

Highlights of AMR trends

- A total of 96 invasive (children <5 years n=32, adult and children > 5 years of age n=64) and 188 non-invasive (Children below the age of 5 years, n= 99; adult and children above 5 years of age, n= 89).
- Pneumosil (PCV10Sii) and PCV13 serotype coverage is 31% and 47% among the serotypes causing disease in children less than 5 years of age. Among the non-pneumosil, PCV13 serotypes, serotypes 3 and 18C together constitute 16% among the children and 13.6 % among the age group >5 years of age.
- Penicillin and cefotaxime demonstrated 100% susceptibility in non-meningeal isolates, whereas only 7 out of 29 cerebrospinal fluid (CSF) isolates were penicillin susceptible, and 22 out of 29 CSF isolates were cefotaxime susceptible.

Clinical relevance

- Non-meningeal isolates of *S. pneumoniae* demonstrated excellent susceptibility to penicillin, but penicillin resistance is a concern in CSF isolates.
- Ceftriaxone and vancomycin should be considered for empirical coverage of pneumococcus in patients with suspected bacterial meningitis.
- Vaccination, as per guidelines, should be done to prevent infections by pneumococcus.

Fungal pathogens

Highlights of AMR trends

- *Candida tropicalis* remains the most frequently isolated *Candida* species, followed by *C. albicans* and *C. parapsilosis*. Notably, *C. auris* continues to show a relatively high isolation rate.
- Fluconazole susceptibility remains high in *C. albicans and C. tropicalis,* whereas near 100% susceptibility was demonstrated to echinocandins in most *Candida* species

except *C. auris* and *Nakaseomyces glabratus (*previously called *C. glabrata),* in which caspofungin resistance was observed in 11.1% of C. auris and 4.3% of Nakaseomyces glabratus (formerly Candida glabrata) isolates, while susceptibility to anidulafungin and micafungin was comparatively higher in these species.

- Among *Aspergillus* isolates, both *A. flavus* and *A. fumigatus* showed nearly 100% susceptibility to voriconazole, with high susceptibility also observed to amphotericin B (92%) and posaconazole (95%).

Clinical relevance

- Echinocandins continue to be the most effective treatment option for most patients with invasive candidiasis upfront with de-escalation to fluconazole, if susceptible.
- Species-level identification and AFST for *candida* isolates is important as *N. glabratus* and *C. auris* often show reduced susceptibility.
- For *Aspergillus* infections, voriconazole remains the drug of choice.

Neonatal sepsis

Highlights of AMR trends

- Among neonates (0–28 days), *Klebsiella pneumoniae* was the predominant isolate followed by *Candida* spp. and *Acinetobacter baumannii*.
- In infants aged 29 days to <12 months, *Candida* spp was the predominant isolate followed by *K. pneumoniae* and *A. baumannii* and among children aged 1–12 years, *Salmonella* spp was the leading isolate followed by *S. aureus K. pneumoniae* .
- Among neonates, *Klebsiella pneumoniae* showed low susceptibility to third-generation cephalosporins and carbapenems. *Escherichia coli* showed a similar pattern, with comparatively higher carbapenem susceptibility. Candida spp. showed high susceptibility to antifungal agents.


TERTIARY-CARE
HOSPITALS

Chapter 1. Summary of isolate distribution

Total number of culture positive isolates studied during the year **2025** was **1, 13,008.** Of these, **24,078** were from blood, **28,629** from urine, **19,568** Lower Respiratory tract (LRT), **18,491** superficial infections**, 10,395** Deep infections, **2,681** Sterile sites (SS), **1,012** Faeces, **1,010** CSF, and **7,144** others. Majority of the isolates were from Enterobacterales except *Salmonella and Shigella* (49.0%) followed by Non fermenting Gram-negative bacilli (NFGNB) (23.1%), staphylococci (13.9%), enterococci (6.7%), fungi (4.2%), Typhoidal *Salmonella* (1.4%), Diarrhoeal bacterial pathogens (0.8%) and streptococci (0.9%) (**Table 1.1).**

In the distribution of major group of organisms in different specimens, member of the Enterobacterales group were the commonest isolates in urine (72.1%), sterile body fluids (SS) (53.9%), deep infections (DI) (50.0%), others (49.3%), superficial infections (SI) (45.7%), LRT (40.2%), blood (32.8%) and CSF (26.9%). Non fermenting Gram-negative bacilli (NFGNB) group were the predominant isolates in the lower respiratory tract (51.6%), CSF (38.6%), deep infection (DI) (24.1%), superficial infections (SI) (22.7%), sterile sites (SS) (20.5%), others (20.3%), blood (17.2%) and urine (9.7%). Staphylococci constituted 27.5 % of the blood infections followed the superficial infections (SI) (22.6%), CSF (21.6%) and deep infection (DI) (19.2%). Enterococci group constituted 12.1% isolates from urine followed by sterile body fluid (10.4%), CSF (6.7%), blood (6.5%), superficial infections (5.5%), and deep infections (4.8%), Typhoidal *Salmonella* group constituted 6.3% of the isolates from blood. Yeast group were significant isolates in the blood infection (8.8%) **(Table 1.1 and Figure 1.1).**

The distribution of top 10 isolates from different specimens is presented in **Table 1.2 and Figure 1.2**. *Escherichia coli* was most commonly isolated (24.4%) followed by the *Klebsiella pneumoniae* (16.9%), *Pseudomonas aeruginosa* (12.2%), *Acinetobacter baumannii* (9.2%) and *Staphylococcus aureus* (8.6%). Among these isolates, *Escherichia coli* was the most predominant isolate from the urine (47.6%), *K. pneumoniae* from the LRT (25.0%), *P. aeruginosa* from LRT (24.7%), *A. baumannii* from LRT (23.9%), *S. aureus* from SI (20.4%), *E. faecalis* and *E. faecium* from urine (5.7%), and (4.1%) respectively.

The relative distribution of the various species isolated from patients in the out-patient department (OPD), admitted to the wards and intensive care unit (ICUs) are presented in **Table 1.3 and Figures 1.3a &1.3b**. Top 5 isolates in descending order in OPD specimen were *E. coli, K. pneumoniae, P. aeruginosa, S. aureus* and *A.baumannii*; in Wards *E. coli, K. pneumoniae, P. aeruginosa, A. baumannii* and *S. aureus*; and in ICU *K. pneumoniae, A. baumannii*, *E. coli, P. aeruginosa* and *S. aureus. Enterococcus faecium* was common isolate from the ICU (3.9%) followed by ward and OPD; whereas, *E. faecalis* was common isolate from the OPD and ward (3.0%) followed by the ICU. (**Table 1.3, Figure 1.3).**

Table 1.1: Specimen wise distribution of major groups of organisms

Isolate	Culture positive																			
	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012		Others n=7144	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Enterobacterales except Salmonella and Shigella	55386 (49)	100	7904 (32.8)	14.3	20636 (72.1)	37.3	7871 (40.2)	14.2	8436 (45.6)	15.2	5197 (50)	9.4	272 (26.9)	0.5	1446 (53.9)	2.6	104 (10.3)	0.2	3520 (49.3)	6.4
NFGNB	26085 (23.1)	100	4140 (17.2)	15.9	2766 (9.7)	10.6	10098 (51.6)	38.7	4191 (22.7)	16.1	2502 (24.1)	9.6	390 (38.6)	1.5	550 (20.5)	2.1	0 (0)	0	1448 (20.3)	5.6
Staphylococci	15749 (13.9)	100	6620 (27.5)	42	550 (1.9)	3.5	1089 (5.6)	6.9	4170 (22.6)	26.5	2001 (19.2)	12.7	218 (21.6)	1.4	228 (8.5)	1.4	0 (0)	0	873 (12.2)	5.5
Enterococci	7516 (6.7)	100	1559 (6.5)	20.7	3464 (12.1)	46.1	0 (0)	0	1015 (5.5)	13.5	496 (4.8)	6.6	68 (6.7)	0.9	280 (10.4)	3.7	0 (0)	0	634 (8.9)	8.4
Fungi	4790 (4.2)	100	2117 (8.8)	44.2	1098 (3.8)	22.9	349 (1.8)	7.3	337 (1.8)	7	123 (1.2)	2.6	53 (5.2)	1.1	159 (5.9)	3.3	1 (0.1)	0	553 (7.7)	11.5
Diarrhoeal bacterial pathogens	898 (0.8)	100	23 (0.1)	2.6	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	875 (86.5)	97.4	0 (0)	0
Typhoidal Salmonella	1615 (1.4)	100	1520 (6.3)	94.1	14 (0)	0.9	2 (0)	0.1	15 (0.1)	0.9	13 (0.1)	0.8	0 (0)	0	3 (0.1)	0.2	32 (3.2)	2	16 (0.2)	1
Streptococci	969 (0.9)	100	195 (0.8)	20.1	101 (0.4)	10.4	159 (0.8)	16.4	327 (1.8)	33.7	63 (0.6)	6.5	9 (0.9)	0.9	15 (0.6)	1.5	0 (0)	0	100 (1.4)	10.3

1. Blood includes: Blood from venepuncture, central catheter, and peripheral catheter.
2. LRT (lower respiratory tract) includes: BAL, sputum, lung aspirate, endotracheal aspirate (ETA) and lung tissue.
3. SSI: Superficial infection includes SST (skin &soft tissue), pus/exudate, wound swab, superficial biopsy and superficial tissue.
4. Deep Infection includes: Abscess aspirate, pus aspirate, deep biopsy and deep tissue. 5. SS (sterile sites) includes: Fluid from sterile spaces, abdominal fluid, intercostal tube fluid, pancreatic drain fluid, pericardial fluid, peritoneal fluid and pleural fluid.

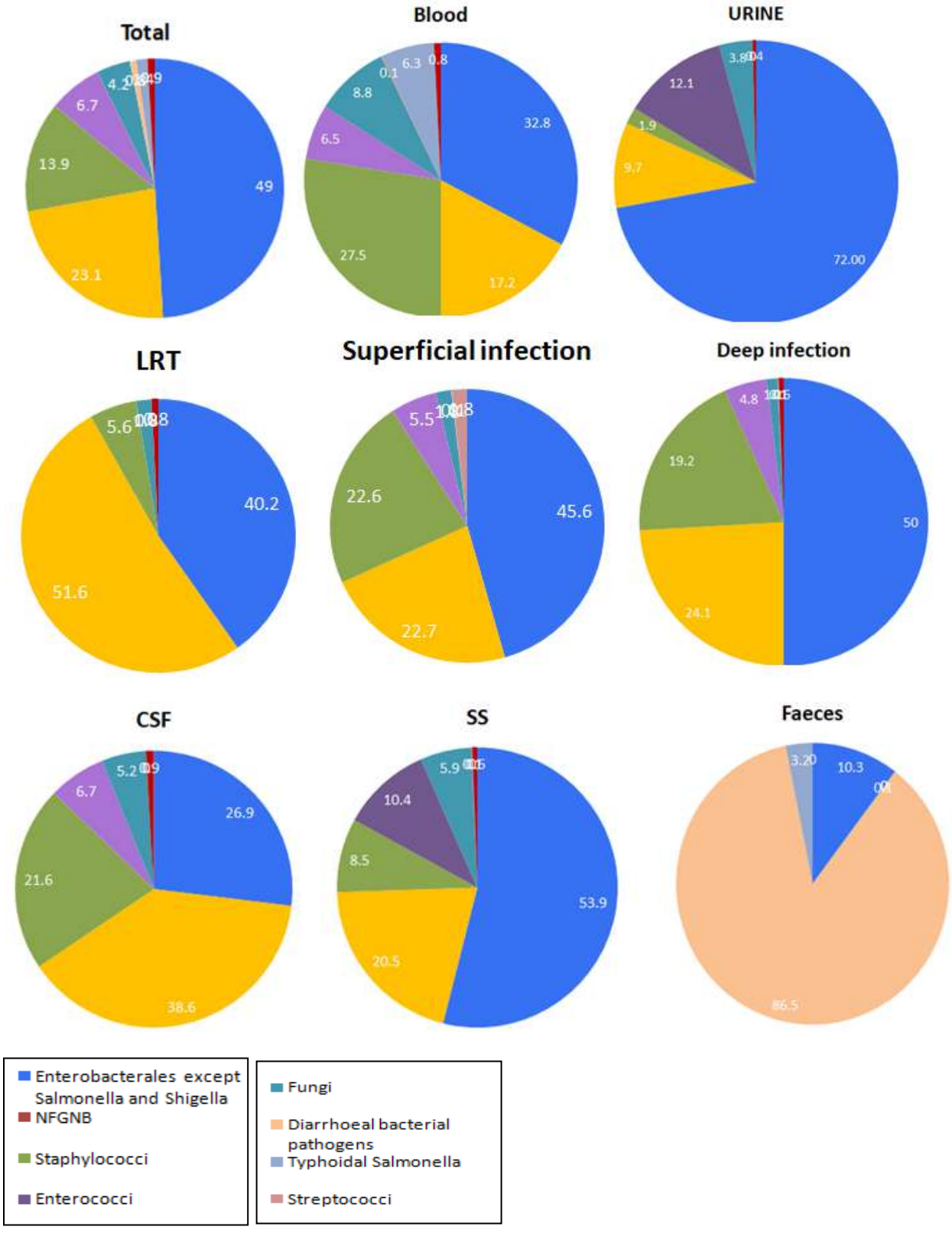


Figure 1.1: Specimen wise distribution of major groups of organisms

Table 1.2: Top 10 isolates overall and their isolation rates from different specimens

Organism	All Specimen	Blood	LRT	Superficial Infection	Deep Infection	SS	Faeces	Urine
Escherichia coli	27588 / 113008 (24.4)	3713 / 24078 (15.4)	1656 / 19568 (8.5)	3654 / 18491 (19.8)	2267 / 10395 (21.8)	760 / 2681 (28.3)	86 / 1012 (8.5)	13626 / 28628 (47.6)
Klebsiella pneumoniae	19134 / 113008 (16.9)	3137 / 24078 (13)	4900 / 19568 (25)	2765 / 18491 (15)	1492 / 10395 (14.4)	491 / 2681 (18.3)	15 / 1012 (1.5)	4958 / 28628 (17.3)
Pseudomonas aeruginosa	13835 / 113008 (12.2)	1384 / 24078 (5.7)	4825 / 19568 (24.7)	2771 / 18491 (15)	1461 / 10395 (14.1)	247 / 2681 (9.2)	0 / 1012 (0)	2181 / 28628 (7.6)
Acinetobacter baumannii	10714 / 113008 (9.2)	2233 / 24078 (9.1)	4852 / 19568 (23.9)	1243 / 18491 (6.5)	971 / 10395 (9.1)	237 / 2681 (8.1)	0 / 1012 (0)	416 / 28628 (1.4)
Staphylococcus aureus	9700 / 113008 (8.6)	1737 / 24078 (7.2)	1011 / 19568 (5.2)	3767 / 18491 (20.4)	1874 / 10395 (18)	173 / 2681 (6.5)	0 / 1012 (0)	362 / 28628 (1.3)
Enterococcus faecalis	3217 / 113008 (2.8)	486 / 24078 (2)	0 / 19568 (0)	537 / 18491 (2.9)	196 / 10395 (1.9)	86 / 2681 (3.2)	0 / 1012 (0)	1623 / 28628 (5.7)
Enterococcus faecium	3128 / 113008 (2.8)	961 / 24078 (4)	0 / 19568 (0)	289 / 18491 (1.6)	212 / 10395 (2)	158 / 2681 (5.9)	0 / 1012 (0)	1162 / 28628 (4.1)
Staphylococcus haemolyticus	1811 / 113008 (1.6)	1515 / 24078 (6.3)	24 / 19568 (0.1)	82 / 18491 (0.4)	40 / 10395 (0.4)	8 / 2681 (0.3)	0 / 1012 (0)	38 / 28628 (0.1)
Staphylococcus epidermidis	1771 / 113008 (1.6)	1493 / 24078 (6.2)	4 / 19568 (0)	84 / 18491 (0.5)	54 / 10395 (0.5)	12 / 2681 (0.4)	0 / 1012 (0)	12 / 28628 (0)
Proteus mirabilis	1754 / 113008 (1.6)	89 / 24078 (0.4)	136 / 19568 (0.7)	566 / 18491 (3.1)	439 / 10395 (4.2)	33 / 2681 (1.2)	0 / 1012 (0)	355 / 28628 (1.2)
Enterobacter cloacae	1660 / 113008 (1.5)	394 / 24078 (1.6)	181 / 19568 (0.9)	322 / 18491 (1.7)	289 / 10395 (2.8)	50 / 2681 (1.9)	2 / 1012 (0.2)	314 / 28628 (1.1)



Figure 1.2: Isolation distribution of the top ten isolates from different specimens

Table 1.3: Distribution of top 10 isolates from all specimens across OPD, ward and ICU

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Escherichia coli	27588 / 113008 (24.4)	10947 / 35193 (31.1)	14117 / 60119 (23.5)	2524 / 17695 (14.3)
Klebsiella pneumoniae	19134 / 113008 (16.9)	5069 / 35193 (14.4)	10219 / 60119 (17)	3846 / 17695 (21.7)
Pseudomonas aeruginosa	13835 / 113008 (12.2)	4859 / 35193 (13.8)	6876 / 60119 (11.4)	2100 / 17695 (11.9)
Acinetobacter baumannii	10714 / 113008 (9.5)	1416 / 35193 (4.0)	5622 / 60119 (9.4)	3676 / 17695 (20.8)
Staphylococcus aureus	9700 / 113008 (8.6)	3978 / 35193 (11.3)	4877 / 60119 (8.1)	845 / 17695 (4.8)
Enterococcus faecalis	3217 / 113008 (2.8)	1060 / 35193 (3)	1809 / 60119 (3)	348 / 17695 (2)
Enterococcus faecium	3128 / 113008 (2.8)	510 / 35193 (1.4)	1929 / 60119 (3.2)	689 / 17695 (3.9)
Staphylococcus haemolyticus	1811 / 113008 (1.6)	352 / 35193 (1)	1049 / 60119 (1.7)	410 / 17695 (2.3)
Staphylococcus epidermidis	1771 / 113008 (1.6)	393 / 35193 (1.1)	1057 / 60119 (1.8)	321 / 17695 (1.8)
Proteus mirabilis	1754 / 113008 (1.6)	709 / 35193 (2)	890 / 60119 (1.5)	155 / 17695 (0.9)
Enterobacter cloacae	1660 / 113008 (1.5)	571 / 35193 (1.6)	929 / 60119 (1.5)	160 / 17695 (0.9)

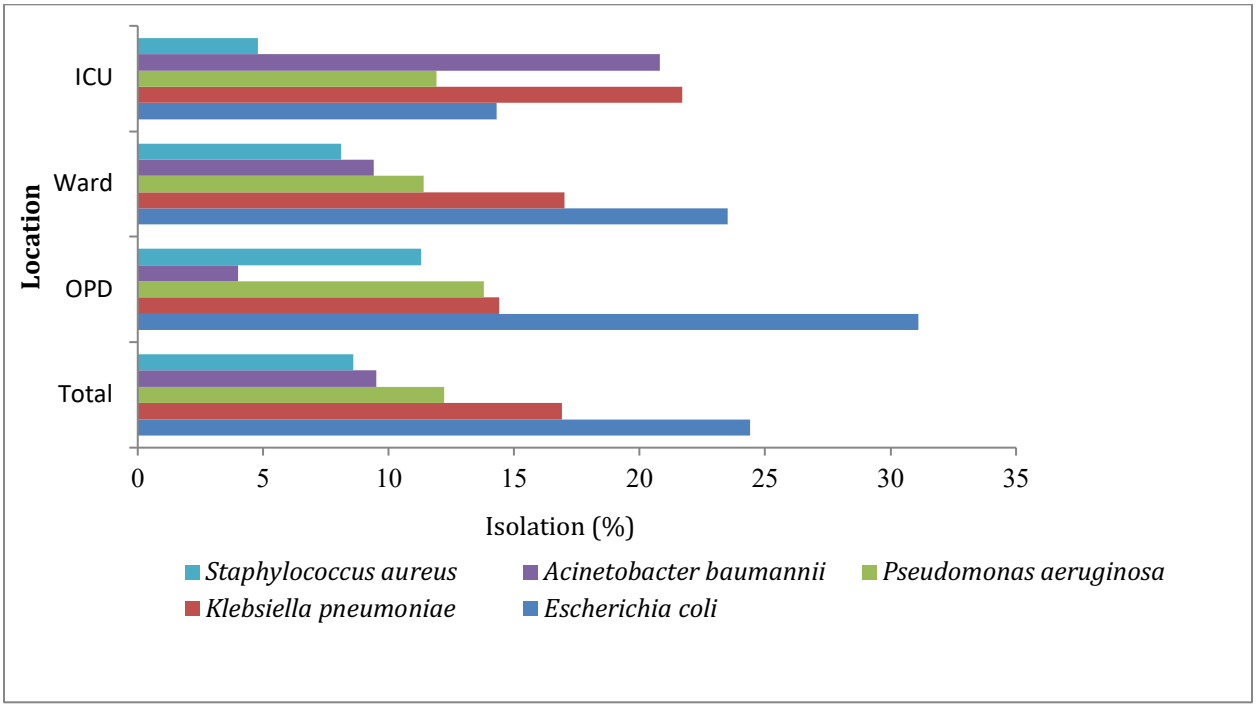


Figure 1.3: Distribution of top 5 isolates from all specimens across OPD, ward and ICU

Yearly isolation rates of top ten isolates from all samples showed a steady increase of *E.coli* from 22.8% to 24.4% and *Klebsiella pneumoniae* from 14.7% in 2017 to 16.9% in 2025 **(Table 1.4, Figure 1.4)** without much change in the isolation rates of the other species.

Table 1.4: Yearly isolation trends of top 10 isolates from all samples

Organism	Year-2017 n(%)	Year-2018 n(%)	Year-2019 n(%)	Year-2020 n(%)	Year-2021 n(%)	Year-2022 n(%)	Year-2023 n(%)	Year-2024 n(%)	Year-2025 n(%)
Escherichia coli	10441 / 45714 (22.8)	19459 / 75182 (25.8)	30953 / 110268 (28.1)	16921 / 68081 (24.8)	23764 / 96836 (24.5)	26804 / 109554 (24.4)	23691 / 102361 (23.14)	25994 / 99027 (26.2)	27588 / 113008 (24.4)
Klebsiella pneumoniae	6743 / 45714 (14.7)	11136 / 75182 (14.8)	18729 / 110268 (16.9)	12173 / 68081 (17.8)	17359 / 96836 (17.9)	19002 / 109554 (17.3)	16664 / 102361 (16.2)	17413 / 99027 (17.5)	19134 / 113008 (16.9)
Pseudomonas aeruginosa	5695 / 45714 (12.4)	8921 / 75182 (11.8)	12650 / 110268 (11.4)	8013 / 68081 (11.7)	11706 / 96836 (12.1)	13388 / 109554 (12.22)	12017 / 102361 (11.74)	11419/ 99027 (11.5)	13835 / 113008 (12.2)
Acinetobacter baumannii	3524 / 45714 (7.7)	5446 / 75182 (7.2)	8839 / 110268 (8.0)	7301 / 68081 (10.7)	12484 / 96836 (12.9)	12176 / 109554 (11.1)	12099 / 102361 (11.8)	10351 / 99027 (10.5)	10714 / 113008 (9.5)
S. aureus	5723 / 45714 (12.5)	8874 / 75182 (11.8)	12625 / 110268 (11.4)	6562 / 68081 (9.6)	8920 / 96836 (9.2)	9477 / 109554 (8.6)	9037 / 102361 (8.8)	8515 / 99027 (8.6)	9700 / 113008 (8.6)
Enterococcus faecalis	1040 / 45714 (2.2)	2022 / 75182 (2.6)	2916 / 110268 (2.6)	2177 / 68081 (3.2)	2405 / 96836 (2.4)	3265 / 109554 (2.9)	3523 / 102361 (3.4)	3002 / 99027 (3.1)	3217 / 113008 (2.8)
Enterococcus faecium	937 / 45714 (2.0)	1479 / 75182 (1.9)	2741 / 110268 (2.4)	2038 / 68081 (2.9)	2486 / 96836 (2.5)	3047 / 109554 (2.7)	2792 / 102361 (2.7)	3002 / 99027 (3.0)	3128 / 113008 (2.8)
Proteus mirabilis	887 / 45714 (1.9)	1289 / 75182 (1.7)	1969 / 110268 (1.8)	1272 / 68081 (1.8)	1646 / 96836 (1.7)	1799 / 109554 (1.6)	1579 / 102361 (1.5)	1800 / 99027 (1.8)	1754 / 113008 (1.6)
Enterobacter cloacae	620 / 45714 (1.3)	1098 / 75182 (1.4)	1514 / 110268 (1.3)	1080 / 68081 (1.6)	1654 / 96836 (1.7)	1780 / 109554 (1.6)	1752 / 102361 (1.7)	1625 / 99027 (1.6)	1660 / 113008 (1.5)
S. haemolyticus	634 / 45714 (1.4)	871 / 75182 (1.1)	827 / 110268 (0.7)	626 / 68081 (0.9)	846 / 96836 (0.8)	2391 / 109554 (2.1)	2274 / 102361 (2.2)	1572 / 99027 (1.5)	1811 / 113008 (1.6)

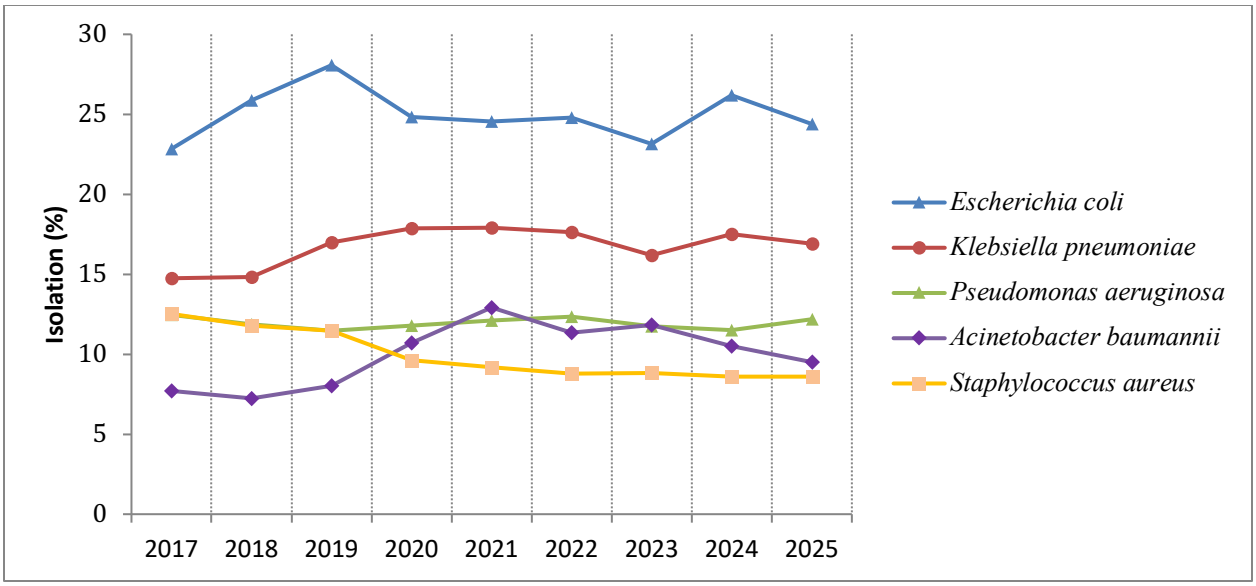


Figure 1.4: Yearly isolation trends of top 5 isolates from all samples

Enterobacterales

Of the total isolates, Enterobacterales isolates (except *Salmonella and Shigella*) constituted a major group (49.0%) **(Table 1.1).** Out of a total of 1,13,008 culture positive isolates, specimen percentage wise distribution of major species within family Enterobacterales is shown in the **Table 1.5 and Figures 1.5.** Overall, *Escherichia coli* was the commonest species (24.4%) followed by *Klebsiella pneumoniae* (16.9%), *Proteus mirabilis* (1.6%) and *Enterobacter cloacae* (1.5%) **(Table 1.5)**. *Escherichia coli* was the most predominant isolate from the urine (47.6%), sterile site (28.3%), Deep infections (21.8%), others (24.3%), superficial infection (19.8%), blood (15.4%) and CSF (8.7%). *Klebsiella pneumoniae* was the most predominant isolate in the lower respiratory tract (25.0%), CSF (15.1%), sterile sites (SS) (18.3%), urine (17.3%), others (17.1%), superficial infection (15.0%), blood (13.0%) and deep infection (DI) (14.4%). *Proteus mirabilis* was common in 4.2 % of deep infections, 2.8% of superficial infections and other specimens (1.8%). *Enterobacter cloacae* constituted 1.9 % of deep infections, 1.7% of superficial infections, 0.7% of CSF and 1.9% of sterile site infection. Isolates from the regional centers (RC 17) had higher percentage isolate rate of *E. coli* and RC 14 had higher *K. pneumoniae*. RC4 had higher percentage isolate rate of *Proteus mirabilis* and RC 7 had higher percentage of *Enterobacter cloacae* than the rest of RCs **(Table 1.6).**

Table 1.5: Specimen wise distributions of major species of Family Enterobacterales except *Salmonella* and *Shigella*

Isolate	Culture positive																			
	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012		Others n=7144	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Escherichia coli	27589 (24.4)	100	3713 (15.4)	13.5	13627 (47.6)	49.4	1656 (8.4)	6	3654 (19.7)	13.2	2267 (21.8)	8.2	88 (8.7)	0.3	760 (28.3)	2.8	86 (8.5)	0.3	1738 (24.3)	6.3
Klebsiella pneumoniae	19134 (16.9)	100	3137 (13.0)	16.4	4958 (17.3)	25.9	4900 (25.0)	25.6	2765 (14.9)	14.5	1492 (14.3)	7.8	153 (15.1)	0.8	491 (18.3)	2.6	15 (1.4)	0.1	1223 (17.1)	6.4
Proteus mirabilis	1754 (1.5)	100	89 (0.3)	5.1	355 (1.2)	20.2	136 (0.7)	7.8	566 (3.0)	32.3	439 (4.2)	25	4 (0.4)	0.2	33 (1.2)	1.9	0 (0)	0	132 (1.8)	7.5
Enterobacter cloacae	1660 (1.4)	100	394 (1.6)	23.7	314 (1.1)	18.9	181 (0.9)	10.9	322 (1.7)	19.4	289 (2.7)	17.4	7 (0.7)	0.4	50 (1.8)	3	2 (0.2)	0.1	101 (1.4)	6.1
Citrobacter koseri	705 (0.6)	100	49 (0.2)	7	258 (0.9)	36.6	91 (0.4)	12.9	185 (1)	26.2	66 (0.6)	9.4	0 (0)	0	14 (0.5)	2	0 (0)	0	42 (0.6)	6
Morganella morganii	657 (0.6)	100	32 (0.1)	4.9	182 (0.6)	27.7	27 (0.1)	4.1	212 (1.1)	32.3	131 (1.2)	19.9	2 (0.2)	0.3	14 (0.5)	2.1	0 (0)	0	57 (0.8)	8.7
Serratia marcescens	504 (0.4)	100	142 (0.6)	28.2	49 (0.1)	9.7	135 (0.7)	26.8	84 (0.4)	16.7	58 (0.5)	11.5	3 (0.3)	0.6	11 (0.4)	2.2	0 (0)	0	22 (0.3)	4.4
Enterobacter spp	465 (0.4)	100	113 (0.4)	24.3	80 (0.2)	17.2	72 (0.3)	15.5	91 (0.5)	19.6	67 (0.6)	14.4	5 (0.5)	1.1	14 (0.5)	3	0 (0)	0	23 (0.3)	4.9
Providencia stuartii	180 (0.1)	100	22 (0.09)	12.2	25 (0.09)	13.9	32 (0.16)	17.8	42 (0.2)	23.3	39 (0.3)	21.7	5 (0.5)	2.8	5 (0.2)	2.8	0 (0)	0	10 (0.14)	5.6

Table 1.6: Regional centre wise distribution of major species of family Enterobacterales (except Salmonella) in all specimens (except faeces)

Regional Centre	*Escherichia coli*	*Klebsiella pneumoniae*	*Proteus mirabilis*	*Enterobacter cloacae*	*Citrobacter koseri*	*Enterobacter spp.*	*Citrobacter spp.*	*Citrobacter freundii*	*Proteus vulgaris*
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	228/966 (23.6)	204/966 (21.1)	2/966 (0.2)	11/966 (1.1)	1/966 (0.1)	3/966 (0.3)	1/966 (0.1)	0/966 (0)	0/966 (0)
RC2	1870/13720 (13.6)	1485/13720 (10.8)	379/13720 (2.8)	240/13720 (1.7)	27/13720 (0.2)	70/13720 (0.5)	44/13720 (0.3)	9/13720 (0.1)	10/13720 (0.1)
RC3	674/4065 (16.6)	482/4065 (11.9)	38/4065 (0.9)	3/4065 (0.1)	15/4065 (0.4)	70/4065 (1.7)	7/4065 (0.2)	4/4065 (0.1)	0/4065 (0)
RC4	923/4512 (20.5)	774/4512 (17.2)	107/4512 (2.4)	57/4512 (1.3)	31/4512 (0.7)	9/4512 (0.2)	0/4512 (0)	0/4512 (0)	0/4512 (0)
RC5	671/2930 (22.9)	548/2930 (18.7)	60/2930 (2)	76/2930 (2.6)	26/2930 (0.9)	0/2930 (0)	14/2930 (0.5)	4/2930 (0.1)	2/2930 (0.1)
RC6	2173/8729 (24.9)	1556/8729 (17.8)	188/8729 (2.2)	35/8729 (0.4)	37/8729 (0.4)	85/8729 (1)	19/8729 (0.2)	13/8729 (0.1)	25/8729 (0.3)
RC7	369/1177 (31.4)	184/1177 (15.6)	14/1177 (1.2)	39/1177 (3.3)	9/1177 (0.8)	2/1177 (0.2)	0/1177 (0)	4/1177 (0.3)	2/1177 (0.2)
RC8	749/3215 (23.3)	727/3215 (22.6)	72/3215 (2.2)	99/3215 (3.1)	36/3215 (1.1)	1/3215 (0)	0/3215 (0)	10/3215 (0.3)	1/3215 (0)
RC9	608/2350 (25.9)	380/2350 (16.2)	1/2350 (0)	0/2350 (0)	145/2350 (6.2)	0/2350 (0)	0/2350 (0)	6/2350 (0.3)	0/2350 (0)
RC10	1536/4994 (30.8)	983/4994 (19.7)	115/4994 (2.3)	148/4994 (3)	109/4994 (2.2)	0/4994 (0)	22/4994 (0.4)	11/4994 (0.2)	12/4994 (0.2)
RC11	428/2004 (21.4)	535/2004 (26.7)	5/2004 (0.2)	58/2004 (2.9)	1/2004 (0)	0/2004 (0)	0/2004 (0)	1/2004 (0)	0/2004 (0)
RC12	618/2159 (28.6)	309/2159 (14.3)	26/2159 (1.2)	53/2159 (2.5)	4/2159 (0.2)	9/2159 (0.4)	7/2159 (0.3)	3/2159 (0.1)	2/2159 (0.1)
RC13	879/3964 (22.2)	655/3964 (16.5)	14/3964 (0.4)	50/3964 (1.3)	1/3964 (0)	11/3964 (0.3)	0/3964 (0)	0/3964 (0)	0/3964 (0)
RC14	2898/8128 (35.7)	1793/8128 (22.1)	17/8128 (0.2)	115/8128 (1.4)	71/8128 (0.9)	64/8128 (0.8)	15/8128 (0.2)	2/8128 (0)	1/8128 (0)
RC16	1849/7187 (25.7)	1452/7187 (20.2)	138/7187 (1.9)	1/7187 (0)	15/7187 (0.2)	4/7187 (0.1)	1/7187 (0)	29/7187 (0.4)	115/7187 (1.6)

Regional Centre	*Escherichia coli*	*Klebsiella pneumoniae*	*Proteus mirabilis*	*Enterobacter cloacae*	*Citrobacter koseri*	*Enterobacter spp.*	*Citrobacter spp.*	*Citrobacter freundii*	*Proteus vulgaris*
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC17	1578/4684 (33.7)	807/4684 (17.2)	61/4684 (1.3)	125/4684 (2.7)	15/4684 (0.3)	5/4684 (0.1)	1/4684 (0)	3/4684 (0.1)	1/4684 (0)
RC19	1355/6086 (22.3)	982/6086 (16.1)	91/6086 (1.5)	51/6086 (0.8)	3/6086 (0)	5/6086 (0.1)	0/6086 (0)	2/6086 (0)	2/6086 (0)
RC20	1235/4213 (29.3)	758/4213 (18)	57/4213 (1.4)	1/4213 (0)	6/4213 (0.1)	2/4213 (0)	4/4213 (0.1)	8/4213 (0.2)	24/4213 (0.6)
RC21	392/1707 (23)	369/1707 (21.6)	29/1707 (1.7)	22/1707 (1.3)	10/1707 (0.6)	1/1707 (0.1)	1/1707 (0.1)	4/1707 (0.2)	2/1707 (0.1)
RC24	582/1745 (33.4)	322/1745 (18.5)	20/1745 (1.1)	14/1745 (0.8)	4/1745 (0.2)	4/1745 (0.2)	7/1745 (0.4)	5/1745 (0.3)	11/1745 (0.6)
RC26	1315/5788 (22.7)	1061/5788 (18.3)	65/5788 (1.1)	150/5788 (2.6)	1/5788 (0)	0/5788 (0)	5/5788 (0.1)	24/5788 (0.4)	1/5788 (0)
RC27	495/2724 (18.2)	520/2724 (19.1)	33/2724 (1.2)	75/2724 (2.8)	42/2724 (1.5)	0/2724 (0)	2/2724 (0.1)	15/2724 (0.6)	2/2724 (0.1)
RC28	569/1904 (29.9)	228/1904 (12)	27/1904 (1.4)	53/1904 (2.8)	4/1904 (0.2)	4/1904 (0.2)	4/1904 (0.2)	3/1904 (0.2)	0/1904 (0)
RC29	144/443 (32.5)	76/443 (17.2)	12/443 (2.7)	10/443 (2.3)	4/443 (0.9)	0/443 (0)	3/443 (0.7)	1/443 (0.2)	2/443 (0.5)
RC30	830/2514 (33)	516/2514 (20.5)	32/2514 (1.3)	68/2514 (2.7)	14/2514 (0.6)	11/2514 (0.4)	0/2514 (0)	5/2514 (0.2)	0/2514 (0)
RC31	709/2197 (32.3)	418/2197 (19)	31/2197 (1.4)	52/2197 (2.4)	21/2197 (1)	3/2197 (0.1)	2/2197 (0.1)	10/2197 (0.5)	2/2197 (0.1)
RC32	830/3074 (27)	500/3074 (16.3)	43/3074 (1.4)	32/3074 (1)	42/3074 (1.4)	19/3074 (0.6)	0/3074 (0)	92/3074 (3)	12/3074 (0.4)
RC33	580/2214 (26.2)	453/2214 (20.5)	51/2214 (2.3)	21/2214 (0.9)	8/2214 (0.4)	67/2214 (3)	2/2214 (0.1)	5/2214 (0.2)	42/2214 (1.9)
RC34	416/2603 (16)	42/2603 (1.6)	26/2603 (1)	0/2603 (0)	3/2603 (0.1)	16/2603 (0.6)	39/2603 (1.5)	0/2603 (0)	6/2603 (0.2)
Total National	27503/111996 (24.6)	19119/111996 (17.1)	1754/111996 (1.6)	1659/111996 (1.5)	705/111996 (0.6)	465/111996 (0.4)	200/111996 (0.2)	273/111996 (0.2)	277/111996 (0.2)

Typhoidal Salmonella

This distribution showed that isolates from the RC28 had higher percentage isolate rate of *Salmonella* Typhi from blood (25.1%) than the rest of RCs **(Table 1.7)**. *Salmonella* Paratyphi A isolate percentage was more in RC 6 (6.3) and in RC 31 (3.7%) as compared to other RCs. The relative distribution of Typhoidal *Salmonella* isolated from blood in the OPD, admitted to the wards and ICUs are presented in **Table 1.8 and Figures 1.6**. Typhoidal *Salmonella* was common isolate from the OPD (14.0%) followed by the wards and was least isolated from the ICU**.** Among Typhoidal Salmonella, *Salmonella* Typhi had higher percentage isolation rate than *Salmonella* Paratyphi A*.* The yearly isolation trend remained stable in 2025, with isolation rates comparable to those reported in 2024 **(Table 1.9 & Figure 1.7).**

Table 1.7: Isolates percentages across Regional Centres of Typhoidal Salmonella isolated from blood

Regional Centre	Total Blood Isolates n(%)	Salmonella Typhi n(%)	Salmonella Paratyphi A n(%)
RC1	264/24078 (1.1)	64/264 (24.2)	1/264 (0.4)
RC2	6662/24078 (27.7)	158/6662 (2.4)	31/6662 (0.5)
RC3	1388/24078 (5.8)	131/1388 (9.4)	25/1388 (1.8)
RC4	635/24078 (2.6)	14/635 (2.2)	0/635 (0)
RC5	588/24078 (2.4)	42/588 (7.1)	14/588 (2.4)
RC6	2020/24078 (8.4)	340/2020 (16.8)	127/2020 (6.3)
RC7	154/24078 (0.6)	2/154 (1.3)	0/154 (0)
RC8	658/24078 (2.7)	0/658 (0)	0/658 (0)
RC9	395/24078 (1.6)	13/395 (3.3)	0/395 (0)
RC10	631/24078 (2.6)	46/631 (7.3)	5/631 (0.8)
RC11	195/24078 (0.8)	0/195 (0)	0/195 (0)
RC12	412/24078 (1.7)	18/412 (4.4)	1/412 (0.2)
RC13	1001/24078 (4.2)	27/1001 (2.7)	29/1001 (2.9)
RC14	1196/24078 (5)	38/1196 (3.2)	5/1196 (0.4)
RC16	421/24078 (1.7)	1/421 (0.2)	0/421 (0)
RC17	1439/24078 (6)	5/1439 (0.3)	1/1439 (0.1)
RC19	1896/24078 (7.9)	0/1896 (0)	0/1896 (0)
RC20	215/24078 (0.9)	10/215 (4.7)	6/215 (2.8)
RC21	337/24078 (1.4)	3/337 (0.9)	1/337 (0.3)
RC24	130/24078 (0.5)	3/130 (2.3)	1/130 (0.8)
RC26	1090/24078 (4.5)	10/1090 (0.9)	4/1090 (0.4)
RC27	402/24078 (1.7)	5/402 (1.2)	2/402 (0.5)
RC28	303/24078 (1.3)	76/303 (25.1)	7/303 (2.3)
RC29	52/24078 (0.2)	0/52 (0)	0/52 (0)
RC30	266/24078 (1.1)	2/266 (0.8)	2/266 (0.8)
RC31	513/24078 (2.1)	43/513 (8.4)	19/513 (3.7)

Regional Centre	Total Blood Isolates n(%)	Salmonella Typhi n(%)	Salmonella Paratyphi A n(%)
RC32	235/24078 (1)	3/235 (1.3)	0/235 (0)
RC33	357/24078 (1.5)	1/357 (0.3)	0/357 (0)
RC34	223/24078 (0.9)	0/223 (0)	0/223 (0)
Total	24078	1055/24078 (4.4)	281/24078 (1.2)

Table 1.8: Location wise distribution of Typhoidal Salmonella isolates from blood

	Total	OPD	Ward	ICU
Total Typhoidal Salmonella	1520 / 24078 (6.3)	855 / 4429 (19.3)	621 / 13974 (4.4)	44 / 5675 (0.8)
Salmonella Typhi	1055 / 24078 (4.4)	619 / 4429 (14)	407 / 13974 (2.9)	29 / 5675 (0.5)
Salmonella Paratyphi A	281 / 24078 (1.2)	155 / 4429 (3.5)	123 / 13974 (0.9)	3 / 5675 (0.1)

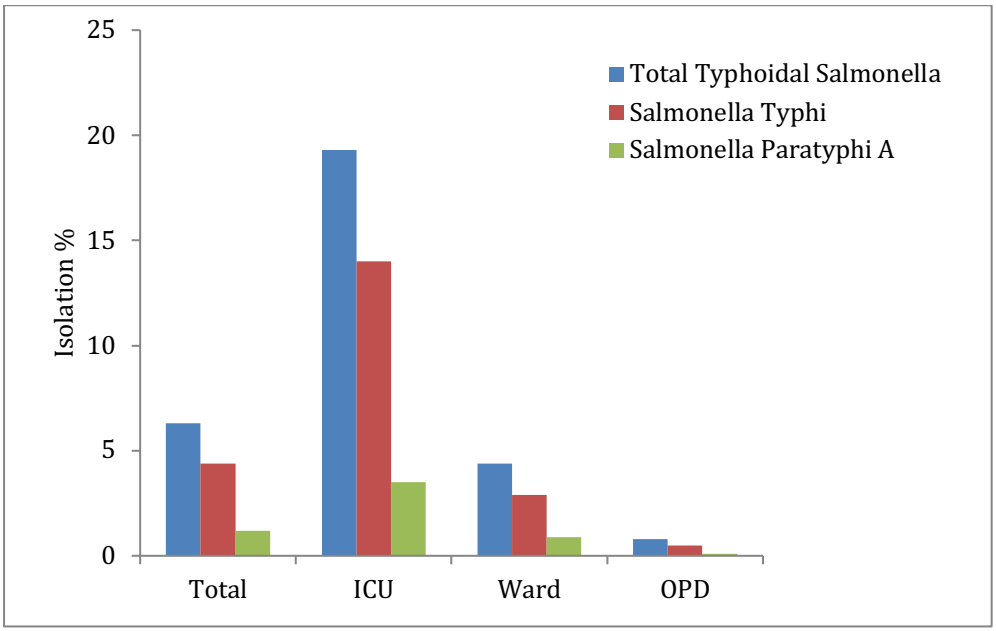


Figure 1.6: Location-wise Isolation pattern of Typhoidal Salmonella isolated from blood across OPD, Ward and ICU

Table 1.9: Yearly-isolation trend of Salmonella Typhi from blood across different regions

	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
North	246/5248 (4.7)	174/4533 (3.8)	47/3479 (1.4)	126/6498 (1.9)	298/12206 (2.4)	498/12083 (4)	451/1042 6 (4.3)	704/1319 8 (5.3)
Central	12/110 (10.9)	36/570 (6.3)	14/448 (3.1)	12/584 (2.1)	51/882 (5.7)	23/785 (2.9)	14/497 (2.8)	21/737 (2.8)
East	2/712 (0.3)	4/1443 (0.3)	1/935 (0.1)	1/1746 (0.1)	3/1568 (0.2)	2/1147 (0.2)	9/1688 (0.5)	6/1734 (0.3)
West	116/2011 (5.8)	164/2761 (5.9)	41/2041 (2)	41/2973 (1.4)	61/3302 (1.8)	47/1835 (2.6)	86/1942 (4.4)	85/2718 (3.1)
South	204/6018 (3.4)	350/8033 (4.4)	103/6206 (1.7)	113/7187 (1.6)	171/6280 (2.7)	528/6332 (8.3)	281/4474 (6.2)	239/5691 (4.2)
Total National	580/ 14099 (4.1)	728/ 17340 (4.2)	206/ 13109 (1.6)	293/ 18988 (1.5)	584 / 24238 (2.41)	1098/ 22182 (4.9)	841/ 19027 (4.4)	1055/ 24078 (4.4)

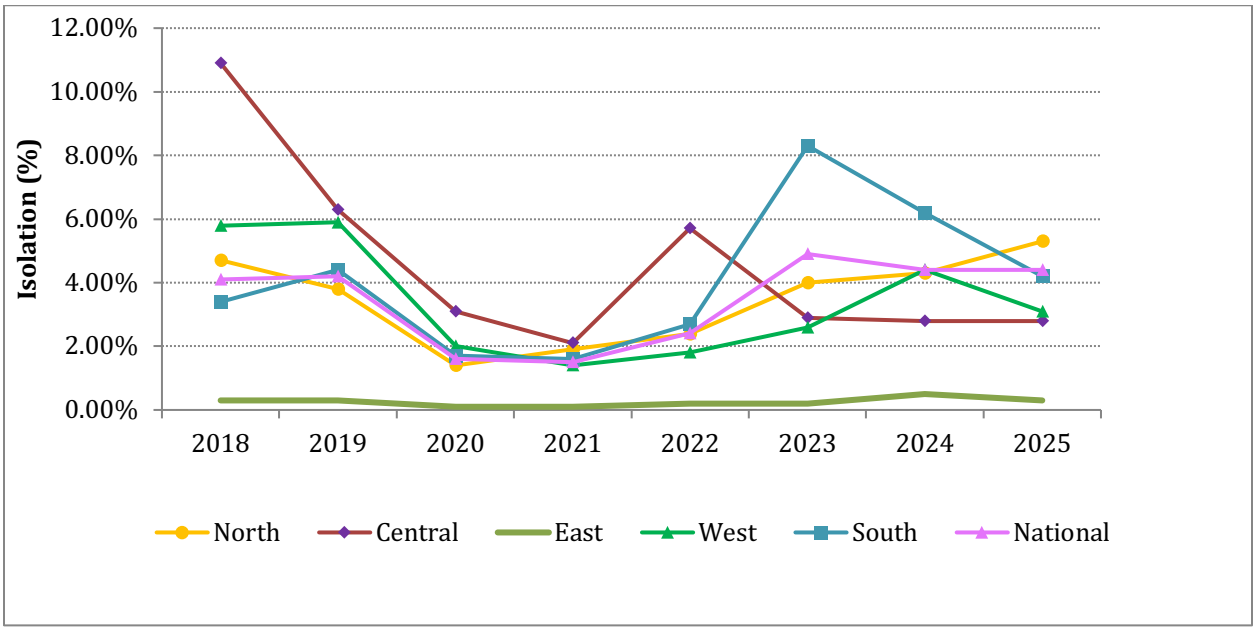


Figure 1.7: Yearly-isolation trends of Salmonella Typhi from blood across different regions

Non-fermenting Gram-negative bacteria

Non-fermenting Gram-negative bacteria (NFGNB) constituted 23.1% of the total isolates (26,085 out of 1,13,008) **(Table 1.1).** Among the NFGNB, *Pseudomonas aeruginosa* (12.2%) was the commonest isolate followed by *Acinetobacter baumannii* (9.5%), *Stenotrophomonas maltophilia* accounted for 0.7% of all isolates respectively. *Pseudomonas aeruginosa* was grossly predominant in LRT (24.7%) followed by superficial infection (15.0%), deep infections (14.1%), and SS (9.2%). *Acinetobacter baumannii* was the predominant isolate from CSF (26.7%) and LRT (24.8%) followed by blood (9.3%) and SS (8.8%) **(Table 1.10).**

Regional center (RC) wise distribution showed that RC 29 had higher percentage isolate rate of *Pseudomonas aeruginosa* and RC 26 had higher percentage isolate rate of *Acinetobacter baumannii* than the rest of RCs **(Table 1.11).** Among clinical settings, *P. aeruginosa* was predominantly isolated in all ward, ICU and OPD (11.9-13.8%) respectively, while *A. baumannii* was predominant in ICU (20.8%), followed by ward (9.3%) and OPD (4.0%) (**Table 1.12a and Figure 1.8).**

The trend analysis over the years 2017 – 2023 shows increase in isolates rates of *A. baumannii* from 7.7% to 12.0% and further decreased isolation rate was observed in 2024 (10.5%) and in 2025 (9.5%). In contrast, stable pattern in the isolation rates of *P. aeruginosa* from 12.4% to 12.2 % in 2017 to 2025 **(Table 1.12b)**. In case of *S. maltophilia,* trend analysis over the years 2017 – 2024 has shown an increased pattern of from 0.3% to 0.7% and in 2025, *n*o changes in the isolation rates have been noted in 2025 (**Figure 1.9).**

Table 1.10: Specimen-wise distribution of NFGNB

Isolate	Culture positive																			
	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012		Others n=7139	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	N	%	n	%	n	%
NFGNB	26085 (23.1)	100	4140 (17.2)	15.9	2766 (9.7)	10.6	10098 (51.6)	38.7	4191 (22.7)	16.1	2502 (24.1)	9.6	390 (38.6)	1.5	550 (20.5)	2.1	0 (0)	0	1448 (20.3)	5.6
Pseudomonas aeruginosa	13835 (12.2)	100	1384 (5.7)	10	2181 (7.6)	15.8	4825 (24.7)	34.9	2771 (15)	20	1461 (14.1)	10.6	90 (8.9)	0.7	247 (9.2)	1.8	0 (0)	0	876 (12.3)	6.3
Acinetobacter baumannii	10714 (9.5)	100	2233 (9.3)	20.8	416 (1.5)	3.9	4852 (24.8)	45.3	1243 (6.7)	11.6	971 (9.3)	9.1	270 (26.7)	2.5	237 (8.8)	2.2	0 (0)	0	492 (6.9)	4.6
Stenotrophomonas maltophilia	794 (0.7)	100	291 (1.2)	36.6	43 (0.2)	5.4	242 (1.2)	30.5	86 (0.5)	10.8	39 (0.4)	4.9	7 (0.7)	0.9	38 (1.4)	4.8	0 (0)	0	48 (0.7)	6

Table 1.11: Isolates percentages across Regional Centres of *Pseudomonas aeruginosa, Acinetobacter baumannii and Stenotrophomonas maltophilia* from all specimens (except faeces)

Regional Centre	Total Isolates	*Pseudomonas aeruginosa*	*Acinetobacter baumannii*	*Stenotrophomonas maltophilia*
	n(%)	n(%)	n(%)	n(%)
RC1	966 (0.9)	163/966 (16.9)	128/966 (13.3)	2/966 (0.2)
RC2	13720 (12.3)	1059/13720 (7.7)	1817/13720 (13.2)	92/13720 (0.7)
RC3	4065 (3.6)	1220/4065 (30)	653/4065 (16.1)	0/4065 (0)
RC4	4512 (4)	517/4512 (11.5)	410/4512 (9.1)	45/4512 (1)
RC5	2930 (2.6)	363/2930 (12.4)	107/2930 (3.7)	40/2930 (1.4)
RC6	8729 (7.8)	1299/8729 (14.9)	522/8729 (6)	112/8729 (1.3)
RC7	1177 (1.1)	120/1177 (10.2)	63/1177 (5.4)	14/1177 (1.2)
RC8	3215 (2.9)	599/3215 (18.6)	95/3215 (3)	77/3215 (2.4)
RC9	2350 (2.1)	380/2350 (16.2)	304/2350 (12.9)	2/2350 (0.1)
RC10	4994 (4.5)	548/4994 (11)	203/4994 (4.1)	46/4994 (0.9)
RC11	2004 (1.8)	192/2004 (9.6)	474/2004 (23.7)	9/2004 (0.4)
RC12	2159 (1.9)	307/2159 (14.2)	241/2159 (11.2)	39/2159 (1.8)
RC13	3964 (3.5)	546/3964 (13.8)	635/3964 (16)	17/3964 (0.4)
RC14	8128 (7.3)	788/8128 (9.7)	303/8128 (3.7)	4/8128 (0)
RC16	7187 (6.4)	495/7187 (6.9)	479/7187 (6.7)	10/7187 (0.1)
RC17	4684 (4.2)	394/4684 (8.4)	592/4684 (12.6)	20/4684 (0.4)
RC19	6086 (5.4)	685/6086 (11.3)	748/6086 (12.3)	23/6086 (0.4)
RC20	4213 (3.8)	370/4213 (8.8)	599/4213 (14.2)	5/4213 (0.1)
RC21	1707 (1.5)	196/1707 (11.5)	346/1707 (20.3)	30/1707 (1.8)
RC24	1745 (1.6)	300/1745 (17.2)	91/1745 (5.2)	5/1745 (0.3)
RC26	5788 (5.2)	922/5788 (15.9)	1155/5788 (20)	106/5788 (1.8)
RC27	2724 (2.4)	333/2724 (12.2)	144/2724 (5.3)	17/2724 (0.6)
RC28	1904 (1.7)	142/1904 (7.5)	117/1904 (6.1)	25/1904 (1.3)
RC29	443 (0.4)	86/443 (19.4)	6/443 (1.4)	3/443 (0.7)
RC30	2514 (2.2)	199/2514 (7.9)	108/2514 (4.3)	3/2514 (0.1)
RC31	2197 (2)	262/2197 (11.9)	107/2197 (4.9)	20/2197 (0.9)
RC32	3074 (2.7)	573/3074 (18.6)	174/3074 (5.7)	8/3074 (0.3)
RC33	2214 (2)	380/2214 (17.2)	120/2214 (5.4)	22/2214 (1)
RC34	2603 (2.3)	411/2603 (15.8)	5/2603 (0.2)	0/2603 (0)
Total National	111996 (100)	13849/111996 (12.4)	10714/111996 (9.6)	796/111996 (0.7)

Table 1.12a: Location-wise isolates percentage of *Pseudomonas aeruginosa, Acinetobacter baumannii and Stenotrophomonas maltophilia* from all samples across OPD, Ward and ICU

Organism	Total	OPD	Ward	ICU
Pseudomonas aeruginosa	13835 / 113008 (12.2)	4859 / 35193 (13.8)	6876 / 60119 (11.4)	2100 / 17695 (11.9)
Acinetobacter baumannii	10714 / 113008 (9.5)	1416 / 35193 (4.0)	5622 / 60119 (9.3)	3676 / 17695 (20.8)
Stenotrophomonas maltophilia	794 / 113008 (0.7)	132 / 35193 (0.4)	447 / 60119 (0.7)	215 / 17695 (1.2)

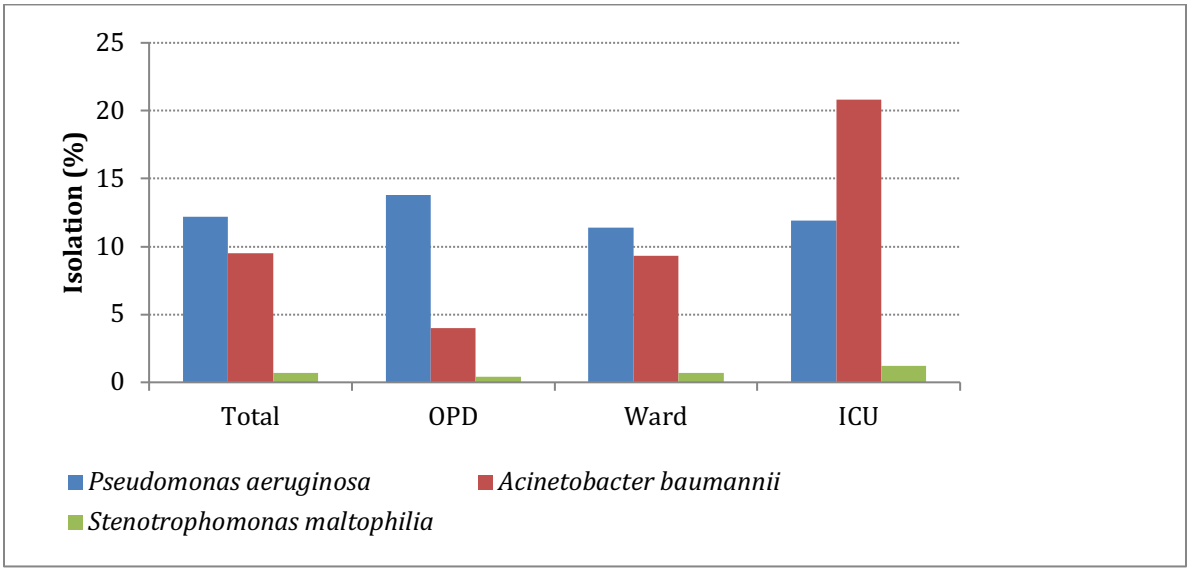


Figure 1.8: Location-wise isolation pattern of *A. baumannii, P. aeruginosa,* and *S. maltophilia* isolated from all samples

Table 1.12b: Yearly isolation trend of *P. aeruginosa, A. baumannii* and *S. maltophilia* isolated from all samples

Bacteria	Year-2017 n(%)	Year-2018 n(%)	Year-2019 n(%)	Year-2020 n(%)	Year-2021 n(%)	Year-2022 n(%)	Year-2023 n(%)	Year-2024 n(%)	Year-2025 n(%)
Pseudomonas aeruginosa	5695 / 45714 (12.4)	8921 / 75182 (11.8)	12650 / 110268 (11.4)	8013 / 68081 (11.7)	11704 / 96650 (12.1)	13151 / 106143 (12.4)	11757 / 99492 (11.8)	11419 / 99027 (11.5)	13835 / 113008 (12.2)
Acinetobacter baumannii	3524 / 45714 (7.7)	5446 / 75182 (7.2)	8839 / 110268 (8.0)	7301 / 68081 (10.7)	12484 / 96650 (12.9)	12110 / 106143 (11.4)	11947 / 99492 (12.0)	10351 / 99027 (10.4)	10714 / 113008 (9.5)
Stenotrophomonas maltophilia	157 / 45714 (0.3)	313 / 75182 (0.4)	382 / 110268 (0.3)	372 / 68081 (0.5)	772 / 96650 (0.8)	826 / 106143 (0.7)	1011 / 99492 (1.02)	726 / 99027 (0.7)	794 / 113008 (0.7)

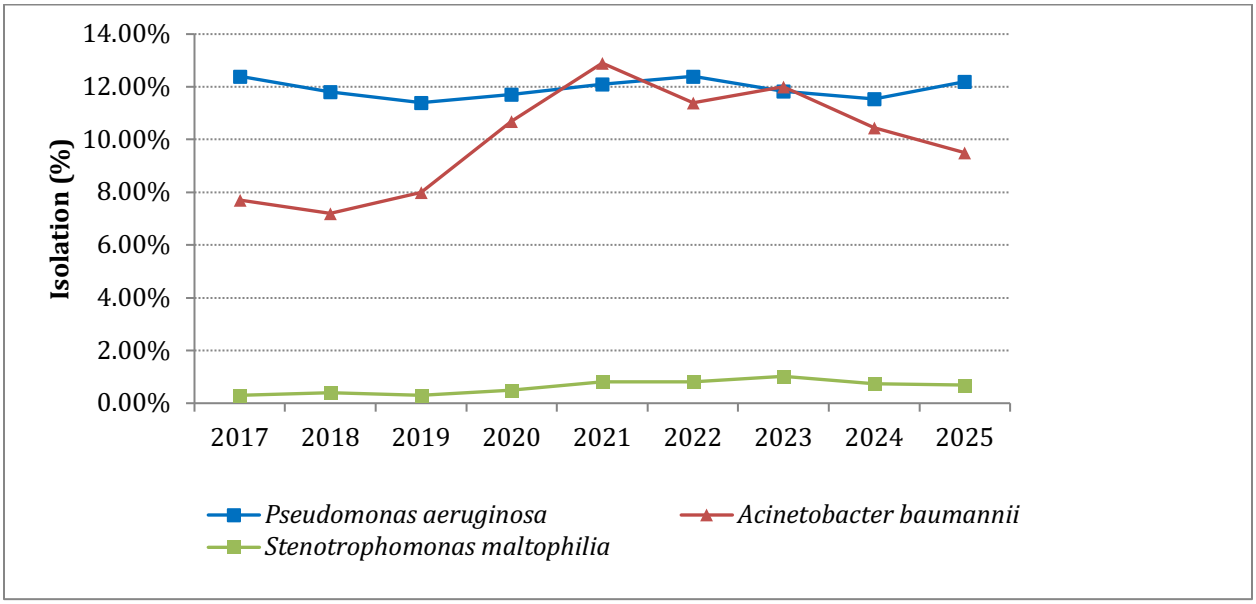


Figure 1.9: Yearly Isolation trend of *P. aeruginosa, A. baumannii and S. maltophilia* isolated from all samples

Staphylococci

Staphylococci constituted 13.9% of the total isolates. *Staphylococcus aureus* was the predominant species in the superficial infections (20.4%) and deep infections (18.0%) followed by others (10.0%), blood (7.2%), sterile body fluids (6.5%), LRT (5.2) and urine (1.3%) **(Table 1.13).**

Coagulase-negative staphylococci (CoNS) are now referred to in clinical and microbiological literature as Staphylococci other than *Staphylococcus aureus* (SOSA). SOSA were the predominant isolates in blood (20.3%) and CSF (15.7%). In blood and CSF, *Staphylococcus epidermidis* isolation rate was 6.2% and 6.3% respectively. Predominant percentage isolation of methicillin resistant *Staphylococcus aureus* (MRSA) was from the superficial infections (SI) 11.7% followed by isolation from deep infection (DI) 11.0%, and 3.9% from blood. Methicillin sensitive *Staphylococcus aureus* (MSSA) were the predominant isolates from the superficial infection (SI) (8.7%), followed by isolation from Deep infections 7.1% and 3.3% from others and blood respectively (**Figure 1.10**). Amongst the SOSA, *S. haemolyticus* (29.9%) were the commonest species followed by *S. epidermidis* (28.2%) and *S. hominis* (24.7%) **(Table1.13).**

Regional centre wise distribution showed the predominance of isolation of *Staphylococcus aureus* in RC28 (18.6%) with MRSA percentage isolation (13.9%) **(Table 1.14).** Among clinical settings, *Staphylococcus aureus* was predominantly isolated in OPD (11.3%), followed by ward (8.1%) and ICU (4.8%), while the coagulase-negative staphylococci (CoNS) was predominant both in ICU (6.1%) and ward (5.9%) then OPD (4.0%) **(Table 1.15 and Figure 1.11).** Trend analysis over the years 2017 – 2025 have shown a steady decline in the isolation rates of *Staphylococcus aureus* from 12.5% to 8.6% in 2025 **(Table 1.16 and Figure 1.12**).

Table 1.13: Specimen wise relative distribution of *S. aureus* and SOSA species

Isolate	Culture positive																			
	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012		Others n=7139	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
No. culture positive	113008 (100)	100	24078 (100)	21.3	28629 (100)	25.3	19568 (100)	17.3	18491 (100)	16.4	10395 (100)	9.2	1010 (100)	0.9	2681 (100)	2.4	1012 (100)	0.9	7139 (100)	6.3
Total Staphylococcus	15749 (13.9)	100	6620 (27.5)	42	550 (1.9)	3.5	1089 (5.6)	6.9	4170 (22.6)	26.5	2001 (19.2)	12.7	218 (21.6)	1.4	228 (8.5)	1.4	0 (0)	0	873 (12.2)	5.5
Staphylococcus aureus	9700 (8.6)	100	1737 (7.2)	17.9	362 (1.3)	3.7	1011 (5.2)	10.4	3767 (20.4)	38.8	1874 (18)	19.3	59 (5.8)	0.6	173 (6.5)	1.8	0 (0)	0	717 (10)	7.4
MSSA	4106 (3.6)	100	788 (3.3)	19.2	153 (0.5)	3.7	442 (2.3)	10.8	1612 (8.7)	39.3	733 (7.1)	17.9	29 (2.9)	0.7	82 (3.1)	2	0 (0)	0	267 (3.7)	6.5
MRSA	5593 (4.9)	100	949 (3.9)	17	209 (0.7)	3.7	568 (2.9)	10.2	2155 (11.7)	38.5	1141 (11)	20.4	30 (3)	0.5	91 (3.4)	1.6	0 (0)	0	450 (6.3)	8
SOSA	6049 (5.4)	100	4883 (20.3)	80.7	188 (0.7)	3.1	78 (0.4)	1.3	403 (2.2)	6.7	127 (1.2)	2.1	159 (15.7)	2.6	55 (2.1)	0.9	0 (0)	0	156 (2.2)	2.6
Staphylococcus haemolyticus	1811 (1.6)	100	1515 (6.3)	83.7	38 (0.1)	2.1	24 (0.1)	1.3	82 (0.4)	4.5	40 (0.4)	2.2	52 (5.1)	2.9	8 (0.3)	0.4	0 (0)	0	52 (0.7)	2.9
Staphylococcus epidermidis	1771 (1.6)	100	1493 (6.2)	84.3	12 (0)	0.7	4 (0)	0.2	84 (0.5)	4.7	54 (0.5)	3	64 (6.3)	3.6	12 (0.4)	0.7	0 (0)	0	48 (0.7)	2.7
Staphylococcus hominis	1496 (1.3)	100	1401 (5.8)	93.6	3 (0)	0.2	2 (0)	0.1	12 (0.1)	0.8	16 (0.2)	1.1	29 (2.9)	1.9	13 (0.5)	0.9	0 (0)	0	20 (0.3)	1.3
Staphylococcus spp.	871 (0.8)	100	459 (1.9)	52.7	86 (0.3)	9.9	48 (0.2)	5.5	202 (1.1)	23.2	11 (0.1)	1.3	12 (1.2)	1.4	18 (0.7)	2.1	0 (0)	0	35 (0.5)	4

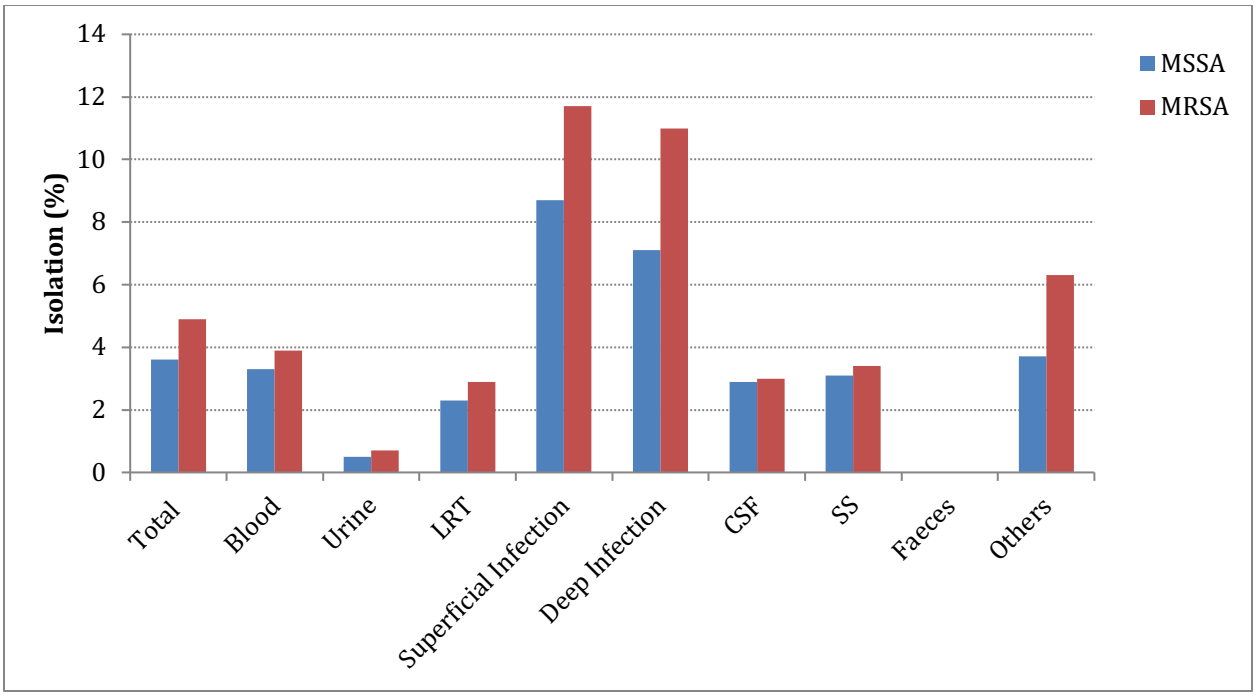


Figure 1.10: Specimen wise relative distributions of MSSA and MRSA

Table 1.14 Isolates percentages across Regional Centres of *S. aureus*, MRSA, MSSA and SOSA species isolated from all samples (Except faeces)

Regional Centre	Total Isolates	*S. aureus*	*MRSA*	*MSSA*	*S.haemolyticus*	*Staphylococcus epidermidis*	*Staphylococcus hominis*	*Staphylococcus lugdunensis*	*Staphylococcus saprophyticus*	*Staphylococcus spp.*
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	966 (0.9)	73/966 (7.6)	30/966 (3.1)	43/966 (4.5)	6/966 (0.6)	0/966 (0)	4/966 (0.4)	0/966 (0)	0/966 (0)	0/966 (0)
RC2	13720 (12.3)	1041/13720 (7.6)	442/13720 (3.2)	599/13720 (4.4)	751/13720 (5.5)	893/13720 (6.5)	742/13720 (5.4)	0/13720 (0)	0/13720 (0)	228/13720 (1.7)
RC3	4065 (3.6)	235/4065 (5.8)	101/4065 (2.5)	134/4065 (3.3)	32/4065 (0.8)	38/4065 (0.9)	40/4065 (1)	0/4065 (0)	0/4065 (0)	20/4065 (0.5)
RC4	4512 (4)	576/4512 (12.8)	221/4512 (4.9)	354/4512 (7.8)	10/4512 (0.2)	8/4512 (0.2)	4/4512 (0.1)	0/4512 (0)	0/4512 (0)	1/4512 (0)
RC5	2930 (2.6)	253/2930 (8.6)	112/2930 (3.8)	141/2930 (4.8)	14/2930 (0.5)	47/2930 (1.6)	22/2930 (0.8)	6/2930 (0.2)	0/2930 (0)	21/2930 (0.7)
RC6	8729 (7.8)	590/8729 (6.8)	334/8729 (3.8)	256/8729 (2.9)	114/8729 (1.3)	92/8729 (1.1)	20/8729 (0.2)	10/8729 (0.1)	21/8729 (0.2)	7/8729 (0.1)
RC7	1177 (1.1)	99/1177 (8.4)	46/1177 (3.9)	53/1177 (4.5)	17/1177 (1.4)	15/1177 (1.3)	9/1177 (0.8)	1/1177 (0.1)	4/1177 (0.3)	0/1177 (0)
RC8	3215 (2.9)	272/3215 (8.5)	94/3215 (2.9)	178/3215 (5.5)	0/3215 (0)	8/3215 (0.2)	3/3215 (0.1)	0/3215 (0)	0/3215 (0)	0/3215 (0)
RC9	2350 (2.1)	237/2350 (10.1)	130/2350 (5.5)	107/2350 (4.6)	0/2350 (0)	0/2350 (0)	0/2350 (0)	0/2350 (0)	0/2350 (0)	0/2350 (0)
RC10	4994 (4.5)	318/4994 (6.4)	94/4994 (1.9)	224/4994 (4.5)	9/4994 (0.2)	26/4994 (0.5)	3/4994 (0.1)	6/4994 (0.1)	5/4994 (0.1)	1/4994 (0)
RC11	2004 (1.8)	167/2004 (8.3)	140/2004 (7)	27/2004 (1.3)	17/2004 (0.8)	3/2004 (0.1)	4/2004 (0.2)	0/2004 (0)	1/2004 (0)	0/2004 (0)
RC12	2159 (1.9)	177/2159 (8.2)	111/2159 (5.1)	66/2159 (3.1)	57/2159 (2.6)	43/2159 (2)	40/2159 (1.9)	0/2159 (0)	1/2159 (0)	23/2159 (1.1)
RC13	3964 (3.5)	358/3964 (9)	273/3964 (6.9)	85/3964 (2.1)	36/3964 (0.9)	47/3964 (1.2)	38/3964 (1)	0/3964 (0)	0/3964 (0)	2/3964 (0.1)
RC14	8128 (7.3)	1290/8128 (15.9)	798/8128 (9.8)	492/8128 (6.1)	7/8128 (0.1)	17/8128 (0.2)	2/8128 (0)	1/8128 (0)	16/8128 (0.2)	0/8128 (0)
RC16	7187 (6.4)	802/7187 (11.2)	619/7187 (8.6)	183/7187 (2.5)	7/7187 (0.1)	4/7187 (0.1)	1/7187 (0)	0/7187 (0)	1/7187 (0)	412/7187 (5.7)

Regional Centre	Total Isolates	*S. aureus*	*MRSA*	*MSSA*	*S.haemolyticus*	*Staphylococcus epidermidis*	*Staphylococcus hominis*	*Staphylococcus lugdunensis*	*Staphylococcus saprophyticus*	*Staphylococcus spp.*
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC17	4684 (4.2)	520/4684 (11.1)	258/4684 (5.5)	262/4684 (5.6)	19/4684 (0.4)	9/4684 (0.2)	10/4684 (0.2)	0/4684 (0)	0/4684 (0)	2/4684 (0)
RC19	6086 (5.4)	94/6086 (1.5)	66/6086 (1.1)	28/6086 (0.5)	331/6086 (5.4)	280/6086 (4.6)	391/6086 (6.4)	1/6086 (0)	0/6086 (0)	14/6086 (0.2)
RC20	4213 (3.8)	584/4213 (13.9)	486/4213 (11.5)	98/4213 (2.3)	27/4213 (0.6)	38/4213 (0.9)	30/4213 (0.7)	0/4213 (0)	0/4213 (0)	7/4213 (0.2)
RC21	1707 (1.5)	79/1707 (4.6)	46/1707 (2.7)	33/1707 (1.9)	25/1707 (1.5)	6/1707 (0.4)	7/1707 (0.4)	0/1707 (0)	0/1707 (0)	1/1707 (0.1)
RC24	1745 (1.6)	144/1745 (8.3)	108/1745 (6.2)	36/1745 (2.1)	31/1745 (1.8)	0/1745 (0)	0/1745 (0)	0/1745 (0)	0/1745 (0)	0/1745 (0)
RC26	5788 (5.2)	256/5788 (4.4)	207/5788 (3.6)	49/5788 (0.8)	158/5788 (2.7)	47/5788 (0.8)	29/5788 (0.5)	0/5788 (0)	4/5788 (0.1)	1/5788 (0)
RC27	2724 (2.4)	231/2724 (8.5)	73/2724 (2.7)	158/2724 (5.8)	9/2724 (0.3)	10/2724 (0.4)	2/2724 (0.1)	1/2724 (0)	0/2724 (0)	4/2724 (0.1)
RC28	1904 (1.7)	354/1904 (18.6)	264/1904 (13.9)	90/1904 (4.7)	0/1904 (0)	0/1904 (0)	0/1904 (0)	0/1904 (0)	0/1904 (0)	0/1904 (0)
RC29	443 (0.4)	22/443 (5)	14/443 (3.2)	8/443 (1.8)	1/443 (0.2)	0/443 (0)	3/443 (0.7)	0/443 (0)	0/443 (0)	1/443 (0.2)
RC30	2514 (2.2)	146/2514 (5.8)	50/2514 (2)	96/2514 (3.8)	86/2514 (3.4)	56/2514 (2.2)	51/2514 (2)	1/2514 (0)	8/2514 (0.3)	19/2514 (0.8)
RC31	2197 (2)	117/2197 (5.3)	76/2197 (3.5)	41/2197 (1.9)	30/2197 (1.4)	36/2197 (1.6)	30/2197 (1.4)	2/2197 (0.1)	7/2197 (0.3)	6/2197 (0.3)
RC32	3074 (2.7)	234/3074 (7.6)	165/3074 (5.4)	69/3074 (2.2)	1/3074 (0)	35/3074 (1.1)	1/3074 (0)	0/3074 (0)	0/3074 (0)	0/3074 (0)
RC33	2214 (2)	167/2214 (7.5)	84/2214 (3.8)	83/2214 (3.7)	8/2214 (0.4)	9/2214 (0.4)	2/2214 (0.1)	0/2214 (0)	3/2214 (0.1)	0/2214 (0)
RC34	2603 (2.3)	264/2603 (10.1)	151/2603 (5.8)	113/2603 (4.3)	8/2603 (0.3)	4/2603 (0.2)	8/2603 (0.3)	0/2603 (0)	0/2603 (0)	101/2603 (3.9)
Total National	111996 (100)	9700/111996 (8.7)	5593/111996 (5)	4106/111996 (3.7)	1811/111996 (1.6)	1771/111996 (1.6)	1496/111996 (1.3)	29/111996 (0)	71/111996 (0.1)	871/111996 (0.8)

Table 1.15: Location-wise isolates percentage of *S. aureus,* MSSA, MRSA and SOSA from all samples across OPD, Ward and ICU

Organism	Total	OPD	Ward	ICU
Total staphylococci	15749 / 113008 (13.9)	5392 / 35193 (15.3)	8454 / 60119 (14.1)	1903 / 17695 (10.8)
Staphylococcus aureus	9700 / 113008 (8.6)	3978 / 35193 (11.3)	4877 / 60119 (8.1)	845 / 17695 (4.8)
MSSA	4106/ 113008 (3.6)	1712/ 35193 (4.9)	2066 / 60119 (3.4)	328/ 17695 (1.8)
MRSA	5593/ 113008 (4.9)	2265/ 35193 (6.4)	2811/ 60119 (4.7)	517/ 17695 (2.9)
SOSA	6049/ 113008 (5.4)	1414 / 35193 (4.0)	3577 / 60119 (5.9)	1058/ 17695 (6.1)

