Annual Report

Antimicrobial Resistance Research and Surveillance Network

January 2024 - December 2024

Division of Descriptive Research

Indian Council of Medical Research, New Delhi

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Annual Report, 2024
ICMR - Antimicrobial Resistance Research & Surveillance Network (AMRSN)
8th edition

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List of acronyms

AFLP	Amplified fragment length polymorphism
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
CAUTI	Catheter-associated urinary tract infections
CLABSI	Central line-associated 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
HAI	Hospital-acquired infections
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
MIC	Minimum inhibitory concentration
MRSA	Methicillin-resistant *Staphylococcus aureus*
MSSA	Methicillin-sensitive *Staphylococcus aureus*
NFGNB	Non-fermenting Gram-negative bacteria
OPD	Outpatient department
R	Resistant
RC	Regional centres
S%	Susceptibility% (Sensitive/Tested)
SDD	Susceptible-dose dependent
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 Network

The Indian Council of Medical Research (ICMR) has been supporting the Antimicrobial Resistance Research & Surveillance Network (AMRSN) since 2013. This is the eighth detailed report from the ICMR AMR surveillance network. The network systematically collects, analyses, and reports data on antimicrobial resistance (AMR) among six key pathogenic groups across India. The network labs undertake susceptibility testing as per the ICMR Standard Operating Practices for Bacteriology and Mycology. This report provides valuable insights into national trends and resistance patterns, as well as the underlying mechanisms of resistance identified through genomic and whole-genome sequencing (WGS) analyses. Since the network collects data from tertiary care hospitals, the data presented in this report is not reflective of the community levels of AMR in the country and should not be extrapolated to community settings.

Highlights of surveillance data 2024:

- This report presents data from January 1st, 2024 to December 31st, 2024. The total number of culture-positive isolates studied during the year 2024 was **99,027**.
- Gram-negative bacteria (GNB) remained the most commonly isolated pathogens from most clinically relevant samples, like blood, urine, CSF, and respiratory tract samples, except for pus/exudate samples.
- *Escherichia coli* was the most commonly isolated pathogen, followed by *Klebsiella pneumoniae*, *Pseudomonas aeruginosa, Acinetobacter baumannii,* and *Staphylococcus aureus*.
- Within healthcare-associated bloodstream infections (BSI), Gram-negative bacteria accounted for 72.1% of all BSI cases, 10.2% were due to fungal pathogens, and 17.7% were from Gram-positive pathogens.
- *Acinetobacter baumannii*, *Klebsiella pneumoniae,* and *Pseudomonas aeruginosa* constituted nearly 80% of causative pathogens for Ventilator-associated Pneumonia (VAP), calling for caution around the empirical use of vancomycin, teicoplanin, and linezolid in most clinical situations.

Enterobacterales

Highlights of AMR trends

- *Escherichia coli* and *Klebsiella pneumoniae* were the most commonly isolated pathogens.
- *E. coli* isolates showed an increase in susceptibility to ceftazidime, from 19.2% in 2023 to 27.5% in 2024. Susceptibility to amikacin, which had declined from 79.2% in 2017 to 68.2% in 2023, showed an increase to 72.5% in 2024. In contrast, a significant decline in susceptibility was observed for carbapenems — from 81.4% in 2017 to 62.7% in 2023 and a further decrease to 57.6% in 2024 for imipenem, and from 73.2% in 2017 to 66% in 2023 and to 62.9% in 2024 for meropenem.
- *K. pneumoniae* showed reduced susceptibility, notably with piperacillin-tazobactam (falling from 42.6% in 2017 to 26% in 2024) and carbapenems (imipenem from 58.5% in 2017 to 31.2% in 2024, and meropenem from 48.1% in 2017 to 35.1% in 2024).
- *K. pneumoniae* also showed an increase in susceptibility to various antibiotics since 2023; cefotaxime, from 17.3% in 2023 to 20.3% in 2024; ceftazidime, from 18.1% in 2023 to 23.7% in 2024; amikacin from 34.5% in 2023 to 39.9% in 2024; ciprofloxacin from 17.1% in 2023 to 20.4% in 2024, and levofloxacin from 17.4% in 2023 to 24.8% in 2024.
- Unlike the previous year, the TEM gene was the predominant gene present in 29.58% of the *E. coli* isolates, followed by IMP in 27.97%, VIM in 19.29%, and NDM-1 in 14.47% of the isolates. The genes encoding for AmpC β-lactamases were the least prevalent.
- In *K. pneumoniae* isolates, the TEM gene was the predominant gene present in 33.66% of the isolates, followed by OXA-48 in 25.57%, and SHV in 22.98% of the isolates. The genes encoding for AmpC β-lactamases were the least prevalent.

Clinical relevance

- Among Enterobacterales, *E. coli* is the predominant pathogen isolated from the urine samples. Fairly good susceptibility was observed for nitrofurantoin and fosfomycin, and therefore, nitrofurantoin or single-dose fosfomycin remains the drug of choice for treating cystitis.
- Ertapenem or amikacin to 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* is ever-increasing. Identification of the carbapenemase (by molecular or immunochromatography tests) is of great

importance as a decent percentage of these isolates are only OXA-48 producers, which can be treated with newer BL-BLI (ceftazidime-avibactam) alone.

- 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

Highlights of AMR trends

- It is important to notice that there was a gradual increase in carbapenem-resistant *P. aeruginosa* from 26% in 2017 to 43% in 2024 (for imipenem) and from 31.3% in 2017 to 38% in 2024 (for meropenem). Fluoroquinolones such as ciprofloxacin showed a susceptibility rate of 57.8% in 2017, which declined to 47.4% in 2022 and then increased to 57% in 2024, indicating an overall similar susceptibility level over the past seven years.
- The molecular profile of carbapenem resistance in *P. aeruginosa* was predominantly driven by MβL genes, particularly NDM and VIM.
- In *A. baumannii*, there is no significant change in the susceptibility trends to the tested antibiotics compared to last year. Resistance to meropenem in *A. baumannii* was recorded as 91.0% in the year 2024, limiting the availability of treatment options.
- Similar to previous years, blaOXA-23 was the only predominant carbapenemase in *A. baumannii* across all the centres, with a rapidly expanding integration of blaNDM, often in co-carriage, which significantly amplifies their resistance potential.

Clinical relevance

- In *P. aeruginosa*, for MβL-producing strains, a combination of aztreonam with ceftazidime/avibactam or aztreonam-avibactam (if synergy has been demonstrated or the isolate is susceptible to aztreonam-avibactam) provides an effective strategy, particularly for co-producers.
- Cefiderocol may be considered if *in vitro* susceptibility is confirmed. Colistin or polymyxin B, preferably in combination with fosfomycin, should be reserved as salvage therapy.
- Susceptibility of *A. baumannii* to minocycline was close to 70% making it the most effective antibiotic after colistin.
- In *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.

- Cefiderocol (if available and susceptible *in vitro*) can be used against both OXA- and NDM-producing *A. baumannii*, while sulbactam/durlobactam (not yet available in India) may provide excellent activity against OXA-type carbapenemases but is ineffective against NDM-producing isolates.

Gram-positive cocci

Highlights of AMR trends

- Methicillin-resistant *Staphylococcus aureus (*MRSA) rates steadily increased over the 8 years of surveillance from 33% in 2017 to nearly 53% in 2024. The anti-MRSA antibiotics such as vancomycin and teicoplanin showed excellent in vitro activity (nearly 100% against MRSA isolates). Linezolid resistance was encountered very rarely; however, being an important anti-TB drug, its use is not encouraged for *Staphylococcus aureus* infections.
- Often dismissed as colonizers, Coagulase-negative *Staphylococcus* (CoNS) - particularly *S. haemolyticus* - are being increasingly recognized as opportunistic pathogens. Importantly, these isolates frequently exhibit multidrug resistance.
- In 2023, *E. faecalis* was the most common species, followed by *E. faecium*. However, this trend reversed in 2024, with *E. faecium* becoming the predominant species.
- Overall, in 2024, vancomycin resistance in enterococci was 22%, slightly higher than in 2023 (17.5%). Notably, the vancomycin resistance rate in *E. faecium* was 10 times higher than in *E. faecalis* (34.2% vs. 3.4%).
- The identification of *Enterococcus* spp. beyond *faecalis* and *faecium* is clinically important, as some of these species are intrinsically resistant to glycopeptides.

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.
- Levonadifloxacin remains very effective against MRSA, as no resistance has been identified on isolates tested till date. It is effective both in acute bacterial skin and skin structure infections, as well as bacteremia and diabetic foot infections.
- 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 option.

Enteric fever pathogens

Highlights of AMR trends

- *Salmonella* Typhi isolates showed very good susceptibility to ceftriaxone (98%), cefixime (97.9%), trimethoprim-sulfamethoxazole (97.7%) and azithromycin (99.5%), and very low susceptibility to fluoroquinolones (>95% resistance). These findings emphasize the limited effectiveness of fluoroquinolones in treating infections caused by this pathogen.

Clinical relevance

- Trimethoprim-sulfamethoxazole (TMP-SMX) and azithromycin remain very good oral options for the treatment of patients with enteric fever, whereas IV ceftriaxone may be used for patients admitted with Enteric fever.
- Use of carbapenems for treating routine enteric fever cases is not recommended.

Diarrheal pathogens

Highlights of AMR trends

- Only 1% of the total isolates were from stool samples, indicating poor representation of the true picture of bacterial diarrhea. Other causes of diarrhea, like viruses, *Entamoeba* and parasites, were not studied for this report.
- The predominant species from these samples was *Salmonella* spp. faecal (20.26%), followed by *Aeromonas* spp. (18.05%), diarrheagenic *Escherichia coli* (17.31%), *Shigella sonnei* (8.93%), and *Vibrio cholerae* (8.38%).

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 diarrhea 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 136 invasive and 148 non-invasive *S. pneumoniae* isolates were included in the analysis for the year 2024.
- Pneumosil (PCV10Sii) percentage serotype coverage is 50% among children less than 5 years of age.
- Among the non-vaccine serotypes, serotypes 3 and 18C constitute 14.7% among the children and 13.4% among the age group >5 years of age.
- Penicillin and cefotaxime demonstrated 100% susceptibility in non-meningeal isolates, whereas only 2 out of 8 cerebrospinal fluid (CSF) isolates were penicillin susceptible, and 7 out of 8 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,* in which resistance was observed in up to 10% of isolates.
- All *Aspergillus flavus* and *A. fumigatus* isolates were susceptible to voriconazole, and amphotericin B resistance was observed in nearly 1/3rd of the *Aspergillus* isolates.

Clinical relevance

- Echinocandins and fluconazole continue to be the most effective treatment options for *Candida* infections. Given their antifungal susceptibility profiles, echinocandins are particularly suitable for treating *C. auris* infections.

- The declining susceptibility of *C. tropicalis* isolates to anidulafungin suggests that the remaining two echinocandins, along with azoles, may be more appropriate for treating infections caused by *C. tropicalis*.
- For *Aspergillus* infections, voriconazole remains the drug of choice. Use of amphotericin B for treating *Aspergillus* should be avoided unless susceptibility to the same has been demonstrated *in vitro*.

Chapter 1. Summary of surveillance data

The total number of culture-positive isolates studied during the year 2024 was **99027.** Of these, **19027** were from blood, **26562** from urine, **16327** from lower respiratory tract (LRT), **13973** from superficial infections (SI)**, 11858** from deep infections (DI), **1994** from sterile sites (SS), **693** from cerebrospinal fluid (CSF), **1086** from faeces, and **7507** from other sites. Majority of the isolates were from Enterobacterales except *Salmonella* and *Shigella* (51.3%) followed by non-fermenting Gram-negative bacteria (NFGNB) (23.0%), staphylococci (13.2%), enterococci (6.8%), fungi (2.7%), typhoidal *Salmonella* (1.4%), diarrheal bacterial pathogens (0.9%), and streptococci (0.5%) (**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 (76.3%), SS (55.2%), DI (49.6%), SI) (47.6%, CSF (37.1%), LRT (36.7%), blood (35.7%), and other sites (50.2%). Non-fermenting Gram-negative bacteria (NFGNB) group were the predominant isolates in the LRT (55.3%), CSF (42.7%), SI (22.9%), DI (22.8%), SS (21.5%), blood (18.6%), urine (6.9%), and other sites (23.6%). *Staphylococci* constituted 26.1% of blood infections, followed by SI (22.3%), DI (21.0%), and CSF (11.6%). Enterococci group constituted 13.0% isolates from urine, followed by sterile body fluid (10.6%), DI (5.5%), SI (5.2%), blood (4.9%), and CSF (3.0%). The typhoidal *Salmonella* group constituted 6.6% of the isolates from blood. Yeast isolates were a significant group in the blood infections (7.5%) **(Table 1.1** and **Figure 1.1).**

The distribution of the top 10 isolates from different specimens is presented in **Table 1.2** and **Figure 1.2**. *Escherichia coli* was most commonly isolated (26.2%), followed by *Klebsiella pneumoniae* (17.5%), *Pseudomonas aeruginosa* (11.5%), *Acinetobacter baumannii* (10.5%), and *Staphylococcus aureus* (8.6%). Among these isolates, *E. coli* was most commonly isolated from the urine (50.7%), *K. pneumoniae* (24.2%), *A. baumannii* (29.4%), and *P. aeruginosa* from LRT (23.7%), *S. aureus* from DI (20.6%), *Enterococcus faecalis* (7.0%), and *Enterococcus faecium* (5.2%) from urine.

The relative distribution of the various species isolated from patients in the out-patient department (OPD), wards and intensive care units (ICUs) is presented in **Table 1.3** and **Figure 1.3**. The top 5 isolates in descending order in OPD specimens were *E. coli,* followed by *K. pneumoniae, S. aureus, P. aeruginosa,* and both *A. baumannii* and *E. faecalis*; in wards, *E. coli, K. pneumoniae, P. aeruginosa, A. baumannii,* and *S. aureus*; and in intensive care units (ICUs), *A. baumannii*, *K. pneumoniae, E. coli, P. aeruginosa,* and *S. aureus. E. faecium* isolates were common from the ICUs (3.6%), followed by the ward and OPD; whereas, *E. faecalis* was a common isolate from the OPDs (4.1%), followed by the wards and the ICUs.