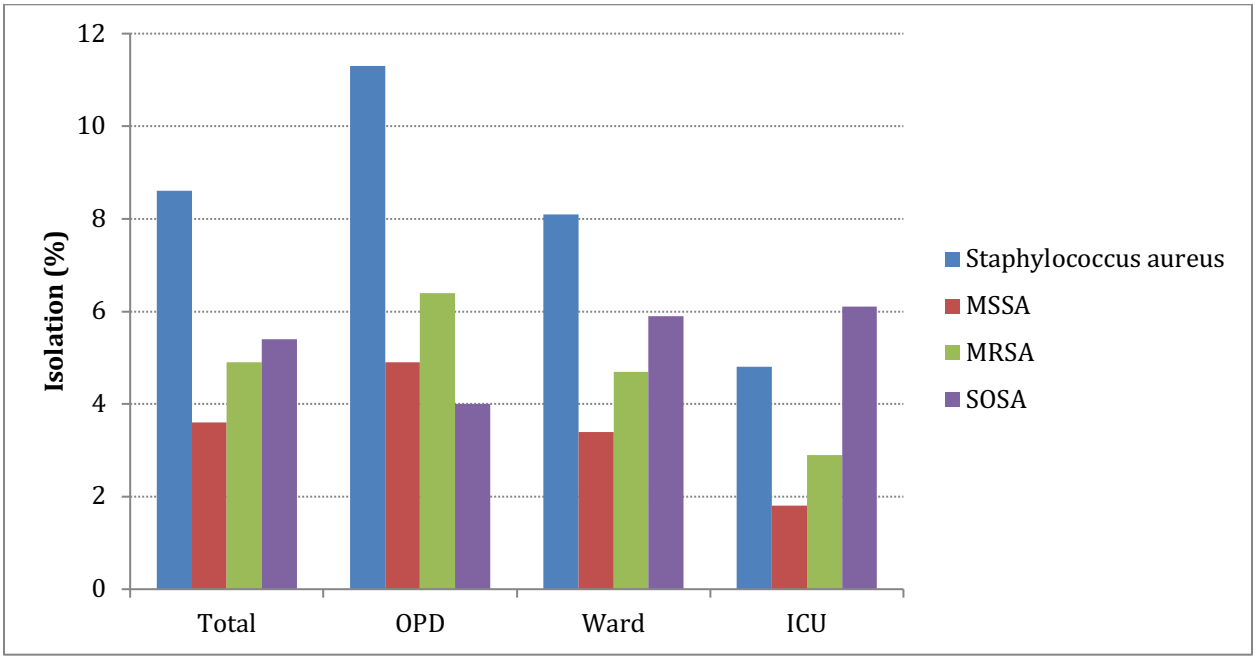


Figure 1.11: Location-wise Isolation pattern of *Staphylococcus aureus*, CoNS, MRSA, MSSA isolated from all samples

Table 1.16: Yearly isolation trend of *Staphylococcus* species

Bacteria	Year 2017 (%)	Year 2018 (%)	Year 2019 (%)	Year 2020 (%)	Year 2021 (%)	Year 2022 (%)	Year 2023 (%)	Year 2024 (%)	Year 2025 (%)
Total staphylococci	8564/ 45714 (18.7)	12950/ 75182 (17.2)	16277/ 110264 (14.8)	8299/ 65561 (12.7)	11482/ 95728 (12)	15748/ 107053 (14.7)	15795 / 99492 (15.8)	13089 / 99027 (13.2)	15749/ 113008 (13.9)
S. aureus	5722/ 45714 (12.5)	8782/ 75182 (11.8)	12623/ 110264 (11.4)	6293/ 65561 (9.6)	8827/ 95728 (9.2)	9415 / 107053 (8.7%)	8900/ 99492 (8.9)	8515 / 99027 (8.6)	9700/ 113008 (8.6)
MRSA	1874/ 45714 (4.1)	3549/ 75182 (4.7)	5353/ 110264 (4.9)	2622/ 65561 (4)	3423/ 95728 (3.6)	4266 / 107053 (4)	4311/ 99492 (4.3)	4262/ 99027 (4.6)	5593/ 113008 (4.9)
MSSA	3820/ 45714 (8.4)	5233/ 75182 (7)	7149/ 110264 (6.5)	3671/ 65561 (5.6)	5273/ 95728 (5.5)	5050/ 107053 (4.7)	4539/ 99492 (4.6)	4253/ 99027 (4.3)	4106/ 113008 (3.6)
SOSA	2842/ 45714 (6.2)	4076/ 75182 (5.4)	3654/ 110264 (3.3)	1966/ 65561 (3.0)	2655/ 95728 (2.8)	6333/ 107053 (6.0)	7314/ 99492 (7.3)	4574/ 99027 (4.6)	6049 / 113008 (5.4)
S. haemolyticus	634/ 45714 (1.4)	871/ 75182 (1.2)	827/ 110264 (0.8)	626/ 65561 (0.9)	836/ 95728 (0.9)	2373 / 107053 (2.2)	2262/ 99492 (2.3)	1572 / 99027 (1.5)	1811 / 113008 (1.6)
S. epidermidis	579/ 45714 (1.3)	912/ 75182 (1.2)	730/ 110264 (0.7)	397/ 65561 (0.6)	595/ 95728 (0.6)	1775/ 107053 (1.6)	2056/ 99492 (2.1)	1269 / 99027 (1.28)	1771 / 113008 (1.6)
S. hominis	383/ 45714 (0.8)	490/ 75182 (0.7)	451/ 110264 (0.4)	313/ 65561 (0.5)	400/ 95728 (0.4)	1473/ 107053 (1.4)	1408/ 99492 (1.4)	1241 / 99027 (1.2)	1496 / 113008 (1.3)
Staphylococcus spp.	1216 / 45714 (2.6)	1717 / 75182 (2.3)	1540 / 110267 (1.4)	657 / 68081 (0.9)	676 / 96658 (0.7)	561 / 107053 (0.5)	1010/ 99492 (1)	425 / 99027 (0.4)	871 / 113008 (0.8)

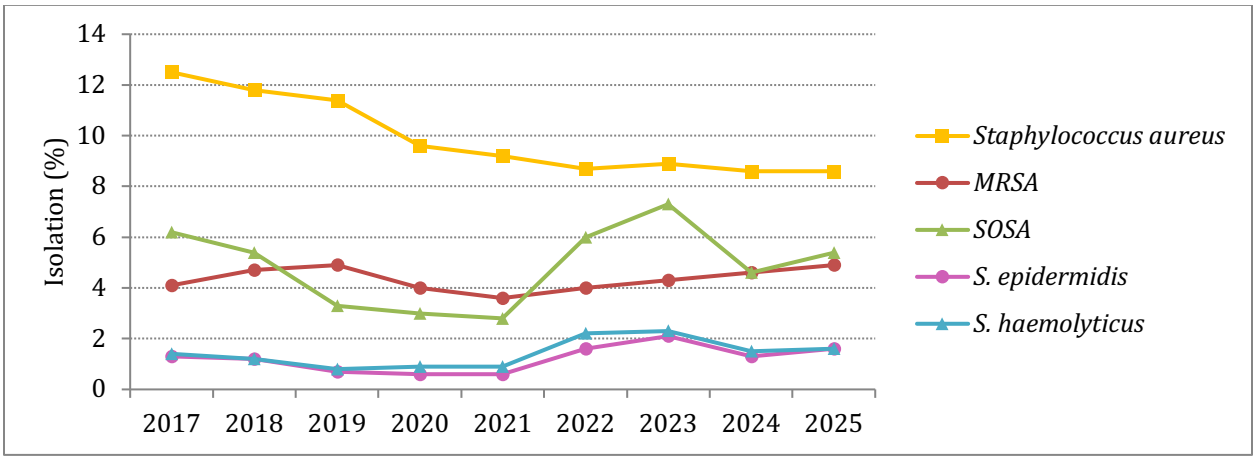


Figure 1.12 Yearly isolation trends of *Staphylococcus* species

Enterococci

Enterococci constituted overall 6.7% of all the isolates **(Table 1.17).** Among the *Enterococcus* species, *E. faecalis* and *E. faecium* accounted for 84.4% of all the total isolates, both *E. faecalis* (42.8%) and *E. faecium* (41.6%) were the predominant species. *E. faecalis* was more frequent in the urine (5.7%) and SS (3.2%) while *E. faecium* was relatively more frequent in the SS (5.9%) and urine (4.1 %) **(Table 1.17 and Figure 1.13).** Regional centre wise distribution showed the predominance of isolation of *E. faecalis* in RC9 (9.1%) and *E. faecium* in RC1 (5.0%) **(Table 1.18).**

Among clinical settings, *E. faecalis* was predominantly isolated in OPD and ward (3.0%), followed by ICU (2.0%), while *E. faecium* was predominant both in ICU (3.9%) and ward (3.2%) then OPD (1.5%) **(Table 1.18 and Figure 1.14).**

Table 1.17: Specimen wise distribution of *Enterococcus* species

	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Enterococci	7516 (6.7)	100	1559 (6.5)	20.7	3464 (12.1)	46.1	0 (0)	0	1015 (5.5)	13.5	496 (4.8)	6.6	68 (6.7)	0.9	280 (10.4)	3.7	0 (0)	0
Enterococcus faecalis	3217 (2.8)	100	486 (2)	15.1	1623 (5.7)	50.5	0 (0)	0	537 (2.9)	16.7	196 (1.9)	6.1	23 (2.3)	0.7	86 (3.2)	2.7	0 (0)	0
Enterococcus faecium	3128 (2.8)	100	961 (4)	30.7	1162 (4.1)	37.1	0 (0)	0	289 (1.6)	9.2	212 (2)	6.8	40 (4)	1.3	158 (5.9)	5.1	0 (0)	0
Enterococcus spp.	1171 (1)	100	112 (0.5)	9.6	679 (2.4)	58	0 (0)	0	189 (1)	16.1	88 (0.8)	7.5	5 (0.5)	0.4	36 (1.3)	3.1	0 (0)	0

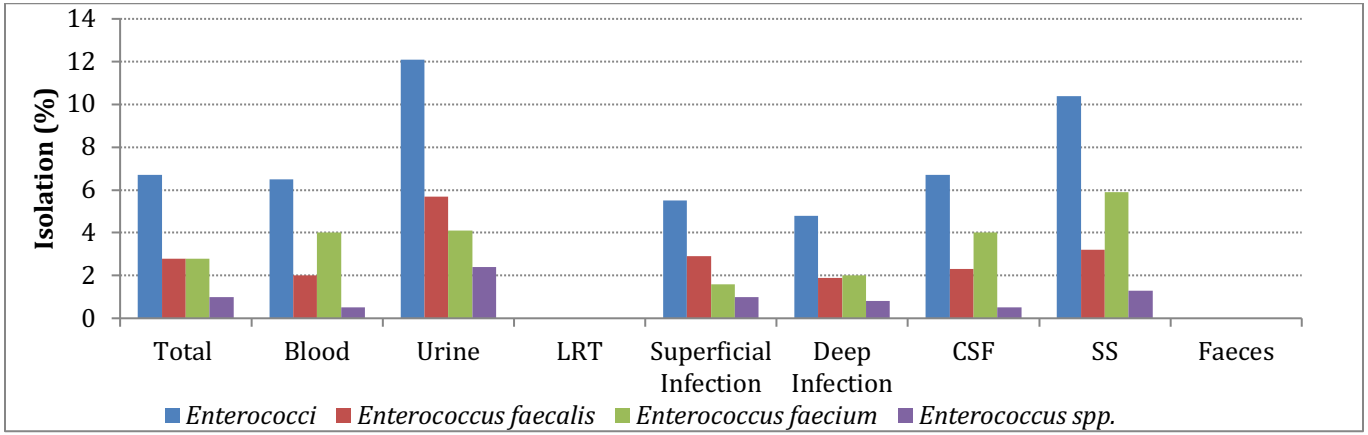


Figure 1.13: Specimen wise distribution of *Enterococcus* species

Table 1.18a: Location-wise isolation of *Enterococcus faecalis, Enterococcus faecium, Enterococcus* spp. from all specimens (Except faeces)

Organism	Total	OPD	Ward	ICU
Enterococcus faecalis	3217 / 111995 (2.9)	1060 / 34802 (3)	1809 / 59520 (3)	348 / 17673 (2)
Enterococcus faecium	3128 / 111995 (2.8)	510 / 34802 (1.5)	1929 / 59520 (3.2)	689 / 17673 (3.9)
Enterococcus spp.	1171 / 111995 (1)	313 / 34802 (0.9)	698 / 59520 (1.2)	160 / 17673 (0.9)

Table 1.18b: Isolates percentages across Regional Centres of *Enterococcus faecalis, Enterococcus faecium, Enterococcus* spp. from all specimen (Except faeces)

Regional Centre	Total Isolates	*Enterococcus faecalis*	*Enterococcus faecium*	*Enterococcus* spp.
	n(%)	n(%)	n(%)	n(%)
RC1	966 (0.9)	14/966 (1.4)	48/966 (5)	4/966 (0.4)
RC2	13720 (12.3)	83/13720 (0.6)	434/13720 (3.2)	100/13720 (0.7)
RC3	4065 (3.6)	25/4065 (0.6)	51/4065 (1.3)	21/4065 (0.5)
RC4	4512 (4)	312/4512 (6.9)	200/4512 (4.4)	12/4512 (0.3)
RC5	2930 (2.6)	55/2930 (1.9)	64/2930 (2.2)	24/2930 (0.8)
RC6	8729 (7.8)	163/8729 (1.9)	370/8729 (4.2)	36/8729 (0.4)
RC7	1177 (1.1)	82/1177 (7)	36/1177 (3.1)	3/1177 (0.3)
RC8	3215 (2.9)	75/3215 (2.3)	133/3215 (4.1)	0/3215 (0)
RC9	2350 (2.1)	213/2350 (9.1)	38/2350 (1.6)	0/2350 (0)
RC10	4994 (4.5)	291/4994 (5.8)	125/4994 (2.5)	48/4994 (1)
RC11	2004 (1.8)	36/2004 (1.8)	58/2004 (2.9)	1/2004 (0)
RC12	2159 (1.9)	25/2159 (1.2)	28/2159 (1.3)	3/2159 (0.1)
RC13	3964 (3.5)	107/3964 (2.7)	194/3964 (4.9)	0/3964 (0)
RC14	8128 (7.3)	195/8128 (2.4)	115/8128 (1.4)	8/8128 (0.1)
RC16	7187 (6.4)	223/7187 (3.1)	166/7187 (2.3)	616/7187 (8.6)
RC17	4684 (4.2)	74/4684 (1.6)	124/4684 (2.6)	1/4684 (0)
RC19	6086 (5.4)	311/6086 (5.1)	277/6086 (4.6)	2/6086 (0)
RC20	4213 (3.8)	164/4213 (3.9)	96/4213 (2.3)	3/4213 (0.1)
RC21	1707 (1.5)	11/1707 (0.6)	26/1707 (1.5)	2/1707 (0.1)
RC24	1745 (1.6)	15/1745 (0.9)	20/1745 (1.1)	101/1745 (5.8)
RC26	5788 (5.2)	102/5788 (1.8)	126/5788 (2.2)	16/5788 (0.3)
RC27	2724 (2.4)	138/2724 (5.1)	72/2724 (2.6)	10/2724 (0.4)
RC28	1904 (1.7)	75/1904 (3.9)	76/1904 (4)	7/1904 (0.4)
RC29	443 (0.4)	24/443 (5.4)	10/443 (2.3)	3/443 (0.7)
RC30	2514 (2.2)	120/2514 (4.8)	73/2514 (2.9)	4/2514 (0.2)

Regional Centre	Total Isolates	*Enterococcus faecalis*	*Enterococcus faecium*	*Enterococcus* spp.
RC31	2197 (2)	27/2197 (1.2)	47/2197 (2.1)	24/2197 (1.1)
RC32	3074 (2.7)	201/3074 (6.5)	26/3074 (0.8)	6/3074 (0.2)
RC33	2214 (2)	42/2214 (1.9)	85/2214 (3.8)	16/2214 (0.7)
RC34	2603 (2.3)	14/2603 (0.5)	10/2603 (0.4)	100/2603 (3.8)
Total National	111996 (100)	3217/111996 (2.9)	3128/111996 (2.8)	1171/111996 (1)

Table 1.19: Yearly isolation trend of *Enterococcus* species

Bacteria	Year 2017 (%)	Year 2018 (%)	Year 2019 (%)	Year 2020 (%)	Year 2021 (%)	Year 2022 (%)	Year 2023 (%)	Year 2024 (%)	Year 2025 (%)
Total Enterococcus	2403/ 45521 (5.3)	4256/ 74295 (5.7)	6767/ 108465 (6.1)	4942/ 65561 (7.5)	5706/ 95728 (5.9)	6965/ 107053 (6.5)	6999/ 99492 (7)	6718/ 99027 (6.7)	7516/ 113008 (6.7)
Enterococcus faecium	937 / 45714 (2.0)	1479 / 75182 (1.9)	2742 / 110268 (2.4)	2038 / 68081 (2.9)	2455 / 96650 (2.5)	3006 / 107053 (2.8)	2753 / 99492 (2.7)	3042 / 99027 (3.0)	3128/ 113008 (2.8)
Enterococcus faecalis	1040 / 45714 (2.2)	2022 / 75182 (2.6)	2916 / 110268 (2.6)	2177 / 68081 (3.2)	2397 / 96650 (2.4)	3241 / 107053 (3.0)	3461 / 99492 (3.4)	3002/99 027 (3.0)	3217/ 113008 (2.8)
Enterococcus spp.	426 / 45714 (0.9)	755 / 75182 (1)	1109 / 110268 (1.0)	727 / 68081 (1.0)	854 / 96650 (0.8)	718 / 107053 (0.6)	785 / 99492 (0.8)	674/ 99027 0.7)	1171/ 113008 (1)

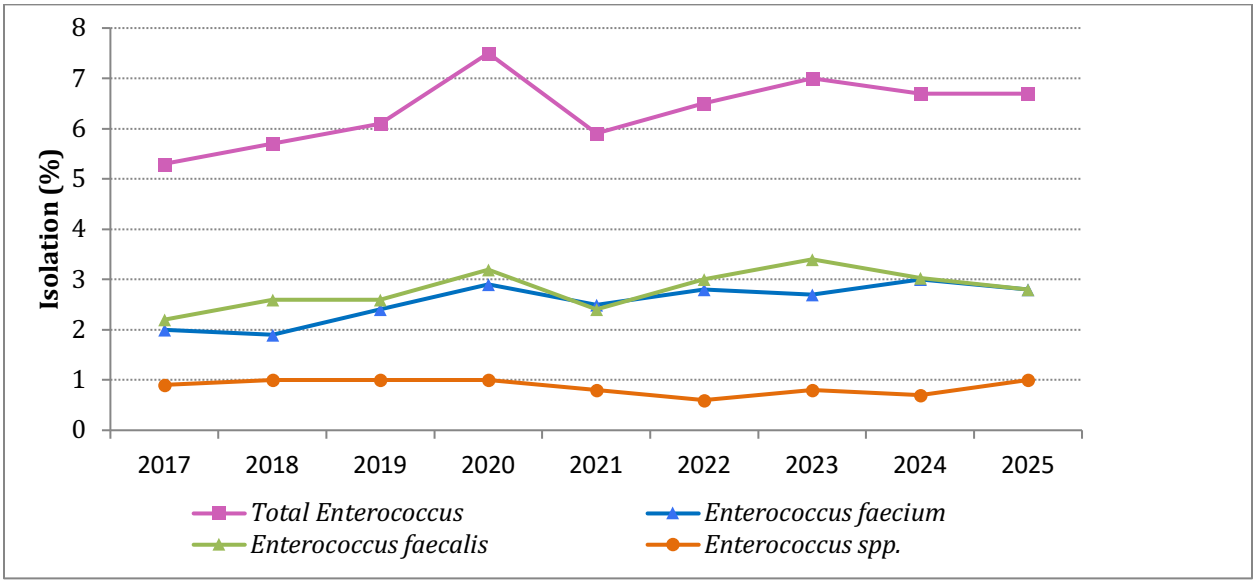


Figure 1.14 Yearly isolation trends of *Enterococcus* species

Fungal species

A total of 4,790 yeast isolates were studied in 2025, of which 2,117 (44.2%) were isolated from blood. *Candida tropicalis* was the most frequently isolated species (n=1,441), followed by *C. albicans* (n=1,169) **(Table 1.20).** *C. tropicalis* was most frequently isolated from blood (3.0%) than from other sterile sites (1.7%), whereas *C. albicans* was most frequently isolated from sterile sites (1.7%) than from blood (1.3%) **(Table 1.20).** In terms of clinical settings, *C. tropicalis* was commonly isolated from ICUs (1.7%) and wards (1.5%) **(Table 1.21 and Figure 1.15).** Among *Aspergillus* species, *A. flavus* was the most frequently isolated, followed by *A. fumigatus* **(Table 1.22).**

Yearly isolation trend showed a steady decline in isolation of *C. tropicalis* from 1.4% in 2017 to 0.8% in 2024 but increased in 2025 (1.3%). Yearly isolation trend *of Candida albicans* showed a stable trend of 1.0% in 2017 and in 2025. *C. parapsilosis* isolates showed an increased trend from 0.2% in 2018 to 0.5% to 2025 **(Table 1.23 & Figure 1.16)**.

Table 1.20: Candida species isolated from different sample types

Isolate	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Fungal isolates	4790 (4.2)	100	2117 (8.8)	44.2	1098 (3.8)	22.9	349 (1.8)	7.3	337 (1.8)	7	123 (1.2)	2.6	53 (5.2)	1.1	159 (5.9)	3.3	1 (0.1)	0
Candida tropicalis	1441 (1.3)	100	727 (3)	50.5	410 (1.4)	28.5	37 (0.2)	2.6	94 (0.5)	6.5	42 (0.4)	2.9	9 (0.9)	0.6	45 (1.7)	3.1	1 (0.1)	0.1
Candida albicans	1169 (1)	100	310 (1.3)	26.5	375 (1.3)	32.1	55 (0.3)	4.7	84 (0.5)	7.2	35 (0.3)	3	13 (1.3)	1.1	45 (1.7)	3.8	0 (0)	0
N. glabratus	435 (0.4)	100	161 (0.7)	37	116 (0.4)	26.7	5 (0)	1.1	51 (0.3)	11.7	11 (0.1)	2.5	4 (0.4)	0.9	28 (1)	6.4	0 (0)	0
Candida auris	321 (0.3)	100	187 (0.8)	58.3	68 (0.2)	21.2	0 (0)	0	18 (0.1)	5.6	3 (0)	0.9	3 (0.3)	0.9	4 (0.1)	1.2	0 (0)	0
Candida parapsilosis	521 (0.5)	100	384 (1.6)	73.7	44 (0.2)	8.4	3 (0)	0.6	33 (0.2)	6.3	18 (0.2)	3.5	4 (0.4)	0.8	11 (0.4)	2.1	0 (0)	0
Candida krusei	96 (0.1)	100	54 (0.2)	56.3	14 (0)	14.6	2 (0)	2.1	7 (0)	7.3	0 (0)	0	1 (0.1)	1	6 (0.2)	6.3	0 (0)	0
Candida kefyr	33 (0)	100	7 (0)	21.2	14 (0)	42.4	2 (0)	6.1	5 (0)	15.2	1 (0)	3	0 (0)	0	1 (0)	3	0 (0)	0
Candida pelliculosa	118 (0.1)	100	114 (0.5)	96.6	3 (0)	2.5	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0
Candida lusitaniae	20 (0)	100	10 (0)	50	5 (0)	25	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0
Candida utilis	23 (0)	100	23 (0.1)	100	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0
Candida	4275 (3.8)	100	2036 (8.5)	47.6	1066 (3.7)	24.9	108 (0.6)	2.5	301 (1.6)	7	111 (1.1)	2.6	34 (3.4)	0.8	143 (5.3)	3.3	1 (0.1)	0

Table 1.21: Candida species isolated from all samples across OPD, Ward and ICUs

Organism	Total	OPD	Ward	ICU
Candida tropicalis	1441 / 113008 (1.3)	213 / 35193 (0.6)	922 / 60119 (1.5)	306 / 17695 (1.7)
Candida albicans	1169 / 113008 (1)	283 / 35193 (0.8)	686 / 60119 (1.1)	200 / 17695 (1.1)
Candida parapsilosis	521 / 113008 (0.5)	56 / 35193 (0.2)	324 / 60119 (0.5)	141 / 17695 (0.8)
Candida auris	321 / 113008 (0.3)	32 / 35193 (0.1)	205 / 60119 (0.3)	84 / 17695 (0.5)
Nakaseomyces *glabratus (C. glabrata)*	435 / 113008 (0.4)	64 / 35193 (0.2)	296 / 60119 (0.5)	75 / 17695 (0.4)
Candida pelliculosa	118 / 113008 (0.1)	9 / 35193 (0)	96 / 60119 (0.2)	13 / 17695 (0.1)
Candida krusei	96 / 113008 (0.1)	11 / 35193 (0)	59 / 60119 (0.1)	26 / 17695 (0.1)
Candida utilis	23 / 113008 (0)	1 / 35193 (0)	17 / 60119 (0)	5 / 17695 (0)
Candida kefyr	33 / 113008 (0)	0 / 35193 (0)	26 / 60119 (0)	7 / 17695 (0)
Candida lusitaniae	20 / 113008 (0)	2 / 35193 (0)	16 / 60119 (0)	2 / 17695 (0)

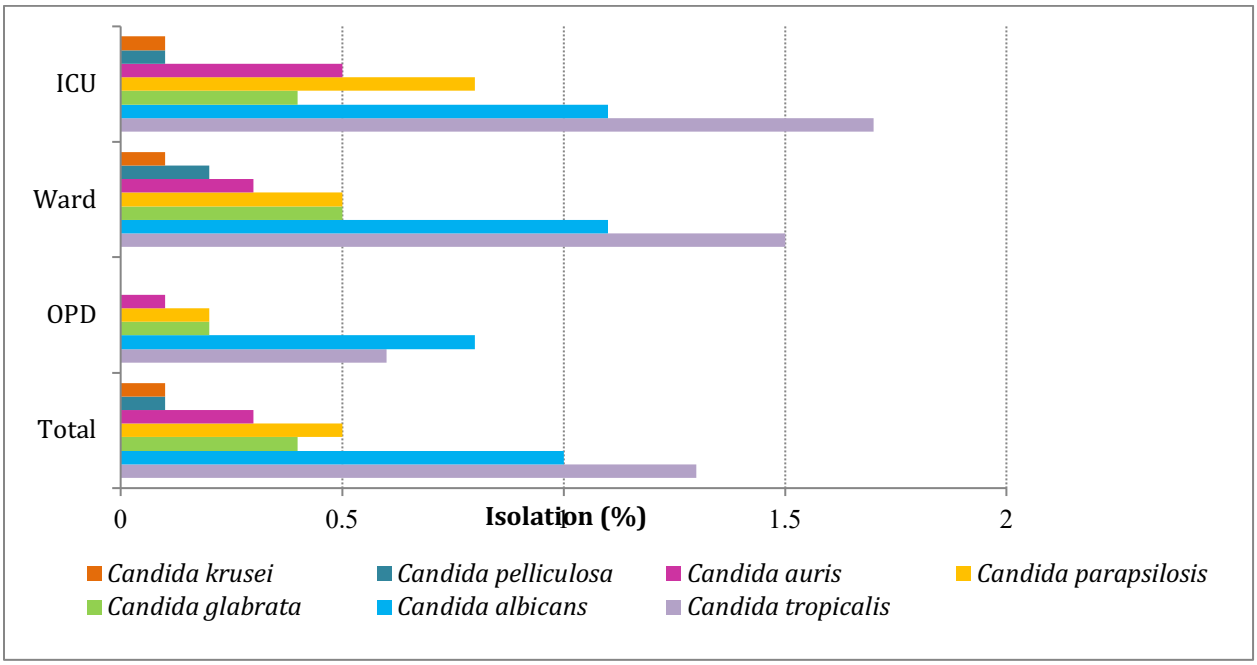


Figure 1.15: Location-wise pattern of *Candida* species isolated from all samples across OPD, Wards and ICUs

Table 1.22: Isolation patterns of *Aspergillus* species from all specimens

Organism	Total n=113008
Aspergillus flavus	202 / 113008 (0.2)
Aspergillus fumigatus	134 / 113008 (0.1)
Aspergillus terreus	16 / 113008 (0)
Aspergillus niger	2 / 113008 (0)

Table 1.23: Yearly trends for isolation of *Candida* species isolated from all samples

Fungal species	Year-2017 n(%)	Year-2018 n(%)	Year-2019 n(%)	Year-2020 n(%)	Year-2021 n(%)	Year-2022 n(%)	Year-2023 n(%)	Year-2024 n(%)	Year-2025 n(%)
Total *Candida*	1498/ 45521 (3.3)	1704/ 74295 (2.3)	2403/ 108465 (2.2)	1869/ 65561 (2.8)	2605/ 95728 (2.7)	2574/ 107053 (2.4)	2394/ 99492 (2.4)	2416/ 99027 (2.4)	4275/1 13008 (3.8)
Candida tropicalis	654 / 45714 (1.4)	500 / 75182 (0.6)	673 / 110268 (0.6)	579 / 68081 (0.8)	889 / 96650 (0.9)	733 / 107053 (0.6)	706/ 99492 (0.7)	822 / 99027 (0.83)	1441 / 113008 (1.3)
Candida albicans	461 / 45714 (1.0)	560 / 75182 (0.7)	687 / 110268 (0.6)	438 / 68081 (0.6)	712 / 96650 (0.7)	719 / 107053 (0.6)	746/ 99492 (0.7)	429 / 99027 (0.43)	1169 / 113008 (1)
Nakaseomyce *sglabratus*	138 / 45714 (0.3)	179 / 75182 (0.2)	205 / 110268 (0.2)	157 / 68081 (0.2)	326 / 96650 (0.3)	322 / 107053 (0.3)	316/ 99492 (0.3)	277 / 99027 (0.28)	435 / 113008 (0.4)
Candida parapsilosis	107 / 45714 (0.2)	134 / 75182 (0.1)	278 / 110268 (0.2)	220 / 68081 (0.3)	306 / 96650 (0.3)	322 / 107053 (0.3)	202/ 99492 (0.2)	329 / 99027 (0.33)	521 / 113008 (0.5)
Candida auris	17 / 45714 (0.0)	56 / 75182 (0.1)	125 / 110268 (0.1)	156 / 68081 (0.2)	220 / 96650 (0.2)	164 / 107053 (0.1)	240/ 99492 (0.2)	293 / 99027 (0.3)	321 / 113008 (0.3)

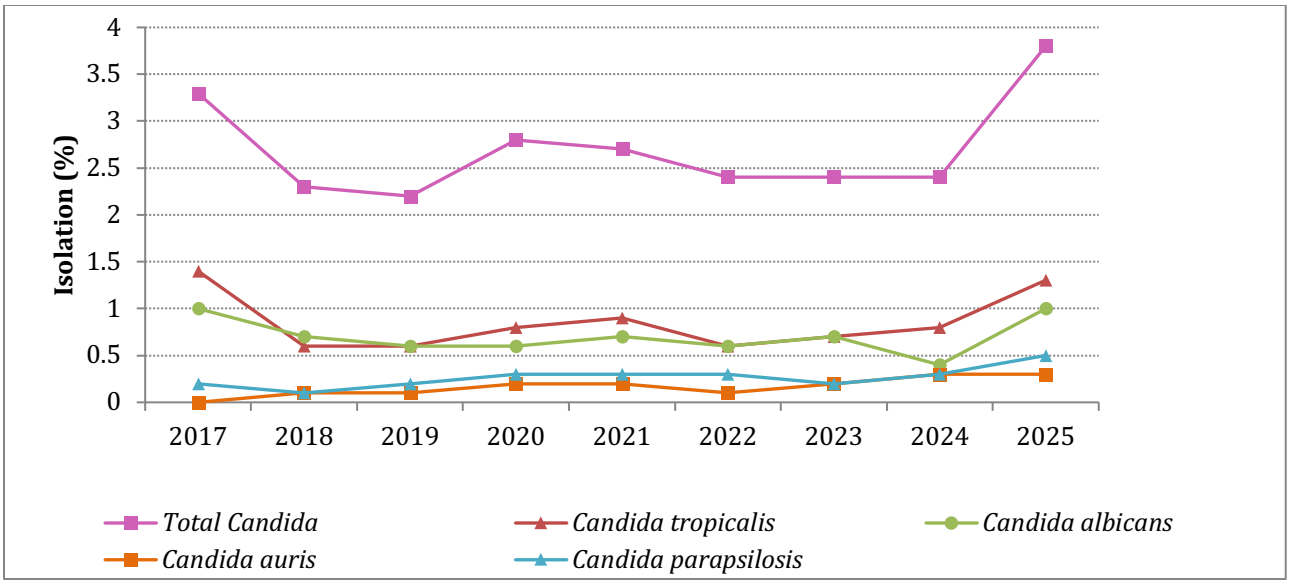


Figure 1.16: Yearly trends for isolation of *Candida* species isolated from all samples

Diarrheal pathogens

A total of 1012 diarrheal pathogen isolates were studied during the year 2025 which constituted 0.9% of total isolates (**Table 1.1**). The predominant species among diarrheal pathogens isolated from faeces sample identified was Salmonella spp faecal (25.6%) followed by *Escherichia coli Diarrheagenic* (15.1%), *Aeromonas* spp. (14.7%) and *Shigella flexneri* (6.7%) (**Table 1.24**).

Table 1.24: Isolation rates of faecal isolates from faeces samples

Isolates	% Isolation from faecal isolates (n= 1012)	% Isolation from total positive cultures (n=113008)
Salmonella spp. faecal	259 / 1012 (25.6)	259 / 113008 (0.2)
Aeromonas spp.	149 / 1012 (14.7)	149 / 113008 (0.1)
Escherichia coli Diarrhoeagenic	153 / 1012 (15.1)	153 / 113008 (0.1)
Salmonella Typhimurium faecal	65 / 1012 (6.4)	65 / 113008 (0.1)
Shigella flexneri	68 / 1012 (6.7)	68 / 113008 (0.1)

Isolates	% Isolation from faecal isolates (n= 1012)	% Isolation from total positive cultures (n=113008)
Shigella sonnei	56 / 1012 (5.5)	56 / 113008 (0)
Vibrio cholerae	40 / 1012 (3.9)	40 / 113008 (0)
Shigella spp.	29 / 1012 (2.9)	29 / 113008 (0)
Campylobacter jejuni	23 / 1012 (2.3)	23 / 113008 (0)
Vibrio spp.	24 / 1012 (2.4)	24 / 113008 (0)
Shigella dysenteriae	4 / 1012 (0.4)	4 / 113008 (0)
Plesiomonas shigelloides	3 / 1012 (0.3)	3 / 113008 (0)
Shigella boydii	3 / 1012 (0.3)	3 / 113008 (0)

Diarrheagenic pathogens were predominantly isolated from patients in OPD and wards **(Table 1.25).** *Escherichia coli* Diarrheagenic was mainly isolated in OPD (28.9%) followed by ward (6.0%) and *Salmonella spp.* faecal was predomiant in ward (30.1%).

Table 1.25: Location-wise Isolation pattern of top 5 faecal isolates isolated from OPD, Ward and ICU

	Total	OPD	Ward	ICU
Salmonella spp. faecal	259 / 1012 (25.6)	74 / 391 (18.9)	180 / 599 (30.1)	5 / 22 (22.7)
Aeromonas spp.	149 / 1012 (14.7)	57 / 391 (14.6)	92 / 599 (15.4)	0 / 22 (0)
Escherichia coli Diarrhoeagenic	153 / 1012 (15.1)	113 / 391 (28.9)	36 / 599 (6)	4 / 22 (18.2)
Salmonella Typhimurium faecal	65 / 1012 (6.4)	10 / 391 (2.6)	53 / 599 (8.8)	2 / 22 (9.1)
Shigella flexneri	68 / 1012 (6.7)	22 / 391 (5.6)	45 / 599 (7.5)	1 / 22 (4.5)

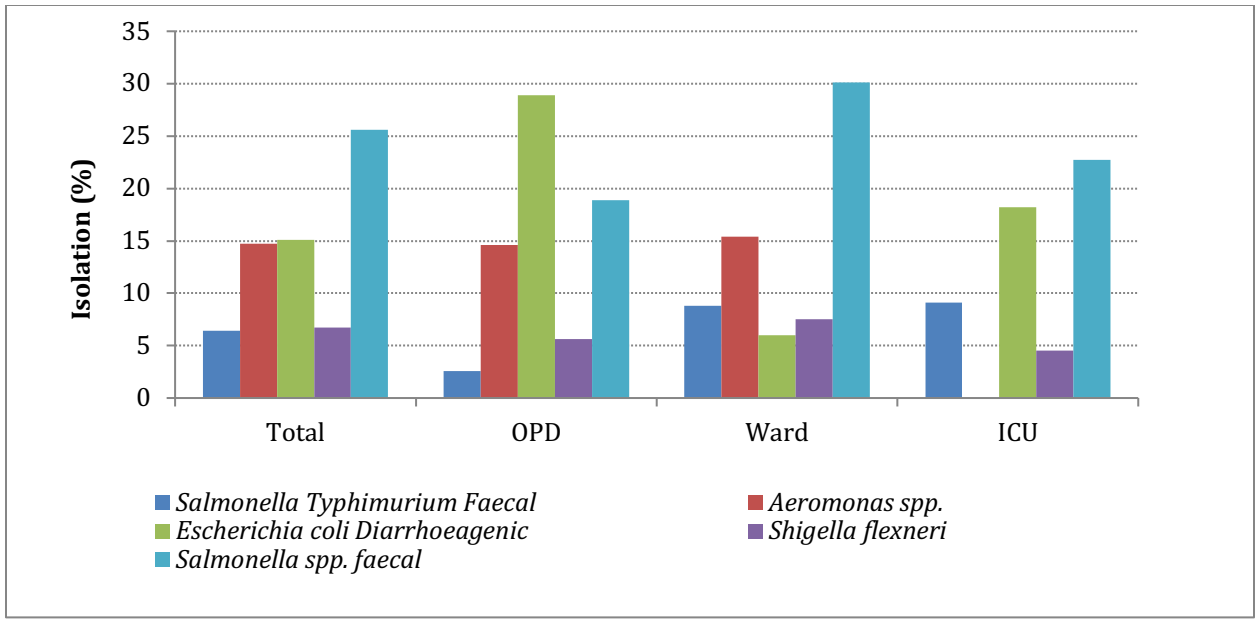


Figure 1.17: Location-wise Isolation pattern of top 5 faecal isolates isolated from faeces across OPD, Ward and ICU

Table 1.27: Yearly Isolation trends of top 5 faecal isolates isolated from faeces

Bacteria	Year 2017 (%)	Year 2018 (%)	Year 2019 (%)	Year 2020 (%)	Year 2021 (%)	Year 2022 (%)	Year 2023 (%)	Year 2024 (%)	Year 2025 (%)
Salmonella spp. faecal	20/501 (4)	39/621 (6.3)	60/1063 (5.6)	24/572 (4.2)	222/651 (34.1)	160/806 (19.9)	307 / 773 (39.7)	220 / 1086 (20.2)	259 / 1012 (25.6)
Escherichia coli Diarrhoeagenic	0/501 (0)	0/621 (0)	134/1063 (12.6)	102/572 (17.8)	88/651 (13.5)	189 / 806 (23.4)	85/773 (10.9)	188 / 1086 (17.3)	153 / 1012 (15.1)
Aeromonas spp.	131/501 (26.1)	114/621 (18.4)	170/1063 (16.0)	77/572 (13.5)	179/651 (27.5)	164 / 806 (20.3)	181/773 (23.4)	196 / 1086 (18.0)	149 / 1012 (14.7)
Shigella flexneri	89/501 (17.8)	47/621 (7.6)	95/1063 (8.9)	55/572 (9.6)	37/651 (5.7)	51 / 806 (6.3)	77 / 773(9.9)	77 / 1086 (7.1)	68 / 1012 (6.7)
Vibrio cholerae	24/501 (4.8)	25/621 (4)	39/1063 (3.7)	31/572 (5.4)	58/651 (8.9)	32 / 806 (3.9)	62 / 773 (8.0)	91/ 1086 (8.3)	40 / 1012 (3.9)

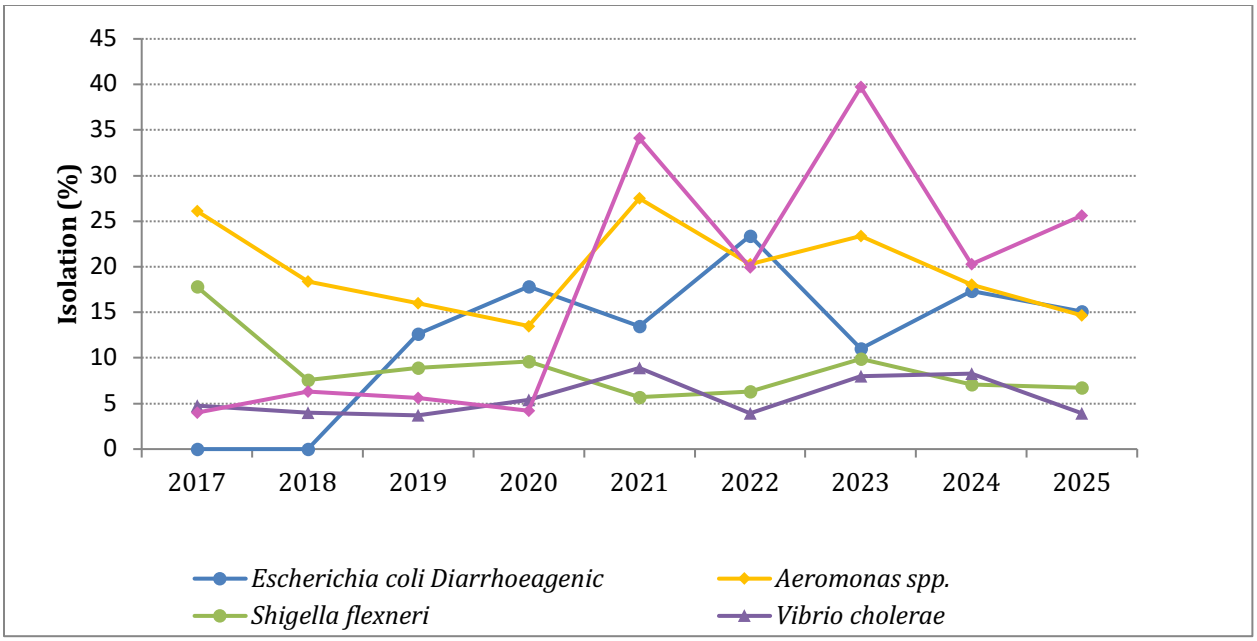


Figure 1.18: Yearly Isolation trends of top faecal isolates isolated from faeces

Streptococcus species

Total number of *Streptococcus* isolates studied during the year 2025 was 969, of those 1.7% were isolated from the upper respiratory tract. Majority of the isolates were from *Streptococcus agalactiae* (n=341) followed by *Streptococcus pneumoniae* (n=296) and *Streptococcus pyogenes* (n=276) (**Table 1.28).** Among clinical settings, *Streptococcus* isolates were common isolates from the OPD (1.1%) followed by ward and ICU (**Table 1.29 and Figure 1.19).**

Table 1.28: Sample-wise Isolation pattern of *Streptococcus* species

Isolate	Total n=113008		Blood n=24078		Urine n=28629		LRT n=19568		Superficial Infection n=18491		Deep Infection n=10395		CSF n=1010		SS n=2681		Faeces n=1012	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Streptococcus	969 (0.9)	100	195 (0.8)	20.1	101 (0.4)	10.4	159 (0.8)	16.4	327 (1.8)	33.7	63 (0.6)	6.5	9 (0.9)	0.9	15 (0.6)	1.5	0 (0)	0
Streptococcus agalactiae	341 (0.3)	100	29 (0.1)	8.5	96 (0.3)	28.2	0 (0)	0	129 (0.7)	37.8	21 (0.2)	6.2	0 (0)	0	2 (0.1)	0.6	0 (0)	0
Streptococcus pneumoniae	296 (0.3)	100	112 (0.5)	37.8	1 (0)	0.3	145 (0.7)	49	13 (0.1)	4.4	7 (0.1)	2.4	3 (0.3)	1	8 (0.3)	2.7	0 (0)	0
Streptococcus pyogenes	276 (0.2)	100	31 (0.1)	11.2	1 (0)	0.4	12 (0.1)	4.3	179 (1)	64.9	30 (0.3)	10.9	0 (0)	0	3 (0.1)	1.1	0 (0)	0
Streptococcus viridans	56 (0)	100	23 (0.1)	41.1	3 (0)	5.4	2 (0)	3.6	6 (0)	10.7	5 (0)	8.9	6 (0.6)	10.7	2 (0.1)	3.6	0 (0)	0

Table 1.29: Location-wise Isolation pattern of *Streptococcus* isolated from all specimens across OPD, Ward and ICU

Organism	Total	OPD	Ward	ICU
Streptococcus agalactiae	341 / 113008 (0.3)	194 / 35193 (0.6)	130 / 60119 (0.2)	17 / 17695 (0.1)
Streptococcus pneumoniae	296 / 113008 (0.3)	72 / 35193 (0.2)	160 / 60119 (0.3)	64 / 17695 (0.4)
Streptococcus pyogenes	276 / 113008 (0.2)	114 / 35193 (0.3)	140 / 60119 (0.2)	22 / 17695 (0.1)
Streptococcus viridans	56 / 113008 (0)	2 / 35193 (0)	39 / 60119 (0.1)	15 / 17695 (0.1)
Streptococcus	969 / 113008 (0.9)	382 / 35193 (1.1)	469 / 60119 (0.8)	118 / 17695 (0.7)

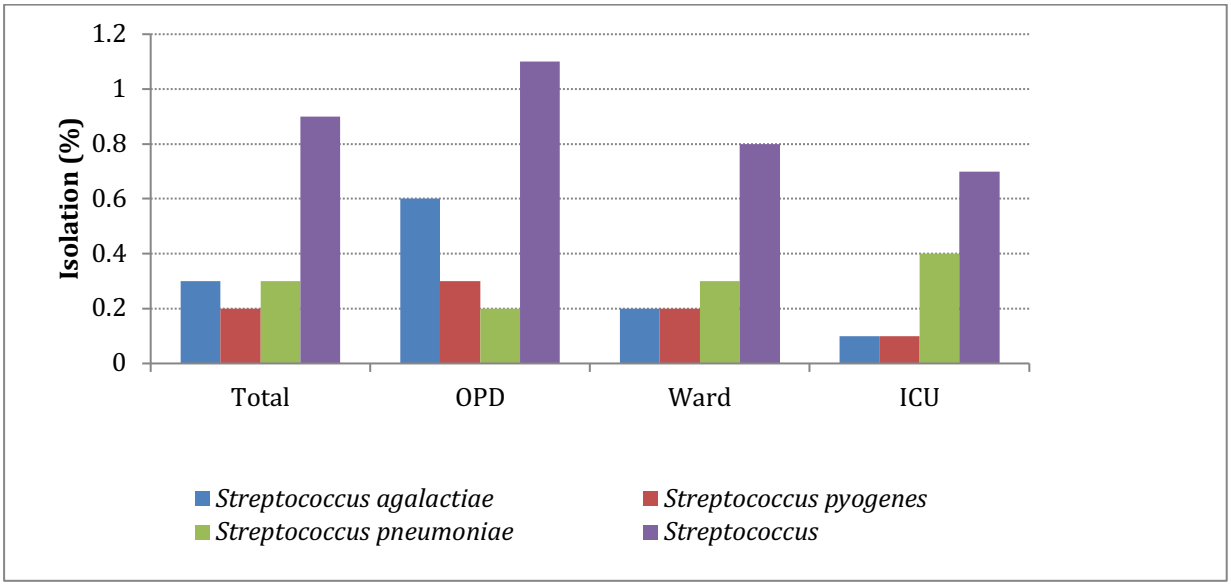


Figure 1.19: Location-wise isolation of *Streptococcus* species

Chapter 2. Enterobacterales

Clinical isolates belonging to various genera and species of Enterobacterales from all specimens (except urine and faeces) were tested for susceptibility to 13 antibiotics, including aminoglycosides (amikacin), cephalosporins (cefotaxime and ceftazidime), fluoroquinolones (ciprofloxacin and levofloxacin), beta-lactam and beta-lactamase inhibitor combination (piperacillin-tazobactam), carbapenems (ertapenem, imipenem and meropenem), polymyxin (colistin), and tetracycline(minocycline and tigecycline). Susceptibility was tested following CLSI guidelines using disc diffusion or automated systems, except for colistin, where a micro-broth dilution test was used.

The antimicrobial susceptibility profile of Enterobacterales isolates shows extensive resistance among the major species, particularly *Escherichia coli* and *Klebsiella pneumonia* **(Table 2.1).** For *E. coli*, only 42.6% of isolates were susceptible to piperacillin-tazobactam, with even lower rates for third-generation cephalosporins such as cefotaxime (18.4%) and ceftazidime (24.7%), suggesting widespread ESBL production. Fluoroquinolone susceptibility was also very poor, with only 9% susceptible to ciprofloxacin and 18.2% to levofloxacin. Some activity was retained with carbapenems (60–65%), though resistance was still concerning. In contrast, amikacin (73%) and colistin (99.8%) demonstrated relatively high susceptibility. Tigecycline demonstrated susceptibility rates of 93.0%, respectively.

Compared to *E. coli*, *K. pneumoniae* showed an alarming resistance profile, with only 29.2% susceptible to piperacillin-tazobactam, 23–27% to third-generation cephalosporins, and just 35–40% to carbapenems, highlighting a high prevalence of carbapenem-resistant strains. Fluoroquinolones were largely ineffective (20–29%), while amikacin susceptibility was limited to 44.5%. Colistin, however, remained highly active, with 98.3% of isolates susceptibleand tigecycline showed 79.3% susceptibility. Other Enterobacterales species showed variable patterns. *Proteus mirabilis* retained higher susceptibility to piperacillin-tazobactam (83.8%) and carbapenems (meropenem and ertapenem, nearly 76%). Similarly, *Morganella morganii* and *Citrobacter koseri* demonstrated better responses to carbapenems (75–80%) and amikacin (>74%). *Proteus, Providencia*, and Morganella spp. may have elevated MICs to imipenem through mechanisms other than the production of carbapenemases. *Enterobacter cloacae* and *Citrobacter freundii* exhibited intermediate resistance, with approximately 40–60% susceptibility across β-lactams and fluoroquinolones, but maintained high susceptibility to amikacin (60–74%) and colistin (98-100%). In contrast, *Providencia stuartii* and *Providencia rettgeri* were significantly resistant, with less than one-third of isolates susceptible to most agents, though amikacin (57–76%) retained partial activity.

On the whole, the data demonstrate substantial multidrug resistance among the major Enterobacterales, with *E. coli* and *K. pneumoniae* showing particularly poor susceptibility to third-generation cephalosporins, fluoroquinolones and carbapenems. *K. pneumoniae* showed the most concerning carbapenem resistance, whereas *E. cloacae* retained comparatively better carbapenem activity. Amikacin remained useful against several species, particularly *E. coli*, *E. cloacae*, *Serratia marcescens* and *Morganella morganii*. Minocycline showed variable activity, with relatively good activity against *E. coli*, *E. cloacae*, and *S. marcescens*. Tigecycline showed high activity against *E. coli*, *E. cloacae* and *S. marcescens*. Colistin remained highly active against *E. coli*, *K. pneumoniae*, *E. cloacae* and *C. koseri*, with susceptibility generally exceeding 97%. Taken together, these findings highlight the high and heterogeneous burden of antimicrobial resistance across *Enterobacterales* and emphasize the need for continued surveillance, species-specific interpretation of susceptibility patterns, and antimicrobial stewardship.

Table 2.1: Species-wise susceptibility of Enterobacterales isolated from all specimens (except urine and faeces)

	E. coli	*K. pneumoniae*	*K. oxytoca*	*Enterobacter aerogenes*	*Klebsiella spp.*	*E. cloacae*	*Enterobacter spp.*	*P. mirabilis*	*C. koseri*	*C. freundii*	*Citrobacter spp.*	*S. marcescens*	*M. morganii*	*P. stuartii*	*P. rettgeri*
	N=13876	N=14161	N=412	N=146	N=741	N=1344	N=385	N=1399	N=447	N=220	N=164	N=455	N=475	N=155	N=76
Piperacillin-tazobactam	5905 / 13850 (42.6)	4120 / 14098 (29.2)	162 / 412 (39.3)	85 / 146 (58.2)	195 / 739 (26.4)	784 / 1341 (58.5)	186 / 384 (48.4)	1168 / 1394 (83.8)	283 / 446 (63.5)	99 / 220 (45)	91 / 164 (55.5)	325 / 441 (73.7)	370 / 473 (78.2)	77 / 155 (49.7)	46 / 77 (59.7)
Cefotaxime	1801 / 9812 (18.4)	2434 / 10218 (23.8)	92 / 362 (25.4)	28 / 88 (31.8)	113 / 721 (15.7)	352 / 816 (43.1)	107 / 325 (32.9)	455 / 986 (46.1)	152 / 327 (46.5)	44 / 168 (26.2)	48 / 123 (39)	171 / 303 (56.4)	153 / 309 (49.5)	35 / 105 (33.3)	22 / 57 (38.6)
Ceftazidime	1444 / 5837 (24.7)	1779 / 6509 (27.3)	113 / 302 (37.4)	19 / 61 (31.1)	163 / 605 (26.9)	223 / 466 (47.9)	56 / 177 (31.6)	302 / 580 (52.1)	131 / 244 (53.7)	48 / 113 (42.5)	18 / 55 (32.7)	102 / 182 (56)	60 / 166 (36.1)	24 / 71 (33.8)	10 / 33 (30.3)
Ertapenem	8165 / 13489 (60.5)	5385 / 13692 (39.3)	215 / 382 (56.3)	110 / 143 (76.9)	352 / 741 (47.5)	884 / 1298 (68.1)	235 / 373 (63)	1044 / 1360 (76.8)	317 / 418 (75.8)	124 / 208 (59.6)	110 / 164 (67.1)	361 / 441 (81.9)	350 / 454 (77.1)	84 / 152 (55.3)	46 / 75 (61.3)
Imipenem	7762 / 12296 (63.1)	4677 / 12806 (36.5)	178 / 387 (46)	96 / 137 (70.1)	309 / 676 (45.7)	791 / 1179 (67.1)	206 / 333 (61.9)	460 / 1045 (44)	302 / 406 (74.4)	103 / 208 (49.5)	88 / 136 (64.7)	276 / 376 (73.4)	92 / 343 (26.8)	35 / 112 (31.3)	20 / 57 (35.1)
Meropenem	9067 / 13877 (65.3)	5699 / 14120 (40.4)	249 / 412 (60.4)	110 / 146 (75.3)	378 / 741 (51)	919 / 1344 (68.4)	247 / 385 (64.2)	1069 / 1399 (76.4)	345 / 447 (77.2)	139 / 220 (63.2)	106 / 164 (64.6)	364 / 455 (80)	375 / 475 (78.9)	89 / 155 (57.4)	44 / 76 (57.9)

	E. coli	*K. pneumoniae*	*K. oxytoca*	*Enterobacter aerogenes*	*Klebsiella spp.*	*E. cloacae*	*Enterobacter spp.*	*P. mirabilis*	*C. koseri*	*C. freundii*	*Citrobacter spp.*	*S. marcescens*	*M. morganii*	*P. stuartii*	*P. rettgeri*
	N=13876	**N=14161**	**N=412**	**N=146**	**N=741**	**N=1344**	**N=385**	**N=1399**	**N=447**	**N=220**	**N=164**	**N=455**	**N=475**	**N=155**	**N=76**
Colistin*	9463/9481 (99.8)	10483/10664 (98.3)	278/278 (100)	95/95 (100)	301/301 (100)	963/990 (97.3)	198/199 (99.5)	-	216/217 (99.5)	131/133 (98.5)	104/105 (99)	-	-	-	-
Amikacin	10132 / 13877 (73)	6293 / 14134 (44.5)	245 / 413 (59.3)	107 / 146 (73.3)	357 / 741 (48.2)	988 / 1344 (73.5)	249 / 385 (64.7)	965 / 1400 (68.9)	334 / 448 (74.6)	134 / 220 (60.9)	125 / 164 (76.2)	352 / 455 (77.4)	358 / 475 (75.4)	89 / 155 (57.4)	58 / 76 (76.3)
Ciprofloxacin	1256 / 13884 (9)	2781 / 14134 (19.7)	134 / 412 (32.5)	89 / 147 (60.5)	193 / 742 (26)	658 / 1348 (48.8)	183 / 385 (47.5)	425 / 1404 (30.3)	259 / 454 (57)	76 / 221 (34.4)	71 / 164 (43.3)	308 / 458 (67.2)	141 / 477 (29.6)	49 / 155 (31.6)	27 / 76 (35.5)
Levofloxacin	1105 / 6088 (18.2)	1960 / 6797 (28.8)	112 / 304 (36.8)	41 / 67 (61.2)	241 / 635 (38)	259 / 457 (56.7)	117 / 188 (62.2)	181 / 557 (32.5)	143 / 253 (56.5)	57 / 137 (41.6)	26 / 54 (48.1)	100 / 151 (66.2)	48 / 162 (29.6)	14 / 69 (20.3)	7 / 35 (20)
Minocycline	4036 / 5982 (67.5)	3220 / 6428 (50.1)	136 / 246 (55.3)	28 / 39 (71.8)	388 / 480 (80.8)	296 / 432 (68.5)	108 / 164 (65.9)	101 / 552 (18.3)	170 / 223 (76.2)	45 / 88 (51.1)	49 / 72 (68.1)	164 / 204 (80.4)	33 / 193 (17.1)	10 / 60 (16.7)	*5/24 (-)
Cefoperazone-sulbactam	6258 / 11750 (53.3)	4429 / 11610 (38.1)	162 / 319 (50.8)	99 / 133 (74.4)	271 / 681 (39.8)	809 / 1194 (67.8)	209 / 342 (61.1)	981 / 1261 (77.8)	252 / 291 (86.6)	106 / 177 (59.9)	100 / 152 (65.8)	295 / 382 (77.2)	287 / 419 (68.5)	69 / 141 (48.9)	45 / 69 (65.2)
Ceftazidime-avibactam	1738 / 3375 (51.5)	1566 / 4152 (37.7)	56 / 143 (39.2)	20 / 36 (55.6)	206 / 324 (63.6)	153 / 282 (54.3)	52 / 108 (48.1)	299 / 400 (74.8)	31 / 55 (56.4)	34 / 71 (47.9)	34 / 51 (66.7)	67 / 99 (67.7)	79 / 118 (66.9)	27 / 55 (49.1)	*21/25 (-)

	E. coli	*K. pneumoniae*	*K. oxytoca*	*Enterobacter aerogenes*	*Klebsiella spp.*	*E. cloacae*	*Enterobacter spp.*	*P. mirabilis*	*C. koseri*	*C. freundii*	*Citrobacter spp.*	*S. marcescens*	*M. morganii*	*P. stuartii*	*P. retigeri*
	N=13876	**N=14161**	**N=412**	**N=146**	**N=741**	**N=1344**	**N=385**	**N=1399**	**N=447**	**N=220**	**N=164**	**N=455**	**N=475**	**N=155**	**N=76**
Tigecycline	7094 / 7632 (93)	6089 / 7681 (79.3)	154 / 227 (67.8)	69 / 74 (93.2)	381 / 533 (71.5)	695 / 732 (94.9)	139 / 155 (89.7)	104 / 306 (34)	185 / 209 (88.5)	64 / 114 (56.1)	69 / 81 (85.2)	165 / 170 (97.1)	-	-	-

* Colistin represents the percentage of intermediate susceptibility

Escherichia coli

Of the total 13,876 *E. coli* isolates, 22% were from OPDs, 64.4% from wards, and 13.6% from ICU **(Table 2.2).** The overall antimicrobial susceptibility profile of *E. coli* demonstrated a high burden of resistance across all hospital locations, with the lowest susceptibility generally observed among ICU isolates.

The overall susceptibility rate for piperacillin-tazobactam was 42.6%, with OPD isolates showing higher susceptibility (51.2%) compared to ward (41%) and ICU (36.5%). Among carbapenems, meropenem showed the highest overall susceptibility (65.3%), with 71.6% in OPD, 64.7% in wards, and 58.2% in ICU. Ertapenem and imipenem demonstrated slightly lower activity, with overall susceptibility rates of 60.5% and 63.1%, respectively, again indicating reduced activity in ICU isolates. Colistin remained highly effective, with near-universal overall susceptibility (99.8%), ranging from 99.7% in OPD to 99.8% in ICU. Amikacin also retained good activity, with 73% overall susceptibility, highest in OPD (75%) and lowest in ICU (66.4%).

In contrast, third-generation cephalosporins and fluoroquinolones showed poor activity. Overall, susceptibility rates for cefotaxime and ceftazidime were 18.4% and 24.7%, respectively, with ICU isolates showing the lowest rates (10.5% and 17.8%). Fluoroquinolones were largely ineffective, with susceptibility rates of 9.0% for ciprofloxacin and 18.2% for levofloxacin. Tigecycline showed 93.0% susceptibility, while cefoperazone-sulbactam showed 53.3% susceptibility.

In summary, *E. coli* isolates from the ICU demonstrated higher resistance, while isolates from the OPD exhibited higher susceptibility, and ward isolates showed intermediate resistance levels. The persistence of colistin activity and partial retention of amikacin and carbapenem susceptibility offer some therapeutic options; however, the high resistance rates observed emphasize the urgent need for strengthened antimicrobial stewardship, the need for ongoing local surveillance and judicious antimicrobial use, especially for ICUs.

Table 2.2: Location-wise susceptibility percentages of *Escherichia coli* isolated from OPD, ward, and ICU isolated from all samples (except faeces and urine)

AMA	Total N=13876 (S%)	OPD N=3060 (S%)	Ward N=8931 (S%)	ICU N=1885 (S%)
Piperacillin-tazobactam	5905 / 13850 (42.6)	1562 / 3053 (51.2)	3656 / 8915 (41)	687 / 1882 (36.5)
Cefotaxime	1801 / 9812 (18.4)	544 / 2223 (24.5)	1127 / 6352 (17.7)	130 / 1237 (10.5)
Ceftazidime	1444 / 5837 (24.7)	439 / 1310 (33.5)	880 / 3823 (23)	125 / 704 (17.8)
Ertapenem	8165 / 13489 (60.5)	2000 / 2979 (67.1)	5202 / 8720 (59.7)	963 / 1790 (53.8)

AMA	Total N=13876 (S%)	OPD N=3060 (S%)	Ward N=8931 (S%)	ICU N=1885 (S%)
Imipenem	7762 / 12296 (63.1)	1826 / 2643 (69.1)	4974 / 7898 (63)	962 / 1755 (54.8)
Meropenem	9067 / 13877 (65.3)	2191 / 3060 (71.6)	5779 / 8932 (64.7)	1097 / 1885 (58.2)
Colistin*	9463/9482 (99.8)	2047/2054 (99.7)	6034/6043 (99.9)	1382/1385 (99.8)
Amikacin	10132 / 13877 (73)	2296 / 3062 (75)	6585 / 8930 (73.7)	1251 / 1885 (66.4)
Ciprofloxacin	1256 / 13884 (9)	354 / 3065 (11.5)	778 / 8931 (8.7)	124 / 1888 (6.6)
Levofloxacin	1105 / 6088 (18.2)	314 / 1375 (22.8)	683 / 3983 (17.1)	108 / 730 (14.8)
Minocycline	4036 / 5982 (67.5)	929 / 1325 (70.1)	2611 / 3859 (67.7)	496 / 798 (62.2)
Cefoperazone-sulbactam	6258 / 11750 (53.3)	1606 / 2607 (61.6)	3949 / 7625 (51.8)	703 / 1518 (46.3)
Ceftazidime-avibactam**	1738 / 3375 (51.5)	400 / 686 (58.3)	1175 / 2279 (51.6)	163 / 410 (39.8)
Tigecycline	7094 / 7632 (93)	1439 / 1571 (91.6)	4741 / 5071 (93.5)	914 / 990 (92.3)

*Colistin represents the percentage of intermediate susceptibility;
** tested selectively on carbapenem-resistant isolates

Klebsiella pneumoniae

Overall, of the total 14,161 *K. pneumoniae* isolates, 19.3% were from OPD, 56.5% from wards, and 24.2% from ICU **(Table 2.3).** The resistance profile of *Klebsiella pneumoniae* was even more concerning than that of *E. coli*, with very low susceptibility across most antibiotic classes, particularly among ICU isolates. Piperacillin-tazobactam resistance was high overall (70.8%), declining from 56.6% in OPD to 71.2% in wards and 81.3% in ICU. Third-generation cephalosporins showed similarly poor activity, with cefotaxime susceptibility of 23.8% overall and only 14.9% in ICU, while ceftazidime susceptibility decreased from 46.3% in OPD to just 13.5% in ICU. Resistance to carbapenems was pronounced, with only 35–40% susceptibility in ward isolates and even lower rates in ICU (ertapenem 26.1%, imipenem 24%, and meropenem 26.3%). Even in OPD isolates, carbapenem susceptibility did not exceed 60%, underscoring the heavy burden of carbapenem resistance. Fluoroquinolones were largely ineffective, with ciprofloxacin susceptibility of only 19.7% overall and 12.0% in ICU, while levofloxacin susceptibility declined from 44.3% in OPD to 17.3% in ICU. Aminoglycoside resistance was notable, with amikacin susceptibility limited to 44.5% overall and falling to 32.1% among ICU isolates. Minocycline demonstrated 50.1% susceptibility overall, decreasing to 40.3% in ICU. Cefoperazone-sulbactam showed limited activity, with 38.1% susceptibility overall

and only 25.7% in ICU. Tigecycline retained relatively good activity, with 79.3% susceptibility overall and 75.7% among ICU isolates. Colistin remained the only consistently effective option, with susceptibility rates exceeding 97% across all locations, although its use is limited by toxicity concerns.

In summary, *K. pneumoniae* showed extremely high resistance across all major drug classes, particularly in ICU isolates where susceptibility to most first-line and reserve antibiotics was critically low.

Table 2.3: Comparison of susceptibility of *Klebsiella pneumoniae* isolated from OPD, ward, and ICU isolated from all samples (except faeces and urine)

AMA	Total N=14161 (S%)	OPD N=2733 (S%)	Ward N=8003 (S%)	ICU N=3425 (S%)
Piperacillin-tazobactam	4120 / 14098 (29.2)	1184 / 2728 (43.4)	2300 / 7975 (28.8)	636 / 3395 (18.7)
Cefotaxime	2434 / 10218 (23.8)	748 / 2047 (36.5)	1352 / 5933 (22.8)	334 / 2238 (14.9)
Ceftazidime	1779 / 6509 (27.3)	603 / 1302 (46.3)	994 / 3862 (25.7)	182 / 1345 (13.5)
Ertapenem	5385 / 13692 (39.3)	1484 / 2631 (56.4)	3048 / 7794 (39.1)	853 / 3267 (26.1)
Imipenem	4677 / 12806 (36.5)	1269 / 2401 (52.9)	2617 / 7224 (36.2)	791 / 3181 (24.9)
Meropenem	5699 / 14120 (40.4)	1637 / 2728 (60)	3166 / 7985 (39.6)	896 / 3407 (26.3)
Colistin*	10481/10635 (98.6)	1914/1925 (99.4)	5899/5965 (98.9)	2668/2745 (97.2)
Amikacin	6293 / 14134 (44.5)	1630 / 2731 (59.7)	3569 / 7992 (44.7)	1094 / 3411 (32.1)
Ciprofloxacin	2781 / 14134 (19.7)	875 / 2732 (32)	1496 / 7992 (18.7)	410 / 3410 (12)
Levofloxacin	1960 / 6797 (28.8)	620 / 1400 (44.3)	1091 / 3955 (27.6)	249 / 1442 (17.3)
Minocycline	3220 / 6428 (50.1)	710 / 1216 (58.4)	1867 / 3615 (51.6)	643 / 1597 (40.3)
Cefoperazone-sulbactam	4429 / 11610 (38.1)	1260 / 2273 (55.4)	2485 / 6673 (37.2)	684 / 2664 (25.7)
Ceftazidime-avibactam**	1566 / 4152 (37.7)	332 / 677 (49)	906 / 2474 (36.6)	328 / 1001 (32.8)
Tigecycline	6089 / 7681 (79.3)	1079 / 1367 (78.9)	3646 / 4512 (80.8)	1364 / 1802 (75.7)

* Colistin represents the percentage of intermediate susceptibility
** tested selectively on carbapenem-resistant isolates

Enterobacter cloacae

Of the total 1,344 *E. cloacae* isolates, 28% were from OPD, 61% from wards, and 11% from ICU **(Table 2.4).** *Enterobacter cloacae* demonstrated a decline in susceptibility among ICU isolates. Susceptibility to piperacillin-tazobactam was only 57.4% in ICU.

Resistance to third-generation cephalosporins was significant, with nearly 45% of ICU isolates susceptible to cefotaxime (45%) and ceftazidime (44%). Carbapenem resistance was also evident, with ertapenem, imipenem, and meropenem susceptibility ranging to nearly 68% in ICU isolates. Among other agents, amikacin showed the highest retained activity, with an overall susceptibility rate of 73.5%, but lower in ICU isolates (63.5%). Resistance to fluoroquinolones was widespread, with ciprofloxacin susceptibility 41.3% and levofloxacin 46.9% in ICU isolates. Minocycline showed 68.5% susceptibility overall and remained relatively consistent across locations (67.7–70.2%). Cefoperazone-sulbactam demonstrated good activity, with 67.8% susceptibility overall, although this declined to 61.3% in ICU isolates. However, overall, the *Enterobacter cloacae* isolates showed good susceptibility to colistin **(Table 2.4).**

To summarise, *E. cloacae* displayed substantial resistance to cephalosporins, fluoroquinolones, and carbapenems, leaving amikacin and colistin as relatively better options, though their effectiveness was also reduced in ICU settings.

Table 2.4: Comparison of susceptibility of *Enterobacter cloacae* isolated from OPD, ward, and ICU isolated from all samples (except faeces and urine)

AMA	Total N=1344 (S%)	OPD N=376 (S%)	Ward N=820 (S%)	ICU N=148 (S%)
Piperacillin-tazobactam	784/1341 (58.5)	249/376 (66)	450/816 (55.1)	85/148 (57.4)
Cefotaxime	352/816 (43.1)	121/246 (49.2)	195/490 (39.8)	36/80 (45)
Ceftazidime	223/466 (47.9)	75/137 (54.7)	126/279 (45.2)	22/50 (44)
Ertapenem	884/1298 (68.1)	269/369 (72.9)	525/791 (66.4)	90/138 (65.2)
Imipenem	791/1179 (67.1)	219/316 (69.3)	484/729 (66.4)	88/134 (65.7)
Meropenem	919/1344 (68.4)	281/376 (74.7)	542/820 (66.1)	96/148 (64.9)
Amikacin	988/1344 (73.5)	291/376 (77.4)	603/820 (73.5)	94/148 (63.5)
Ciprofloxacin	658/1348 (48.8)	208/376 (55.3)	388/820 (47.2)	62/148 (41.3)
Levofloxacin	259/457 (56.7)	83/129 (64.3)	153/279 (54.8)	23/49 (46.9)
Minocycline	296/432 (68.5)	87/124 (70.2)	176/260 (67.7)	33/48 (68.8)
Cefoperazone-sulbactam	809/1194 (67.8)	248/337 (73.6)	485/733 (66.2)	76/124 (61.3)
Ceftazidime-avibactam	153/282 (54.3)	38/68 (55.9)	104/184 (56.5)	11/30 (36.7)
Tigecycline	695/732 (94.9)	159/167 (95.2)	464/486 (95.5)	72/79 (91.1)

Citrobacter koseri

Of the total 447 *C. koseri* isolates, 32.4% were from OPD, 52.1% from wards, and 15.4% from ICU **(Table 2.5).** These isolates showed comparatively lower resistance than other *Enterobacterales*, except for ICU isolates, which demonstrated a high resistance rate.Piperacillin-tazobactam susceptibility was 63.5% overall, but only 36.2% of the isolates obtained from ICUs were susceptible. Third-generation cephalosporins showed reduced activity, with cefotaxime susceptibility at 31.8% and ceftazidime at 33.3% in ICU isolates. Carbapenems retained reasonable activity, though resistance was notable in ICU cases, where ertapenem, imipenem, and meropenem susceptibility declined to nearly 45%. Among other agents, amikacin remained the most reliable option with 74.6% overall susceptibility. Fluoroquinolone resistance in ICU isolates was also evident, with ciprofloxacin and levofloxacin susceptibility below 60%.

Overall, while *C. koseri* showed better susceptibility than other *Enterobacterales*, ICU isolates exhibited substantial resistance across multiple drug classes, underscoring the need for continued monitoring and stewardship interventions.

Table 2.5: Comparison of susceptibility of *Citrobacter koseri* isolated from OPD, ward, and ICU from all samples (except faeces and urine)

AMA	Total N= 447 (S%)	OPD N= 145 (S%)	Ward N=233 (S%)	ICU N=69 (S%)
Piperacillin-tazobactam	283 / 446 (63.5)	108 / 145 (74.5)	150 / 232 (64.7)	25 / 69 (36.2)
Cefotaxime	152 / 327 (46.5)	51 / 92 (55.4)	80 / 169 (47.3)	21 / 66 (31.8)
Ceftazidime	131 / 244 (53.7)	39 / 60 (65)	74 / 130 (56.9)	18 / 54 (33.3)
Ertapenem	317 / 418 (75.8)	111 / 136 (81.6)	179 / 222 (80.6)	27 / 60 (45)
Imipenem	302 / 406 (74.4)	104 / 123 (84.6)	168 / 216 (77.8)	30 / 67 (44.8)
Meropenem	345 / 447 (77.2)	126 / 145 (86.9)	187 / 233 (80.3)	32 / 69 (46.4)
Amikacin	334 / 447 (74.6)	124 / 145 (85.5)	176 / 233 (75.5)	34 / 69 (48.6)
Ciprofloxacin	259 / 447 (57.9)	95 / 150 (63.3)	142 / 233 (60.7)	22 / 69 (31.4)
Levofloxacin	143 / 253 (56.5)	42 / 61 (68.9)	84 / 135 (62.2)	17 / 57 (29.8)
Minocycline	170 / 223 (76.2)	45 / 54 (83.3)	92 / 120 (76.7)	33 / 49 (67.3)
Cefoperazone-sulbactam	252 / 291 (86.6)	99 / 112 (88.4)	141 / 160 (88.1)	*12/19 (-)
Ceftazidime-avibactam	31 / 55 (56.4)	*12/21 (-)	*15/24 (-)	*4/10 (-)
Tigecycline	185 / 209 (88.5)	54 / 62 (87.1)	99 / 106 (93.4)	32 / 41 (78)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Yearly susceptibility trends of different *Enterobacterales*

Analysis of surveillance data from 2017 to 2025 revealed a progressive decline in antimicrobial susceptibility across the major *Enterobacterales* species (*E. coli, K. pneumoniae, Enterobacter* spp., and *Citrobacter* spp.)

E. coli

Over the last nine years (2017–2025), *Escherichia coli* isolates demonstrated a steady decline in susceptibility across most antibiotics. Susceptibility to piperacillin-tazobactam fell from 56.8% in 2017 to 42.6% in 2025. Third-generation cephalosporins remained largely ineffective, with ceftazidime showing persistently poor activity throughout the study period, remaining below 30%, with susceptibility fluctuating from approximately 23% in 2017 to 24% in 2025. Carbapenem susceptibility showed a concerning decline. Imipenem decreased from approximately 80% in 2017 to 63% in 2025, while meropenem declined from 74% to 65% over the same period. Amikacin susceptibility remained relatively high, ranging from approximately 67–81%, although it declined from around 80% in 2017 to 72% in 2025. Fluoroquinolone susceptibility was consistently very low, with ciprofloxacin ranging between approximately 9–22% and declining to around 9% in 2025 **(Table 2.6 and Figure 2.1).**

Overall, *E. coli* demonstrated sustained high resistance to ceftazidime and ciprofloxacin, accompanied by a gradual decline in susceptibility to carbapenems and amikacin over 2017–2025. Amikacin and carbapenems remained comparatively more effective options, although the declining trend highlights the need for continued antimicrobial resistance surveillance and stewardship.

Table 2.6: Yearly susceptibility trend of *E. coli* isolated from all samples (except faeces and urine)

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=6282	N=9187	N=13133	N=8198	N=13533	N=14728	N=13026	N=12445	N=13876
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	3424/6030 (56.8)	4857/8961 (54.2)	6620/12121 (54.6)	4211/7890 (53.4)	6126/12935 (47.4)	5170/14728 (35.1)	3205/7559 (42.4)	4818/11679 (41.3)	5905 / 13850 (42.6)
Cefazolin	*0/8 (-)	*2/6 (-)	*0/1 (-)	*0/4 (-)	*0/1 (-)	5/22 (-)	8/18 (-)	21/94 (22.3)	*2/5 (-)
Cefotaxime	879/5747 (15.3)	1274/7817 (16.3)	1537/10646 (14.4)	1063/6835 (15.6)	1656/10613 (15.6)	2311/12718 (18.1)	1021/6833 (14.9)	1629/10279 (15.9)	1801 / 9812 (18.4)
Ceftazidime	1295/5513 (23.5)	1398/5956 (23.5)	1501/7540 (19.9)	943/5072 (18.6)	1220/6786 (18)	1697/8988 (18.8)	935/4859 (19.2)	1237/4500 (27.5)	1444 / 5837 (24.7)
Ertapenem	3104/4605 (67.4)	4528/6877 (65.8)	6633/9335 (71.1)	4067/5729 (71)	5334/7933 (67.2)	6257/9965 (62.7)	3364/5625 (59.8)	6457/10484 (61.6)	8165 / 13489 (60.5)
Imipenem	4699/5773 (81.4)	6453/8874 (72.7)	6497/10254 (63.4)	5176/7191 (72)	7903/12338 (64.1)	9211/13921 (66.1)	4686/7472 (62.7)	6715/11662 (57.6)	7762 / 12296 (63.1)
Meropenem	4158/5678 (73.2)	5873/8404 (69.9)	9110/12167 (74.9)	5683/7499 (75.8)	8872/12774 (69.5)	9980/14304 (69.7)	5006/7582 (66.0)	7587/12061 (62.9)	9067 / 13877 (65.3)
Amikacin	4788/6048 (79.2)	7071/8912 (79.3)	9936/12549 (79.2)	6451/7935 (81.3)	10326/13209 (78.2)	11138/14477 (76.9)	5196/7611 (68.2)	9024/12445 (72.5)	10132 / 13877 (73)
Ciprofloxacin	1028/5368 (19.2)	1889/8451 (22.4)	2427/11700 (20.7)	1580/7092 (22.3)	2287/12013 (19)	1797/14564 (12.3)	969/7597 (12.76)	1312/12361 (10.6)	1256 / 13884 (9)
Levofloxacin	140/889 (15.7)	600/3493 (17.2)	1145/6050 (18.9)	717/3762 (19.1)	866/5143 (16.8)	969/6199 (15.6)	567/3500 (16.2)	676/4269 (15.8)	1105 / 6088 (18.2)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

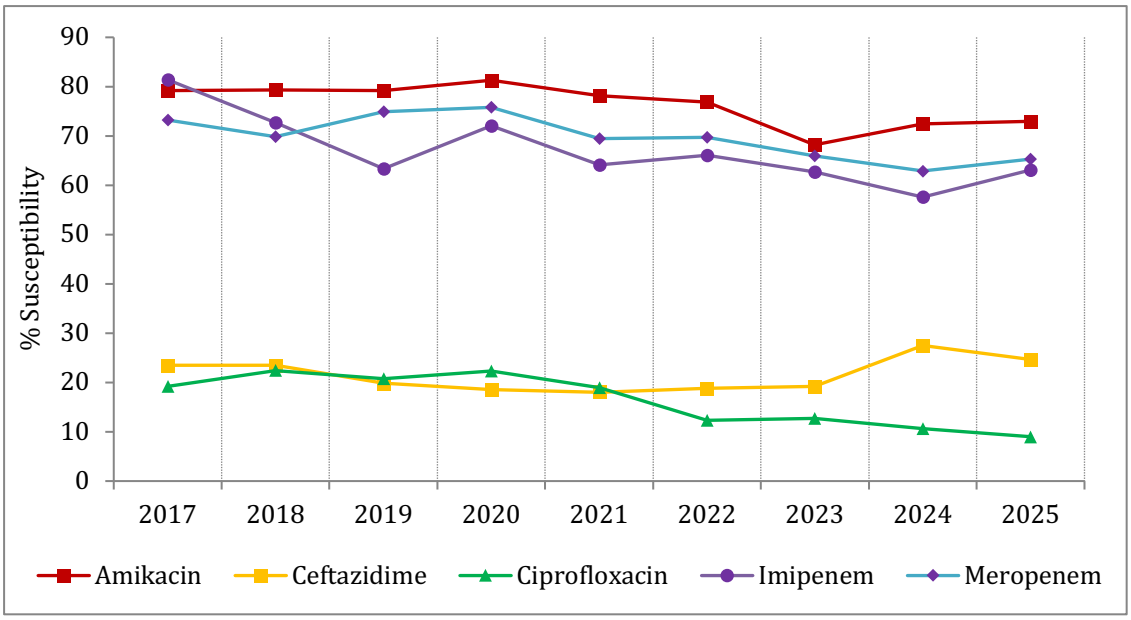


Figure 2.1: Yearly susceptibility trend of *E. coli* isolated from all samples (except faeces and urine)

Klebsiella pneumoniae

Over the last nine years (2017–2025), *Klebsiella pneumoniae* isolates showed a continuous decline in susceptibility across most antibiotic classes **(Table 2.7, Figure 2.2).** Susceptibility to piperacillin-tazobactam dropped from 42.6% in 2017 to 29.2% in 2025. Susceptibility towards third-generation cephalosporins remained consistently below 30% and declined further in recent years. Carbapenem susceptibility also showed an overall downward trend. Imipenem decreased from approximately 59% in 2017 to 36% in 2025, while meropenem declined from around 48% to 39% over the same period, with the lowest susceptibility observed around 2023–2024.Amikacin susceptibility remained relatively stable at approximately 34–51%, declining from around 49% in 2017 to 45% in 2025, although a marked decrease was observed in 2023. Fluoroquinolone susceptibility remained low throughout the period, with ciprofloxacin decreasing from 32% to 19.7%. In summary, *K. pneumoniae* has demonstrated persistently high resistance to ceftazidime and ciprofloxacin, accompanied by a concerning decline in carbapenem susceptibility. Amikacin retained comparatively better activity, although susceptibility remained below 50% for most years.

Table 2.7: Yearly susceptibility trend of *K. pneumoniae* isolated from all samples (except faeces and urine)

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=5389	N=8394	N=13381	N=8932	N=13633	N=15008	N=12795	N=12517	N=14161
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	2207/5179 (42.6)	3256/8223 (39.6)	4872/12502 (39)	3165/8669 (36.5)	4393/13185 (33.3)	3300/14953 (22.0)	1939/7312 (26.5)	3024/11650 (26.0)	4120 / 14098 (29.2)
Cefazolin	*0/3 (-)	*0/0 (-)	*0/1 (-)	*0/3 (-)	*1/3 (-)	5/16 (-)	*2/12 (-)	12/36 (33.3)	1 / 2 (-)
Cefotaxime	1109/5092 (21.8)	1577/7158 (22)	2400/11292 (21.3)	1472/7658 (19.2)	2217/10879 (20.4)	2754/12919 (21.3)	1119/6479 (17.3)	2038/10032 (20.3)	2434 / 10218 (23.8)
Ceftazidime	1320/4790 (27.6)	1488/5503 (27)	1985/7908 (25.1)	1147/5334 (21.5)	1452/7507 (19.3)	1852/9500 (19.4)	915/5063 (18.1)	1280/5404 (23.7)	1779 / 6509 (27.3)
Ertapenem	2022/4456 (45.4)	3189/6667 (47.8)	4362/9650 (45.2)	2560/6255 (40.9)	3526/8298 (42.5)	3978/9845 (40.4)	1803/5275 (34.18)	3762/10212 (36.8)	5385 / 13692 (39.3)
Imipenem	3136/5360 (58.5)	4257/8223 (51.8)	5039/11031 (45.7)	3771/8392 (44.9)	5474/12660 (43.2)	6115/14474 (42.2)	2568/7211 (35.6)	3634/11641 (31.2)	4677 / 12806 (36.5)
Meropenem	2478/5147 (48.1)	3832/7591 (50.5)	6081/12164 (50)	3660/7771 (47.1)	5707/12678 (45)	6404/14619 (43.8)	2764/7335 (37.6)	4276/12189 (35.1)	5699 / 14120 (40.4)
Amikacin	2583/5286 (48.9)	4204/8276 (50.8)	6507/13018 (50)	4171/8828 (47.2)	6174/13451 (45.9)	6838/14888 (45.9)	2539/7357 (34.5)	4994/12517 (39.9)	6293 / 14134 (44.5)
Ciprofloxacin	1667/5213 (32)	2766/7688 (36)	4144/11560 (35.8)	2420/7218 (33.5)	3621/11712 (30.9)	3016/14827 (20.3)	1258/7341 (17.1)	2502/12271 (20.4)	2781 / 14134 (19.7)
Levofloxacin	254/898 (28.3)	967/3333 (29)	2596/7432 (34.9)	1391/4913 (28.3)	1830/6101 (30)	1712/6782 (25.2)	647/3709 (17.4)	1270/5113 (24.8)	1960 / 6797 (28.8)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

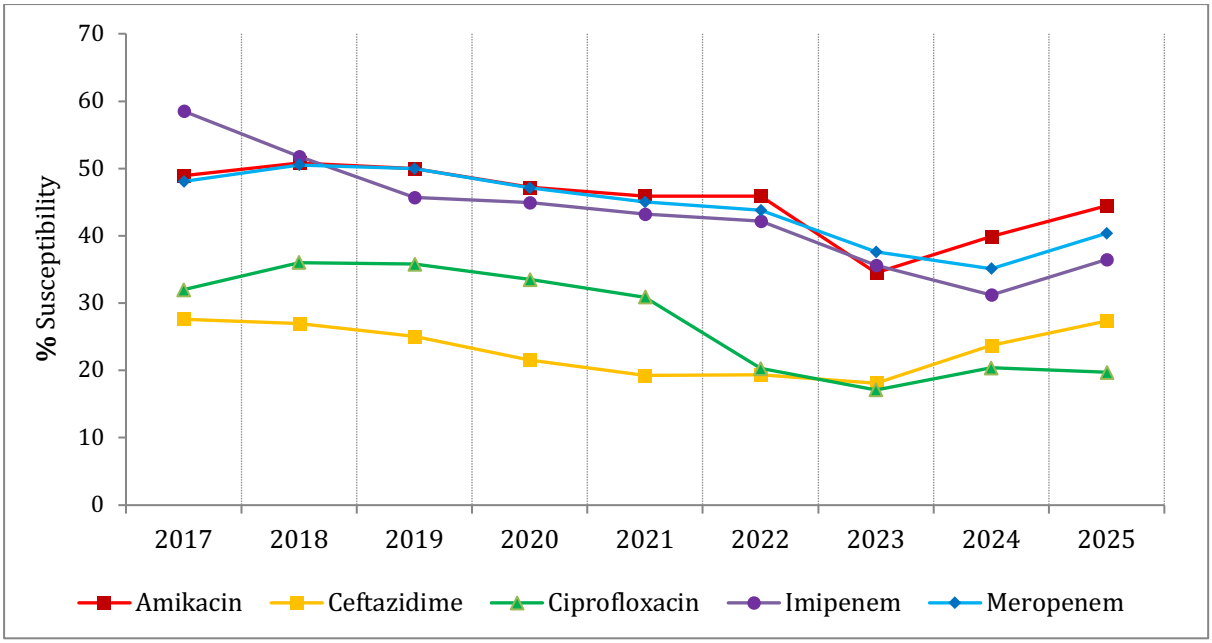


Figure 2.2: Yearly susceptibility trend of *K. pneumoniae* isolated from all samples (except faeces and urine)

Enterobacter species

Over the last nine years (2017–2025), *Enterobacter* species showed fluctuating but overall declining susceptibility trends across multiple antibiotics **(Table 2.8, Figure 2.3).** Piperacillin-tazobactam susceptibility fluctuated substantially, declining from 66.0% in 2017 to 38.2% in 2022, followed by an increase to 48.4% in 2025. Third-generation cephalosporins showed consistently poor activity, with cefotaxime susceptibility ranging from 13.1–35.7% and ceftazidime from 21.2–35.8%, remaining below 40% throughout the period.Carbapenems continued to be the most active agents against *Enterobacter* species; however, a progressive decline in susceptibility was observed over theperiod. Ertapenem susceptibility decreased from 66.1% in 2017 to 59.0% in 2024, with a slight recovery to 63.0% in 2025. Imipenem declined from 70.5% in 2017 to 61.9% in 2025, while meropenem decreased from 69.9% to 64.2%. Amikacin remained relatively effective, with susceptibility fluctuating between 62.3% and 75.8% and reaching 68.7% in 2025. Fluoroquinolones showed variable activity, with ciprofloxacin declining from 53.1% in 2017 to 47.5% in 2025, while levofloxacin remained comparatively higher at 62.8% in 2024 and 62.3% in 2025.In summary, *Enterobacter* species exhibited moderate susceptibility to carbapenems and aminoglycosides; however, a declining trend was evident over the years. In contrast, resistance to third-generation cephalosporins and fluoroquinolones remained consistently high, underscoring their limited therapeutic utility against these isolates.

Table 2.8: Yearly susceptibility trend of *Enterobacter* species isolated from all samples (except faeces and urine)

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=1140	N=1600	N=2071	N=1287	N=393	N=324	N=194	N=229	N=385
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	682/1092 (62.5)	961/1567 (61.3)	1253/1908 (65.7)	781/1225 (63.8)	234/369 (63.4)	122/319 (38.2)	56/120 (46.6)	82/199 (41.2)	186 / 384 (48.4)
Cefotaxime	310/1093 (28.4)	448/1423 (31.5)	576/1590 (36.2)	391/1094 (35.7)	78/290 (26.9)	65/251 (25.9)	13/99 (13.1)	42/179 (23.5)	107 / 325 (32.9)
Ceftazidime	363/1013 (35.8)	424/1159 (36.6)	494/1305 (37.9)	281/823 (34.1)	69/251 (27.5)	66/225 (29.3)	24/113 (21.2)	32/100 (32)	56 / 177 (31.6)
Ertapenem	613/929 (66)	855/1170 (73.1)	950/1281 (74.2)	562/783 (71.8)	171/216 (79.2)	135/176 (76.7)	60/79 (75.9)	95/161 (59.0)	235 / 373 (63)
Imipenem	851/1133 (75.1)	1111/1575 (70.5)	1117/1662 (67.2)	826/1148 (72)	191/281 (68)	188/266 (70.6)	83/122 (68.0)	104/198 (52.5)	206 / 333 (61.9)
Meropenem	735/1051 (69.9)	1068/1503 (71.1)	1497/1990 (75.2)	918/1211 (75.8)	262/378 (69.3)	230/296 (77.7)	87/122 (71.3)	123/206 (59.7)	247 / 385 (64.2)
Amikacin	734/1059 (69.3)	1119/1572 (71.2)	1446/1965 (73.6)	948/1250 (75.8)	267/371 (72)	221/306 (72.2)	76/122 (62.3)	151/229 (65.9)	249 / 385 (64.7)
Ciprofloxacin	578/1088 (53.1)	837/1369 (61.1)	1147/1836 (62.5)	699/1080 (64.7)	189/272 (69.5)	166/319 (52.0)	61/122 (50.0)	105/226 (46.5)	183 / 385 (47.5)
Levofloxacin	93/150 (62)	289/550 (52.5)	587/959 (61.2)	334/554 (60.3)	113/170 (66.5)	69/116 (59.4)	43/69 (62.3)	54/86 (62.8)	117 / 188 (62.2)

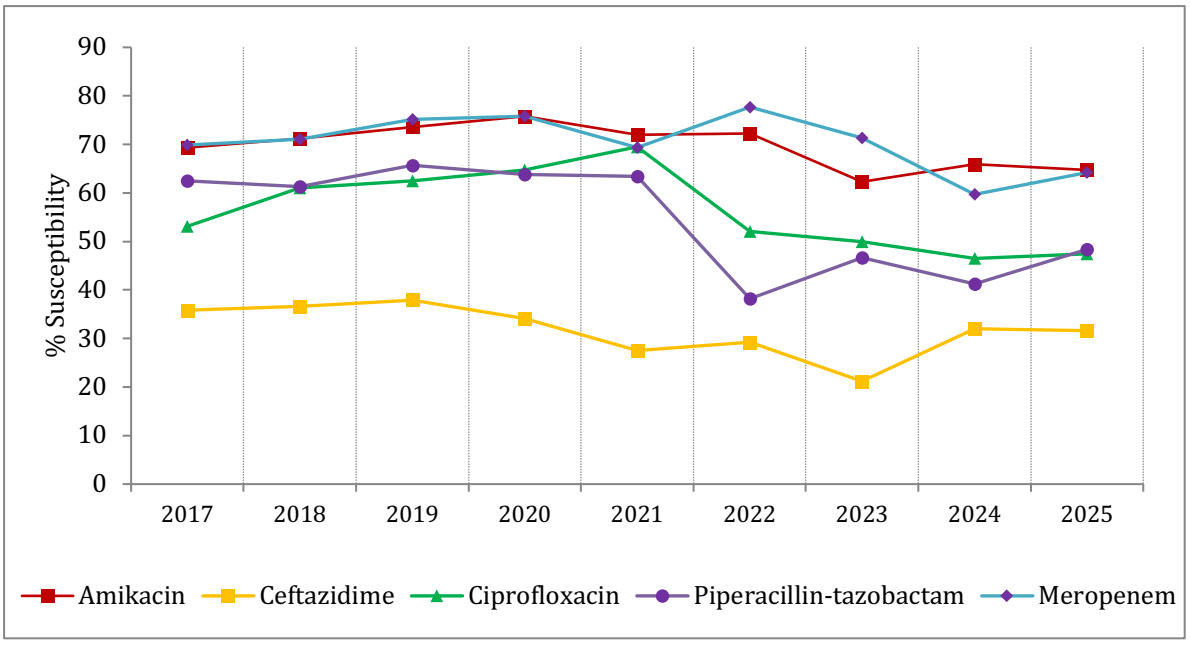


Figure 2.3: Yearly susceptibility trend of *Enterobacter* species isolated from all samples (except faeces and urine)

Citrobacter species

Citrobacter species demonstrated variable but overall declining susceptibility across most antibiotics **(Table 2.9, Figure 2.4).** Susceptibility to piperacillin-tazobactam reduced from 57.8% in 2017 to 48.1% in 2025. Third-generation cephalosporins showed consistently limited activity. Cefotaxime susceptibility ranged from 30.7% to 49.5%, while ceftazidime remained below 40% throughout the period, declining from 38.6% in 2017 to 32.7% in 2025.

Carbapenems retained moderate activity, though their susceptibility showed a gradual reduction over time. Imipenem susceptibility declined from 65.3% in 2017 to 64.7% in 2025, while meropenem susceptibility decreased from 65.8% to 64.6%. Amikacin remained relatively effective, with susceptibility ranging from 60.9% to 76.3%, although it declined to 61.1% in 2024 before recovering to 76.2% in 2025. In contrast, fluoroquinolone resistance remained high, with ciprofloxacin susceptibility declining from 46.8% in 2017 to 43.3% in 2025. In summary, *Citrobacter* species retained moderate susceptibility to carbapenems and amikacin, both of which showed a declining trend. Third-generation cephalosporins and fluoroquinolones consistently exhibited poor activity, highlighting narrowing treatment options.

Table 2.9: Yearly susceptibility trend of *Citrobacter* species isolated from all samples (except faeces and urine)

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=321	N=613	N=796	N=447	N=136	N=139	N=77	N=126	N=164
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	178/308 (57.8)	365/603 (60.5)	458/760 (60.3)	252/427 (59)	73/114 (64.0)	60/139 (43.2)	25/42 (59.5)	59/122 (48.4)	91/164 (55.5)
Cefotaxime	94/306 (30.7)	193/556 (34.7)	228/654 (34.9)	144/388 (37.1)	35/87 (40.2)	50/101 (49.5)	16/34 (47.0)	41/116 (35.3)	48/123 (39)
Ceftazidime	110/285 (38.6)	168/474 (35.4)	201/577 (34.8)	105/295 (35.6)	15/48 (31.3)	23/58 (39.6)	5/17 (-)	*11/24 (-)	18/55 (32.7)
Ertapenem	161/263 (61.2)	336/522 (64.4)	381/597 (63.8)	224/334 (67.1)	81/93 (87.1)	71/88 (80.6)	29/36 (80.5)	61/102 (59.8)	110/164 (67.1)
Imipenem	198/303 (65.3)	369/594 (62.1)	403/679 (59.4)	270/421 (64.1)	71/111 (64)	71/104 (68.2)	26/37 (70.2)	63/126 (50)	88/136 (64.7)
Meropenem	187/284 (65.8)	396/580 (68.3)	505/765 (66)	299/427 (70)	81/131 (61.8)	91/123 (73.9)	31/42 (73.8)	75/126 (59.5)	106/164 (64.6)
Amikacin	212/318 (66.7)	416/604 (68.9)	509/763 (66.7)	312/438 (71.2)	89/128 (69.5)	92/125 (73.6)	31/42 (73.8)	77/126 (61.1)	125/164 (76.2)
Ciprofloxacin	138/295 (46.8)	324/599 (54.1)	430/740 (58.1)	256/410 (62.4)	72/121 (59.5)	67/135 (49.6)	24/42 (57.1)	40/126 (31.8)	71/164 (43.3)
Levofloxacin	44/86 (51.2)	145/319 (45.5)	296/512 (57.8)	132/236 (55.9)	27/34 (79.4)	16/36 (44.4)	5/12 (-)	*11/15 (-)	26/54 (48.1)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

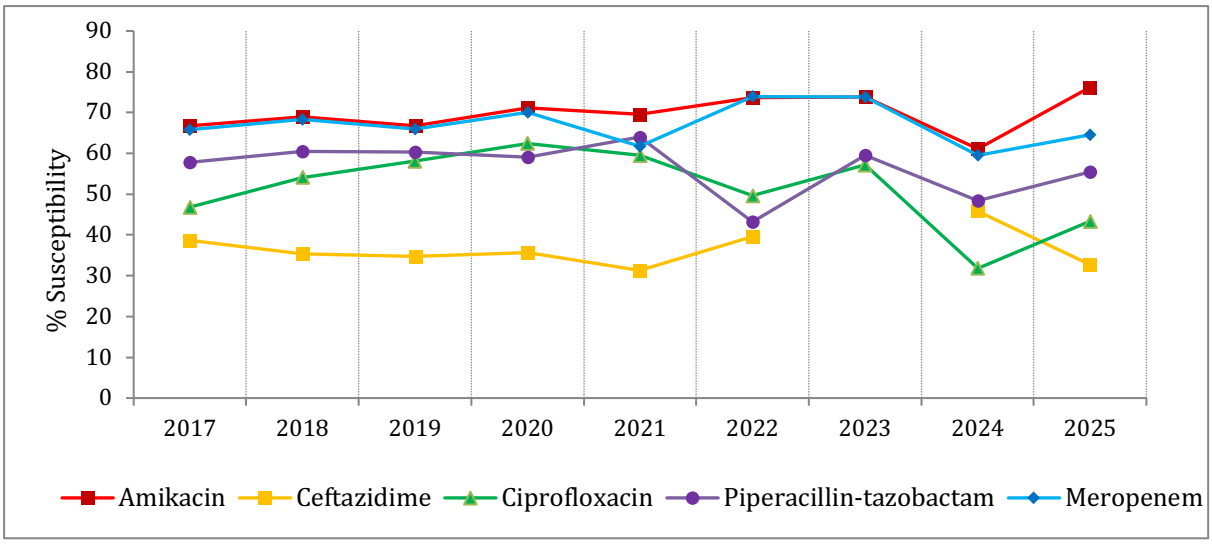


Figure 2.4: Yearly susceptibility trend of *Citrobacter* species isolated from all samples (except faeces and urine)

Analysis of results from individual Regional Centers (RCs)

Twenty-nine regional centers (RCs) from different parts of the country, representing both public and private sectors, participated in the surveillance. While overall susceptibility analysis included results from all centers for the designated organisms and antibiotics, RC-wise analysis was restricted to drug–pathogen combinations with at least 30 isolates tested to ensure robustness of the data.

Escherichia coli

Across all regional centers (RCs), *E. coli* isolates demonstrated consistently low susceptibility to third-generation cephalosporins and fluoroquinolones, while moderate activity was retained with carbapenems, amikacin and minocycline, and high susceptibility was observed with tigecycline **(Table 2.10).** Overall susceptibility was 42.6% to piperacillin-tazobactam, 18.3% to cefotaxime and 24.7% to ceftazidime. Carbapenem susceptibility was comparatively higher, with 60.5% for ertapenem, 63.2% for imipenem and 65.4% for meropenem, while amikacin showed 73.0% susceptibility. Fluoroquinolones were largely ineffective, with only 9.0% and 18.2% susceptibility to ciprofloxacin and levofloxacin, respectively. Tigecycline remained highly active; with 92.9% overall susceptibility. Marked inter-centre variation was observed. RC4, RC6, RC8, RC10 and RC20 demonstrated relatively higher carbapenem and amikacin susceptibility, with several centers reporting ≥75% susceptibility to carbapenems and >85% to amikacin. In contrast, RC1, RC2, RC12, RC19, RC21 and several other centers showed markedly low susceptibility across multiple agents, particularly cephalosporins and fluoroquinolones. Some centers reported 0% susceptibility to ciprofloxacin or levofloxacin.

Table 2.10: RC-wise Antimicrobial Susceptibility (AMS) percentages of *Escherichia coli* from total samples (except faeces & urine)

RC	Piperacillin-tazobactam (N=13842)	Cefotaxime (N=9819)	Ceftazidime (N=5840)	Ertapenem (N=13493)	Imipenem (N=12284)	Meropenem (N=13869)	Amikacin (N=13876)	Ciprofloxacin (N=13876)	Levofloxacin (N=6094)	Minocycline (N=5988)	Cefoperazone-sulbactam (N=11750)	Ceftazidime-avibactam (N=3374)	Tigecycline (N=7638)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	22/111 (19.8)	15/111 (13.5)	11/74 (14.9)	31/111 (27.9)	27/89 (30.3)	35/111 (31.5)	63/111 (56.8)	14/111 (12.6)	17/63 (27)	0/5* (-)	44/105 (41.9)	1/3* (-)	12/24* (-)
RC2	674/1871 (36)	667/1861 (35.8)	118/317 (37.2)	892/1843 (48.4)	406/931 (43.6)	933/1870 (49.9)	1591/1870 (85.1)	117/1870 (6.3)	40/128 (31.3)	204/293 (69.6)	934/1804 (51.8)	-	1/1* (-)
RC3	203/670 (30.3)	148/673 (22)	153/673 (22.7)	577/674 (85.6)	569/668 (85.2)	573/674 (85)	302/674 (44.8)	172/674 (25.5)	200/658 (30.4)	424/502 (84.5)	412/534 (77.2)	0/3* (-)	380/391 (97.2)
RC4	311/497 (62.6)	0/4* (-)	0/10* (-)	374/495 (75.6)	110/148 (74.3)	374/496 (75.4)	360/496 (72.6)	122/498 (24.5)	5/19* (-)	49/65 (75.4)	328/494 (66.4)	18/107 (16.8)	226/230 (98.3)
RC5	272/443 (61.4)	3/255 (1.2)	1/2* (-)	321/441 (72.8)	348/441 (78.9)	347/443 (78.3)	387/443 (87.4)	37/443 (8.4)	0/0 * (-)	16/68 (23.5)	268/404 (66.3)	0/0 * (-)	231/232 (99.6)
RC6	457/1066 (42.9)	77/677 (11.4)	2/4* (-)	629/1066 (59)	701/1062 (66)	700/1067 (65.6)	776/1067 (72.7)	31/1067 (2.9)	0/8 * (-)	703/1053 (66.8)	435/854 (50.9)	159/266 (59.8)	832/844 (98.6)
RC7	72/130 (55.4)	6/27* (-)	3/19* (-)	82/127 (64.6)	97/128 (75.8)	100/130 (76.9)	112/130 (86.2)	8/130 (6.2)	1/19* (-)	16/19* (-)	55/90 (61.1)	1/2* (-)	85/85 (100)
RC8	310/561 (55.3)	135/562 (24)	178/558 (31.9)	382/562 (68)	432/560 (77.1)	427/563 (75.8)	507/563 (90.1)	31/563 (5.5)	43/562 (7.7)	438/563 (77.8)	331/473 (70)	1/1* (-)	475/475 (100)
RC9	141/225 (62.7)	56/225 (24.9)	73/228 (32)	141/217 (65)	132/229 (57.6)	176/229 (76.9)	156/229 (68.1)	48/229 (21)	60/223 (26.9)	181/223 (81.2)	0/2 * (-)	0/0 * (-)	36/42 (85.7)

RC	Piperacillin-tazobactam (N=13842)	Cefotaxime (N=9819)	Ceftazidime (N=5840)	Ertapenem (N=13493)	Imipenem (N=12284)	Meropenem (N=13869)	Amikacin (N=13876)	Ciprofloxacin (N=13876)	Levofloxacin (N=6094)	Minocycline (N=5988)	Cefoperazone-sulbactam (N=11750)	Ceftazidime-avibactam (N=3374)	Tigecycline (N=7638)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC10	349/601 (58.1)	19/74 (25.7)	0/1 (-)	489/599 (81.6)	504/599 (84.1)	499/600 (83.2)	459/602 (76.2)	95/610 (15.6)	0/1 (-)	63/108 (58.3)	389/535 (72.7)	1/1 * (-)	2/2 * (-)
RC11	94/310 (30.3)	36/310 (11.6)	51/310 (16.5)	122/292 (41.8)	154/305 (50.5)	161/310 (51.9)	175/310 (56.5)	21/310 (6.8)	35/306 (11.4)	177/308 (57.5)	29/97 (29.9)	0/0 * (-)	24/24* (-)
RC12	109/354 (30.8)	21/86 (24.4)	44/309 (14.2)	177/345 (51.3)	185/357 (51.8)	198/349 (56.7)	224/349 (64.2)	8/348 (2.3)	24/332 (7.2)	177/305 (58)	134/344 (39)	139/261 (53.3)	331/335 (98.8)
RC13	173/502 (34.5)	30/422 (7.1)	74/265 (27.9)	182/383 (47.5)	220/463 (47.5)	253/512 (49.4)	226/509 (44.4)	53/508 (10.4)	56/298 (18.8)	102/215 (47.4)	182/437 (41.6)	77/233 (33)	355/392 (90.6)
RC14	678/1238 (54.8)	209/1183 (17.7)	135/423 (31.9)	838/1240 (67.6)	926/1239 (74.7)	920/1240 (74.2)	1067/1240 (86)	70/1240 (5.6)	145/685 (21.2)	325/326 (99.7)	672/1082 (62.1)	66/246 (26.8)	1066/1072 (99.4)
RC16	115/472 (24.4)	69/472 (14.6)	123/471 (26.1)	279/472 (59.1)	124/471 (26.3)	325/472 (68.9)	381/472 (80.7)	84/472 (17.8)	117/472 (24.8)	263/435 (60.5)	163/292 (55.8)	132/191 (69.1)	67/219 (30.6)
RC17	371/722 (51.4)	18/154 (11.7)	44/157 (28)	468/721 (64.9)	523/719 (72.7)	522/723 (72.2)	639/723 (88.4)	39/723 (5.4)	16/112 (14.3)	82/123 (66.7)	387/628 (61.6)	47/209 (22.5)	597/598 (99.8)
RC19	132/400 (33)	2/304 (0.7)	21/210 (10)	162/402 (40.3)	189/402 (47)	204/402 (50.7)	203/402 (50.5)	20/402 (5)	44/400 (11)	28/145 (19.3)	52/280 (18.6)	0/89 (0)	5/31 (16.1)
RC20	243/603 (40.3)	82/603 (13.6)	214/603 (35.5)	367/603 (60.9)	403/603 (66.8)	410/603 (68)	540/603 (89.6)	70/603 (11.6)	97/603 (16.1)	362/603 (60)	36/389 (9.3)	28/113 (24.8)	335/392 (85.5)

RC	Piperacillin-tazobactam (N=13842)	Cefotaxime (N=9819)	Ceftazidime (N=5840)	Ertapenem (N=13493)	Imipenem (N=12284)	Meropenem (N=13869)	Amikacin (N=13876)	Ciprofloxacin (N=13876)	Levofloxacin (N=6094)	Minocycline (N=5988)	Cefoperazone-sulbactam (N=11750)	Ceftazidime-avibactam (N=3374)	Tigecycline (N=7638)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC21	21/164 (12.8)	2/163 (1.2)	12/158 (7.6)	42/109 (38.5)	60/166 (36.1)	63/167 (37.7)	60/167 (35.9)	4/167 (2.4)	15/167 (9)	42/49 (85.7)	37/122 (30.3)	4/68 (5.9)	24/31 (77.4)
RC24	91/249 (36.5)	17/248 (6.9)	17/151 (11.3)	147/249 (59)	78/146 (53.4)	159/249 (63.9)	104/249 (41.8)	15/249 (6)	29/178 (16.3)	92/144 (63.9)	114/248 (46)	133/234 (56.8)	214/238 (89.9)
RC26	265/840 (31.5)	1/10* (-)	5/43 (11.6)	405/828 (48.9)	476/842 (56.5)	481/842 (57.1)	579/842 (68.8)	14/842 (1.7)	0/53 (0)	23/31 (74.2)	338/822 (41.1)	22/75 (29.3)	670/691 (97)
RC27	207/259 (79.9)	52/138 (37.7)	10/10* (-)	230/259 (88.8)	237/258 (91.9)	237/259 (91.5)	232/259 (89.6)	51/259 (19.7)	9/9* (-)	12/12* (-)	226/259 (87.3)	0/1* (-)	255/258 (98.8)
RC28	72/203 (35.5)	0/0* (-)	0/1* (-)	89/203 (43.8)	102/192 (53.1)	97/203 (47.8)	125/203 (61.6)	1/203 (0.5)	1/6* (-)	0/0* (-)	81/203 (39.9)	4/16 * (-)	192/192 (100)
RC29	40/72 (55.6)	14/63 (22.2)	17/60 (28.3)	43/72 (59.7)	49/71 (69)	51/72 (70.8)	57/72 (79.2)	6/72 (8.3)	1/4* (-)	57/62 (91.9)	44/72 (61.1)	12/22 * (-)	58/58 (100)
RC30	84/195 (43.1)	27/140 (19.3)	2/9 * (-)	127/195 (65.1)	131/191 (68.6)	133/195 (68.2)	153/196 (78.1)	18/195 (9.2)	2/15* (-)	2/2* (-)	105/196 (53.6)	6/14 * (-)	184/188 (97.9)
RC31	133/254 (52.4)	21/233 (9)	10/98 (10.2)	168/253 (66.4)	176/255 (69)	178/256 (69.5)	195/256 (76.2)	8/256 (3.1)	1/99 (1)	27/32 (84.4)	151/255 (59.2)	6/74 (8.1)	247/247 (100)
RC32	85/347 (24.5)	29/326 (8.9)	35/263 (13.3)	94/236 (39.8)	160/344 (46.5)	194/348 (55.7)	95/348 (27.3)	22/348 (6.3)	56/256 (21.9)	48/134 (35.8)	80/237 (33.8)	23/127 (18.1)	63/169 (37.3)

RC	Piperacillin-tazobactam (N=13842)	Cefotaxime (N=9819)	Ceftazidime (N=5840)	Ertapenem (N=13493)	Imipenem (N=12284)	Meropenem (N=13869)	Amikacin (N=13876)	Ciprofloxacin (N=13876)	Levofloxacin (N=6094)	Minocycline (N=5988)	Cefoperazone-sulbactam (N=11750)	Ceftazidime-avibactam (N=3374)	Tigecycline (N=7638)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC33	109/303 (36)	36/300 (12)	51/255 (20)	200/303 (66)	151/244 (61.9)	200/303 (66)	248/303 (81.8)	45/303 (14.9)	40/246 (16.3)	0/0 * (-)	145/303 (47.9)	17/90 (18.9)	0/0* (-)
RC34	72/188 (38.3)	9/188 (4.8)	40/155 (25.8)	107/189 (56.6)	92/173 (53.2)	117/189 (61.9)	116/189 (61.4)	32/189 (16.9)	51/166 (30.7)	123/157 (78.3)	86/189 (45.5)	64/100 (64)	127/171 (74.3)
Total	5905/ 13842 (42.6)	1801/ 9819 (18.3)	1444/ 5840 (24.7)	8165/ 13493 (60.5)	7762/ 12284 (63.2)	9067/ 13869 (65.4)	10132/ 13876 (73)	1256/ 13876 (9)	1105/ 6094 (18.2)	4036/ 5988 (67.4)	6258/ 11750 (53.3)	1738/ 3374 (51.5)	7094/ 7638 (92.9)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Klebsiella pneumoniae

Klebsiella pneumoniae isolates across RCs showed very low susceptibility, with overall rates of 29.2% for piperacillin-tazobactam, 23.7–27.2% for third-generation cephalosporins, 36–40% for carbapenems, 44.5% for amikacin, and <30% for fluoroquinolones **(Table 2.11).** Tigecycline showed comparatively better activity (79.1%), while minocycline demonstrated moderate susceptibility (49.8%). Most RCs showed a uniformly resistant profile; however, RC8, RC10 and particularly RC29 demonstrated comparatively higher susceptibility to carbapenems (≈54–73%) and amikacin (≈62–75%). RC9 also showed relatively higher fluoroquinolone susceptibility, particularly levofloxacin (54.9%). In contrast, RC11, RC19, RC21, RC26 and RC28 exhibited very low susceptibility across most major drug classes, with carbapenem susceptibility generally below 30% and fluoroquinolone susceptibility often below 10%.

Table 2.11: RC-wise AMS percentages of *K. pneumoniae* from total samples (except faeces & urine)

RC	Piperacillin-tazobactam (N=14130)	Cefotaxime (N=10250)	Ceftazidime (N=6544)	Ertapenem (N=13731)	Imipenem (N=12836)	Meropenem (N=14154)	Amikacin (N=14160)	Ciprofloxacin (N=14160)	Levofloxacin (N=6833)	Minocycline (N=6463)	Cefoperazone-sulbactam (N=11641)	Ceftazidime-avibactam (N=4153)	Tigecycline (N=7697)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	36/158 (22.8)	18/155 (11.6)	20/95 (21.1)	40/157 (25.5)	26/122 (21.3)	40/157 (25.5)	49/157 (31.2)	24/157 (15.3)	19/89 (21.3)	1/3 (-)	48/145 (33.1)	1/3 (-)	18/27 (-)
RC2	329/1485 (22.2)	636/1484 (42.9)	92/392 (23.5)	463/1474 (31.4)	189/899 (21)	397/1485 (26.7)	926/1485 (62.4)	196/1485 (13.2)	35/124 (28.2)	150/265 (56.6)	468/1449 (32.3)	-	1/1 (-)
RC3	102/482 (21.2)	171/481 (35.6)	176/482 (36.5)	256/482 (53.1)	256/480 (53.3)	257/482 (53.3)	193/482 (40)	184/482 (38.2)	200/482 (41.5)	122/183 (66.7)	202/394 (51.3)	3/3 (-)	2/4 (-)

RC	Piperacillin-tazobactam (N=14130)	Cefotaxime (N=10250)	Ceftazidime (N=6544)	Ertapenem (N=13731)	Imipenem (N=12836)	Meropenem (N=14154)	Amikacin (N=14160)	Ciprofloxacin (N=14160)	Levofloxacin (N=6833)	Minocycline (N=6463)	Cefoperazone-sulbactam (N=11641)	Ceftazidime-avibactam (N=4153)	Tigecycline (N=7697)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC4	239/617 (38.7)	0/0 (-)	1/24 (-)	300/618 (48.5)	71/186 (38.2)	298/617 (48.3)	274/617 (44.4)	184/617 (29.8)	15/45 (33.3)	17/49 (34.7)	271/617 (43.9)	43/302 (14.2)	358/376 (95.2)
RC5	234/414 (56.5)	32/225 (14.2)	0/0 (-)	271/413 (65.6)	267/409 (65.3)	273/414 (65.9)	296/415 (71.3)	168/414 (40.6)	0/0 (-)	11/76 (14.5)	246/379 (64.9)	0/0 (-)	284/311 (91.3)
RC6	229/113 2 (20.2)	88/682 (12.9)	0/2 (0)	287/113 5 (25.3)	294/113 8 (25.8)	299/113 8 (26.3)	327/113 8 (28.7)	111/113 8 (9.8)	0/18 (-)	452/112 6 (40.1)	221/825 (26.8)	125/367 (34.1)	657/819 (80.2)
RC7	25/97 (25.8)	6/26 (-)	4/21 (-)	33/92 (35.9)	34/96 (35.4)	38/97 (39.2)	48/97 (49.5)	17/97 (17.5)	3/20 (-)	11/19 (-)	25/53 (47.2)	0/0 (-)	41/47 (87.2)
RC8	318/630 (50.5)	246/628 (39.2)	275/630 (43.7)	358/629 (56.9)	341/628 (54.3)	362/630 (57.5)	392/630 (62.2)	218/630 (34.6)	219/626 (35)	449/630 (71.3)	326/559 (58.3)	0/0 (-)	505/562 (89.9)
RC9	127/267 (47.6)	95/267 (35.6)	101/270 (37.4)	112/258 (43.4)	117/270 (43.3)	135/271 (49.8)	134/271 (49.4)	98/271 (36.2)	147/268 (54.9)	211/266 (79.3)	0/0 (-)	0/0 (-)	57/76 (75)
RC10	267/631 (42.3)	30/81 (37)	1/1 (-)	343/629 (54.5)	353/629 (56.1)	350/629 (55.6)	351/629 (55.8)	190/642 (29.6)	0/0 (-)	89/281 (31.7)	292/556 (52.5)	1/4 (-)	3/4 (-)
RC11	49/392 (12.5)	40/391 (10.2)	38/391 (9.7)	62/338 (18.3)	84/390 (21.5)	82/393 (20.9)	60/393 (15.3)	16/393 (4.1)	22/387 (5.7)	67/384 (17.4)	28/115 (24.3)	1/5 (-)	27/34 (79.4)
RC12	57/231 (24.7)	9/66 (13.6)	30/208 (14.4)	68/223 (30.5)	56/228 (24.6)	73/227 (32.2)	72/227 (31.7)	29/227 (12.8)	40/217 (18.4)	84/199 (42.2)	63/226 (27.9)	70/178 (39.3)	189/222 (85.1)

RC	Piperacillin-tazobactam (N=14130)	Cefotaxime (N=10250)	Ceftazidime (N=6544)	Ertapenem (N=13731)	Imipenem (N=12836)	Meropenem (N=14154)	Amikacin (N=14160)	Ciprofloxacin (N=14160)	Levofloxacin (N=6833)	Minocycline (N=6463)	Cefoperazone-sulbactam (N=11641)	Ceftazidime-avibactam (N=4153)	Tigecycline (N=7697)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC13	99/445 (22.2)	33/393 (8.4)	63/255 (24.7)	112/355 (31.5)	114/408 (27.9)	141/449 (31.4)	96/451 (21.3)	39/449 (8.7)	57/272 (21)	73/204 (35.8)	119/393 (30.3)	57/218 (26.1)	279/348 (80.2)
RC14	577/1252 (46.1)	399/1214 (32.9)	178/449 (39.6)	699/1251 (55.9)	694/1251 (55.5)	735/1251 (58.8)	713/1251 (57)	361/1251 (28.9)	249/694 (35.9)	341/349 (97.7)	596/1101 (54.1)	68/379 (17.9)	1002/1095 (91.5)
RC16	202/857 (23.6)	212/857 (24.7)	279/856 (32.6)	412/857 (48.1)	209/857 (24.4)	462/857 (53.9)	512/857 (59.7)	209/857 (24.4)	348/856 (40.7)	370/789 (46.9)	325/585 (55.6)	221/369 (59.9)	85/520 (16.3)
RC17	143/615 (23.3)	31/266 (11.7)	37/274 (13.5)	198/616 (32.1)	182/615 (29.6)	182/616 (29.5)	335/616 (54.4)	102/616 (16.6)	39/167 (23.4)	126/189 (66.7)	154/549 (28.1)	40/315 (12.7)	489/540 (90.6)
RC19	141/624 (22.6)	0/472 (0)	24/386 (6.2)	154/625 (24.6)	185/625 (29.6)	182/625 (29.1)	152/625 (24.3)	50/625 (8)	130/624 (20.8)	57/292 (19.5)	41/333 (12.3)	0/156 (0)	15/83 (18.1)
RC20	173/617 (28)	82/617 (13.3)	209/617 (33.9)	224/617 (36.3)	235/617 (38.1)	248/617 (40.2)	252/618 (40.8)	104/617 (16.9)	144/617 (23.3)	313/616 (50.8)	51/406 (12.6)	28/106 (26.4)	328/406 (80.8)
RC21	23/276 (8.3)	8/276 (2.9)	35/265 (13.2)	39/210 (18.6)	41/281 (14.6)	45/281 (16)	37/281 (13.2)	27/281 (9.6)	40/269 (14.9)	91/118 (77.1)	36/215 (16.7)	15/114 (13.2)	65/87 (74.7)
RC24	73/251 (29.1)	22/250 (8.8)	24/132 (18.2)	100/249 (40.2)	46/128 (35.9)	108/252 (42.9)	81/252 (32.1)	18/252 (7.1)	31/163 (19)	73/125 (58.4)	93/252 (36.9)	105/230 (45.7)	222/237 (93.7)
RC26	154/864 (17.8)	2/12 (-)	4/28 (-)	213/859 (24.8)	199/862 (23.1)	218/865 (25.2)	235/866 (27.1)	72/865 (8.3)	4/105 (3.8)	4/16 (-)	209/850 (24.6)	43/177 (24.3)	560/731 (76.6)

RC	Piperacillin-tazobactam (N=14130)	Cefotaxime (N=10250)	Ceftazidime (N=6544)	Ertapenem (N=13731)	Imipenem (N=12836)	Meropenem (N=14154)	Amikacin (N=14160)	Ciprofloxacin (N=14160)	Levofloxacin (N=6833)	Minocycline (N=6463)	Cefoperazone-sulbactam (N=11641)	Ceftazidime-avibactam (N=4153)	Tigecycline (N=7697)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC27	141/373 (37.8)	48/191 (25.1)	11/12 (-)	172/375 (45.9)	176/373 (47.2)	181/374 (48.4)	205/375 (54.7)	106/375 (28.3)	10/10 (-)	10/10 (-)	161/375 (42.9)	0/0 (-)	345/370 (93.2)
RC28	24/94 (25.5)	0/0 (-)	0/2 (-)	25/94 (26.6)	25/93 (26.9)	24/94 (25.5)	28/94 (29.8)	16/94 (17)	0/4 (-)	0/0 (-)	26/94 (27.7)	1/15 (-)	71/73 (97.3)
RC29	36/51 (70.6)	24/50 (48)	24/44 (54.5)	37/51 (72.5)	36/50 (72)	39/51 (76.5)	38/51 (74.5)	23/51 (45.1)	1/2 (50)	40/43 (93)	38/51 (74.5)	9/15 (-)	38/41 (92.7)
RC30	92/304 (30.3)	46/219 (21)	2/10 (-)	119/301 (39.5)	103/301 (34.2)	115/308 (37.3)	124/312 (39.7)	72/308 (23.4)	2/35 (5.7)	0/4 (-)	103/308 (33.4)	9/39 (23.1)	244/282 (86.5)
RC31	56/223 (25.1)	33/209 (15.8)	12/81 (14.8)	64/222 (28.8)	66/219 (30.1)	72/223 (32.3)	73/227 (32.2)	25/223 (11.2)	4/153 (2.6)	2/5 (-)	63/218 (28.9)	33/149 (22.1)	151/201 (75.1)
RC32	82/374 (21.9)	75/366 (20.5)	80/294 (27.2)	88/220 (40)	167/361 (46.3)	205/375 (54.7)	118/375 (31.5)	40/375 (10.7)	94/264 (35.6)	35/162 (21.6)	94/220 (42.7)	41/124 (33.1)	34/159 (21.4)
RC33	86/317 (27.1)	43/315 (13.7)	51/263 (19.4)	127/317 (40.1)	103/265 (38.9)	128/317 (40.4)	160/317 (50.5)	81/317 (25.6)	88/261 (33.7)	0/0 (-)	122/317 (38.5)	30/176 (17)	0/0 (-)
RC34	6/25 (-)	5/25 (-)	8/25 (-)	9/25 (-)	8/25 (-)	10/25 (-)	12/25 (-)	1/25 (-)	19/25 (-)	21/25 (-)	8/25 (-)	25/25 (-)	19/25 (-)
Total	4120/ 14130 (29.2)	2434/ 10250 (23.7)	1779/ 6544 (27.2)	5385/ 13731 (39.2)	4677/ 12836 (36.4)	5699/ 14154 (40.3)	6293/ 14160 (44.5)	2781/ 14160 (19.6)	1960/ 6833 (28.7)	3220/ 6463 (49.8)	4429/ 11641 (38.0)	1566/ 4153 (37.7)	6089/ 7697 (79.1)

Proteus mirabilis

Proteus mirabilis isolates showed high overall susceptibility to piperacillin-tazobactam (83.8%), ertapenem (76-77%) and meropenem, and amikacin (68.9%), whereas susceptibility to cephalosporins (46.1–52.1%), imipenem (44%), ciprofloxacin (30%), and levofloxacin (32.5%) was considerably lower **(Table 2.12).** Cefoperazone-sulbactam (77.8%) retained good activity. Marked inter-RC variation was observed. RC8, RC10, RC17, RC26, RC27, RC31 and RC29 demonstrated relatively high susceptibility to piperacillin-tazobactam and carbapenems, whereas RC11, RC19, RC21 and RC32 showed substantially lower susceptibility across multiple agents. Fluoroquinolone susceptibility was particularly poor in several centers, including RC6, RC19, RC20, RC26 and RC31.

Table 2.12: RC-wise AMS percentages of *Proteus mirabilis* from total samples (except faeces & urine)

RC	Piperacillin-tazobactam (N=1393)	Cefotaxime (N=986)	Ceftazidime (N=580)	Ertapenem (N=1359)	Imipenem (N=1044)	Meropenem (N=1399)	Amikacin (N=1399)	Ciprofloxacin (N=1399)	Levofloxacin (N=557)	Cefoperazone-sulbactam (N=1261)	Ceftazidime-avibactam (N=400)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC2	322/379 (85)	196/379 (51.7)	61/135 (45.2)	226/377 (59.9)	40/192 (20.8)	216/379 (57)	343/379 (90.5)	109/379 (28.8)	32/112 (28.6)	304/367 (82.8)	-
RC3	30/38 (78.9)	23/38 (60.5)	23/38 (60.5)	36/38 (94.7)	36/38 (94.7)	37/38 (97.4)	22/38 (57.9)	21/38 (55.3)	19/37 (51.4)	34/36 (94.4)	0/0 (-)
RC4	94/99 (94.9)	0/0 (-)	0/2 (-)	89/99 (89.9)	1/3 (-)	89/99 (89.9)	62/99 (62.6)	48/99 (48.5)	0/1 (-)	83/99 (83.8)	2/12 (-)
RC5	29/36 (80.6)	8/19 (-)	0/0 (-)	29/35 (82.9)	10/15 (-)	30/36 (83.3)	21/36 (58.3)	9/36 (25)	0/0 (-)	25/33 (75.8)	0/0 (-)

RC	Piperacillin-tazobactam (N=1393)	Cefotaxime (N=986)	Ceftazidime (N=580)	Ertapenem (N=1359)	Imipenem (N=1044)	Meropenem (N=1399)	Amikacin (N=1399)	Ciprofloxacin (N=1399)	Levofloxacin (N=557)	Cefoperazone-sulbactam (N=1261)	Ceftazidime-avibactam (N=400)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC6	133/139 (95.7)	41/70 (58.6)	0/0 (-)	121/139 (87.1)	86/139 (61.9)	121/139 (87.1)	95/139 (68.3)	37/139 (26.6)	0/0 (-)	95/113 (84.1)	26/35 (74.3)
RC7	9/10 (-)	2/3 (-)	1/1 (-)	7/10 (-)	0/10 (-)	6/10 (-)	8/10 (-)	4/10 (-)	1/1 (-)	3/6 (-)	0/0 (-)
RC8	61/61 (100)	50/61 (82)	53/60 (88.3)	61/62 (98.4)	14/55 (25.5)	60/61 (98.4)	53/61 (86.9)	26/61 (42.6)	23/61 (37.7)	50/51 (98)	0/0 (-)
RC10	74/80 (92.5)	9/13 (-)	0/0 (-)	84/84 (100)	72/77 (93.5)	84/84 (100)	51/84 (60.7)	26/89 (29.2)	0/0 (-)	66/71 (93)	0/0 (-)
RC12	18/21 (-)	5/10 (-)	5/18 (-)	15/17 (-)	1/20 (-)	10/20 (-)	11/20 (-)	8/20 (-)	6/19 (-)	8/20 (-)	12/13 (-)
RC16	34/64 (53.1)	43/64 (67.2)	54/64 (84.4)	51/64 (79.7)	12/64 (18.8)	51/64 (79.7)	60/64 (93.8)	32/64 (50)	42/64 (65.6)	45/48 (93.8)	37/41 (90.2)
RC17	45/52 (86.5)	4/26 (-)	9/26 (-)	43/52 (82.7)	28/51 (54.9)	48/52 (92.3)	42/52 (80.8)	15/52 (28.8)	7/18 (-)	41/48 (85.4)	5/18 (-)
RC19	56/65 (86.2)	0/46 (0)	10/41 (24.4)	45/65 (69.2)	40/65 (61.5)	52/65 (80)	11/65 (16.9)	5/65 (7.7)	8/65 (12.3)	22/53 (41.5)	0/14 (-)
RC20	37/50 (74)	15/50 (30)	24/50 (48)	32/50 (64)	26/50 (52)	33/50 (66)	45/50 (90)	5/50 (10)	5/50 (10)	6/39 (15.4)	7/14 (-)
RC21	9/22 (-)	1/24 (-)	8/24 (-)	5/11 (-)	5/24 (-)	9/24 (-)	4/24 (-)	3/24 (-)	5/24 (-)	5/20 (-)	4/14 (-)

RC	Piperacillin-tazobactam (N=1393)	Cefotaxime (N=986)	Ceftazidime (N=580)	Ertapenem (N=1359)	Imipenem (N=1044)	Meropenem (N=1399)	Amikacin (N=1399)	Ciprofloxacin (N=1399)	Levofloxacin (N=557)	Cefoperazone-sulbactam (N=1261)	Ceftazidime-avibactam (N=400)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC24	9/12 (-)	3/12 (-)	4/7 (-)	10/12 (-)	3/7 (-)	10/12 (-)	2/12 (-)	4/12 (-)	3/9 (-)	8/12 (-)	7/11 (-)
RC26	59/61 (96.7)	0/0 (-)	0/1 (-)	56/60 (93.3)	17/60 (28.3)	57/61 (93.4)	32/61 (52.5)	18/61 (29.5)	0/3 (-)	56/61 (91.8)	0/0 (-)
RC27	26/26 (-)	11/13 (-)	1/1 (-)	26/26 (-)	5/23 (-)	26/26 (-)	23/26 (-)	11/26 (-)	1/1 (-)	24/26 (-)	0/0 (-)
RC30	19/22 (-)	4/15 (-)	0/0 (-)	12/22 (-)	4/21 (-)	9/22 (-)	9/23 (-)	7/22 (-)	0/1 (0)	8/22 (-)	0/1 (0)
RC31	21/23 (-)	9/22 (-)	5/13 (-)	20/23 (-)	2/23 (-)	20/23 (-)	12/23 (-)	6/23 (-)	1/10 (-)	21/23 (-)	1/6 (-)
RC32	23/38 (60.5)	10/37 (27)	11/26 (-)	10/20 (-)	22/37 (59.5)	32/38 (84.2)	9/38 (23.7)	8/38 (21.1)	6/21 (-)	10/20 (-)	2/8 (-)
RC33	24/42 (57.1)	6/39 (15.4)	10/30 (33.3)	28/42 (66.7)	14/23 (-)	28/42 (66.7)	27/42 (64.3)	5/42 (11.9)	6/30 (20)	30/42 (71.4)	4/9 (-)
RC34	10/23 (-)	6/23 (-)	14/22 (-)	14/23 (-)	10/21 (-)	15/23 (-)	10/23 (-)	9/23 (-)	13/21 (-)	15/23 (-)	14/19 (-)
Total	1168/1393 (83.8)	455/986 (46.1)	302/580 (52.1)	1044/1359 (76.8)	460/1044 (44)	1069/1399 (76.4)	965/1399 (68.9)	425/1399 (30.3)	181/557 (32.5)	981/1261 (77.8)	299/400 (74.8)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Enterobacter cloacae

Enterobacter cloacae isolates across RCs showed moderate-to-high susceptibility to several antimicrobial classes, with national rates of 58.5% for piperacillin-tazobactam, 43.1–47.9% for third-generation cephalosporins, 67–68% for carbapenems, 73.5% for amikacin, 48.9–56.7% for fluoroquinolones, 68.5% for minocycline, 67.8% for cefoperazone-sulbactam, 54.3% for ceftazidime-avibactam, and 94.9% for tigecycline **(Table 2.13).** Several RCs, particularly RC8 and RC27, demonstrated comparatively higher susceptibility across most drug classes, with carbapenem susceptibility generally >85%, aminoglycoside susceptibility ~88–96%, and fluoroquinolone susceptibility ~64–80%. RC29 also showed very high susceptibility across nearly all agents, although the number of isolates was small. In contrast, RC12, RC19, RC21, RC24, and RC32 exhibited comparatively reduced susceptibility across multiple antimicrobial classes, particularly to cephalosporins, carbapenems, aminoglycosides, and fluoroquinolones. RC12 and RC24 showed particularly low carbapenem susceptibility (approximately 35–42% and 11–42%, respectively), while RC19 demonstrated low susceptibility to cephalosporins (3.7–15.8%) and amikacin (50%). Tigecycline retained the highest overall activity nationally (94.9%), with susceptibility ≥90% in most RCs, although lower activity was observed in RC20, RC32, and RC33.

Table 2.13: RC-wise AMS percentages of *Enterobacter cloacae* from total samples (except faeces & urine)

RC	Piperacillin-tazobactam (N=1340)	Cefotaxime (N=816)	Ceftazidime (N=466)	Ertapenem (N=1298)	Imipenem (N=1178)	Meropenem (N=1344)	Amikacin (N=1344)	Ciprofloxacin (N=1344)	Levofloxacin (N=457)	Minocycline (N=432)	Cefoperazone-sulbactam (N=1193)	Ceftazidime-avibactam (N=281)	Tigecycline (N=732)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC2	103/240 (42.9)	96/238 (40.3)	28/77 (36.4)	120/240 (50)	48/128 (37.5)	112/240 (46.7)	189/240 (78.8)	85/240 (35.4)	10/29 (-)	30/53 (56.6)	133/236 (56.4)	99/108 (91.7)	0/0 (-)
RC4	34/42 (81)	0/0 (-)	0/0 (-)	38/42 (90.5)	13/14 (-)	38/42 (90.5)	34/42 (81)	31/42 (73.8)	0/0 (-)	3/6 (-)	37/42 (88.1)	0/4 (-)	16/17 (-)

RC	Piperacillin-tazobactam (N=1340)	Cefotaxime (N=816)	Ceftazidime (N=466)	Ertapenem (N=1298)	Imipenem (N=1178)	Meropenem (N=1344)	Amikacin (N=1344)	Ciprofloxacin (N=1344)	Levofloxacin (N=457)	Minocycline (N=432)	Cefoperazone-sulbactam (N=1193)	Ceftazidime-avibactam (N=281)	Tigecycline (N=732)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC5	52/66 (78.8)	0/20 (-)	0/0 (-)	57/63 (90.5)	58/64 (90.6)	60/66 (90.9)	57/66 (86.4)	36/66 (54.5)	0/0 (-)	0/2 (-)	50/58 (86.2)	0/0 (-)	41/41 (100)
RC6	14/27 (-)	5/20 (-)	0/0 (-)	18/27 (-)	20/27 (-)	20/27 (-)	19/27 (-)	9/27 (-)	0/0 (-)	18/27 (-)	16/24 (-)	5/8 (-)	20/23 (-)
RC7	23/28 (-)	2/5 (-)	2/3 (-)	23/27 (-)	22/27 (-)	25/29 (-)	27/29 (-)	19/29 (-)	3/4 (-)	2/2 (-)	18/20 (-)	0/0 (-)	19/20 (-)
RC8	77/92 (83.7)	63/92 (68.5)	73/92 (79.3)	78/92 (84.8)	80/92 (87)	79/92 (85.9)	81/92 (88)	61/92 (66.3)	68/91 (74.7)	84/92 (91.3)	67/79 (84.8)	0/0 (-)	78/79 (98.7)
RC10	71/105 (67.6)	11/16 (-)	0/0 (-)	87/105 (82.9)	87/105 (82.9)	87/105 (82.9)	80/105 (76.2)	66/109 (60.6)	0/0 (-)	13/18 (-)	72/91 (79.1)	0/1 (-)	0/1 (-)
RC11	22/51 (43.1)	19/51 (37.3)	19/51 (37.3)	21/45 (46.7)	24/49 (49)	23/51 (45.1)	15/51 (29.4)	18/51 (35.3)	20/50 (40)	22/50 (44)	7/13 (-)	0/0 (-)	5/5 (-)
RC12	12/48 (25)	5/17 (-)	8/47 (17)	19/45 (42.2)	17/48 (35.4)	22/47 (46.8)	21/47 (44.7)	14/47 (29.8)	19/45 (42.2)	30/43 (69.8)	13/46 (28.3)	14/35 (40)	44/45 (97.8)
RC13	12/30 (40)	4/18 (-)	4/9 (-)	10/16 (-)	12/27 (-)	16/30 (53.3)	14/30 (46.7)	9/30 (30)	5/11 (-)	2/6 (-)	13/25 (-)	5/8 (-)	18/18 (-)
RC14	60/92 (65.2)	53/87 (60.9)	16/20 (-)	69/92 (75)	71/92 (77.2)	71/92 (77.2)	73/92 (79.3)	53/92 (57.6)	48/66 (72.7)	15/15 (-)	58/81 (71.6)	4/15 (-)	80/80 (100)

RC	Piperacillin-tazobactam (N=1340)	Cefotaxime (N=816)	Ceftazidime (N=466)	Ertapenem (N=1298)	Imipenem (N=1178)	Meropenem (N=1344)	Amikacin (N=1344)	Ciprofloxacin (N=1344)	Levofloxacin (N=457)	Minocycline (N=432)	Cefoperazone-sulbactam (N=1193)	Ceftazidime-avibactam (N=281)	Tigecycline (N=732)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC17	74/105 (70.5)	6/28 (-)	18/28 (-)	75/106 (70.8)	80/106 (75.5)	81/106 (76.4)	92/106 (86.8)	68/106 (64.2)	15/21 (-)	22/22 (-)	65/90 (72.2)	5/29 (-)	89/91 (97.8)
RC19	10/28 (-)	1/27 (-)	3/19 (-)	13/28 (-)	13/26 (-)	12/28 (-)	14/28 (-)	15/28 (-)	16/27 (-)	5/17 (-)	4/19 (-)	0/9 (-)	3/5 (-)
RC21	8/22 (-)	7/21 (-)	6/20 (-)	7/20 (-)	9/22 (-)	9/22 (-)	10/22 (-)	6/22 (-)	6/21 (-)	17/19 (-)	7/20 (-)	5/16 (-)	16/17 (-)
RC24	4/12 (-)	3/12 (-)	1/9 (-)	4/12 (-)	1/9 (-)	5/12 (-)	2/12 (-)	1/12 (-)	1/11 (-)	2/11 (-)	5/12 (-)	4/11 (-)	9/12 (-)
RC26	64/129 (49.6)	4/8 (-)	8/16 (-)	82/125 (65.6)	80/130 (61.5)	86/130 (66.2)	93/130 (71.5)	37/130 (28.5)	6/16 (-)	10/12 (-)	82/124 (66.1)	4/11 (-)	105/114 (92.1)
RC27	43/51 (84.3)	21/32 (65.6)	0/0 (-)	46/51 (90.2)	46/50 (92)	48/51 (94.1)	49/51 (96.1)	41/51 (80.4)	3/3 (-)	1/1 (-)	45/51 (88.2)	0/0 (-)	49/51 (96.1)
RC28	22/33 (66.7)	0/0 (-)	1/1 (-)	24/33 (72.7)	24/32 (75)	25/33 (75.8)	25/33 (75.8)	14/33 (42.4)	0/0 (-)	0/0 (-)	25/33 (75.8)	0/2 (0)	29/29 (-)
RC29	6/6 (-)	3/3 (-)	2/2 (-)	6/6 (-)	6/6 (-)	6/6 (-)	6/6 (-)	5/6 (-)	1/1 (-)	2/2 (-)	6/6 (-)	0/1 (-)	5/5 (-)
RC30	18/34 (52.9)	12/25 (-)	0/2 (-)	24/34 (70.6)	20/32 (62.5)	21/35 (60)	21/35 (60)	19/35 (54.3)	1/1 (-)	1/1 (-)	21/34 (61.8)	1/1 (-)	31/32 (96.9)
RC31	28/40 (70)	21/40 (52.5)	12/24 (-)	30/39 (76.9)	30/40 (75)	32/40 (80)	35/40 (87.5)	26/40 (65)	13/18 (-)	11/15 (-)	29/40 (72.5)	1/7 (-)	34/38 (89.5)

RC	Piperacillin-tazobactam (N=1340)	Cefotaxime (N=816)	Ceftazidime (N=466)	Ertapenem (N=1298)	Imipenem (N=1178)	Meropenem (N=1344)	Amikacin (N=1344)	Ciprofloxacin (N=1344)	Levofloxacin (N=457)	Minocycline (N=432)	Cefoperazone-sulbactam (N=1193)	Ceftazidime-avibactam (N=281)	Tigecycline (N=732)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC32	9/25 (-)	6/21 (-)	9/18 (-)	10/15 (-)	13/25 (-)	18/25 (-)	10/25 (-)	7/25 (-)	6/13 (-)	3/14 (-)	12/15 (-)	3/7 (-)	3/8 (-)
RC33	11/21 (-)	6/21 (-)	10/20 (-)	13/21 (-)	11/18 (-)	13/21 (-)	11/21 (-)	10/21 (-)	10/20 (-)	0/0 (-)	14/21 (-)	2/8 (-)	0/0 (-)
Total	784/ 1340 (58.5)	352/ 816 (43.1)	223/ 466 (47.9)	884/ 1298 (68.1)	791/ 1178 (67.1)	919/ 1344 (68.4)	988/ 1344 (73.5)	658/ 1344 (48.9)	259/ 457 (56.7)	296/ 432 (68.5)	809/ 1193 (67.8)	153/ 281 (54.3)	695/ 732 (94.9)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Species-wise susceptibility of Enterobacterales from urine

The antimicrobial susceptibility of Enterobacterales isolated from urine samples revealed marked variability across species **(Table 2.14),** highlighting the importance of species-specific antimicrobial selection for the management of urinary tract infections. *Escherichia coli* was the predominant uropathogen and demonstrated relatively high susceptibility to fosfomycin (96.5%) and nitrofurantoin (79.1%). In contrast, susceptibility to commonly used agents such as cefazolin (10.2%), ciprofloxacin (14.5%), cefotaxime (20.8%) and levofloxacin (28.3%) was low. Moderate susceptibility was observed for amikacin (74.7%) and carbapenems, including ertapenem (76.7%) and meropenem (77.7%), while imipenem showed comparatively lower susceptibility (70.2%). The second most frequently isolated species, *Klebsiella pneumoniae*, exhibited substantially reduced susceptibility across most antimicrobial classes, with susceptibility of only 44.8% to imipenem, 51.8% to meropenem and 52.4% to ertapenem; however, fosfomycin retained comparatively better activity (67.4%). *Klebsiella oxytoca* showed a variable susceptibility profile, with relatively better activity observed for fosfomycin (77.1%) and meropenem (59.7%), while susceptibility to imipenem was low (31.1%). Among the less frequently isolated species, *Enterobacter cloacae* demonstrated comparatively favourable susceptibility to meropenem (78.7%), ertapenem (78.7%), imipenem (74.1%) and amikacin (79.0%), although susceptibility to ciprofloxacin remained moderate (60.3%). *Proteus mirabilis* showed high susceptibility to meropenem (84.9%), ertapenem (82.7%) and piperacillin-tazobactam (83.5%), consistent with its limited utility against this organism. *Citrobacter koseri* demonstrated one of the most favourable susceptibility profiles, with high susceptibility to fosfomycin (95.8%), meropenem (95.9%), amikacin (95.0%), imipenem (91.2%) and cefoperazone-sulbactam (98.1%). *Citrobacter freundii* showed moderate susceptibility to carbapenems and aminoglycosides, with meropenem susceptibility of 68.2% and amikacin susceptibility of 62.3%. *Morganella morganii* demonstrated relatively high susceptibility to meropenem (88.9%), ertapenem (86.4%) and piperacillin-tazobactam (80.8%), whereas susceptibility to fosfomycin (29.5%) and nitrofurantoin (15.9%) was low.

In summary, *E. coli* remained the predominant uropathogen and showed high susceptibility to fosfomycin and nitrofurantoin but substantial resistance to cephalosporins and fluoroquinolones. *K. pneumoniae* exhibited a considerably more resistant profile, with limited susceptibility to carbapenems and most commonly used agents. Other Enterobacterales, including *Enterobacter*, *Proteus*, *Citrobacter* and *Morganella*, demonstrated species-specific susceptibility patterns, with carbapenems and amikacin generally retaining greater activity in several species.

Table 2.14: Species-wise susceptibility of Enterobacterales isolated from urine

AMA	*Escherichia coli* (N=13627)	*Klebsiella pneumoniae* (N=4958)	*Klebsiella oxytoca* (N=200)	*Klebsiella spp.* (N=338)	*Enterobacter cloacae* (N=314)	*Enterobacter spp.* (N=80)	*Proteus mirabilis* (N=355)	*Citrobacter koseri* (N=258)	*Citrobacter freundii* (N=53)	*Morganella morganii* (N=182)	*Providencia rettgeri* (N=25)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	7854 / 13575 (57.9)	1922 / 4937 (38.9)	79 / 200 (39.5)	74 / 338 (21.9)	211 / 313 (67.4)	38 / 79 (48.1)	294 / 352 (83.5)	222 / 258 (86)	22 / 53 (41.5)	147 / 182 (80.8)	*15/25 (-)
Cefazolin	351 / 3437 (10.2)	150 / 1198 (12.5)	7 / 97 (7.2)	63 / 213 (29.6)	4 / 34 (11.8)	*2/6 (-)	7 / 51 (13.7)	9 / 34 (26.5)	*0/7 (-)	*0/17 (-)	*0/4 (-)
Cefotaxime	1905 / 9165 (20.8)	853 / 3265 (26.1)	44 / 179 (24.6)	40 / 334 (12)	68 / 152 (44.7)	25 / 70 (35.7)	111 / 232 (47.8)	123 / 169 (72.8)	11 / 35 (31.4)	38 / 96 (39.6)	*8/11 (-)
Ceftazidime	3012 / 7553 (39.9)	1020 / 2769 (36.8)	70 / 174 (40.2)	93 / 282 (33)	103 / 149 (69.1)	14 / 45 (31.1)	107 / 191 (56)	92 / 118 (78)	19 / 35 (54.3)	34 / 70 (48.6)	*3/12 (-)
Ertapenem	10048 / 13096 (76.7)	2488 / 4744 (52.4)	108 / 190 (56.8)	124 / 338 (36.7)	237 / 301 (78.7)	51 / 80 (63.8)	287 / 347 (82.7)	238 / 255 (93.3)	30 / 51 (58.8)	152 / 176 (86.4)	*19/24 (-)
Imipenem	7876 / 11222 (70.2)	1838 / 4104 (44.8)	56 / 180 (31.1)	104 / 301 (34.6)	169 / 228 (74.1)	46 / 72 (63.9)	147 / 287 (51.2)	198 / 217 (91.2)	19 / 37 (51.4)	66 / 131 (50.4)	*10/22 (-)
Meropenem	9619 / 12373 (77.7)	2378 / 4592 (51.8)	114 / 191 (59.7)	141 / 329 (42.9)	199 / 253 (78.7)	49 / 77 (63.6)	281 / 331 (84.9)	231 / 241 (95.9)	30 / 44 (68.2)	144 / 162 (88.9)	*17/24 (-)
Amikacin	10178 / 13627 (74.7)	2590 / 4949 (52.3)	127 / 200 (63.5)	155 / 338 (45.9)	249 / 315 (79)	48 / 80 (60)	211 / 354 (59.6)	245 / 258 (95)	33 / 53 (62.3)	139 / 182 (76.4)	*14/25 (-)
Ciprofloxacin	1983 / 13636 (14.5)	1270 / 4951 (25.7)	55 / 200 (27.5)	58 / 338 (17.2)	190 / 315 (60.3)	30 / 80 (37.5)	107 / 355 (30.1)	209 / 258 (81)	14 / 53 (26.4)	53 / 182 (29.1)	*7/25 (-)
Levofloxacin	1857 / 6565 (28.3)	836 / 2439 (34.3)	56 / 156 (35.9)	99 / 303 (32.7)	54 / 98 (55.1)	13 / 31 (41.9)	72 / 170 (42.4)	67 / 92 (72.8)	*12/22 (-)	17 / 54 (31.5)	*3/12 (-)
Trimethoprim-sulfamethoxazole	6126 / 12808 (47.8)	2188 / 4643 (47.1)	97 / 191 (50.8)	165 / 295 (55.9)	218 / 279 (78.1)	36 / 73 (49.3)	139 / 341 (40.8)	227 / 250 (90.8)	25 / 51 (49)	91 / 173 (52.6)	*7/21 (-)

AMA	*Escherichia coli* (N=13627)	*Klebsiella pneumoniae* (N=4958)	*Klebsiella oxytoca* (N=200)	*Klebsiella spp.* (N=338)	*Enterobacter cloacae* (N=314)	*Enterobacter spp.* (N=80)	*Proteus mirabilis* (N=355)	*Citrobacter koseri* (N=258)	*Citrobacter freundii* (N=53)	*Morganella morganii* (N=182)	*Providencia rettgeri* (N=25)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Fosfomycin	11761 / 12188 (96.5)	2568 / 3809 (67.4)	145 / 188 (77.1)	287 / 331 (86.7)	153 / 218 (70.2)	47 / 57 (82.5)	214 / 264 (81.1)	161 / 168 (95.8)	38 / 46 (82.6)	38 / 129 (29.5)	*13/21 (-)
Nitrofurantoin	9683 / 12239 (79.1)	1131 / 4480 (25.2)	101 / 194 (52.1)	205 / 333 (61.6)	101 / 288 (35.1)	22 / 69 (31.9)	-	167 / 233 (71.7)	33 / 51 (64.7)	-	-
Norfloxacin	3540 / 10026 (35.3)	1617 / 3643 (44.4)	70 / 154 (45.5)	238 / 315 (75.6)	196 / 266 (73.7)	32 / 58 (55.2)	140 / 229 (61.1)	162 / 184 (88)	21 / 42 (50)	78 / 151 (51.7)	*8/18 (-)
Minocycline	3984 / 5496 (72.5)	1044 / 2025 (51.6)	67 / 119 (56.3)	212 / 264 (80.3)	44 / 69 (63.8)	*17/27 (-)	22 / 163 (13.5)	77 / 90 (85.6)	*8/17 (-)	12 / 32 (37.5)	*1/11 (-)
Cefoperazone-sulbactam	5397 / 7920 (68.1)	1412 / 2849 (49.6)	68 / 118 (57.6)	121 / 318 (38.1)	126 / 173 (72.8)	34 / 50 (68)	189 / 237 (79.7)	154 / 157 (98.1)	*17/25 (-)	84 / 112 (75)	*12/15 (-)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Escherichia coli* from urine

Fosfomycin demonstrated the highest overall susceptibility among the tested antibiotics, with 96.5% of isolates remaining sensitive, followed by nitrofurantoin (79.1%), meropenem (77.7%), ertapenem (76.7%) and amikacin (74.7%). However, marked resistance was observed to commonly use oral agents, particularly cefazolin (13.9%), ciprofloxacin (14.5%), cefotaxime (20.8%) and levofloxacin (28.3%). Susceptibility to trimethoprim-sulfamethoxazole was also limited (47.8%). Considerable inter-regional variation was evident, with fosfomycin susceptibility remaining consistently high across most RCs (89.7–100%), while susceptibility to ciprofloxacin was generally low, ranging from 2.5% to 40.1%. Carbapenem susceptibility also varied substantially, with meropenem susceptibility ranging from 30.3% in RC1 to 91.7% in RC17. Piperacillin-tazobactam showed moderate overall susceptibility (57.9%), but regional values ranged from 12.7% to 77.2%. Cefoperazone-sulbactam demonstrated 68.1% overall susceptibility, while ceftazidime-avibactam showed 52.9%, with substantial regional variation **(Table 2.15).**

Table 2.15: RC-wise AMS percentages of *Escherichia coli* from urine

RC	Piperacillin-tazobactam (N=13565)	Cefazolin (N=5040)	Cefotaxime (N=9166)	Ertapenem (N=13097)	Imipenem (N=11217)	Meropenem (N=12373)	Amikacin (N=13627)	Ciprofloxacin (N=13627)	Levofloxacin (N=6568)	Trimethoprim-sulfamethoxazole (N=12808)	Fosfomycin (N=12189)	Nitrofurantoin (N=12238)	Norfloxacin (N=10027)	Minocycline (N=5497)	Cefoperazone sulbactam (N=7920)	Ceftazidime avibactam (N=639)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	35/117 (29.9)	18/40 (45)	24/116 (20.7)	46/117 (39.3)	30/107 (28)	33/109 (30.3)	61/117 (52.1)	19/117 (16.2)	26/69 (37.7)	22/43 (51.2)	94/117 (80.3)	98/116 (84.5)	55/117 (47)	3/8 (37.5)	22/35 (62.9)	0/0 (-)
RC4	314/429 (73.2)	0/0 (-)	1/3 (-)	367/429 (85.5)	4/4 (-)	367/429 (85.5)	309/429 (72)	153/429 (35.7)	6/8 (-)	74/143 (51.7)	429/429 (100)	305/429 (71.1)	192/429 (44.8)	0/2 (-)	327/421 (77.7)	0/0 (-)
RC5	131/228 (57.5)	0/0 (-)	5/201 (2.5)	151/225 (67.1)	173/228 (75.9)	171/228 (75)	197/228 (86.4)	14/228 (6.1)	0/0 (-)	109/227 (48)	74/77 (96.1)	146/208 (70.2)	0/0 (-)	0/0 (-)	123/194 (63.4)	0/0 (-)
RC6	717/1102 (65.1)	1/1 (-)	132/659 (20)	888/1104 (80.4)	914/1105 (82.7)	909/1107 (82.1)	870/1106 (78.7)	42/1106 (3.8)	0/1 (-)	436/1080 (40.4)	1071/1097 (97.6)	881/1091 (80.8)	65/228 (28.5)	816/1097 (74.4)	633/836 (75.7)	1/2 (-)
RC7	156/238 (65.5)	1/3 (-)	12/48 (25)	183/232 (78.9)	44/60 (73.3)	113/132 (85.6)	189/241 (78.4)	44/239 (18.4)	7/34 (20.6)	104/230 (45.2)	228/234 (97.4)	159/200 (79.5)	85/156 (54.5)	23/32 (71.9)	27/37 (73)	0/0 (-)
RC8	126/184 (68.5)	0/0 (-)	44/185 (23.8)	150/185 (81.1)	159/184 (86.4)	161/185 (87)	169/185 (91.4)	8/186 (4.3)	8/185 (4.3)	92/184 (50)	180/182 (98.9)	8/8 (-)	4/8 (-)	146/185 (78.9)	107/123 (87)	0/0 (-)
RC9	287/372 (77.2)	124/353 (35.1)	154/377 (40.8)	302/371 (81.4)	298/375 (79.5)	331/378 (87.6)	288/379 (76)	152/379 (40.1)	168/375 (44.8)	201/345 (58.3)	338/364 (92.9)	292/370 (78.9)	109/235 (46.4)	302/372 (81.2)	0/1 (-)	0/0 (-)
RC10	680/938 (72.5)	0/0 (-)	42/114 (36.8)	832/937 (88.8)	851/936 (90.9)	843/936 (90.1)	755/938 (80.5)	238/947 (25.1)	0/0 (-)	499/938 (53.2)	2/2 (-)	799/935 (85.5)	251/823 (30.5)	58/104 (55.8)	704/820 (85.9)	0/0 (-)

RC	Piperacillin-tazobactam (N=13565)	Cefazolin (N=5040)	Cefotaxime (N=9166)	Ertapenem (N=13097)	Imipenem (N=11217)	Meropenem (N=12373)	Amikacin (N=13627)	Ciprofloxacin (N=13627)	Levofloxacin (N=6568)	Trimethoprim-sulfamethoxazole (N=12808)	Fosfomycin (N=12189)	Nitrofurantoin (N=12238)	Norfloxacin (N=10027)	Minocycline (N=5497)	Cefoperazone sulbactam (N=7920)	Ceftazidime avibactam (N=639)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC11	50/118 (42.4)	0/0 (-)	21/117 (17.9)	64/98 (65.3)	63/118 (53.4)	59/118 (50)	55/118 (46.6)	6/118 (5.1)	10/116 (8.6)	36/114 (31.6)	87/92 (94.6)	74/116 (63.8)	10/68 (14.7)	62/115 (53.9)	4/7 (-)	0/0 (-)
RC12	143/280 (51.1)	31/228 (13.6)	23/29 (-)	204/267 (76.4)	190/277 (68.6)	204/263 (77.6)	198/269 (73.6)	18/269 (6.7)	45/257 (17.5)	117/267 (43.8)	255/259 (98.5)	200/265 (75.5)	74/267 (27.7)	5/8 (-)	173/261 (66.3)	9/30 (30)
RC13	167/358 (46.6)	53/131 (40.5)	50/293 (17.1)	171/265 (64.5)	217/368 (59)	232/371 (62.5)	157/370 (42.4)	70/371 (18.9)	93/350 (26.6)	149/326 (45.7)	336/358 (93.9)	250/361 (69.3)	108/345 (31.3)	110/160 (68.8)	83/155 (53.5)	0/0 (-)
RC14	1144/1657 (69)	1/3 (-)	420/1536 (27.3)	1350/1657 (81.5)	1405/1657 (84.8)	1391/1656 (84)	1405/1658 (84.7)	195/1658 (11.8)	252/805 (31.3)	882/1657 (53.2)	1644/1658 (99.2)	1005/1188 (84.6)	408/1188 (34.3)	417/417 (100)	958/1248 (76.8)	7/7 (-)
RC16	484/1376 (35.2)	186/1356 (13.7)	303/1376 (22)	1013/1377 (73.6)	405/1377 (29.4)	1095/1377 (79.5)	1155/1377 (83.9)	323/1377 (23.5)	457/1375 (33.2)	705/1357 (52)	1327/1377 (96.4)	1054/1377 (76.5)	418/989 (42.3)	890/1255 (70.9)	668/910 (73.4)	226/295 (76.6)
RC17	589/845 (69.7)	2/2 (-)	132/478 (27.6)	757/852 (88.8)	784/853 (91.9)	784/855 (91.7)	794/855 (92.9)	53/855 (6.2)	268/407 (65.8)	487/844 (57.7)	666/668 (99.7)	403/440 (91.6)	421/440 (95.7)	354/437 (81)	650/778 (83.5)	2/15 (-)
RC19	463/948 (48.8)	52/915 (5.7)	4/437 (0.9)	552/951 (58)	568/953 (59.6)	594/951 (62.5)	644/953 (67.6)	109/953 (11.4)	156/933 (16.7)	307/902 (34)	846/927 (91.3)	812/947 (85.7)	187/941 (19.9)	52/182 (28.6)	14/184 (7.6)	2/125 (1.6)
RC20	410/625 (65.6)	50/625 (8)	118/625 (18.9)	473/625 (75.7)	403/524 (76.9)	407/523 (77.8)	579/625 (92.6)	83/625 (13.3)	128/625 (20.5)	249/623 (40)	601/625 (96.2)	462/625 (73.9)	92/422 (21.8)	411/625 (65.8)	55/417 (13.2)	0/0 (-)

RC	Piperacillin-tazobactam (N=13565)	Cefazolin (N=5040)	Cefotaxime (N=9166)	Ertapenem (N=13097)	Imipenem (N=11217)	Meropenem (N=12373)	Amikacin (N=13627)	Ciprofloxacin (N=13627)	Levofloxacin (N=6568)	Trimethoprim-sulfamethoxazole (N=12808)	Fosfomycin (N=12189)	Nitrofurantoin (N=12238)	Norfloxacin (N=10027)	Minocycline (N=5497)	Cefoperazone sulbactam (N=7920)	Ceftazidime avibactam (N=639)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC21	27/212 (12.7)	17/285 (6)	4/221 (1.8)	48/75 (64)	90/222 (40.5)	112/225 (49.8)	39/225 (17.3)	27/225 (12)	48/224 (21.4)	101/220 (45.9)	213/223 (95.5)	154/224 (68.8)	23/72 (31.9)	1/4 (-)	34/93 (36.6)	10/43 (23.3)
RC24	142/333 (42.6)	17/210 (8.1)	33/333 (9.9)	218/333 (65.5)	93/165 (56.4)	226/331 (68.3)	141/333 (42.3)	22/333 (6.6)	37/198 (18.7)	81/184 (44)	307/324 (94.8)	287/332 (86.4)	71/312 (22.8)	114/162 (70.4)	176/331 (53.2)	54/76 (71.1)
RC26	277/472 (58.7)	0/0 (-)	0/2 (-)	407/471 (86.4)	98/113 (86.7)	104/162 (64.2)	335/473 (70.8)	59/473 (12.5)	0/13 (-)	202/467 (43.3)	459/462 (99.4)	353/463 (76.2)	114/462 (24.7)	1/5 (-)	2/4 (-)	0/0 (-)
RC27	177/236 (75)	39/227 (17.2)	44/142 (31)	196/224 (87.5)	213/236 (90.3)	212/236 (89.8)	207/236 (87.7)	32/236 (13.6)	2/7 (-)	125/234 (53.4)	219/220 (99.5)	208/233 (89.3)	82/234 (35)	0/0 (-)	199/233 (85.4)	0/0 (-)
RC28	202/366 (55.2)	0/0 (-)	0/0 (-)	257/366 (70.2)	174/258 (67.4)	189/286 (66.1)	270/366 (73.8)	24/366 (6.6)	0/0 (-)	147/365 (40.3)	359/364 (98.6)	151/183 (82.5)	36/183 (19.7)	0/1 (0)	162/271 (59.8)	0/0 (-)
RC29	33/72 (45.8)	6/55 (10.9)	9/71 (12.7)	42/72 (58.3)	45/67 (67.2)	36/63 (57.1)	51/72 (70.8)	4/72 (5.6)	11/62 (17.7)	28/67 (41.8)	71/71 (100)	53/72 (73.6)	16/72 (22.2)	55/64 (85.9)	31/66 (47)	0/0 (-)
RC30	437/635 (68.8)	0/0 (-)	126/385 (32.7)	574/635 (90.4)	11/14 (-)	15/29 (-)	500/635 (78.7)	127/635 (20)	1/13 (-)	418/635 (65.8)	630/635 (99.2)	537/625 (85.9)	236/625 (37.8)	4/4 (-)	11/14 (-)	0/3 (-)
RC31	306/453 (67.5)	0/0 (-)	101/445 (22.7)	372/453 (82.1)	70/84 (83.3)	363/439 (82.7)	324/453 (71.5)	67/453 (14.8)	1/40 (2.5)	204/447 (45.6)	448/453 (98.9)	361/454 (79.5)	126/454 (27.8)	2/2 (-)	12/17 (-)	3/9 (-)