Table 1.1: Specimen-wise distribution of major groups of organisms

Isolate	Culture positive																			
	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086		Others N=7507	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Enterobacterales except *Salmonella* and *Shigella*	50787 (51.29)	100	6789 (35.68)	13.4	20257 (76.26)	39.9	5985 (36.66)	11.8	6647 (47.57)	13.1	5882 (49.6)	11.6	257 (37.09)	0.5	1101 (55.22)	2.2	103 (9.48)	0.2	3766 (50.17)	7.4
NFGNB	22831 (23.06)	100	3531 (18.56)	15.5	1855 (6.98)	8.1	9031 (55.31)	39.6	3212 (22.99)	14.1	2699 (22.76)	11.8	296 (42.71)	1.3	429 (21.51)	1.9	3 (0.28)	0	1775 (23.64)	7.8
Staphylococci	13089 (13.22)	100	4964 (26.09)	37.9	389 (1.46)	3	917 (5.62)	7	3113 (22.28)	23.8	2491 (21.01)	19	80 (11.54)	0.6	166 (8.32)	1.3	0 (0)	0	969 (12.91)	7.4
Enterococci	6718 (6.78)	100	927 (4.87)	13.8	3438 (12.94)	51.2	68 (0.42)	1	732 (5.24)	10.9	655 (5.52)	9.7	21 (3.03)	0.3	212 (10.63)	3.2	3 (0.28)	0	662 (8.82)	9.9
Fungi	2729 (2.76)	100	1419 (7.46)	52	534 (2.01)	19.6	219 (1.34)	8	80 (0.57)	2.9	74 (0.62)	2.7	34 (4.91)	1.2	79 (3.96)	2.9	3 (0.28)	0.1	287 (3.82)	10.5
Diarrheal bacterial pathogens	944 (0.95)	100	22 (0.12)	2.3	12 (0.05)	1.3	5 (0.03)	0.5	10 (0.07)	1.1	5 (0.04)	0.5	1 (0.14)	0.1	3 (0.15)	0.3	878 (80.85)	93	8 (0.11)	0.8
Typhoidal *Salmonella*	1395 (1.41)	100	1257 (6.61)	90.1	18 (0.07)	1.3	3 (0.02)	0.2	5 (0.04)	0.4	10 (0.08)	0.7	1 (0.14)	0.1	1 (0.05)	0.1	96 (8.84)	6.9	4 (0.05)	0.3
Streptococci	534 (0.54)	100	118 (0.62)	22.1	59 (0.22)	11	99 (0.61)	18.5	174 (1.25)	32.6	42 (0.35)	7.9	3 (0.43)	0.6	3 (0.15)	0.6	0 (0)	0	36 (0.48)	6.7

Note:

1. Blood includes: Blood from venepuncture, blood from central catheter, and blood from a peripheral catheter.
2. LRT (Lower Respiratory Tract) includes: Bronchoalveolar lavage (BAL), sputum, lung aspirate, endotracheal aspirate (ETA) and lobectomy tissue (lung tissue).
3. SI (Superficial infection) includes: SST (skin & soft tissue), pus/exudate, wound swab, superficial biopsy and superficial tissue.
4. DI (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.

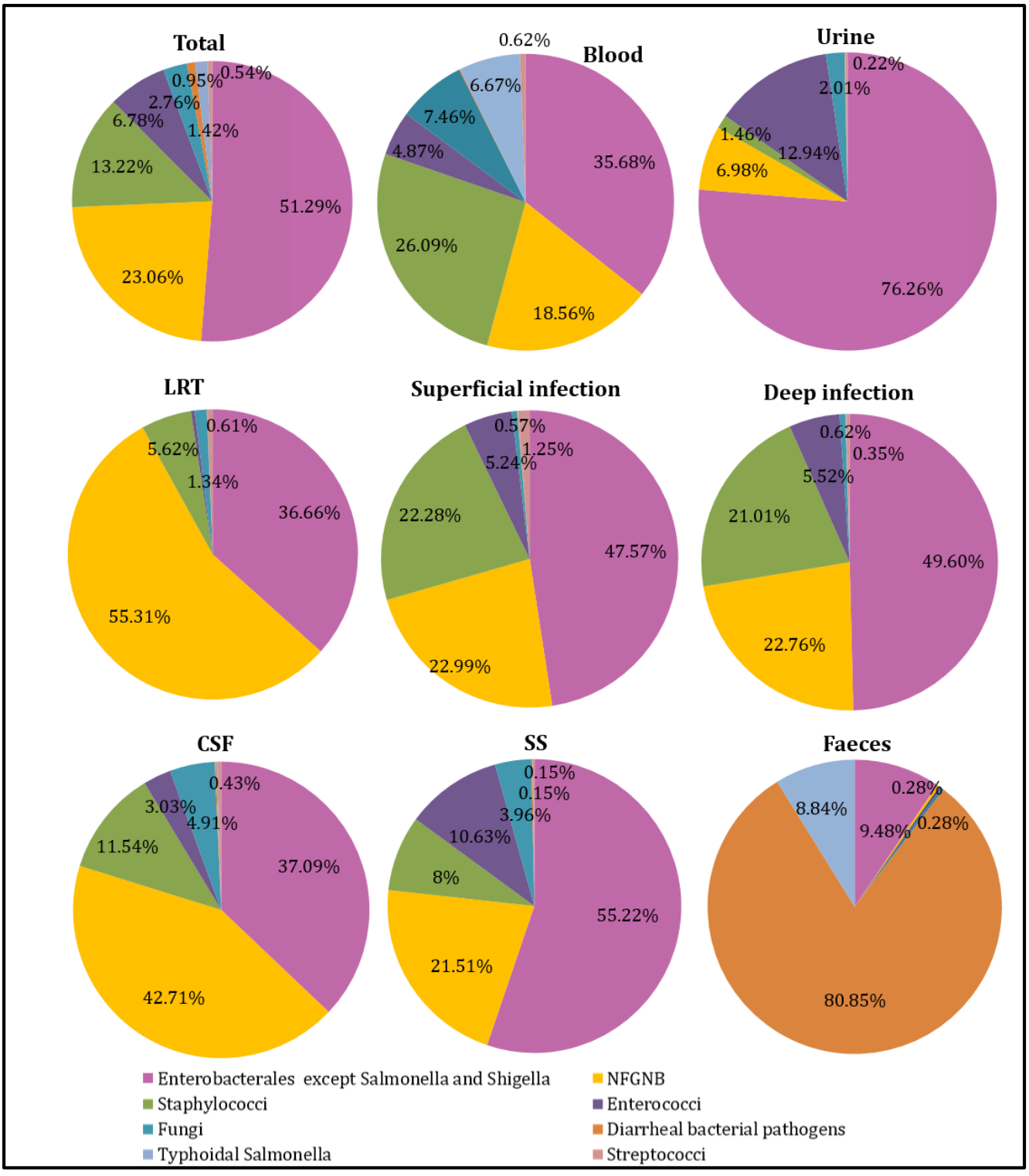


Figure 1.1: Specimen-wise distribution of major groups of organisms

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

Organism	All Specimens n(%)	Blood n(%)	LRT n(%)	SI n(%)	DI n(%)	SS n(%)	Faeces n(%)	Urine n(%)
Escherichia coli	26001 / 99027 (26.2)	3236 / 19027 (17.01)	1143 / 16327 (7.0)	2889 / 13973 (20.68)	2714 / 11858 (22.89)	570/ 1994 (28.59)	80/ 1086 (7.37)	13476 / 26562 (50.73)
Klebsiella pneumoniae	17413 / 99027 (17.5)	2779 / 19027 (14.61)	3952/ 16327 (24.2)	2221 / 13973 (15.89)	1685 / 11858 (14.2)	402 / 1994 (20.16)	21/ 1086 (1.93)	4875 / 26562 (18.35)
Pseudomonas aeruginosa	11419 / 99027 (11.5)	1026 / 19027 (5.4)	3858/ 16327 (23.7)	2032 / 13973 (14.5)	1678 / 11858 (14.2)	218/ 1994 (10.9)	1 / 1086 (0.1)	1534 / 26562 (5.8)
Acinetobacter baumannii	10351 / 99027 (10.5)	2142 / 19027 (11.26)	4804 / 16327 (29.4)	1112/ 13973 (8.0)	940 / 11858 (7.9)	168 / 1994 (8.4)	1 /1086 (0.1)	289 / 26562 (1.1)
Staphylococcus aureus	8515 / 99027 (8.6)	1067 / 19027 (5.61)	891/ 16327 (5.5)	2850 / 13973 (20.4)	2438 /11858 (20.6)	136 /1994 (6.8)	0 / 1086 (0)	289 / 26562 (1.1)
Enterococcus faecalis	3042 / 99027 (3.07)	276 / 19027 (1.5)	31 / 16327 (0.2)	378/ 13973 (2.7)	188/ 11858 (1.6)	57/ 1994 (2.9)	0 / 1086 (0)	1862 / 26562 (7.0)
Enterococcus faecium	3002 / 99027 (3.03)	603 / 19027 (3.17)	22 / 16327 (0.1)	233 / 13973 (1.7)	293/ 11858 (2.5)	131/ 1994 (6.6)	3 / 1086 (0.3)	1372 / 26562 (5.2)
Proteus mirabilis	1800 / 99027 (1.82)	62 / 19027 (0.33)	150 / 16327 (0.9)	492 / 13973 (3.52)	519/ 11858 (4.38)	18/ 1994 (0.9)	0 / 1086 (0)	383/ 26562 (1.44)
Enterobacter cloacae	1625 / 99027 (1.64)	321 / 19027 (1.7)	156 / 16327 (0.96)	301/ 13973 (2.2)	364/ 11858 (3.07)	39/ 1994 (1.96)	1/ 1086 (0.09)	318/ 26562 (1.2)
Staphylococcus haemolyticus	1572 / 99027 (1.59)	1380/ 19027 (7.3)	7 / 16327 (0)	104 /13973 (0.7)	11 / 11858 (0.1)	11 / 1994 (0.16)	0 / 1086 (0)	13/ 26562 (0)

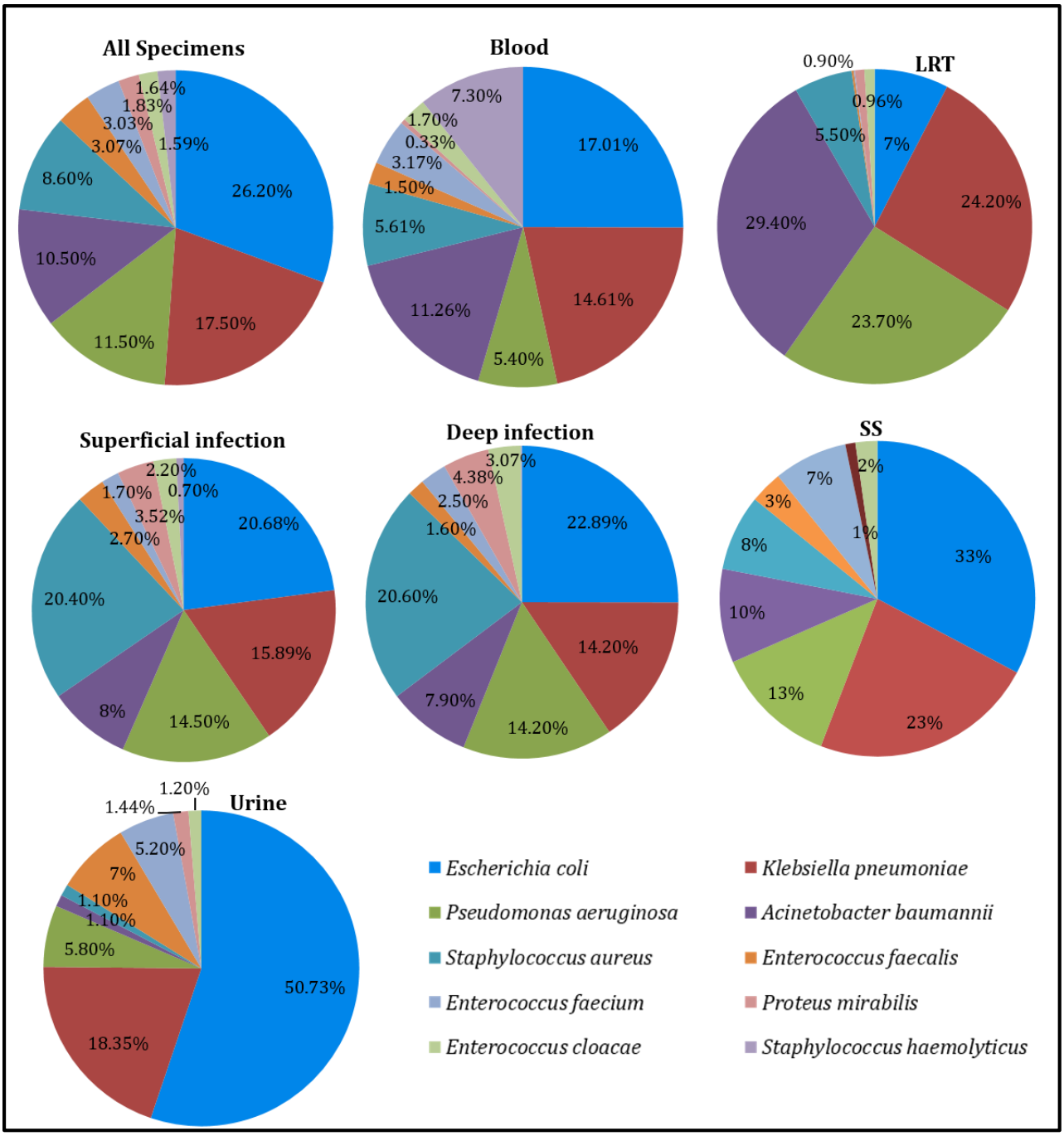


Figure 1.2: Isolation distribution of the top 10 isolates from different specimens