RC	Piperacillin-tazobactam (N=13565)	Cefazolin (N=5040)	Cefotaxime (N=9166)	Ertapenem (N=13097)	Imipenem (N=11217)	Meropenem (N=12373)	Amikacin (N=13627)	Ciprofloxacin (N=13627)	Levofloxacin (N=6568)	Trimethoprim-sulfamethoxazole (N=12808)	Fosfomycin (N=12189)	Nitrofurantoin (N=12238)	Norfloxacin (N=10027)	Minocycline (N=5497)	Cefoperazone sulbactam (N=7920)	Ceftazidime avibactam (N=639)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC32	185/478 (38.7)	32/448 (7.1)	54/470 (11.5)	133/271 (49.1)	300/481 (62.4)	352/482 (73)	143/482 (29.7)	12/482 (2.5)	56/245 (22.9)	146/472 (30.9)	427/476 (89.7)	232/476 (48.7)	111/473 (23.5)	23/81 (28.4)	111/218 (50.9)	0/0 (-)
RC33	108/277 (39)	0/0 (-)	29/276 (10.5)	179/277 (64.6)	161/250 (64.4)	180/275 (65.5)	211/277 (76.2)	38/277 (13.7)	2/26 (-)	91/243 (37.4)	254/277 (91.7)	211/275 (76.7)	64/277 (23.1)	0/0 (-)	14/30 (46.7)	0/0 (-)
RC34	64/226 (28.3)	72/158 (45.6)	20/226 (8.8)	119/227 (52.4)	113/206 (54.9)	136/227 (59.9)	132/227 (58.1)	44/227 (19.4)	75/197 (38.1)	114/194 (58.8)	196/217 (90.3)	188/226 (83.2)	182/206 (88.3)	135/174 (77.6)	97/216 (44.9)	24/34 (70.6)
Total	7854/ 13565 (57.9)	702/ 5040 (13.9)	1905/ 9166 (20.8)	10048/ 13097 (76.7)	7876/11222 (70.2)	9619/12373 (77.7)	10178/13627 (74.7)	1983/13627 (14.5)	1857/6568 (28.3)	6126/12808 (47.8)	11761/ 12189 (96.5)	9683/12238 (79.1)	3540/10027 (35.3)	3984/5497 (72.5)	5397/7920 (68.1)	338/639 (52.9)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Klebsiella pneumoniae* from urine

Klebsiella pneumoniae isolates from urine demonstrated low susceptibility to commonly used agents, particularly cefazolin (18.3%), cefotaxime (26.1%), ciprofloxacin (25.7%), and nitrofurantoin (25.3%). Carbapenems demonstrated only moderate activity, with susceptibility rates of 52.4% for ertapenem, 44.8% for imipenem, and 51.8% for meropenem, indicating substantial carbapenem resistance. Amikacin retained moderate activity (52.3%), while trimethoprim-sulfamethoxazole showed susceptibility of 47.1%. Regional variation was pronounced, with several centers showing particularly low susceptibility to β-lactams, fluoroquinolones, and carbapenems, whereas higher susceptibility was observed in selected centers. Cefoperazone-sulbactam showed moderate overall activity (49.6%), while minocycline demonstrated 51.6% susceptibility. Ceftazidime-avibactam showed relatively limited overall susceptibility (39.5%), although interpretation should consider the smaller number of isolates tested. These findings indicate a multidrug-resistant *K. pneumoniae* population with limited therapeutic options, highlighting the importance of species-specific susceptibility data to guide appropriate management of urinary tract infections **(Table 2.16).**

Table 2.16: RC-wise AMS percentages of *Klebsiella pneumoniae* from urine

RC	Piperacillin-tazobactam (N=4932)	Cefazolin (N=1805)	Cefotaxime (N=3265)	Ertapenem (N=4744)	Imipenem (N=4102)	Meropenem (N=4592)	Amikacin (N=4947)	Ciprofloxacin (N=4947)	Levofloxacin (N=2439)	Trimethoprim-sulfamethoxazole	Fosfomycin (N=3809)	Nitrofurantoin (N=4479)	Norfloxacin (N=3642)	Minocycline (N=2025)	Cefoperazone sulbactam (N=2848)	Ceftazidime avibactam (N=339)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	6/47 (12.8)	4/14 (-)	6/47 (12.8)	10/47 (21.3)	6/43 (14)	7/44 (15.9)	12/47 (25.5)	4/47 (8.5)	6/32 (18.8)	9/19 (-)	33/44 (75)	28/47 (59.6)	12/47 (25.5)	1/3 (-)	7/16 (-)	0/0 (-)
RC4	88/154 (57.1)	0/0 (-)	0/1 (0)	107/154 (69.5)	¾ (-)	107/154 (69.5)	78/154 (50.6)	67/154 (43.5)	3/8 (-)	23/44 (52.3)	148/154 (96.1)	43/154 (27.9)	93/154 (60.4)	0/0 (-)	95/151 (62.9)	0/0 (-)
RC5	55/134 (41)	0/0 (-)	12/74 (16.2)	72/133 (54.1)	76/132 (57.6)	77/134 (57.5)	81/134 (60.4)	36/134 (26.9)	0/0 (-)	62/131 (47.3)	46/70 (65.7)	21/131 (16)	0/0 (-)	0/0 (-)	58/118 (49.2)	0/0 (-)
RC6	110/417 (26.4)	0/0 (-)	48/255 (18.8)	148/417 (35.5)	156/417 (37.4)	161/417 (38.6)	150/417 (36)	65/417 (15.6)	0/0 (-)	159/410 (38.8)	225/409 (55)	53/411 (12.9)	21/98 (21.4)	185/414 (44.7)	106/307 (34.5)	2/10 (-)
RC7	44/86 (51.2)	0/2 (-)	8/21 (-)	53/84 (63.1)	16/28 (-)	46/58 (79.3)	59/88 (67)	32/88 (36.4)	5/17 (-)	55/86 (64)	57/87 (65.5)	27/68 (39.7)	43/53 (81.1)	9/16 (-)	11/22 (-)	0/0 (-)
RC8	34/90 (37.8)	0/0 (-)	26/90 (28.9)	43/90 (47.8)	41/90 (45.6)	44/90 (48.9)	48/90 (53.3)	19/90 (21.1)	20/90 (22.2)	33/90 (36.7)	65/90 (72.2)	0/2 (-)	1/1 (-)	56/90 (62.2)	29/61 (47.5)	0/0 (-)
RC9	69/105 (65.7)	38/96 (39.6)	50/102 (49)	61/97 (62.9)	62/105 (59)	74/106 (69.8)	60/106 (56.6)	47/106 (44.3)	56/103 (54.4)	57/102 (55.9)	76/99 (76.8)	34/101 (33.7)	41/70 (58.6)	79/105 (75.2)	1/1 (-)	0/0 (-)

RC	Piperacillin-tazobactam (N=4932)	Cefazolin (N=1805)	Cefotaxime (N=3265)	Ertapenem (N=4744)	Imipenem (N=4102)	Meropenem (N=4592)	Amikacin (N=4947)	Ciprofloxacin (N=4947)	Levofloxacin (N=2439)	Trimethoprim-sulfamethoxazole	Fosfomycin (N=3809)	Nitrofurantoin (N=4479)	Norfloxacin (N=3642)	Minocycline (N=2025)	Cefoperazone sulbactam (N=2848)	Ceftazidime avibactam (N=339)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC10	166/354 (46.9)	0/0 (-)	19/42 (45.2)	222/354 (62.7)	228/354 (64.4)	228/354 (64.4)	219/355 (61.7)	110/357 (30.8)	0/0 (-)	190/353 (53.8)	0/0 (-)	46/352 (13.1)	112/310 (36.1)	48/131 (36.6)	172/309 (55.7)	0/0 (-)
RC11	11/113 (9.7)	0/0 (-)	11/113 (9.7)	15/65 (23.1)	20/112 (17.9)	18/113 (15.9)	15/113 (13.3)	6/113 (5.3)	9/111 (8.1)	26/111 (23.4)	14/38 (36.8)	5/112 (4.5)	9/55 (16.4)	14/112 (12.5)	1/4 (-)	0/0 (-)
RC12	38/86 (44.2)	19/61 (31.1)	4/7 (-)	50/80 (62.5)	46/84 (54.8)	49/82 (59.8)	47/82 (57.3)	24/82 (29.3)	24/76 (31.6)	39/81 (48.1)	54/74 (73)	18/78 (23.1)	36/75 (48)	2/2 (-)	45/80 (56.3)	6/21 (-)
RC13	59/203 (29.1)	46/118 (39)	28/168 (16.7)	68/168 (40.5)	75/206 (36.4)	86/206 (41.7)	51/206 (24.8)	34/206 (16.5)	51/203 (25.1)	78/186 (41.9)	76/165 (46.1)	34/202 (16.8)	67/192 (34.9)	50/108 (46.3)	44/105 (41.9)	0/0 (-)
RC14	275/542 (50.7)	1/1 (-)	222/505 (44)	313/541 (57.9)	315/541 (58.2)	324/542 (59.8)	330/542 (60.9)	186/542 (34.3)	124/267 (46.4)	296/541 (54.7)	450/536 (84)	141/400 (35.3)	190/400 (47.5)	131/131 (100)	244/414 (58.9)	1/3 (-)
RC16	158/595 (26.6)	93/588 (15.8)	175/594 (29.5)	284/595 (47.7)	114/594 (19.2)	321/595 (53.9)	349/595 (58.7)	151/595 (25.4)	232/595 (39)	307/585 (52.5)	396/595 (66.6)	189/595 (31.8)	236/463 (51)	254/524 (48.5)	242/437 (55.4)	97/159 (61)
RC17	105/188 (55.9)	0/0 (-)	25/106 (23.6)	135/191 (70.7)	137/191 (71.7)	138/191 (72.3)	168/191 (88)	65/191 (34)	54/79 (68.4)	102/170 (60)	108/130 (83.1)	64/81 (79)	78/81 (96.3)	66/83 (79.5)	120/165 (72.7)	2/9 (-)
RC19	143/356 (40.2)	40/336 (11.9)	2/168 (1.2)	159/356 (44.7)	160/357 (44.8)	174/357 (48.7)	154/357 (43.1)	53/357 (14.8)	114/349 (32.7)	121/336 (36)	108/216 (50)	143/355 (40.3)	117/350 (33.4)	14/58 (24.1)	13/84 (15.5)	0/44 (-)

RC	Piperacillin-tazobactam (N=4932)	Cefazolin (N=1805)	Cefotaxime (N=3265)	Ertapenem (N=4744)	Imipenem (N=4102)	Meropenem (N=4592)	Amikacin (N=4947)	Ciprofloxacin (N=4947)	Levofloxacin (N=2439)	Trimethoprim-sulfamethoxazole	Fosfomycin (N=3809)	Nitrofurantoin (N=4479)	Norfloxacin (N=3642)	Minocycline (N=2025)	Cefoperazone sulbactam (N=2848)	Ceftazidime avibactam (N=339)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC20	41/135 (30.4)	7/135 (5.2)	27/135 (20)	48/135 (35.6)	49/113 (43.4)	50/114 (43.9)	55/ 135 (40.7)	23/ 135 (17)	35/ 135 (25.9)	47/ 135 (34.8)	89/ 135 (65.9)	28/ 135 (20.7)	27/91 (29.7)	63/ 135 (46.7)	13/87 (14.9)	0/0 (-)
RC21	9/86 (10.5)	11/115 (9.6)	2/87 (2.3)	23/41 (56.1)	24/87 (27.6)	27/88 (30.7)	12/88 (13.6)	12/88 (13.6)	32/88 (36.4)	49/84 (58.3)	32/86 (37.2)	18/86 (20.9)	20/39 (51.3)	0/1 (0)	14/49 (28.6)	6/2 9 (-)
RC24	22/70 (31.4)	4/48 (8.3)	4/70 (5.7)	31/70 (44.3)	18/43 (41.9)	35/70 (50)	17/70 (24.3)	8/70 (11.4)	12/50 (24)	15/44 (34.1)	22/51 (43.1)	23/70 (32.9)	18/65 (27.7)	22/43 (51.2)	25/69 (36.2)	11/27 (-)
RC26	93/193 (48.2)	1/1 (100)	0/2 (-)	139/19 3 (72)	15/24 (-)	32/86 (37.2)	126/1 94 (64.9)	64/19 4 (33)	0/14 (-)	89/18 6 (47.8)	138/1 83 (75.4)	24/18 9 (12.7)	98/18 9 (51.9)	1/1 (-)	0/2 (0)	0/1 (0)
RC27	57/145 (39.3)	25/135 (18.5)	23/75 (30.7)	74/139 (53.2)	83/145 (57.2)	85/145 (58.6)	85/14 5 (58.6)	38/14 5 (26.2)	0/0 (-)	67/14 4 (46.5)	92/13 0 (70.8)	35/14 5 (24.1)	43/14 5 (29.7)	0/0 (-)	71/13 9 (51.1)	1/1 (-)
RC28	60/133 (45.1)	0/0 (-)	0/0 (-)	70/134 (52.2)	50/108 (46.3)	48/109 (44)	74/13 4 (55.2)	36/13 4 (26.9)	0/0 (-)	57/13 3 (42.9)	100/1 32 (75.8)	23/64 (35.9)	34/64 (53.1)	0/0 (-)	47/10 7 (43.9)	0/0 (-)
RC29	10/25 (-)	8/22 (-)	11/25 (-)	15/25 (-)	14/24 (-)	14/25 (-)	16/25 (-)	5/25 (-)	11/21 (-)	10/22 (-)	20/22 (-)	10/25 (-)	14/25 (-)	21/21 (-)	11/21 (-)	0/0 (-)
RC30	134/ 208 (64.4)	0/0 (-)	73/115 (63.5)	165/ 208 (79.3)	3/6 (-)	4/43 (9.3)	168/ 208 (80.8)	109/ 208 (52.4)	1/18 (-)	147/ 208 (70.7)	11/11 (-)	33/20 5 (16.1)	136/ 203 (67)	0/0 (-)	0/3 (-)	5/15 (-)

RC	Piperacillin-tazobactam (N=4932)	Cefazolin (N=1805)	Cefotaxime (N=3265)	Ertapenem (N=4744)	Imipenem (N=4102)	Meropenem (N=4592)	Amikacin (N=4947)	Ciprofloxacin (N=4947)	Levofloxacin (N=2439)	Trimethoprim-sulfamethoxazole	Fosfomycin (N=3809)	Nitrofurantoin (N=4479)	Norfloxacin (N=3642)	Minocycline (N=2025)	Cefoperazone sulbactam (N=2848)	Ceftazidime avibactam (N=339)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC31	74/195 (37.9)	0/0 (-)	48/190 (25.3)	99/195 (50.8)	14/32 (43.8)	98/193 (50.8)	98/ 195 (50.3)	47/ 195 (24.1)	2/80 (2.5)	70/ 194 (36.1)	128/ 189 (67.7)	21/ 195 (10.8)	76/19 5 (39)	0/1 (0)	1/5 (-)	2/19 (-)
RC32	32/124 (25.8)	19/108 (17.6)	22/120 (18.3)	32/79 (40.5)	71/125 (56.8)	80/125 (64)	50/12 5 (40)	8/125 (6.4)	31/71 (43.7)	50/ 120 (41.7)	62/ 122 (50.8)	28/ 124 (22.6)	46/ 125 (36.8)	13/29 (-)	29/62 (46.8)	0/0 (-)
RC33	24/136 (17.6)	0/0 (-)	6/136 (4.4)	46/136 (33.8)	38/122 (31.1)	44/134 (32.8)	56/ 136 (41.2)	17/ 136 (12.5)	4/15 (-)	20/11 1 (18)	10/24 (-)	29/ 136 (21.3)	36/ 136 (26.5)	0/0 (-)	7/14 (-)	0/0 (-)
RC34	5/17 (-)	15/25 (-)	1/17 (-)	6/17 (-)	4/17 (-)	7/17 (-)	12/17 (-)	4/17 (-)	10/17 (-)	10/17 (-)	8/17 (-)	13/17 (-)	13/17 (-)	15/17 (-)	6/17 (-)	1/1 (-)
Total	1922/ 4932 (38.9)	331/ 1805 (18.3)	853/ 3265 (26.1)	2488/ 4744 (52.4)	1838/ 4102 (44.8)	2378/ 4592 (51.8)	2590/ 4947 (52.3)	1270/ 4947 (25.7)	836/2 439 (34.3)	2188/ 4643 (47.1)	2568/ 3809 (67.4)	1131/ 4479 (25.3)	1617/ 3642 (44.4)	1044/ 2025 (51.6)	1412/ 2848 (49.6)	134/ 339 (39.5)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Yearly susceptibility trends of different Enterobacterales from urine samples

Over the nine-year period from 2017 to 2025, urinary isolates of *Escherichia coli* and *Klebsiella pneumoniae* demonstrated substantial antimicrobial resistance, with generally low susceptibility to third-generation cephalosporins and fluoroquinolones and a progressive decline in susceptibility to several key antimicrobial agents **(Tables 2.17-2.18 and Figure 2.5-2.6).** In *E. coli*, susceptibility to piperacillin-tazobactam declined from 73.7% in 2017 to 57.9% in 2025, while cefazolin remained consistently low, declining from 23.7% to 10.2%. Cefotaxime susceptibility remained poor throughout the period, ranging from 20.8% to 28.7%, whereas ceftazidime showed an apparent increase in susceptibility from 21.8% in 2022 to 39.9% in 2025. Carbapenems retained comparatively higher activity, although susceptibility to imipenem decreased from 88.3% in 2017 to 70.2% in 2025, while meropenem decreased from 80.8% to 77.7%. Amikacin susceptibility also declined from 86.4% in 2017 to 74.7% in 2025. Fluoroquinolone susceptibility remained low, with ciprofloxacin declining from 24.0% to 14.5%, while levofloxacin showed a relatively stable but poor susceptibility of 28.3% in 2025. In contrast, trimethoprim-sulfamethoxazole showed a gradual improvement from 35.4% to 47.8%. Fosfomycin remained highly active, with susceptibility increasing from 82.2% in 2017 to 96.5% in 2025, while nitrofurantoin, despite a decline from 88.3% to 79.1%, continued to retain better efficacy.

In *K. pneumoniae*, susceptibility was generally lower than that observed in *E. coli*, particularly for β-lactams, carbapenems, aminoglycosides, and urinary antimicrobials. Piperacillin-tazobactam susceptibility decreased from 52.5% in 2017 to 38.9% in 2025, while cefazolin remained consistently poor, with susceptibility of only 18.4% in 2025. Cefotaxime susceptibility remained low throughout, ranging between 21.9% and 29.1%, although ceftazidime showed an increase to 36.7% in 2025. Carbapenem susceptibility demonstrated a marked decline compared with 2017 levels: imipenem decreased from 70.8% to 44.7%, while meropenem declined from 56.3% to 51.7%. Amikacin susceptibility also remained relatively low, decreasing from 56.9% in 2017 to 52.3% in 2025. Fluoroquinolone susceptibility was poor, with ciprofloxacin declining from 33.5% in 2017 to 25.6% in 2025, whereas levofloxacin, after reaching a low of 14.7% in 2023, increased to 34.2% in 2025. Trimethoprim-sulfamethoxazole showed moderate susceptibility (47.1%), while nitrofurantoin remained ineffective with susceptibility declining from 37.6% in 2017 to 25.2% in 2025.

In summary, *E. coli* demonstrated higher antimicrobial susceptibility than *K. pneumoniae* for most of the commonly tested agents. Both organisms showed concerning reductions in susceptibility to piperacillin-tazobactam, carbapenems, and amikacin over the study period, while fluoroquinolone susceptibility remained consistently low. In 2025*, K. pneumoniae* showed relatively high susceptibility to tigecycline (84.8%) but moderate susceptibility to ceftazidime-avibactam (39.5%); these findings should be interpreted according to their clinical use and are not directly comparable with routine oral UTI treatment options.

Table 2.17: Yearly susceptibility trend of *E. coli* isolated from urine

AMA	Year-2017 N=4087 (S%)	Year-2018 N=9972 (S%)	Year-2019 N=17291 (S%)	Year-2020 N=8201 (S%)	Year-2021 N=10096 (S%)	Year-2022 N=11781 (S%)	Year-2023 N=10042 (S%)	Year-2024 N=13476 (S%)	Year-2025 N=13627 (S%)
Piperacillin-tazobactam	2966/4024 (73.7)	6407/9586 (66.8)	10945/15900 (68.8)	5184/7660 (67.7)	6110/9648 (63.3)	6600/11723 (56.3)	3277/5845 (56.1)	5182/9269 (55.9)	7854 / 13575 (57.9)
Cefazolin	448/1890 (23.7)	1472/5282 (27.9)	1442/6071 (23.8)	606/2720 (22.3)	661/3169 (20.9)	964/4794 (20.1)	255/2446 (10.4)	453/3727 (12.2)	351 / 3437 (10.2)
Cefotaxime	976/3982 (24.5)	2239/8981 (24.9)	3553/14042 (25.3)	1584/6664 (23.8)	1933/7852 (24.6)	3194/11123 (28.7)	1253/5356 (23.4)	1913/7422 (25.8)	1905 / 9165 (20.8)
Ceftazidime	*1/10 (-)	*0/2 (-)	*0/3 (-)	*1/2 (-)	*1/2 (-)	701/3222 (21.8)	727/3289 (22.1)	1600/4722 (33.9)	3012 / 7553 (39.9)
Ertapenem	3216/3960 (81.2)	6518/9014 (72.3)	10265/13597 (75.5)	5133/6541 (78.5)	6156/7881 (78.1)	6997/9306 (75.2)	3639/4972 (73.2)	6975/9066 (76.9)	10048 / 13096 (76.7)
Imipenem	3533/3999 (88.3)	7109/9655 (73.6)	10630/14658 (72.5)	6206/7785 (79.7)	7398/9595 (77.1)	9105/11577 (78.6)	4055/5630 (72.0)	5989/8708 (68.8)	7876 / 11222 (70.2)
Meropenem	3234/4002 (80.8)	6716/9222 (72.8)	12608/15418 (81.8)	6007/7279 (82.5)	7443/9122 (81.6)	9513/11564 (82.3)	4526/5859 (77.2)	7476/10241 (73)	9619 / 12373 (77.7)
Amikacin	3524/4081 (86.4)	8018/9657 (83)	13598/16448 (82.7)	6834/8131 (84)	8384/10043 (83.5)	10058/11743 (85.7)	4163/5858 (71.1)	10221/13476 (75.8)	10178 / 13627 (74.7)
Ciprofloxacin	952/3971 (24)	2523/9069 (27.8)	4176/15441 (27)	2105/7364 (28.6)	2514/8986 (28)	2151/11680 (18.4)	1050/5858 (17.9)	3020/13476 (22.4)	1983 / 13636 (14.5)
Levofloxacin	675/2375 (28.4)	1700/6440 (26.4)	2166/8348 (25.9)	945/3676 (25.7)	1081/4408 (24.5)	1192/5151 (23.1)	517/2752 (18.8)	951/4330 (22.0)	1857 / 6565 (28.3)
Trimethoprim-sulfamethoxazole	1396/3946 (35.4)	3486/8807 (39.6)	6569/15285 (43)	2863/6656 (43)	3621/8509 (42.6)	4433/10383 (42.7)	2334/4954 (47.1)	4486/9094 (49.3)	6126 / 12808 (47.8)
Fosfomycin	678/825 (82.2)	2739/3103 (88.3)	7466/7657 (97.5)	3599/3691 (97.5)	4192/4319 (97.1)	6862/7101 (96.6)	3477/3711 (93.7)	6288/6821 (92.2)	11761 / 12188 (96.5)
Nitrofurantoin	3556/4025 (88.3)	8389/9745 (86.1)	13892/16727 (83.1)	6572/7935 (82.8)	7490/9064 (82.6)	9282/10287 (90.2)	4289/4999 (85.8)	8981/11119 (80.8)	9683 / 12239 (79.1)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

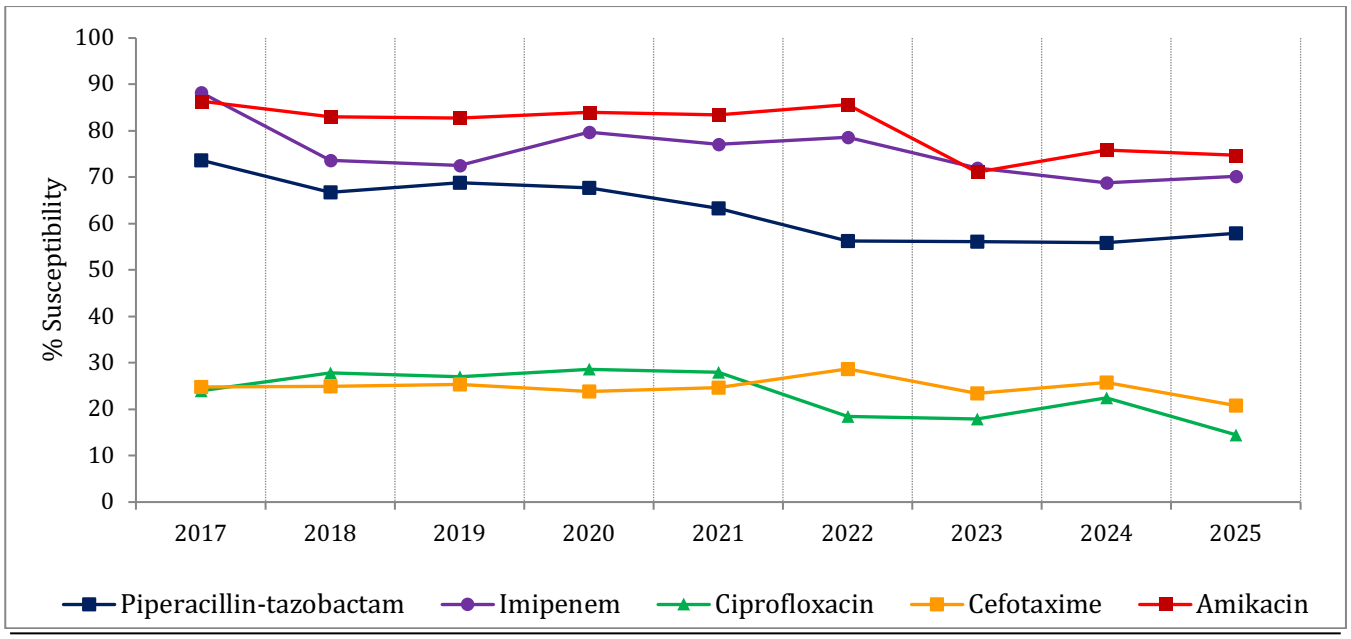


Figure 2.5: Yearly susceptibility trends of *E. coli* isolated from urine

Table 2.18: Yearly susceptibility trends of *K. pneumoniae* isolated from urine

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=1336	N=2626	N=5027	N=2860	N=3583	N=3825	N=3496	N=4875	N=4958
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	692/1317 (52.5)	1180/2527 (46.7)	2290/4602 (49.8)	1241/2655 (46.7)	1405/3403 (41.3)	1396/3806 (36.7)	671/1998 (33.6)	1182/3499 (33.8)	1923/4942 (38.9)
Cefazolin	141/531 (26.6)	371/1315 (28.2)	472/1756 (26.9)	184/893 (20.6)	1970/3560 (55.3)	347/1521 (22.8)	72/824 (8.7)	169/1283 (13.2)	332/1806 (18.4)
Cefotaxime	353/1292 (27.3)	646/2378 (27.2)	1189/4080 (29.1)	592/2250 (26.3)	756/2653 (28.5)	1017/3490 (29.1)	390/1782 (21.9)	799/2764 (28.9)	853/3274 (26.1)
Ceftazidime	*2/10 (-)	*0/1 (-)	*0/2 (-)	*0/3 (-)	*1/10 (-)	281/1202 (23.4)	214/1193 (17.9)	468/1858 (25.2)	1020/2778 (36.7)
Ertapenem	714/1287 (55.5)	1270/2428 (52.3)	2293/4114 (55.7)	1228/2304 (53.3)	1447/2834 (51.1)	1504/3018 (49.8)	744/1712 (43.5)	1637/3305 (49.5)	2489/4754 (52.4)
Imipenem	927/1310 (70.8)	1546/2570 (60.2)	2652/4386 (60.5)	1603/2708 (59.2)	1841/3387 (54.4)	2019/3741 (54)	796/1931 (41.2)	1388/3244 (42.8)	1838/4111 (44.7)
Meropenem	739/1312 (56.3)	1305/2380 (54.8)	2731/4311 (63.3)	1489/2419 (61.6)	1776/3180 (55.8)	2096/3736 (56.1)	903/2006 (45.0)	1981/4078 (48.6)	2379/4601 (51.7)
Amikacin	758/1333 (56.9)	1535/2555 (60.1)	2924/4808 (60.8)	1664/2823 (58.9)	1970/3560 (55.3)	2165/3808 (56.9)	890/2006 (44.4)	2435/4871 (50.0)	2591/4956 (52.3)
Ciprofloxacin	445/1327 (33.5)	884/2364 (37.4)	1766/4353 (40.6)	991/2461 (40.3)	1121/3047 (36.8)	944/3787 (24.9)	410/2005 (20.4)	1363/4850 (28.1)	1271/4957 (25.6)
Levofloxacin	295/662 (44.6)	594/1631 (36.4)	971/2517 (38.6)	440/1348 (32.6)	483/1687 (28.6)	503/1771 (28.4)	159/1078 (14.7)	415/1656 (25.1)	836/2447 (34.2)
Trimethoprim-sulfamethoxazole	443/1291 (34.3)	969/2417 (40.1)	1962/4545 (43.2)	946/2330 (40.6)	1258/3117 (40.4)	1406/3427 (41)	689/1722 (40.0)	1537/3417 (45.0)	2191/4652 (47.1)
Nitrofurantoin	491/1307 (37.6)	954/2566 (37.2)	1541/4856 (31.7)	896/2716 (33)	841/3123 (26.9)	1297/3272 (39.6)	607/1655 (36.7)	736/3479 (21.2)	1132/4487 (25.2)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

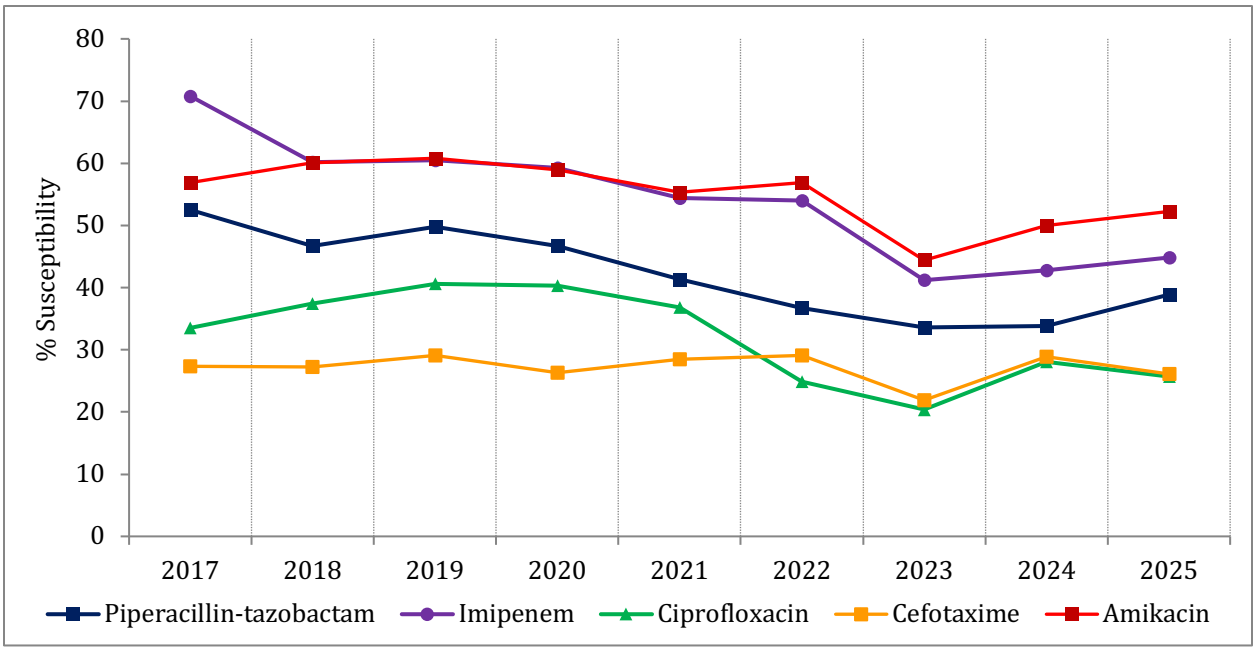


Figure 2.6: Yearly susceptibility trend of *K. pneumoniae* isolated from urine

Molecular characterisation

Six hundred six (606) *E. coli* isolates were subjected to four multiplex PCRs and three monoplex PCRs for OXA-48, CTXM-15 and NDM. Overall, TEM (21%) was the most common, followed by CTXM-1 (13.0%), OXA-1, OXA-48 and NDM-1 (12.0% each), SHV (6.0%), VIM (6.0%) IMP (4.0%), CTXM-2 (4.0%), CTXM-9 (3.0%), MOX (2.0%), DHA (2.0%), ACC and FOX (1.0% each) and KPC (1.0%) **(Figures 2.7, Table 2.19 and Figure 2.8).** The *E. coli* isolates received from RC1 were mainly positive for CTXM-1 (36.4%), TEM (27.3%); and VIM (18.2%); the remaining genes showed less than 10% presence. The isolates from RC2 also showed maximum positivity for CTXM-1 (30%), TEM (26.7%), OXA-48 (16.7%), CTXM-9 (13.3%), NDM-1 (11.7%), and SHV, OXA-1, CTXM-2, ACC, FOX, MOX, DHA, IMP, VIM, AND KPC, at less than 10%. The majority of RC3 isolates were positive for TEM (40%), NDM (22.5%), OXA-48 (16.3%), OXA-1 (12.5%), and CTXM-1 (11.1%), with the remaining genes detected in fewer than 10% of isolates.

Similarly, the RC4 isolates were found to be less than 10%. RC5 isolates showed only NDM (37.5%), TEM (34.4%), OXA-48 (18.8%), CTXM-9 (15.6%), CTXM (12.5%) and other genes at less than 10%. RC6 isolates showed OXA-1 (18.9%), followed by VIM (17.6%), TEM (13.5%) and CTXM-1 (12.2%) with the remaining genes detected in fewer than 10% of isolates. The RC8 isolates were positive for TEM (28.9%), OXA-48 (15.6%), and DHA (11.1%) with the remaining genes detected in fewer than 10% of isolates. In RC9, TIM was detected in 23.3% of isolates, CTXM-2 in 18.3%, SHV in 11.7%, and other are less than 10%. RC11 showed high positivity for OXA-48 (33.3%), TEM (28.6%), followed by NDM, IMP and CTXM-1 (23.8%) and VIM (14.3%). RC12 isolates were maximally positive for OXA-1 (57.8%), followed by CTXM-1 (31.1%), TEM (22.2%), NDM-1 (15.6%) and CTXM-2 and SHV (11.1%). The RC14 isolates showed positivity for OXA-48 (29.8%), TEM (43%), NDM (17.4%) and OXA-1 (12.8%), and the remaining genes showed lower prevalence (less than 10%). In RC17 isolates, CTXM-1 (20.7%) was the most common, followed by OXA-48 (13.8%) and the remaining genes showed lower prevalence (less than 10%). In RC19 samples, OXA-48, TEM and NDM (25% each) had the highest prevalence. Among the RC20 samples, the TEM resistance gene was found in 20% of cases, while NDM, and TEM resistance genes were present in 13.3% of isolates. In the RC21 samples, TEM (30%), followed by OXA-48, VIM and KPC at 20% and remaining genes are less than 10%. In the RC27 samples, VIM had the highest prevalence at 31.6% each, followed by IMP (26.3%), CTXM-1 (21.1%) and TEM and NDM at 10.5% each.The predominant resistance genes in RC18 samples were NDM-1 (80%), followed by CTXM-15 and SHV at 13% each. RC28 samples showed a higher prevalence of OXA-1 (54.5%), TEM (50%), followed by CTXM-1 (40.9%), and NDM (18.2%). And the last RC30 isolates showed the presence of VIM (50%), IMP (41.7%), and OXA-48 at 25% each.

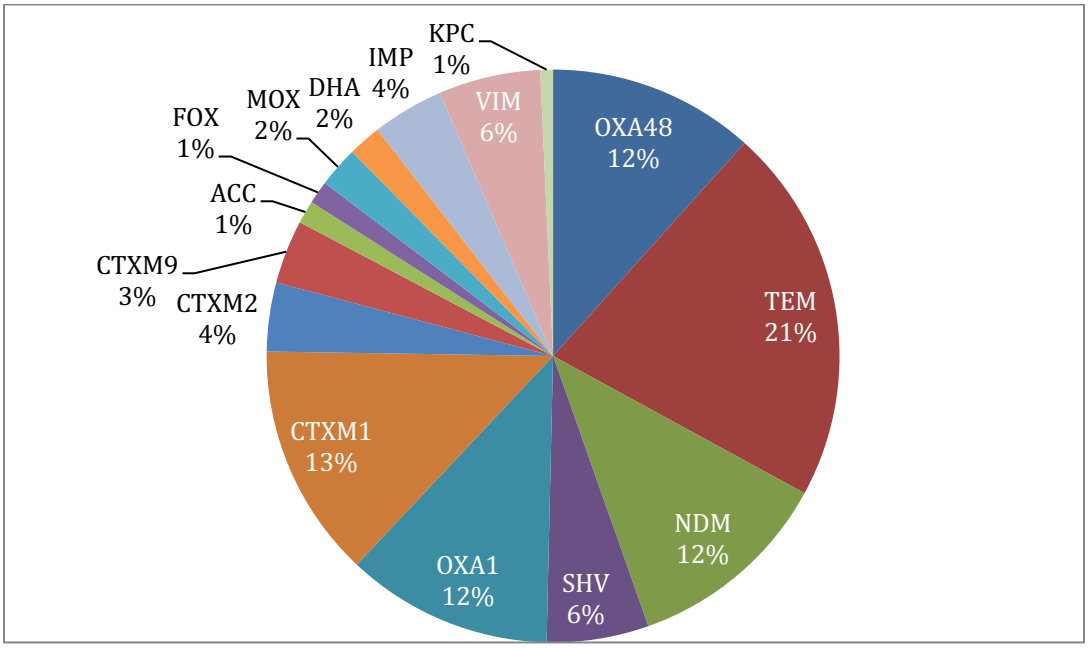
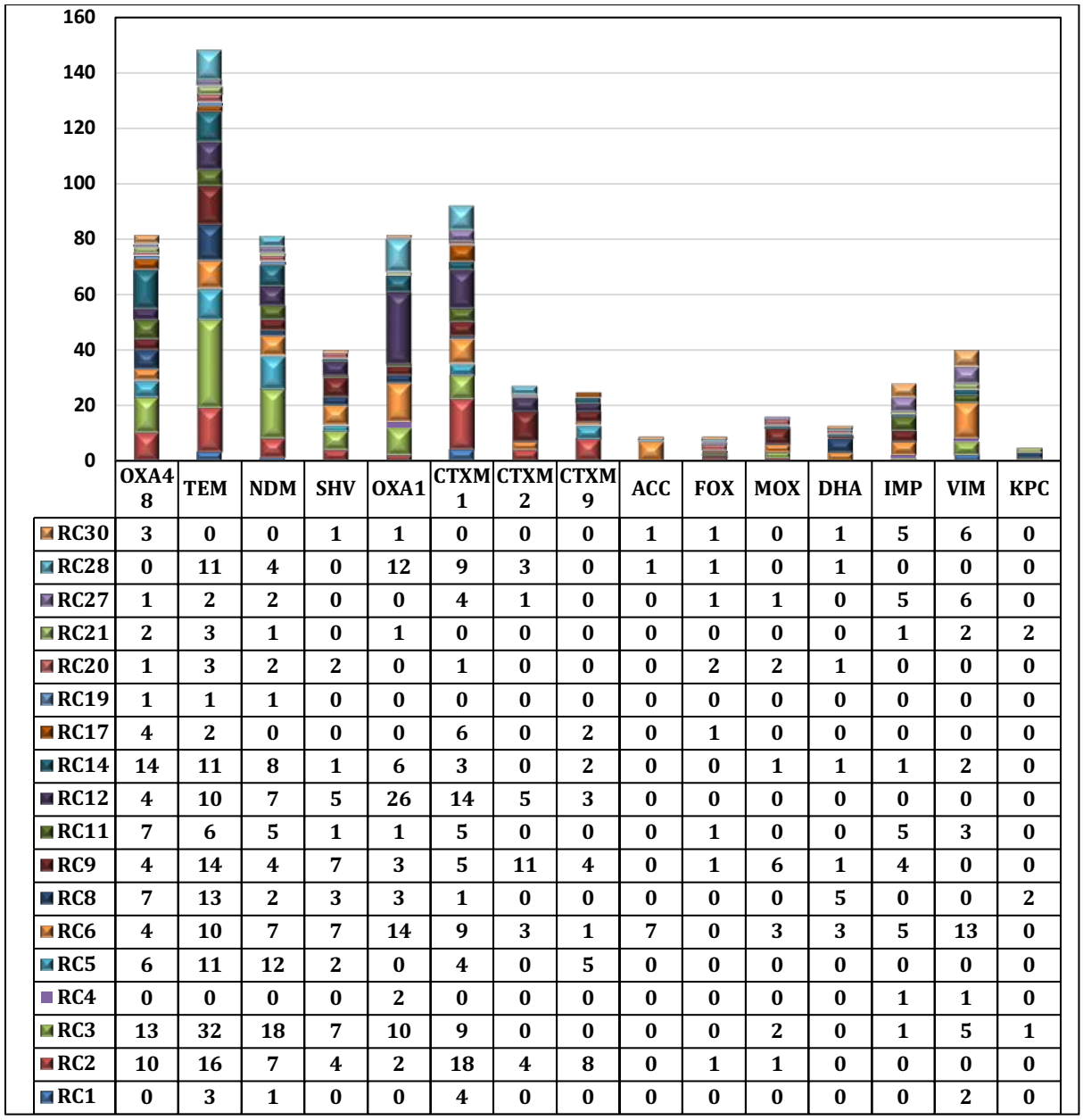


Figure 2.7: Percentage positivity of AMR associated genetic determinants in *E. coli* (2025)

In *E. coli* isolates, TEM gene was the predominant gene present in 21% of the isolates, CTXM-1 in 13% followed by NDM and OXA 48 in 12% of the isolates. The genes encoding for AmpC β-lactamases were the least prevalent.

Table 2.19: Percentage positivity of resistant genes in *E. coli* from each centre

RC	Antimicrobial Resistance Genes														
	OXA 48	TEM	NDM	SHV	OXA 1	CTX M1	CTX M2	CTX M9	ACC	FOX	MOX	DHA	IMP	VIM	KPC
RC1	0	27.3	9.1	0.0	0.0	36.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	18.2	0
RC2	16.7	26.7	11.7	6.7	3.3	30.0	6.7	13.3	0.0	1.7	1.7	0.0	0.0	0.0	0
RC3	16.3	40	22.5	8.75	12.5	11.2	0	0	0.0	0.0	2.5	0.0	1.3	6.3	1.3
RC4	0	0	0	0	10	0	0	0	0.0	0.0	0.0	0.0	5.0	5.0	0
RC5	18.8	34.4	37.5	6.25	0	12.5	0	15.6	0.0	0.0	0.0	0.0	0.0	0.0	0
RC6	5.4	13.5	9.5	9.5	18.9	12.2	4.1	1.4	9.5	0.0	4.1	4.1	6.8	17.6	0
RC8	15.6	28.9	4.4	6.7	6.7	2.2	0.0	0.0	0.0	0.0	0.0	11.1	0.0	0.0	4.4
RC9	6.7	23.3	6.7	11.7	5.0	8.3	18.3	6.7	0.0	1.7	10.0	1.7	6.7	0.0	0
RC11	33.3	28.6	23.8	4.8	4.8	23.8	0.0	0.0	0.0	4.8	0.0	0.0	23.8	14.3	0
RC12	8.9	22.2	15.6	11.1	57.8	31.1	11.1	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0
RC14	29.8	23.4	17.0	2.1	12.8	6.4	0.0	4.3	0.0	0.0	2.1	2.1	2.1	4.3	0
RC17	13.8	6.9	0.0	0.0	0.0	20.7	0.0	6.9	0.0	3.4	0.0	0.0	0.0	0.0	0
RC19	25	25	25	0	0	0	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0
RC20	6.7	20.0	13.3	13.3	0.0	6.7	0	0	0.0	13.3	13.3	6.7	0.0	0.0	0
RC21	20	30	10	0	10	0	0	0	0.0	0.0	0.0	0.0	10.0	20.0	20
RC27	5.3	10.5	10.5	0.0	0.0	21.1	5.3	0	0.0	5.3	5.3	0.0	26.3	31.6	0
RC28	0.0	50.0	18.2	0.0	54.5	40.9	13.6	0	4.5	4.5	0.0	4.5	0.0	0.0	0
RC30	25.0	0.0	0.0	8.3	8.3	0.0	0.0	0	8.3	8.3	0.0	8.3	41.7	50.0	0



	OXA48	TEM	NDM	SHV	OXA1	CTXM1	CTXM2	CTXM9	ACC	FOX	MOX	DHA	IMP	VIM	KPC
RC30	3	0	0	1	1	0	0	0	1	1	0	1	5	6	0
RC28	0	11	4	0	12	9	3	0	1	1	0	1	0	0	0
RC27	1	2	2	0	0	4	1	0	0	1	1	0	5	6	0
RC21	2	3	1	0	1	0	0	0	0	0	0	0	1	2	2
RC20	1	3	2	2	0	1	0	0	0	2	2	1	0	0	0
RC19	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
RC17	4	2	0	0	0	6	0	2	0	1	0	0	0	0	0
RC14	14	11	8	1	6	3	0	2	0	0	1	1	1	2	0
RC12	4	10	7	5	26	14	5	3	0	0	0	0	0	0	0
RC11	7	6	5	1	1	5	0	0	0	1	0	0	5	3	0
RC9	4	14	4	7	3	5	11	4	0	1	6	1	4	0	0
RC8	7	13	2	3	3	1	0	0	0	0	0	5	0	0	2
RC6	4	10	7	7	14	9	3	1	7	0	3	3	5	13	0
RC5	6	11	12	2	0	4	0	5	0	0	0	0	0	0	0
RC4	0	0	0	0	2	0	0	0	0	0	0	0	1	1	0
RC3	13	32	18	7	10	9	0	0	0	0	2	0	1	5	1
RC2	10	16	7	4	2	18	4	8	0	1	1	0	0	0	0
RC1	0	3	1	0	0	4	0	0	0	0	0	0	0	2	0

Figure 2.8: Various resistance genes found in *E. coli* isolates from different regional centres across India (2025)

The stacked bar graph represents the prevalence of resistant genes in *E. coli* isolates received from the regional centres (RC = 18) in the year 2025. Each colour on the bar graph represents a different regional centre.

Molecular characterisation of *K. pneumoniae* isolates

Six hundred seventy three (673) *K. pneumoniae* isolates were subjected to five multiplex PCRs and one monoplex PCR for OXA-48. Overall, TEM gene was the most prevalent, present in 20% of the isolates, followed by SHV in 19%, OXA-48 in 17%, NDM in 13%, CTXM-1 in 12%, OXA 1 in 8%, and others are less than 10% **(Figures 2.9, Table 2.20 and Figure 2.10).** Among the RC1 isolates, the most prevalent resistance genes were TEM (56.3%), followed by CTXM-1 and SHV (43.8%), NDM (31.3%), IMP and KPC (18.8%), and OXA 48 (12.5%). The isolates from RC2 showed maximum positivity for CTXM-1 (59%) followed by TEM (47.5%), OXA-48 (44.3%), NDM (27.9%), OXA-1 (26.2%) and SHV (16%) and others are less than 10%. In the RC3 samples, TEM had the highest prevalence at 40.7%, followed by SHV (23.5%), OXA-48 (14.8%), NDM and OXA-1 (12.3%), whereas the rest genes were less than 10%. The RC4 isolates were majorly positive for SHV (30%), NDM and OXA-48 (25% each), followed by TEM (15%) and OXA-1, ACC and FOX (15%). Within RC5 isolates, OXA-48 (51.3%) was the predominant resistance gene, followed by NDM, SHV and TEM (35.9%), OXA-1 (30.8%), and CTXM-1 (23.1%). RC6 samples also exhibited high prevalence for OXA-48 (39.2%), NDM (36.5%), TEM (35.1%), SHV (27%), CTXM-1 (23%), OXA-1 (21.6%) and FOX (13.5%). The RC8 isolates were positive for TEM (55.6%), followed by SHV (22.2%), OXA-48 (20%), and FOX (17.8%). The RC9 samples showed a high prevalence of SHV (48.3%), followed by OXA-48, TEM, CTXM-1 (16.7%) and NDM (15%).

The RC11 isolates were positive for OXA-48 (60%), TEM and NDM (42%) other than that SHV (38%) and CTXM 1 (30%). The RC12 isolates showed maximum positivity for TEM (63.6%), NDM (40.9%), OXA-48 (36.4%), and CTXM-1 (20.5%). Within RC14 samples exhibited a high prevalence of SHV (46.9%), TEM and OXA-48 (30.6%), CTXM-1 (22.4%) and NDM (16.3%). Among the RC17 isolates, SHV (43.3%), OXA-48 (33.3%), CTXM-1 (30%), OXA-1 (23.3%) and TEM and NDM (13.3%) were the most common resistance genes.In RC19 samples, SHV, NDM, VIM, KPC and TEM (25%) were prevalent. RC20 isolates showed a major proportion of isolates positive for SHV (69.2%), followed by OXA 48 and KPC (23.1%).Other resistant marker genes were less than 20%. RC21 samples showed varying prevalence for different resistance genes, with SHV (44.7%), TEM (28.9%), NDM and OXA-1 (21.1%) being notable. Others like VIM, KPC and CTXM-1 were detected at lower levels (lesser than 20%) or were absent. Within RC27 isolates, 17.6% of the isolates were positive for CTXM-1, followed by TEM and FOX (11.8%). In RC28, 75% of the isolates showed the presence of SHV, followed by OXA-1 in 40% of the isolates and TEM and NDM in 20% and others are less than 10%. In RC30, 66.7% of the isolates showed the presence of SHV, followed by OXA-48 and OXA-1 in 25% of the isolates and CTXM-1(16.7%).

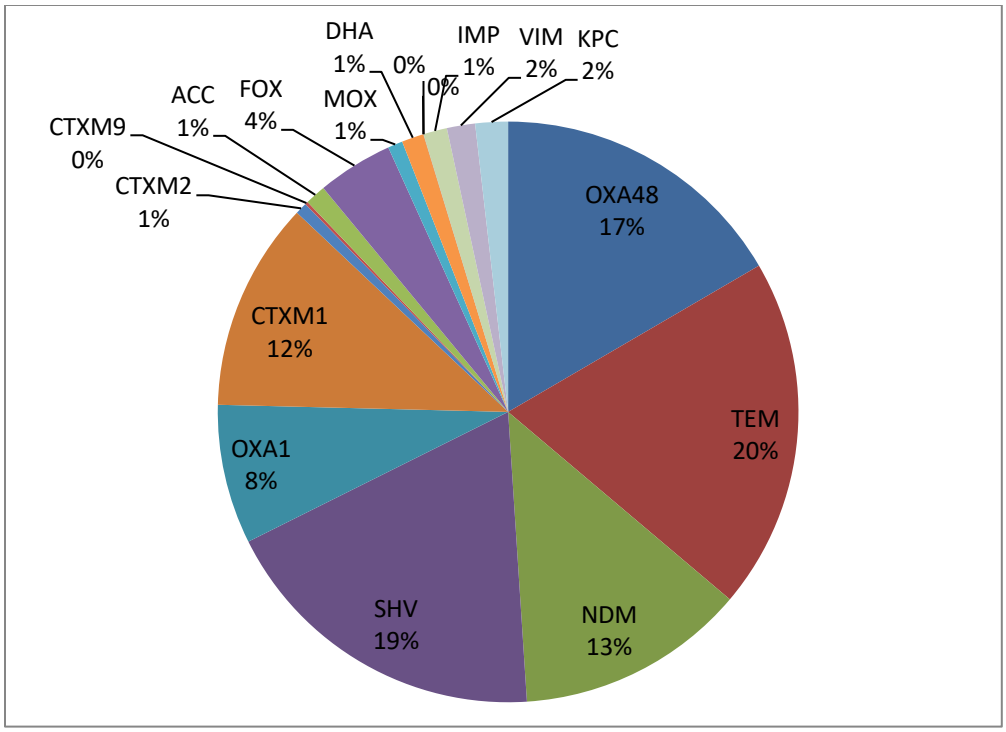


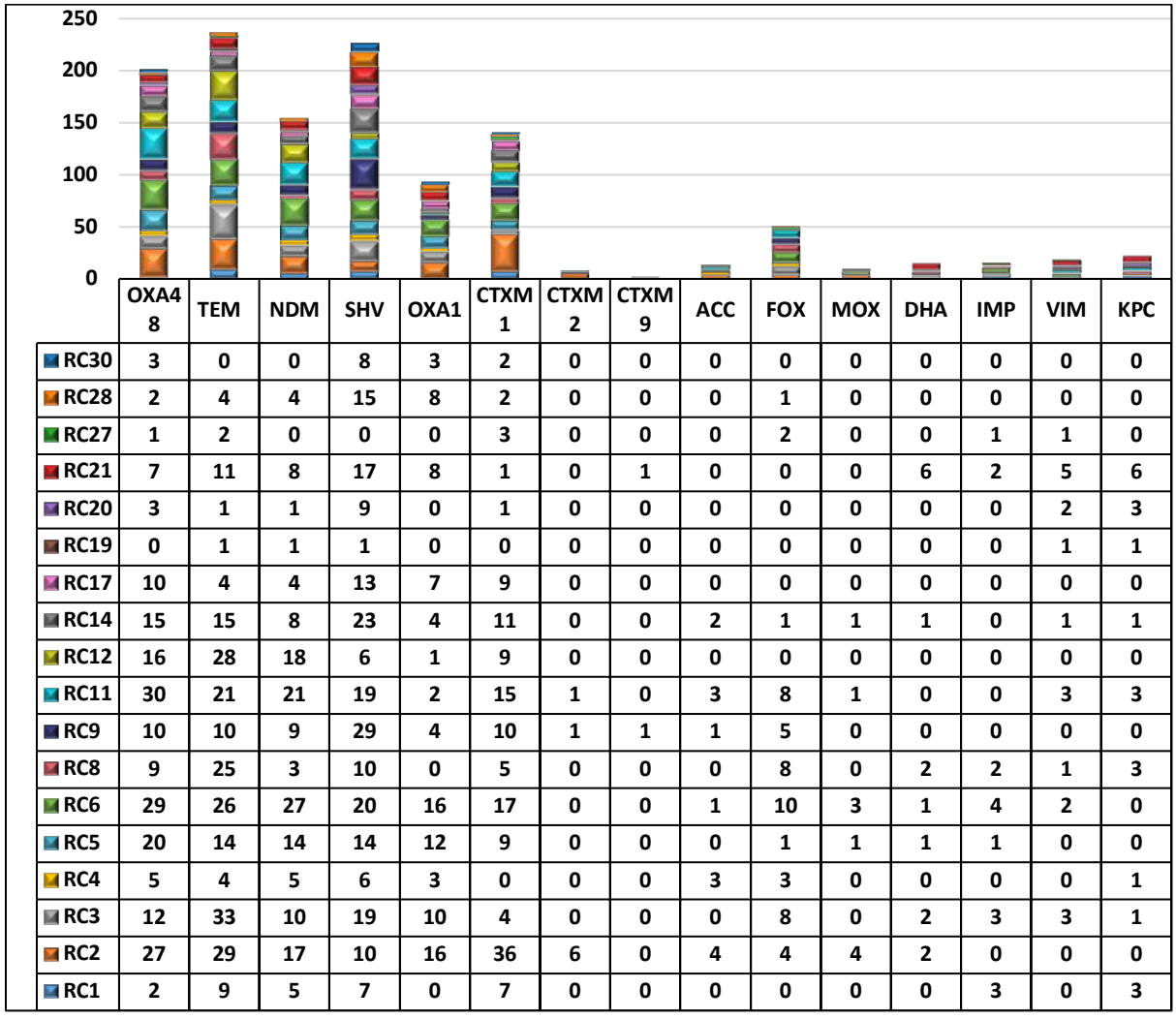
Figure 2.9: Percentage positivity of AMR associated genetic determinants in *K. pneumoniae* (2025)

In *K. pneumoniae* isolates, TEM gene was the predominant gene present in 20% of the isolates followed by SHV in 19% of the isolates and OXA-48 in 17% of the isolates. The genes encoding for AmpC β-lactamases were the least prevalent genes.

Table 2.20: Percentage positivity of resistant genes in *K. pneumoniae* from each centre

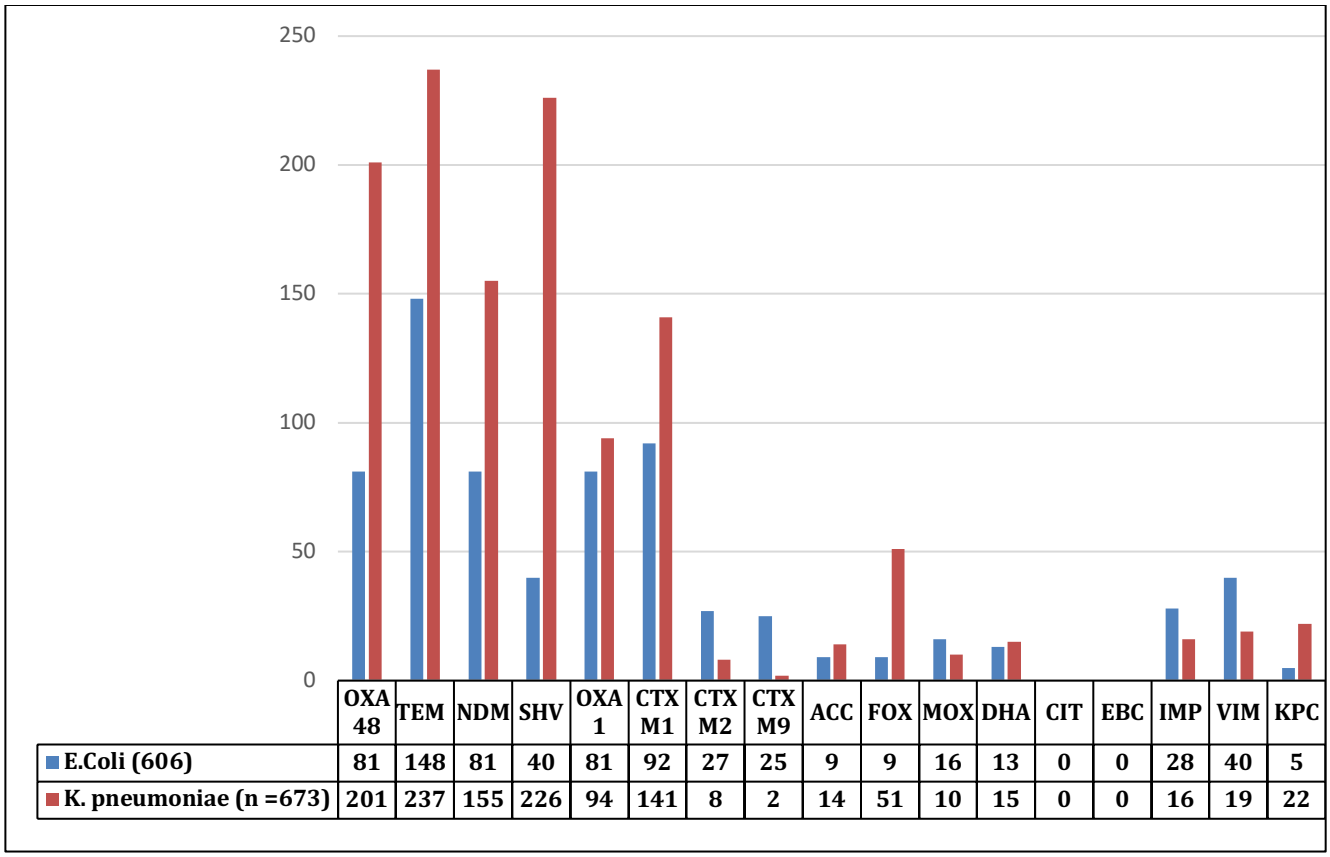
RC	Antimicrobial Resistance genes														
	OXA 48	TEM	NDM	SHV	OXA 1	CTX M1	CTX M2	CTX M9	ACC	FOX	MOX	DHA	IMP	VIM	KPC
RC1	12.5	56.3	31.3	43.8	0.0	43.8	0.0	0.0	0.0	0.0	0.0	0.0	18.8	0.0	18.8
RC2	44.3	47.5	27.9	16.4	26.2	59.0	9.8	0.0	6.6	6.6	6.6	3.3	0.0	0.0	0.0
RC3	14.8	40.7	12.3	23.5	12.3	4.9	0.0	0.0	0.0	9.9	0.0	2.5	3.7	3.7	1.2
RC4	25.0	20.0	25.0	30.0	15.0	0.0	0.0	0.0	15.0	15.0	0.0	0.0	0.0	0.0	5.0
RC5	51.3	35.9	35.9	35.9	30.8	23.1	0.0	0.0	0.0	2.6	2.6	2.6	2.6	0.0	0.0
RC6	39.2	35.1	36.5	27.0	21.6	23.0	0.0	0.0	1.4	13.5	4.1	1.4	5.4	2.7	0.0
RC8	20.0	55.6	6.7	22.2	0.0	11.1	0.0	0.0	0.0	17.8	0.0	4.4	4.4	2.2	6.7
RC9	16.7	16.7	15.0	48.3	6.7	16.7	1.7	1.7	1.7	8.3	0.0	0.0	0.0	0.0	0.0
RC11	60.0	42.0	42.0	38.0	4.0	30.0	2.0	0.0	6.0	16.0	2.0	0.0	0.0	6.0	6.0
RC12	36.4	63.6	40.9	13.6	2.3	20.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
RC14	30.6	30.6	16.3	46.9	8.2	22.4	0.0	0.0	4.1	2.0	2.0	2.0	0.0	2.0	2.0
RC17	33.3	13.3	13.3	43.3	23.3	30.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
RC19	0.0	25.0	25.0	25.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	25.0	25.0

RC	Antimicrobial Resistance genes														
	OXA 48	TEM	NDM	SHV	OXA 1	CTX M1	CTX M2	CTX M9	ACC	FOX	MOX	DHA	IMP	VIM	KPC
RC20	23.1	7.7	7.7	69.2	0.0	7.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	15.4	23.1
RC21	18.4	28.9	21.1	44.7	21.1	2.6	0.0	2.6	0.0	0.0	0.0	15.8	5.3	13.2	15.8
RC27	5.9	11.8	0.0	0.0	0.0	17.6	0.0	0.0	0.0	11.8	0.0	0.0	5.9	5.9	0.0
RC28	10.0	20.0	20.0	75.0	40.0	10.0	0.0	0.0	0.0	5.0	0.0	0.0	0.0	0.0	0.0
RC30	25.0	0.0	0.0	66.7	25.0	16.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0



	OXA48	TEM	NDM	SHV	OXA1	CTXM1	CTXM2	CTXM9	ACC	FOX	MOX	DHA	IMP	VIM	KPC
RC30	3	0	0	8	3	2	0	0	0	0	0	0	0	0	0
RC28	2	4	4	15	8	2	0	0	0	1	0	0	0	0	0
RC27	1	2	0	0	0	3	0	0	0	2	0	0	1	1	0
RC21	7	11	8	17	8	1	0	1	0	0	0	6	2	5	6
RC20	3	1	1	9	0	1	0	0	0	0	0	0	0	2	3
RC19	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1
RC17	10	4	4	13	7	9	0	0	0	0	0	0	0	0	0
RC14	15	15	8	23	4	11	0	0	2	1	1	1	0	1	1
RC12	16	28	18	6	1	9	0	0	0	0	0	0	0	0	0
RC11	30	21	21	19	2	15	1	0	3	8	1	0	0	3	3
RC9	10	10	9	29	4	10	1	1	1	5	0	0	0	0	0
RC8	9	25	3	10	0	5	0	0	0	8	0	2	2	1	3
RC6	29	26	27	20	16	17	0	0	1	10	3	1	4	2	0
RC5	20	14	14	14	12	9	0	0	0	1	1	1	1	0	0
RC4	5	4	5	6	3	0	0	0	3	3	0	0	0	0	1
RC3	12	33	10	19	10	4	0	0	0	8	0	2	3	3	1
RC2	27	29	17	10	16	36	6	0	4	4	4	2	0	0	0
RC1	2	9	5	7	0	7	0	0	0	0	0	0	3	0	3

Figure 2.10: Various resistance genes found in *K. pneumoniae* isolates from different regional centres across India (2025)



	OXA 48	TEM	NDM	SHV	OXA 1	CTX M1	CTX M2	CTX M9	ACC	FOX	MOX	DHA	CIT	EBC	IMP	VIM	KPC
E.Coli (606)	81	148	81	40	81	92	27	25	9	9	16	13	0	0	28	40	5
K. pneumoniae (n =673)	201	237	155	226	94	141	8	2	14	51	10	15	0	0	16	19	22

Figure 2.11: Comparison of resistance genes present in *E. coli* and *K. pneumoniae* isolates from regional centres across India (2025)

The comparison between the *E. coli* (n= 606) and *K. pneumoniae* (n=673) isolates received from regional centres (n = 18) in 2025 revealed the presence of resistance genes in *Klebsiella* isolates than *E. coli*.

Clinical relevance

Antimicrobial susceptibility patterns from 2025 demonstrate a substantial and persistent burden of antimicrobial resistance (AMR) among Enterobacterales, particularly *Escherichia coli* and *Klebsiella pneumoniae*. These organisms account for a large proportion of urinary tract infections (UTIs), bloodstream infections (BSIs), ventilator-associated pneumonia (VAP), intra-abdominal infections, and neonatal sepsis. The increasing prevalence of multidrug-resistant (MDR) strains, including extended-spectrum β-lactamase (ESBL)-producing and carbapenem-resistant Enterobacterales (CRE), has substantially reduced the effectiveness of commonly used antibiotics. Persistently low susceptibility to third-generation cephalosporins and fluoroquinolones, alongside declining carbapenem susceptibility, indicates a narrowing range of reliable therapeutic options. These findings

have important implications for empirical treatment, antimicrobial stewardship (AMS), infection prevention and control (IPC), and regional treatment guidelines.

The resistance burden was particularly pronounced for *K. pneumoniae*. In 2025, susceptibility was only 29.2% to piperacillin-tazobactam, 23.8–27.3% to third-generation cephalosporins, 36.5–40.4% to carbapenems, and 44.5% to amikacin, while remaining below 30% for fluoroquinolones. Among ICU isolates, susceptibility to ertapenem, imipenem, and meropenem was only 26.1%, 24.9%, and 26.3%, respectively. These findings suggest that conventional β-lactams, fluoroquinolones, and even carbapenems may provide inadequate empirical coverage for severe *K. pneumoniae* infections in high-resistance settings.

A similar, although comparatively less severe, pattern was observed for *E. coli*. Overall susceptibility in 2025 was 42.6% to piperacillin-tazobactam, 18.4% to cefotaxime, 24.7% to ceftazidime, 60.5% to ertapenem, 63.1% to imipenem, and 65.3% to meropenem. Fluoroquinolone susceptibility remained particularly poor, at 9.0% for ciprofloxacin and 18.2% for levofloxacin. For both organisms, ICU isolates demonstrated substantially greater resistance across major antimicrobial classes than outpatient (OPD) and ward isolates. This may reflect antimicrobial selection pressure, greater healthcare exposure, and transmission of resistant organisms within critical-care settings, with direct implications for empirical treatment in critically ill patients.

Long-term susceptibility trends from 2017–2025 further highlight the increasing resistance burden. In *E. coli*, imipenem susceptibility declined from approximately 80% in 2017 to 63% in 2025, while meropenem susceptibility decreased from 74% to 65%. The decline was more pronounced in *K. pneumoniae*, with imipenem susceptibility falling from 58.5% to 36.5% and meropenem susceptibility from 48.1% to 40.4%. These trends indicate that carbapenem resistance is becoming an increasingly important component of the overall resistance profile of Enterobacterales, challenging their traditional role as reliable agents for severe Gram-negative infections.

Molecular findings provide further evidence of the clinical importance of this resistance burden. Among regional-centre isolates in 2025, *K. pneumoniae* demonstrated a greater burden of resistance-associated genes than E. coli, with TEM, SHV, OXA-48, NDM, and CTX-M among the commonly detected determinants. Carbapenemase genes, including NDM, OXA-48, IMP, VIM, and KPC, are particularly concerning because they constrain treatment options. Metallo-β-lactamases, such as NDM, IMP, and VIM, are not inhibited by avibactam, limiting the activity of ceftazidime-avibactam against these organisms. Furthermore, resistance determinants may be carried on mobile genetic elements, facilitating dissemination among Enterobacterales and other Gram-negative organisms. Marked inter-centre variation in resistance-gene profiles underscores the importance of local epidemiology in developing empirical treatment and infection-control strategies.

The data also highlight the importance of preserving currently active and last-line agents. Colistin retained high in-vitro activity against *E. coli* and *K. pneumoniae*; however, its toxicity, last-resort status, and emergence of resistance in some ICU isolates support cautious,

targeted use rather than routine empirical reliance. Amikacin retained useful activity against *E. coli* but demonstrated considerably lower activity against *K. pneumoniae*, particularly among ICU isolates.

The variable activity of newer agents also has important implications. Ceftazidime-avibactam susceptibility was only 37.7% among *K. pneumoniae* and 51.5% among E. coli isolates, demonstrating that newer agents cannot automatically be considered reliable empirical options without local susceptibility data. Tigecycline retained comparatively higher activity against both organisms; however, its use should be guided by the infection site and established pharmacological limitations.

Urinary isolate data further demonstrate the need for site-specific antimicrobial interpretation. *E. coli* remained the predominant urinary pathogen and retained comparatively good susceptibility to fosfomycin and nitrofurantoin, although susceptibility to several commonly used agents declined during 2017–2025. In contrast, *K. pneumoniae* demonstrated a substantially more resistant urinary profile, with lower susceptibility to piperacillin-tazobactam, carbapenems, amikacin, and fluoroquinolones.

Taken together, the 2025 surveillance data demonstrate a sustained narrowing of effective antimicrobial choices, driven particularly by the high resistance burden in *E. coli* and *K. pneumoniae* and declining carbapenem susceptibility. Treatment of CRE infections increasingly requires consideration of newer agents, including ceftazidime-avibactam, aztreonam-based strategies, and cefiderocol, or combination regimens in selected settings. Appropriate therapy depends on the underlying resistance mechanism, clinical indication, and infection site, highlighting the importance of rapid molecular diagnostics to guide targeted treatment and reduce unnecessary exposure to broad-spectrum and reserve antibiotics.

Strengthening national AMR surveillance, expanding access to rapid molecular diagnostics, enhancing AMS programmes, and improving IPC practices remain key priorities. Regional variation in phenotypic susceptibility and resistance determinants supports continued multicentre genomic surveillance to identify emerging resistance patterns, monitor dissemination, and enable timely modification of empirical treatment recommendations. Integrating microbiological, molecular, and clinical data will be essential to inform evidence-based treatment guidelines and preserve the effectiveness of available antimicrobial agents.

Chapter 3. Non-fermenting Gram-negative Bacteria (NFGNB)

A total of 26,085 non-fermenting Gram-negative bacilli (NFGNB) isolates were collected across multiple clinical settings in India during 2025. *Pseudomonas aeruginosa* constituted the largest share with 13,835 isolates (53%), followed by *Acinetobacter baumannii* with 10,714 isolates (41%), and *Stenotrophomonas maltophilia* with 794 isolates (3%). Surveillance from 2017–2025 continues to show high resistance to carbapenems, cephalosporins, and fluoroquinolones in *A. baumannii* and *P. aeruginosa*, while colistin and minocycline remain largely effective agents against these two organisms. *S. maltophilia* shows stable susceptibility to minocycline, levofloxacin and trimethoprim-sulfamethoxazole. Overall, the 2025 data confirm a persistently challenging resistance landscape among NFGNB in Indian healthcare settings, reinforcing the continued need for antimicrobial stewardship, molecular surveillance, and judicious use of reserve agents such as colistin.

Pseudomonas aeruginosa

In 2025, a total of 13,835 *Pseudomonas aeruginosa* isolates were collected from multiple centres across India, including outpatient (n=4,859), ward (n=6,876) and ICU (n=2,100) settings. Location-wise analysis (**Table 3.1**) showed that colistin remained the most active agent overall (97.5% susceptibility), closely followed by polymyxin B (97.3%) and amikacin (72.7%). Among the β-lactams, piperacillin-tazobactam and meropenem each showed 68.4% and 67.9% susceptibility respectively, cefepime 67.9%, and ceftazidime 67.2%, while imipenem showed comparatively lower activity at 64.4%. OPD isolates generally showed higher susceptibility than ward and ICU isolates across nearly every agent, with ICU isolates showing the lowest susceptibility, including imipenem (47.4%), ciprofloxacin (46.9%) and levofloxacin (45.1%). Sample-wise analysis (**Table 3.2**) indicated that lower respiratory tract (LRT) and sterile-site (SI) specimens generally had higher susceptibility, whereas urine isolates showed the lowest susceptibility across most agents [e.g., piperacillin-tazobactam (53.5%), ceftazidime (50.7%)]. Colistin retained consistently high susceptibility (≥95%) across all sample types, including CSF (100%, n=90). Fluoroquinolones remained the weakest-performing class overall, with ciprofloxacin at 56.6% and levofloxacin at 56.8%. Temporal analysis over the last nine years (**Table 3.3, Figure 3.1**) revealed relatively stable susceptibility for most agents, with ciprofloxacin showing the greatest year-on-year volatility and a partial recovery by 2025, while cefoperazone-sulbactam and ceftazidime-avibactam were introduced to the testing panel only in 2025 (61.4% and 57.2% respectively), reflecting expanding use of newer β-lactam/β-lactamase-inhibitor combinations.

Table 3.1: Location-wise susceptibility percentages of *Pseudomonas aeruginosa* isolated from all samples (except faeces) across OPD, Ward and ICU

AMA	Total N=13835 (S%)	OPD N=4859 (S%)	Ward N=6876 (S%)	ICU N=2100 (S%)
Piperacillin-tazobactam	9463 / 13835 (68.4)	3766 / 4859 (77.5)	4529 / 6876 (65.9)	1168 / 2100 (55.6)
Cefepime	8491 / 12497 (67.9)	3460 / 4397 (78.7)	4028 / 6195 (65)	1003 / 1905 (52.7)
Ceftazidime	9297 / 13835 (67.2)	3748 / 4859 (77.1)	4447 / 6876 (64.7)	1102 / 2100 (52.3)
Imipenem	8909 / 13835 (64.4)	3653 / 4859 (75.2)	4260 / 6876 (61.9)	996 / 2100 (47.4)
Meropenem	9402 / 13835 (67.9)	3813 / 4859 (78.5)	4486 / 6876 (65.2)	1103 / 2100 (52.5)
Colistin*	8818 / 9040 (97.5)	2869 / 2940 (97.6)	4540 / 4636 (97.9)	1409 / 1464 (96.2)
Amikacin	8146 / 11211 (72.7)	3199 / 4035 (79.3)	4076 / 5667 (71.9)	871 / 1509 (57.7)
Tobramycin	5007 / 6948 (72.1)	2122 / 2732 (77.7)	2316 / 3260 (71)	569 / 956 (59.5)
Ciprofloxacin	7832 / 13826 (56.6)	3003 / 4856 (61.8)	3843 / 6870 (55.9)	986 / 2100 (46.9)
Levofloxacin	7082 / 12466 (56.8)	2681 / 4297 (62.4)	3574 / 6335 (56.4)	827 / 1834 (45.1)
Polymixin B*	2323 / 2388 (97.3)	841 / 865 (97.2)	1158 / 1185 (97.7)	324 / 338 (95.8)
Cefoperazone-sulbactam	5620 / 9149 (61.4)	2244 / 3183 (70.5)	2721 / 4570 (59.5)	655 / 1396 (46.9)
Ceftazidime-avibactam	1711 / 2993 (57.2)	583 / 907 (64.3)	914 / 1602 (57.1)	214 / 484 (44.2)

*Colistin & Polymixin B represents the percentage of intermediate susceptibility

Table 3.2: Sample-wise susceptibility percentages of *Pseudomonas aeruginosa*

AMA	Blood N=1384	LRT N=4825	SI N=2771	DI N=1461	CSF N=90	Urine N=2181
Piperacillin-tazobactam	1003/1384 (72.5)	3585/4825 (74.3)	1875/2771 (67.7)	1027/1460 (70.3)	44/90 (48.9)	1166/2180 (53.5)
Cefepime	865/1220 (70.9)	3249/4449 (73)	1684/2472 (68.1)	1027/1369 (75)	25/66 (37.9)	970/1953 (49.7)
Ceftazidime	990/1384 (71.5)	3481/4825 (72.1)	1924/2770 (69.5)	1005/1461 (68.8)	31/90 (34.4)	1105/2181 (50.7)
Imipenem	858/1384 (62)	3320/4825 (68.8)	1886/2771 (68.1)	991/1461 (67.8)	41/90 (45.6)	1075/2181 (49.3)
Meropenem	970/1384 (70.1)	3467/4825 (71.9)	2012/2771 (72.6)	1040/1461 (71.2)	34/90 (37.8)	1124/2181 (51.5)
Colistin*	1005/1026 (97.9)	2569/2632 (97.6)	1980/2019 (98.1)	928/944 (98.3)	73/73 (100)	1524/1594 (95.6)
Amikacin	917/1183 (77.5)	2909/3782 (76.9)	1631/2114 (77.2)	774/1000 (77.4)	48/79 (60.8)	1167/2119 (55.1)
Levofloxacin	858/1228 (69.9)	2788/4488 (62.1)	1514/2505 (60.4)	586/1170 (50.1)	31/85 (36.5)	756/1940 (39)

*Colistin represents percentage of intermediate susceptibility

Table 3.3: Yearly susceptibility trend of *Pseudomonas aeruginosa* isolated from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=5687 (S%)	N=8880 (S%)	N=12634 (S%)	N=7839 (S%)	N=11622 (S%)	N=13228 (S%)	N=11757 (S%)	N=11419 (S%)	N=13835 (S%)
Piperacillin-tazobactam	3757/5450 (68.9)	6034/8499 (71)	8416/11430 (73.6)	5012/7418 (67.6)	7548/10835 (69.7)	9017/13156 (68.5)	4483/6525 (68.7)	7242/10443 (69.3)	9463 / 13875 (68.2)
Cefepime	3074/5003 (61.4)	5259/8284 (63.5)	7660/12038 (63.6)	4497/7355 (61.1)	7263/11233 (64.7)	7887/12625 (62.4)	4057/6380 (63.6)	6964/10317 (67.5)	8491 / 12497 (67.9)
Ceftazidime	3602/5504 (65.4)	5663/8598 (65.9)	7545/11977 (63)	4647/7635 (60.9)	6914/11028 (62.7)	7528/12767 (58.9)	3988/6525 (61.1)	7306/11381 (64.2)	9297 / 13857 (67.1)
Imipenem	4059/5514 (73.6)	5627/8377 (67.2)	6425/10230 (62.8)	4411/7036 (62.7)	6749/10389 (65)	8183/12795 (63.9)	4010/6525 (61.5)	5944/10443 (56.9)	8909 / 13888 (64.1)
Meropenem	3490/5083 (68.7)	5736/8292 (69.2)	8255/12242 (67.4)	4955/7661 (64.7)	7581/11280 (67.2)	8524/12898 (66.1)	4275/6525 (65.5)	6730/10857 (62)	9402 / 13842 (67.9)
Colistin*	1727/1738 (99.4)	983/1075 (91.4)	1767/1899 (93)	1291/1355 (95.3)	2226/2298 (96.9)	6675/6885 (96.9)	2923/3037 (96.3)	5281/5408 (97.7)	8818/9040 (97.5)
Amikacin	3864/5609 (68.9)	6019/8747 (68.8)	8340/12329 (67.6)	5276/7723 (68.3)	7990/11480 (69.6)	9000/13133 (68.5)	4334/6202 (69.9)	7017/9578 (73.3)	8146 / 11211 (72.7)
Gentamicin	2526/4249 (59.4)	4077/6462 (63.1)	5820/9383 (62)	3241/5341 (60.7)	5277/8311 (63.5)	6321/9896 (63.8)	2844/4398 (64.7)	2373/3399 (69.8)	1086/1537 (70.6)
Tobramycin	2954/4365 (67.7)	3809/5603 (68)	4627/6783 (68.2)	2907/4331 (67.1)	4148/6015 (69)	4364/6379 (68.4)	2523/3957 (63.8)	3099/4522 (68.5)	5007 / 6948 (72.1)
Ciprofloxacin	2930/5069 (57.8)	4814/8026 (60)	6281/10945 (57.4)	3768/6541 (57.6)	6126/10159 (60.3)	6039/12719 (47.4)	3313/6525 (50.8)	6397/11222 (57)	7832 / 13834 (56.6)
Levofloxacin	3236/5351 (60.5)	4794/8217 (58.3)	6148/10922 (56.3)	3771/6743 (55.9)	5863/10123 (57.9)	5635/11048 (51.0)	2769/5771 (48)	4537/8407 (54)	7082 / 12466 (56.8)

*Colistin represents percentage intermediate susceptibility

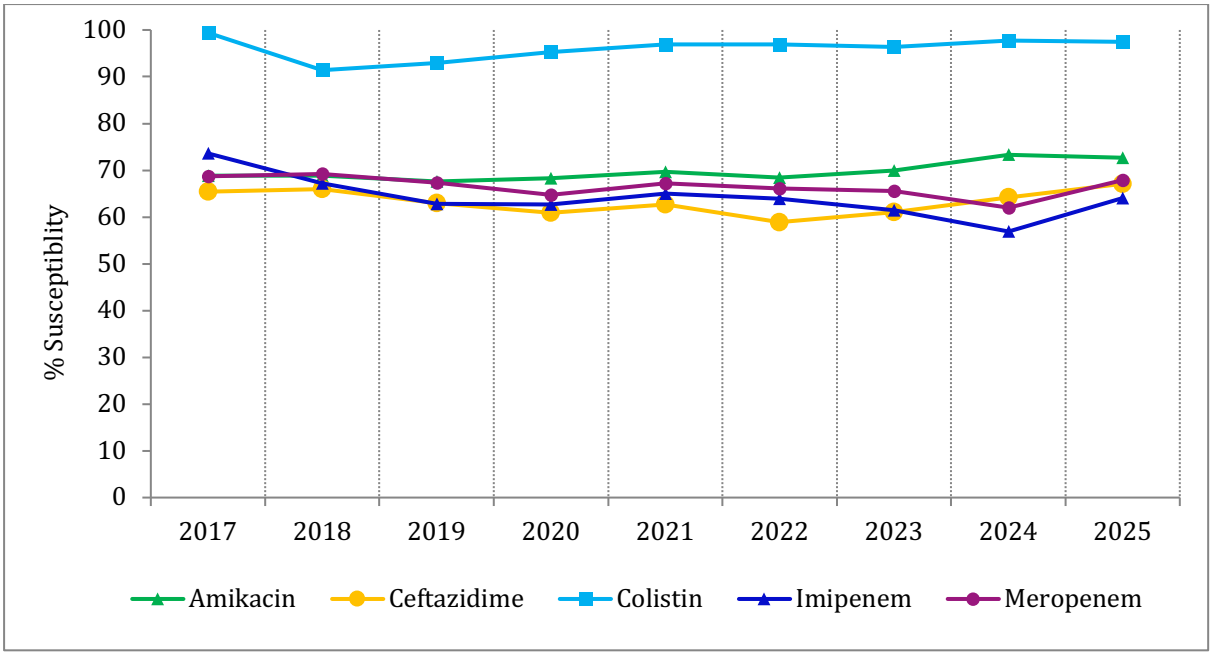


Figure 3.1: Yearly susceptibility trend of *Pseudomonas aeruginosa* isolated from all samples

Acinetobacter baumannii

In 2025, a total of 10,714 *Acinetobacter baumannii* isolates were collected from multiple centres across India, including outpatient (n=1,416), ward (n=5,622), and ICU (n=3,676) settings. Location-wise analysis (**Table 3.4**) confirmed colistin as the only reliably active agent, with 98.5% overall susceptibility, followed at a distance by minocycline (57.4%). All other agents tested showed markedly limited activity: piperacillin-tazobactam (13.6%), amikacin (15.7%), ceftazidime (11.7%), meropenem (12.8%), cefepime (11.8%) and imipenem (11.3%). β-lactams and carbapenems tended to show higher susceptibility in OPD isolates, whereas amikacin, minocycline and levofloxacin showed higher susceptibility in ICU isolates, a pattern that may reflect differences in the isolate mix and prior antibiotic exposure between these agent classes. Sample-wise analysis (**Table 3.5**) showed that colistin remained highly active (≥96% intermediate susceptibility) across all specimen types. Notably, urine isolates showed markedly higher susceptibility than blood or LRT isolates for most β-lactams and aminoglycosides (e.g., piperacillin-tazobactam: urine 42.9% vs. blood 16.3%; meropenem: urine 45.2% vs. blood 15.4%), while minocycline was most active in deep-infection specimens (77.6%). Temporal analysis over nine years (**Table 3.6, Figure 3.2**) showed persistently low susceptibility to β-lactams, carbapenems and aminoglycosides throughout the period, with carbapenem susceptibility declining from 2017 to a trough around 2023–2024 before a partial rebound in 2025. Colistin and minocycline remained the most reliable agents across the surveillance window, underscoring the sustained multidrug-resistance challenge posed by *A. baumannii* in Indian healthcare settings.

Table 3.4: Location-wise susceptibility percentages of *A. baumannii* isolated from all samples except faeces across OPD, Ward and ICU

AMA	Total N=10714 (S%)	OPD N=1416 (S%)	Ward N=5622 (S%)	ICU N=3676 (S%)
Piperacillin-tazobactam	1452/10703 (13.6)	38/1415 (2.7)	89/5620 (1.6)	50/3668 (1.4)
Cefepime	1157/9836 (11.8)	52/1258 (4.1)	249/5169 (4.8)	114/3409 (3.3)
Ceftazidime	1252/10705 (11.7)	36/1416 (2.5)	124/5620 (2.2)	39/3669 (1.1)
Imipenem	1214/10705 (11.3)	14/1417 (1.0)	34/5620 (0.6)	13/3668 (0.4)
Meropenem	1375/10704 (12.8)	29/1416 (2.0)	101/5620 (1.8)	39/3668 (1.1)
Colistin*	9062/9202 (98.5)	1156/1177 (98.2)	4753/4825 (98.5)	3153/3200 (98.5)
Amikacin	1678/10704 (15.7)	48/1415 (3.4)	227/5621 (4.0)	193/3668 (5.3)
Minocycline	5933/10345 (57.4)	67/1327 (5.0)	395/5425 (7.3)	378/3593 (10.5)
Levofloxacin	1331/8853 (15.0)	82/1178 (7.0)	442/4682 (9.4)	283/2993 (9.5)

*Colistin represents percentage intermediate susceptibility of *Acinetobacter* spp.

Table 3.5: Sample-wise susceptibility percentages of *A. baumannii*

AMA	Blood N=2233 (S%)	LRT N=4852 (S%)	SI N=1243 (S%)	DI N=971 (S%)	CSF N=270 (S%)	Urine N=416 (S%)
Piperacillin-tazobactam	364/2231 (16.3)	493/4846 (10.2)	139/1243 (11.2)	109/971 (11.2)	42/270 (15.6)	177/413 (42.9)
Cefepime	311/1980 (15.7)	403/4566 (8.8)	97/1076 (9)	83/921 (9)	34/227 (15)	126/378 (33.3)
Ceftazidime	337/2231 (15.1)	420/4847 (8.7)	128/1243 (10.3)	94/971 (9.7)	18/271 (6.6)	134/413 (32.4)
Imipenem	319/2231 (14.3)	390/4849 (8)	133/1242 (10.7)	92/971 (9.5)	22/270 (8.1)	152/413 (36.8)
Meropenem	344/2232 (15.4)	431/4846 (8.9)	158/1242 (12.7)	98/971 (10.1)	32/270 (11.9)	187/414 (45.2)
Colistin*	1960/1996 (98.2)	3917/3967 (98.7)	1103/1115 (98.9)	883/900 (98.1)	248/258 (96.1)	346/355 (97.5)
Amikacin	434/2232 (19.4)	550/4847 (11.3)	173/1242 (13.9)	119/971 (12.3)	42/270 (15.6)	194/413 (47)
Minocycline	1446/2159 (67)	2263/4704 (48.1)	679/1216 (55.8)	716/923 (77.6)	176/263 (66.9)	226/358 (63.1)
Levofloxacin	317/1557 (20.4)	485/4187 (11.6)	146/1114 (13.1)	75/749 (10)	49/225 (21.8)	149/369 (40.4)

*Colistin represents percentage intermediate susceptibility of *Acinetobacter* spp.

Table 3.6: Yearly susceptibility trend of *A. baumannii* isolated from all samples (except faeces)

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=3359 (S%)	N=4549 (S%)	N= 8531 (S%)	N=6849 (S%)	N= 12393 (S%)	N= 12142 (S%)	N= 11948 (S%)	N= 10351 (S%)	N= 10714 (S%)
Piperacillin tazobactam	484/3187 (15.2)	760/4494 (16.9)	1245/8010 (15.5)	770/6724 (11.5)	1327/12052 (11)	1578/12124 (13.0)	936/7260 (12.9)	1148/9852 (11.7)	1452/10703 (13.6)
Cefepime	368/3300 (11.2)	587/4457 (13.2)	1040/8271 (12.6)	587/6571 (8.9)	1086/11986 (9.1)	1280/11900 (10.7)	808/7240 (11.2)	869/9741 (8.9)	1157/9836 (11.8)
Ceftazidime	355/3202 (11.1)	575/4164 (13.8)	905/7453 (12.1)	546/6441 (8.5)	890/10395 (8.6)	1023/11197 (9.1)	635/7260 (8.7)	1081/10351 (10.4)	1252/10705 (11.7)
Imipenem	501/3346 (15)	818/4517 (18.1)	1098/7272 (15.1)	744/6702 (11.1)	1445/11934 (12.1)	1456/11918 (12.2)	745/7260 (10.3)	826/9852 (8.4)	1214/10705 (11.3)
Meropenem	615/3287 (18.7)	953/4178 (22.8)	1742/8399 (20.7)	779/6747 (11.5)	1516/12083 (12.5)	1690/11910 (14.2)	877/7260 (12.1)	924/10304 (9)	1375/10704 (12.8)
Colistin*	28/31 (90.3)	36/38 (94.7)	103/108 (95.4)	91/94 (96.8)	4553/4758 (95.7)	7362/7700 (95.6)	4914/4970 (98.9)	5194/5331 (97.4)	9062/9202 (98.5)
Amikacin	638/3312 (19.3)	877/3795 (23.1)	1429/7016 (20.4)	1014/5863 (17.3)	1925/10734 (17.9)	2053/11892 (17.2)	1194/7260 (16.4)	1638/10351 (15.8)	1678/10704 (15.7)
Minocycline	926/1380 (67.1)	2393/3725 (64.2)	3893/6431 (60.5)	2794/5139 (54.4)	5547/10185 (54.5)	6207/10542 (58.8)	4018/5579 (72)	5873/8368 (70.2)	5933/10345 (57.4)
Levofloxacin	886/3040 (29.1)	959/4047 (23.7)	1500/7841 (19.1)	825/6181 (13.3)	1382/9919 (13.9)	1755/10013 (17.5)	749/6221 (12)	830/6809 (12.2)	1331/8853 (15.0)

*Colistin represents percentage intermediate susceptibility of *Acinetobacter* spp.

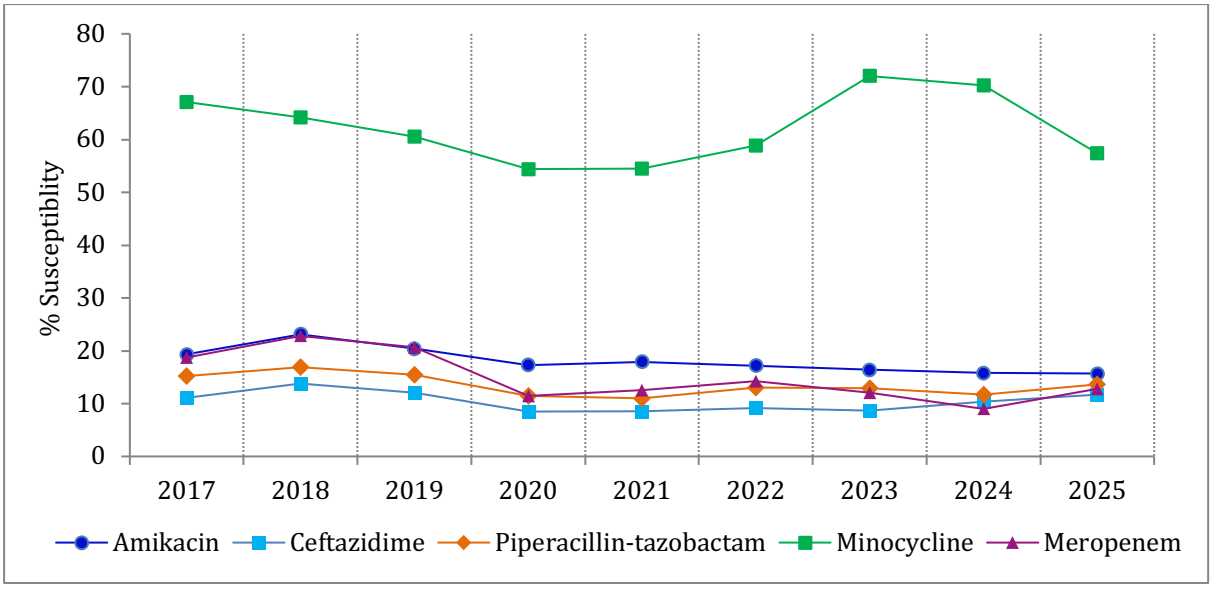


Figure 3.2: Yearly susceptibility trend of *A. baumannii* isolated from all samples (except faeces)

Stenotrophomonas maltophilia

In 2025, a total of 794 *Stenotrophomonas maltophilia* isolates were collected across ward (n=447), ICU (n=215), and OPD (n=132) settings. Location-wise analysis (**Table 3.7**) showed that levofloxacin (87%) and minocycline (85.6%) demonstrated the highest overall susceptibility, followed by trimethoprim-sulfamethoxazole (82.3%). Susceptibility to these three principal agents was broadly comparable across OPD, ward and ICU settings. Ticarcillin-clavulanic acid and chloramphenicol were tested on very small numbers of isolates (7 and 19 respectively) and susceptibility percentages are therefore not reported for these two agents, consistent with inadequate sample size for reliable estimation. Sample-wise analysis (**Table 3.8**) confirmed these trends, with minocycline, levofloxacin and trimethoprim-sulfamethoxazole retaining comparable activity (roughly 74–90%) across blood, LRT, superficial-infection, deep-infection and urine specimens, without a specimen type standing out as markedly more resistant. Temporal analysis over nine years (**Table 3.9, Figure 3.3**) showed that levofloxacin and trimethoprim-sulfamethoxazole susceptibility remained stable (82–91%) throughout 2017–2025. Minocycline susceptibility was consistently ≥91% from 2017 to 2024 but declined to 85.5% in 2025a change due to CLSI-M100 breakpoints changes otherwise. Overall, minocycline, levofloxacin and trimethoprim-sulfamethoxazole remain the most dependable therapeutic options for *S. maltophilia* infections in Indian healthcare settings.

Table 3.7: Location-wise susceptibility percentages of *Stenotrophomonas maltophilia* isolated from all samples across OPD, Ward and ICU

AMA	Total N=794 (S%)	Ward N=447 (S%)	ICU N=215 (S%)	OPD N=132 (S%)
Ticarcillin-clavulanic acid	*5/7 (-)	*1/3 (-)	*3/3 (-)	*1/1 (-)
Minocycline	680 / 794 (85.6)	377 / 447 (84.3)	185 / 215 (86)	118 / 132 (89.4)
Levofloxacin	691 / 794 (87)	382 / 447 (85.5)	188 / 215 (87.4)	121 / 132 (91.7)
Trimethoprim-sulfamethoxazole	648 / 787 (82.3)	356 / 441 (80.7)	175 / 214 (81.8)	117 / 132 (88.6)
Chloramphenicol	*16/19 (-)	*7/8 (-)	*6/8 (-)	*3/3 (-)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Table 3.8: Sample-wise susceptibility percentages of *Stenotrophomonas maltophilia*

AMA	All Specimens (except faeces)	Blood	LRT	SI	DI	Urine
	N=794 (S%)	N=291 (S%)	N=242 (S%)	N=86 (S%)	N=39 (S%)	N=43 (S%)
Ticarcillin-clavulanic acid	*5/7 (-)	*5/5 (-)	*0/0 (-)	*0/1 (-)	*0/0 (-)	*0/1 (-)
Minocycline	680/794 (85.6)	256/291 (88)	210/242 (86.8)	70/86 (81.4)	34/39 (87.2)	33/43 (76.7)
Levofloxacin	691/794 (87)	258/291 (88.7)	214/242 (88.4)	73/86 (84.9)	35/39 (89.7)	35/43 (81.4)
Trimethoprim-sulfamethoxazole	648/787 (82.3)	247/288 (85.8)	197/240 (82.1)	68/85 (80)	35/39 (89.7)	31/42 (73.8)
Chloramphenicol	*16/19 (-)	*14/16 (-)	*1/1 (-)	*1/1 (-)	*0/0 (-)	*0/1 (-)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Table 3.9: Yearly susceptibility trend of *Stenotrophomonas maltophilia* isolated from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=157 (S%)	N=310 (S%)	N=374 (S%)	N=360 (S%)	N=766 (S%)	N=827 (S%)	N=1011 (S%)	N=726 (S%)	N=794 (S%)
Ticarcillin-clavulanic acid	19/26 (73.1)	45/60 (75)	59/68 (86.8)	28/33 (84.8)	34/39 (87.2)	*11/12 (-)	*1/2 (-)	*1/4 (-)	*5/7 (-)
Ceftazidime	15/27 (55.6)	42/63 (66.7)	46/73 (63)	41/73 (56.2)	42/84 (50)	159/211 (75.3)	173/226 (76.5)	21/36 (58.3)	-
Minocycline	143/151 (94.7)	272/299 (91)	331/350 (94.6)	332/346 (96)	717/739 (97)	776/803 (96.6)	516/533 (96.8)	693/726 (95.45)	680 / 794 (85.5)
Levofloxacin	126/152 (82.9)	225/257 (87.5)	225/261 (86.2)	324/358 (90.5)	694/764 (90.8)	741/820 (90.3)	487/533 (91.4)	642/725 (88.55)	691 / 794 (87)
Trimethoprim-sulfamethoxazole	132/150 (88)	255/308 (82.8)	333/372 (89.5)	318/359 (88.6)	674/765 (88.1)	704/817 (86.1)	379/416 (91.1)	501/573 (87.43)	648 / 787 (82.3)
Chloramphenicol	*0/0 (-)	*1/2 (-)	*3/3 (-)	*8/9 (-)	*2/2 (-)	*4/5 (-)	21/35 (60)	27/50 (54)	*16/19 (-)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

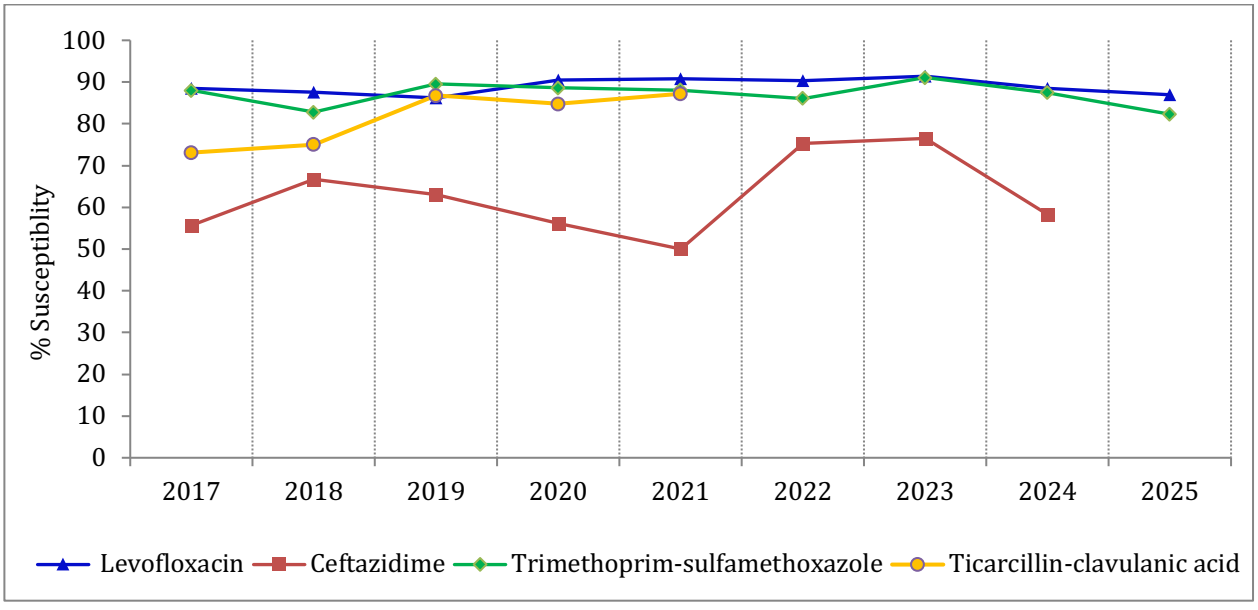


Figure 3.3: Yearly susceptibility trend of *Stenotrophomonas maltophilia* isolated from all samples

Molecular mechanism of resistance

Pseudomonas aeruginosa

In this multicentre surveillance analysis, a total of 468 revived *Pseudomonas aeruginosa* isolates collected from 13 Indian centres during 2025 were evaluated for carbapenem resistance and underlying molecular mechanisms **(Table 3.10)**. Of these, 419 isolates were tested, comprising 84 isolates (20.0%) that were carbapenem-resistant (CR) and 335 isolates (80.0%) were carbapenem-susceptible (CS). PCR-based molecular screening identified metallo-β-lactamases (MβL*s*) as the predominant carbapenemase determinants. NDM was detected in 22 isolates (5.3%), while VIM was detected in 10 isolates (2.4%). Among Class A carbapenemases, KPC was detected in 5 isolates (1.2%) and GES in3 isolates (0.7%). Extended-spectrum β-lactamase determinants included TEM in 4 isolates (1.0%) and VEB in 4 isolates (1.0%). No SPM, IMP or OXA-48-like carbapenemase was detected among theisolates screened. 15 Co-production of resistance determinants was observed in 34 isolates. The major co-production patterns included NDM with VEB, KPC with VEB, KPC with NDM, VIM with VEB and VIM with TEM. NDM-VEB co-production was observed across several regional centres, while KPC-VEB and KPC-NDM combinations were also identified. These findings demonstrate the presence of multiple β-lactamase determinants occurring either individually or in combination among the characterized isolates. Notably, 337 isolates (80.4%) were PCR-negative for all the screened resistance determinants. The high proportion of PCR-negative *P. aeruginosa* isolates indicates that the targeted carbapenemase genes were not detected in a substantial proportion of isolates. However, molecular testing was performed on the overall *P. aeruginosa* isolate population and was not restricted to carbapenem-resistant isolates. Therefore, the molecular findings cannot be directly correlated with the carbapenem resistance phenotype, and the contribution of alternative resistance mechanisms cannot be established from the present data. Overall, the molecular profile observed in 2025 was predominantly characterized by metallo-β-lactamase (MBL) determinants, particularly NDM and VIM, while KPC, GES, TEM and VEB were detected at lower frequencies.

Table 3.10: Yearly evaluation of molecular resistance mechanisms in *Pseudomonas aeruginosa*

Regional Centres	Total (Revived)	*CR	*CS	ESBL			Class A Carbapenemase		Class B Carbapenemase (MβL's)				Class D carbapenemase	Co-producers (n)	PCR Negative (From revived)
				SHV	TEM	VEB	KPC	GES	SPM	IMP	VIM	NDM	OXA-48 LIKE		
RC 13	13(9)	8	1	-	-	-	-	-	-	-	1	2	-	NDM+VEB (2), KPC+NDM (3)	1
RC1	16(14)	3	11	-	-	-	-	1	-	-	-	-	-	NDM+VEB (1)	12
RC 14	30(29)	3	26	-	-	-	1	-	-	-	-	2	-	-	26
SH 49	13	3	10	-	-	-	-	-	-	-	-	2	-	-	11
RC 9	60(57)	4	53	-	2	-	1	-	-	-	3	3	-	VIM+TEM (1)	47
RC 17	77(73)	8	65	-	-	-	1	1	-	-	-	-	-	KPC+VEB (5), NDM+VEB (2)	64
RC 5	45(40)	6	34	-	-	-	-	-	-	-	-	3	-	NDM+VEB (5)	32
RC 2	30(12)	2	10	-	1	-	1	-	-	-	1	-	-	NDM+VEB (1)	8
Rc 16	60(56)	11	45	-	1		1	-	-	-	1	3		VIM+VEB (1), KPC+VEB (2)	47
RC 20	30(26)	8	18	-	-	-	-	-	-	-	2	1	-	-	23
RC 6	60	15	45	-	-	2	-	1	-	-	1	3	-	NDM+VEB (5)	48
RC 8	34(30)	13	17	-	-	2	-	-	-	-	1	3	-	NDM+VEB (6)	18
Total Centres-12	**468(419)**	**84**	**335**		**4**	**4**	**5**	**3**			**10**	**22**		**34**	**337**

*CR - Carbapenem Resistant
*CS - Carbapenem Susceptible

Acinetobacter baumannii

A total of 360 revived *Acinetobacter baumannii* isolates from 11 centres across India were tested for molecular resistance genes **(Table 3.11).** Of these, 328 (91.1%) were carbapenem-resistant (CRAB), while 32 (8.9%) were carbapenem-susceptible. Molecular characterization demonstrated a clear predominance of Class D carbapenemase-mediated resistance, particularly *bla*OXA-23. A total of 104 isolates were reported with OXA-23-associated profiles, making OXA-23 the major acquired carbapenemase detected across the participating centres. The most prominent molecular pattern was the frequent co-occurrence of OXA-23 and NDM, with additional isolates carrying OXA-23 + PER, OXA-23 + NDM + PER, and less frequently OXA-23 + TEM. These findings demonstrate the accumulation of multiple β-lactam resistance determinants within individual CRAB isolates and indicate increasing molecular complexity of carbapenem resistance. The combination of a Class D carbapenemase such as OXA-23 with a Class B metallo-β-lactamase such as NDM is of particular concern because it can substantially compromise the activity of conventional β-lactam agents and further restrict therapeutic options. OXA-58 was detected in a small number of isolates and was identified in combination with OXA-23 and/or NDM, whereas other tested carbapenemases, including Class A determinants and the Class B carbapenemases IMP, VIM and SIM, were not prominently detected in the surveillance dataset. ESBL-associated determinants, particularly PER and TEM, were observed mainly as co-producers with OXA-23, further contributing to the multidrug-resistant phenotype.

In addition, PCR-negative isolates were classified as carbapenem-susceptible. Among the 29 revived isolates, a very small number were PCR-negative for all resistance determinants included in the molecular panel, suggesting that mechanisms other than the targeted carbapenemases may contribute to carbapenem resistance. This finding suggests that carbapenem resistance in these isolates may be mediated by mechanisms other than the targeted carbapenemases, including ISAba1-mediated overexpression of intrinsic OXA-51-like enzymes, ADC/AmpC overexpression, efflux-pump upregulation, porin or other outer-membrane alterations, and other chromosomal or regulatory mechanisms. OXA-51 was detected in all isolates and was used as a genomic marker for confirmation of *A. baumannii*. Collectively, the multicentric 2025 surveillance data demonstrate that carbapenem resistance among Indian *A. baumannii* isolates is overwhelmingly associated with OXA-23-mediated Class D carbapenemase production, with widespread occurrence of OXA-23 + NDM co-producers and additional PER/TEM-associated resistance determinants. The continued detection of these complex resistance profiles across geographically diversecentres highlights the need for sustained molecular surveillance and integration of phenotypic and genotypic resistance data for effective clinical management and infection-control strategies.

Table 3.11: Yearly evaluation of molecular resistance mechanisms in *Acinetobacter baumannii*

Regional Centres	Total (Revived)	*CR	*CS	ESBL				Class A		Class B carbapenemase (MβLs)				Class D carbapenemase			Co-producers (No.of isolates)	PCR Negative from revived
				SHV	TEM	VEB	PER	KPC	GES	IMP	VIM	NDM	SIM	OXA-23	OXA-24	OXA-58		
RC 1	16 (13)	13	-	-	-	-	-	-	-	-	-	-	-	7	-	-	OXA-23 + PER (1), OXA-23 + NDM (4), OXA-23 + NDM + PER (1)	-
RC 13	17 (13)	13	-	-	-	-	1	-	-	-	-	-	-	4	-	-	OXA-23 + PER (3), OXA-23 + NDM (4), OXA-23 + OXA-58 + NDM + PER (1)	-
RC 14	35 (29)	28	1	-	-	-	-	-	-	-	-	1		10	-	-	OXA-23 + PER (2), OXA-23 + NDM (15),	-
RC 9	60 (55)	53	2	-	-	-	-	-	-	-	-	-	-	11	-	-	OXA-23 + TEM (1), OXA-23 + PER (15), OXA-23 + NDM (19), OXA-23 + NDM + PER (8)	1
RC 17	74 (59)	59	-	-	-	-	-	-	-	-	-	-	-	16	-	-	OXA-23 + TEM (2), OXA-23 + NDM (35), OXA-23 + NDM + PER (6)	-
RC 5	40 (34)	23	11	-	-	-	1	-	-	-	-	2	-	8	-	-	OXA-23 + PER (1) OXA-23 + NDM (12), OXA-23 + OXA-58 + PER (1)	9
RC 2	32 (9)	9	-	-	-	-	-	-	-	-	-	-	-	3	-	-	OXA-23 + NDM (4), OXA-23 + NDM + TEM (1)	1
RC 16	60 (55)	47	8	-	-	-	1	-	-	-	-	-	-	18	-	-	OXA-23 + PER (1) OXA-23 + NDM (22) OXA-23 + NDM + TEM (4) OXA-23 + OXA-58 + NDM (2)	7
RC 20	30 (25)	21	4	-	-	-	-	-	-	-	-	-	-	10	-	-	OXA-23 + TEM (2) OXA-23 + PER (2) OXA-23 + NDM (4) OXA-23 + NDM + TEM (4)	3
RC 6	60 (59)	56	3	-	-	-	1	-	-	-	-	-	-	17	-	-	OXA-23 + PER (12) OXA-23 + NDM (16) OXA-23 + NDM + PER (7) OXA-23 + OXA-58 + NDM (1)	5
RC 8	11 (9)	6	3	-	-	-	-	-	-	-	-	-	-	-	-	-	OXA-23 + NDM (5) OXA-23 + NDM + PER (1)	3
Total Centres - 11	**435 (360)**	**328**	**32**				**4**					**3**		**104**			**220**	**29**

*CR - Carbapenem Resistant; *CS - Carbapenem Susceptible [OXA-51 was detected in all isolates and used as a genomic marker for the confirmation of *A.*

Clinical relevance and treatment guidance

Pseudomonas aeruginosa

Among the 419 *Pseudomonas aeruginosa* isolates tested, 84 (20.0%) were carbapenem-resistant, representing a significant therapeutic concern. NDM (5.3%) and VIM (2.4%) were the predominant carbapenemase determinants, with additional detection of KPC, GES, TEM and VEB, including several co-production patterns. The presence of MβL-producing isolates may substantially limit conventional β-lactam treatment options; therefore, carbapenem therapy should be guided by isolate-specific AST rather than used empirically for suspected CR *P. aeruginosa* infections.The high proportion of PCR-negative isolates (80.4%) indicates that carbapenem resistance may also involve non-carbapenemase mechanisms such as efflux-pump overexpression and porin alterations. Treatment should be guided by antimicrobial susceptibility testing, CLSI/EUCAST breakpoint and, where available, molecularcharacterization. For difficult-to-treat *P. aeruginosa*, newer β-lactams such as ceftolozane-tazobactam, ceftazidime-avibactam, imipenem-relebactam and cefiderocol should be selectedaccording to susceptibility. Cefiderocol is preferred for MBL-producing isolates when susceptible.Routine combination therapy is not recommended when an active preferred β-lactam is available.Overall, these findings emphasize the need for reliable AST, early recognition of resistancemechanisms and antimicrobial stewardship to support appropriate therapy and preserve theeffectiveness of newer antipseudomonal agents.

Acinetobacter baumannii

A high prevalence of carbapenem resistance was observed among *A. baumannii*, with 91.1% of revived isolates exhibiting carbapenem resistance, highlighting a substantial therapeutic and infection-control challenge. OXA-23 was the predominant carbapenemase determinant, with frequent detection of OXA-23 + NDM co-profiles, while PER and TEM ESBL determinants were also identified among several OXA-23-positive isolates. These findings highlight the complex β-lactam resistance profile of CRAB and the limited reliability of carbapenems for empirical treatment in severe infections. Molecular characterizationtherefore complement phenotypic antimicrobial susceptibility testing to guide appropriate therapy. For serious CRAB infections, sulbactam-containing regimens, including sulbactam-durlobactam where available, are important therapeutic options, while high-dose ampicillin-sulbactam, cefiderocol and other active agents may be considered according to susceptibility results and clinical circumstances. In NDM-producing isolates, ceftazidime-avibactam should not be used solely on the basis of carbapenemase detection because avibactam lacks activity against metallo-β-lactamases. Overall, these findings emphasize the importance of routine antimicrobial susceptibility testing, molecular surveillance, antimicrobial stewardship and strengthened infection-prevention measures for effective management of CRAB in Indian healthcare settings.

Stenotrophomonas maltophilia

Minocycline and levofloxacin remain the preferred first-line agents for *S. maltophilia* infections based on the 2025 susceptibility data, with trimethoprim-sulfamethoxazole as a reliable alternative. The modest decline in minocycline susceptibility observed in 2025 due to CLSI M100 breakpoints changes (85.5%, down from >91% in prior years). Combination therapy is generally not required outside severe sepsis or confirmed resistance to first-line agents, and empirical therapy should continue to prioritize minocycline or levofloxacin, guided by local susceptibility trends.

Chapter 4. Typhoidal Salmonella

Typhoid fever continues to pose a significant public health challenge, despite being a preventable and treatable disease in India and evolved from treatable bacterial infection to complicated disease by the emergence of antimicrobial resistance (AMR) over the time. *Salmonella enterica* serovar Typhi (hereafter *S*. Typhi) and *Salmonella enterica* serovar Paratyphi A (hereafter *S*. Paratyphi A), causative organism for enteric fever, have sequentially acquired resistance to majority class of antibiotics introduced for the treatment including first-line antibiotics- ampicillin, chloramphenicol, and cotrimoxazole, fluoroquinolones, followed by third-generation cephalosporins.

The emergence of extensively drug-resistant (XDR) *S*. Typhi has further restricted therapeutic options. More recently, reports on azithromycin resistance has raised additional concerns.This increased resistance has narrowed therapeutic options, increased the risk of treatment failure, and threatened the effective clinical management of typhoid fever. At the same time, the re-emergence of susceptibility to first-line antibiotics across various countries highlights the dynamic nature of antimicrobial resistance and underscores the importance of continued surveillance. In view of this, the Indian Council of Medical Research Antimicrobial Resistance Surveillance Network (ICMR-AMRSN) has been monitoring antimicrobial susceptibility patterns of typhoidal *Salmonella* across participating centres in different geographical regions of India. The antimicrobial susceptibility data generated through this nationwide surveillance are presented below to provide an overview of the current resistance landscape and regional variations among *S.* Typhi and *S.* Paratyphi A.

Antimicrobial susceptibility testing in typhoidal *Salmonella* demonstrated high susceptibility to most of the first-line antibiotics and third-generation cephalosporins among both *S.*Typhi and *S.* Paratyphi A isolates **(Table 4.1).** *S.* Typhi showed highest susceptibility to azithromycin (1048/1054; 99.4%), ceftriaxone (1013/1049; 96.6%), trimethoprim-sulfamethoxazole (1012/1042; 97.1%), chloramphenicol (953/989; 96.4%), and ampicillin (953/1018; 93.6%). Similarly, *S.* Paratyphi A showed high susceptibility to ceftriaxone (277/281; 98.6%), chloramphenicol (274/276; 99.3%), trimethoprim-sulfamethoxazole (281/281; 100%), and ampicillin (272/280; 97.1%).

In contrast, fluoroquinolone susceptibility was observed to be lowest. Ciprofloxacin susceptibility was observed in only 21/1075 (2.0%) *S.* Typhi and 1/281 (0.4%) *S.* Paratyphi A isolates. None of the isolates were observed susceptible against levofloxacin (0/58 for *S.* Typhi and 0/21 for *S.* Paratyphi A) or ofloxacin (0/105 and 0/18, respectively). Ciprofloxacin was tested in a much larger number of isolates than levofloxacin and ofloxacin; therefore, the absence of susceptible isolates in the levofloxacin and ofloxacin groups does not indicate lower activity of these agents compared with ciprofloxacin .Overall, widespread fluoroquinolone non-susceptibility among both *S.* Typhi and *S.* Paratyphi A, despite the high susceptibility retained by several conventional first-line agents and ceftriaxone highlights the continued therapeutic

challenge posed by fluoroquinolone resistance and the dynamic evolution of antimicrobial resistance in typhoidal *Salmonella*.

Table 4.1: Susceptibility pattern of *Salmonella* species from blood

AMA	Blood	
	***S.* Typhi N*=1055 (S%)**	***S.*Paratyphi A N*=281 (S%)**
Ampicillin	953/1018 (93.6)	272/280 (97.1)
Azithromycin*	1048/1054 (99.4)	NT**
Cefotaxime	581/642 (90.5)	168 / 177 (95.0)
Ceftriaxone	1013/1049 (96.6)	277/281 (98.6)
Chloramphenicol	953/989 (96.4)	274/276 (99.3)
Ciprofloxacin	21/1055 (2)	1/281 (0.4)
Levofloxacin	0/58 (0)	0/21* (-)
Ofloxacin	0/105 (0)	0/18* (-)
Trimethoprim-sulfamethoxazole	1012/1042 (97.1)	281/281 (100)

***N**in the column heading represents the total number of isolates included in the analysis. The denominator for each antibiotic represents the number of isolates actually tested for that antibiotic and may therefore differ between antibiotics. Susceptibility percentages were calculated using the number of isolates tested for the respective antibiotic as the denominator.*
***NT**- Not Tested as azithromycin susceptibility cut-off values are not given in CLSI for S.Paratyphi A.*
***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

S. Typhi demonstrated highest susceptibility to azithromycin (1048/1054; 99.4%), ceftriaxone (1013/1049; 96.6%), trimethoprim-sulfamethoxazole (1012/1042; 97.1%), chloramphenicol (953/989; 96.4%), cefixime (95.3%), and ampicillin (953/1018; 93.6%) **(Table 4.2**). However, ceftriaxone susceptibility was high in the North (98.4%) and South (96.7%) but was comparatively lower in the West and Central regions (83.3% each). Similarly, susceptibility to ampicillin and chloramphenicol was lower in the West and Central regions than in the North and South. Cefixime showed regional variation, with susceptibility ranging from 97.7% in the North to 50% in the West; however, these regional estimates were based on relatively small numbers of tested isolates.

Azithromycin demonstrated consistently highest activity across all regions, with susceptibility ≥95% in every region and 100% susceptibility in the West and East. Trimethoprim-sulfamethoxazole also retained high activity nationally and across most regions. In contrast, fluoroquinolone susceptibility remained extremely low. Only 21/1055 (2.0%) *S.* Typhi isolates were susceptible to ciprofloxacin nationally, with

susceptibility ranging from 0.3% in the North to 6.1% in the South, while no susceptible isolates were detected in the Central region. No susceptible isolates were observed among those tested for levofloxacin (0/58; 0% nationally). Overall, the regional findings demonstrate persistent and widespread fluoroquinolone non-susceptibility, susceptibility to azithromycin and ceftriaxone, and regional pockets of reduced susceptibility to ceftriaxone and older first-line antibiotics.

Table 4.2: Susceptibility pattern of *S.* Typhi from blood across different regions of India

AMA	National (N=1055) (S%)	North (N=704) (S%)	South (N=239) (S%)	West (N*=85) (S%)	Central (N=21) (S%)	East (N=6) (S%)
Ceftriaxone	1013/1049 (96.6)	692/703 (98.4)	231/239 (96.7)	70/84 (83.3)	15/18* (-)	5/5* (-)
Azithromycin	1048/1054 (99.4)	702/704 (99.7)	236/239 (98.7)	85/85 (100)	20/21* (-)	5/5* (-)
Cefixime	302/317 (95.3)	254/260 (97.7)	43/48 (89.6)	3/6* (-)	0/0 (-)	2/3* (-)
Ampicillin	953/1018 (93.6)	669/703 (95.2)	224/238 (94.1)	39/50 (78)	17/21* (-)	4/6* (-)
Chloramphenicol	953/989 (96.4)	677/693 (97.7)	187/195 (95.9)	67/77 (87)	18/20* (-)	4/4* (-)
Trimethoprim-sulfamethoxazole	1012/1042 (97.1)	683/697 (98)	232/239 (97.1)	71/79 (89.9)	20/21* (-)	6/6* (-)
Levofloxacin	0/58 (0)	0/36 (0)	0/17* (0)	0/0 (-)	0/2* (0)	0/6* (-)
Ciprofloxacin	21/1055 (2)	2/704 (0.3)	15/239 (6.2)	4/85 (4.7)	0/23* (0)	0/6* (-)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Year-wise antimicrobial susceptibility surveillance of *S.* Typhi from 2017 to 2025 demonstrated that ceftriaxone susceptibility remained high throughout the surveillance period (93.8–99.6%), with a transient decline to 93.8% in 2022 followed by recovery to 98.0% in 2024 and 96.6% in 2025 **(Table 4.3, Figure 4.1).** Cefixime showed a similar pattern, with susceptibility remaining above 96% during most years, declining to 94.5% in 2022 and 95.3% in 2025. Azithromycin exhibited a progressive improvement in susceptibility, increasing from 95.7% in 2017 to approximately 99% in recent years and reaching 99.4% in 2025.

Susceptibility to the traditional first-line agents was also high. Ampicillin susceptibility increased from 91.9% in 2017 to 97.5% in 2020 and remained at 97.5% in 2024, although a decline to 93.6% was observed in 2025. Chloramphenicol and trimethoprim-sulfamethoxazole remained consistently active, with susceptibility of 96.4% and 97.1%, respectively, in 2025. In contrast, ciprofloxacin susceptibility showed a decline, from 11.6% in 2017 to 2.0% in 2025, with susceptibility remaining below 3% since 2022 except for the earlier transient increase observed in 2021. Levofloxacin susceptibility was

also low and variable, with no susceptible isolate detected among the 58 isolates tested in 2025.

Overall, the nine-year surveillance data demonstrate persistent fluoroquinolone non-susceptibility in *S.* Typhi, and high susceptibility to azithromycin, ceftriaxone and first-line antibiotics. The re-emergence of susceptibility to older first-line drugs reflects reduced antimicrobial selection pressure following their decreased use, whereas the continued low susceptibility to fluoroquinolones highlights their limited therapeutic utility for empirical treatment of enteric fever.

Table 4.3: Yearly susceptibility trends of *S.* Typhi from blood

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year - 2022	Year-2023	Year-2024	Year-2025
	N=345 (S%)	N=580 (S%)	N=728 (S%)	N=206 (S%)	N=293 (S%)	N=584 (S%)	N=1098 (S%)	N=841 (S%)	N=1055 (S%)
Ampicillin	305/ 332 (91.9)	551/ 576 (95.7)	658/ 703 (93.6)	192/ 197 (97.5)	278/ 290 (95.9)	510/ 542 (94.1)	619/ 635 (97.5)	748/ 767 (97.5)	953/ 1018 (93.6)
Ceftriaxone	329/ 334 (98.5)	531/ 541 (98.2)	645/ 658 (98)	192/ 193 (99.5)	280/ 281 (99.6)	534/ 569 (93.8)	640/ 661 (96.8)	824/ 841 (98)	1013/ 1049 (96.6)
Cefixime	221/ 223 (99.1)	344/ 349 (98.6)	434/ 448 (96.9)	157/ 158 (99.4)	209/ 212 (98.6)	416/ 440 (94.5)	549/ 570 (96.3)	614/ 627 (97.9)	302/ 317 (95.3)
Azithromycin	266/ 278 (95.7)	497/ 506 (98.2)	547/ 568 (96.3)	163/ 166 (98.2)	212/ 213 (99.5)	520/ 537 (96.8)	640/ 657 (97.4)	837/ 841 (99.5)	1048/ 1054 (99.4)
Ciprofloxacin	35/ 302 (11.6)	29/ 440 (6.6)	35/ 501 (7)	8/ 162 (4.9)	40/ 204 (19.6)	18/ 590 (3.0)	14/ 674 (2.1)	11/ 841 (1.3)	21/ 1055 (2)
Levofloxacin	*0/3 (-)	*5/18 (-)	3/35 (8.6)	*4/12 (-)	9/30 (30)	7/108 (6.4)	10/55 (18.2)	*1/22 (-)	0/58 (0)
Trimethoprim-sulfamethoxazole	322/ 341 (94.4)	552/ 575 (96)	693/ 718 (96.5)	194/ 202 (96)	266/ 278 (95.7)	537/ 578 (92.9)	634/ 655 (96.8)	812/ 831 (97.7)	1012/ 1042 (97.1)
Chloramphenicol	267/ 278 (96)	541/ 560 (96.6)	582/ 611 (95.3)	180/ 185 (97.3)	246/ 257 (95.7)	473/ 499 (94.7)	597/ 608 (98.2)	578/ 592 (97.6)	953/ 989 (96.4)

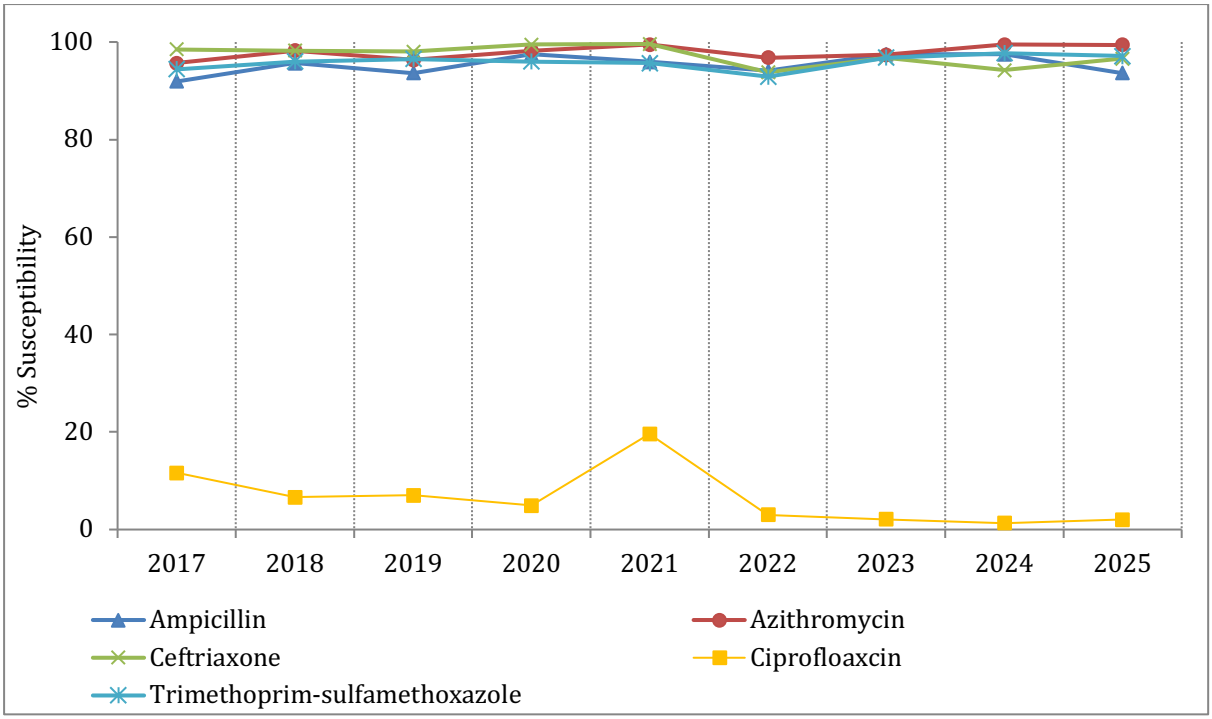


Figure 4.1: Year-wise antimicrobial susceptibility trends among *S.* Typhi isolates recovered from blood, 2017–2025

Year-wise antimicrobial susceptibility surveillance of *S.* Paratyphi A from 2017 to 2025 demonstrated consistently high susceptibility to ceftriaxone, cefixime, ampicillin, trimethoprim-sulfamethoxazole and chloramphenicol, with the occasional fluctuations **(Table 4.4, Figure 4.2).** Ceftriaxone susceptibility remained high throughout the surveillance period, ranging from 95.0% to 100%, and was 98.6% in 2025. Cefixime susceptibility was also high, ranging from 90.0% to 100%, with a transient decline to 90.0% in 2022 followed by recovery to 98.9% in 2025. Ampicillin susceptibility ranged from 90.6% in 2019 to 100% in 2023 and remained high at 97.1% in 2025. Trimethoprim-sulfamethoxazole and chloramphenicol demonstrated good activity against *S.* Paratyphi A. Susceptibility to trimethoprim-sulfamethoxazole was ≥95.9% throughout the study period and reached 100% in 2025, while chloramphenicol susceptibility remained ≥94.7%, reaching 99.3% in 2025.

While, ciprofloxacin susceptibility remained extremely low; declining from 10.0% in 2017 to 0.4% in 2025. Although transient increases were observed in 2021 (8.7%) and 2023 (6.9%), susceptibility subsequently declined to 1.2% in 2024 and 0.4% in 2025. In case of levofloxacin; no susceptible isolates were detected among the 21 isolates tested in 2025.

Overall, these results highlight the fluoroquinolone non-susceptibility in *S.* Paratyphi A, despite the high susceptibility to ceftriaxone, cefixime, trimethoprim-sulfamethoxazole, chloramphenicol and ampicillin.

Table 4.4: Year-wise antimicrobial susceptibility trends among *S.*Paratyphi A isolates recovered from blood, 2017–2025

AMA	Year- 2017	Year- 2018	Year- 2019	Year- 2020	Year -2021	Year-2022	Year- 2023	Year-2024	Year-2025
	N=41 (S%)	N=125 (S%)	N=147 (S%)	N=52 (S%)	N=58 (S%)	N=118 (S%)	N=240 (S%)	N=346 (S%)	N=281 (S%)
Ampicillin	38/40 (95)	122/125 (97.6)	125/138 (90.6)	42/46 (91.3)	55/57 (96.5)	109/113 (96.4)	93/93 (100)	319/324 (98.5)	272/280 (97.1)
Ceftriaxone	38/40 (95)	121/124 (97.6)	139/142 (97.9)	47/47 (100)	57/57 (100)	111/115 (96.5)	96/96 (100)	342/346 (98.8)	277/281 (98.6)
Cefixime	26/27 (96.3)	105/105 (100)	105/107 (98.1)	32/32 (100)	45/45 (100)	72/80 (90.0)	70/73 (95.9)	275/281 (97.9)	93/94 (98.9)
Ciprofloxacin	4/40 (10)	1/111 (0.9)	1/86 (1.2)	1/31 (3.2)	4/46 (8.7)	1/121 (0.8)	7/101 (6.9)	4/346 (1.2)	1/281 (0.4)
Levofloxacin	*0/2 (-)	*0/5 (-)	0/25 (0)	*0/9 (-)	*0/8 (-)	*1/6 (-)	4/19 (21.1)	*0/5 (-)	0/21 (-)
Trimethoprim-sulfamethoxazole	41/41 (100)	123/123 (100)	144/145 (99.3)	47/49 (95.9)	54/55 (98.2)	117/118 (99.1)	95/95 (100)	342/343 (99.7)	281/281 (100)
Chloramphenicol	30/30 (100)	121/121 (100)	128/128 (100)	48/49 (98)	54/57 (94.7)	107/109 (98.1)	86/87 (98.9)	265/266 (99.6)	274/276 (99.3)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

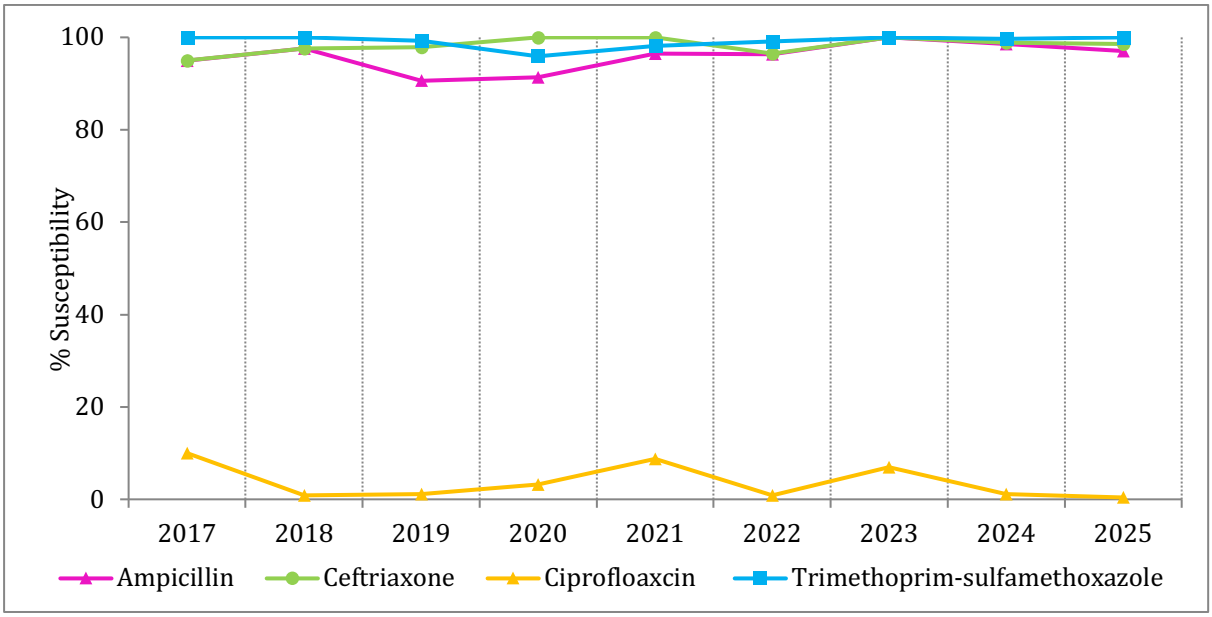


Figure 4.2: Year-wise antimicrobial susceptibility trends among *S.*Paratyphi A isolates recovered from blood, 2017–2025

Comparison of susceptibility in *S.* Typhi and *S.* Paratyphi A

S. Paratyphi A shows morepreservation of susceptibility to the older first-line drugs than *S.* Typhi. In 2025, *S.* Paratyphi A had 97.1% ampicillin, 99.3% chloramphenicol and 100% trimethoprim-sulfamethoxazole susceptibility, compared with 93.6%, 96.4% and 97.1%, respectively, for *S.* Typhi. However, ciprofloxacin susceptibility was almost completely absent in both serovars—0.4% in *S.* Paratyphi A versus 2.0% in *S.* Typhi.

Molecular mechanism of resistance

Genotypic resistance determinants were compared with phenotypic susceptibility profiles **(Table 4.5).** Susceptibility was assessed by disk diffusion for first-line antibiotics (co-trimoxazole, amoxicillin, chloramphenicol), fluoroquinolones (ciprofloxacin, pefloxacin), third-generation cephalosporins (cefixime, ceftriaxone), and azithromycin, according to CLSI guidelines. Multiple drug resistance (MDR) was defined as resistance to ampicillin, chloramphenicol, and co-trimoxazole.

A total of 104 *Salmonella* isolates underwent whole genome sequencing (WGS), comprising 79 (76.0%) *S.* Typhi, 13 (12.5%) *S.* Paratyphi A, and 12 (11.5%) non-typhoidal *Salmonella* (NTS). Among *S.* Typhi, H58 lineage (genotype 4.3.1) predominated, particularly sublineages 4.3.1.2 (n=22), 4.3.1.2.1 (n=27), and 4.3.1.1 (n=12). Other isolates belonged to genotypes 2.2, 2.2.2, 2.5, 3.2, 3.2.2, 3.3.1, and 3.3.2. *S.* Paratyphi A predominantly belonged to ST129 (n=9), followed by ST85 (n=4). NTS comprised *S.* Kentucky (n=3), *S.* Agona (n=2), and one isolate each of *S.* Virchow, Braenderup, Newport, Typhimurium, Enteritidis, Anatum, and an unclassified *Salmonella enterica* isolate.

Most *S.* Typhi isolates exhibited low ampicillin MICs, indicating re-emerging susceptibility. However, 6/79 (7.6%) isolates demonstrated resistance associated with *bla*TEM-family genes. Five carried *bla*TEM-1D, alone or with *bla*SHV-12, while one harboured *bla*TEM-1D/*bla*TEM-116. These genes occurred predominantly in MDR isolates and frequently co-occurred with *catA1*, *sul1/sul2*, *dfrA7*, and ESBL determinants, indicating persistence of classical ampicillin resistance despite reduced clinical use.

Chloramphenicol resistance was detected in 4/79 (5.1%) *S.* Typhi isolates carrying *catA1*. All belonged to H58 lineage and concurrently harboured *bla*TEM-1D, *sul1/sul2*, and *dfrA7*, representing the classical MDR phenotype. None of the *S.* Paratyphi A or NTS isolates carried *catA1*. The low prevalence suggests re-emerging susceptibility following reduced clinical use.

Most isolates remained susceptible to co-trimoxazole. Resistance for co-trimoxazole was identified in 4/79 (5.1%) *S.* Typhi isolates all also carrying *bla*TEM-1 D and *catA1*. Additionally, *dfrA14* occurred in two *S.* Typhi and two NTS isolates (*S.* Newport and Kentucky), while *dfrA15* with *sul1* was detected in *S.* Braenderup. No *S.* Paratyphi A isolates carried *sul1*, *sul2*, or *dfrA7*. The co-occurrence of these determinants suggests their association with MDR gene clusters and potentially mobile genetic elements.

Fluoroquinolone resistance was the most prominent resistance phenotype. Among *S.* Typhi, 27/79 (34.2%) carried triple QRDR mutations (*gyrA* S83F/D87N with *parC* S80I), predominantly within H58 genotype 4.3.1.2.1. These isolates exhibited high-level resistance, with ciprofloxacin MICs of 32 to >256 µg/mL and increased levofloxacin and ofloxacin MICs. Other mutations included *gyrA* S83F alone (30.4%), S83Y (13.9%), S83F with *parC* S80I (5.1%), and S83F with *parE* L416F (5.1%). Less frequent mutations involved *gyrA* D87G/D87N, *parC* E84G, *gyrB* S464F, and *parE* D420N.

Among *S.* Paratyphi A, 12/13 (92.3%) carried *gyrA* S83F with *parC* T57S, while one carried S83Y with T57S. All were associated with reduced fluoroquinolone susceptibility.

NTS isolates demonstrated diverse resistance mechanisms. All three *S.* Kentucky isolates carried multiple QRDR mutations associated with high-level resistance. *S.* Agona also harboured multiple mutations, while *S.* Newport and Braenderup carried plasmid-mediated *qnrS13* and *qnrB7*, respectively. *S.* Typhimurium and Enteritidis lacked QRDR mutations and remained susceptible. Overall, chromosomal QRDR mutations predominated in typhoidal *Salmonella*, whereas NTS exhibited both chromosomal and plasmid-mediated mechanisms.

Most isolates exhibited susceptible ceftriaxone MICs (0.032–0.125 µg/mL). However, 9/104 (8.7%) carried ESBL genes. Among *S.* Typhi, 5/79 (6.3%) were resistant: three carried *bla*SHV-12, one *bla*CTX-M-15, and one *bla*CTX-M-15 with *bla*NDM-5, resulting in ceftriaxone MICs ≥32 µg/mL. No ESBL genes were detected in *S.* Paratyphi A. Among NTS, one *S.* Newport carried *bla*CTX-M-15 and three *S.* Kentucky carried *bla*CTX-M-55. These genes were associated with transferable plasmids, including IncX3, IncH12/IncH12A, and IncFIB. ESBL-producing *Salmonella* poses a clinical concern because ceftriaxone remains central to treating severe enteric fever and invasive salmonellosis.

Two *S.* Typhi isolates (2.5%) carried *acrB* R717Q, although both remained phenotypically susceptible to azithromycin. One *S.* Newport isolate carried plasmid-mediated *mph(A)* (MIC 8 µg/mL). These findings strongly emphasise the need for continued, integrated genomic and phenotypic surveillance of typhoidal and non-typhoidal Salmonella.

Table 4.5: Genotypic and phenotypic details of isolates selected for molecular characterization

S.N	LAB ID	organism	ST	Haplotype	Mutation	Plasmid	CTR	FIX	AZM	CIP	LEV	OFL	SXT	CHL	AMP
1	220/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	34	8	12	6	16	34	32	26
2	11815/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	30	6	6	12	12	31	29	22
3	24307/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.032	0.125	22	8	12	16	36	37	27
4	27367/ RC1	S Typhi	ST1	4.3.1.2	gyr AS83Y		0.064	0.38	16	0.19	0.5	0.25	32	26	31
5	24096/ RC1	S Typhi	ST1	4.3.1	gyr AS83Y		0.19	0.25	16	0.75	0.25	0.75	34	31	30
6	304/ RC1	S Typhi	ST1	4.3.1.2	gyr AS83Y		0.064	0.19	16	0.19	0.5	0.5	31	29	25
7	17373/ RC1	S Typhi	ST1	4.3.1.1	gyr AS83Y		0.064	0.25	16	0.75	1	1	34	31	29
8	23948/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.047	0.5	6	64	3	16	28	30	28
9	20479/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.5	8	64	4	16	30	30	27
10	221/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.75	6	32	2	16	27	29	19
11	24370/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.38	12	>256	>32	24	34	28	19
12	27131/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.047	0.094	3	>256	6	3	35	28	25
13	12729/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.38	4	16	16	16	29	30	17
14	12376/ RC1	S Typhi	ST2	3.2	gyrA D87G		0.064	0.125	4	0.064	0.032	0.19	30	32	31
15	211/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.5	12	>256	>32	>32	31	27	29
16	8494/21 RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I	Col (pHAD28)	0.064	0.38	6	96	8	24	30	30	28
17	17288/22 RC1	S Typhi	ST1	4.3.1.2	gyr AS83F/D87N;parCS80I		0.094	0.38	16	0.25	0.38	0.25	33	36	27
18	661005/ RC5	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I, acrB R717Q		32	32	14	11	13		35	34	31
19	697510/ RC5	S Typhi	ST1	4.3.1.2	gyr AS83F		0.094	0.125	8	0.25	0.5	0.75	33	31	6
20	697540/ RC5	S Typhi	ST2	2.5	gyr AS83F		0.094	0.125	12	0.5	0.75	0.75	38	36	6
21	699077/ RC6	S Typhi	ST2	3.3.1	gyr AS83F;parE L416F		0.19	0.25	12	0.125	0.19	0.19	48	36	12
22	707791/ RC17	S Typhi	ST1	4.3.1.1	gyr AS83F		0.094	0.125	8	2	3	4	28	32	6
23	707609// RC17	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.125	8	4	2	4	26	28	24

S.N	LAB ID	organism	ST	Haplotype	Mutation	Plasmid	CTR	FIX	AZM	CIP	LEV	OFL	SXT	CHL	AMP
24	724026/ RC3	S Typhi	ST1	4.3.1.2	gyr AS83F; parCS80I		0.064	0.125	8	0.25	0.25	0.38	37	34	34
25	727239/ RC3	S Typhi	ST1	4.3.1.2	gyr AS83F		0.047	0.094	8	0.125	0.25	0.25	43	34	39
26	734723/ RC3	S Typhi	ST1	4.3.1.1	gyr AS83Y		0.047	0.19	12	0.125	0.25	0.25	42	34	37
27	664937/Rc16	S Typhi	ST1	4.3.1.2	gyr AS83F		0.064	0.125	8	0.125	0.25	0.38	37	33	22
28	790686/RC17	S Typhi	ST1	4.3.1.1	gyr A S83F		0.094	0.38	8	0.25	0.38	0.38	30	30	30
29	790688/RC17	S Typhi	ST1	4.3.1.1	gyr A S83Y		0.064	0.25	8	0.19	0.25	0.25	34	34	33
30	66557/ RC14	S Typhi	ST1	4.3.1.2	gyr AS83F;parC S80I		0.064	0.025	8	0.094	0.19	0.19	32	30	6
31	670208/ RC14	S Typhi	ST1	4.3.1.2	gyr AS83F		0.047	0.125	12	0.125	0.25	0.25	32	33	30
32	791982/ RC14	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		32	32	48	>256	>32	>32	6	6	6
33	791992/ RC14	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.25	12	>256	>32	>32	34	34	31
34	720493/ RC14	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.19	8	32	32	32	33	34	30
35	791236/ RC14	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.19	8	>256	>32	>32	29	33	30
36	791250/ RC14	S Typhi	ST1	4.3.1.2	gyr AS83F		0.094	0.25	12	0.38	0.75	0.75	34	23	25
37	38200/25/ RC1	S Typhi	ST2	2.2.2	gyr AS83F	IncFIB(pHCM2)	0.094	0.19	2	0.094	0.125	0.25	35	33	34
38	38892/25/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.5	4	48	12	16	31	32	30
39	38529/25/ RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.75	2	32	12	12	32	32	30
40	854676/ RC2	S Typhi	ST2	2.5	gyrA S83F	IncFIB(pHCM2)	0.064	0.25	8	0.25	0.38	0.5	34	31	30
41	854683/ RC2	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.25	12	96	24	24	29	34	30
42	854691/ RC2	S Typhi	ST1	4.3.1.2	gyr AS83F;parC E84G		0.047	0.094	8	96	24	24	30	31	24
43	854699/ RC2	S Typhi	ST2	2.5	gyrA S83F		0.064	0.25	12	0.25	0.38	0.38	24	29	26
44	854704/ RC2	S Typhi	ST1	4.3.1.2	gyr A S83F		0.047	0.094	12	0.25	0.38	0.38	21	31	26
45	796275/ RC5	S Typhi	ST1	4.3.1.1	gyr A S83Y		0.064	0.125	8	0.25	0.25	0.38	33	30	26
46	796305/ RC5	S Typhi	ST2	3.3.2	No mutation		0.047	0.094	4	0.047	0.047	0.064	35	30	31
47	796927/ RC5	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.5	12	>256	>32	>32	30	33	28
48	791310/ RC14	S Typhi	ST1	4.3.1.2	gyr AS83F		0.094	0.125	8	96	24	24	23	28	17
49	791311/ RC14	S Typhi	ST1	4.3.1.2	gyr AS83F/D87N;parCS80I		0.094	0.125	12	>32	32	32	26	25	19

S.N	LAB ID	organism	ST	Haplotype	Mutation	Plasmid	CTR	FIX	AZM	CIP	LEV	OFL	SXT	CHL	AMP
50	B-40367/25/ RC1	S Typhi	ST1	4.3.1.1	blaTEM-1D;CatA1;gyr B S464F; Sul1;Sul2; dfrA7; acrB R717Q	IncQ1 aph(6)-d,aph(3")-lb	0.125	0.25	12	0.094	0.094	0.25	6	6	6
51	B-40689/25/ RC1	S Typhi	ST2	2.2	gyr AS83F		0.032	0.125	3	0.25	0.125	0.19	33	31	22
52	793667/RC6	S Typhi	ST1	4.3.1.2	gyr AS83F		0.047	0.094	12	0.19	0.25	0.38	31	33	30
53	793673/ RC6	S Typhi	ST2	3.3.1	gyr AS83F;parE L416F		0.094	0.38	8	0.25	0.38	0.5	25	29	24
54	794657/ RC6	S Typhi	ST2	3.3.1	gyr AS83F;parE L416F		0.094	0.38	12	0.25	0.38	0.5	29	30	24
55	794669/ RC6	S Typhi	ST1	4.3.1.2	gyr AS83F;parCS80I		0.094	0.5	8	0.25	0.38	0.5	30	30	24
56	795917/ RC6	S Typhi	ST1	4.3.1.1	gyr AS83F		0.064	0.125	12	0.19	0.38	0.5	30	31	26
57	832168/ RC6	S Typhi	ST1	4.3.1.1	blaSHV-12;blaTEM-1D;CatA1;gyrA S83Y;parE D420N; Sul1;Sul2; dfrA7	IncX3 (blaSHV-12 contig); IncQ1 (aph(6)-Id,aph(3)-lb contig)	>32	>32	4	0.19	0.5	0.75	6	6	6
58	753422/RC5	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.25	8	32	32	32	34	32	29
59	753549/RC5	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.047	0.125	12	96	16	16	34	36	31
60	796459/RC5	S Typhi	ST1	4.3.1.2	gyr A S83Y; blaSHV-12	IncX3	32		4	0.125	0.19	0.25	34	31	29
61	802314/ RC5	S Typhi	ST1	4.3.1.2	gyr AS83F; qnrS;blaCTX-M-15_23;Sul2;dfrA14;tetA	Inc FIB(PHCM2); Inc FIB (K); Inc X1	>32	>32	4	1	3	4	6	28	6
62	796146/ RC16	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.5	12	>256	>32	>32	33	35	29
63	838838/RC8	S Typhi	ST2	3.2.2	gyr AS83F		0.094	0.38	8	0.25	0.38	0.5	33	32	31
64	2365/ RC1	S Typhi	ST1	4.3.1.1	gyr AS83F	Inc FIB(PHCM2)	0.125	0.38	6	0.19	0.125	0.38	36	33	28
65	843469/RC9	S Typhi	ST1	4.3.1.1	blaSHV-12;blaTEM-1D;CatA1;gyrA S83Y;parE D420N; Sul1;Sul2; dfrA7	IncX3 (blaSHV-12 contig); IncQ1 (aph(6)-Id,aph(3)-lb contig)	32		12	0.25	0.38	0.38	6	6	6
66	839436/RC14	S Typhi	ST1	4.3.1.2.1	blaTEM-1D;gyrA S83F/D87N; parC S80I		0.064	0.19	12	96	24	24	34	31	29
67	876826/RC14	S Typhi	ST1	4.3.1.1	bla CTX-M-15_23; tetA; gyrA S83Y; qnrS; blaNDM5	IncX3; Inc FIB(K)	>32	>256	8	32	16	16	28	32	6
68	874807/SH49	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.5	8	>32	16	16	31	32	20

S.N	LAB ID	organism	ST	Haplotype	Mutation	Plasmid	CTR	FIX	AZM	CIP	LEV	OFL	SXT	CHL	AMP
69	845632/ SH49	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.064	0.25	12	0.125	0.25	0.25	32	32	28
70	844974/ SH49	S Typhi	ST1	4.3.1.1	gyr AS83Y		0.047	0.125	8	32	16	16	35	31	24
71	841821/RC27	S Typhi	ST2	2.2	gyr AS83F		0.047	0.094	4	0.125	0.25	0.38	34	35	25
72	880878/RC27	S Typhi	ST1	4.3.1	gyr AS83Y		0.094	0.5	12	0.25	0.25	0.38	30	31	21
73	866906/RC4	S Typhi	ST1	4.3.1.1	blaTEM-1D/blaTEM-116; gyrA S83Y		0.047	0.094	12	0.25	0.25	0.38	32	27	24
74	866319/RC26	S Typhi	ST1	4.3.1.2	gyr A S83Y		0.064	0.125	2	0.125	0.125	0.125	34	32	28
75	899222/ RC26	S Typhi	ST2	3.3.1	gyr AS83F;parE L416F		0.047	0.094	1	0.125	0.19	0.125	35	30	30
76	859597/ RC26	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.5	2	24	4	3	34	32	26
77	11477/26/RC1	S Typhi	ST1	4.3.1.1	gyrA D87N		0.064	0.25	8	0.19	0.19	0.19	30	32	24
78	8410/26/RC1	S Typhi	ST1	4.3.1.2.1	gyr AS83F/D87N;parCS80I		0.094	0.38	6	48	8	12	31	29	19
79	11182/26/RC1	S Typhi	ST2	2.2	gyr AS83F		0.047	0.125	4	0.25	0.25	0.19	34	34	24
80	735/RC1	S Para A	ST129	2.4.2	gyr AS83F		0.064	29	12	0.38	0.75	2	6	30	20
81	742/ RC1	S Para A	ST129	2.4.2	**gyr AS83F**		0.064	29	12	0.5	0.75	2	6	31	20
82	66081/ RC5	S Para A	ST129		gyr AS83F; ParC T57S		0.094	0.125	14	26	21	24	34	31	26
83	661125/ RC5	S Para A	ST129		gyr AS83F; ParC T57S		0.094	0.125	17	29	24	24	35	26	24
84	698551/RC5	S Para A	ST85		gyr A S83Y; parC T57S		0.064	0.125	8	0.25	0.38	0.5	35	34	6
85	724028/ RC3	S Para A	ST129		gyr AS83F; ParC T57S		0.094	0.19	12	0.38	0.5	0.5	36	29	23
86	772290/RC17	S Para A	ST129		gyr AS83F; ParC T57S		0.064	0.25	12	0.25	0.38	0.38	30	30	25
87	796431/ RC5	S Para A	ST85		gyr AS83F; parC T57S	Col (PHAD28)	0.094	0.38	12	0.125	0.25	0.38	32	29	26
88	2450/RC1	S Para A	ST85		gyr AS83F; parC T57S	Col(PHAD28)	0.125	0.25	16	0.25	1	1	31	29	22
89	842126/RC27	S Para A	ST129		gyr AS83F; ParC T57S		0.047	0.125	12	0.25	0.38	0.5	32	30	14
90	877060/RC30	S Para A	ST129		gyr AS83F; ParC T57S		0.064	0.125	12	0.25	0.5	0.38	33	32	26
91	11314/26/RC1	S Para A	ST129		gyr AS83F; ParC T57S		0.125	0.38	12	0.75	1.5	1	32	26	23
92	8958/26/RC1	S Para A	ST85		gyr AS83F; parC T57S		0.064	0.25	12	0.25	1	1.5	32	30	20
93	665594/ RC5	S. Virchow	ST1750		parC T57S	IncFIB(pHCM2)	32	32	16	35	32		34	29	27
94	792025/RC8	S. Braenderup	ST22		parC;T57S;qnrB7;sul1;dfrA15	IncX3	0.094	0.25	8	0.19	0.25	0.25	6	32	29

S.N	LAB ID	organism	ST	Haplotype	Mutation	Plasmid	CTR	FIX	AZM	CIP	LEV	OFL	SXT	CHL	AMP
95	809972/ RC8	S.Newport			parC T57S;qnrS13; blaCTX-M-15;mph(A); dfrA14; tetB	IncH12/IncH12A	>32	>256	8	0.19	0.19	0.25	6	30	6
96	809975/ RC8	S. Agona			tetA; Sul 1; gyrA S83F/D87N;parC T57S/S80I		0.064	0.19	8	8	8	4	32	30	30
97	796435/ RC5	S. Agona	ST13		gyr AS83F/D87N;parC T57S/S80I; tet A; sul1		0.094	0.5	8	>32	32	32	30	30	30
98	831259/RC14	S. Typhimurium	ST36		Inc FII(S)		0.047	0.125	12	0.0047	0.064	0.064	30	29	22
99	753392/RC5	S. Kentucky	ST198		gyr AS83F/D87Y;parC T57S/S80I; tetA;blaCTX-M-55; blaTEM-141; bla TEM-1B; bla TEM-206	Inc FIB(PHCM2)	>32	>32	8	32	32	32	31	28	6
100	753484/RC5	S. enteritidis	ST 11		No mutation	Inc FIB(S)/Inc FII(S); Inc FIB(S)/Inc FII(S); Col (PHAD 28)	0.064	0.25	8	0.047	0.047	0.064	38	32	30
101	753607/RC5	S. Kentucky	ST198		gyr AS83F/D87Y;parC T57S/S80I; tetA;blaCTX-M-55; blaTEM-141; bla TEM-1B; bla TEM-206	Inc FIB(PHCM2)	>32	>32	12	>256	32	32	26	27	6
102	811380/RC16	S. Enterica	No file				0.064	0.25	8	0.094	0.19	0.25	34	31	29
103	878872/RC9	S Anatum	ST64		blaTEM-116; parC T57S		0.064	0.125	12	0.064	0.064	0.094	34	28	19
104	876839/RC14	S. Kentucky	ST198		gyr AS83F/D87Y;parC T57S/S80I; tetA;blaCTX-M-55; blaTEM-141; bla TEM-1B; bla TEM-206, floR; dfrA14; sul3		0.047	0.19	12	96	24	24	6	6	6

MLST (Multiple locus sequence typing)

Multilocus sequence typing (MLST) characterises bacterial isolates through seven conserved housekeeping genes: *thrA, purE, sucA, hisD, aroC, hemD,* and *dnaN*. Unique allele combinations define sequence types (STs), enabling comparison of bacterial population structure and epidemiology.

Among 104 whole-genome sequenced *Salmonella* isolates, ST1 predominated among 79 *S.* Typhi isolates (62/79; 78.5%), followed by ST2 (17/79; 21.5%). ST1 was exclusively associated with the H58 lineage, encompassing genotypes 4.3.1, 4.3.1.1, 4.3.1.2, and 4.3.1.2.1, and comprised most MDR, XDR, and fluoroquinolone-resistant isolates. ST2 was associated with non-H58 genotypes and generally exhibited lower resistance. Among 13 *S.* Paratyphi A isolates, ST129 predominated (9/13; 69.2%), followed by ST85 (4/13; 30.8%). Both harboured QRDR mutations associated with reduced fluoroquinolone susceptibility. The 12 non-typhoidal *Salmonella* (NTS) isolates demonstrated greater ST diversity. *S.* Kentucky ST198 carried multiple resistance determinants, including *bla*CTX-M-55, *bla*TEM variants, *tetA*, and QRDR mutations.

Isolation and identification of Ceftriaxone *Salmonella* Typhi

During ICMR-AMRSN surveillance (2023–2026), three ceftriaxone- and cefixime-resistant *S. Typhi* isolates exhibiting concurrent resistance to ampicillin, chloramphenicol, co-trimoxazole, and fluoroquinolones were identified at a tertiary healthcare centre in North India. Isolates were identified using the White–Kauffmann–Le Minor scheme, Vitek 2 Compact, and conventional biochemical methods. Blood culture bottles flagged positive by BACT/ALERT were subcultured for identification and further phenotypic and genomic characterisation.Genome assemblies ranged from 4.85–4.91 Mb, comprising 2–18 contigs. All isolates showed 87 SNPs relative to the reference genome, indicating close genetic relatedness within genotype 4.3.1.1.

All three XDR isolates were recovered from blood cultures between 2023 and 2025, involving two female patients (18 and 27 years) and one 7-year-old male child. Ceftriaxone MICs were 32 µg/mL and cefixime MICs 256 µg/mL. All were resistant to ampicillin and co-trimoxazole. Ciprofloxacin MICs ranged from 0.19–16 µg/mL. Despite their XDR phenotype, all remained susceptible to azithromycin (MICs 3–8 µg/mL) **(Tables 4.6 and 4.7).**

Table 4.6: Phenotypic Characterization of extensively drug-resistant *S.* Typhi

	MIC (µg/ml)					Disk Diffusion (mm)													
Year of Isolation	FIX	AZM	CIP	OFL	LEV	OFL	LEV	CIP	PFL	CTR	FIX	SXT	CHL	AMP	AZM	NA	IMI	MEM	ETP	TAX
S34/ 15291	256	8	16	3	3	17	17	18	19	10	6	6	6	6	19	10	35	36	34	25
S35/32483	256	6	1.5	2	2	20	25	27	20	18	6	6	6	6	20	6	34	35	33	24
S36/8072	256	3	0.19	0.75	0.5	27	28	29	19	20	6	6	6	6	23	6	35	34	34	26

Abbreviations: FIX, cefixime; AZM, azithromycin; CIP, ciprofloxacin; OFL, ofloxacin; LEV, levofloxacin; PFL, pefloxacin; CTR, ceftriaxone; SXT, trimethoprim-sulfamethoxazole; CHL, chloramphenicol; AMP, ampicillin; NA, nalidixic acid; IMI, imipenem; MEM, meropenem; ETP, ertapenem; TAX, cefotaxime.

Table 4.7: Genotypic Characterization of extensively drug-resistant *S.* Typhi

	Genotypic Characterization (Pathogenwatch)											
	Ampicillin	Broad Spectrum Cephalosporins	Chloram phenicol	Ciprofloxacin	Sulfonamides	Trimethoprim	Co-Trimoxazole	Sequence Type	Genotype	Plasmid	No. of Contigs	Genome length
S34/ 15291	blaCTX-M-15_23;blaTEM-1D	blaCTX-M-15_23	catA1	aac6-lb-cr;gyrB_S464F;qnrB	sul1; sul2	dfrA14;dfrA7	dfrA14;dfrA7; sul1; sul2	ST1	4.3.1.1	IncR	2	4914464
S35/ 32483	blaSHV-12;blaTEM-1D	blaSHV-12	catA1	gyrA_S83Y;parE_D420N	sul1; sul2	dfrA7	dfrA7; sul1; sul2	ST1	4.3.1.1	IncX3	10	4850146
S36/8072	blaSHV-12;blaTEM-1D	blaSHV-13	catA2	gyrA_S83Y;parE_D420N	sul1; sul2	dfrA7	dfrA7; sul1; sul3	ST1	4.3.1.1	IncX3	18	4849876

Genotypic characterization

Whole-genome sequencing revealed that all three isolates belonged to sequence type ST1 and the globally disseminated genotype 4.3.1.1 (H58 lineage). This lineage is strongly associated with the global spread of multidrug-resistant and XDR *S. Typhi*. All isolates carried multiple antimicrobial resistance genes consistent with their phenotypic profiles. β-lactam resistance was mediated by blaTEM-1D together with an ESBL gene, namely blaCTX-M-15 in isolate no. 34 and blaSHV-12 in isolates no. 35 and 36. These genes are responsible for resistance to third-generation cephalosporins. Resistance to ampicillin was mediated by blaTEM-1D, while chloramphenicol resistance was associated with catA1 (isolates 34 and 35) and catA2 (isolate 36). Resistance to trimethoprim-sulfamethoxazole was mediated by dfrA7/dfrA14 together with sul1, sul2, or sul3.
Fluoroquinolone resistance mechanisms differed among the isolates. Isolate no 34 possessed plasmid-mediated quinolone resistance genes (qnrB and aac (6′)-Ib-cr) along with the chromosomal mutation gyrB_S464F, corresponding to its high ciprofloxacin MIC (16 µg/mL). In contrast, isolates 35 and 36 carried the QRDR mutations gyrA_S83Y and parE_D420N, with reduced fluoroquinolone susceptibility. No acquired resistance genes for azithromycin were detected.

Plasmid analysis

Distinct plasmid replicons were identified among the isolates. Isolate 34 harbored an IncR plasmid, whereas isolates 35 and 36 contained IncX3 plasmids. These plasmids are responsible for the acquisition and dissemination of antimicrobial resistance genes, including ESBL determinants.