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

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Escherichia coli	26001 / 99027 (26.26)	11125 / 32729 (33.99)	12509 / 48648 (25.71)	2367 / 17650 (13.41)
Klebsiella pneumoniae	17413 / 99027 (17.58)	4763 / 32729 (14.55)	8789 / 48648 (18.07)	3861 / 17650 (21.88)
Pseudomonas aeruginosa	11419 / 99027 (11.53)	3781 / 32729 (11.55)	5673 / 48648 (11.66)	1965 / 17650 (11.13)
Acinetobacter baumannii	10351 / 99027 (10.45)	1341 / 32729 (4.1)	4901 / 48648 (10.07)	4109 / 17650 (23.28)
Staphylococcus aureus	8515 / 99027 (8.6)	3779 / 32729 (11.55)	3942 / 48648 (8.1)	794 / 17650 (4.5)
Enterococcus faecalis	3042 / 99027 (3.07)	1345 / 32729 (4.11)	1394 / 48648 (2.87)	303 / 17650 (1.72)
Enterococcus faecium	3002 / 99027 (3.03)	570 / 32729 (1.74)	1793 / 48648 (3.69)	639 / 17650 (3.62)
Proteus mirabilis	1800 / 99027 (1.82)	773 / 32729 (2.36)	825 / 48648 (1.7)	202 / 17650 (1.14)
Enterobacter cloacae	1625 / 99027 (1.64)	521 / 32729 (1.59)	855 / 48648 (1.76)	249 / 17650 (1.41)
Staphylococcus haemolyticus	1572 / 99027 (1.59)	372 / 32729 (1.14)	752 / 48648 (1.55)	448 / 17650 (2.54)

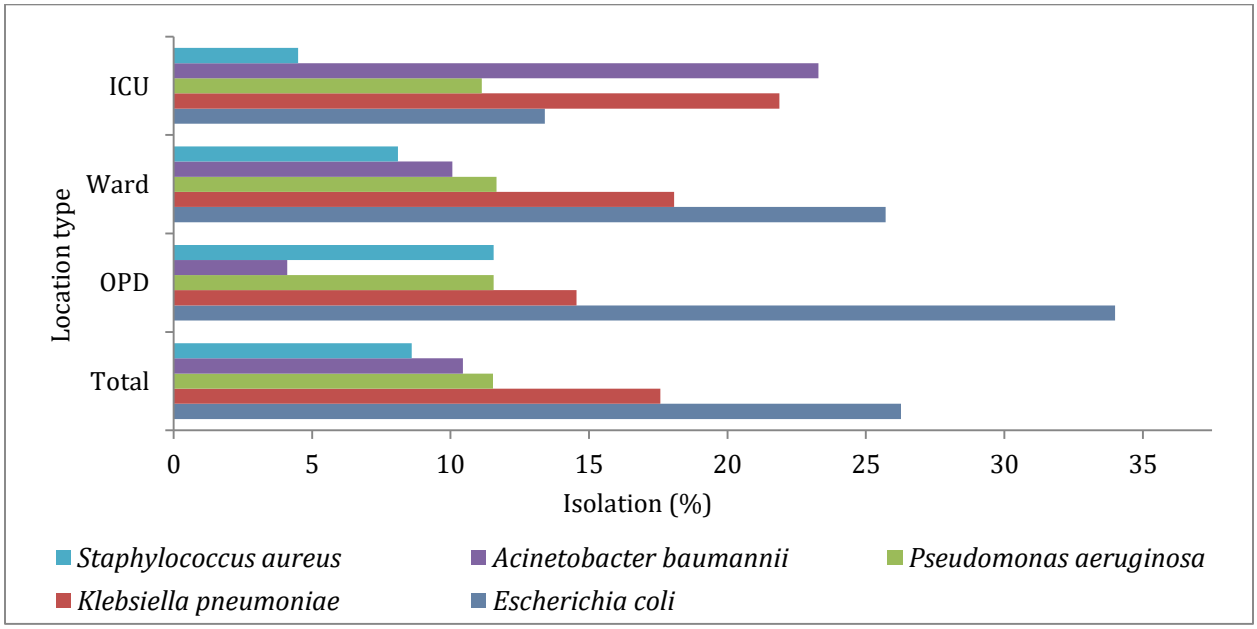


Figure 1.3: Distribution of the top 5 isolates from all specimens across OPD, ward and ICU

Yearly isolation rates of the top ten isolates from all samples showed a steady increase of *E. coli* from 22.8% in 2017 to 26.2% in 2024 and *K. pneumoniae* from 14.8% in 2017 to 17.7% in 2024 **(Table 1.4** and **Figure 1.4)** without much change in the isolation rates of the other species. There was also a decline in the isolation rates of *S. aureus* from 12.5% in 2017 to 8.6% in 2024.

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

Rank	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(%)
1	*Escherichia coli*	10441 / 45714 (22.84)	19459 / 75182 (25.88)	30953 / 110268 (28.07)	16921 / 68081 (24.85)	23764 / 96836 (24.54)	26804 / 109554 (24.47)	23691 / 102361 (23.14)	25994 / 99027 (26.2)
2	*Klebsiella pneumoniae*	6743 / 45714 (14.75)	11136 / 75182 (14.81)	18729 / 110268 (16.98)	12173 / 68081 (17.88)	17359 / 96836 (17.93)	19002 / 109554 (17.34)	16664 / 102361 (16.28)	17413 / 99027 (17.5)
3	*Pseudomonas aeruginosa*	5695 / 45714 (12.46)	8921 / 75182 (11.87)	12650 / 110268 (11.47)	8013 / 68081 (11.77)	11706 / 96836 (12.09)	13388 / 109554 (12.22)	12017 / 102361 (11.74)	11419/ 99027 (11.5)
4	*Acinetobacter baumannii*	3524 / 45714 (7.71)	5446 / 75182 (7.24)	8839 / 110268 (8.02)	7301 / 68081 (10.72)	12484 / 96836 (12.89)	12176 / 109554 (11.11)	12099 / 102361 (11.82)	10351 / 99027 (10.5)
5	*Staphylococcus aureus*	5723 / 45714 (12.52)	8874 / 75182 (11.8)	12625 / 110268 (11.45)	6562 / 68081 (9.64)	8920 / 96836 (9.21)	9477 / 109554 (8.65)	9037 / 102361 (8.83)	8515 / 99027 (8.6)
6	*Enterococcus faecalis*	1040 / 45714 (2.28)	2022 / 75182 (2.69)	2916 / 110268 (2.64)	2177 / 68081 (3.2)	2405 / 96836 (2.48)	3265 / 109554 (2.98)	3523 / 102361 (3.44)	3002 / 99027 (3.07)
7	*Enterococcus faecium*	937 / 45714 (2.05)	1479 / 75182 (1.97)	2741 / 110268 (2.49)	2038 / 68081 (2.99)	2486 / 96836 (2.57)	3047 / 109554 (2.78)	2792 / 102361 (2.73)	3002 / 99027 (3.03)
8	*Proteus mirabilis*	887 / 45714 (1.94)	1289 / 75182 (1.71)	1969 / 110268 (1.79)	1272 / 68081 (1.87)	1646 / 96836 (1.7)	1799 / 109554 (1.64)	1579 / 102361 (1.54)	1800 / 99027 (1.82)
9	*Enterobacter cloacae*	620 / 45714 (1.36)	1098 / 75182 (1.46)	1514 / 110268 (1.37)	1080 / 68081 (1.59)	1654 / 96836 (1.71)	1780 / 109554 (1.62)	1752 / 102361 (1.71)	1625 / 99027 (1.64)
10	*Staphylococcus haemolyticus*	634 / 45714 (1.39)	871 / 75182 (1.16)	827 / 110268 (0.75)	626 / 68081 (0.92)	846 / 96836 (0.87)	2391 / 109554 (2.18)	2274 / 102361 (2.22)	1572 / 99027 (1.5)

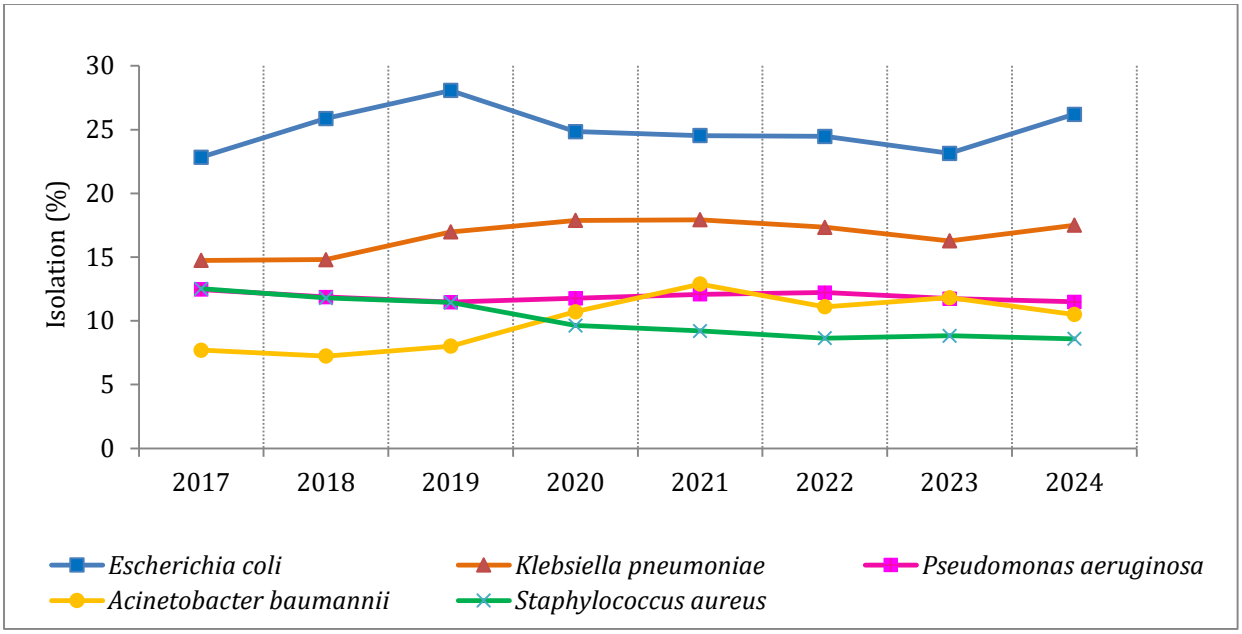


Figure 1.4: Yearly isolation trends of the top 5 isolates from all samples

Enterobacterales

Of the overall isolates, Enterobacterales (except *Salmonella* and *Shigella*) constituted a major group (51.3%) **(Table 1.1)**. Out of a total of 99,027 culture-positive isolates, specimen percentage-wise distribution of major species within the family Enterobacterales is shown in **Table 1.5** and **Figure 1.5.** Overall, *E. coli* was the commonest species (26.2%) followed by *K. pneumoniae* (17.5%), *P. mirabilis* (1.8%) and *E. cloacae* (1.6%) **(Table 1.5)**. *E. coli* was predominantly isolated from urine (50.7%), SS (28.6%), DI (22.9%), SI (20.7%), blood (17.0%), CSF (9.1%), and other sites (24.4%). *K. pneumoniae* was the most frequently isolated in the LRT (24.2%), CSF (22.4%), sterile sites (SS) (20.2%), urine (18.4%), SI (15.9%), blood (14.6%), DI (14.2%), and other sites (17.6%). *P. mirabilis* was common in DI (4.4%), SI (3.5%), and infections of the other sites (2.2%). *E. cloacae* constituted 3.1% of DI, 2.2% of SI, 2.02% of CSF, and 1.96% of SS infections. Isolates from the regional centre 1 (RC1) had a higher percentage isolation rate of *E. coli* and *K. pneumoniae*. RC2 had a higher percentage isolation rate of *P. mirabilis,* and RC11 had a higher percentage of *E. cloacae* than the rest of the RCs **(Table 1.6).**

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

Isolate	Culture positive																			
	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086		Others N=7502	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Escherichia coli	26001 (26.2)	100	3236 (17.01)	12.4	13476 (50.73)	51.8	1143 (7)	4.4	2889 (20.68)	11.1	2714 (22.89)	10.4	63 (9.09)	0.2	570 (28.59)	2.2	80 (7.37)	0.3	1830 (24.38)	7
Klebsiella pneumoniae	17413 (17.5)	100	2779 (14.61)	16	4875 (18.35)	28	3952 (24.21)	22.7	2221 (15.89)	12.8	1685 (14.21)	9.7	155 (22.37)	0.9	402 (20.16)	2.3	21 (1.93)	0.1	1323 (17.62)	7.6
Proteus mirabilis	1800 (1.82)	100	62 (0.33)	3.4	383 (1.44)	21.3	150 (0.92)	8.3	492 (3.52)	27.3	519 (4.38)	28.8	9 (1.3)	0.5	18 (0.9)	1	0 (0)	0	167 (2.22)	9.3
Enterobacter cloacae	1625 (1.64)	100	321 (1.69)	19.8	318 (1.2)	19.6	156 (0.96)	9.6	301 (2.15)	18.5	364 (3.07)	22.4	14 (2.02)	0.9	39 (1.96)	2.4	1 (0.09)	0.1	111 (1.48)	6.8
Citrobacter koseri	779 (0.79)	100	48 (0.25)	6.2	405 (1.52)	52	67 (0.41)	8.6	163 (1.17)	20.9	56 (0.47)	7.2	0 (0)	0	7 (0.35)	0.9	0 (0)	0	33 (0.44)	4.2
Morganella morganii	608 (0.61)	100	45 (0.24)	7.4	154 (0.58)	25.3	21 (0.13)	3.5	129 (0.92)	21.2	180 (1.52)	29.6	2 (0.29)	0.3	11 (0.55)	1.8	0 (0)	0	66 (0.88)	10.9
Serratia marcescens	578 (0.58)	100	111 (0.58)	19.2	118 (0.44)	20.4	160 (0.98)	27.7	68 (0.49)	11.8	72 (0.61)	12.5	4 (0.58)	0.7	11 (0.55)	1.9	1 (0.09)	0.2	33 (0.44)	5.7
Enterobacter spp.	316 (0.32)	100	57 (0.3)	18	87 (0.33)	27.5	44 (0.27)	13.9	45 (0.32)	14.2	45 (0.38)	14.2	3 (0.43)	0.9	10 (0.5)	3.2	0 (0)	0	25 (0.33)	7.9
Providencia stuartii	203 (0.2)	100	31 (0.16)	15.3	17 (0.06)	8.4	45 (0.28)	22.2	38 (0.27)	18.7	41 (0.35)	20.2	0 (0)	0	0 (0)	0	0 (0)	0	31 (0.41)	15.3