Summary

Typhoidal *Salmonella* remains a significant therapeutic challenge in India, primarily due to fluoroquinolone resistance and the emergence of extensively drug-resistant (XDR) *S.* Typhi*.* Nationally, S. Typhi retained high susceptibility to azithromycin (99.4%), ceftriaxone (96.6%), co-trimoxazole (97.1%), chloramphenicol (96.4%), and ampicillin (93.6%). *S.* Paratyphi A similarly demonstrated high susceptibility to conventional agents. However, ciprofloxacin susceptibility was only 2.0% and 0.4%, respectively. Between 2017 and 2025, susceptibility to older first-line antibiotics re-emerged, while fluoroquinolone susceptibility remained persistently low.
Whole-genome sequencing of 104 isolates revealed the genetic basis of resistance. *S.* Typhi predominantly belonged to the H58 lineage (genotype 4.3.1), with ST1 accounting for 78.5% of isolates. *S.* Paratyphi A was predominantly ST129 (69.2%). Fluoroquinolone resistance was primarily associated with chromosomal QRDR mutations, particularly *gyrA* S83F/D87N and *parC* S80I. Classical multidrug resistance was associated with *bla*TEM-1D, *catA1*, *sul1/sul2*, and *dfrA7*. ESBL-mediated resistance involved *bla*SHV-12, *bla*CTX-M-15, and *bla*CTX-M-55.

Three XDR *S.* Typhi isolates belonged to ST1 and H58 genotype 4.3.1.1. They carried combinations of *bla*TEM-1D with *bla*CTX-M-15 or *bla*SHV-12, alongside resistance to chloramphenicol and co-trimoxazole. IncR and IncX3 plasmids were identified. All three isolates remained susceptible to azithromycin.

Overall, the findings highlight the continued dissemination of H58-ST1, near-complete loss of fluoroquinolone susceptibility, and emergence of MDR/XDR clones. Sustained national antimicrobial susceptibility testing and WGS-based surveillance are essential to monitor emerging resistance and guide treatment and public-health interventions.

Clinical relevance and treatment guidance

Treatment of enteric fever should be individualised according to disease severity, patient characteristics, regional resistance patterns, and microbiological results. The high susceptibility to azithromycin and ceftriaxone supports their continued use as important therapeutic options for enteric fever. Azithromycin remains an important oral option for uncomplicated enteric fever.

The predominantly extracellular activity and limited intracellular penetration of β-lactams, including amoxicillin and ceftriaxone, may influence treatment outcomes. Azithromycin combined with ceftriaxone remains an important therapeutic option, particularly for hospitalized patients with complicated enteric fever or relevant travel historydepending on clinical presentation and antimicrobial susceptibility patterns.

Cefixime has limited intracellular bacteriostatic activity, potentially contributing to variable treatment outcomes, and is no longer included among recommended agents for *Salmonella* susceptibility testing/reporting in CLSI M100, 36th edition (2026). Fluoroquinolones should be used only when susceptibility is confirmed by antimicrobial susceptibility testing (AST) and should not be considered appropriate for empirical treatment of suspected typhoid or paratyphoid fever, given the high resistance reported.

The detection of ESBL-producing *S.* Typhi carrying *bla*SHV-12, *bla*CTX-M-15, or *bla*CTX-M-55 is clinically concerning because ceftriaxone remains central to enteric fever treatment. Although national susceptibility remains high, regional variation and emerging resistance underscore the need for susceptibility-guided treatment. Carbapenem-based therapy guided by AST is recommended for complicated infections caused by ceftriaxone-resistant or XDR *S.* Typhi.

The three XDR isolates identified in this surveillance combined resistance to multiple conventional antimicrobial classes with ESBL genes, while retaining azithromycin susceptibility. IncR and IncX3 plasmids highlight the potential dissemination of clinically important resistance determinants. The detection of *acrB* R717Q-associated reduced azithromycin susceptibility, despite high national susceptibility, represents an early warning. Carbapenem-resistant *S.* Typhi, particularly *bla*NDM-5-producing strains, represents an emerging global threat, emphasising the need for novel therapeutics and strengthened stewardship.

Overall, empirical treatment should reflect national and regional resistance patterns, while definitive therapy should be guided by culture and AST wherever possible. Integration of phenotypic testing with whole-genome sequencing can provide early warning of emerging MDR/XDR lineages and inform evidence-based treatment recommendations. Sustainable control requires genomic surveillance, rapid diagnostics, and strengthened infection prevention measures.

Chapter 5. Diarrheal pathogens

This chapter summarizes the antimicrobial susceptibility profiles and longitudinal resistance trends among major diarrheal bacterial pathogens isolated from faecal specimens during 2025. The surveillance included *Aeromonas* spp., *Shigella* spp. (*Shigella flexneri* and *Shigella sonnei*), *Vibrio cholerae*, and diarrhoeagenic *Escherichia coli* (DEC).

Aeromonas spp.

Among *Aeromonas* spp. isolated from faecal specimens during 2025 (n = 149), the highest susceptibility was observed to trimethoprim-sulfamethoxazole (91.3%), followed by meropenem (81.3%), cefixime (78.6%), ceftriaxone (77.9%), and tetracycline (77.6%). Carbapenems continued to demonstrate good activity against *Aeromonas* isolates, although meropenem exhibited higher susceptibility than imipenem, with only 59.7% of isolates remaining susceptible to the latter. Third-generation cephalosporins also retained good *in vitro* activity, with cefixime and ceftriaxone demonstrating comparable susceptibility rates. In contrast, ciprofloxacin susceptibility remained poor (16.8%), indicating that fluoroquinolones continue to have limited effectiveness against Aeromonas infections **(Table 5.1).**

Table 5.1: Susceptibility pattern of *Aeromonas spp*

AMA	Faeces N=149 (S%)
Cefixime	110/140 (78.6)
Ceftriaxone	116/149 (77.9)
Ciprofloxacin	25/149 (16.8)
Imipenem	83/139 (59.7)
Meropenem	113/139 (81.3)
Tetracycline	66/85 (77.6)
Trimethoprim-sulfamethoxazole	136/149 (91.3)

Analysis of the yearly susceptibility trends from 2017 to 2025 demonstrates that *Aeromonas* spp. have maintained relatively stable susceptibility to several key antimicrobial agents despite moderate year-to-year fluctuations. Meropenem susceptibility improved steadily from 54.2% in 2017 to reach its highest level of 89.0% in 2023 before declining marginally to

87.8% in 2024 and further to 81.3% in 2025. Despite this recent reduction, meropenem continues to demonstrate consistently superior activity compared with imipenem throughout the surveillance period. Imipenem susceptibility gradually improved from 43.5% in 2017 to approximately 60–64% during recent years and remained relatively stable at 59.7% in 2025. Tetracycline susceptibility showed minimal variation over the surveillance period, remaining consistently above 75% with no evidence of progressive decline, thereby reinforcing its continued therapeutic utility. Ciprofloxacin susceptibility remained persistently poor throughout the surveillance period, fluctuating between 5.4% and 20.9%, with only a modest improvement observed during 2025. Collectively, these findings indicate sustained activity of carbapenems and tetracycline against *Aeromonas* spp., while continued poor susceptibility to ciprofloxacin highlights persistent fluoroquinolone resistance and support the need for susceptibility-guided therapy **(Table 5.2; Figure 5.1).**

Table 5.2: Yearly susceptibility trends of *Aeromonas* spp.from faeces

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=131	N=114	N=170	N=77	N=179	N=164	N=181	N=196	N=149
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefixime	*0/0 (-)	23/36 (63.9)	*0/0 (-)	*0/0 (-)	*0/0 (-)	132/164 (80.4)	*0/0 (-)	*0/1 (-)	110/140 (78.6)
Imipenem	20/46 (43.5)	53/109 (48.6)	*1/2 (-)	*0/0 (-)	77/154 (50)	104/164 (63.4)	53/83 (63.9)	117/189 (61.9)	83/139 (59.7)
Meropenem	26/48 (54.2)	71/109 (65.1)	*1/2 (-)	*0/0 (-)	118/153 (77.1)	138/164 (84.1)	73/82 (89)	166/189 (87.8)	113/139 (81.3)
Tetracycline	104/126 (82.5)	97/113 (85.8)	134/169 (79.3)	58/77 (75.3)	145/178 (81.5)	141/164 (85.9)	66/85 (77.6)	159/194 (82)	66/85 (77.6)
Ciprofloxacin	8/78 (10.3)	11/112 (9.8)	20/169 (11.8)	4/74 (5.4)	22/177 (12.4)	14/164 (8.5)	18/86 (20.9)	20/196 (10.2)	25/149 (16.8)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

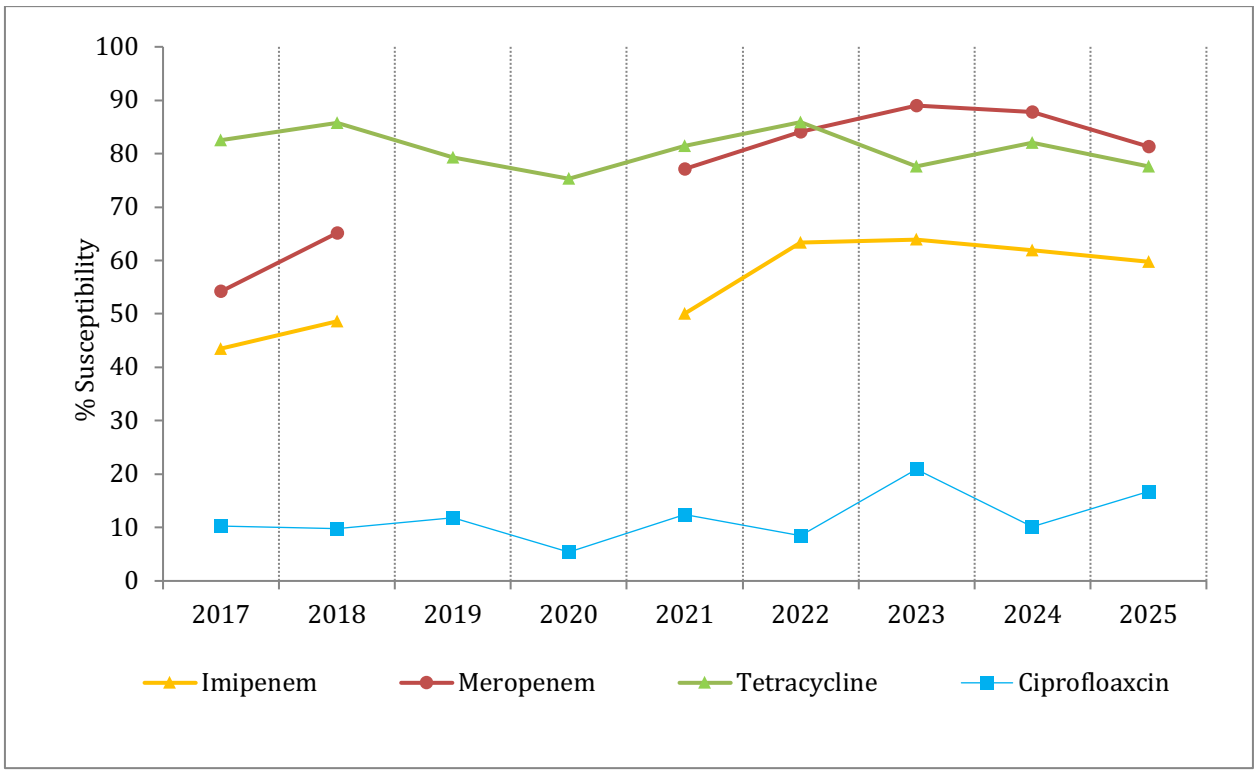


Figure 5.1: Yearly susceptibility trends of *Aeromonas* spp.

Shigella spp

Shigella flexneri

Among *Shigella flexneri* isolates recovered during 2025 (n = 68), chloramphenicol demonstrated the highest susceptibility (77.8%), followed by cefotaxime (71.9%), ceftriaxone (70.1%) and cefixime (64.1%). Trimethoprim-sulfamethoxazole exhibited moderate activity, with 57.4% of isolates remaining susceptible. In contrast, susceptibility to ampicillin was markedly low (13.2%), while ciprofloxacin demonstrated extremely poor activity, with only 7.5% susceptible isolates. These findings indicate that third-generation cephalosporins continue to retain useful activity against *S. flexneri*, whereas ampicillin and fluoroquinolones are unlikely to provide reliable empirical coverage. The uniformly poor susceptibility to nalidixic acid further supports the widespread occurrence of quinolone resistance among circulating isolates (**Table 5.3**).

Table 5.3: Susceptibility pattern of *Shigella* species

AMA	All specimens	
	Shigella flexneri **N=68 (S%)**	***Shigella sonnei*** **N=56 (S%)**
Ampicillin	9/68 (13.2)	32/54 (59.3)
Cefixime	25/39 (64.1)	20/30 (66.7)
Cefotaxime	46/64 (71.9)	33/45 (73.3)
Ceftriaxone	47/67 (70.1)	41/55 (74.5)
Chloramphenicol	49/63 (77.8)	44/45 (97.8)
Ciprofloxacin	5/67 (7.5)	5/56 (8.9)
Nalidixic acid	*0/6 (-)	*0/6 (-)
Trimethoprim-sulfamethoxazole	39/68 (57.4)	20/55 (36.4)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

The longitudinal surveillance data from 2017 to 2025 reveal substantial changes in the antimicrobial susceptibility profile of *S. flexneri*. Ampicillin susceptibility declined progressively over the surveillance period, falling from 44.9% in 2017 to only 13.2% in 2025, indicating sustained loss of activity against this pathogen. Cefixime maintained moderate to good activity throughout the study period, with susceptibility generally ranging between 64% and 88%. Although susceptibility declined from 74.7% in 2024 to 64.1% in 2025, cefixime remains among the most effective oral agents evaluated. Trimethoprim-sulfamethoxazole demonstrated marked temporal variation. Following low susceptibility during the earlier surveillance years, susceptibility increased progressively from 2021 onwards, reaching a peak of 79.2% in 2023 before declining to 53.5% in 2024 and remaining relatively stable at 57.4% in 2025. Overall, the yearly trends indicate continuing multidrug resistance in *S. flexneri*, with third-generation cephalosporins retaining the most consistent activity while resistance to older first-line agents remains widespread (**Table 5.4; Figure 5.2**).

Table 5.4: Yearly susceptibility trends of *Shigella flexneri*

AMA	Year-2017 N=89 (S%)	Year-2018 N=47 (S%)	Year-2019 N=95 (S%)	Year-2020 N=55 (S%)	Year-2021 N=37 (S%)	Year-2022 N=51 (S%)	Year-2023 N=25 (S%)	Year-2024 N=77 (S%)	Year-2025 N=68 (S%)
Ampicillin	40/89 (44.9)	12/47 (25.5)	24/94 (25.5)	9/54 (16.7)	7/37 (18.9)	6/51 (11.8)	4/25 (16)	21/77 (27.3)	9/68 (13.2)
Cefixime	56/69 (81.2)	38/46 (82.6)	73/92 (79.3)	45/51 (88.2)	25/37 (67.6)	25/47 (53.2)	16/25 (64)	56/75 (74.7)	25/39 (64.1)
Nalidixic acid	0/24 (0)	*0/15 (-)	2/35 (5.7)	*2/13 (-)	*0/8 (-)	*0/8 (-)	*0/5 (-)	*1/18 (-)	*0/6 (-)
Trimethoprim-sulfamethoxazole	7/72 (9.7)	14/47 (29.8)	22/95 (23.2)	9/55 (16.4)	14/37 (37.8)	26/50 (52.0)	19/24 (79.2)	38/71 (53.5)	39/68 (57.4)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

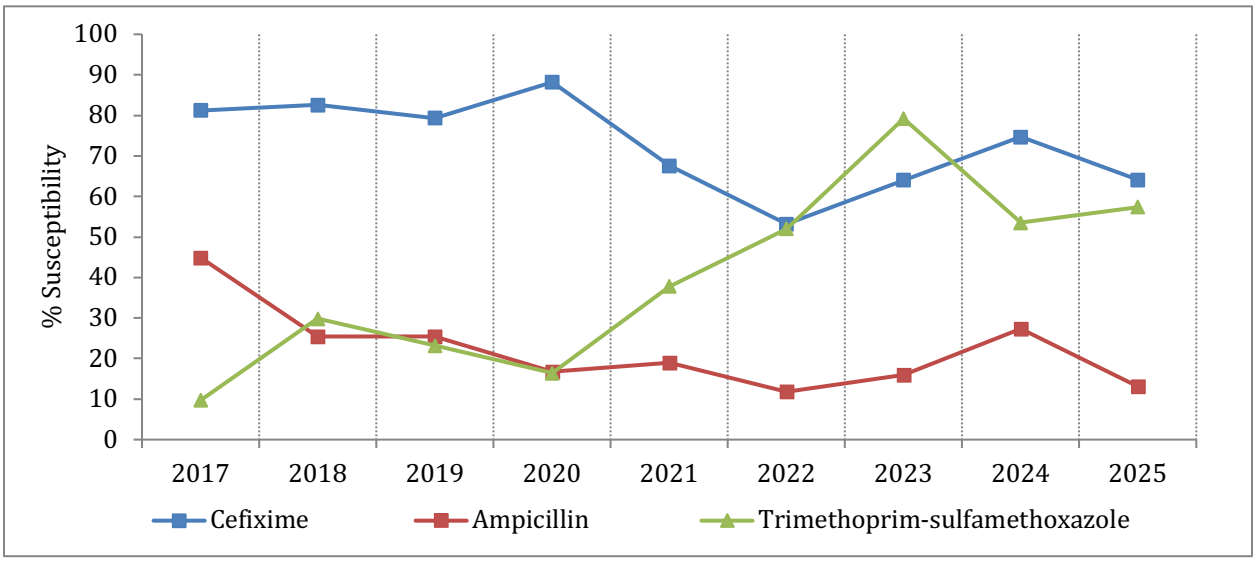


Figure 5.2: Yearly susceptibility trends of *Shigella flexneri*

Shigella sonnei

Among *Shigella sonnei* isolates (n = 56), chloramphenicol exhibited excellent activity, with 97.8% susceptibility, followed by ceftriaxone (74.5%), cefotaxime (73.3%) and cefixime (66.7%). Ampicillin susceptibility was moderate (59.3%), whereas trimethoprim-sulfamethoxazole demonstrated lower activity (36.4%). Similar to *S. flexneri*, ciprofloxacin susceptibility remained extremely poor, with only 8.9% of isolates susceptible. These findings indicate that cephalosporins continue to provide useful therapeutic activity against *S. sonnei*, whereas fluoroquinolones are unlikely to be effective for empirical treatment. The

persistently poor susceptibility to ciprofloxacin further supports the widespread resistance to quinolone-class antimicrobials among Shigella isolates.

Year-wise analysis from 2017 to 2025 demonstrates greater fluctuation in antimicrobial susceptibility among *S. sonnei* than observed for *S. flexneri*. Cefixime maintained consistently high activity during the earlier surveillance years, exceeding 90% susceptibility between 2017 and 2019, before declining to approximately 80% during 2021–2024 and further to 66.7% in 2025. Ampicillin susceptibility varied considerably during the surveillance period, increasing progressively to 82.5% in 2024 before declining to 59.3% during the current year. Trimethoprim-sulfamethoxazole also demonstrated marked year-to-year variation, improving gradually from very low susceptibility during the earlier surveillance years to 51.6% in 2024 before decreasing to 36.4% in 2025. Overall, the longitudinal surveillance data indicate that while susceptibility to several antimicrobial agents has fluctuated over time, third-generation cephalosporins continue to retain useful activity against *S. sonnei*, whereas fluoroquinolone resistance remains firmly established (**Table 5.5; Figure 5.3**).

Table 5.5: Yearly susceptibility trends of *Shigella sonnei*

AMA	Year-2017 N=52 (S%)	Year-2018 N=26 (S%)	Year-2019 N=57 (S%)	Year-2020 N=*14 (S%)	Year-2021 N= 41 (S%)	Year-2022 N=39 (S%)	Year-2023 N=*15 (S%)	Year-2024 N=97 (S%)	Year-2025 N=56 (S%)
Ampicillin	35/52 (67.3)	18/24 (75)	42/57 (73.7)	*10/14 (-)	22/40 (55)	30/39 (76.9)	*14/15 (-)	80/97 (82.5)	32/54 (59.3)
Cefixime	47/50 (94)	25/26 (96.2)	52/57 (91.2)	*12/13 (-)	31/39 (79.5)	31/39 (79.5)	*13/14 (-)	81/94 (86.2)	20/30 (66.7)
Nalidixic acid	*0/8 (-)	*0/1 (-)	*0/8 (-)	*0/0 (-)	*0/7 (-)	*0/4 (-)	*0/1 (-)	*0/17 (-)	*0/6 (-)
Trimethoprim-sulfamethoxazole	4/52 (7.7)	0/25 (-)	5/57 (8.8)	*1/13 (-)	9/41 (22)	9/39 (23.1)	*6/15 (-)	49/95 (51.6)	20/55 (36.4)

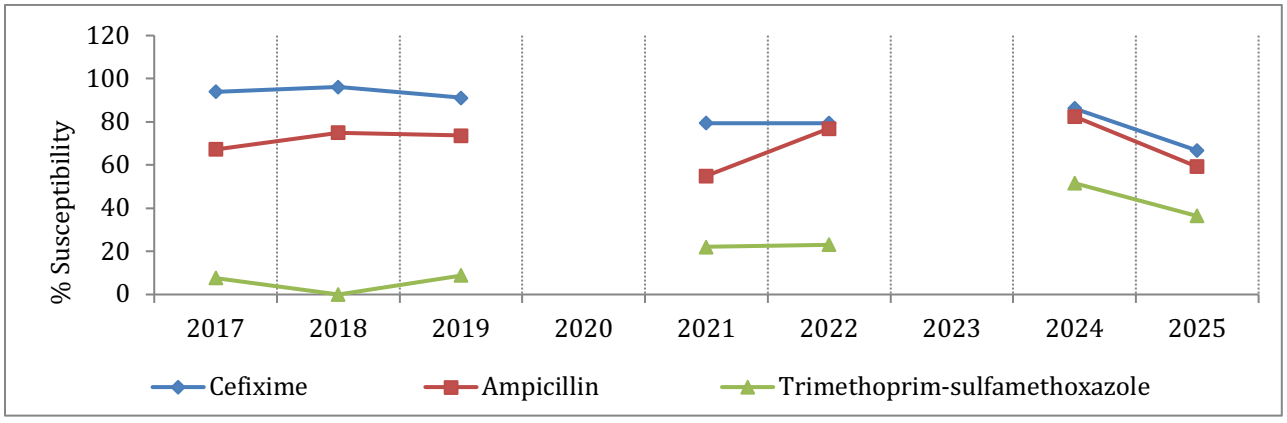


Figure 5.3: Yearly susceptibility trends of *Shigella sonnei*

Vibrio cholerae

Among *Vibrio cholerae* isolates recovered from faecal specimens during 2025 (n = 40), tetracycline demonstrated the highest *in vitro* activity, with 97.5% of isolates remaining susceptible. Ampicillin also exhibited excellent activity, with susceptibility of 92.5%, representing one of the highest susceptibility rates observed. In contrast, trimethoprim-sulfamethoxazole demonstrated only moderate activity, with 47.5% susceptibility, indicating that resistance to this agent remains common among circulating isolates. No nalidixic acid susceptibility results were available during the current surveillance year. Overall, the 2025 susceptibility profile indicates that tetracycline continues to provide excellent therapeutic coverage for *V. cholerae*, while ampicillin retains high activity. However, the comparatively lower susceptibility to trimethoprim-sulfamethoxazole suggests that this antimicrobial should be used cautiously and preferably following susceptibility testing (**Table 5.6**).

Table 5.6: Susceptibility pattern of *Vibrio cholerae*

AMA	*Vibrio cholerae* N=40 (S%)
Ampicillin	37/40 (92.5)
Nalidixic acid	*0/0 (-)
Tetracycline	39/40 (97.5)
Trimethoprim-sulfamethoxazole	19/40 (47.5)

Analysis of the yearly susceptibility trends from 2017 to 2025 demonstrates remarkable stability in the antimicrobial susceptibility profile of *V. cholerae*, particularly for tetracycline. Throughout the surveillance period, tetracycline susceptibility consistently exceeded 90%, ranging from 90.5% to 100%, and remained at 97.5% during both 2024 and 2025, confirming its sustained effectiveness against circulating isolates. Ampicillin susceptibility exhibited greater temporal variation. Following moderate susceptibility during 2017–2019, activity declined to its lowest level (39.3%) in 2020 before increasing substantially over subsequent years, reaching 84.3% in 2022, 79.8% in 2024 and further improving to 92.5% in 2025. This represents the highest ampicillin susceptibility observed during the surveillance period and suggests improved activity against recent *V. cholerae* isolates. In contrast, trimethoprim-sulfamethoxazole susceptibility fluctuated considerably over time, varying between 17.2% and 50.0%, with moderate susceptibility (47.5%) observed during the current year. Overall, the surveillance data demonstrate sustained effectiveness of tetracycline, improving

susceptibility to ampicillin during recent years, and persistently variable activity of trimethoprim-sulfamethoxazole. **(Table 5.7; Figure 5.4).**

Table 5.7: Yearly susceptibility trends of *Vibrio cholerae*

AMA	Year-2017 N=24 (S%)	Year-2018 N=25 (S%)	Year-2019 N=39 (S%)	Year-2020 N=31 (S%)	Year-2021 N=58 (S%)	Year-2022 N=32 (S%)	Year-2023 N=17 (S%)	Year-2024 N=94 (S%)	Year-2025 N=40 (S%)
Ampicillin	17/24 (70.8)	17/24 (70.8)	22/39 (56.4)	11/28 (39.3)	44/51 (86.3)	27/32 (84.3)	*12/17 (-)	71/89 (79.8)	37/40 (92.5)
Tetracycline	19/21 (90.5)	*7/10 (-)	36/38 (94.7)	31/31 (100)	55/58 (94.8)	29/32 (90.6)	*15/17 (-)	79/81 (97.5)	39/40 (97.5)
Nalidixic acid	*1/8 (-)	*0/4 (-)	*0/5 (-)	*1/1 (-)	*0/0 (-)	*0/1 (-)	*0/0 (-)	*1/1 (-)	*0/0 (-)
Trimethoprim-sulfamethoxazole	10/24 (41.7)	6/24 (25)	18/38 (47.4)	13/31 (41.9)	10/58 (17.2)	16/32 (50.0)	*7/17 (-)	22/93 (23.7)	19/40 (47.5)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

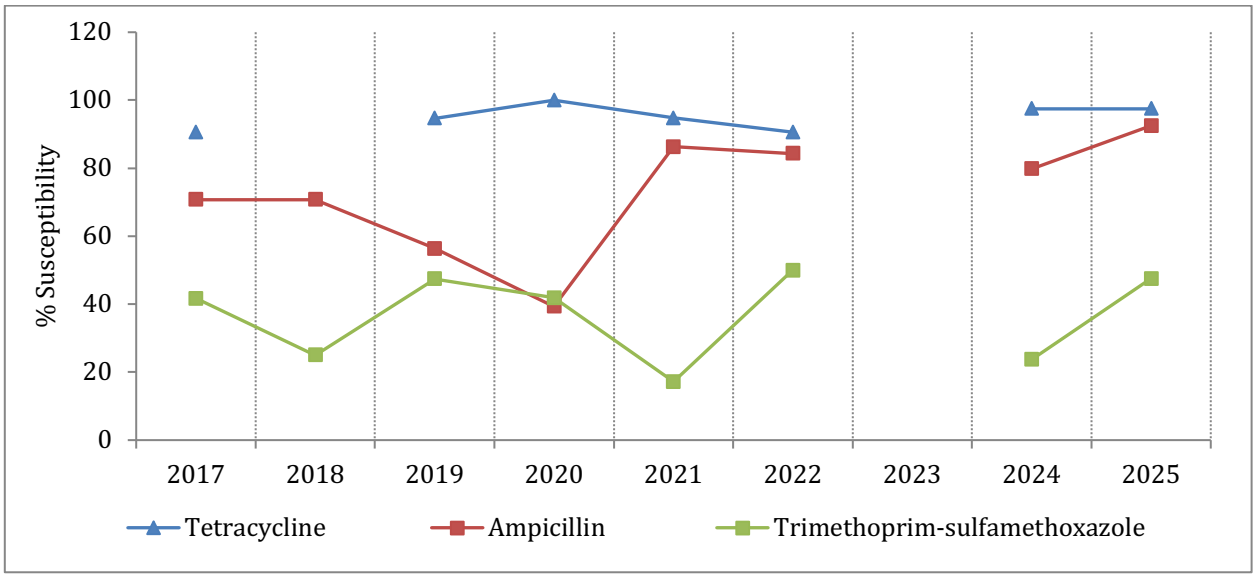


Figure 5.4: Yearly susceptibility trends of *Vibrio cholera*

Diarrhoeagenic *Escherichia coli* (DEC)

Among diarrhoeagenic *Escherichia coli* (DEC) isolates recovered during 2025 (n = 153), chloramphenicol demonstrated the highest susceptibility (90.8%), followed by trimethoprim-sulfamethoxazole (40.4%), although the latter exhibited only moderate activity. Susceptibility

to ampicillin (14.4%), nalidixic acid (15.9%), cefixime (4.6%) and ciprofloxacin (0.7%) remained extremely low, indicating widespread resistance to several commonly prescribed antimicrobial agents. The near-complete loss of ciprofloxacin activity is particularly concerning, while the poor susceptibility observed for cefixime suggests diminishing effectiveness of this oral third-generation cephalosporin. Overall, the current susceptibility profile indicates that DEC isolates continue to exhibit extensive multidrug resistance, thereby limiting available therapeutic options **(Table 5.8).**

Table 5.8: Susceptibility pattern of DEC

AMA	Diarrheagenic *Escherichia coli* N=153 (S%)
Ampicillin	22/153 (14.4)
Azithromycin	*0/0 (-)
Cefixime	5/108(4.6)
Chloramphenicol	139/153(90.8)
Ciprofloxacin	1/146(0.7)
Nalidixic acid	17/107(15.9)
Trimethoprim-sulfamethoxazole	61/151(40.4)

The yearly susceptibility trends from 2019 to 2025 demonstrate the persistence of multidrug resistance among DEC isolates. Ampicillin susceptibility remained consistently poor throughout the surveillance period, varying between 0% and 14.4%, with only a modest increase observed during 2024 and 2025. Similarly, cefixime susceptibility declined progressively from 13.2% in 2019 to only 4.6% in 2025, indicating a gradual reduction in susceptibility over time. Nalidixic acid susceptibility remained uniformly low, fluctuating between approximately 8% and 17%, reflecting sustained resistance to quinolone-class antimicrobials. Trimethoprim-sulfamethoxazole demonstrated the greatest temporal variation, remaining around 30–36% during 2019–2022 before increasing markedly to 68.6% in 2024 and subsequently declining to 40.4% in 2025. Although susceptibility during the current year was considerably lower than that observed in 2024, trimethoprim-sulfamethoxazole continued to exhibit greater activity than the other commonly tested oral antimicrobial agents. Overall, the surveillance data indicate persistent multidrug resistance among DEC isolates with little evidence of sustained improvement in susceptibility to β-lactams or fluoroquinolones (**Table 5.9; Figure 5.5).**

Table 5.9: Yearly susceptibility trend of DEC

AMA	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=134 (S%)	N=102 (S%)	N=88 (S%)	N=189 (S%)	N=33 (S%)	N=188 (S%)	N=153 (S%)
Ampicillin	6/132 (4.5)	1/102 (1)	0/87 (0)	6/189 (3.2)	1/33 (3)	22/188 (11.7)	22/153 (14.4)
Cefixime	17/129 (13.2)	11/100 (11)	12/87 (13.8)	6/189 (3.2)	1/33 (3)	12/188 (6.4)	5/108 (4.6)
Nalidixic acid	14/122 (11.5)	11/98 (11.2)	7/87 (8)	15/164 (9.1)	5/32 (15.6)	32/188 (17)	17/107 (15.9)
Trimethoprim-sulfamethoxazole	45/133 (33.8)	32/102 (31.4)	32/88 (36.4)	56/186 (30.1)	7/33 (21.2)	129/188 (68.6)	61/151 (40.4)

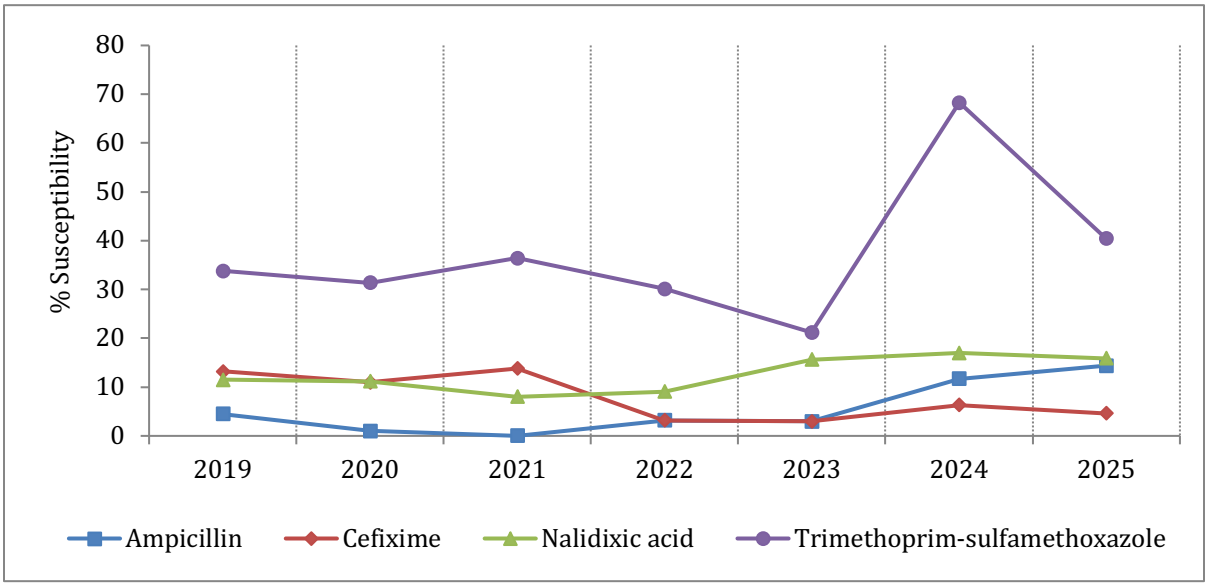


Figure 5.5: Yearly susceptibility trend of DEC

Summary

The 2025 antimicrobial resistance surveillance of diarrhoeal bacterial pathogens demonstrates substantial variation in susceptibility profiles, highlighting the importance of continued surveillance to guide empirical treatment.

Among *Aeromonas* spp., trimethoprim-sulfamethoxazole, meropenem, cefixime, ceftriaxone, and tetracycline retained high *in vitro* activity, whereas ciprofloxacin susceptibility remained

consistently low. Carbapenems and tetracycline demonstrated sustained effectiveness throughout the surveillance period.

Both *Shigella flexneri* and *S. sonnei* exhibited persistent fluoroquinolone resistance, with ciprofloxacin susceptibility below 10% in 2025. Third-generation cephalosporins retained moderate to high activity, although cefixime susceptibility declined in recent years. Ampicillin susceptibility was substantially lower in *S. flexneri* than in *S. sonnei*, while trimethoprim-sulfamethoxazole demonstrated variable, moderate activity.

Among *Vibrio cholerae*, tetracycline maintained excellent activity and remained the most reliable antimicrobial agent. Ampicillin susceptibility improved considerably, whereas trimethoprim-sulfamethoxazole retained moderate activity, supporting continued monitoring of susceptibility trends.

Diarrhoeagenic *Escherichia coli* (DEC) demonstrated extensive multidrug resistance, with poor susceptibility to ampicillin, cefixime, ciprofloxacin, and nalidixic acid. Chloramphenicol retained excellent activity, while trimethoprim-sulfamethoxazole demonstrated moderate susceptibility, indicating narrowing therapeutic options.

Overall, the findings highlight persistent fluoroquinolone resistance across multiple enteric pathogens and declining susceptibility to selected β-lactams. Continued laboratory-based surveillance, judicious antimicrobial use, and periodic revision of empirical treatment guidelines are essential to inform evidence-based clinical management and strengthen national antimicrobial stewardship programmes.

Molecular mechanism of resistance

As part of the antimicrobial resistance (AMR) surveillance programme, representative diarrhoeal bacterial isolates received from participating centres were molecularly characterized to investigate acquired resistance determinants. Genomic DNA was extracted using standardized protocols and quality-assessed before analysis. Conventional multiplex PCR assays standardized under ICMR-AMRSN were used to detect clinically important resistance genes, including ESBL determinants (*bla*CTX-M groups 1, 2 and 9, *bla*TEM, *bla*SHV and *bla*OXA-1-like), plasmid-mediated AmpC genes (*bla*CMY and *bla*DHA), and non-β-lactam resistance genes (*dfrA, sul1/sul2, qnrB, qnrS, mphA* and *ermB*). Positive and negative controls were included, and amplification products were confirmed by agarose gel electrophoresis.

Among 47 diarrhoeagenic *Escherichia coli* isolates, acquired resistance genes were frequent **(Table 5.10).** *bla*OXA-1 was most prevalent (48.9%), followed by *bla*TEM (36.2%) and *bla*CTX-M (31.9%), indicating a substantial burden of ESBL-associated resistance. The plasmid-mediated AmpC gene *bla*CMY was detected in 6.4%. Among non-β-lactam determinants, *sul* and *dfrA* genes were detected in 36.2% and 31.9%, respectively, while

qnrS/qnrB genes were identified in 8.5%. Co-occurrence of multiple determinants indicated circulation of multidrug-resistant *E. coli* with diverse resistance mechanisms.

In 29 *Salmonella* spp. isolates, acquired resistance genes were comparatively limited. *bla*TEM was detected in 27.6%, while *bla*CTX-M, *bla*OXA-1 and *bla*CMY were not identified. *dfrA* and *sul* genes were each detected in 6.9%; plasmid-mediated quinolone resistance genes were absent. These findings were consistent with the comparatively favourable phenotypic susceptibility profile, including preserved susceptibility to third-generation cephalosporins.

Among 18 *Shigella* spp. isolates, *bla*OXA-1 and *bla*CMY were each detected in 27.8%, and *bla*TEM in 16.7%; *bla*CTX-M was not detected. Folate pathway resistance genes were also observed, with *dfrA* in 33.3% and *sul* in 22.2%. Plasmid-mediated quinolone resistance genes (*qnrS/qnrB*) were identified in 11.1%, supporting the observed reduced fluoroquinolone susceptibility.

Overall, molecular findings broadly concorded with phenotypic susceptibility profiles. Integrating molecular characterization into routine surveillance can improve understanding of circulating resistance mechanisms and support interpretation of AMR patterns across diarrhoeagenic pathogens.

Table 5.10: Summary of molecular characterization of antimicrobial resistance determinants among diarrhoeal pathogens

Pathogen	Predominant AMR genes detected (% isolates)	Correlation with phenotypic resistance	Interpretation
Diarrhoeagenic *E. coli*	blaOXA-1 (48.9%), blaTEM (36.2%), blaCTX-M (31.9%), sul (36.2%), dfrA (31.9%), qnrS/B (8.5%), blaCMY (6.4%)	High resistance to β-lactams, trimethoprim-sulfamethoxazole and fluoroquinolones	Highest burden of acquired resistance determinants, indicating widespread multidrug resistance among diarrhoeagenic *E. coli.*
Salmonella spp.	blaTEM (27.6%), dfrA (6.9%), sul (6.9%); blaCTX-M, blaOXA-1, blaCMY and qnr not detected	Preserved susceptibility to third-generation cephalosporins and relatively lower multidrug resistance	Lowest prevalence of acquired AMR genes among the pathogens studied, consistent with favourable antimicrobial susceptibility patterns.
Shigella spp.	blaOXA-1 (27.8%), blaCMY (27.8%), dfrA (33.3%), sul (22.2%), blaTEM (16.7%), qnrS/B (11.1%); blaCTX-M not detected	Correlates with resistance to ampicillin, trimethoprim-sulfamethoxazole and fluoroquinolones while maintaining moderate	Intermediate resistance burden with multiple co-existing resistance mechanisms contributing to the multidrug-resistant phenotype.

		cephalosporin susceptibility	

Clinical relevance and treatment guidelines

Antimicrobial resistance surveillance highlights evolving resistance among bacterial pathogens causing diarrhoeal illness in India, with substantial inter-species variation. Empirical treatment should therefore reflect local pathogen epidemiology and be periodically revised using regional surveillance data. High resistance to fluoroquinolones and β-lactams reinforces the importance of culture-guided therapy and antimicrobial stewardship. AST is particularly important in severe, persistent or invasive infections.

General recommendations

- Reserve empirical antimicrobial therapy for severe diarrhoea, dysentery, suspected invasive infection or patients at high risk of complications, in accordance with national guidelines.
- Use current regional susceptibility data to guide treatment and modify therapy promptly when culture and AST results become available.
- Avoid empirical fluoroquinolones, given low susceptibility among *Aeromonas* spp., *Shigella* spp. and diarrhoeagenic *Escherichia coli* (DEC).
- Integrate phenotypic AST and molecular surveillance to detect emerging resistance and inform treatment recommendations.
- Restrict reserve agents, particularly carbapenems, to preserve their effectiveness.

Pathogen-specific recommendations

Aeromonas spp.

Trimethoprim-sulfamethoxazole, meropenem, cefixime, ceftriaxone and tetracycline retain good *in vitro* activity, while ciprofloxacin susceptibility remains poor. For severe or invasive infections, carbapenems may be considered in selected patients; third-generation cephalosporins and tetracyclines are alternatives guided by AST. Monitor carbapenem susceptibility given the recent decline in meropenem activity.

Shigella spp.

Persistent fluoroquinolone resistance makes empirical ciprofloxacin unreliable. Third-generation cephalosporins remain consistent options for moderate to severe infections. *Shigella sonnei* retains greater ampicillin susceptibility than *S. flexneri*. Use trimethoprim-

sulfamethoxazole only when susceptibility is confirmed, and continue monitoring cephalosporin and azithromycin activity.

Vibrio cholerae

Tetracycline remains a preferred agent when antibiotics are indicated; doxycycline is an option for adults under national recommendations. Ampicillin susceptibility has improved, but this trend requires continued monitoring. Trimethoprim-sulfamethoxazole is not preferred empirically. Rehydration remains central to cholera management.

Diarrhoeagenic *Escherichia coli* (DEC)

Extensive multidrug resistance and low susceptibility to ampicillin, cefixime, nalidixic acid and ciprofloxacin preclude their empirical use. Chloramphenicol retained high *in vitro* activity and trimethoprim-sulfamethoxazole moderate activity; treatment should be individualized and guided by AST when indicated.

Sustained laboratory surveillance, molecular characterization, periodic prescribing review, infection prevention and stewardship are essential to update treatment guidance and limit resistance spread.

Chapter 6. Staphylococci and Enterococci

A total of 9700 *Staphylococcus aureus*, 6048 *Staphylococci* other than *Staphylococcus aureus* (SOSA) and 6345 enterococcal isolates collected across India were analysed in the year 2025.

Staphylococcus aureus

A total of 9700 isolates of *S. aureus* were reported from different centres across India. The proportion of MRSA in 2025 (57.7%) was slightly higher than the rates reported in 2024 (50.1%). Identification of MRSA was done by testing susceptibility to cefoxitin (4833) or oxacillin (2839). The overall proportion of MRSA was 56.8% and 52.7% based on the 2 methods respectively. There was a discrepancy in the MRSA rates detected by oxacillin MIC and cefoxitin DD/MIC which could be because of the different number of isolates tested by both methods. Moreover the same isolates may not have been tested by both the methods. As per CLSI guidelines an isolate of *S.aureus* may be identified as MRSA using either cefoxitin and /or oxacillin. On some occasions, only one of the two methods may be positive for eg: *mec*C isolates may sometimes be cefoxitin resistant but oxacillin sensitive.

Susceptibility to tetracycline, clindamycin, co-trimoxazole, erythromycin and ciprofloxacin was higher among MSSA when compared to MRSA. The anti MRSA antibiotics such as vancomycin, teicoplanain and tigecycline showed excellent in vitro activity (100% against MRSA isolates) although susceptibility rate of tigecycline against SOSA was much lower (71.6%). Linezolid resistance was encountered in MRSA, MSSA as well as SOSA isolates (6.5%, 3.9% and 5.4% respectively) **(Table 6.1)**.

Table 6.1: Percentage susceptibility of *S. aureus*, MSSA, MRSA and SOSA isolated from all samples

AMA	All Specimens			
	S. aureus N=9700 (S%)	MSSA N=4106 (S%)	MRSA N=5593 (S%)	SOSA N=6048 (S%)
Cefoxitin	3679/8512 (43.2)	3679/3679 (100)	0/4833 (0)	518/2436 (21.3)
Oxacillin	2549/5388 (47.3)	2549/2549 (100)	0/2839 (0)	816/4053 (20.1)
Vancomycin	9398/9398 (100)	3823/3823 (100)	5575/5575 (100)	5999/5999 (100)
Teicoplanin	5433/5433 (100)	2321/2322 (100)	3111/3111 (100)	2806/2806 (100)
Erythromycin	3398/9657 (35.2)	1940/4078 (47.6)	1458/5579 (26.1)	966/5990 (16.1)
Tetracycline	8343/9178 (90.9)	3594/3802 (94.5)	4749/5376 (88.3)	4595/5783 (79.5)
Tigecycline	3826/3826 (100)	1470/1470 (100)	2356/2356 (100)	1087/1519 (71.6)
Ciprofloxacin	2100/9692 (21.7)	1319/4101 (32.2)	781/5591 (14.0)	1768/6047 (29.2)
Clindamycin	7102/9123 (77.8)	3185/3807 (83.7)	3917/5316 (73.7)	2094/5530 (37.9)
Trimethoprim-sulfamethoxazole	7780/9694 (80.3)	3561/4102 (86.8)	4219/5592 (75.4)	3995/6027 (66.3)
Linezolid	9174/9699 (94.6)	3945/4106 (96.1)	5229/5593 (93.5)	5719/6047 (94.6)

The susceptibility pattern of *S. aureus* and SOSA across different hospital locations are presented in **Table 6.2.** As expected, the overall MRSA rates among *S. aureus* were higher in the ICU isolates than in OPD and ward isolates although the difference was not significant. Susceptibility to most antibiotics was least among ICU isolates and highest among OPD isolates of *S.aureus* including MRSA and SOSA. Linezolid resistance rates among MRSA were 6.3%, SOSA 5.2% and MSSA 3.9% which were higher than the 2024 rates (3.4%, 1.9% and 1.5% respectively). No teicoplanin resistance was observed among MRSA, MSSA and SOSA.

Center wise analysis

There were significant differences in MRSA rates observed between the various regional centres, the highest rate in the isolates from RC11 and RC20 while the lowest MRSA rates were observed from the RC30 and RC10 based on cefoxitin test results **(Table 6.3).** Ciprofloxacin susceptibility was extremely low across all the centres except RC03 and RC16. The susceptibility rate of other antibiotics varied widely between the centres for many of the antibiotics. Linezolid resistance was highest among isolates from RC 34, RC12 and RC13. Overall susceptibility rates to erythromycin, clindamycin, ciprofloxacin, co-trimoxazole were more evident in MSSA when compared to MRSA **(Table 6.4 and Fig 6.1).**

Table 6.2: Location-wise susceptibility of *S. aureus*, MSSA, MRSA and SOSA from all samples (except urine and faeces)

AMA	*Staphylococcus aureus*				MSSA				MRSA				SOSA			
	Total n=9338	OPD n=3780	Ward n=4729	ICU n=829	Total n=3953	OPD n=1632	Ward n=2002	ICU n=319	Total n=5384	OPD n=2147	Ward n=2727	ICU n=510	Total n=5861	OPD n=1313	Ward n=3495	ICU n=1053
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	3556/8220 (43.3)	1537/3513 (43.8)	1726/3988 (43.3)	293/719 (40.8)	3556/3556 (100)	1537/1537 (100)	1726/1726 (100)	293/293 (100)	0/4664 (0)	0/1976 (0)	0/2262 (0)	0/426 (0)	477/2311 (20.6)	155/642 (24.1)	267/1291 (20.7)	55/378 (14.6)
Oxacillin	2470/5224 (47.3)	994/1994 (49.8)	1288/2762 (46.6)	188/468 (40.2)	2470/2470 (100)	994/994 (100)	1288/1288 (100)	188/188 (100)	0/2754 (0)	0/1000 (0)	0/1474 (0)	0/280 (0)	790/3968 (19.9)	186/738 (25.2)	496/2456 (20.2)	108/774 (14)
Vancomycin	9039/9039 (100)	3738/3738 (100)	4525/4525 (100)	776/776 (100)	3673/3673 (100)	1595/1595 (100)	1808/1808 (100)	270/270 (100)	5366/5366 (100)	2143/2143 (100)	2717/2717 (100)	506/506 (100)	5812/5812 (100)	1309/1309 (100)	3463/3463 (100)	1040/1040 (100)
Teicoplanin	5242/5242 (100)	2029/2092 (100)	2688/2688 (100)	462/462 (100)	2228/2229 (100)	940/940 (100)	1127/1127 (100)	162/162 (100)	3013/3013 (100)	1152/1152 (100)	1561/1561 (100)	300/300 (100)	2713/2713 (100)	495/495 (100)	1633/1633 (100)	585/585 (100)
Erythromycin	3278/9319 (35.2)	1342/3776 (35.5)	1666/4715 (35.3)	270/828 (32.6)	1876/3941 (47.6)	777/1629 (47.7)	936/1993 (47)	163/319 (51.1)	1402/5378 (26.1)	565/2147 (26.3)	730/2722 (26.8)	107/509 (21)	928/5820 (15.9)	237/1304 (18.2)	551/3467 (15.9)	140/1049 (13.3)
Tetracycline	8042/8830 (91.1)	3240/3545 (91.4)	4129/4545 (90.8)	673/740 (90.9)	3469/3661 (94.8)	1425/1501 (94.9)	1780/1888 (94.3)	264/272 (97.1)	4573/5169 (88.5)	1815/2044 (88.8)	2349/2657 (88.4)	409/468 (87.4)	4453/5603 (79.5)	934/1225 (76.2)	2736/3361 (81.4)	783/1017 (77)
Tigecycline	3646/3646 (100)	1532/1532 (100)	1908/1908 (100)	206/206 (100)	1390/1390 (100)	609/609 (100)	730/730 (100)	51/51 (100)	2256/2256 (100)	923/923 (100)	1178/1178 (100)	155/155 (100)	997/1392 (71.6)	197/311 (63.3)	600/819 (73.3)	200/262 (76.3)

Ciprofloxacin	1969/ 9330 (21.1)	776/ 3778 (20.5)	1019/ 4723 (21.6)	174/ 829 (21)	1252/ 3948 (31.7)	496/ 1631 (30.4)	646/ 1998 (32.3)	110/ 319 (34.5)	717/ 5382 (13.3)	280/ 2147 (13)	373/ 2725 (13.7)	64/ 510 (12.5)	1663/ 5860 (28.4)	424/ 1313 (32.3)	1038/ 3494 (29.7)	201/ 1053 (19.1)
Clindamycin	6850/ 8773 (78.1)	2850/ 3563 (80)	3445/ 4459 (77.3)	555/ 751 (73.9)	3068/ 3660 (83.8)	1268/ 1508 (84.1)	1567/ 1869 (83.8)	233/ 283 (82.3)	3782/ 5113 (74)	1582/ 2055 (77)	1878/ 2590 (72.5)	322/ 468 (68.8)	1996/ 5354 (37.3)	560/ 1210 (46.3)	1194/ 3185 (37.5)	242/ 959 (25.2)
Trimethoprim-sulfamethoxazole	7486/ 9332 (80.2)	3066/ 3779 (81.1)	3796/ 4724 (80.4)	624/ 829 (75.3)	3426/ 3949 (86.8)	1417/ 1632 (86.8)	1737/ 1998 (86.9)	272/ 319 (85.3)	4060/ 5383 (75.4)	1649/ 2147 (76.8)	2059/ 2726 (75.5)	352/ 510 (69)	3857/ 5839 (66.1)	835/ 1308 (63.8)	2326/ 3478 (66.9)	696/ 1053 (66.1)
Linezolid	8843/ 9337 (94.7)	3583/ 3779 (94.8)	4482/ 4729 (94.8)	778/ 829 (93.8)	3800/ 3953 (96.1)	1578/ 1632 (96.7)	1913/ 2002 (95.6)	309/ 319 (96.9)	5043/ 5384 (93.7)	2005/ 2147 (93.4)	2569/ 2727 (94.2)	469/ 510 (92)	5554/ 5859 (94.8)	1247/ 1313 (95)	3309/ 3493 (94.7)	998/ 1053 (94.8)

Table 6.3: RC-wise AMS percentages of *S. aureus* from all samples (except faeces and urine)

RC/ AMA	Cefoxitin (N=8220)	Oxacillin (N=5224)	Vancomycin (N=9039)	Teicoplanin (N=5242)	Erythromycin (N=9324)	Tetracycline (N=8831)	Tigecycline (N=3646)	Ciprofloxacin (N=9342)	Clindamycin (N=8829)	Trimethoprim-sulfamethoxazole (N=9341)	Linezolid (N=9340)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Total	3556/ 8220 (43.3)	2470/ 5224 (47.3)	90394/ 9039 (100)	5242/ 5242 (100)	3278/ 9324 (35.2)	8042/ 8831 (91.1)	3646/ 3646 (100)	1969/ 9342 (21.1)	6850/ 8829 (77.6)	7486/ 9341 (80.1)	8843/ 9340 (94.7)
RC1	42/72 (58.3)	1/1 (-)	69/69 (100)	6/6 (100)	36/72 (50)	55/72 (76.4)	0/0 (Null)	27/72 (37.5)	46/59 (78)	45/72 (62.5)	64/72 (88.9)
RC2	582/847 (68.7)	598/1035 (57.8)	1040/1040 (100)	352/352 (100)	369/1041 (35.4)	1024/1031 (99.3)	1/1 (-)	121/1040 (11.6)	343/675 (50.8)	895/ 1036 (86.4)	1041/ 1041 (100)
RC3	134/235 (57)	0/0 (Null)	201/201 (100)	0/0 (Null)	111/234 (47.4)	217/224 (96.9)	0/0 (Null)	156/229 (68.1)	109/171 (63.7)	228/235 (97)	197/235 (83.8)
RC4	346/564 (61.3)	65/226 (28.8)	565/565 (100)	232/232 (100)	285/568 (50.2)	515/566 (91)	230/230 (100)	198/568 (34.9)	479/618 (77.5)	525/573 (91.6)	562/567 (99.1)
RC5	107/166 (64.5)	139/248 (56)	135/135 (100)	131/131 (100)	109/253 (43.1)	232/250 (92.8)	44/44 (100)	31/253 (12.3)	240/253 (94.9)	202/253 (79.8)	253/253 (100)
RC6	249/572 (43.5)	195/447 (43.6)	576/576 (100)	567/567 (100)	217/576 (37.7)	502/565 (88.8)	123/123 (100)	40/576 (6.9)	365/574 (63.6)	330/576 (57.3)	572/576 (99.3)
RC7	8/11 (-)	44/84 (52.4)	85/85 (100)	86/86 (100)	36/84 (42.9)	80/86 (93)	84/84 (100)	10/88 (11.4)	73/84 (86.9)	61/87 (70.1)	85/87 (97.7)

RC8	169/258 (65.5)	168/256 (65.6)	263/263 (100)	262/262 (100)	104/257 (40.5)	256/263 (97.3)	263/263 (100)	60/263 (22.8)	257/263 (97.7)	212/263 (80.6)	263/263 (100)
RC9	105/233 (45.1)	0/0 (Null)	208/208 (100)	0/0 (Null)	70/231 (30.3)	221/231 (95.7)	1/1 (-)	42/233 (18)	212/231 (91.8)	214/233 (91.8)	216/233 (92.7)
RC10	212/304 (69.7)	17/92 (18.5)	304/304 (100)	298/298 (100)	127/304 (41.8)	4/4 (-)	0/0 (Null)	81/312 (26)	258/304 (84.9)	274/305 (89.8)	301/304 (99)
RC11	27/165 (16.4)	27/133 (20.3)	166/166 (100)	166/166 (100)	58/166 (34.9)	141/166 (84.9)	3/3 (-)	8/166 (4.8)	143/163 (87.7)	86/166 (51.8)	156/166 (94)
RC12	24/51 (47.1)	65/169 (38.5)	177/177 (100)	172/172 (100)	72/179 (40.2)	167/177 (94.4)	152/152 (100)	8/177 (4.5)	137/179 (76.5)	100/177 (56.5)	140/177 (79.1)
RC13	85/353 (24.1)	2/9 (-)	329/329 (100)	9/9 (-)	91/357 (25.5)	283/358 (79.1)	19/19 (100)	137/358 (38.3)	197/354 (55.6)	293/358 (-)	268/358 (74.9)
RC14	475/1249 (38)	475/996 (47.7)	1252/1252 (100)	1248/1248 (100)	492/1253 (39.3)	1215/1253 (97)	908/908 (100)	320/1253 (25.5)	1208/1250 (96.6)	1018/1253 (81.2)	1253/1253 (100)
RC16	146/674 (21.7)	0/0 (Null)	674/674 (100)	3/3 (-)	170/673 (25.3)	600/674 (89)	255/255 (100)	308/674 (45.7)	500/674 (74.2)	573/674 (85)	545/674 (80.9)
RC17	20/24 (-)	233/464 (50.2)	478/478 ((100))	470/470 (100)	198/477 (41.5)	458/477 (96)	462/462 (100)	67/478 (14)	384/477 (80.5)	446/478 (93.3)	478/478 (100)
RC19	27/93 (29)	0/0 (Null)	92/92 (100)	0/0 (Null)	16/93 (17.2)	27/86 (31.4)	0/0 (Null)	12/93 (12.9)	33/92 (35.9)	76/93 (81.7)	88/93 (94.6)

RC20	97/566 (17.1)	11/26 (-)	580/580 (100)	26/26 (-)	141/580 (24.3)	492/580 (84.8)	340/340 (100)	33/580 (5.7)	472/580 (81.4)	544/580 (93.8)	556/580 (95.9)
RC21	33/76 (43.4)	33/74 (44.6)	76/76 (100)	76/76 (100)	15/77 (19.5)	70/77 (90.9)	73/73 (100)	7/77 (9.1)	71/77 (92.2)	56/77 (72.7)	77/77 (100)
RC24	36/138 (26.1)	1/1 (-)	136/136 (100)	2/2 (-)	40/138 (29)	120/138 (87)	14/14 (-)	9/138 (6.5)	72/108 (66.7)	122/138 (88.4)	124/138 (89.9)
RC26	36/192 (18.8)	46/230 (20)	239/239 (100)	239/239 (100)	60/246 (24.4)	215/246 (87.4)	99/99 (100)	13/246 (5.3)	205/245 (83.7)	111/246 (45.1)	243/246 (98.8)
RC27	148/216 (68.5)	111/119 (93.3)	219/219 (100)	212/212 (100)	91/218 (41.7)	203/217 (93.5)	13/13 (100)	98/220 (44.5)	150/184 (81.5)	175/220 (79.5)	220/220 (100)
RC28	87/339 (25.7)	87/299 (29.1)	341/341 (100)	341/341 (100)	105/341 (30.8)	301/341 (88.3)	335/335 (100)	1/341 (0.3)	331/336 (98.5)	248/341 (72.7)	341/341 (100)
RC29	6/15 (-)	4/14 (-)	17/17 (-)	15/15 (-)	4/17 (-)	17/17 (-)	14/14 (-)	2/17 (-)	10/13 (-)	12/17 (-)	17/17 (-)
RC30	61/62 (98.4)	85/127 (66.9)	125/125 (100)	115/115 (100)	44/127 (34.6)	120/127 (94.5)	23/23 (-)	24/128 (18.8)	92/118 (78)	104/128 (81.3)	125/128 (97.7)
RC31	39/105 (37.1)	40/96 (41.7)	117/117 (100)	116/116 (100)	54/117 (46.2)	108/114 (94.7)	115/115 (100)	11/117 (9.4)	113/117 (96.6)	73/117 (62.4)	117/117 (100)
RC32	67/225 (29.8)	12/54 (22.2)	228/228 (100)	69/69 (100)	41/230 (17.8)	59/76 (77.6)	3/3 (-)	19/230 (8.3)	116/230 (50.4)	110/230 (47.8)	200/230 (87)

RC33	80/164 (48.8)	0/0 (Null)	98/98 (100)	0/0 (-)	69/164 (42.1)	148/164 (90.2)	0/0 (Null)	34/164 (20.7)	105/149 (70.5)	148/164 (90.2)	156/164 (95.1)
RC34	108/251 (43)	11/24 (-)	249/249 (100)	29/29 (-)	53/251 (21.1)	192/251 (76.5)	72/72 (100)	92/251 (36.7)	129/251 (51.4)	205/251 (81.7)	185/252 (73.4)
Total	3556/8220 (43.3)	2470/5224 (47.3)	9039 /9039 (100)	5242/5242 (100)	3278/9324 (35.2)	8042/8831 (91.1)	3646/3646 (100)	1969/9342 (21.1)	6850/8829 (77.6)	7486/9341 (80.1)	8843/9340 (94.7)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Table 6.4: Year-wise susceptibility trends of *S. aureus* from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=5708	N=8644	N=12320	N=6281	N=8827	N=9415	N=8900	N=8515	N=9700
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	3805/5668 (67.1)	4863/7919 (61.4)	6272/10835 (57.9)	3394/5787 (58.6)	3869/6740 (57.4)	4657/8387 (55.5)	3954/7017 (56.3)	2233/4690 (47.6)	3679 / 8512 (43.2)
Oxacillin	314/438 (71.7)	1218/2196 (55.5)	2280/3773 (60.4)	1140/1869 (61)	2440/3685 (66.2)	1709/3036 (56.3)	1737/4071 (42.7)	3075/5910 (52.0)	2549 / 5388 (47.3)
Vancomycin	2602/2602 (100)	4640/4640 (100)	6996/6996 (100)	3846/3846 (100)	6203/6204 (100)	7684/7731 (99.4)	8810/8850 (99.5)	7968/7968 (100.0)	9398 / 9398 (100)
Teicoplanin	5233/5257 (99.5)	6544/6697 (97.7)	6194/6269 (98.8)	2043/2050 (99.7)	3351/3356 (99.9)	3450/3466 (99.5)	4272/4277 (99.9)	3377/3377 (100.0)	5433 / 5433 (100)
Erythromycin	2755/5570 (49.5)	3593/8102 (44.3)	4803/11975 (40.1)	2594/6096 (42.6)	3617/8355 (43.3)	3586/9282 (38.6)	3226/8126 (39.7)	2967/8274 (35.8)	3398 / 9662 (35.1)
Tetracycline	3492/3860 (90.5)	6255/7050 (88.7)	9269/10329 (89.7)	4734/5284 (89.6)	5686/6400 (88.8)	6963/8144 (85.5)	5667/6530 (86.8)	3765/4241 (88.7)	8343 / 9179 (90.8)
Tigecycline	433/435 (99.5)	1529/1536 (99.5)	2902/2914 (99.6)	1559/1559 (100)	2113/2131 (99.2)	2314/2452 (94.4)	2365/2470 (95.7)	2846/2846 (100.0)	3826 / 3826 (100)
Ciprofloxacin	1224/5260 (23.3)	1497/8094 (18.5)	1990/11200 (17.8)	1101/5845 (18.8)	1455/8341 (17.4)	1948/9050 (21.5)	1972/8850 (22.3)	1473/8035 (18.3)	2100 / 9705 (21.6)
Clindamycin	4235/5475 (77.4)	6460/8456 (76.4)	9153/11984 (76.4)	4645/6084 (76.3)	6334/8579 (73.8)	6815/9154 (74.4)	6464/8786 (73.6)	6000/8255 (72.6)	7102 / 9179 (77.3)
Trimethoprim-sulfamethoxazole	3064/4306 (71.2)	4764/7565 (63)	7927/11401 (69.5)	3926/5821 (67.4)	4718/6954 (67.8)	6374/8620 (73.9)	6645/8850 (75.1)	6118/7968 (76.7)	7780 / 9703 (80.1)
Linezolid	5424/5445 (99.6)	8054/8148 (98.8)	11461/11547 (99.3)	5846/5877 (99.5)	8233/8236 (100)	8934/9055 (98.7)	8794/8850 (99.4)	7951/8159 (97.4)	9174 / 9702 (94.5)

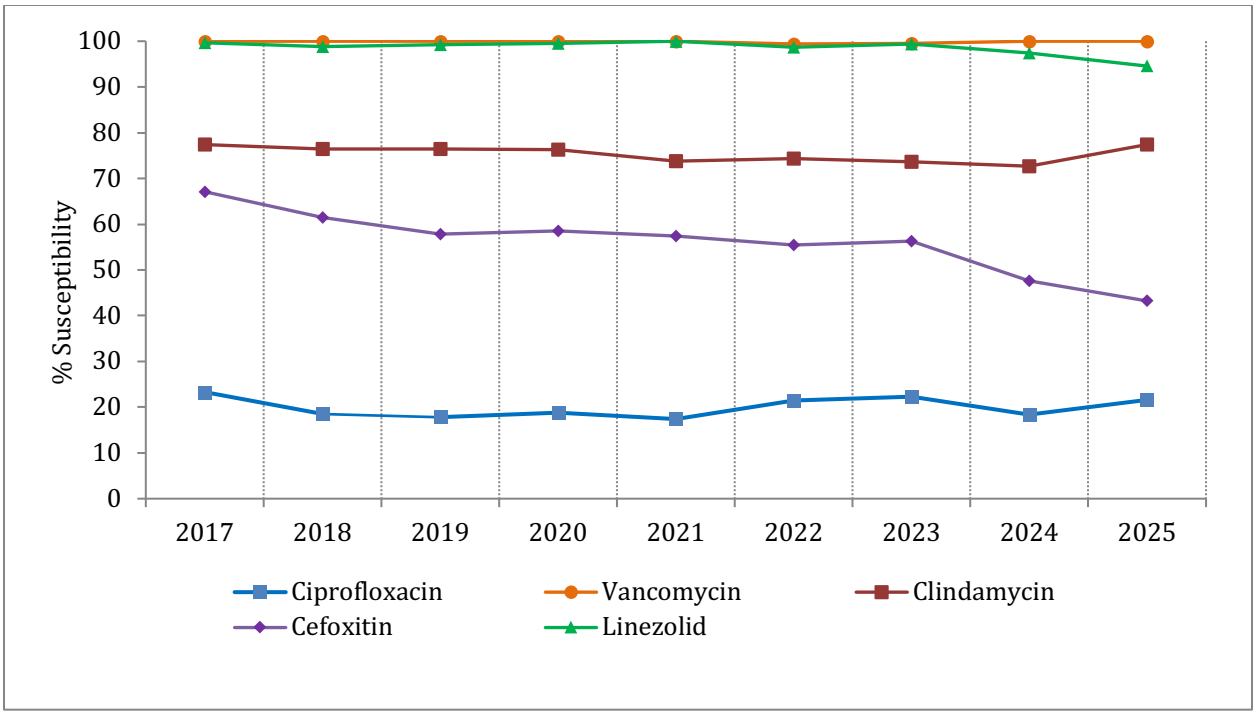


Figure 6.1: Year-wise susceptibility trends of *S. aureus* from all samples

Most of the *S. aureus* isolates were obtained from superficial infections (n=3767) followed by deep infection (n=1874) and blood stream infections (n=1737) **(Tables 6.5-6.7).** MRSA rates differed based on the source of isolation, with isolates from deep and superficial infection demonstrating highest rates (around 60%) while those from blood showed the lowest rates (49.7%). Although overall *S. aureus* showed increasing trends of resistance to most antibiotics over the years, no such prominent trend could be observed with MSSA isolates. MRSA rates steadily increased over the 9 years of study from 33% in 2017 to nearly 56.8% in 2025 **(Tables 6.5-6.7)**.

Table 6.5: Susceptibility percentages of staphylococci isolated from blood

AMA	Blood			
	S. aureus N=1737 (S%)	MSSA N=788 (S%)	MRSA N=949 (S%)	SOSA N=4883 (S%)
Cefoxitin	663 / 1317 (50.3)	663/663 (100)	0/654 (0)	326/1678 (19.4)
Oxacillin	567 / 1156 (49)	567/567 (100)	0/589 (0)	665/3516 (18.9)
Vancomycin	1679 / 1679 (100)	735/735 (100)	944/944 100)	4848/4848 (100)
Teicoplanin	1018 / 1018 (100)	450/450 (100)	568/568 (100)	2142/2235 (95.8)
Erythromycin	600 / 1732 (34.6)	371/784 (47.3)	229/946 (24.2)	740/4846 (15.3)
Tetracycline	1484 / 1642 (90.4)	705/740 (95.3)	779/902 (86.4)	3789/4665 (81.2)
Tigecycline	555 / 555 (100)	237/237 (100)	318/318 (100)	600/873 (68.7)
Ciprofloxacin	428 / 1737 (24.6)	272/784 (34.7)	156/948 (16.5)	1288/4883 (26.4)
Clindamycin	1120 / 1608 (69.7)	560/706 (79.3)	560/883 (63.4)	1526/4425 (34.5)
Trimethoprim-sulfamethoxazole	1382 / 1735 (79.7)	687/784 (87.6)	695/948 (73.3)	3278/4862 (67.4)
Linezolid	1641 / 1737 (94.5)	754/788 (95.7)	887/949 (93.5)	4678/4882 (95.8)

Table 6.6: Susceptibility percentages of staphylococci isolated from Superficial Infections

AMA	Superficial Infections			
	S. aureus N=3767 (S%)	MSSA N=1612 (S%)	MRSA N=2155 (S%)	SOSA N=403 (S%)
Cefoxitin	1451 / 3387 (42.8)	1451/1451 (100)	0/1936 (0)	75/280 (26.8)
Oxacillin	961 / 2057 (46.7)	961/961 (100)	0/1096 (0)	46/206 (22.3)
Vancomycin	3649 / 3649 (100)	1504/1504 (100)	2145/2145 (100)	400/400 (100)
Teicoplanin	2429 / 2430 (100)	1055/1055 (100)	1375/1375 (100)	189/189 (100)
Erythromycin	1408 / 3765 (37.4)	792/1609 (49.2)	616/2154 (28.6)	79/402 (19.7)
Tetracycline	3349 / 3621 (92.5)	1431/1505 (95.1)	1918/2115 (90.7)	276/389 (71)
Tigecycline	1623 / 1623 (100)	629/629 (100)	994/994 (100)	190/264 (72)
Ciprofloxacin	883 / 3771 (23.4)	546/1612 (33.9)	337/2155 (15.6)	178/403 (44.2)
Clindamycin	3060 / 3725 (82.1)	1387/1577 (88)	1673/2120 (78.9)	208/390 (53.3)
Trimethoprim-sulfamethoxazole	3026 / 3773 (80.2)	1397/1612 (86.7)	1629/2155 (75.6)	243/403 (60.3)
Linezolid	3546 / 3769 (94.1)	1548/1612 (96)	1998/2155 (92.7)	332/403 (82.4)

Table 6.7: Susceptibility percentages of staphylococci isolated from Deep Infections

AMA	Deep Infections			
	S. aureus N=1874 (S%)	MSSA N=733 (S%)	MRSA N=1141 (S%)	SOSA N=127 (S%)
Cefoxitin	705 / 1773 (39.8)	705/705 (100)	0/1068 (0)	19/109 (17.4)
Oxacillin	485 / 1030 (47.1)	485/485 (100)	0/545 (0)	15/52 (28.8)
Vancomycin	1837 / 1837 (100)	696/696 (100)	1141/1141 (100)	126/126 (100)
Teicoplanin	968 / 968 (100)	392/392 (100)	576/576 (100)	50/50 (100)
Erythromycin	598 / 1871 (32)	320/730 (43.8)	278/1140 (24.4)	17/127 (13.4)
Tetracycline	1490 / 1685 (88.4)	602/642 (93.8)	888/1043 (85.1)	66/116 (56.9)
Tigecycline	737 / 737 (100)	270/270 (100)	467/467 (100)	35/42 (83.3)
Ciprofloxacin	180 / 1875 (9.6)	120/733 (16.4)	60/1141 (5.3)	39/127 (30.7)
Clindamycin	1367 / 1820 (75.1)	566/712 (79.5)	801/1104 (72.6)	54/125 (43.2)
Trimethoprim-sulfamethoxazole	1465 / 1874 (78.2)	620/733 (84.6)	845/1141 (74.1)	63/127 (49.6)
Linezolid	1780 / 1874 (95)	708/733 (96.6)	1072/1141 (94)	121/127 (95.3)

As per **Table 6.8 and Figure 6.2**, there was not much variation of susceptibility to different antibiotics among MSSA isolates over the different years under study. Susceptibility to ciprofloxacin was extremely low, to erythromycin was moderate while that to clindamycin and tetracycline remained high with hardly any change. Susceptibility to co-trimoxazole showed an upward trend for the last 3 years.

Similar to MSSA, MRSA susceptibility rates to different antibiotics also did not show much variation (**Table 6.9 and Figure 6.3**). Fortunately anti MRSA antibiotics like vancomycin, teicoplanin and tigecycline continued to show excellent activity. However a worrisome finding was the doubling in linezolid resistance among 2025 isolates compared to 2024 (6.5% vs 3.4%)

Table 6.8: Year-wise susceptibility trends of MSSA from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=3819	N=5135	N=7029	N=3655	N=5273	N=5050	N=4539	N=4262	N=4106
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	3801/3801 (100)	4857/4857 (100)	6255/6255 (100)	3388/3388 (100)	3845/3845 (100)	4525/4525 (100)	3901/3901 (100.0)	2183/2183 (100.0)	3679/3679 (100)
Oxacillin	306/306 (100)	1187/1187 (100)	2195/2195 (100)	1100/1100 (100)	2399/2399 (100)	1670/1670 (100)	1689/1689 (100.0)	3002/3002 (100.0)	2549/2549 (100)
Vancomycin	1935/1935 (100)	3041/3041 (100)	3986/3986 (100)	2153/2153 (100)	4010/4010 (100)	4323/4335 (99.7)	4524/4539 (99.7)	3896/3896 (100.0)	3823/3823 (100)
Teicoplanin	3509/3517 (99.8)	3642/3682 (98.9)	3391/3419 (99.2)	1074/1075 (99.9)	1945/1949 (99.8)	1720/1724 (99.8)	1875/1875 (100.0)	1751/1751 (100.0)	2321/2322 (100)
Erythromycin	2251/3739 (60.2)	2757/4841 (57)	3527/6895 (51.2)	1962/3570 (55)	2665/4975 (53.6)	2557/4983 (51.3)	2299/4299 (53.5)	1908/4119 (46.3)	1940/4078 (47.6)
Tetracycline	2508/2665 (94.1)	3809/4137 (92.1)	5383/5791 (93)	2838/3047 (93.1)	3297/3579 (92.1)	3889/4291 (90.6)	3278/3552 (92.3)	1765/1920 (91.9)	3594/3802 (94.5)
Tigecycline	300/302 (99.3)	902/902 (100)	1608/1613 (99.7)	861/861 (100)	1102/1112 (99.1)	1091/1136 (96)	1054/1106 (95.3)	1306/1306 (100.0)	1470/1470 (100)
Ciprofloxacin	1051/3524 (29.8)	1167/4816 (24.2)	1587/6452 (24.6)	888/3386 (26.2)	1112/4971 (22.4)	1412/4879 (28.9)	1568/4553 (34.4)	1022/3937 (26.0)	1319/4101 (32.2)
Clindamycin	3162/3666 (86.3)	4341/5021 (86.5)	5837/6839 (85.3)	3021/3548 (85.1)	4057/5137 (79)	4081/4913 (83.1)	3811/4506 (84.6)	3330/4122 (80.8)	3185/3807 (83.7)
Trimethoprim-sulfamethoxazole	2202/2959 (74.4)	3030/4499 (67.3)	4750/6475 (73.4)	2425/3344 (72.5)	2884/3927 (73.4)	3555/4547 (78.2)	3853/4539 (84.9)	3102/3896 (79.6)	3561/4102 (86.8)
Linezolid	3630/3636 (99.8)	4775/4800 (99.5)	6433/6448 (99.8)	3343/3349 (99.8)	4838/4839 (100)	4761/4789 (99.4)	4528/4539 (99.8)	3882/3942 (98.5)	3945/4106 (96.1)

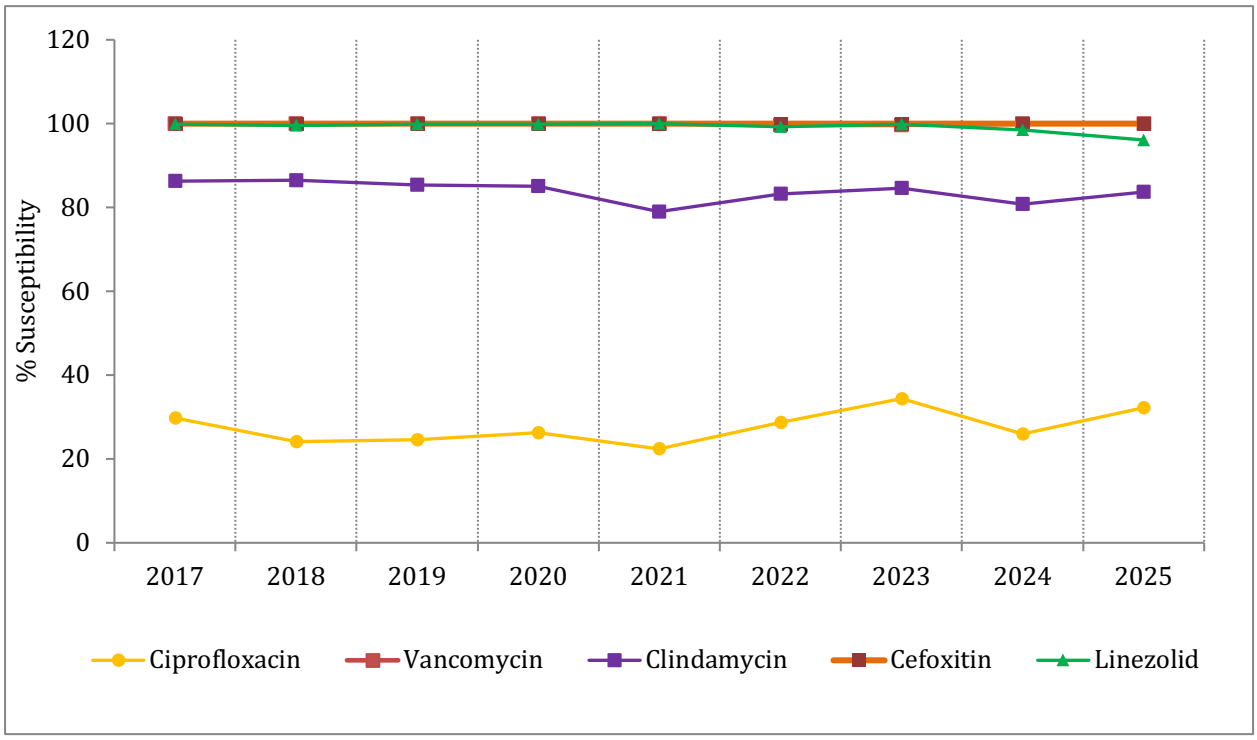


Figure 6.2: Year-wise susceptibility trends of MSSA from all samples

Table 6.9: Year-wise susceptibility trends of MRSA from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=1870	N=3445	N=5185	N=2582	N=3423	N=4266	N=4311	N=4253	N=5593
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	0/1867 (0)	0/3062 (0)	0/4578 (0)	0/2399 (0)	24/2895 (0.8)	132/3862 (3.4)	53/3116 (1.7)	0/2505 (0)	0/4833 (0)
Oxacillin	8/132 (6.1)	31/1009 (3.1)	85/1578 (5.4)	40/769 (5.2)	41/1286 (3.2)	39/1366 (2.9)	48/2383 (2.0)	0/2908 (0)	0/2839 (0)
Vancomycin	667/667 (100)	1581/1581 (100)	2960/2960 (100)	1676/1676 (100)	2153/2154 (100)	3315/3348 (99)	4286/4311 (99.4)	4072/4072 (100.0)	5575/5575 (100)
Teicoplanin	1719/1735 (99.1)	2848/2956 (96.3)	2729/2775 (98.3)	948/953 (99.5)	1369/1370 (99.9)	1690/1700 (99.4)	2397/2402 (99.8)	1626/1626 (100.0)	3111/3111 (100)
Erythromycin	494/1813 (27.2)	822/3228 (25.5)	1251/4988 (25.1)	621/2490 (24.9)	917/3274 (28)	1009/4230 (23.9)	927/3834 (24.2)	1059/4153 (25.5)	1458/5579 (26.1)
Tetracycline	983/1193 (82.4)	2397/2859 (83.8)	3829/4473 (85.6)	1885/2223 (84.8)	2348/2772 (84.7)	3007/3782 (79.5)	2389/2978 (80.2)	2000/2321 (86.2)	4749/5376 (88.3)
Tigecycline	133/133 (100)	627/634 (98.9)	1280/1286 (99.5)	694/694 (100)	990/998 (99.2)	1195/1281 (93.3)	1311/1364 (96.1)	1540/1540 (100.0)	2356/2356 (100)
Ciprofloxacin	165/1718 (9.6)	323/3222 (10)	397/4654 (8.5)	204/2417 (8.4)	328/3257 (10.1)	524/4096 (12.8)	404/4311 (9.4)	454/4104 (11.1)	781/5591 (14)
Clindamycin	1067/1802 (59.2)	2083/3373 (61.8)	3248/5044 (64.4)	1598/2497 (64)	2228/3362 (66.3)	2671/4181 (63.9)	2653/4280 (62.0)	2670/4132 (64.6)	3917/5316 (73.7)
Trimethoprim-sulfamethoxazole	851/1332 (63.9)	1701/3006 (56.6)	3127/4848 (64.5)	1484/2449 (60.6)	1796/2961 (60.7)	2771/4013 (69.1)	2792/4311 (64.8)	3016/4072 (74.1)	4219/5592 (75.4)
Linezolid	1779/1794 (99.2)	3228/3296 (97.9)	4936/5001 (98.7)	2476/2500 (99)	3317/3319 (99.9)	4084/4173 (97.9)	4266/4311 (99.0)	4069/4212 (96.6)	5229/5593 (93.5)

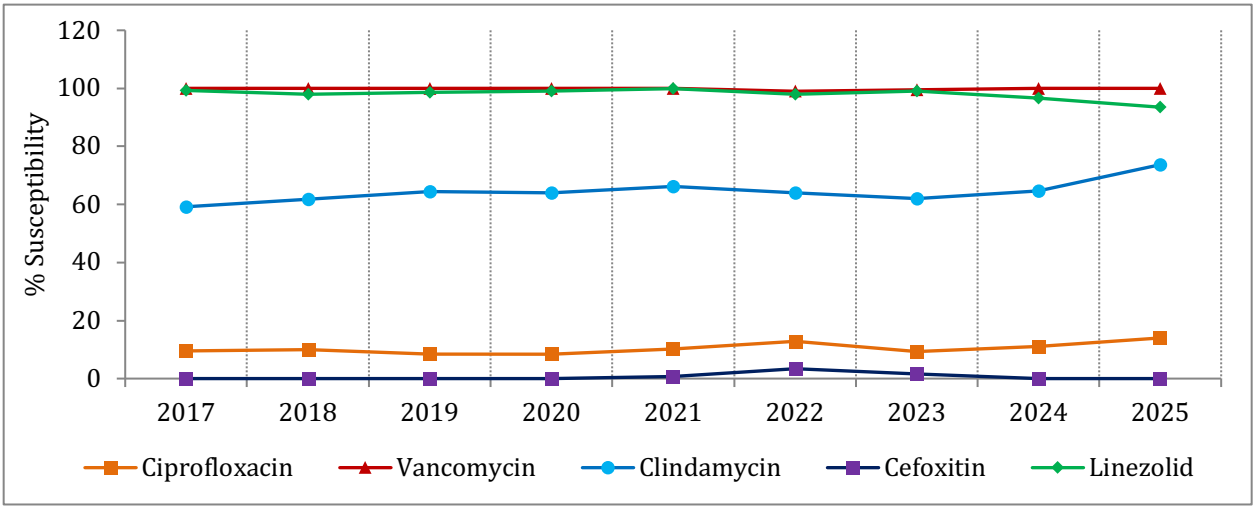


Figure 6.3: Year-wise susceptibility trends of MRSA from all samples

Staphylococci other than *Staphylococcus aureus* (SOSA)

The common species were *S.haemolyticus, S.epidermidis, S.hominis, S.saprophyticus and S. lugdunensis*. Cefoxitin resistance was highest in *S.haemolyticus*, followed by *S.epidermidis* and *S.hominis.* With the exception of teicoplanin, and vancomycin, *S.haemolyticus* exhibited much lower rates of susceptibility to all antibiotics when compared to the other species. Linezolid resistance rates remained unchanged in *S.epidermidis and S.hominis* while it was slightly higher among *S.haemolyticus* (2.1 to 6.3%) **(Table 6.10).** The only species which showed 100% susceptibility to linezolid was *S. lugdunensis*.

The rate of methicillin resistance among SOSA across all the years under study steadily increased from 67% in 2017 – nearly 79 % during 2025 **(Table 6.11 and Figure 6.4).** Erythromycin susceptibility showed a significant decline from 2017 (27.7%) to 2025(16.1%). Tetracycline susceptibility trends improved from 42.2% in 2024 to 79.5% in 2025 while clindamycin susceptibility reduced from 58% in 2017 to 38 % in 2025. Susceptibility to higher antibiotics such as vancomycin, tigecycline remained excellent through all the years of study, while linezolid resistance increased from 1.9% in 2024 to 5.4% in 2025.

Table 6.10: Susceptibility percentages of SOSA isolated from all specimens

AMA	All Specimens					
	***S. haemolyticus* N=1810 (S%)**	***S. epidermidis* N=1769 (S%)**	***S. hominis* N=1495 (S%)**	***Staphylococcus* spp. N=870 (S%)**	***S. lugdunensis* N=28 (S%)**	***S. saprophyticus* N=70 (S%)**
Cefoxitin	55/642 (8.6)	106/604 (17.5)	159/543 (29.3)	153/582 (26.3)	23/27 (-)	22/38 (-)
Vancomycin	1807/1807 (100)	1748/1748 (100)	1484/1484 (100)	865/865 (100)	26/26 (-)	69/69 (100)
Teicoplanin	973/973 (100)	944/944 (100)	611/611 (100)	191191 (100)	24/24 (-)	63/63 (100)
Erythromycin	189/1796 (10.5)	303/1757 (17.2)	219/1483 (14.8)	216/870 (24.8)	22/29 (-)	17/55 (30.9)
Tetracycline	1284/1750 (73.4)	1380/1658 (83.2)	1129/1427 (79.1)	720/861 (83.6)	20/22 (-)	62/65 (95.4)
Ciprofloxacin	245/1811 (13.5)	541/1770 (30.6)	478/1496 (32)	412/871 (47.3)	27/29 (-)	65/70 (92.9)
Clindamycin	350/1643 (21.3)	625/1634 (38.2)	651/1320 (49.3)	419/843 (49.7)	22/28 (-)	27/62 (43.5)
Linezolid	1697/1811 (93.7)	1732/1769 (97.9)	1453/1496 (97.1)	738/871 (84.7)	29/29 (-)	70/71 (98.6)
Trimethoprim-sulfamethoxazole	1017/1803 (56.4)	1271/1761 (72.2)	965/1494 (64.6)	652/869 (75)	29/29 (-)	61/71 (85.9)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Table 6.11: Year-wise susceptibility trends of SOSA from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=2830	N=4016	N=3571	N=2018	N=2655	N=6333	N=6895	N=4574	N=6049
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	930/2810 (33.1)	982/3574 (27.5)	921/3298 (27.9)	487/1907 (25.5)	566/2444 (23.2)	883/4049 (21.8)	705/3500 (20.1)	423/1780 (23.8)	518/2437 (21.3)
Vancomycin	718/718 (100)	1619/1679 (96.4)	1681/1691 (99.4)	890/890 (100)	1374/1377 (99.8)	5633/5680 (99.2)	6746/6895 (97.8)	4574/4574 (100)	6000/6000 (100)
Teicoplanin	2212/2236 (98.9)	2912/3083 (94.5)	1324/1379 (96)	229/238 (96.2)	497/518 (95.9)	1701/1771 (96)	2727/2914 (93.6)	1178/1178 (100)	2807/2807 (100)
Erythromycin	742/2679 (27.7)	755/3459 (21.8)	815/3514 (23.2)	396/1999 (19.8)	455/2608 (17.4)	875/6267 (14)	684/4720 (14.5)	328/2444 (13.4)	966/5991 (16.1)
Tetracycline	1177/1358 (86.7)	2236/2811 (79.5)	2658/3269 (81.3)	1582/1916 (82.6)	1809/2537 (71.3)	248/358 (69.3)	1788/3747 (47.7)	802/1902 (42.2)	4595/5783 (79.5)
Ciprofloxacin	986/2236 (44.1)	1145/3015 (38)	1178/2798 (42.1)	563/1597 (35.3)	778/2210 (35.2)	1980/6015 (32.9)	1958/6895 (28.4)	1323/4574 (28.9)	1768/6048 (29.2)
Clindamycin	1613/2782 (58)	2151/3952 (54.4)	2058/3509 (58.6)	1057/2005 (52.7)	1363/2626 (51.9)	2273/6019 (37.8)	2326/6895 (33.7)	1474/4574 (32.2)	2095/5531 (37.9)
Linezolid	2638/2680 (98.4)	3796/3900 (97.3)	3340/3429 (97.4)	1958/1978 (99)	2600/2614 (99.5)	4347/4356 (99.7)	6849/6895 (99.3)	4487/4574 (98.1)	5720/6048 (94.6)
Trimethoprim-sulfamethoxazole	923/1940 (47.6)	1579/3452 (45.7)	1687/3428 (49.2)	861/1935 (44.5)	1224/2610 (46.9)	5502/5550 (99.1)	3789/6895 (55)	2279/4574 (49.8)	3995/6028 (66.3)

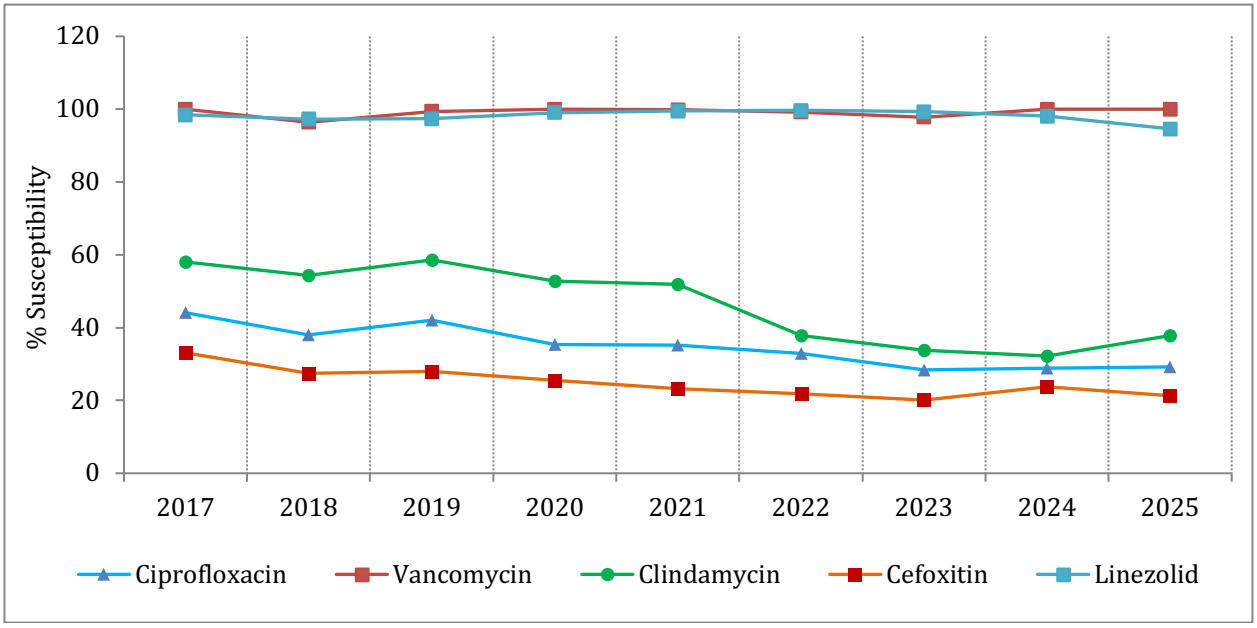


Figure 6.4: Year-wise susceptibility trends of SOSA from all samples

Enterococci

E. faecalis is usually the commonest species followed by *E. faecium*. However in 2024 and 2025, *E. faecium* was found to be the predominant species. The susceptibility rate in *E. faecium* was significantly lower for ampicillin, high level gentamicin and vancomycin than in *E. faecalis*. Overall vancomycin resistance in enterococci was 20 %, slightly lower than 22% in 2024. However, the rate was 7.5 times higher in *E. faecium* compared *to E. faecalis* (33% vs 4.4%). Isolates from blood (both the species) appear to be more resistant when compared to isolates from superficial infections except ampicillin. Although the numbers are too small for significance, vancomycin resistance among CSF isolates was much higher than the overall rate **(Table 6.12).** The susceptibility to all the antibiotics was higher among *E. faecalis* isolates when compared to *E. faecium*. Among urine sample, the difference was particularly marked for ampicillin and nitrofurantoin. Linezolid resistance was encountered more frequently among *E. faecium* isolates (5.8%) than the *E. faecalis* (3.1%) **(Table 6.13).** Among location wise, as expected, most antibiotics showed lower susceptibility rates among ICU isolates when compared to ward isolates. This difference was noted in *E. faecalis* species except for ciprofloxacin where the rates were lower in ward and OPD isolates than the ICU isolates **(Table 6.14).**

Table 6.12: Susceptibility patterns of enterococci from all samples (except urine)

AMA	All Specimens (except urine)		Blood		Superficial Infection		Deep Infection		CSF	
	E. faecalis N=1594 (S%)	*E. faecium* N=1957 (S%)	*E. faecalis* N=486 (S%)	*E. faecium* N=956 (S%)	*E. faecalis* N=537 (S%)	*E. faecium* N=288 (S%)	*E. faecalis* N=196 (S%)	*E. faecium* N=212 (S%)	*E. faecalis* N=*23 (S%)	*E. faecium* N=40 (S%)
Ampicillin	1011/1330 (76)	353/1611 (21.9)	309/427 (72.4)	200/828 (24.2)	346/448 (77.2)	47/242 (19.4)	132/161 (82)	37/169 (21.9)	*12/18 (-)	*4/18 (-)
Vancomycin	1524/1594 (95.6)	1312/1957 (67)	449/486 (92.4)	586/956 (61.3)	530/537 (98.7)	223/288 (77.4)	186/196 (94.9)	149/212 (70.3)	20/23 (87)	20/40 (50)
Teicoplanin	1445/1529 (94.5)	1194/1783 (67)	407/449 (90.6)	533/856 (62.3)	518/528 (98.1)	215/285 (75.4)	179/192 (93.2)	146/207 (70.5)	18/20 (90)	14/37 (37.8)
Gentamicin HL	800/1383 (57.8)	699/1819 (38.4)	252/458 (55)	345/903 (38.2)	277/484 (57.2)	123/268 (45.9)	85/148 (57.4)	57/181 (31.5)	9/20 (45)	9/39 (23.1)
Linezolid	1553/1594 (97.4)	1770/1957 (90.4)	469/486 (96.5)	858/956 (89.7)	523/537 (97.4)	267/288 (92.7)	192/196 (98)	193/212 (91)	23/23 (-)	26/40 (65)

Table 6.13: Susceptibility patterns of enterococci from urine

AMA	Urine	
	Enterococcus faecalis N=1613 (S%)	*Enterococcus faecium* N=1151 (S%)
Ampicillin	884/1470 (60.1)	192/1010 (19)
Vancomycin	1486/1613 (92.1)	938/1151 (81.5)
Teicoplanin	1437/1579 (91)	890/1136 (78.3)
Ciprofloxacin	287/1581 (18.2)	76/1125 (6.8)
Nitrofurantoin	1249/1573 (79.4)	323/1066 (30.3)
Linezolid	1563/1613 (96.9)	1084/1151 (94.2)

Table 6.14: Susceptibility pattern of Enterococci from all samples across OPD, Ward and ICU

AMA	*Enterococcus faecalis*				*Enterococcus faecium*			
	Total N=3217	OPD N=1060	Ward N=1809	ICU N=348	Total N=3128	OPD N=510	Ward N=1929	ICU N=689
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Ampicillin	1895 / 2801 (67.7)	681 / 956 (71.2)	1024 / 1544 (66.3)	190 / 301 (63.1)	545 / 2624 (20.8)	136 / 456 (29.8)	329 / 1629 (20.2)	80 / 539 (14.8)
Vancomycin	3010 / 3240 (92.9)	996 / 1067 (93.3)	1699 / 1824 (93.1)	315 / 349 (90.3)	2250 / 3165 (71.1)	410 / 526 (77.9)	1451 / 1958 (74.1)	389 / 681 (57.1)
Teicoplanin	2882 / 3109 (92.7)	956 / 1031 (92.7)	1629 / 1747 (93.2)	297 / 331 (89.7)	2084 / 2923 (71.3)	374 / 486 (77)	1350 / 1802 (74.9)	360 / 635 (56.7)
Gentamicin HL	1440 / 2603 (55.3)	478 / 792 (60.4)	828 / 1527 (54.2)	134 / 284 (47.2)	995 / 2621 (38)	189 / 399 (47.4)	624 / 1644 (38)	182 / 578 (31.5)
Ciprofloxacin	308 / 1666 (18.5)	143 / 706 (20.3)	141 / 855 (16.5)	24 / 105 (22.9)	82 / 1195 (6.9)	28 / 284 (9.9)	46 / 739 (6.2)	8 / 172 (4.7)
Nitrofurantoin	1303 / 1630 (79.9)	584 / 701 (83.3)	651 / 832 (78.2)	68 / 97 (70.1)	324 / 1070 (30.3)	113 / 253 (44.7)	179 / 669 (26.8)	32 / 148 (21.6)
Linezolid	3116 / 3207 (97.2)	1030 / 1057 (97.4)	1753 / 1804 (97.2)	333 / 346 (96.2)	2854 / 3110 (91.8)	483 / 510 (94.7)	1795 / 1921 (93.4)	576 / 679 (84.8)

Table 6.15 and **Figure 6.5** depict the year wise susceptibility rates of *E. faecalis* from 2017 to 2025. The susceptibility rates showed a slightly decreasing trend for almost all the antibiotics in 2025 when compared to 2024.

Table 6.15: Year-wise susceptibility trends of *Enterococcus faecalis* from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=1034	N=2014	N=2895	N=2101	N=2373	N=3240	N=3461	N=3042	N=3217
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Ampicillin	633/987 (64.1)	1338/1813 (73.8)	1993/2467 (80.8)	1606/1942 (82.7)	1609/2127 (75.6)	2011/2832 (71.0)	2413/3347 (72.1)	2204/2874 (76.69)	1895/2801 (67.7)
Vancomycin	978/1016 (96.3)	1921/2000 (96.1)	2791/2860 (97.6)	2018/2073 (97.3)	2242/2335 (96)	3043/3209 (94.8)	3267/3461 (94.4)	2274/2370 (95.95)	3010/3240 (92.9)
Teicoplanin	992/1030 (96.3)	1889/1970 (95.9)	2582/2633 (98.1)	2001/2039 (98.1)	2235/2310 (96.8)	2995/3141 (95.4)	3080/3328 (92.5)	2151/2281 (94.3)	2882/3109 (92.7)
Gentamicin HL	512/993 (51.6)	982/1890 (52)	1411/2458 (57.4)	1059/1818 (58.3)	1015/1825 (55.6)	1579/2764 (57.1)	1578/3126 (50.5)	964/1694 (56.91)	1440/2603 (55.3)
Ciprofloxacin	41/358 (11.5)	87/641 (13.6)	162/982 (16.5)	127/586 (21.7)	126/646 (19.5)	385/1431 (26.9)	205/1805 (11.4)	397/1951 (20.35)	308/1666 (18.5)
Nitrofurantoin	352/375 (93.9)	710/763 (93.1)	1293/1421 (91)	812/895 (90.7)	757/878 (86.2)	1259/1425 (88.4)	1321/1651 (80)	1600/1816 (88.11)	1303/1630 (79.9)
Linezolid	998/1011 (98.7)	1832/1863 (98.3)	2727/2753 (99.1)	1874/1897 (98.8)	2207/2222 (99.3)	3098/3169 (97.8)	3360/3461 (97.1)	2473/2526 (97.9)	3116/3207 (97.2)

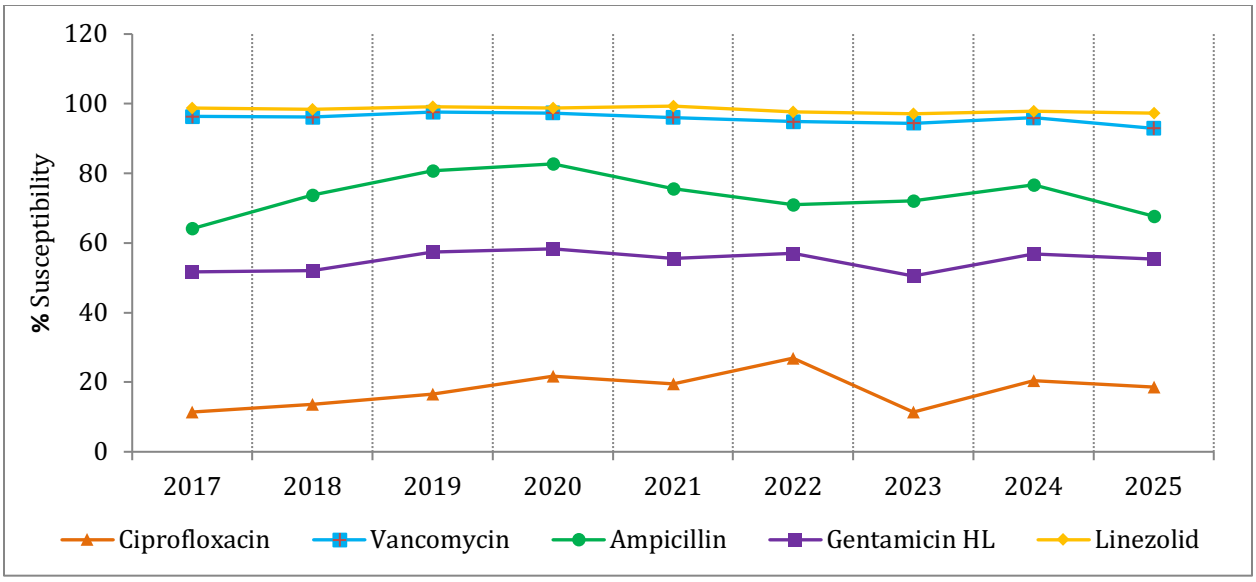


Figure 6.5: Year-wise susceptibility trends of *Enterococcus faecalis* from all samples

Among RC wise analysis, in *Enterococcus faecalis* the susceptibility rates to vancomycin ranged from 60.9% in RC32 to 100 % in several regional centres. There were significant differences observed between the various regional centres, the highest VRE rate in the isolates from RC 32.. Susceptibility to linezolid was high (>90%) in most centres except RC 34 (75%) and RC9 (87.6%) Susceptibility to ampicillin ranged from 39 -100%, while susceptibility to high level gentamicin ranged between 22% in RC1 to 96% in RC 17 (**Table 6.16.**

Table 6.16: RC-wise AMS percentages of *Enterococcus faecalis* from total (except faeces & urine)

RC/ Antibiotics	Ampicillin (N=1330)	Vancomycin (N=1594)	Teicoplanin (N=1529)	Gentamicin HL (N=1383)	Linezolid (N=1594)
	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	4/9 (-)	9/13 (-)	1/4 (-)	2/9 (-)	8/9 (-)
RC2	62/83 (74.7)	72/83 (86.7)	41/46 (89.1)	34/83 (41)	83/83 (100)
RC3	21/25 (-)	24/25 (-)	24/25 (-)	20/25 (-)	24/25 (-)
RC4	109/184 (59.2)	181/184 (98.4)	178/184 (96.7)	89/184 (48.4)	184/184 (100)
RC5	0/0 (Null)	48/50 (96)	48/50 (96)	5/8 (-)	50/50 (100)
RC6	102/109 (93.6)	101/113 (89.4)	102/113 (90.3)	49/112 (43.8)	108/113 (95.6)
RC7	13/13 (-)	15/15 (-)	15/15 (-)	11/12 (-)	14/15 (-)
RC8	2/2 (-)	33/34 (97.1)	33/34 (97.1)	26/34 (76.5)	34/34 (100)
RC9	64/111 (57.7)	108/113 (95.6)	101/110 (91.8)	76/112 (67.9)	99/113 (87.6)
RC10	192/193 (99.5)	192/193 (99.5)	191/193 (99)	43/48 (89.6)	192/193 (99.5)
RC11	26/31 (83.9)	31/32 (96.9)	32/32 (100)	11/26 (-)	32/32 (100)
RC12	17/19 (-)	20/20 (-)	20/20 (-)	9/18 (-	20/20 (-)

RC/ Antibiotics	Ampicillin (N=1330)	Vancomycin (N=1594)	Teicoplanin (N=1529)	Gentamicin HL (N=1383)	Linezolid (N=1594)
	(S%)	(S%)	(S%)	(S%)	(S%)
RC13	26/33 (78.8)	34/34 (100)	30/33 (90.9)	20/33 (60.6)	32/34 (94.1)
RC14	58/71 (81.7)	70/70 (100)	70/70 (100)	42/70 (60)	68/70 (97.1)
RC16	17/57 (29.8)	53/57 (93)	53/57 (93)	36/57 (63.2)	54/57 (94.7)
RC17	52/52 (100)	58/59 (98.3)	57/57 (100)	50/52 (96.2)	58/58 (100)
RC19	38/73 (52.1)	69/84 (82.1)	57/71 (80.3)	27/73 (37)	73/74 (98.6)
RC20	37/67 (55.2)	63/67 (94)	62/67 (92.5)	59/67 (88.1)	67/67 (100)
RC21	8/9 (-)	9/10 (-)	9/10 (-)	4/10 (-)	10/10 (-)
RC24	4/8 (-)	7/8 (-)	6/6 (-)	2/8 (-)	8/8 (-)
RC26	2/2 (-)	88/92 (95.7)	89/92 (96.7)	27/89 (30.3)	87/92 (94.6)
RC27	98/103 (95.1)	116/116 (100)	112/112 (100)	78/116 (67.2)	116/116 (100)
RC28	0/0 (Null)	24/25 (-)	24/25 (-)	6/25 (-)	24/25 (-)
RC29	3/6 (-)	6/6 (-)	6/6 (-)	3/6 (-)	6/6 (-)
RC30	29/31 (93.5)	44/45 (97.8)	39/39 (100)	28/45 (62.2)	44/45 (97.8)
RC31	1/2 (-)	10/11 (-)	10/11 (-)	10/11 (-)	11/11 (-)
RC32	6/11 (-)	14/23 (-)	13/22 (-)	19/23 (-)	22/23 (-)
RC33	16/23 (-)	22/23 (-)	19/21 (-)	10/23 (-)	22/23 (-)
RC34	4/4 (-)	3/4 (-)	3/4 (-)	4/4 (-)	3/4 (-)
Total	1011/1330 (76)	1524/1594 (95.6)	1445/1529 (94.5)	800/1383 (57.8)	1553/1594 (97.4)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Year-wise susceptibility trends of *Enterococcus faecium* from all samples from 2017-2025 is shown (**Table 6.17 and Figure 6.6**). Higher susceptibility trends were observed for all antibiotics in 2025 isolates when compared to 2024 except for nitrofurantoin. Ampicillin and ciprofloxacin susceptibility rates were extremely low all through the study years. However, susceptibility to high level gentamicin went up from 25.6% in 2017 to 38% in 2025.

Among RC wise analysis, in *Enterococcus faecium*, the susceptibility rates of vancomycin ranged from 47.2% in RC6 to 97.5% in RC27. Susceptibility to linezolid was high in most of the centres in the range between 90% to 100% except in RC26 (60.2%) and RC6 (69.4%) (**Table: 6.18).**

Table 6.17: Year-wise susceptibility trends of *Enterococcus faecium* from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024	Year-2025
	N=937	N=1476	N=2700	N=1994	N=2422	N=2998	N=2746	N=3002	N=3128
Ampicillin	172/860 (20)	214/1213 (17.6)	414/2290 (18.1)	200/1810 (11)	269/2154 (12.5)	400/2580 (15.5)	479/2599 (18.4)	464/2756 (16.8)	545/2624 (20.8)
Vancomycin	697/914 (76.3)	1139/1465 (77.7)	2214/2683 (82.5)	1546/1966 (78.6)	1830/2372 (77.2)	2229/2984 (74.7)	1957/2746 (71.3)	1783/2538 (70.3)	2250/3165 (71.1)
Teicoplanin	740/926 (79.9)	1148/1461 (78.6)	2206/2638 (83.6)	1570/1947 (80.6)	1849/2342 (78.9)	2207/2917 (75.7)	1797/2475 (72.6)	1723/2442 (70. 6)	2084/2923 (71.3)
Gentamicin HL	208/812 (25.6)	360/1247 (28.9)	836/2392 (34.9)	577/1696 (34)	612/1701 (36)	1008/2571 (39.2)	914/2492 (36.7)	807/2106 (38.3)	995/2621 (38)
Ciprofloxacin	10/230 (4.3)	26/446 (5.8)	79/984 (8)	38/544 (7)	47/640 (7.3)	140/1141 (12.3)	50/1112 (4.5)	75/1429 (5.3)	82/1195 (6.9)
Nitrofurantoin	181/251 (72.1)	259/509 (50.9)	559/1221 (45.8)	319/779 (40.9)	342/791 (43.2)	449/918 (48.9)	318/878 (36.2)	431/1252 (34.4)	324/1070 (30.3)
Linezolid	860/910 (94.5)	1352/1411 (95.8)	2562/2644 (96.9)	1813/1896 (95.6)	2216/2320 (95.5)	2670/2909 (91.8)	2544/2746 (92.6)	2575/2832 (90.9)	2854/3110 (91.8)

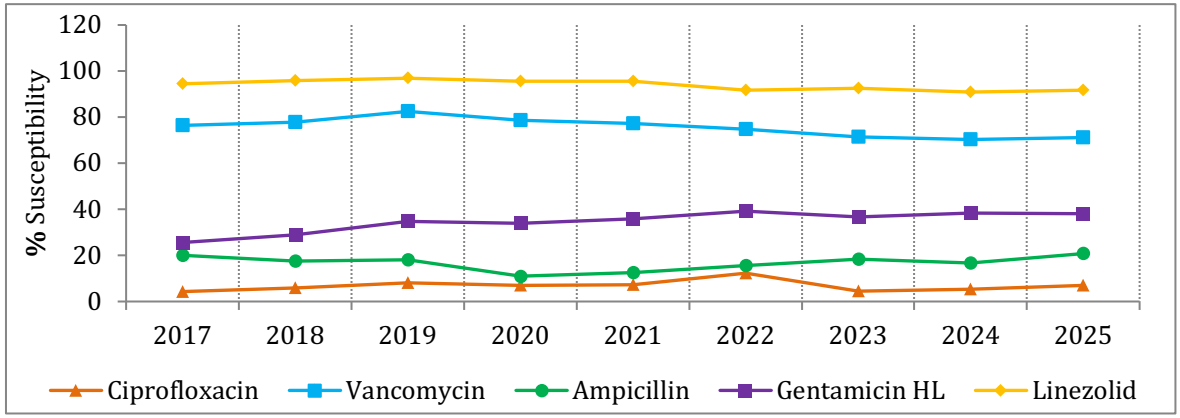


Figure 6.6: Year-wise susceptibility trends of *Enterococcus faecium* from all samples

Table 6.18: RC-wise AMS percentages of *Enterococcus faecium* from total samples (except faeces & urine)

RC/ Antibiotics	Ampicillin (N=1616)	Vancomycin (N=1966)	Teicoplanin (N=1792)	Gentamicin_HL (N=1823)	Linezolid (N=1966)
	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	17/44 (38.6)	32/52 (61.5)	22/40 (55)	23/44 (52.3)	41/44 (93.2)
RC2	83/435 (19.1)	240/434 (55.3)	163/278 (58.6)	120/434 (27.6)	428/434 (98.6)
RC3	5/50 (10)	29/50 (58)	35/50 (70)	18/50 (36)	46/50 (92)
RC4	9/112 (8)	85/112 (75.9)	80/114 (70.2)	37/114 (32.5)	108/112 (96.4)
RC5	0/0 (Null)	39/51 (76.5)	38/50 (76)	3/9 (-)	50/51 (98)
RC6	25/271 (9.2)	136/288 (47.2)	148/288 (51.4)	68/287 (23.7)	200/288 (69.4)
RC7	4/4 (-)	4/5 (-)	5/5 (-)	4/4 (-)	5/5 (-)
RC8	0/15 (-)	64/91 (70.3)	65/90 (72.2)	31/91 (34.1)	82/91 (90.1)
RC9	15/22 (-)	21/22 (95.5)	21/22 (-)	14/22 (-)	21/22 (-)
RC10	8/81 (9.9)	57/81 (70.4)	57/81 (70.4)	33/37 (89.2)	81/81 (100)
RC11	4/47 (8.5)	28/47 (59.6)	29/47 (61.7)	7/26 (-)	47/47 (100)
RC12	0/17 (-)	11/18 (-)	11/18 (-)	7/18 (-)	15/18 (-)
RC13	22/100 (22)	81/113 (71.7)	61/109 (56)	52/94 (55.3)	103/111 (92.8)
RC14	4/57 (7)	46/57 (80.7)	47/57 (82.5)	16/57 (28.1)	55/57 (96.5)
RC16	4/26 (-)	23/26 (-)	22/26 (-)	14/26 (-)	25/26 (-)
RC17	99/100 (99)	100/112 (89.3)	96/107 (89.7)	97/100 (97)	105/107 (98.1)
RC19	10/73 (13.7)	69/82 (84.1)	51/73 (69.9)	17/73 (23.3)	71/73 (97.3)
RC20	6/38 (15.8)	30/38 (78.9)	28/38 (73.7)	30/38 (78.9)	35/38 (92.1)
RC21	3/18 (-)	16/22 (-)	16/22 (-)	8/22 (-)	20/22 (-)
RC26	2/3 (-)	52/103 (50.5)	55/103 (53.4)	18/102 (17.6)	62/103 (60.2)
RC27	11/34 (32.4)	39/40 (97.5)	38/39 (97.4)	27/40 (67.5)	40/40 (100)
RC28	0/0 (Null)	28/38 (73.7)	29/38 (76.3)	15/35 (42.9)	37/38 (97.4)
RC30	3/18 (-)	22/25 (-)	21/23 (-)	14/25 (-)	22/25 (-)
RC31	0/3 (-)	17/24 (-)	18/24 (-)	9/24 (-)	21/24 (-)
RC32	2/2 (-)	5/5 (-)	5/5 (-)	4/5 (-)	5/5 (-)
RC33	14/36 (38.9)	31/38 (81.6)	29/33 (87.9)	7/37 (18.9)	37/37 (100)
Total	353/1616 (21.9)	1312/1966 (66.2)	1194/1792 (66.9)	699/1823 (38.4)	1770/1966 (90.4)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Clinical relevance and treatment guidance

The proportion of MRSA and VRE was found to be high among blood isolates which is a cause for concern. Although vancomycin susceptibility remains very high among MRSA isolates, the occurrence of hVISA which is not usually detected in most clinical laboratories is worrisome as it may lead to therapeutic failure. Although vancomycin may continue to be used for serious MRSA infections, it is better to use alternate drugs if the MIC value is close to the break point as such isolates are likely to be hVISA. As susceptibility to daptomycin is 100% and linezolid continues to be more than 90% among MRSA isolates, these antimicrobials may be considered as alternative agents besides vancomycin. This may also remove some of the selection pressure on antimicrobial resistance genes exerted by vancomycin. The decision to start vancomycin empirically for serious *S. aureus* infections depends on the MRSA rates in that centre.

In centres where MRSA rates are high, vancomycin or linezolid may be used as empirical therapy with de-escalation if required. On the other hand, in centres where MRSA rates are low, Beta lactams may be used as empirical therapy with escalation to glycopeptides/ linezolid/ daptomycin as required. For skin and soft tissue infections, the possibility of using tetracyclines and or clindamycin may be considered as susceptibility rates to these two antibiotics continue to be high. The new drug, Levonadifloxacin appears to be a very effective antibiotic against MRSA as no resistance has been identified on isolates tested in our centre and other regional centres till date (100% susceptibility among a total of 565 MRSA isolates). As per available literature, it appears to be highly efficient against acute bacterial skin and skin structure infections, as well as bacteraemia and diabetic foot infections.

While it is relatively easy to assign clinical significance to *S. aureus* and *Enterococcus* species, the same is not true for SOSA. They are often dismissed as colonizers though they are being increasingly recognized as opportunistic pathogens, particularly *S.haemolyticus*. Another feature of importance is that these isolates are often multi drug resistant; the genes are carried on mobile elements which make transfer of resistance a distinct possibility. In cases where there is a strong possibility of SOSA being pathogens, it may be prudent to use either vancomycin or linezolid as the rates of resistance to beta lactams are extremely high. The numbers of *E. faecium* was almost equal to *E. faecalis* across most centres of India. This could signify a worrisome trend as this species is far more drug resistant when compared to *E. faecalis*. In serious infections, such as meningitis or bacteraemia, linezolid may be tried as empirical therapy, with de-escalation if indicated. In centres which reported linezolid resistance in enterococci, daptomycin may be considered an alternative. The detection of *Enterococcus* species other than faecalis and faecium is also significant as some of these species are intrinsically resistant to glycopeptides. Hence speciation of enterococci is of clinical significance and is not just an academic exercise.

Molecular characterisation reports of Staphylococcal and Enterococcal isolates from the Regional Centre

Staphylococcus aureus

A total of 671 *S. aureus* isolates were received during 2025 from various regional centres and their associated hospitals. Of these, 53 isolates (7.9%) were contaminated and were excluded from further analysis. Therefore, a total of 618 isolates (92.1%) were processed for further analysis, comprising 343 MRSA isolates (55.5%) and 275 MSSA isolates (44.5%). All MRSA isolates were found to be positive for the *mecA* gene, whereas all MSSA isolates were negative for *mecA* gene.

Among the 618 isolates tested, 371 (60.0%) were erythromycin-resistant. Of these, 181 (48.8%) exhibited the $iMLS_B$ phenotype, followed by 166 (44.7%) isolates exhibiting the MS phenotype and 24 (6.5%) exhibiting the $cMLS_B$ phenotype. A total of 247 isolates (40.0%) were susceptible to erythromycin and were classified as a sensitive phenotype (SP).

Regarding erythromycin resistance-associated genes, *ermC* was the most commonly detected gene, being identified in 220 of 371(59.3%) erythromycin-resistant isolates. *ermA* was detected in 1 isolate (0.3%), while a combination of *ermA + ermC* was detected in 1 isolate (0.3%). A total of 149 isolates (40.2%) were negative for all the *erm* genes tested. This may be due to the presence of other resistance mechanisms, such as the *msrAB* gene, which was not tested in these isolates. A total of 36 unusual linezolid-resistant or intermediate isolates were identified from some regional centres (RCs). None of the isolates were found to be positive for the *cfrA* gene. All 36 isolates were found to be susceptible to linezolid by both disc diffusion and MIC methods. All 343 MRSA isolates were found to be susceptible to daptomycin and tigecycline by the E-test method.

Staphylococci other than *S. aureus* (SOSA)

A total of 233 SOSA isolates were received during 2025 from various regional centres and their associated hospitals. Of these, 35 isolates (15%) were contaminated and were excluded from further analysis. Therefore, a total of 198 isolates (85%) were processed for further analysis, comprising 131 MR-SOSA isolates (66.2%) and 67 MS-SOSA isolates (33.8%). All MR-SOSA isolates were found to be positive for the *mecA* gene, whereas all MS-SOSA isolates were negative for the *mecA* gene.

A total of 20 unusual linezolid-resistant or intermediate isolates were identified from some regional centres (RCs). Of these, 3 isolates were positive for the *cfrA* gene and were resistant to linezolid by both E-test and disc diffusion methods. The remaining 17 isolates were negative for the *cfrA* gene and were found to be susceptible to linezolid either by disc diffusion and MIC methods.

***Enterococcus* species:**

A total of 734 *Enterococcus* isolates were received during 2025 from various regional centres and their associated hospitals. Of these, 106 isolates (14.4%) were contaminated and were excluded from further analysis. Therefore, a total of 628 isolates (85.6%) were processed for further analysis, comprising 328 *E. faecalis* isolates (52.2%)**,** 299 *E. faecium* isolates (47.6%), and 1 *Enterococcus* spp. isolate (0.2%).

Among the 628 *Enterococcus* isolates, 101 (16.1%) were identified as vancomycin-resistant enterococci (VRE). The *vanA* gene was detected in all VRE isolates, while all were negative for the vanB gene. The remaining 527 isolates (83.9%) were susceptible to vancomycin and were negative for both *vanA* and *vanB* genes.

A total of 15 isolates were found to be resistant to fosfomycin by the disc diffusion method.

Linezolid resistance-associated genes were tested in all VRE isolates and unusual linezolid-resistant isolates. A total of 138 isolates were tested for linezolid resistance (LR) genes. Among these, 35 isolates carried the *cfrD* gene alone, 9 isolates carried *optrA*, and 5 isolates harboured a combination of *cfrD* and *optrA*. The remaining 89 isolates were negative for all the tested LR genes.

Interestingly, 2 isolates were found to be resistant or intermediate to linezolid by both disc diffusion and E-test methods but were negative by PCR for all the tested resistance genes. This finding may be due to the presence of other linezolid resistance mechanisms that were not investigated in this study. Additionally, 7 isolates were found to be susceptible to linezolid by disc diffusion; however, all 7 isolates were classified as intermediate or resistant by the E-test method and were positive for the *cfrD* gene.

Chapter 7. Fungal pathogens

A total of 4790 yeast isolates were studied during the year 2025. Antifungal susceptibility testing of these isolates revealed that *C. tropicalis* and *C. albicans* remain largely susceptible to all the antifungal drugs (**Table 7.1**). Against these two species, echinocandins showed very good activity, with resistance of ~2%; echinocandin resistance was appreciably higher in some other species. *Nakaseomyces glabratus* (Previously called *C. glabrata)* showed reduced susceptibility to echinocandins, with up to 4.29% resistance to caspofungin. Fluconazole resistance was 6.0% in *N. glabratus* isolates. *C. parapsilosis* exhibited excellent susceptibility against echinocandins, while fluconazole resistance was 17.7%. The most concerning resistance patterns were observed in *C. auris,* with up to 11.1% resistance to caspofungin and 96.5% resistance to fluconazole. These findings highlight *C. auris* as a multidrug-resistant species. *C. krusei* demonstrated 6.3% resistance to caspofungin and 4.2% against voriconazole. Echinocandin resistance in *N. glabratus* and fluconazole resistance in *C. parapsilosis* warrant continued surveillance.

Antifungal susceptibility patterns in blood and urine isolates were broadly similar (**Tables 7.2 and 7.3**). *C. tropicalis* and *C. albicans* from both sources showed high susceptibility to echinocandins. Fluconazole resistance in *C. tropicalis* was similar in the two sources (2.8% in blood and 2.9% in urine); in *C. albicans,* it was higher in urine isolates (4.2%) than in blood isolates (2.9%). Echinocandin susceptibility was comparable in urine and blood isolates of *N. glabratus*, but fluconazole resistance was higher in urine isolates of *N. glabratus*. Fluconazole resistance was higher in blood isolates of *C. parapsilosis*, while echinocandin susceptibility was comparable among blood and urine isolates. *C. auris* showed the most concerning susceptibility profile in both the sample types. Overall, echinocandins retained good activity against most *Candida* isolates from blood and urine, whereas fluconazole resistance was particularly high in *C. auris* and *C. parapsilosis*.

Table 7.1: Susceptibility pattern of *Candida* species isolated from all samples

AMA		*C.tropicalis* n=1446	*C. albicans* n=1169	*N. glabratus* n= 435	*C.parapsilosis* n=521	*C. auris*[#] n=321	*C. krusei* n=96
Anidulafungin	S	574/578 (99.3)	390/399 (97.7)	213/223 (95.5)	248/248 (100)	163/189 (86.2)	48/50 (96.0)
	I	3/578 (0.5)	7/399 (1.7)	4/223 (1.8)	0	14/189 (7.4)	1/50 (2.0)
	R	1/578 (0.2)	2/399 (0.5)	6/223 (2.7)	0	12/189 (6.3)	1/50 (2.0)
Caspofungin	S	1342/1363 (98.4)	1141/1155 (98.8)	334/416 (79.7)	503/508 (99.0)	241/314 (76.7)	70/95 (73.7)
	I	13/1363 (0.9)	10/1155 (0.8)	64/416 (15.3)	1/508 (0.2)	38/314 (12.1)	19/95 (20.0)
	R	8/1363 (0.6)	4/1155 (0.3)	18/416 (4.3)	4/508 (0.8)	35/314 (11.1)	6/95 (6.3)
Fluconazole	S	1383/1446 (95.6)	1079/1164 (92.7)	355/381 (93.2)[$]	413/518 (79.7)	10/319 (3.1)	*
	SDD	24/1446 (1.6)	25/1164 (2.1)	3/381 (0.8)	13/518 (2.5)	1/319 (0.3)	
	R	39/1446 (2.7)	60/1164 (5.1)	23/381 (6.0)	92/518 (17.7)	308/319 (96.5)	
Micafungin	S	1353/1368 (98.9)	1023/1039 (98.4)	364/402 (90.5)	504/509 (99.0)	286/307 (93.1)	89/93 (95.7)
	I	11/1368 (0.8)	12/1039 (1.2)	22/402 (5.4)	2/509 (0.4)	7/307 (2.3)	4/93 (4.3)
	R	4/1368 (0.3)	4/1039 (0.4)	16/402 (4.0)	3/509 (0.6)	14/307 (4.5)	0
Voriconazole	S	1375/1441 (95.4)	1047/1148 (91.1)	WT=352/401 (87.78)[^]	438/507 (86.4)	**	85/94 (90.4)
	I	43/1441 (3.0)	60/1148 (5.2)	-	52/507 (10.2)		5/94 (5.3)
	R	23/1441 (1.6)	41/1148 (3.5)	NWT=49/401 (12.22)[^]	17/507 (3.3)		4/94 (4.2)

Footnotes:

S=Susceptible, SDD=Susceptible-Dose Dependent, I=Intermediate, R=Resistant, WT=Wild-type, NWT=Non-wild-type

[$] Only Susceptible dose dependent (≤32 mg/L) and Resistant (≥64 mg/L) categories are defined by CLSI for fluconazole against *N. glabratus*. Isolates with MICs below the SDD are provided here only for analytical purposes and should not be interpreted as the CLSI-defined susceptible category.

[#]Tentative MIC breakpoints (mg/L) established by the CDC were used for the interpretation of antifungal susceptibility testing of *Candida auris*.

*Isolates of *C. krusei* are intrinsically resistant to fluconazole. MIC testing is therefore unnecessary, and isolates should always be reported as resistant or intrinsically resistant.

**Voriconazole breakpoints or epidemiological cut-off values arenot available for *C. auris*.

[^]Interpretation of *N. glabratus* as wild-type (WT) or Non-wild-type (NWT) for voriconazole is done as per epidemiological cut-off values given in CLSI document M57S, 4th edition.

Table 7.2: Susceptibility pattern of *Candida* species isolated from blood

AMA		*C.tropicalis* n=730	*C. albicans* n=310	*N.glabratus* n=161	*C. parapsilosis* n=384	*C. auris* #n=187	*C.krusei* n=54
Anidulafungin	S	349/351 (99.4)	160/164 (97.5)	76/82 (92.7)	188/188 (100)	77/96 (80.2)	29/30 (96.6)
	I	1/351 (0.3)	3/164 (1.8)	2/82 (2.4)	0	13/96 (13.5)	0
	R	1/351 (0.3)	1/164 (0.6)	4/82 (4.9)	0	6/96 (6.2)	1/30 (3.3)
Caspofungin	S	651/666 (97.7)	297/302 (98.3)	128/156 (82.0)	367/372 (98.6)	133/183 (72.7)	43/53 (81.14
	I	9/666 (1.3)	4/302 (1.3)	22/156 (14.1)	1/372 (0.3)	27/183 (14.7)	8/53 (15.1)
	R	6/666 (0.9)	1/302 (0.3)	6/156 (3.9)	4/372 (1.1)	23/183 (12.5)	2/53 (3.7)
Fluconazole	S	697/730 (95.5)	290/308 (94.1)	122/129 (94.5)$	295/382 (77.2)	7/185 (3.7)	*
	SDD	12/730 (1.64)	9/308 (2.9)	1/129 (0.8)	12/382 (3.1)	0	
	R	21/730 (2.9)	9/308 (2.9)	6/129 (4.6)	75/382 (19.6)	178/185 (96.2)	
Micafungin	S	681/691 (98.5)	287/295 (97.3)	134/153 (87.6)	373/377 (98.9)	160/174 (91.9)	51/53 (96.2)
	I	6/691 (0.8)	5/295 (1.7)	13/153 (8.5)	1/377 (0.3)	7/174 (4.0)	2/53 (3.7)
	R	4/691 (0.6)	3/295 (1.0)	6/153 (3.9)	3/377 (0.8)	7/174 (4.0)	0
Voriconazole	S	689/729 (94.5)	285/301 (94.7)	WT=141/152 (92.76)^	319/373 (85.5)	**	46/53 (86.8)
	I	27/729 (3.7)	10/301 (3.3)	0	40/373 (10.7)		5/53 (9.4)
	R	13/729 (1.8)	6/301 (2.0)	NWT=11/152 (7.24)^	14/373 (3.7)		2/53 (3.7)

Footnotes:

S=Susceptible, SDD=Susceptible-Dose Dependent, I=Intermediate, R=Resistant, WT=Wild-type, NWT=Non-wild-type

$ Only Susceptible dose dependent (≤32 mg/L) and Resistant (≥64 mg/L) categories are defined by CLSI for fluconazole against *N. glabratus*. Isolates with MICs below the SDD are provided here only for analytical purposes and should not be interpreted as the CLSI-defined susceptible category.

Tentative MIC breakpoints (mg/L) established by the CDC were used for the interpretation of antifungal susceptibility testing of *Candida auris*.

* Isolates of *C. krusei* are intrinsically resistant to fluconazole. MIC testing is therefore unnecessary, and isolates should always be reported as resistant or intrinsically resistant.

**Voriconazole breakpoints or epidemiological cut-off values are not available for *C. auris*.

^ Interpretation of *N. glabratus* as wild-type (WT) or Non-wild-type (NWT) for voriconazole is done as per epidemiological cut-off values given in CLSI document M57S, 4th edition.

Table 7.3: Susceptibility pattern of *Candida* species isolated from urine

AMA		*C.tropicalis* n=410	*C. albicans* n=375	*N. glabratus* n=116	*C. parapsilosis* n=44	*C. auris*[#] n=68	*C. krusei* n=14
Anidulafungin	S	123/124 (99.2)	127/129 (98.4)	52/55 (94.5)	16/16 (-)	44/48 (91.6)	6/7 (-)
	I	1/124 (0.8)	1/129 (0.7)	1/55 (1.8)	0	0	1/7 (-)
	R	0	1/129 (0.7)	2/55 (3.6)	0	4/48 (8.3)	0
Caspofungin	S	402/405 (99.2)	367/373 (98.4)	86/104 (82.7)	43/43 (100)	54/65 (83.1)	10/14 (-)
	I	2/405 (0.5)	4/373 (1.1)	13/104 (12.5)	0	5/65 (7.7)	3/14 (-)
	R	1/405 (0.2)	2/373 (0.5)	5/104 (4.8)	0	6/65 (9.2)	1/14 (-)
Fluconazole	S	394/410 (96.1)	352/375 (93.8)	93/104 (89.4)[$]	38/44 (86.3)	2/68 (2.9)	*
	SDD	4/410 (1.0)	7/375 (1.8)	1/104 (0.9)	0	0	
	R	12/410 (2.9)	16/375 (4.2)	10/104 (9.6)	6/44 (13.6)	66/68 (97.0)	
Micafungin	S	387/388 (99.7)	290/292 (99.3)	98/102 (96.0)	39/40 (97.5)	64/68 (94.1)	11/12 (-)
	I	1/388 (0.2)	2/292 (0.8)	4/102 (3.9)	1/40 (2.5)	0	1/12 (-)
	R	0	0	0	0	4/68 (5.8)	0
Voriconazole	S	393/407 (96.5)	343/371 (92.4)	WT=76/101 (75.25)[^]	39/43 (90.7)	**	13/14 (-)
	I	7/407 (1.7)	16/371 (4.3)	0	4/43 (9.3)		0
	R	7/407 (1.7)	12/371 (3.2)	WT=25/101 (24.75)[^]	0		1/14 (-)

Footnotes:

S=Susceptible, SDD=Susceptible-Dose Dependent, I=Intermediate, R=Resistant, WT=Wild-type, NWT=Non-wild-type

[$] Only Susceptible dose dependent (≤32 mg/L) and Resistant (≥64 mg/L) categories are defined by CLSI for fluconazole against *N. glabratus*. Isolates with MICs below the SDD are provided here only for analytical purposes and should not be interpreted as theCLSI-defined susceptible category.

[#] Tentative MIC breakpoints (mg/L) established by the CDC were used for the interpretation of antifungal susceptibility testing of *Candida auris*.

* Isolates of *C. krusei* are intrinsically resistant to fluconazole. MIC testing is therefore unnecessary, and isolates should always be reported as resistant or intrinsically resistant

**Voriconazole breakpoints or epidemiological cut-off values are not available for *C. auris*.

[^] Interpretation of *N. glabratus* as wild-type (WT) or Non-wild-type (NWT) for voriconazole is done as per epidemiological cut-off values given in CLSI document M57S, 4th edition.

Antifungal susceptibility of *Aspergillus* isolates

The antifungal susceptibility profiles of *Aspergillus flavus* and *Aspergillus fumigatus* isolated from all samples are shown in **Table 7.4**. Almost all isolates of both species were susceptible to voriconazole (99.500% of *A. flavus* isolates and 100% of *A. fumigates* isolates).

Table 7.4: Susceptibility pattern of *Aspergillus* species isolated from all samples

AMA	*Aspergillus flavus* (WT%)	*Aspergillus fumigatus* (WT%)
Amphotericin B	186/201 (92.54)	124/134 (92.53)
Caspofungin	196/200 (98)	126/129 (97.67)
Itraconazole	197/202 (97.52)	123/134 (91.79)
Posaconazole	193/202 (95.54)	*
Voriconazole	199/200 (99.50)	133/133 (100)

Note: WT=Wild-type; * - Epidemiological cut-off values not available

Susceptibility trend over last five years

Susceptibility pattern over last five years showed that most *Candida* species remained highly susceptible to the echinocandins, with susceptibility generally remaining above 80% throughout the years. However, some variation was observed across species and years. *C. auris* showed consistently lower susceptibility to fluconazole and voriconazole, while echinocandin susceptibility remained comparatively high. *C. albicans* also showed variable susceptibility to fluconazole and voriconazole. In contrast, *N. glabratus* and *C. parapsilosis* maintained relatively stable susceptibility to the echinocandins, although fluconazole susceptibility was lower. It indicates that echinocandins continued to show good in-vitro activity against the major *Candida* species, whereas azole susceptibility was more variable and warrants continued surveillance. *A. flavus* and *A. fumigatus* have shown generally high and stable susceptibility patterns over the last five years. Figures 7.1a-7.1d are showing susceptibility trends of *Candida* species over last five years.

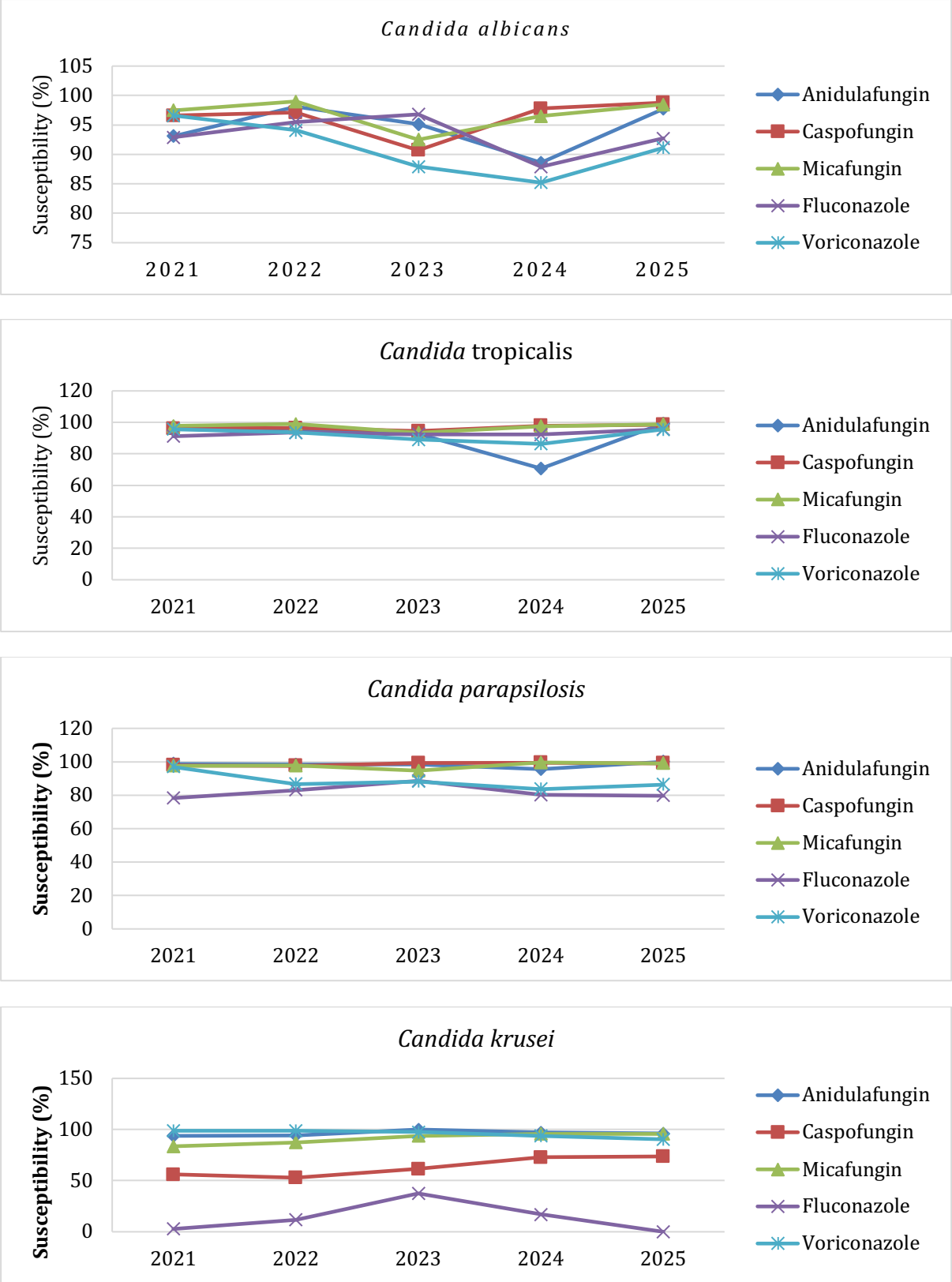


Figure 7.1a-d: Susceptibility trend of *Candida* over the years

a: Candida albicans, *b: Candida tropicalis*, c: *Candida parapsilosis*, d: *Candida krusei*

Characterisation of the resistance mechanism

Molecular Characterization of *ERG11* in fluconazole-resistant *Candida* Isolates

As part of ongoing antifungal resistance surveillance, *ERG11* gene sequencing was performed on selected *Candida* isolates (with increased fluconazole MICs) from the surveillance network. The analysis was done to identify mutations in the *ERG11* gene that could be associated with reduced susceptibility to azole antifungal agents.

A total of 59 *Candida* isolates were resistant to fluconazole, including 49 *C. auris*, 3 *C. albicans*, and 7*C. parapsilosis*. Species-specific overlapping primers were used to amplify and sequence the *ERG11* gene. The sequences were then examined for nucleotide changes and the corresponding amino acid substitutions.

The Y132F amino acid substitution in *ERG11* was detected in 48 *C. auris* isolates, and the K143R mutation was present in one isolate. All *C. albicans* isolates carried the A114V and F145L mutations in the *ERG11* gene. One isolate of *C. parapsilosis* had Y132F and I398R mutations, while five other isolates hadthe K143R mutation; no mutation was found in one isolate **(Table 7. 5)**. These amino acid substitutions have been reported tobe associated with reduced azole susceptibility or fluconazole resistance in *Candida* species.

Table 7.5: Details of fungal isolates received from different regional centres

Regional Centre	Fungal Isolates Sent to Nodal Centre	Resistant Isolates	Mutations identified in Resistant isolates
RC 6	199	*C. auris* (n=26)	Y132F (n=25) K143R (n=1)
		C. parapsilosis (n=6)	K143R (n=4) Y132F and I398R (n=1) No mutation (n=1)
		Candida albicans (n=3)	A114V andF145L (n=3)
RC 17	85	*C. auris* (n=3)	Y132F (n=3)
RC 8	56	*C. auris* (n=6)	Y132F (n=6)
RC 5	34	*C. auris* (n=9)	Y132F (n=9)
RC 9	17	*C. parapsilosis* (n=1)	K143R (n=1)
RC 14	15	No resistant isolates	-
RC 12	7	No resistant isolates	-
RC 19	7	*C. auris* (n=5)	Y132F (n=5)
RC 33	5	No resistant isolates	-

Mutation analysis in the *cyp51* gene of *Aspergillus fumigatus* with raised voriconazole MIC

One isolate of *A. fumigatus* with a raised voriconazole MIC (2 mg/L) was sequenced for mutations in the cyp51 gene. Overlapping primers were designed for the *A. fumigatus* cytochrome P450 sterol 14 alpha-demethylase (*cyp51*) gene.

Sanger sequencing was performed by capillary electrophoresis. Contigs were prepared from forward and reverse sequences with SeqMan software and aligned against the reference sequence to detect single-nucleotide polymorphisms in the gene. Alignment of the deduced protein sequence of this isolate against the reference sequence revealed no mutations in the Cyp51protein **(Figure 7.2).**



Figure 7.2: Alignment of the Cyp51protein sequence of the isolate with a raised voriconazole MIC against the reference sequence.

Clinical relevance and treatment guidance

Consistent with last year's trends, *C. tropicalis* remains the most commonly isolated *Candida* species, followed by *C. albicans* and *C. parapsilosis*. Isolation rates of *C. auris* remain consistently high, underscoring its clinical significance.

Echinocandins, which show good activity against all *Candida* species, remain the most reliable empirical drugs for invasive candidiasis. However, species-level identification and AFST are important in *N. glabratus* and *C. auris* infections, which showed reduced susceptibility. Echinocandins should be preferred initially; with subsequent de-escalation to fluconazole if the isolate is susceptible. This is important in case of *C. auris* infection, where fluconazole should not be given empirically. Despite the excellent categorical susceptibility reported here, *C. parapsilosis* typically has higher echinocandin MICs than other *Candida* species, and AFST is necessary before treatment is chosen, particularly because fluconazole resistance in this species is also relatively high.

Isolation of *Candida* from urine generally represents colonisation, and treatment may be unnecessary in asymptomatic patients. However, patients with symptomatic *Candida* UTI may require treatment. Susceptibility patterns of urine isolates cannot be extrapolated directly to the treatment of invasive candidiasis.

Multidrug resistance in *C. auris* underlines the need for rapid identification and susceptibility testing. Echinocandins are generally preferred for the initial treatment whenever the isolate is susceptible. Overall, the findings support species-directed and

susceptibility-guided therapy, as routine fluconazole use may be ineffective, particularly against *C. auris*, *C. krusei* and fluconazole-resistant *C. parapsilosis.* The susceptibility patterns of *Aspergillus* isolates make voriconazole the drug of choice for treating these infections. Unlike in the Netherlands, the UK, and the USA, azole resistance in *Aspergillus fumigatus* remained very low in India.

Chapter 8. Streptococcus pneumoniae

Serotype distribution and antimicrobial susceptibility profile of invasive and non-invasive *S. pneumoniae* in India

As part of national reference laboratory, we receive *S. pneumoniae* isolates from various hospitals within India. The invasive isolates include, *S.pneumoniae isolated* from sterile specimens such as CSF, blood and other sterile body fluids. The non-invasive isolates include, *S. pneumoniae isolated* from respiratory specimens (Sputum, BAL and other respiratory specimens).

Serotype distribution

A total of 96 invasive (Children below the age of 5 years n=32, adult and children above 5 years of age n=64) and 188 non-invasive (Children below the age of 5 years, n= 99; adult and children above 5 years of age, n= 89). *S. pneumoniae i*solated in the year 2025 were included in the analysis. The serotype distribution among the invasive and non-invasive isolates of *S. pneumoniae*is depicted **(Figure 8.1** and **Table 8.1)**. Overall, the most common serotypes were serotypes 3, 19F, and 15B, all of which were predominant among non-invasive infections. Serotypes 11A and 35B, although equal in number (n=15), were the next most predominant serotypes in non-invasive infections. The serotypes causing invasive infections were more diverse, with the top seven comprising PCV13 serotypes 3, 19A, 19F, 1, 5, 18C, and 14. These were followed by the non-vaccine serotypes 11A, 15B, and 23B.

Serotype percentage covered by Pneumosil (PCV10 Sii) was 31% and 39% for children less than 5 years (n=131) and for adults and children above 5 years of age (n=153), respectively (**Table 8.2).** Serotype percentage covered by Pneumosil (PCV10 Sii) was 47% and 30% among the invasive and non-invasive isolates. Among the serotypes not included in the Pneumosil (PCV10Sii), the serotype 4 constitute 0.3% (n=1/284), 3 constitute 11% (n=31/284) and 18C constitute 3.9% (11/284) of the total isolates. The majority of serotype 3 was observed among the non-invasive infections (8%, n=23/284), though they were present in equal numbers in both the age groups. Over all the predominant other non-Pneumosil serotypes were serotype 23A, 15B/C, 11A, and 35B.

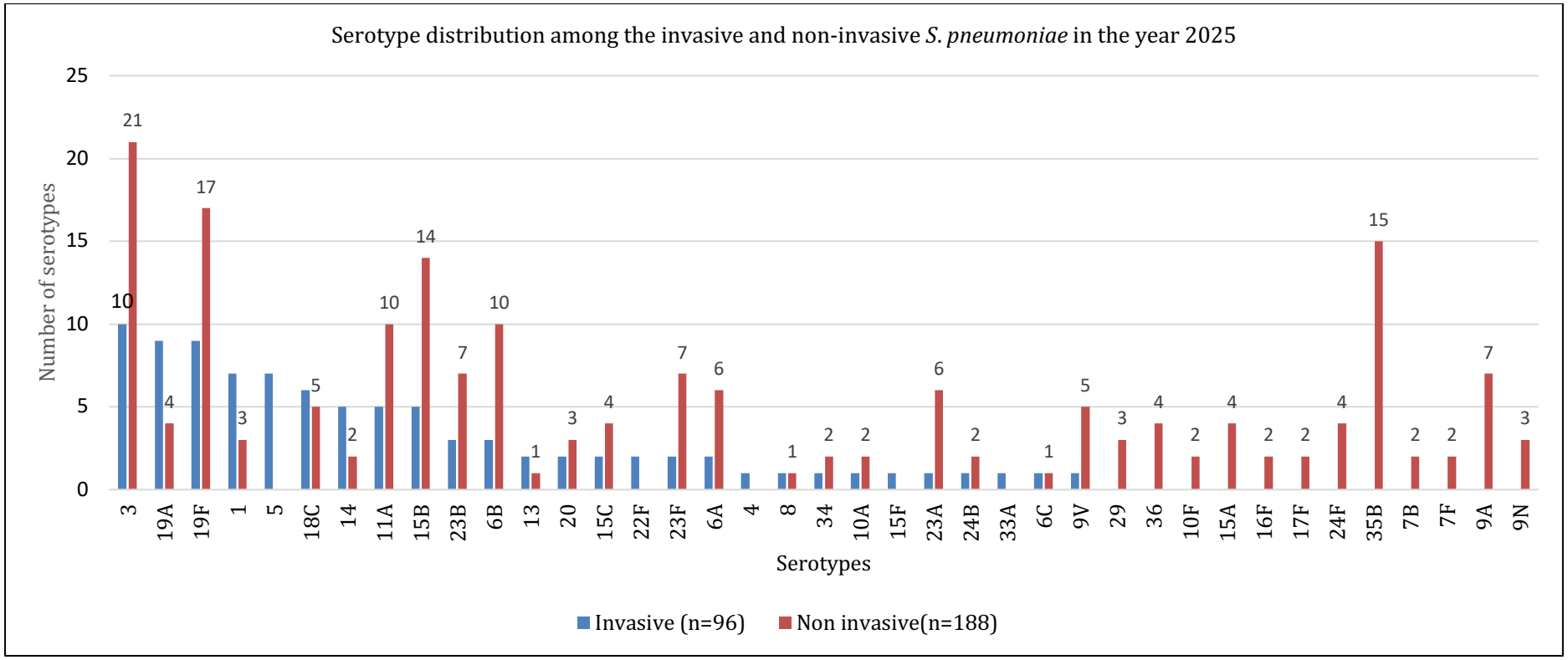


Figure 8.1: The serotype distribution of invasive (n=96) and non-invasive (n=188) isolates of *S. pneumoniae*

Table 8.1: Serotype distribution of *Streptococcus pneumoniae* among invasive and non-invasive isolates

Serotypes*	Invasive (n=96)	Non invasive(n=188)	Grand Total
3	10	21	31
19A	9	4	13
19F	9	17	26
1	7	3	10
5	7		7
18C	6	5	11
14	5	2	7
11A	5	10	15
15B	5	14	19
23B	3	7	10
6B	3	10	12
13	2	1	3
20	2	3	5
15C	2	4	6
22F	2		2
23F	2	7	9
6A	2	6	8
4	1		1
8	1	1	2
34	1	2	3
10A	1	2	3
15F	1		1
23A	1	6	7
24B	1	2	3
33A	1		1
6C	1	1	2
9V	1	5	6
29		3	3
36		4	4
10F		2	2
15A		4	4
16F		2	2
17F		2	2
24F		4	4
35B	1	14	15
7B		2	2
7F		2	2

Pneumosil serotypes

PCV13 serotypes

9A		7	7
9N		3	3

*One each of serotype 38, 45, 12F and 31in invasive; 17A, 25F, 11B, 11C, 35C and 10Bin non-invasive infections.

Table 8.2: Comparison of *Streptococcus pneumoniae* serotype distribution between age groups below 5 years and above 5 years

Row Labels	<5 Years (n=131)	>5 Years (n=154)
3	15	16
19F	12	14
15B	9	10
35B	8	6
11A	7	8
18C	6	5
19A	6	7
23B	5	5
6B	5	8
9A	5	2
23F	4	5
6A	4	4
14	3	4
10A	3	
23A	3	4
9V	3	3
5	2	5
20	2	3
29	2	1
34	2	1
36	2	2
15A	2	2
15C	2	4
17F	2	
24B	2	1
1	1	9
13	1	2
38	1	
45	1	
10B	1	
11C	1	
17A	1	
22F	1	1

Pneumosil Serotypes

PCV13 Serotypes

Row Labels	<5 Years (n=131)	>5 Years (n=154)
24F	1	3
25F	1	
35C	1	
6C	1	1
7B	1	1
7F	1	1
9N	1	2
4		1
8		2
31		1
35		1
10F		2
11B		1
12F		1
15F		1
16F		2
33A		1

Antimicrobial Susceptibility Profile

The penicillin and cefotaxime antimicrobial susceptibility percentage of invasive *S. pneumoniae* isolates (n=95) were calculated based on meningeal or non-meningeal criteria (**Figure 8.2** and **Table 8.3**). The penicillin and cefotaxime non-susceptibility was high in meningeal isolates compared to the non-meningeal isolates.

The antimicrobial susceptibility profile for antibiotics other than penicillin and cefotaxime, for invasive isolates is given below **(Figure 8.3).** The atimicrobial susceptibility profile of non invasive isolates is depicted **(Figure 8.4).**

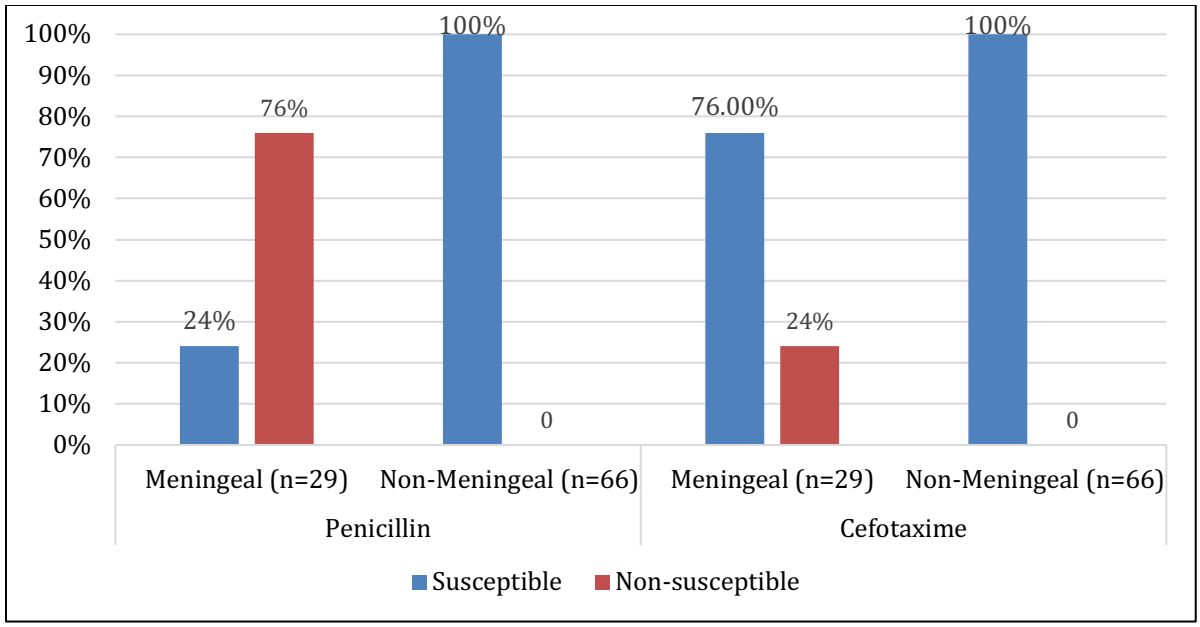


Figure 8.2: Penicillin and cefotaxime antimicrobial susceptibility of invasive isolates of *S. pneumoniae*. Due to the limited number of isolates fulfilling the meningeal criteria, the results should be interpreted with caution.

Table 8.3: Number of *S. pneumoniae* invasive isolates susceptible to penicillin and cefotaxime

Organism	Penicillin		Cefotaxime	
	Meningeal (n=29)	**Non-Meningeal (n=66)**	**Meningeal (n=29)**	**Non-Meningeal (n=66)**
	S% (N/D)	S% (N/D)	S% (N/D)	S% (N/D)
S.pneumoniae	24% (7/29)	100% (66/66)	76% (22/29)	100% (66/66)

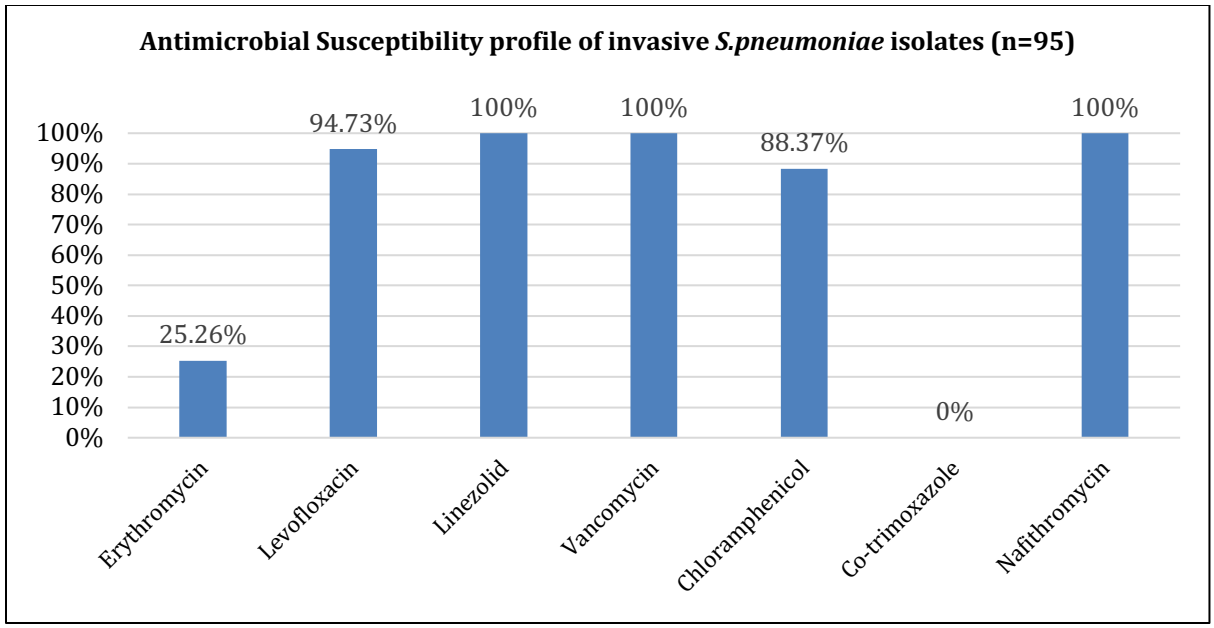


Figure 8.3: Antimicrobial susceptibility profile of invasive *S. pneumoniae* isolatesfor antibiotics other than penicillin and cefotaxime

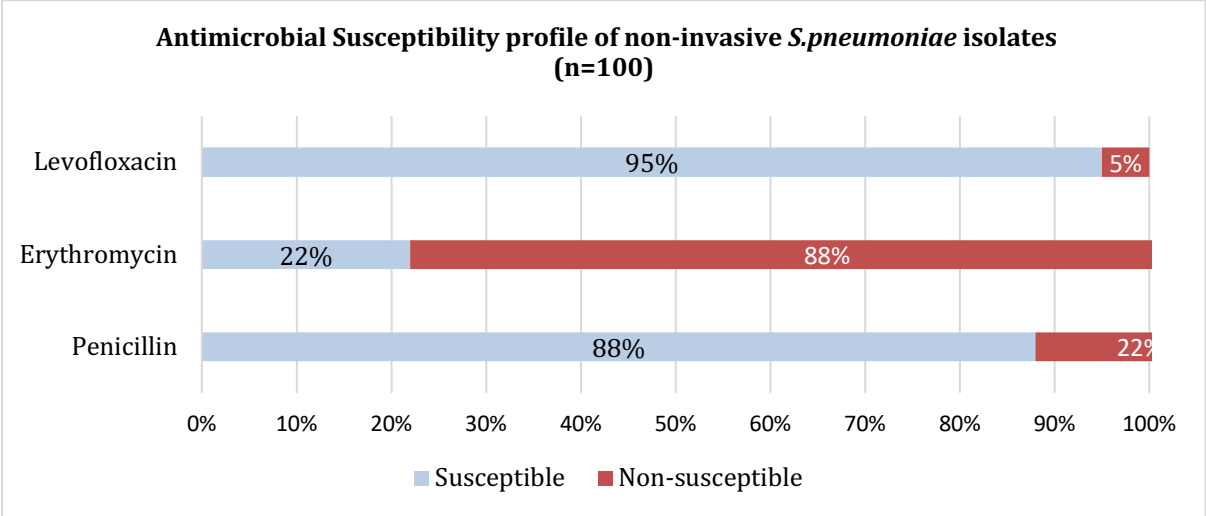


Figure 8.4: Antimicrobial susceptibility profile of non-invasive *S. pneumonia* isolates

Summary

Pneumosil (PCV10Sii) and PCV13 serotype coverage is 31% and 47% among the serotypes causing disease in children less than 5 years of age. Among the non-pneumosil PCV13 serotypes, serotypes 3 and 18C together constitute 16% among the children and 13.6 % among the age group >5 years of age. In adults and children, serotype 3 was major cause of non-invasive infections. The new higher valent vaccine, PCV 20 provides a serotype coverage

of 62.6% in children less than 5 years of age. Continued monitoring of serotypes 3 and 18C is important, as they are predominant among both Children, adults, invasive and non-invasive isolates. The antimicrobial susceptibility to penicillin and cefotaxime in meningeal isolates is decreasing gradually. Similarly, decrease in erythromycin susceptiblity is alarming in invasive and non-invasive isolates.

Chapter 9. Neonatal sepsis and Paediatric blood stream infections

Bloodstream infections are an important cause of morbidity and mortality among neonates, infants and children. The bacterial pathogens associated with these infections and their antimicrobial resistance profiles may vary across different paediatric age groups. Understanding the distribution of these pathogens and their antimicrobial susceptibility patterns is essential for informing empirical antibiotic therapy and guiding clinical management.

For the first time, the ICMR Annual Antimicrobial Resistance Surveillance Report presents age-stratified data on bacterial isolates associated with neonatal sepsis and blood stream infections and their antimicrobial susceptibility patterns. The analysis covers three age groups: neonates (0–28 days), infants (29 days to <1 year) and children (1–12 years).

Coagulase-negative staphylococci (CoNS), now referred to as *Staphylococcus* species other than *S. aureus* (SOSA), have been excluded from this analysis because, based on the available surveillance data, it is not possible to reliably distinguish true bloodstream infections from blood culture contamination. The data collection system does not capture information on the number of positive blood culture sets, which may help assess the clinical significance of CoNS isolation. Therefore, the available data are insufficient to determine whether CoNS isolates represent true infections or contaminants. Accordingly, CoNS isolates have been excluded, and all pathogen distribution and antimicrobial susceptibility percentages have been calculated using denominators that exclude CoNS isolates

Distribution of bacterial isolates

The distribution of bacterial isolates from blood cultures varied across the four age groups. Among neonates (0–28 days; n=1,075), *Klebsiella pneumoniae* was the most frequently isolated pathogen (25.1%), followed by Candida spp.(17.7%), *Acinetobacter baumannii* (14.4%) and *Escherichia coli* (8.1%) **(Table 9.1).** In infants aged 29 days to <12 months (n=1,069), *Candida* spp (17.4%) followed by *K. pneumoniae* (16.2%) and *A. baumannii* (15.9%) were the predominant isolates, followed by *E. coli* (10.2%) and *Staphylococcus aureus* (9.5%) **(Table 9.2)**. Among children aged 1–12 years (n=1,641), *Salmonella* spp was the leading isolate (27.1%), followed by *S. aureus* (11.0%), *K. pneumoniae* (10.4%) and *A. baumannii* (10.3%) **(Table 9.3**).