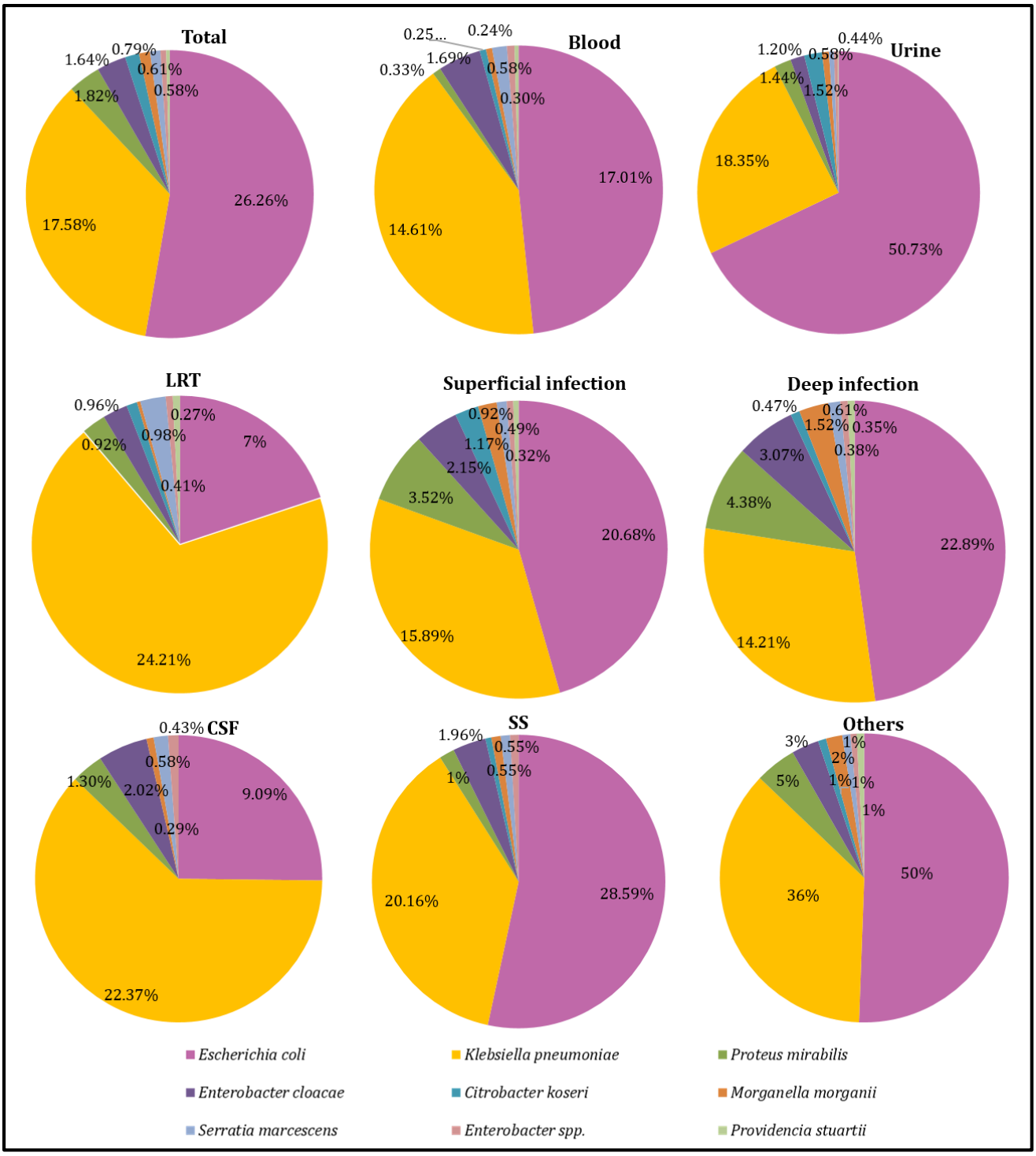


Figure 1.5: Specimen-wise distribution of the major species of Family Enterobacterales except *Salmonella* and *Shigella*

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	77/144 (53.47)	53/144 (36.81)	1/144 (0.69)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0(-)	*0/0 (-)
RC2	4041/23241 (17.39)	3341/23241 (14.38)	638/23241 (2.75)	452/23241 (1.94)	45/23241 (0.19)	90/23241 (0.39)	81/23241 (0.35)	26/23241 (0.11)	33/23241 (0.14)
RC3	492/2944 (16.71)	240/2944 (8.15)	10/2944 (0.34)	1/2944 (0.03)	5/2944 (0.17)	40/2944 (1.36)	4/2944 (0.14)	0/2944 (0.00)	0/2944 (0.00)
RC4	4877/11369 (42.90)	2184/11369 (19.21)	228/11369 (2.01)	185/11369 (1.63)	179/11369 (1.57)	88/11369 (0.77)	1/11369 (0.01)	19/11369 (0.17)	17/11369 (0.15)
RC5	938/3161 (29.67)	710/3161 (22.46)	53/3161 (1.68)	55/3161 (1.74)	27/3161 (0.85)	18/3161 (0.57)	5/3161 (0.16)	8/3161 (0.25)	5/3161 (0.16)
RC6	1691/7199 (23.49)	1403/7199 (19.49)	137/7199 (1.90)	59/7199 (0.82)	26/7199 (0.36)	13/7199 (0.18)	16/7199 (0.22)	5/7199 (0.07)	8/7199 (0.11)
RC7	815/3054 (26.69)	568/3054 (18.60)	56/3054 (1.83)	84/3054 (2.75)	19/3054 (0.62)	15/3054 (0.49)	1/3054 (0.03)	18/3054 (0.59)	1/3054 (0.03)
RC8	998/3976 (25.10)	901/3976 (22.66)	84/3976 (2.11)	99/3976 (2.49)	41/3976 (1.03)	9/3976 (0.23)	2/3976 (0.05)	10/3976 (0.25)	0/3976 (0.00)
RC9	1004/3466 (28.97)	655/3466 (18.90)	5/3466 (0.14)	9/3466 (0.26)	159/3466 (4.59)	0/3466 (0.00)	0/3466 (0.00)	2/3466 (0.06)	3/3466 (0.09)
RC10	2641/9383 (28.15)	1585/9383 (16.89)	220/9383 (2.34)	250/9383 (2.66)	185/9383 (1.97)	0/9383 (0.00)	24/9383 (0.26)	20/9383 (0.21)	37/9383 (0.39)
RC11	429/2531 (16.95)	553/2531 (21.85)	15/2531 (0.59)	157/2531 (6.20)	2/2531 (0.08)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC12	283/949 (29.82)	194/949 (20.44)	*0/0 (-)	45/949 (4.74)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC13	67/391 (17.14)	91/391 (23.27)	*0/0 (-)	2/391 (0.51)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC14	1711/4560 (37.52)	902/4560 (19.78)	21/4560 (0.46)	144/4560 (3.16)	63/4560 (1.38)	5/4560 (0.11)	4/4560 (0.09)	5/4560 (0.11)	*0/0 (-)
RC16	2176/7345 (29.63)	1493/7345 (20.33)	152/7345 (2.07)	8/7345 (0.11)	22/7345 (0.30)	27/7345 (0.37)	3/7345 (0.04)	27/7345 (0.37)	101/7345 (1.38)

RC17	1008/3262 (30.90)	534/3262 (16.37)	*0/0 (-)	2/3262 (0.06)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC18	32/199 (16.08)	24/199 (12.06)	*0/0 (-)	1/199 (0.50)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	2/199 (1.01)
RC19	1063/5358 (19.84)	960/5358 (17.92)	107/5358 (2.00)	28/5358 (0.52)	3/5358 (0.06)	5/5358 (0.09)	2/5358 (0.04)	5/5358 (0.09)	1/5358 (0.02)
RC20	1323/3887 (34.04)	667/3887 (17.16)	55/3887 (1.41)	1/3887 (0.03)	5/3887 (0.13)	4/3887 (0.10)	5/3887 (0.13)	8/3887 (0.21)	26/3887 (0.67)
RC21	330/1522 (21.68)	409/1522 (26.87)	24/1522 (1.58)	46/1522 (3.02)	2/1522 (0.13)	*0/0 (-)	*0/0 (-)	*0/0 (-)	1/1522 (0.07)
Total National	25996/97941 (26.54)	17467/97941 (17.83)	1806/97941 (1.84)	1628/97941 (1.66)	783/97941 (0.80)	317/97941 (0.32)	148/97941 (0.15)	153/97941 (0.16)	235/97941 (0.24)

Typhoidal *Salmonella*

The distribution across regional centres showed that RC6 had a higher percentage isolation rate of *Salmonella* Typhi from blood (17.1%) than the rest of the RCs **(Table 1.7)**. *Salmonella* Paratyphi A isolate percentage was higher in RC6 (9.8%) and in RC3 (4.3%) as compared to other RCs. The relative distribution of Typhoidal *Salmonella* isolated from blood in the OPD, admitted to the wards and ICUs is presented in **Table 1.8** and **Figure 1.6**. Typhoidal *Salmonella* was most commonly isolated from the OPD (22.4%), followed by the wards, and was least isolated from the ICU **(Table 1.8)**. Among Typhoidal *Salmonella*, *Salmonella* Typhi had a higher percentage isolation rate (4.4%) than *Salmonella* Paratyphi A (1.8%). Yearly isolation trends showed a decline in isolation rates of *Salmonella* Typhi from 2018 to 2022 from all over India, but showed an increased isolation rate in 2023 and 2024 **(Table 1.9** and **Figure 1.7)**.

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

Regional Centre	Total Blood Isolates	*Salmonella* Typhi	*Salmonella* Paratyphi A
	n(%)	n(%)	n(%)
RC1	0*0/0 (-)	*0/0 (-)	*0/0 (-)
RC2	6603/19027 (34.70)	103/6603 (1.56)	30/6603 (0.45)
RC3	1009/19027 (5.30)	150/1009 (14.87)	43/1009 (4.26)
RC4	29/19027 (0.15)	*0/0 (-)	*0/0 (-)
RC5	691/19027 (3.63)	59/691 (8.54)	17/691 (2.46)
RC6	2030/19027 (10.67)	348/2030 (17.14)	198/2030 (9.75)
RC7	550/19027 (2.89)	10/550 (1.82)	2/550 (0.36)
RC8	773/19027 (4.06)	*0/0 (-)	1/773 (0.13)
RC9	607/19027 (3.19)	15/607 (2.47)	1/607 (0.16)
RC10	1456/19027 (7.65)	94/1456 (6.46)	37/1456 (2.54)
RC11	315/19027 (1.66)	0/315 (0.00)	*0/0 (-)
RC12	182/19027 (0.96)	14/182 (7.69)	*0/0 (-)
RC13	94/19027 (0.49)	2/94 (2.13)	*0/0 (-)
RC14	539/19027 (2.83)	34/539 (6.31)	8/539 (1.48)
RC16	401/19027 (2.11)	4/401 (1.00)	*0/0 (-)
RC17	1441/19027 (7.57)	3/1441 (0.21)	5/1441 (0.35)
RC18	29/19027 (0.15)	*0/29 (-)	*0/0 (-)
RC19	1740/19027 (9.14)	*0/0 (-)	*0/0 (-)
RC20	53/19027 (0.28)	*0/0 (-)	*0/0 (-)
RC21	485/19027 (2.55)	5/485 (1.03)	4/485 (0.82)
Total National	19027	841/19027 (4.42)	346/19027 (1.82)

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

	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Total Typhoidal *Salmonella*	1257 / 19027 (6.61)	722 / 3218 (22.44)	496 / 9285 (5.34)	39 / 6524 (0.6)
Salmonella Typhi	841 / 19027 (4.42)	462 / 3218 (14.36)	358 / 9285 (3.86)	21 / 6524 (0.32)
Salmonella Paratyphi A	346 / 19027 (1.82)	239 / 3218 (7.43)	102 / 9285 (1.1)	5 / 6524 (0.08)

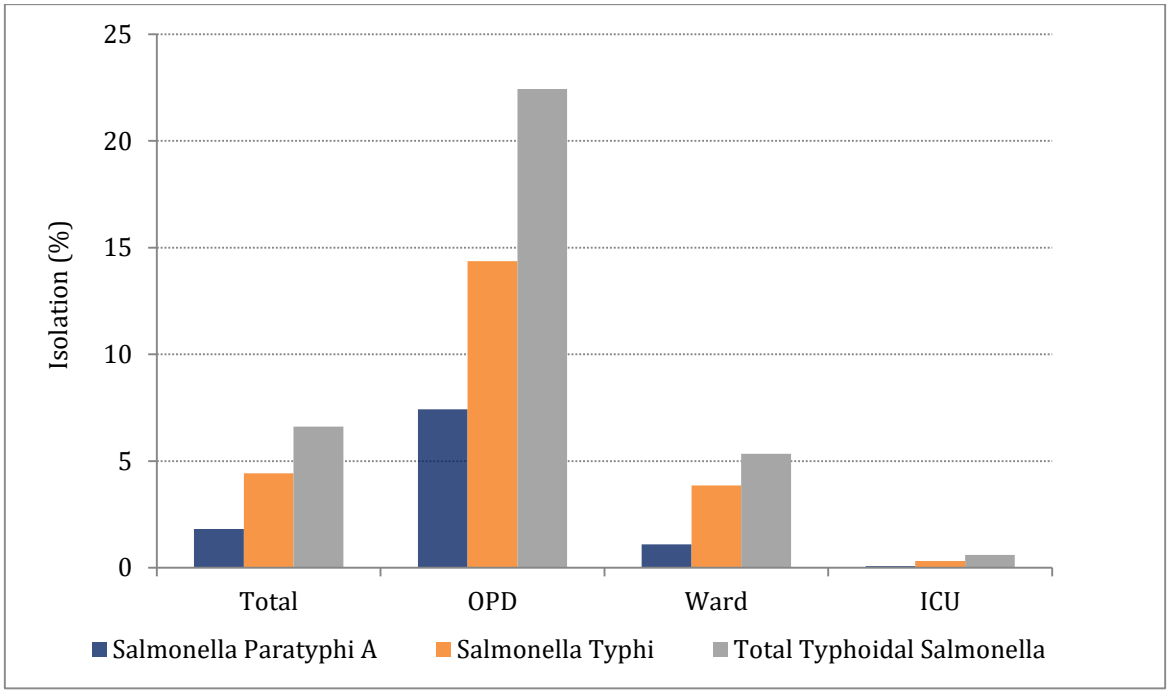


Figure 1.6: Location-wise isolation pattern of Typhoidal *Salmonella* isolated from blood across OPD, Ward and ICU

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
	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)	451/10426 (4.33)
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 (2.82)
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 (0.53)
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 (4.43)
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 (6.28)
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 (4.42)