Table 9.1: Distribution of top bacterial isolates (%) from blood cultures among neonates (0–28 days)

Organism	Blood N=1075
Klebsiella pneumoniae	270 (25.1)
Candida spp	191 (17.7)
Acinetobacter baumannii	155 (14.4)
Escherichia coli	87 (8.1)
Enterococcus spp.	82 (7.6)
Staphylococcus aureus	57 (5.3)
Pseudomonas aeruginosa	49 (4.5)
Klebsiella spp.	46 (4.2)
Enterobacter spp.	33(3.0)
Acinetobacter spp.	31 (2.8)
Salmonella spp	14 (1.3)
Streptococcus spp	5 (0.4)
Yeast other than Candida	5 (0.4)
Others Gram-negative bacteria	50 (4.6)

Table 9.2: Distribution of top bacterial isolates (%) from blood cultures among infants (29 days- <12 months)

Organism	Blood (N=1069)
Candida spp.	186 (17.4)
Klebsiella pneumoniae	173 (16.2)
Acinetobacter baumannii	170 (15.9)
Escherichia coli	109 (10.2)
Staphylococcus aureus	102 (9.5)
Pseudomonas aeruginosa	90 (8.4)
Enterococcus spp.	69 (6.5)
Salmonella spp.	43 (4.0)
Enterobacter spp.	29 (2.7)
Acinetobacter spp.	15 (1.4)
Yeast other than Candida	13 (1.2)
Streptococcus spp.	9 (0.8)

Klebsiella spp.	8 (0.7)
Other Gram-negative bacteria	53 (5.0)

Table 9.3: Distribution of bacterial isolates (%) from blood cultures among children (1 -12 years)

Organism	Blood (N=1641)
Salmonella spp.	442 (27.0)
Staphylococcus aureus	180 (11.0)
Klebsiella pneumoniae	170 (10.4)
Acinetobacter baumannii	169 (10.3)
Pseudomonas aeruginosa	135 (8.2)
Escherichia coli	134 (8.2)
Candida spp.	139 (8.5)
Enterococcus spp.	84 (5.1)
Acinetobacter spp.	60 (3.7)
Enterobacter spp.	39 (2.4)
Streptococcus spp.	21 (1.3)
Klebsiella spp.	5 (0.3)
Yeast *other than Candida*	2 (0.1)
Other Gram-negative bacteria	61 (3.7)

Antimicrobial susceptibility profile

Antimicrobial susceptibility of top isolates from blood cultures among neonates (0–28 days)

The antimicrobial susceptibility patterns of predominant bloodstream isolates among neonates (0–28 days) showed low susceptibility to several commonly used antibiotics. Among Gram-negative bacteria, *Klebsiella pneumoniae* exhibited low susceptibility to third-generation cephalosporins (11.5%), ciprofloxacin (13.7%) and carbapenems (23.5%). *Escherichia coli* showed a similar susceptibility pattern, although susceptibility to carbapenems was comparatively higher at 45%. Similarly, *Acinetobacter baumannii* demonstrated low susceptibility to most tested antibiotics, including carbapenems (14.5%), amikacin (17.5%) and third-generation cephalosporins (13.6%). Susceptibility to minocycline was higher, at 66.7%. Among *Candida* spp., susceptibility to antifungal agents

was high, with 97% susceptibility to caspofungin, 84.4% to fluconazole and 90.2% to voriconazole.

Antimicrobial susceptibility of top isolates from blood cultures among infants (29 days-12 months)

Among *Candida* spp., susceptibility to antifungal agents was high, with 97% susceptibility to caspofungin, 85.7% to fluconazole and 96.4% to voriconazole. *Klebsiella pneumoniae* isolates exhibited low susceptibility to most tested antibiotics, particularly ciprofloxacin (11.0%), third-generation cephalosporins (16.1%), carbapenems (31.0%) and amikacin (34.7%). *Escherichia coli* showed a similar susceptibility pattern, with third-generation cephalosporins (20%), susceptibility to carbapenems was comparatively higher (60%). *Acinetobacter baumannii* also showed low susceptibility to most tested antibiotics, including carbapenem (21.3%), amikacin (23.7%) and third-generation cephalosporins (22.1%).
Among Gram-positive isolates, *Staphylococcus aureus* showed Cefoxitin susceptibility of 48.6%, however, 100% susceptibility was observed to vancomycin, teicoplanin, daptomycin and tigecycline, while linezolid showed 98.0% susceptibility.

Antimicrobial susceptibility of top isolates from blood cultures among children (1 -12 yrs)

Salmonella spp was the leading isolate in this age group and among *Salmonella Typhi* isolates, high susceptibility was observed to most tested antibiotics, including azithromycin (99.4%), cefixime (96.6%), ceftriaxone (97.8%), chloramphenicol (96.5%), and ampicillin (93.4%). However, susceptibility to ciprofloxacin was markedly low (0.9%), indicating widespread fluoroquinolone resistance.
Among Gram-positive isolates, *Staphylococcus aureus* showed relatively low susceptibility. Cefoxitin susceptibility was 60.4%, 100% susceptibility was observed to vancomycin and teicoplanin.
Among Gram-negative bacteria, *Klebsiella pneumoniae* demonstrated low susceptibility to most tested antibiotics, particularly ciprofloxacin (19.4%), ceftazidime (21.3%), cefepime (25.6%), ceftriaxone (26.3%) and ceftazidime-avibactam (26.8%). Carbapenem susceptibility was approximately 41% across ertapenem, imipenem and meropenem.


SECONDARY-CARE
HOSPITALS

Chapter 10. Summary of isolate distribution

The 2025 ICMR-AMRSN annual report marks an important expansion of national AMR surveillance with the inclusion of secondary-care hospitals**.** To account for differences in hospital capacity and patient volume, the participating secondary-care hospitals were stratified into three bed-size categories: Category I (≤ 200 beds), Category II (201–499 beds), and Category III (≥500 beds)**.** A total of 34 secondary-care hospitals contributed data in 2025, (8 hospitals in category I, 18 hospitals in category II, and 8 hospitals in category III). Across the three categories, 2,732, 11,709, and 6,088 culture-positive isolates, respectively, were studied during the year.

Isolates distribution:

A total of 20,529 isolates were analysed across three hospital categories based on bed capacity: Category I (n=2,732), Category II (n=11,709), and Category III (n=6,088). The distribution of isolates by specimen differed markedly between categories **(Table 10.1 and Figure 10.1).**

Urine was the most common source in category I (61.9%) and category II (49.2%), but fell to 24.0% in category III. Blood isolates increased steadily with hospital size, from 9.3% in category I to 12.0% in category II and 22.1% in category III. Lower respiratory tract (LRT) isolates followed a similar trend, rising from 7.1% to 11.7% and 13.4%. Deep infections were the largest group (28.5 %) in category III compared with other groups. Superficial infections were similar in categories I and II (15.2% and 14.7%) but lower in category III (4.9%). CSF (0.1-0.5%) and SS (0.7-1.3%) isolates accounted for a small share in all categories.

Overall, smaller hospitals mostly reported urine isolates as they sent more urine cultures, while larger hospitals showed a more varied distribution of isolates, with a higher share of bloodstream, respiratory, and deep infections.

Table 10.1: Distribution of isolates by site of infection across hospital bed-size categories

	Total	Blood	Urine	LRT	Superficial Infection	Deep Infection	CSF	SS
Category I (≤ 200 Beds)	2732	254 (9.3)	1690 (61.9)	193 (7.1)	416 (15.2)	30 (1.1)	14 (0.5)	26 (1)
Category II (201-499 Beds)	11709	1406 (12)	5763 (49.2)	1367 (11.7)	1723 (14.7)	829 (7.1)	16 (0.1)	86 (0.7)
Category III (>500 Beds)	6088	1348 (22.1)	1460 (24)	818 (13.4)	299 (4.9)	1735 (28.5)	5 (0.1)	77 (1.3)

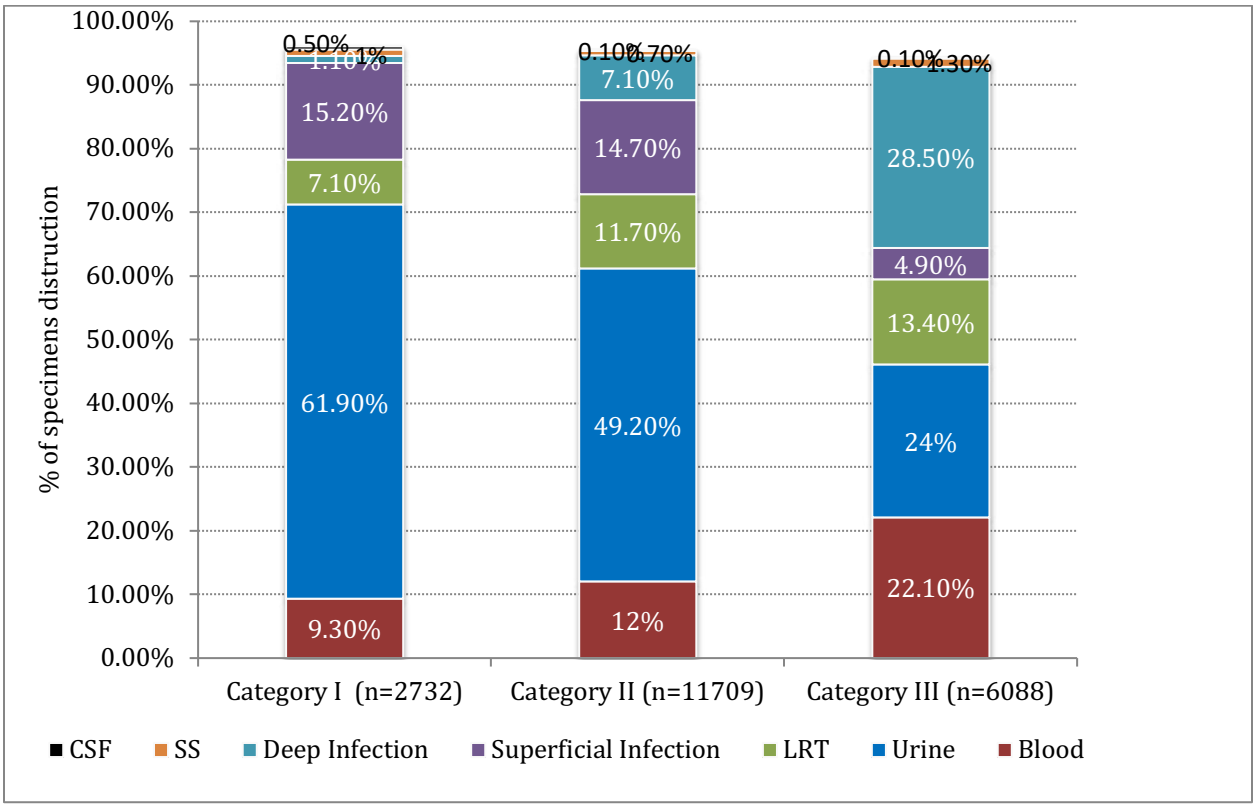


Figure 10.1: Distribution of isolates by site of infection across hospital bed-size categories
LRT: lower respiratory tract; CSF: cerebrospinal fluid; SS: Sterile site

Distribution of pathogen groups

Like tertiary-care hospitals, *Escherichia coli* was the most frequently isolated organism in categories I and II, but its proportion decreased to 22.8% in category III. In contrast, *Staphylococcus aureus* was more common in category III hospitals (20.4%) than in categories I (13.2%) and II (9.9%). *Klebsiella pneumoniae* also showed an increasing trend with hospital size, rising from 9.2% in category I to 14.8% in category II and 15.3% in category III. Similarly, the proportions of *Pseudomonas aeruginosa* (7.2%, 10.2%, and 13.2%) and *Acinetobacter baumannii* (0.8%, 3.0%, and 4.2%) increased across the three categories **(Table 10.2 and Figure 10.2).**

Overall, smaller hospitals mainly see community-type urinary infections dominated by *E. coli* whereas larger hospitals showed a more varied pathogen distribution, with higher proportions of *S. aureus* and non-fermenting Gram-negative bacilli, including *P. aeruginosa* and *A. baumannii*. These findings indicate differences in the distribution of major pathogens across hospital bed-size categories.

In blood cultures, *Escherichia coli* was more frequent in category II hospitals (18.9%) than in category I (16.5%) and category III (9.1%). In contrast, *Staphylococcus aureus* was markedly more common in category III hospitals (29.3%). The proportion of *Klebsiella pneumoniae* was also higher in larger hospitals, increasing from 12.9% in category I to 14.5% in category III, while *Salmonella* Typhi decreased from 14.9% to 3.5% across these categories **(Table 10.3 and Figure 10.3).**

In urine cultures, *E. coli* was the predominant pathogen across all three categories, accounting for 45.9%, 51.3%, and 42.8% of isolates, respectively. *K. pneumoniae* increased from 7.5% in category I to 15.1% in category III, whereas *Pseudomonas aeruginosa* showed a relatively stable distribution (5.0–6.5%). *S. aureus* accounted for a small proportion of urine isolates (4.0–7.1%) in categories II and III (**Table 10.4 and Figure 10.4).**

In lower respiratory tract (LRT) samples, *K. pneumoniae* was the most frequently reported pathogen in all three categories (27.3–30.8%), followed by *P. aeruginosa* (25.5–27.8%). The proportions of *E. coli* and *Acinetobacter baumannii* were higher in category III hospitals (14.0% and 12.0%, respectively) than in category I hospitals (8.8% and 7.7%), indicating differences in the pathogen profile of respiratory infections across hospital sizes (**Table 10.5 and Figure 10.5).** In superficial infection samples, *Staphylococcus aureus* predominated in category I (39.0%) and remained common in categories II (22.2%) and III (23.1%). *P. aeruginosa* showed a higher proportion in category III (32.4%) than in categories I (10.5%) and II (16.6%). The proportion of *E. coli* decreased from 17.0% in category I to 12.7% in category III, while *K. pneumoniae* accounted for 8.6–11.1% of isolates in the three categories (**Table 10.6 and Figure 10.6).**

Overall, the findings highlight specimen-specific differences in pathogen distribution across hospital bed-size categories. Increasing isolation rates of non-fermenters (*Acinetobacter baumannii* and *Pseudomonas aeruginosa*) from smaller to larger hospitals suggest increasing

proportion of hospital acquired infections. Also higher proportion of *E. coli*, both in blood and urine and also *Salmonella Typhi* from blood suggest that smaller hospitals represent community infections. Higher isolation of *Staphylococcus aureus* in larger hospitals may be due to higher numbers of blood culture sent as compared to smaller hospitals. These differences may be reflected of variations in patient case mix, referral patterns, and healthcare exposure across hospital categories and should be interpreted in the context of the available culture-positive isolates.

Table 10.2: Distribution of pathogens across hospital bed-size categories from all specimens

Category	*Escherichia coli*	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Klebsiella spp.*	*Acinetobacter baumannii*
Category I (≤ 200 Beds)	960 (35.14)	251 (9.2%)	197 (7.2%)	360 (13.2%)	424 (15.5%)	22 (0.8%)
Category II (201-499 Beds)	3924 (33.51)	1733 (14.8%)	1195 (10.2%)	1162 (9.9%)	398 (3.4%)	358 (3.0%)
Category III (>500 Beds)	1389 (22.82)	932 (15.3%)	806 (13.2%)	1242 (20.4%)	141 (2.3%)	258 (4.2%)

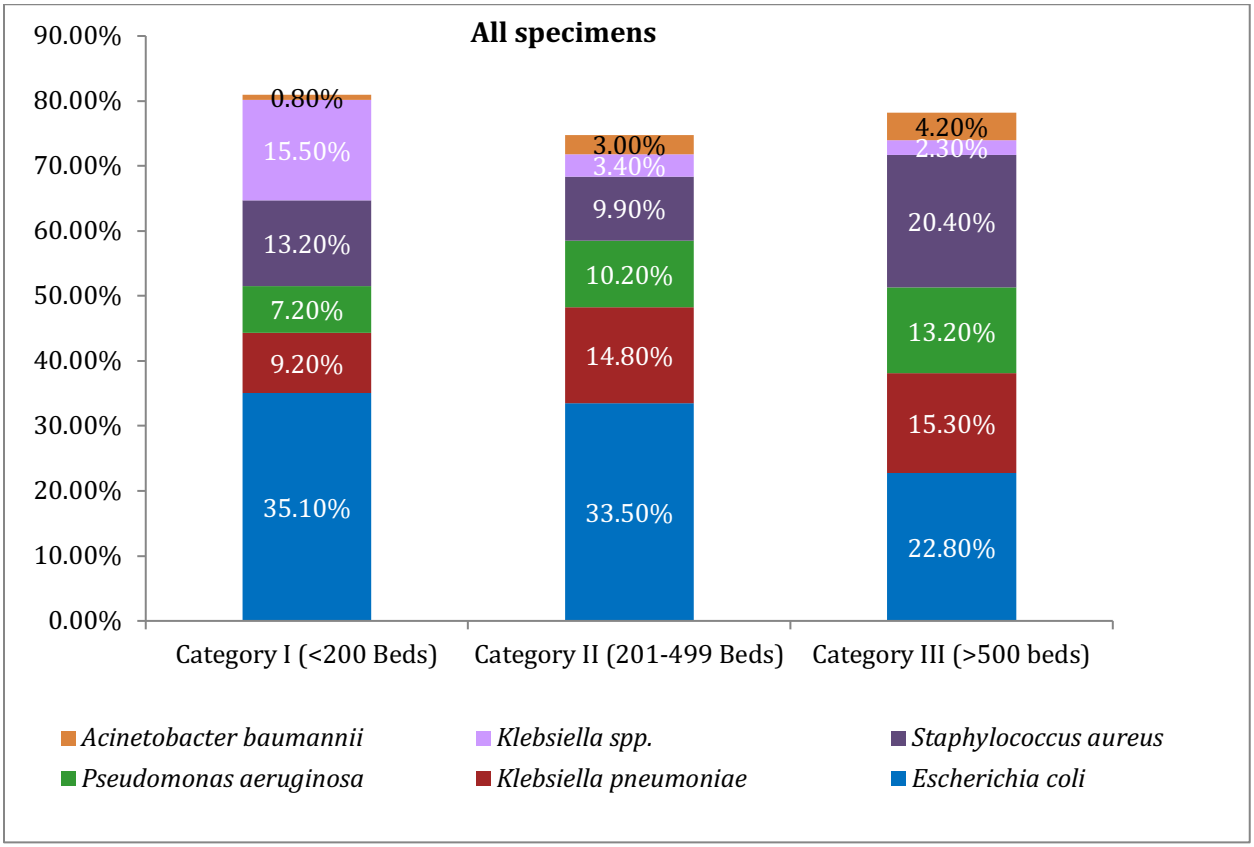


Figure 10.2: Distribution of pathogens across hospital bed-size categories from all specimens

Table 10.3: Distribution of pathogens across hospital bed-size categories from blood

Category	*Total isolates*	*Escherichia coli*	*Klebsiella pneumoniae*	*Staphylococcus aureus*	*Salmonella* Typhi
Category I (≤ 200 Beds)	254	42 (16.5%)	33 (12.9%)	44 (17.3%)	38 (14.9%)
Category II (201-499 Beds)	1406	266 (18.9%)	175 (12.4%)	165 (11.7%)	135 (9.6%)
Category III (>500 Beds)	1348	123 (9.1%)	196 (14.5%)	395 (29.3%)	47 (3.5%)

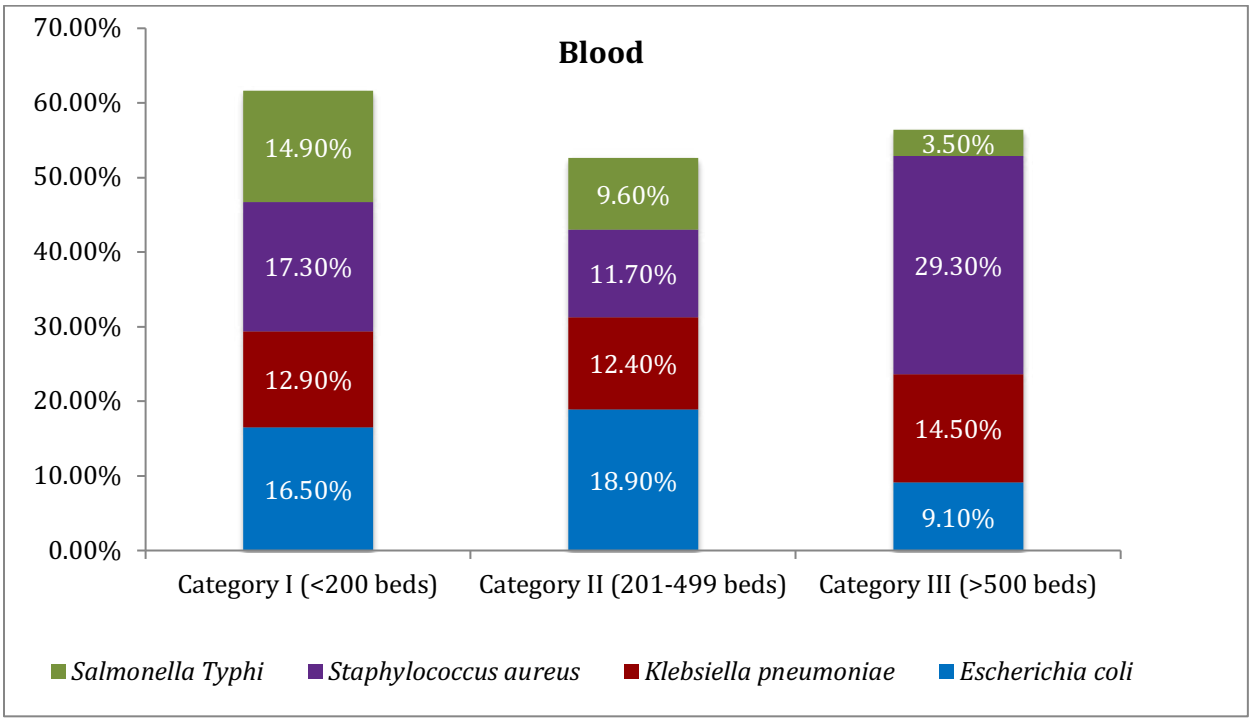


Figure 10.3: Distribution of pathogens across hospital bed-size categories from blood

Table 10.4: Distribution of pathogens across hospital bed-size categories from urine

Category	Total isolates	*Escherichia coli*	*Klebsiella pneumoniae*	*P.aeruginosa*	*Staphylococcus aureus*	Klebsiella spp
Category I (≤ 200 Beds)	1690	777 (45.9%)	127 (7.5%)	109 (6.4%)	85 (5.0%)	344 (20.3%)
Category II (201-499 Beds)	5763	2959 (51.3%)	732 (12.7%)	289 (5.0%)	232 (4.0%)	227 (3.9%)
Category III (>500 Beds)	1460	625 (42.8%)	220 (15.1%)	95 (6.5%)	104 (7.1%)	58 (4.0%)

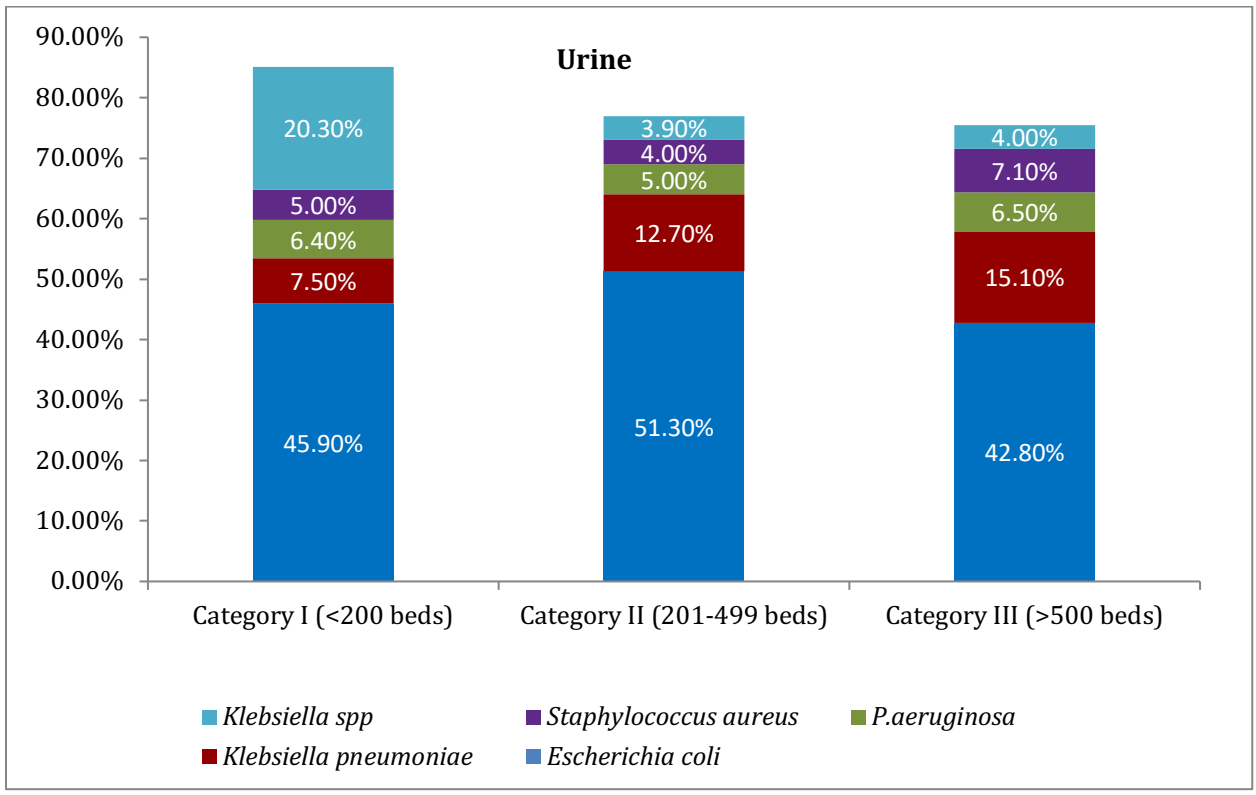


Figure 10.4: Distribution of pathogens across hospital bed-size categories from urine

Table 10.5: Distribution of pathogens across hospital bed-size categories from LRT samples

Category	Total isolates	*Klebsiella pneumoniae*	*P. aeruginosa*	*Escherichia coli*	*A. baumannii*	*S. pneumoniae*
Category I (≤ 200 Beds)	193	43 (22.2%)	32 (16.5%)	14 (7.2%)	6 (3.0%)	26 (13.4%)
Category II (201-499 Beds)	1367	422 (30.8%)	349 (25.5%)	138 (10.1%)	132 (9.6%)	22 (1.6%)
Category III (>500 Beds)	818	224 (27.3%)	213 (26.0%)	114 (14.0%)	98 (12.0%)	7 (0.8%)

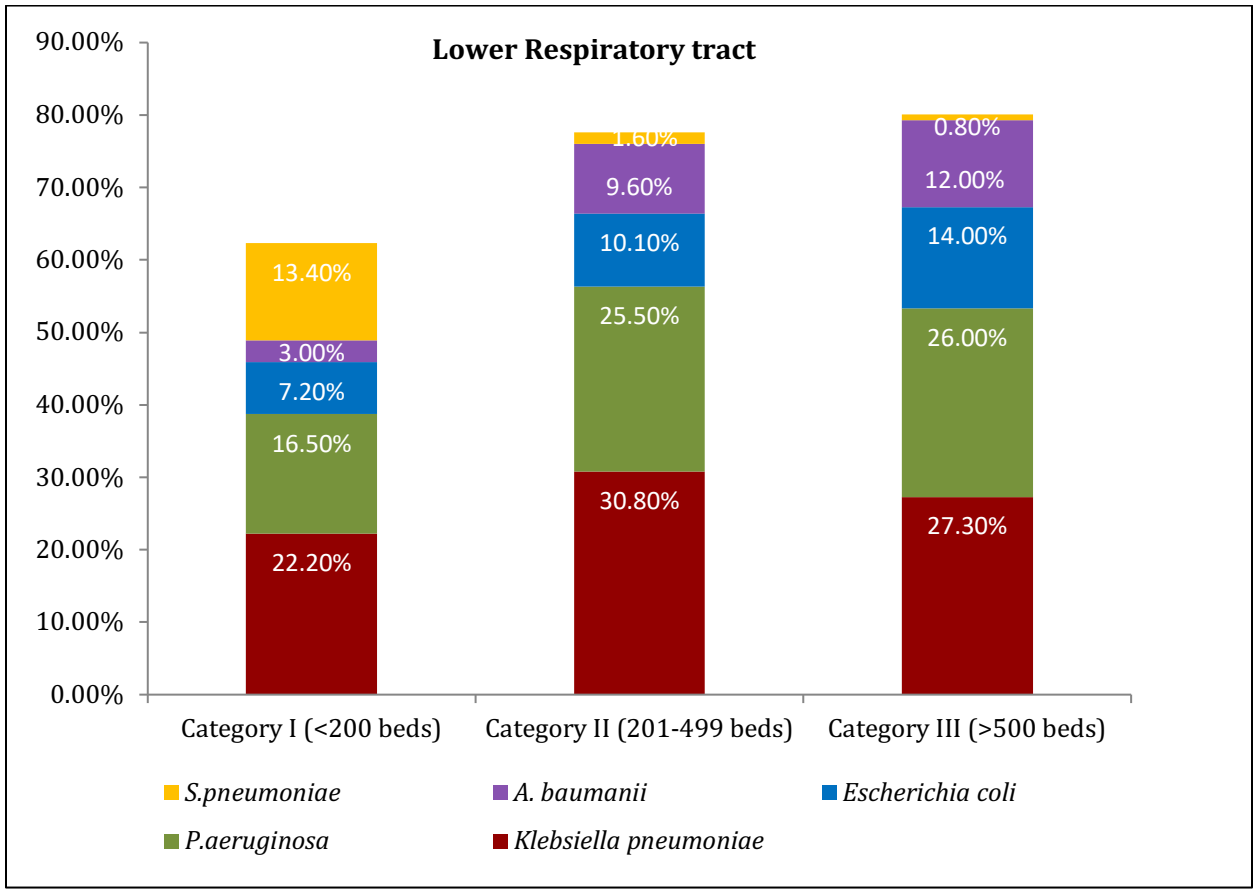


Figure 10.5: Distribution of pathogens across hospital bed-size categories from LRT samples

Table 10.6: Distribution of pathogens across hospital bed-size categories from Superficial Infection samples

Category	Total isolates	*S.aureus*	*Escherichia coli*	*P .aeruginosa*	*Klebsiella pneumoniae*
Category I (≤ 200 Beds)	416	162 (39.0%)	71 (17.0%)	44 (10.5%)	36 (8.6%)
Category II (201-499 Beds)	1723	384 (22.2%)	289 (16.7%)	287 (16.6%)	192 (11.1%)
Category III (>500 Beds)	299	69 (23.1%)	38 (12.7%)	97 (32.4%)	30 (10.0%)

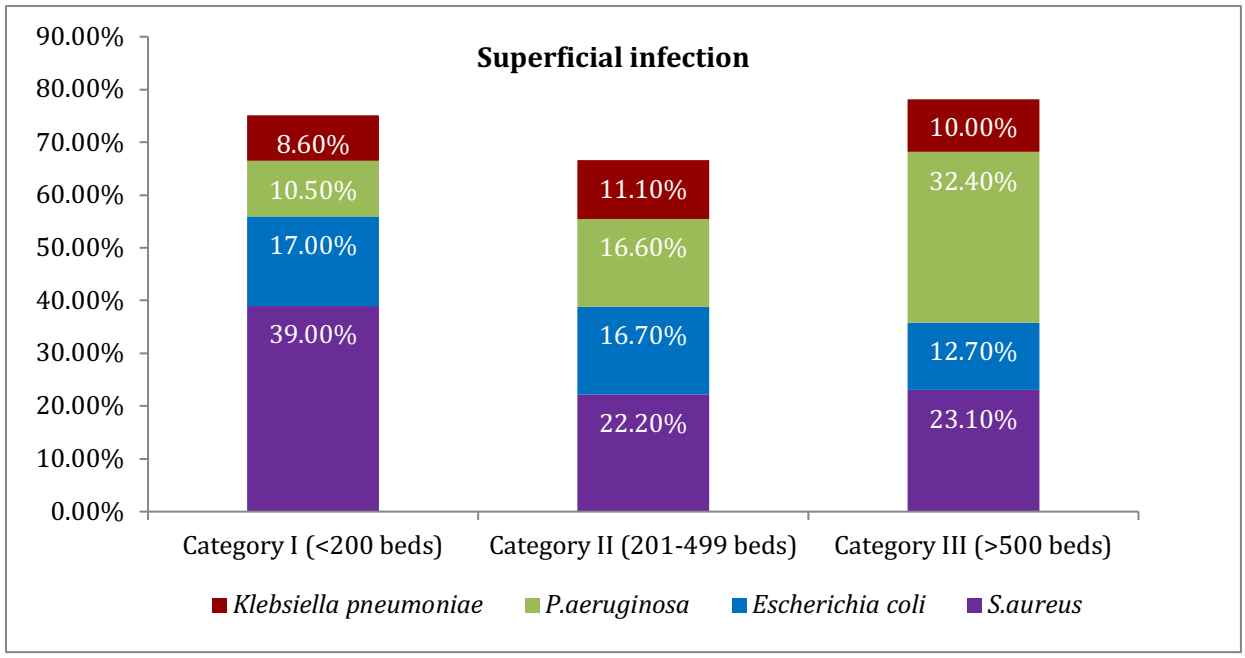


Figure 10.6: Distribution of pathogens across hospital bed-size categories from Superficial Infection samples

Chapter 11. Enterobacterales

Escherichia coli

The susceptibility data show a graded decline in the susceptibility of *E. coli* to several antimicrobial agents across hospital bed- size categories, from small hospitals (Category I, ≤200 beds) to medium-sized hospitals (Category II, 201–499 beds) and large hospitals (Category III, >500 beds).

The most pronounced declines were observed for the third-generation cephalosporins and the fluoroquinolones. Cefotaxime susceptibility declined from 39.8% in Category I to 24.9% in Category II and 4.9% in Category III. Ceftriaxone fell from 39.8% to 28.0% and 11.5%, while ceftazidime fell from 53.8% to 40.7% and 24.1%. Ciprofloxacin susceptibility was low across all categories (21.0%, 16.5% and 6.2% in all categories), whereas levofloxacin showed low susceptibility without a clear gradient among hospital categories (36.7%, 30.0% and 30.5%). These findings raise concerns regarding the cephalosporins and fluoroquinolones suitability for empirical therapy, particularly in larger institutions **(Table 11.1 and Figure 11.1)**.

Of particular concern was the reduced susceptibility to carbapenems and β-lactam/β-lactamase inhibitor combinations, which are important therapeutic options for serious infections. Meropenem susceptibility was 80.3% in Category I and 77.5% in Category II but declined to 67.1% in Category III. Imipenem declined steadily from 84.2% to 72.8% and 60.9% and ertapenem from 76.9% and 74.8% to 54.4% in respective categories. Susceptibility to piperacillin–tazobactam declined from 66.4% to 55.8% and 31.0%, while that to cefoperazone–sulbactam decreased from 74.8% to 66.3% and 44.7%. Amikacin retained comparatively higher activity, with susceptibility rates of 85.4%, 72.1% and 65.0% across the three categories, respectively.

Table 11.1: Susceptibility % of *E. coli* isolates from all samples except urine and feces across hospital bed-size categories

	E. coli		
AMA	**Category I** (≤ 200 beds)	**Category II (201-499 beds)**	**Category III (>500 beds)**
	N=157	N=949	N=763
Amikacin	134 / 157 (85.4)	685 / 950 (72.1)	496 / 763 (65)
Cefotaxime	37 / 93 (39.8)	153 / 614 (24.9)	21 / 429 (4.9)
Ceftazidime	28 / 52 (53.8)	210 / 516 (40.7)	57 / 237 (24.1)
Ceftriaxone	37 / 93 (39.8)	260 / 929 (28)	81 / 704 (11.5)
Cefoperazone-sulbactam	107 / 143 (74.8)	558 / 842 (66.3)	295 / 660 (44.7)
Ertapenem	120 / 156 (76.9)	686 / 917 (74.8)	409 / 752 (54.4)

AMA	*E. coli*		
	Category I (≤ 200 beds)	**Category II (201-499 beds)**	**Category III (>500 beds)**
	N=157	N=949	N=763
Imipenem	101 / 120 (84.2)	655 / 900 (72.8)	426 / 699 (60.9)
Meropenem	126 / 157 (80.3)	735 / 948 (77.5)	512 / 763 (67.1)
Ciprofloxacin	33 / 157 (21)	156 / 948 (16.5)	47 / 760 (6.2)
Levofloxacin	55 / 150 (36.7)	207 / 690 (30)	136 / 446 (30.5)
Piperacillin-tazobactam	101 / 152 (66.4)	504 / 903 (55.8)	235 / 759 (31)

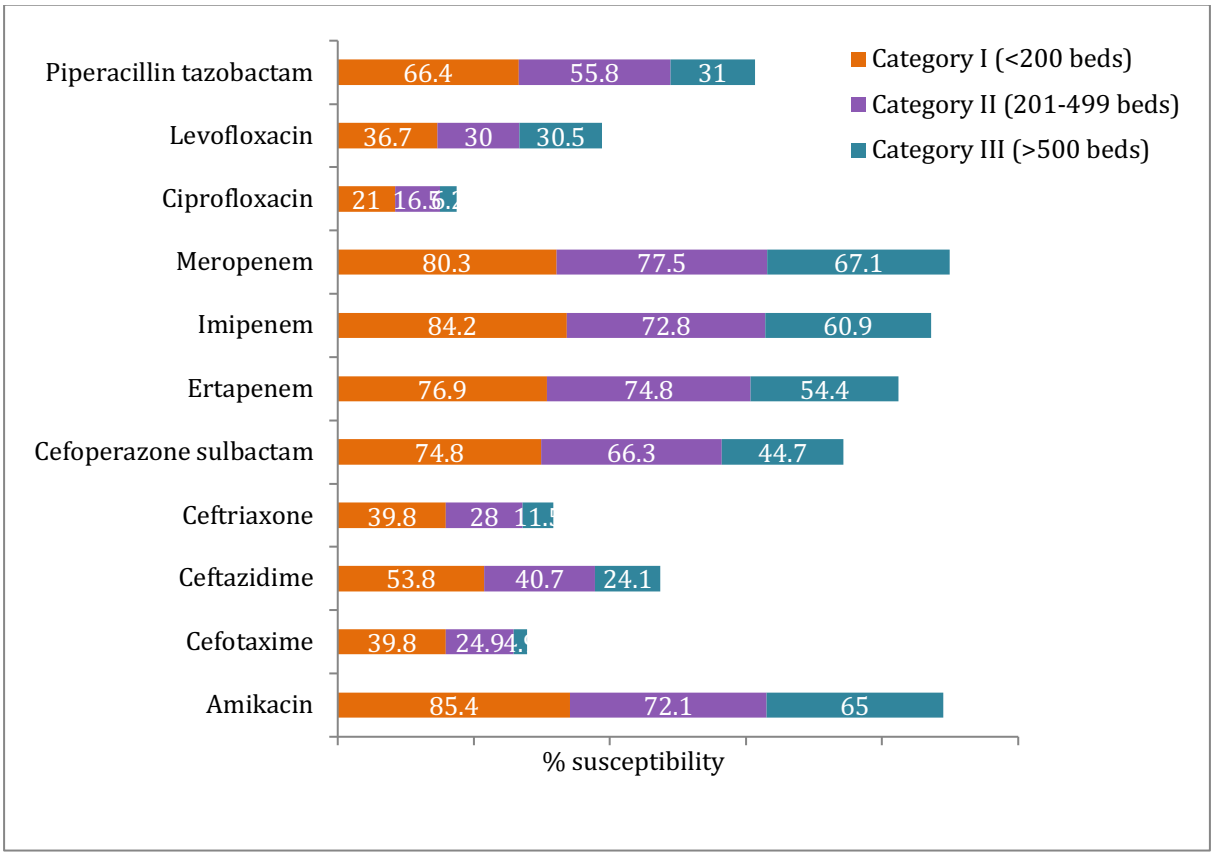


Figure 11.1: Comparison of antimicrobial susceptibility in *E. coli* isolates from all specimen types, excluding faecal and urine samples, across hospital bed-size categories

In conclusion, *E. coli* susceptibility was generally higher in smaller hospitals and lower in larger hospitals, particularly those with ≥500 beds. This variation may reflect differences in patient case complexity, duration of hospitalisation and antimicrobial exposure, although these factors cannot be established from the susceptibility data alone. Amikacin and carbapenems retained comparatively better activity; however, susceptibility varied across individual agents and hospital categories.

Klebseilla pneumoniae

K. pneumoniae exhibited low susceptibility to most antimicrobial agents, with generally lower susceptibility in larger hospitals. Susceptibility to cefotaxime declined from 38.3% in category I to 29.0% in category II and 10.9% in category III. Similarly, ceftriaxone susceptibility decreased from 47.5% to 33.4% and 17.5%, while ceftazidime susceptibility declined from 43.8% to 36.5% and 24.9%, respectively. Ciprofloxacin also showed a marked decline, with susceptibility decreasing from 47.1% in category I to 39.7% in category II and 13.7% in category III.

Of particular concern was the reduced susceptibility to carbapenems, which are important treatment options for serious infections. Meropenem susceptibility was 70.2% in category I, 56.1% in category II and 60.5% in category III, a similar pattern was observed for imipenem. Amikacin showed the highest susceptibility among the agents reported; however, this declined substantially from 73.6% in category I to 49.9% in category II and 47.4% in category III. Susceptibility to piperacillin–tazobactam also decreased across the categories, from 60.3% to 42.8% and 29.1%, while cefoperazone–sulbactam susceptibility declined from 66.9% to 55.1% and 41.9%, respectively **(Table 11.2 and Figure 11.2).**

Table 11.2: Susceptibility % of *Klebsiella pneumoniae* isolates from all samples except urine and feces across hospital bed-size categories

	Klebsiella pneumoniae		
AMA	Category I ≤ 200 beds	Category II 201-499beds	Category III >500 beds
	N=121	N=997	N=712
Amikacin	89 / 121 (73.6)	498 / 997 (49.9)	338 / 713 (47.4)
Cefotaxime	23 / 60 (38.3)	181 / 624 (29)	57 / 522 (10.9)
Ceftazidime	14 / 32 (43.8)	214 / 586 (36.5)	44 / 177 (24.9)
Ceftriaxone	57 / 120 (47.5)	325 / 972 (33.4)	110 / 630 (17.5)
Cefoperazone-sulbactam	79 / 118 (66.9)	158 / 287 (55.1)	251 / 599 (41.9)
Ertapenem	83 / 120 (69.2)	540 / 957 (56.4)	366 / 706 (51.8)
Imipenem	78 / 108 (72.2)	467 / 918 (50.9)	354 / 628 (56.4)

AMA	*Klebsiella pneumoniae*		
	Category I ≤ 200 beds	Category II 201-499beds	Category III >500 beds
	N=121	N=997	N=712
Meropenem	85 / 121 (70.2)	560 / 999 (56.1)	431 / 712 (60.5)
Levofloxacin	61 / 116 (52.6)	264 / 994 (26.6)	160 / 516 (31)
Ciprofloxacin	57 / 121 (47.1)	309 / 778 (39.7)	97 / 710 (13.7)
Piperacillin-tazobactam	73 / 121 (60.3)	410 / 958 (42.8)	206 / 707 (29.1)

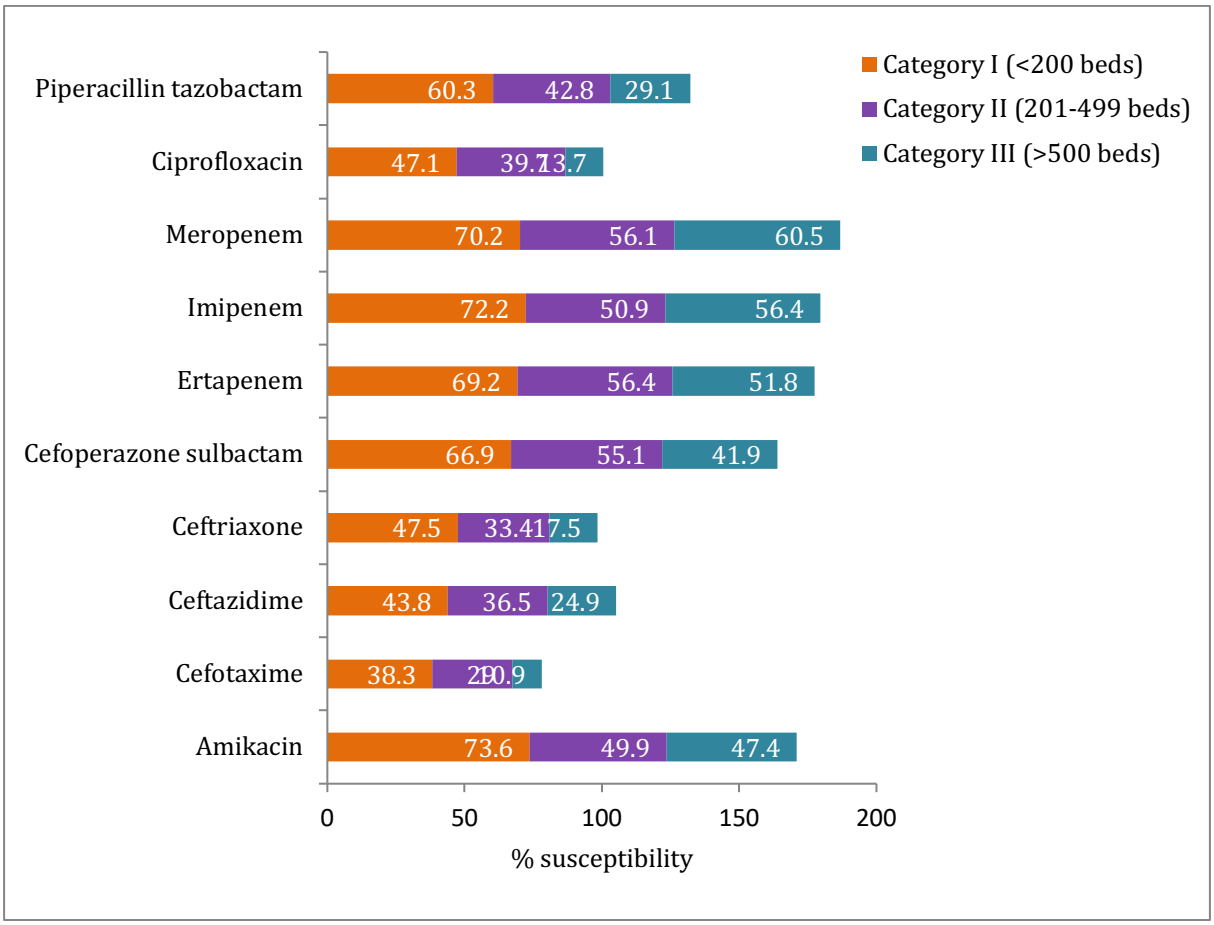


Figure 11.2: Comparison of antimicrobial susceptibility in *K. pneumoniae* isolates from all specimen types, excluding faecal and urine samples, across hospital bed-size categories

Susceptibility of *E. coli* isolates from urine across hospital bed-size categories

Urinary *E. coli* isolates showed a general decline in antimicrobial susceptibility with increasing hospital bed size. Third-generation cephalosporins and fluoroquinolones exhibited low susceptibility, particularly in category III hospitals. Cefotaxime

susceptibility declined from 42.0% in category I to 7.9% in category III, while ciprofloxacin susceptibility decreased from 23.8% to 11.5%. Carbapenems, nitrofurantoin and amikacin retained comparatively higher activity in smaller hospitals, although susceptibility was lower in category III. Nitrofurantoin susceptibility declined from 84.8% to 59.3%, while meropenem susceptibility decreased from 87.5% to 69.9% **(Table 11.3 and Figure 11.3).** Marked declines were also observed for piperacillin–tazobactam and cefoperazone–sulbactam. In conclusion, oral options such as the fluoroquinolones and cotrimoxazole are unreliable for empirical therapy, particularly in larger hospitals. Carbapenems and nitrofurantoin retain the best activity.

Table 11.3: Susceptibility % *E. coli* isolates from urine across hospital bed-size categories

AMA	Category I ≤ 200 beds	Category II 201-499 beds	Category III >500 beds
	N=777	N=2959	N=625
Amikacin	663 / 777 (85.3)	2291 / 2967 (77.2)	262 / 625 (41.9)
Cefazolin (Complicated UTI)	*13/22 (-)	73 / 468 (15.6)	3 / 107 (2.8)
Cefazolin (Uncomplicated UTI)	*5/6 (-)	81 / 160 (50.6)	68 / 175 (38.9)
Cefotaxime	169 / 402 (42)	670 / 2178 (30.8)	45 / 573 (7.9)
Ceftazidime	190 / 355 (53.5)	806 / 1694 (47.6)	74 / 293 (25.3)
Ceftriaxone	317 / 777 (40.8)	983 / 2832 (34.7)	71 / 538 (13.2)
Piperacillin-tazobactam	567 / 777 (73)	1903 / 2968 (64.1)	186 / 599 (31.1)
Cefoperazone-sulbactam	587 / 693 (84.7)	1442 / 1865 (77.3)	108 / 366 (29.5)
Ciprofloxacin	185 / 777 (23.8)	678 / 2970 (22.8)	72 / 625 (11.5)
Levofloxacin	218 / 579 (37.7)	519 / 1422 (36.5)	154 / 561 (27.5)
Ertapenem	676 / 777 (87)	2399 / 2860 (83.9)	338 / 601 (56.2)
Imipenem	461 / 541 (85.2)	1648 / 2153 (76.5)	324 / 564 (57.4)
Meropenem	674 / 770 (87.5)	1973 / 2411 (81.8)	435 / 622 (69.9)
Nitrofurantoin	643 / 758 (84.8)	2350 / 2880 (81.6)	370 / 624 (59.3)
Norfloxacin	303 / 587 (51.6)	1363 / 2806 (48.6)	191 / 600 (31.8)
Trimethoprim-sulfamethoxazole	347 / 692 (50.1)	1373 / 2559 (53.7)	203 / 481 (42.2)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

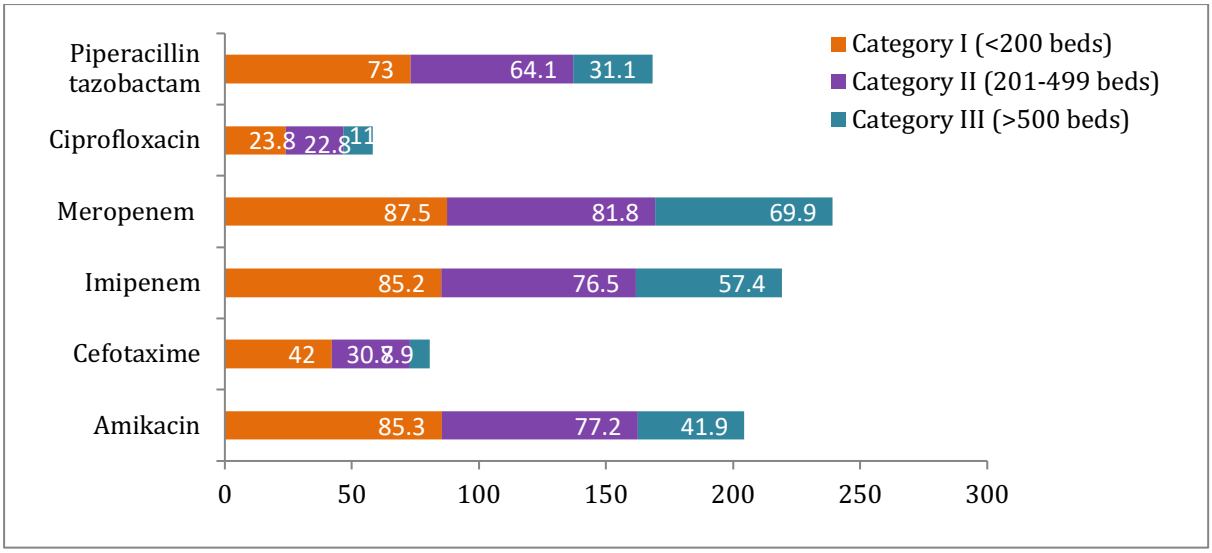


Figure 11.3: Comparison of antimicrobial susceptibility in *E. coli* isolates from all specimen types, excluding faecal and urine samples, across hospital bed-size categories

Susceptibility of *K. pneumoniae* isolates from urine across hospital categories

Urinary *K. pneumoniae* isolates showed generally lower antimicrobial susceptibility with increasing hospital bed size, particularly to cephalosporins and fluoroquinolones. Cefotaxime susceptibility declined from 60.3% in category I to 9.2% in category III, while ceftriaxone and ciprofloxacin susceptibility fell to 13.8% and 10.5%, respectively. Levofloxacin showed no significant difference across hospital categories. Norfloxacin susceptibility was 66.3% in smaller hospitals but declined to 61.9% and 34.4% in other categories **(Table 11.4 and Figure 11.4).**

Among the reserve agents, amikacin declined from 76.6% to 61.7% and 41.8% in respective categories; piperacillin-tazobactam from 64.6% to 36.9% and cefoperazone-sulbactam from 74.8% to 35.4%. Among carbapenems, meropenem declined from 78.7% to 54.2% and 66.1%. Trimethoprim-sulfamethoxazole declined from 69.7% to 56.6% and 51.4%. Nitrofurantoin showed better susceptibility in category III, but lower in tertiary centres (25.2%) **(Table 11.4).**

Table 11.4: Susceptibility % *of K. pneumoniae* isolates from urine across hospital bed-size categories

	Category I ≤ 200 beds	Category II 201-499beds	Category III >500 beds
AMA	N=127	N=732	N=220
Amikacin	98 / 128 (76.6)	455 / 738 (61.7)	92 / 220 (41.8)
Cefazolin (Uncomplicated UTI)	*1/3 (-)	*2/3 (-)	41 / 89 (46.1)
Cefazolin (Complicated UTI)	*0/0 (-)	12 / 91 (13.2)	3 / 61 (4.9)

	Category I ≤ 200 beds	Category II 201-499beds	Category III >500 beds
Cefotaxime	35 / 58 (60.3)	143 / 431 (33.2)	20 / 218 (9.2)
Ceftazidime	14 / 36 (38.9)	195 / 419 (46.5)	16 / 100 (16)
Ceftriaxone	66 / 127 (52)	285 / 726 (39.3)	20 / 145 (13.8)
Piperacillin-tazobactam	82 / 127 (64.6)	343 / 733 (46.8)	69 / 187 (36.9)
Cefoperazone-sulbactam	89 / 119 (74.8)	252 / 510 (49.4)	40 / 113 (35.4)
Ciprofloxacin	61 / 127 (48)	214 / 733 (29.2)	23 / 220 (10.5)
Levofloxacin	56 / 103 (54.4)	194 / 443 (43.8)	92 / 202 (45.5)
Ertapenem	94 / 127 (74)	423 / 714 (59.2)	106 / 219 (48.4)
Imipenem	67 / 98 (68.4)	289 / 594 (48.7)	114 / 208 (54.8)
Meropenem	100 / 127 (78.7)	343 / 633 (54.2)	144 / 218 (66.1)
Nitrofurantoin	50 / 121 (41.3)	281 / 695 (40.4)	113 / 216 (52.3)
Norfloxacin	65 / 98 (66.3)	419 / 677 (61.9)	65 / 189 (34.4)
Trimethoprim-sulfamethoxazole	85 / 122 (69.7)	359 / 634 (56.6)	91 / 177 (51.4)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

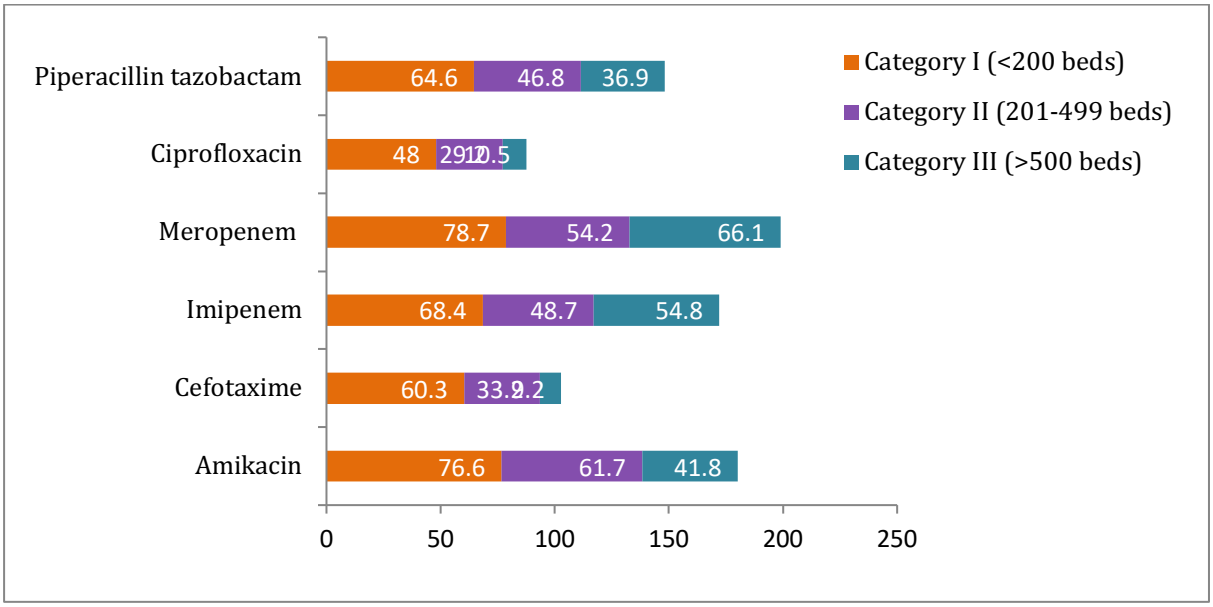


Figure 11.4: Comparison of antimicrobial susceptibility in *K. pneumoniae* isolates from all specimen types, excluding faecal and urine samples, across hospital bed-size categories

Chapter 12. Non-fermenting Gram-negative Bacteria (NFGNB)

A total of 2,893 clinically significant non-fermenting Gram-negative bacterial (NFGNB) isolates, comprising 2,198 *Pseudomonas aeruginosa* and 695 *Acinetobacter baumannii*, recovered from clinical specimens (except faeces), were included in the antimicrobial susceptibility analysis. The susceptibility profiles were assessed across three hospital bed-size categories: Category I (≤ 200 beds), Category II (201-499 beds), and Category III (>500 beds). Antimicrobial susceptibility data were analysed for 10 antibiotics against *P. aeruginosa* and 11 antibiotics against *A. baumannii*, representing baseline antimicrobial classes, including aminoglycosides, cephalosporins, beta-lactam/beta-lactamase inhibitor combinations, fluoroquinolones, and carbapenems. Minocycline and trimethoprim-sulfamethoxazole were additionally evaluated against *A. baumannii*.
The analysis revealed distinct susceptibility patterns between the two organisms, with *A. baumannii* exhibiting substantially lower susceptibility to most antimicrobial agents compared with *P. aeruginosa*. Differences were also observed across hospital bed-size categories, with isolates from larger hospitals generally demonstrating less favourable susceptibility profiles.

Pseudomonas aeruginosa

Of the 2,198 *P. aeruginosa* isolates, 54.3% were reported by category II hospitals, followed by category III (36.7%) and category I (9.0%) hospitals. Carbapenems retained relatively high activity against *P.aeruginosa*, with overall susceptibility rates of 78.4% for meropenem and 75.2% for imipenem. Notably, carbapenem susceptibility remained largely comparable across hospital categories, ranging from 78.2% to 80.2% for meropenem and 75.0% to 76.6% for imipenem. Piperacillin-tazobactam also demonstrated relatively favourable activity, although susceptibility declined progressively from 79.2% in category I to 68.1% in category III hospitals. Among aminoglycosides, amikacin exhibited an overall susceptibility of 76.1%, with lower susceptibility observed in Category III hospitals (68.8%) compared with category I (81.6%) and category II (79.8%) hospitals. Tobramycin susceptibility was 86.3% and 68.0% in categories II and III, respectively. Susceptibility percentages were not calculated for category I hospitals owing to the limited number of isolates tested (n=22)
(Table 12.1 and Figure 12.1).
A similar declining trend was observed among cephalosporins. Overall susceptibility to cefepime, ceftazidime, and cefoperazone-sulbactam was 73.4%, 68.4%, and 67.9%, respectively. For all three agents, the lowest susceptibility was observed in Category III hospitals, with corresponding rates of 67.1%, 61.7%, and 62.6%. Fluoroquinolones demonstrated comparatively lower activity, with overall susceptibility rates of 56.7% for ciprofloxacin and 58.4% for levofloxacin. The decline was particularly pronounced for ciprofloxacin, for which susceptibility decreased from 69.0% in category I to 43.8% in category III hospitals. A similar pattern was observed for levofloxacin, with susceptibility

declining from 70.6% to 49.7% across the corresponding categories. Overall, *P. aeruginosa* isolates from category III hospitals exhibited lower susceptibility to most antimicrobial agents compared with those from category I and category II hospitals. However, carbapenem susceptibility remained relatively stable across all three hospital categories, in contrast to the declining susceptibility observed for fluoroquinolones, cephalosporins, and aminoglycosides **(Table 12.1)**.

Table 12.1: Susceptibility % *of P. aeruginosa* isolated from all specimens (except faeces) across hospital bed-size categories

AMA	Category I ≤ 200 beds	Category II 201-499 beds	Category III >500 beds
	N=197	N=1195	N=806
Amikacin	160 / 196 (81.6)	835 / 1046 (79.8)	465 / 676 (68.8)
Cefepime	106 / 128 (82.8)	764 / 1001 (76.3)	444 / 662 (67.1)
Cefoperazone-sulbactam	130 / 157 (82.8)	486 / 717 (67.8)	275 / 439 (62.6)
Ceftazidime	151 / 197 (76.6)	856 / 1195 (71.6)	497 / 806 (61.7)
Ciprofloxacin	136 / 197 (69)	754 / 1190 (63.4)	351 / 801 (43.8)
Levofloxacin	137 / 194 (70.6)	707 / 1135 (62.3)	387 / 778 (49.7)
Imipenem	151 / 197 (76.6)	897 / 1194 (75.1)	600 / 800 (75)
Meropenem	158 / 197 (80.2)	934 / 1195 (78.2)	630 / 805 (78.3)
Piperacillin-tazobactam	156 / 197 (79.2)	913 / 1194 (76.5)	549 / 806 (68.1)
Tobramycin	*17/22 (-)	472 / 547 (86.3)	270 / 397 (68)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

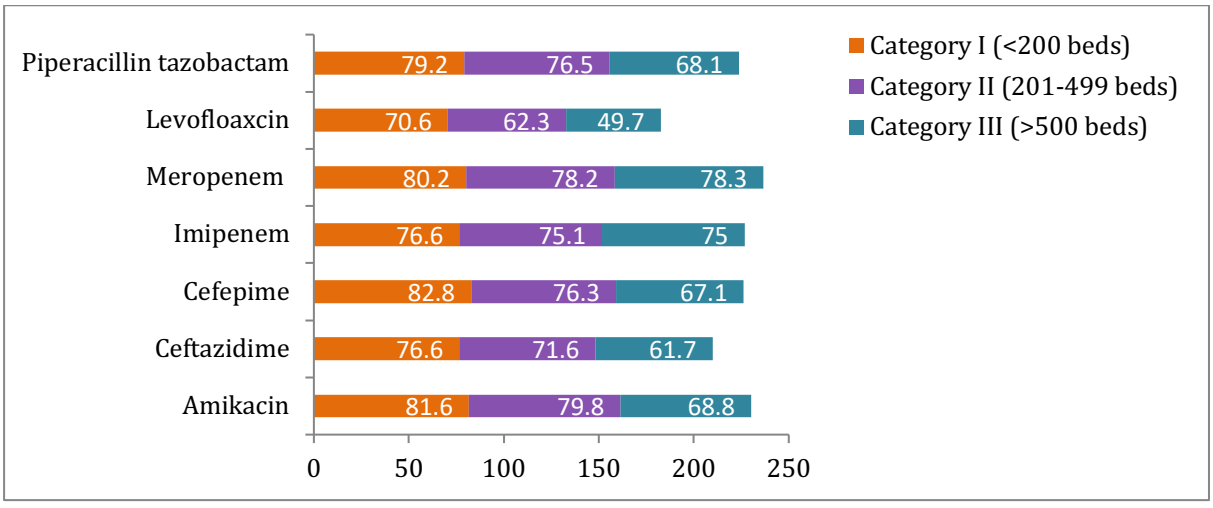


Figure 12.1: Susceptibility % *of P. aeruginosa* isolated from all specimens (except faeces) across hospital bed-size categories

Acinetobacter baumannii

Among the 695 *A. baumannii* isolates included in the analysis, the majority were reported from category II hospitals (59.0%), followed by category III (37.8%) and category I (3.2%) hospitals. Owing to the limited number of isolates from category I hospitals (n=22), susceptibility percentages were not calculated for this category. In contrast to *P. aeruginosa*, *A. baumannii* demonstrated markedly reduced susceptibility across most antimicrobial classes, particularly among isolates recovered from category III hospitals.

Carbapenem susceptibility was substantially lower, with overall rates of 34.5% for meropenem and 31.7% for imipenem. A marked difference was observed between category II and category III hospitals, with meropenem susceptibility declining from 43.4% to 20.5% and imipenem susceptibility from 41.3% to 16.5%, respectively. Among cephalosporins, overall susceptibility to cefepime and ceftazidime was 27.0% and 28.4%, respectively. Susceptibility to both agents was considerably lower in category III hospitals (12.9% and 14.4%, respectively) than in category II hospitals (36.1% and 37.3%, respectively) **(Table 12.2).**

In beta-lactam/beta-lactamase inhibitor combinations, cefoperazone-sulbactam demonstrated an overall susceptibility of 36.5%, with rates of 40.9% in category II and 29.3% in category III hospitals. Piperacillin-tazobactam exhibited an overall susceptibility of 32.7%, declining from 43.9% in category II to 15.2% in category III hospitals. Amikacin and levofloxacin also demonstrated limited activity, with overall susceptibility rates of 27.9% and 30.0%, respectively. For both agents, susceptibility was substantially lower in category III hospitals. Trimethoprim-sulfamethoxazole exhibited an overall susceptibility of 40.5%, with a marked reduction from 52.9% in category II to 20.1% in category III hospitals. Minocycline demonstrated the highest overall susceptibility against *A. baumannii* (56.1%). Nevertheless, considerable variation was observed across hospital categories, with susceptibility declining from 64.2% in category II to 43.5% in category III hospitals.

Table 12.2: Susceptibility % *of A. baumannii* isolated from all specimens (except faeces) across hospital bed-size categories

AMA	Category I ≤ 200 beds	Category II 201-499 beds	Category III >500 beds
	N=22	**N=410**	**N=263**
Amikacin	*16/22 (-)	143 / 410 (34.9)	45 /263 (17.1)
Ampicillin-sulbactam	-	67 / 135 (49.6)	3 /11 (-)
Cefepime	*12/20 (-)	135 / 374 (36.1)	31 /241 (12.9)
Cefoperazone-sulbactam	*16/22 (-)	165 / 403 (40.9)	72 /246 (29.3)
Ceftazidime	*14/22 (-)	153 / 410 (37.3)	38 /263 (14.4)

Imipenem	*16/21 (-)	167 / 404 (41.3)	42 /255 (16.5)
Levofloxacin	*9/17 (-)	134 / 368 (36.4)	42 /219 (19.2)
Meropenem	*16/22 (-)	178 / 410 (43.4)	54 /263 (20.5)
Piperacillin-tazobactam	*13/22 (-)	180 / 410 (43.9)	40 /263 (15.2)
Minocycline	*10/18 (-)	255 / 397 (64.2)	111 /255 (43.5)
Trimethoprim-sulfamethoxazole	*6/9 (-)	157 / 297 (52.9)	36 /179 (20.1)

***** *Fewer than 30 isolates tested; percentage susceptibility not calculated*

Collectively, these findings indicate a substantial burden of antimicrobial resistance among *A. baumannii* isolates, with particularly low susceptibility to carbapenems, cephalosporins, aminoglycosides, and fluoroquinolones in category III hospitals. Although minocycline retained comparatively higher activity, fewer than half of the isolates from category III hospitals were susceptible, highlighting the limited antimicrobial options against this pathogen **(Table 12.2).**

Summary

The surveillance findings demonstrate substantial differences in antimicrobial susceptibility between the two major non-fermenting Gram-negative pathogens. *P. aeruginosa* retained relatively higher susceptibility to carbapenems and selected beta-lactam agents, whereas *A. baumannii* exhibited consistently lower susceptibility across most antimicrobial classes.

A notable finding was the lower susceptibility observed among isolates recovered from category III hospitals (>500 beds), particularly for *A. baumannii*. While carbapenem susceptibility in *P. aeruginosa* remained relatively consistent across hospital categories, a marked reduction was observed in *A. baumannii*, with susceptibility to both imipenem and meropenem falling to approximately 16% to 21% in category III hospitals.

These findings underscore the importance of continued antimicrobial resistance surveillance, particularly in larger healthcare facilities, and reinforce the need for institution-specific antibiograms, susceptibility-guided antimicrobial therapy, and strengthened antimicrobial stewardship programmes.

Chapter 13. Staphylococci and Enterococci

The susceptibility profiles of *S. aureus* were assessed across three hospital bed-size categories: Category I (≤ 200 beds), Category II (201-499 beds), and Category III (>500 beds). Antimicrobial susceptibility data were analysed for 11 antibiotics against *S. aureus.* The MRSA rates based on cefoxitin susceptibility differed significantly across the different categories of secondary hospitals. It ranged from 46.4% in category I hospitals increasing to 54.1% in the 2nd category and raising sharply to 86% among the secondary hospitals with over 500 beds. While susceptibility to antibiotics like erythromycin, tetracycline, clindamycin and ciprofloxacin remained almost similar between category I and II hospitals, category III hospitals showed marked decrease in susceptibility to these antibiotics. There was a paradoxical increase in susceptibility to co-trimoxazole among the category II hospitals compared to category I **(Table 13.1).**

Antibiotics like vancomycin, tigecycline and teicoplanin showed 100% susceptibility across all the categories. A finding of concern is the number of linezolid resistant isolates encountered in all the categories although the rates were slightly more in category III hospitals.

The data showed that only tetracycline showed good susceptibility **(Table 13.2 and 13.3)**. Erythromycin and ciprofloxacin demonstrated very low susceptibility among the MRSA isolates when compared to MSSA isolates in category I and II hospitals.

Table 13.1: Susceptibility % of *S. aureus* from all specimens except urine and faeces across hospital bed-size categories

AMA	Category I (≤ 200 beds)	Category II (201-499 beds)	Category III (>500 beds)
	N=253	N=894	N=1080
Cefoxitin	98/183 (53.6)	353/769 (45.9)	116/827 (14)
Oxacillin	101/213 (47.4)	165/348 (47.4)	125/710 (17.6)
Vancomycin	244/244 (100)	816/816 (100)	1053/1053 (100)
Teicoplanin	206/206 (100)	387/387 (100)	710/710 (100)
Erythromycin	89/233 (38.2)	306/871 (35.1)	173/1061 (16.3)
Tetracycline	199/231 (86.1)	678/776 (87.4)	590/972 (60.7)
Ciprofloxacin	77/252 (30.6)	260/878 (29.6)	208/1059 (19.6)
Clindamycin	196/251 (78.1)	679/871 (78)	765/1070 (71.4)
Linezolid	248/253 (98.0)	875/894 (97.9)	1039/1079 (96.3)
Tigecycline	160/160 (100)	267/267 (100)	22/22 (100)
Trimethoprim-sulfamethoxazole	158/245 (64.5)	659/858 (76.8)	595/1061 (56.1)

Table 13.2: Susceptibility % of MSSA from all specimens except urine and faeces across hospital bed-size categories

MSSA			
AMA	Category I **(≤ 200 beds)**	Category II (201-499 beds)	Category III (>500 beds)
	N=125	**N=401**	**N=222**
Cefoxitin	98/98 (100)	353/353 (100)	116/116 (100)
Oxacillin	101/101 (100)	165/165 (100)	125/125 (100)
Vancomycin	120/120 (100)	328/328 (100)	199/199 (100)
Teicoplanin	100/100 (100)	193/193 (100)	125/125 (100)
Erythromycin	64/120 (53.3)	185/396 (46.7)	80/218 (36.7)
Tetracycline	116/121 (95.9)	314/341 (92.1)	184/210 (87.6)
Ciprofloxacin	56/125 (44.8)	178/394 (45.2)	41/216 (19)
Clindamycin	111/125 (88.8)	319/389 (82)	180/221 (81.4)
Linezolid	122/125 (97.6)	390/401 (97.3)	212/222 (95.5)
Tigecycline	83/83 (100)	125/125 (100)	6/6 (-)
Trimethoprim-sulfamethoxazole	93/120 (77.5)	321/385 (83.4)	134/216 (62)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

Table 13.3: Susceptibility % of MRSA from all specimens except urine and faeces across hospital bed-size categories

MRSA			
AMA	Category I **(≤ 200 beds)**	Category II (201-499 beds)	Category III (>500 beds)
	N=128	**N=493**	**N=858**
Cefoxitin	0/85 (0)	0/416 (0)	0/711 (0)
Oxacillin	0/112 (0)	0/183 (0)	0/585 (0)
Vancomycin	124/124 (100)	488/488 (100)	854/854 (100)
Teicoplanin	106/106 (100)	194/194 (100)	585/585 (100)
Erythromycin	25/113 (22.1)	121/475 (25.5)	93/843 (11)
Tetracycline	93/110 (84.5)	364/435 (83.7)	406/762 (53.3)
Tigecycline	77/77 (100)	142/142 (100)	16/16 (-)
Ciprofloxacin	21/127 (16.5)	82/484 (16.9)	167/843 (19.8)

MRSA			
AMA	Category I **(≤ 200 beds)**	Category II (201-499 beds)	Category III (>500 beds)
	N=128	**N=493**	**N=858**
Clindamycin	85/126 (67.5)	360/482 (74.7)	335/849 (39.5)
Trimethoprim-sulfamethoxazole	65/125 (52)	338/473 (71.5)	461/845 (54.6)
Linezolid	116/128 (90.6)	428/493 (86.8)	826/857 (96.4)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

Table 13.4 shows the susceptibility pattern of Staphylococci other than *S. aureus* (SOSA) as per the category of the hospital. Compared to *S. aureus,* susceptibility of SOSA to almost all the antibiotics were significantly lower with isolates from category III hospitals showing the least susceptibility. Cefoxitin resistance is extremely high ranging from 76% in category I to 93.3% in category III. Susceptibility to linezolid was similar across all the categories of hospitals.

Table 13.4: Susceptibility % of SOSA from all specimens except urine and faeces across hospital bed-size categories

SOSA			
AMA	Category I **(≤ 200 beds)**	Category II (201-499 beds)	Category III (>500 beds)
	N=65	**N=325**	**N=226**
Cefoxitin	5/21 (-)	31/156 (19.9)	14/209 (6.7)
Oxacillin	12/45 (26.7)	48/209 (23)	42/126 (33.3)
Vancomycin	65/65 (100)	314/314 (100)	224/224 (100)
Teicoplanin	44/44 (100)	194/194 (100)	123/123 (100)
Erythromycin	19/53 (35.8)	72/322 (22.4)	16/221 (7.2)
Tetracycline	38/50 (76)	229/305 (75.1)	70/172 (40.7)
Ciprofloxacin	31/63 (49.2)	127/321 (39.6)	45/216 (20.8)
Clindamycin	39/65 (60)	159/316 (50.3)	51/220 (23.2)
Trimethoprim-sulfamethoxazole	33/48 (68.8)	207/319 (64.9)	109/189 (57.7)
Linezolid	63/65 (96.9)	313/324 (96.6)	216/226 (95.6)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

Enterococci

Vancomycin resistance among *Enterococcus faecalis* was almost similar at around 5% among category I and II while no VRE was encountered in category III hospitals. Occasional resistance to linezolid was observed in *Enterococcus faecalis,* with slightly higher rates among category III when compared to category I and II **(Table 13.5).**

Table 13.5: Susceptibility % of *Enterococcus faecalis* from all specimens across hospital bed-size categories

Enterococcus faecalis			
AMA	Category I **(≤ 200 beds)**	Category II (201-499 beds)	Category III (>500 beds)
	N=43	**N=354**	**N=51**
Ampicillin	*21/22 (-)	273 / 311 (87.8)	*13/25 (-)
Vancomycin	41 / 43 (95.3)	336 / 354 (94.9)	51 / 51 (100)
Teicoplanin	41 / 43 (95.3)	300 / 316 (94.9)	44 / 49 (89.8)
Gentamicin_HL	20 / 32 (62.5)	118 / 195 (60.5)	*20/25 (-)
Ciprofloxacin	16 / 36 (44.4)	44 / 200 (22)	*3/23 (-)
Nitrofurantoin	25 / 30 (83.3)	198 / 222 (89.2)	*18/23 (-)
Fosfomycin	*3/3 (-)	22 / 51 (43.1)	*13/18 (-)
Linezolid	42 / 43 (97.6)	344 / 354 (97.1)	48 / 51 (94.1)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

Vancomycin resistance was higher among *Enterococcus faecium* both from category II (26.8%) and category III (24.3%) hospitals. Lower resistance rates to linezolid was observed among *Enterococcus faecium* compared to *Enterococcus faecalis* with isolates from both category II and III hospitals exhibiting close to 3% resistance **(Table 13.6).**

Table 13.6: Susceptibility % of *Enterococcus faecium* from all specimens across hospital bed-size categories

Enterococcus faecium			
AMA	Category I **(≤ 200 beds)**	Category II (201-499 beds)	Category III (>500 beds)
	N=15	**N=250**	**N=70**
Ampicillin	*3/8 (-)	51 / 196 (26)	*10/27 (-)
Vancomycin	*13/15 (-)	186 / 250 (74.4)	53 / 70 (75.7)
Teicoplanin	*14/15 (-)	188 / 246 (76.4)	44 / 65 (67.7)
Gentamicin_HL	*8/12 (-)	84 / 167 (50.3)	*7/20 (-)
Ciprofloxacin	*2/12 (-)	14 / 144 (9.7)	*4/21 (-)
Nitrofurantoin	*1/8 (-)	46 / 138 (33.3)	*18/22 (-)
Linezolid	*15/15 (-)	242 / 249 (97.1)	66 / 68 (97.1)

** Fewer than 30 isolates tested; percentage susceptibility not calculated*

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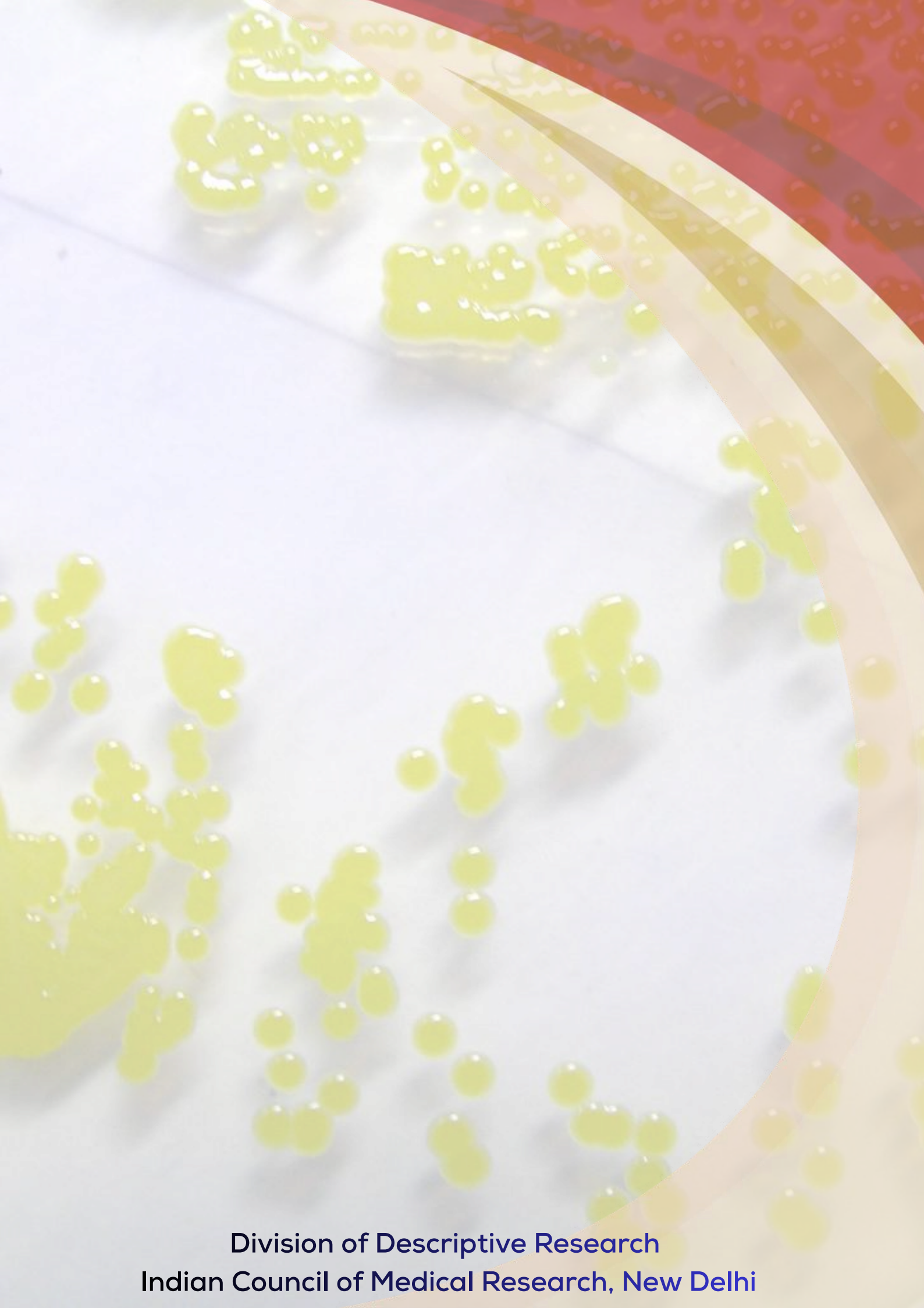
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