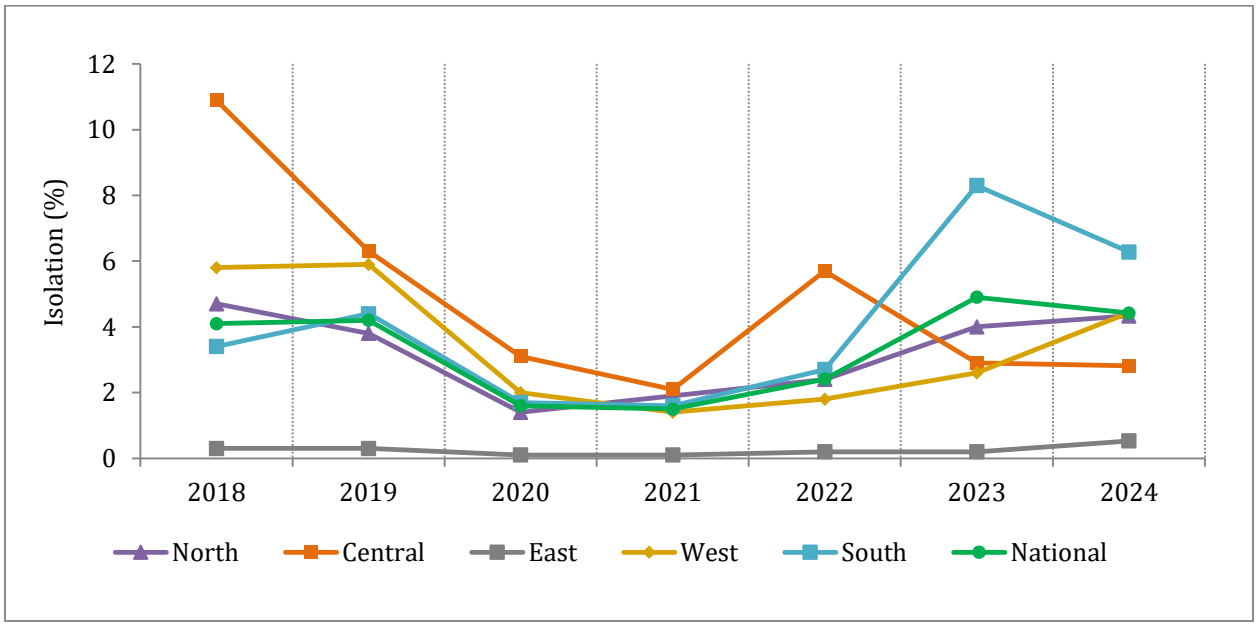


Figure 1.7: Yearly isolation trends of *Salmonella* Typhi from blood across different regions

Non-fermenting Gram-negative bacteria

Non-fermenting Gram-negative bacteria (NFGNB) constituted 23.1% of the total isolates (22,831 out of 99027) **(Table 1.1)**. Among the NFGNB, *P. aeruginosa* (11.5%) was the commonest isolate, followed by *A. baumannii* (10.5%), *Stenotrophomonas maltophilia,* and *Burkholderia cepacia,* which accounted for 0.7% and 0.3% of all isolates, respectively. *P. aeruginosa* was grossly predominant in LRT (23.6%), followed by SI (14.5%), DI (14.2%), and SS (10.9%). *A. baumannii* was the predominant isolate from CSF (32.5%) and LRT (29.4%), followed by blood (11.3%) and SS (8.4%) **(Table 1.10)**.

Regional centre (RC)-wise distribution showed a higher percentage isolation rate of *A. baumannii* in RC11 (28.68%) and RC13 (28.13%), and of *P. aeruginosa* (33.15%) in RC3 than the rest of the RCs **(Table 1.11)**. Among clinical settings, *P. aeruginosa* was predominantly isolated in all wards, ICU, and OPD (11.1-11.7%), respectively, while *A. baumannii* was predominant in the ICU (23.3%), followed by the ward (10.1%) and OPD (4.1%) **(Table 1.12a** and **Figure 1.8)**.

The trend analysis over the years 2017–2023 has shown an increased isolation rate of *A. baumannii* from 7.7% to 12.0%, though a decreased isolation rate was observed in 2024 (10.5%). In contrast, a stable pattern in the isolation rates of *P. aeruginosa* of 12.4% was observed from 2017 to 2022; however, a decreased isolation rate was observed in 2024 (11.5%) **(Table 1.12b)**. In the case of *S. maltophilia* and *B. cepacia,* no significant changes in the isolation rates were noted across the eight years of analysis (**Figure 1.9).**

Table 1.10: Specimen-wise distribution of NFGNB

Isolate	Culture positive																			
	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086		Others N=7502	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
NFGNB	22831 (23.1)	100	3531 (18.6)	15.5	1855 (7)	8.1	9031 (55.3)	39.6	3212 (23)	14.1	2699 (22.8)	11.8	296 (42.7)	1.3	429 (21.5)	1.9	3 (0.3)	0	1773 (23.6)	7.8
Pseudomonas aeruginosa	11419 (11.5)	100	1026 (5.4)	9	1534 (5.8)	13.4	3858 (23.6)	33.8	2032 (14.5)	17.8	1678 (14.2)	14.7	64 (9.2)	0.6	218 (10.9)	1.9	0 (0)	0	1007 (13.4)	8.8
Acinetobacter baumannii	10351 (10.5)	100	2142 (11.3)	20.7	289 (1.1)	2.8	4804 (29.4)	46.4	1112 (8)	10.7	940 (7.9)	9.1	225 (32.5)	2.2	168 (8.4)	1.6	1 (0.1)	0	670 (8.9)	6.5
Stenotrophomonas maltophilia	726 (0.7)	100	173 (0.9)	23.8	21 (0.1)	2.9	306 (1.9)	42.1	53 (0.4)	7.3	63 (0.5)	8.7	6 (0.9)	0.8	30 (1.5)	4.1	2 (0.2)	0.3	72 (1)	9.9
Burkholderia cepacia complex	334 (0.3)	100	190 (1.0)	56.8	11 (0)	3.2	63 (0.3)	18.8	15 (0.1)	4.4	18 (0.1)	5.3	0 (0)	0	13 (0.7)	3.8	0 (0)	0	24 (0.3)	7.1

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

Regional Centre	Total Isolates	*Pseudomonas aeruginosa*	*Acinetobacter baumannii*	*Stenotrophomonas maltophilia*	*Burkholderia cepacia*
	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	144 (0.15)	13/144 (9.03)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC2	23241 (23.73)	2627/23241 (11.30)	3822/23241 (16.45)	267/23241 (1.15)	48/23241 (0.21)
RC3	2944 (3.01)	976/2944 (33.15)	560/2944 (19.02)	*0/0 (-)	*0/0 (-)
RC4	11369 (11.61)	976/1369 (8.6)	497/11369 (4.54)	74/11369 (0.69)	11/11369 (0.10)
RC5	3161 (3.23)	369/3161 (11.67)	93/3161 (2.94)	46/3161 (1.46)	53/3161 (1.68)
RC6	7199 (7.35)	1002/7199 (13.92)	465/7199 (6.46)	103/7199 (1.43)	48/7199 (0.67)
RC7	3054 (3.12)	323/3054 (10.58)	176/3054 (5.76)	10/3054 (0.33)	101/3054 (3.31)
RC8	3976 (4.06)	680/3976 (17.10)	159/3976 (4.00)	55/3976 (1.38)	12/3976 (0.30)
RC9	3466 (3.54)	337/3466 (9.72)	607/3466 (17.51)	0/3466 (0.00)	*0/0 (-)
RC10	9383 (9.58)	1006/9383 (10.72)	444/9383 (4.73)	96/9383 (1.02)	56/9383 (0.60)
RC11	2531 (2.58)	333/2531 (13.16)	726/2531 (28.68)	3/2531 (0.12)	*0/0 (-)
RC12	949 (0.97)	148/949 (15.60)	48/949 (5.06)	1/949 (0.11)	*0/0 (-)
RC13	391 (0.40)	67/391 (17.14)	110/391 (28.13)	*0/0 (-)	1/391 (0.26)
RC14	4560 (4.66)	465/4560 (10.20)	59/4560 (1.29)	*0/0 (-)	*0/0 (-)
RC16	7345 (7.50)	610/7345 (8.30)	568/7345 (7.73)	26/7345 (0.35)	*0/0 (-)
RC17	3262 (3.33)	366/3262 (11.22)	420/3262 (12.88)	*0/0 (-)	*0/0 (-)
RC18	199 (0.20)	18/199 (9.05)	11/199 (5.53)	11/199 (5.53)	*0/0 (-)
RC19	5358 (5.47)	452/5358 (8.44)	907/5358 (16.93)	14/5358 (0.26)	*0/0 (-)
RC20	3887 (3.97)	443/3887 (11.40)	513/3887 (13.20)	*0/0 (-)	*0/0 (-)
RC21	1522 (1.55)	208/1522 (13.67)	165/1522 (10.84)	18/1522 (1.18)	7/1522 (0.46)
Total National	97941	11419/97941 (11.65)	10350/97941 (10.5)	724/97941 (0.74)	334/97941 (0.34)

Table 1.12a: Location-wise isolate percentage of *P. aeruginosa, A. baumannii, S. maltophilia* and *B. cepacia* from all samples across OPD, Ward and ICU

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Pseudomonas aeruginosa	11419 / 99027 (11.53)	3781 / 32729 (11.55)	5673 / 48648 (11.66)	1965 / 17650 (11.13)
Acinetobacter baumannii	10351 / 99027 (10.45)	1341 / 32729 (4.1)	4901 / 48648 (10.07)	4109 / 17650 (23.28)
Stenotrophomonas maltophilia	726 / 99027 (0.73)	120 / 32729 (0.37)	350 / 48648 (0.72)	256 / 17650 (1.45)
Burkholderia cepacia complex	334 / 99027 (0.33)	33/ 32729 (0.1)	116 / 48648 (0.23)	185 / 17650 (1.0)

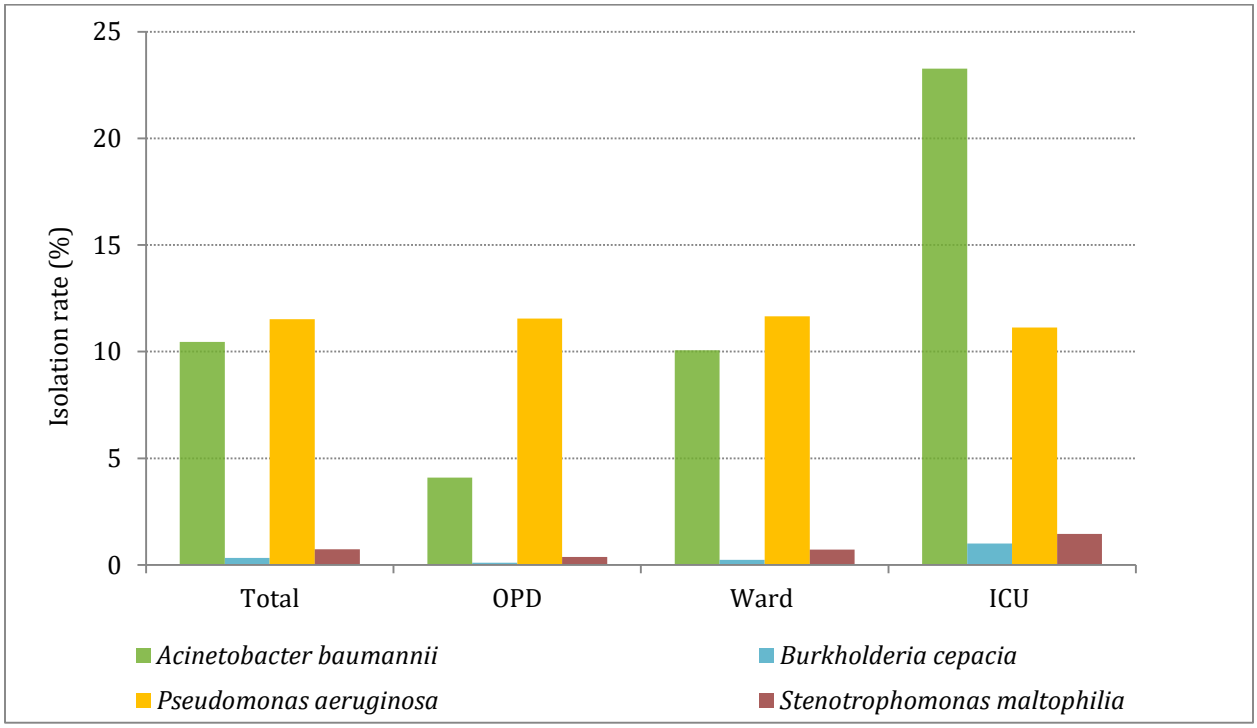


Figure 1.8: Location-wise isolation pattern of *A. baumannii, B. cepacia, P. aeruginosa,* and *S. maltophilia* isolated from all samples

Table 1.12b: Yearly isolation trend of *P. aeruginosa, A. baumannii, S. maltophilia* and *B. cepacia* 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(%)
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 (11.82)	11419 / 99027 (11.53)
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 (12.01)	10351 / 99027 (10.45)
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 (0.73)
Burkholderia cepacia complex	120 / 45714 (0.2)	213 / 75182 (0.2)	233/ 110267 (0.2)	239 / 68081 (0.3)	389 / 96658 (0.4)	370/ 107053 (0.35)	178 / 99492 (0.18)	334 / 99027 (0.3)

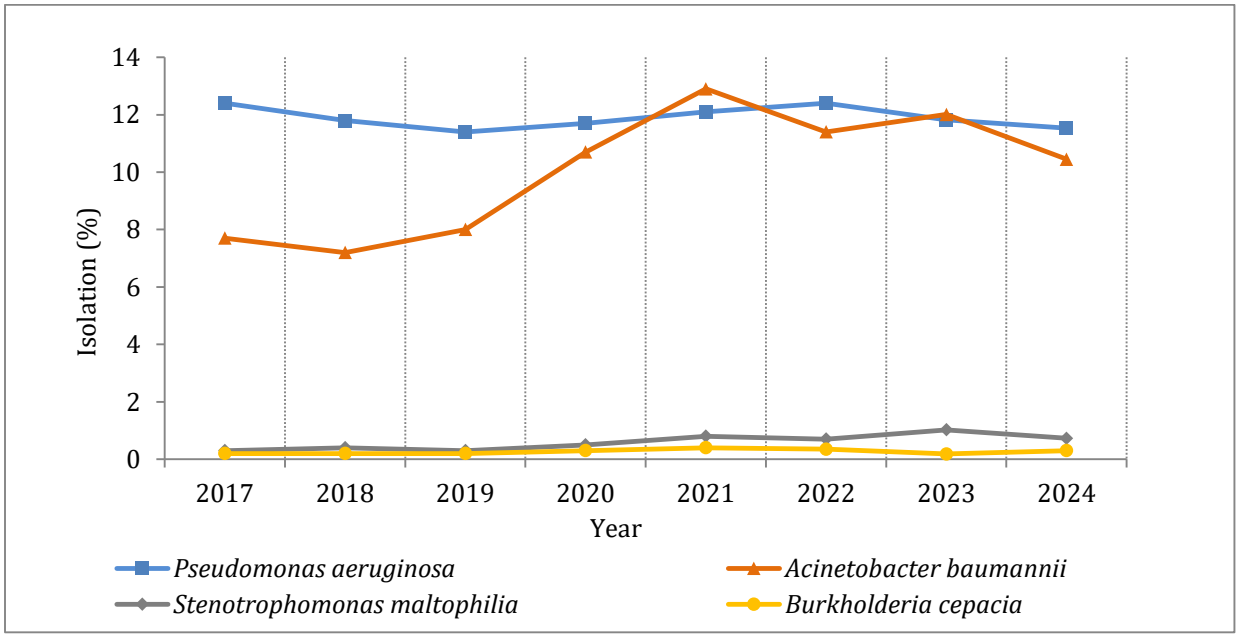


Figure 1.9: Yearly isolation trend of *P. aeruginosa, A. baumannii, S. maltophilia* and *B. cepacia* isolated from all samples

Staphylococci

Staphylococci constituted 13.2% of the total isolates **(Table 1.13)**. *S. aureus* was the predominant species in the DI (20.6%) and SI (20.4%), followed by others (10.7%), sterile body fluids (6.8%), blood (5.6%), LRT (5.5%) and urine (1.1%) **(Table 1.13)**. Coagulase-negative staphylococci (CoNS) were the predominant isolates in blood (20.5%) and CSF (6.1%), reflecting the high incidence of shunt infections and intravascular device-associated infections, respectively. In blood and CSF, *S. epidermidis* isolation rate was 5.7% and 2.9% respectively, reflecting the ability of the species to form biofilms and high incidence of shunt-associated and dialysis-associated infections. Predominant percentage isolation of methicillin-resistant *Staphylococcus aureus* (MRSA) was from SI (10.7%), followed by isolation from DI (10.3%), 3.9% from CSF, 3.6% from sterile body sites, and 2.7% from blood. Methicillin-sensitive *Staphylococcus aureus* (MSSA) was the predominant isolate from DI (10.3%), followed by isolation from SI (9.8%), other sites (5.8%), and blood (2.9%), respectively (**Figure 1.10**). Amongst the CoNS, *S. haemolyticus* (34.4%) was the commonest species, followed by *S. epidermidis* (27.7%) and *S. hominis* (27.1%) (**Table 1.13)**. Regional centre-wise distribution is shown in **Table 1.14**.

Among clinical settings, *S. aureus* was predominantly isolated in the OPDs (11.6%), followed by the wards (8.1%) and the ICUs (4.5%), while the coagulase-negative staphylococci (CoNS) were predominant in ICUs (6.7%), wards (4.8%), and then OPDs (3.3%) **(Table 1.15** and **Figure 1.11)**. Trend analysis over the years 2017–2024 has shown a steady decline in the isolation rates of *S. aureus* from 12.5% in 2017 to 8.6% in 2024 **(Table 1.16** and **Figure 1.12)**.

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

Isolate	Culture positive																			
	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086		Others N=7502	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
No. culture positive	99027 (100)	100	19027 (100)	19.2	26562 (100)	26.8	16327 (100)	16.5	13973 (100)	14.1	11858 (100)	12	693 (100)	0.7	1994 (100)	2	1086 (100)	1.1	7502 (100)	7.6
Total Staphylococcus	13089 (13.2)	100	4964 (26.1)	37.9	389 (1.5)	3	917 (5.6)	7	3113 (22.3)	23.8	2491 (21)	19	80 (11.5)	0.6	166 (8.3)	1.3	0 (0)	0	969 (12.9)	7.4
Staphylococcus aureus	8515 (8.6)	100	1067 (5.6)	12.5	289 (1.1)	3.4	891 (5.5)	10.5	2850 (20.4)	33.5	2438 (20.6)	28.6	38 (5.5)	0.4	136 (6.8)	1.6	0 (0)	0	806 (10.7)	9.5
MSSA	4262 (4.3)	100	559 (2.9)	13.1	152 (0.6)	3.6	460 (2.8)	10.9	1364 (9.8)	32.1	1223 (10.3)	28.6	11 (1.6)	0.3	65 (3.3)	1.5	0	0	428 (5.8)	10.1
MRSA	4253 (4.3)	100	508 (2.7)	11.9	137 (0.5)	3.2	431 (2.6)	10.1	1486 (10.7)	34.9	1215 (10.3)	28.5	27 (3.9)	0.6	71 (3.6)	1.7	0	0	378 (5.1)	8.9
CoNS	4574 (4.6)	100	3897 (20.5)	85.2	100 (0.4)	2.2	26 (0.2)	0.6	263 (1.9)	5.7	53 (0.4)	1.2	42 (6.1)	0.9	30 (1.5)	0.7	0 (0)	0	163 (2.2)	3.6
Staphylococcus haemolyticus	1572 (1.6)	100	1380 (7.3)	87.8	13 (0)	0.8	7 (0)	0.4	104 (0.7)	6.6	11 (0.1)	0.7	12 (1.7)	0.8	11 (0.6)	0.7	0 (0)	0	34 (0.5)	2.2
Staphylococcus epidermidis	1269 (1.3)	100	1090 (5.7)	85.9	6 (0)	0.5	5 (0)	0.4	49 (0.4)	3.9	23 (0.2)	1.8	20 (2.9)	1.6	4 (0.2)	0.3	0 (0)	0	72 (1)	5.7
Staphylococcus hominis	1241 (1.3)	100	1186 (6.2)	95.6	5 (0)	0.4	0 (0)	0	22 (0.2)	1.8	9 (0.1)	0.7	2 (0.3)	0.2	4 (0.2)	0.3	0 (0)	0	13 (0.2)	1
Staphylococcus spp.	425 (0.4)	100	222 (1.2)	52.2	49 (0.2)	11.5	13 (0.1)	3.1	73 (0.5)	17.2	6 (0.1)	1.4	8 (1.2)	1.9	10 (0.5)	2.4	0 (0)	0	44 (0.6)	10.4

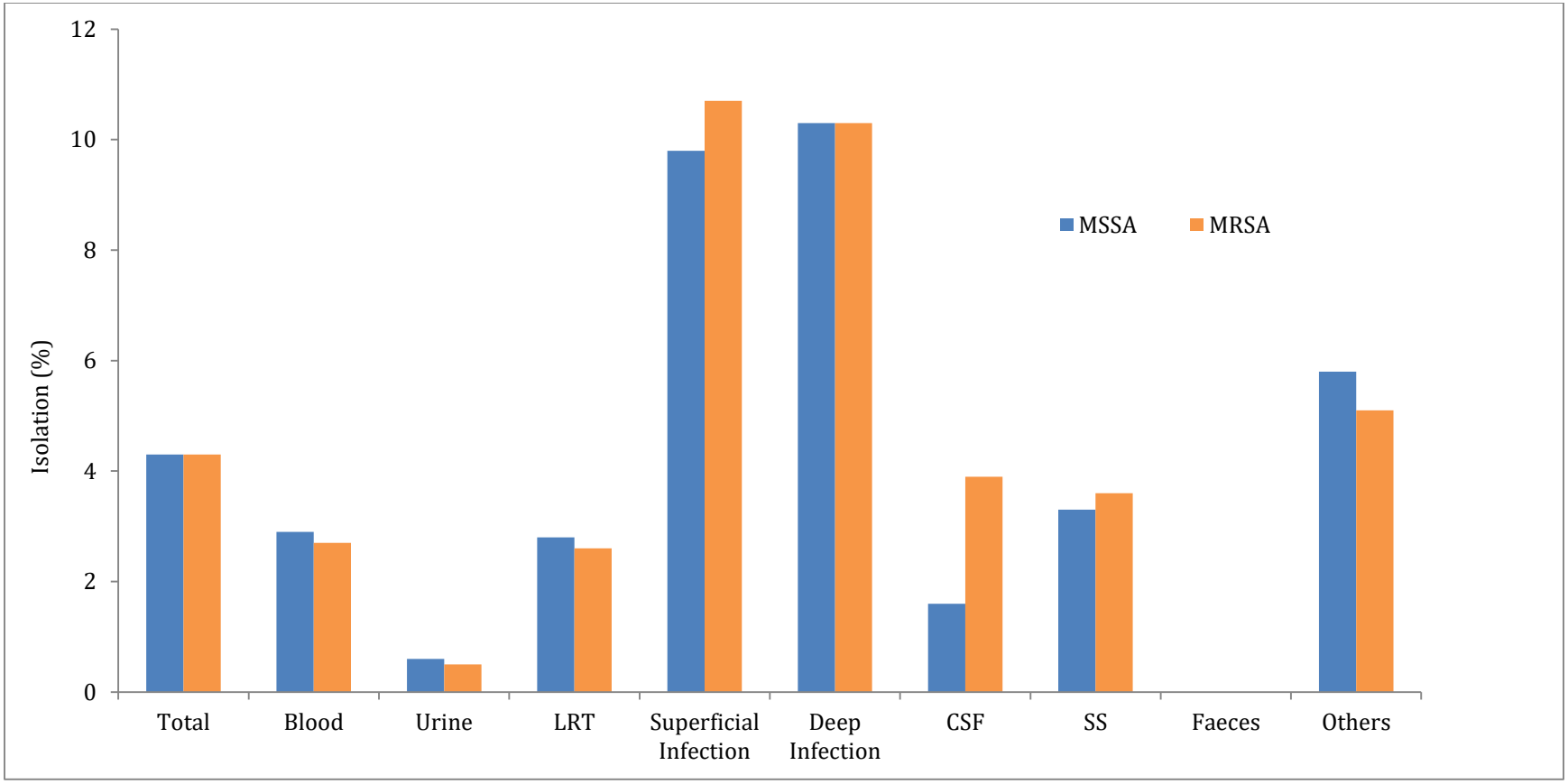


Figure 1.10: Specimen-wise relative distributions of MSSA and MRSA

Table 1.14: Regional Centre-wise isolate percentages of *S. aureus*, MRSA, MSSA and CoNS species isolated from all samples (except faeces)

Regional Centre	Total Isolates	*S. aureus*	MRSA	MSSA	*S. haemolyticus*	*S. epidermidis*	*S. hominis*	*S. lugdunensis*	*S. saprophyticus*	*Staphylococcus spp.*
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC2	23241 (23.73)	2962/23241 (12.74)	1448/23241 (6.23)	1514/23241 (6.51)	845/23241 (3.64)	740/23241 (3.18)	749/23241 (3.22)	*0/0 (-)	*0/0 (-)	175/23241 (0.75)
RC3	2944 (3.01)	153/2944 (5.20)	58/2944 (1.97)	95/2944 (3.23)	10/2944 (0.34)	14/2944 (0.48)	11/2944 (0.37)	*0/0 (-)	*0/0 (-)	16/2944 (0.54)
RC4	11369 (11.61)	593/11369 (5.2)	183/11369 (1.6)	410/11369 (3.6)	1/11369 (0.01)	1/11369 (0.01)	*0/0 (-)	*0/0 (-)	*0/0 (-)	1/11369 (0.01)
RC5	3161 (3.23)	171/3161 (5.41)	152/3161 (4.81)	19/3161 (0.60)	27/3161 (0.85)	50/3161 (1.58)	21/3161 (0.66)	*0/0 (-)	*0/0 (-)	21/3161 (0.66)
RC6	7199 (7.35)	408/7199 (5.67)	238/7199 (3.31)	170/7199 (2.36)	104/7199 (1.44)	100/7199 (1.39)	26/7199 (0.36)	5/7199 (0.07)	9/7199 (0.13)	11/7199 (0.15)
RC7	3054 (3.12)	216/3054 (7.07)	120/3054 (3.93)	96/3054 (3.14)	76/3054 (2.49)	59/3054 (1.93)	38/3054 (1.24)	*0/0 (-)	14/3054 (0.46)	2/3054 (0.07)
RC8	3976 (4.06)	328/3976 (8.25)	115/3976 (2.89)	213/3976 (5.36)	5/3976 (0.13)	6/3976 (0.15)	4/3976 (0.10)	*0/0 (-)	1/3976 (0.03)	*0/0 (-)
RC9	3466 (3.54)	345/3466 (9.95)	168/3466 (4.85)	177/3466 (5.11)	2/3466 (0.06)	*0/0 (-)	0/3466 (0.00)	*0/0 (-)	0/3466 (0.00)	*0/0 (-)
RC10	9383 (9.58)	707/9383 (7.53)	261/9383 (2.78)	446/9383 (4.75)	28/9383 (0.30)	52/9383 (0.55)	8/9383 (0.09)	14/9383 (0.15)	10/9383 (0.11)	5/9383 (0.05)
RC11	2531 (2.58)	183/2531 (7.23)	122/2531 (4.82)	61/2531 (2.41)	6/2531 (0.24)	3/2531 (0.12)	2/2531 (0.08)	0/2531 (0.00)	*0/0 (-)	*0/0 (-)
RC12	949 (0.97)	105/949 (11.06)	69/949 (7.27)	36/949 (3.79)	7/949 (0.74)	1/949 (0.11)	3/949 (0.32)	0/949 (0.00)	*0/0 (-)	*0/0 (-)
RC13	391 (0.40)	3/391 (0.77)	3/391 (0.77)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC14	4560 (4.66)	810/4560 (17.76)	381/4560 (8.36)	429/4560 (9.41)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC16	7345 (7.50)	594/7345 (8.09)	432/7345 (5.88)	162/7345 (2.21)	29/7345 (0.39)	67/7345 (0.91)	33/7345 (0.45)	1/7345 (0.01)	2/7345 (0.03)	182/7345 (2.48)
RC17	3262 (3.33)	296/3262 (9.07)	53/3262 (1.62)	243/3262 (7.45)	25/3262 (0.77)	1/3262 (0.03)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)

RC18	199 (0.20)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC19	5358 (5.47)	166/5358 (3.10)	96/5358 (1.79)	70/5358 (1.31)	374/5358 (6.98)	148/5358 (2.76)	336/5358 (6.27)	*0/0 (-)	2/5358 (0.04)	8/5358 (0.15)
RC20	3887 (3.97)	351/3887 (9.03)	274/3887 (7.05)	77/3887 (1.98)	2/3887 (0.05)	9/3887 (0.23)	6/3887 (0.15)	*0/0 (-)	4/3887 (0.10)	1/3887 (0.03)
RC21	1522 (1.55)	124/1522 (8.15)	80/1522 (5.26)	44/1522 (2.89)	31/1522 (2.04)	18/1522 (1.18)	4/1522 (0.26)	*0/0 (-)	1/1522 (0.07)	3/1522 (0.20)
Total National	97941	8515/97941 (8.71)	4253/9794 1 (4.3)	4262/97941 (4.3)	1572/97941 (1.6)	1269/9794 1 (1.3)	1241/9794 1 (1.3)	20/97941 (0.02)	43/97941 (0.04)	425/97941 (0.4)

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

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Total Staphylococci	13089 / 99027 (13.2)	4845 / 32729 (14.8)	6272 / 48648 (12. 9)	1972 / 17650 (11.2)
Staphylococcus aureus	8515 / 99027 (8.6)	3779 / 32729 (11.6)	3942 / 48648 (8.1)	794 / 17650 (4.5)
MSSA	4262/99027 (4.3)	2002/32729 (6.1)	1910/48648 (3.9)	350/17650 (2.1)
MRSA	4253/99027 (4.3)	1777/32729 (5.4)	2032/48648 (4.2)	444/17650 (2.5)
CoNS	4574/99027 (4.6)	1066/32729 (3.3)	2330/48648 (4.8)	1178/17650 (6.7)

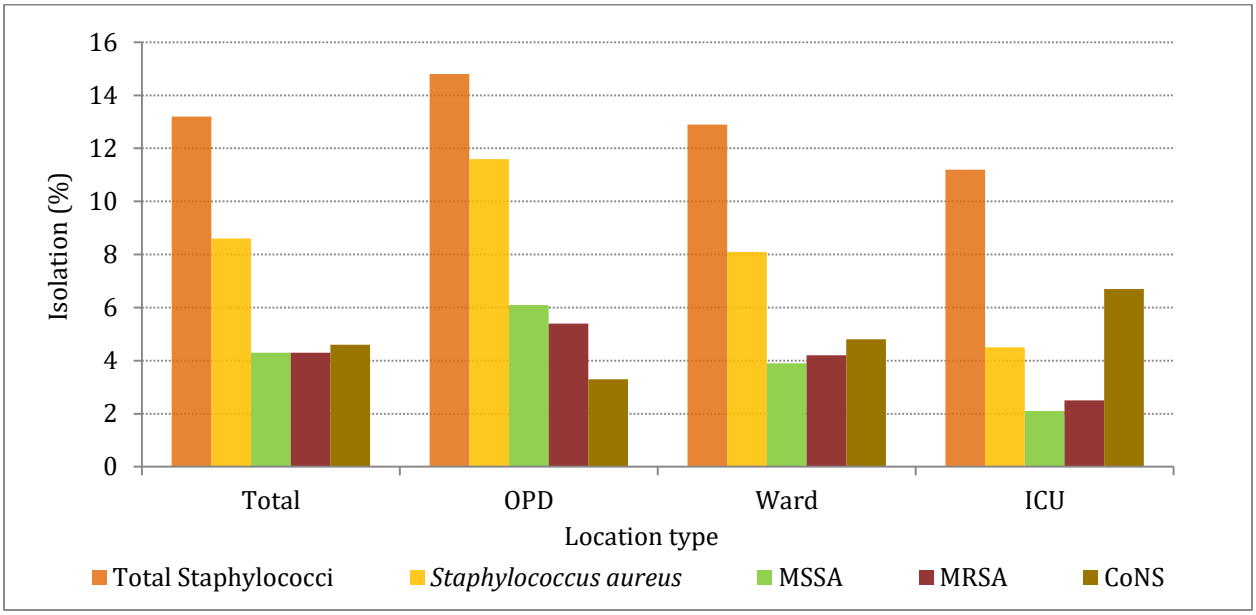


Figure 1.11: Location-wise isolation pattern of total Staphylococci, *S. aureus*, MSSA, MRSA and CoNS isolated from all samples

Table 1.16: Yearly isolation trend of *Staphylococcus* species

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(%)
Total Staphylococci	8564/ 45714 (18.7)	12950/ 75182 (17.2)	16277/ 110264 (14.8)	5163/ 65561 (12.7)	11482/ 95728 (12)	15748/ 107053 (14.7)	15795 / 99492 (15.9)	13089 / 99027 (13.2)
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)
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 (4.3)
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)
CoNS	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)
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 (1.6)
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 (1.3)
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 (1.3)
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)

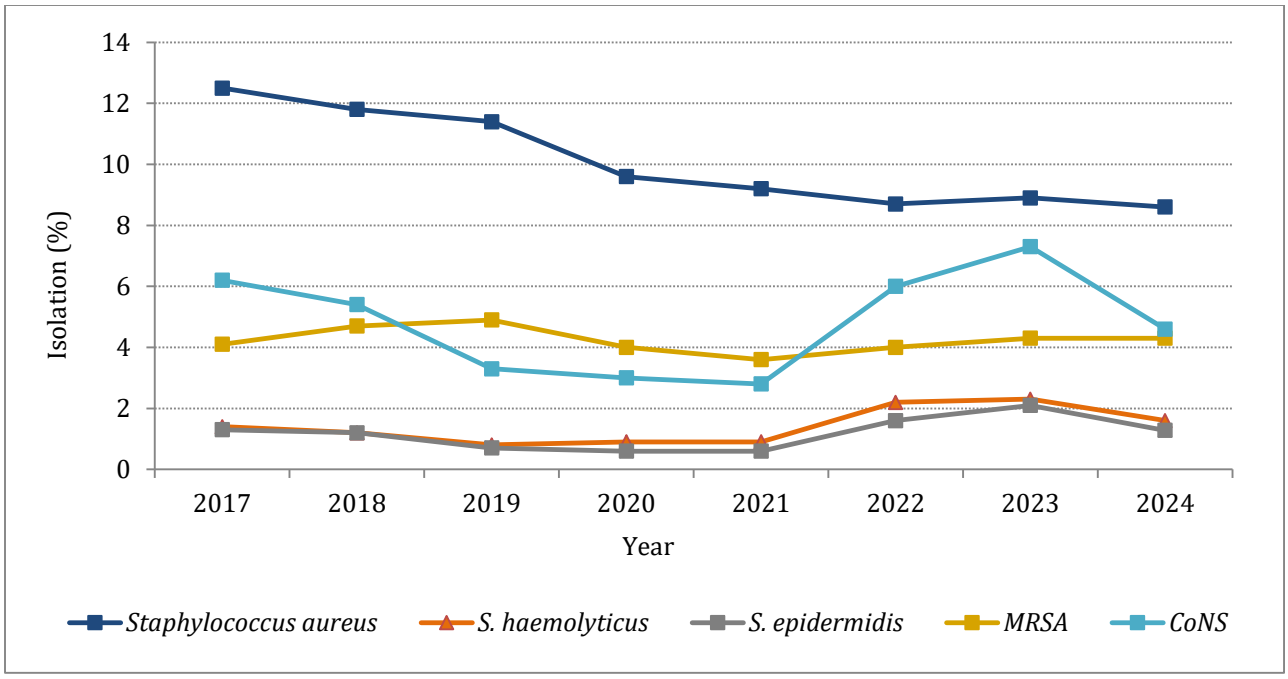


Figure 1.12: Yearly isolation trends of *Staphylococcus* species

Enterococci

Enterococci constituted overall 6.8% of all isolates **(Table 1.17)**. Among the *Enterococcus* species, *E. faecalis* (45.3%) and *E. faecium* (44.6%) were the predominant species, accounting for 89.9% of the total isolates. *E. faecalis* was more frequent in the urine (7.0%) and SS (2.9%), while *E. faecium* was relatively more frequent in the SS (6.6%) and urine (5.2%) **(Table 1.17** and **Figure 1.13)**.

Among clinical settings, *E. faecalis* was predominantly isolated in OPD (4.17%), followed by ward (2.9%) and ICU (1.72%), while *E. faecium* was predominant both in the ward (3.73%) and ICU (3.63%), followed by OPD (1.76%) **(Table 1.18a** and **Figure 1.14).** RC-wise distribution showed the predominance of *E. faecalis* (16.6%) and *E. faecium* (29.2%) isolation in RC18 **(Table 1.18b)**.

The trend analysis over the years has shown stable isolation rates of *E. faecium* from 2.0% in 2017 to 2.8% in 2023 and an observed increase in isolates in 2024 (3.1%), whereas in *E. faecalis* an increase from 2.2% to 3.5% was observed from 2017 to 2023 respectively, with a decrease observed in 2024 (3.03%) **(Table 1.19** and **Figure 1.14)**.

Table 1.17: Specimen-wise distribution of *Enterococcus* species

	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Enterococci	6718 (6.8)	100	927 (4.9)	13.8	3438 (12.9)	51.2	68 (0.4)	1	732 (5.2)	10.9	655 (5.5)	9.7	21 (3)	0.3	212 (10.6)	3.2	3 (0.3)	0
Enterococcus faecalis	3042 (3.1)	100	276 (1.5)	9.1	1862 (7)	61.2	31 (0.2)	1	378 (2.7)	12.4	188 (1.6)	6.2	7 (1)	0.2	57 (2.9)	1.9	0 (0)	0
Enterococcus faecium	3002 (3)	100	603 (3.2)	20.1	1372 (5.2)	45.7	22 (0.1)	0.7	233 (1.7)	7.8	293 (2.5)	9.8	12 (1.7)	0.4	131 (6.6)	4.4	3 (0.3)	0.1
Enterococcus spp.	674 (0.7)	100	48 (0.3)	7.1	204 (0.8)	30.3	15 (0.1)	2.2	121 (0.9)	18	174 (1.5)	25. 8	2 (0.3)	0.3	24 (1.2)	3.6	0 (0)	0

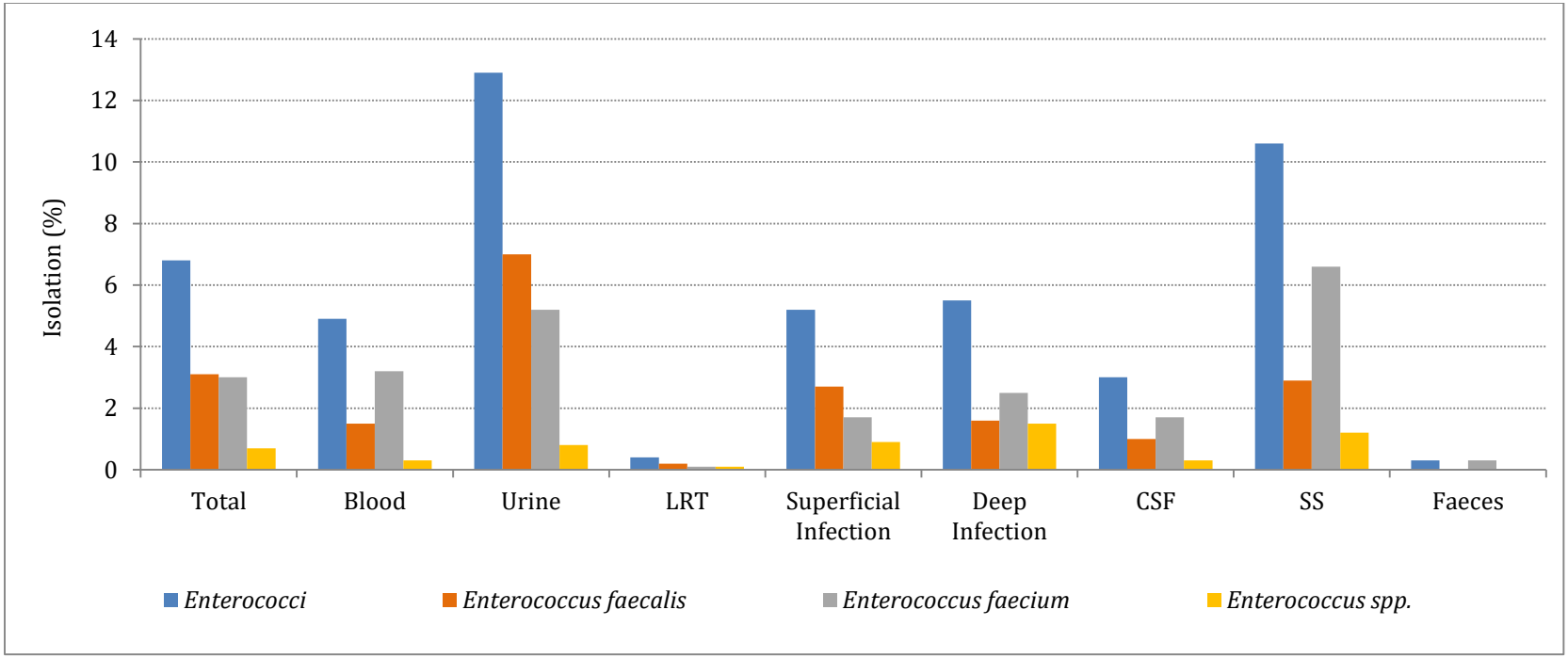


Figure 1.13: Specimen-wise distribution of *Enterococcus* species

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

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Enterococcus faecalis	3042 / 97941 (3.11)	1345 / 32289 (4.17)	1394 / 48035 (2.9)	303 / 17617 (1.72)
Enterococcus faecium	2999 / 97941 (3.06)	569 / 32289 (1.76)	1791 / 48035 (3.73)	639 / 17617 (3.63)
Enterococcus spp.	674 / 97941 (0.69)	207 / 32289 (0.64)	391 / 48035 (0.81)	76 / 17617 (0.43)

Table 1.18b: Isolate percentages across Regional Centres of *Enterococcus faecalis, Enterococcus faecium, Enterococcus* spp. from all specimens (except faeces)

Regional Centre	Total isolates	*Enterococcus faecalis*	*Enterococcus faecium*	*Enterococcus* spp.
	n(%)	n(%)	n(%)	n(%)
RC1	144 (0.15)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC2	23241 (23.73)	76/23241 (0.33)	452/23241 (1.94)	247/23241 (1.06)
RC3	2944 (3.01)	21/2944 (0.71)	36/2944 (1.22)	16/2944 (0.54)
RC4	11369 (11.61)	724/11369 (6.4)	493/11369 (4.3)	40/11369 (0.4)
RC5	3161 (3.23)	1/3161 (0.03)	*0/0 (-)	*0/0 (-)
RC6	7199 (7.35)	125/7199 (1.74)	325/7199 (4.51)	19/7199 (0.26)
RC7	3054 (3.12)	179/3054 (5.86)	62/3054 (2.03)	13/3054 (0.43)
RC8	3976 (4.06)	106/3976 (2.67)	136/3976 (3.42)	7/3976 (0.18)
RC9	3466 (3.54)	172/3466 (4.96)	125/3466 (3.61)	*0/0 (-)
RC10	9383 (9.58)	672/9383 (7.16)	385/9383 (4.10)	103/9383 (1.10)
RC11	2531 (2.58)	39/2531 (1.54)	51/2531 (2.02)	3/2531 (0.12)
RC12	949 (0.97)	14/949 (1.48)	24/949 (2.53)	*0/0 (-)
RC13	391 (0.40)	9/391 (2.30)	26/391 (6.65)	2/391 (0.51)
RC14	4560 (4.66)	65/4560 (1.43)	28/4560 (0.61)	*0/0 (-)
RC16	7345 (7.50)	331/7345 (4.51)	294/7345 (4.00)	213/7345 (2.90)
RC17	3262 (3.33)	77/3262 (2.36)	159/3262 (4.87)	3/3262 (0.09)
RC18	199 (0.20)	33/199 (16.58)	58/199 (29.15)	*0/0 (-)
RC19	5358 (5.47)	211/5358 (3.94)	107/5358 (2.00)	1/5358 (0.02)
RC20	3887 (3.97)	176/3887 (4.53)	187/3887 (4.81)	4/3887 (0.10)

RC21	1522 (1.55)	11/1522 (0.72)	51/1522 (3.35)	3/1522 (0.20)
Total	97941	3042/97941 (3.1)	2999/97941 (3.1)	674/97941 (0.7)

Table 1.19: Yearly isolation trend of *Enterococcus* species

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(%)
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)	6718/99 027 (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 (2.76)	3042 / 99027 (3.07)
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 (3.48)	3002 / 99027 (3.03)
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 (0.79)	674/ 99027 (0.68)

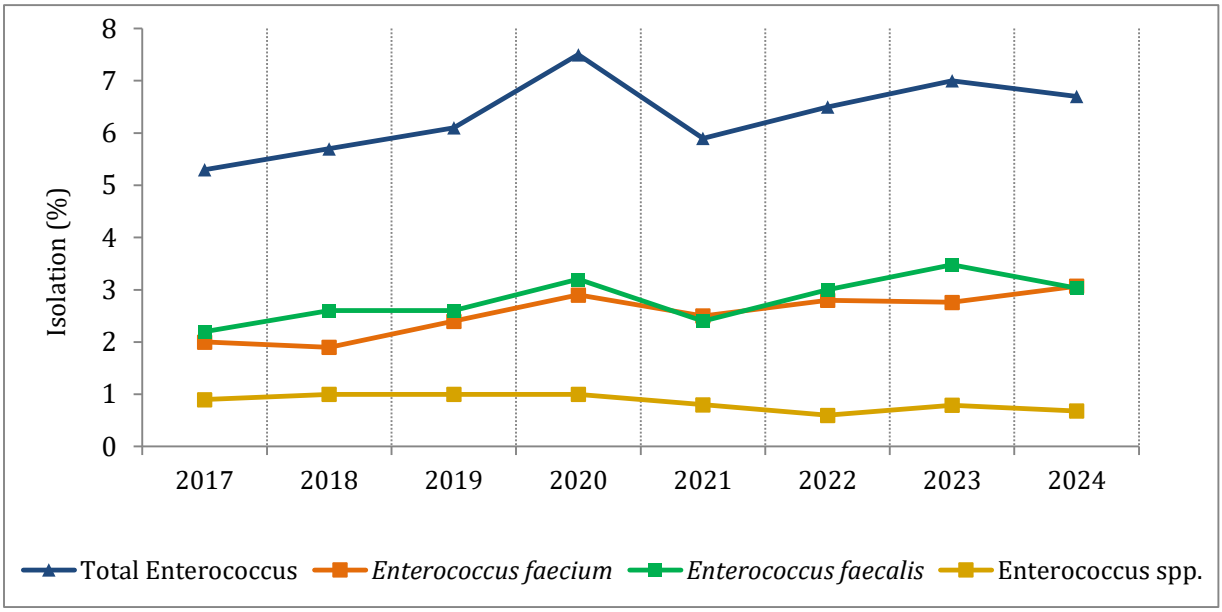


Figure 1.14: Yearly isolation trends of *Enterococcus* species

Fungal species

The total number of yeast isolates studied during the year 2024 was 2729, of which 52% (1419) were isolated from blood. The majority of the isolates were from *Candida tropicalis* (n=822), followed by *Candida albican*s (n=429) **(Table 1.20)**. In the distribution of fungi species in different specimens, *C. tropicalis* was predominantly isolated from blood (2.8%), followed by sterile sites (1.2%), and *C. albican*s was predominantly isolated from sterile sites (0.9%), followed by blood (0.8%) **(Table 1.20)**. In clinical settings, in ICUs, *C. tropicalis* was a common isolate from the ICU (1.68%) and ward (0.85%) **(Table 1.21** and **Figure 1.15)**. Among *Aspergillus* species, *A. flavus* was the predominant isolate, followed by *A. fumigatus* **(Table 1.22)**.

Yearly isolation trends show a steady decline in isolation of *C. tropicalis* from 1.4% in 2017 to 0.7% in 2023 and a slight increase in 2024 (0.8%). Yearly isolation trend *of C. albican*s shows a steady decline from 1.0% in 2017 to 0.4% in 2024. Both *C. auris and C. parapsilosis* isolates show a stable trend from 2020 to 2024 **(Table 1.23** and **Figure 1.16)**.

Table 1.20: *Candida* species isolated from different sample types (except faeces)

Isolate	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Fungal isolates	2729 (2.8)	100	1419 (7.5)	52	534 (2)	19.6	219 (1.3)	8	80 (0.6)	2.9	74 (0.6)	2.7	34 (4.9)	1.2	79 (4)	2.9	3 (0.3)	0.1
Candida tropicalis	822 (0.8)	100	533 (2.8)	64.8	163 (0.6)	19.8	4 (0)	0.5	23 (0.2)	2.8	15 (0.1)	1.8	4 (0.6)	0.5	23 (1.2)	2.8	1 (0.1)	0.1
Candida albicans	429 (0.4)	100	148 (0.8)	34.5	149 (0.6)	34.7	3 (0)	0.7	19 (0.1)	4.4	16 (0.1)	3.7	4 (0.6)	0.9	17 (0.9)	4	1 (0.1)	0.2
Candida glabrata	277 (0.3)	100	117 (0.6)	42.2	88 (0.3)	31.8	0 (0)	0	11 (0.1)	4	11 (0.1)	4	3 (0.4)	1.1	10 (0.5)	3.6	0 (0)	0
Candida auris	293 (0.3)	100	182 (1)	62.1	65 (0.2)	22.2	1 (0)	0.3	14 (0.1)	4.8	16 (0.1)	5.5	3 (0.4)	1	7 (0.4)	2.4	0 (0)	0
Candida parapsilosis	329 (0.3)	100	278 (1.5)	84.5	22 (0.1)	6.7	1 (0)	0.3	2 (0)	0.6	3 (0)	0.9	4 (0.6)	1.2	1 (0.1)	0.3	0 (0)	0
Candida krusei	48 (0)	100	24 (0.1)	50	9 (0)	18.8	1 (0)	2.1	1 (0)	2.1	1 (0)	2.1	2 (0.3)	4.2	7 (0.4)	14.6	1 (0.1)	2.1
Candida kefyr	14 (0)	-	3 (0)	-	5 (0)	-	0 (0)	-	1 (0)	-	0 (0)	-	1 (0.1)	-	2 (0.1)	-	0 (0)	-
Candida pelliculosa	63 (0.1)	100	54 (0.3)	85.7	0 (0)	0	0 (0)	0	1 (0)	1.6	0 (0)	0	0 (0)	0	2 (0.1)	3.2	0 (0)	0
Candida lusitaniae	9 (0)	-	4 (0)	-	1 (0)	-	0 (0)	-	2 (0)	-	0 (0)	-	0 (0)	-	1 (0.1)	-	0 (0)	-
Candida utilis	24 (0)	100	21 (0.1)	87.5	1 (0)	4.2	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0

Total *Candida*	2343 (2.4)	100	1386 (7.3)	59.2	508 (1.9)	21.7	11 (0.1)	0.5	75 (0.5)	3.2	64 (0.5)	2.7	21 (3)	0.9	70 (3.5)	3	3 (0.3)	0.1

Notes:

1. Percentages are out of a particular specimen (column).
2. Percentages in rows below Culture positive are out of Culture positive in respective columns.
3. Blood includes: Blood-central catheter, Blood-peripheral and Peripheral catheter-blood.
4. LRT (Lower Respiratory Tract) includes: BAL, Sputum, Lung aspirate, Endotracheal aspirate (ETA) and Lobectomy tissue (Lung tissue).
5. SI (Superficial Infection) includes: SST (Skin & Soft Tissue), Pus/exudate, Wound swab, Superficial Biopsy and Superficial Tissue.
6. DI (Deep Infection) includes: Abscess aspirate, Pus aspirate, Deep Biopsy and Deep Tissue.
7. SS (Sterile sites) includes: Fluid from sterile spaces, Abdominal fluid, Intracostal tube fluid, Pancreatic drain fluid, Pericardial fluid, Peritoneal fluid and Pleural fluid.

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

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Candida tropicalis	822 / 99027 (0.83)	111 / 32729 (0.34)	414 / 48648 (0.85)	297 / 17650 (1.68)
Candida albicans	429 / 99027 (0.43)	58 / 32729 (0.18)	255 / 48648 (0.52)	116 / 17650 (0.01)
Candida parapsilosis	329 / 99027 (0.33)	47 / 32729 (0.14)	188 / 48648 (0.39)	94 / 17650 (0.53)
Candida auris	293 / 99027 (0.3)	44 / 32729 (0.13)	110 / 48648 (0.23)	139 / 17650 (0.79)
Candida glabrata	277 / 99027 (0.28)	22 / 32729 (0.07)	188 / 48648 (0.39)	67 / 17650 (0.38)
Candida pelliculosa	63 / 99027 (0.06)	2 / 32729 (0)	50 / 48648 (0.1)	11 / 17650 (0.06)
Candida krusei	48 / 99027 (0.05)	4 / 32729 (0.01)	26 / 48648 (0.05)	18 / 17650 (0.1)
Candida utilis	24 / 99027 (0.02)	12 / 32729 (0.04)	4 / 48648 (0)	8 / 17650 (0.05)
Candida kefyr	14 / 99027 (0.01)	1 / 32729 (0)	7 / 48648 (0.01)	6 / 17650 (0.03)
Candida lusitaniae	9 / 99027 (0.01)	0 / 32729 (0)	7 / 48648 (0.01)	2 / 17650 (0)

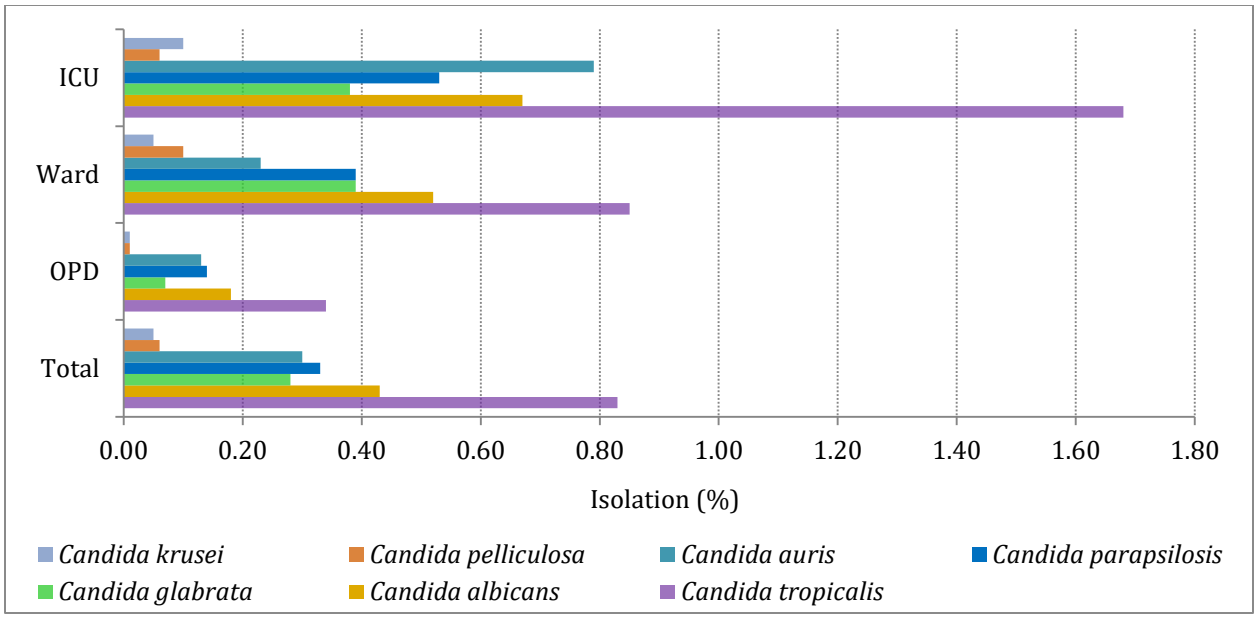


Figure 1.15: Location-wise pattern of *Candida* species isolated from all samples across OPD, Wards and ICUs

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

Organism	Total n(%)
Aspergillus flavus	186/99027 (0.18)
Aspergillus fumigatus	111/99027 (0.11)
Aspergillus terreus	11 / 99027 (0.01)
Aspergillus niger	5/ 99027 (0.005)

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(%)
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)
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)
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)
Candida glabrata	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)
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)
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)

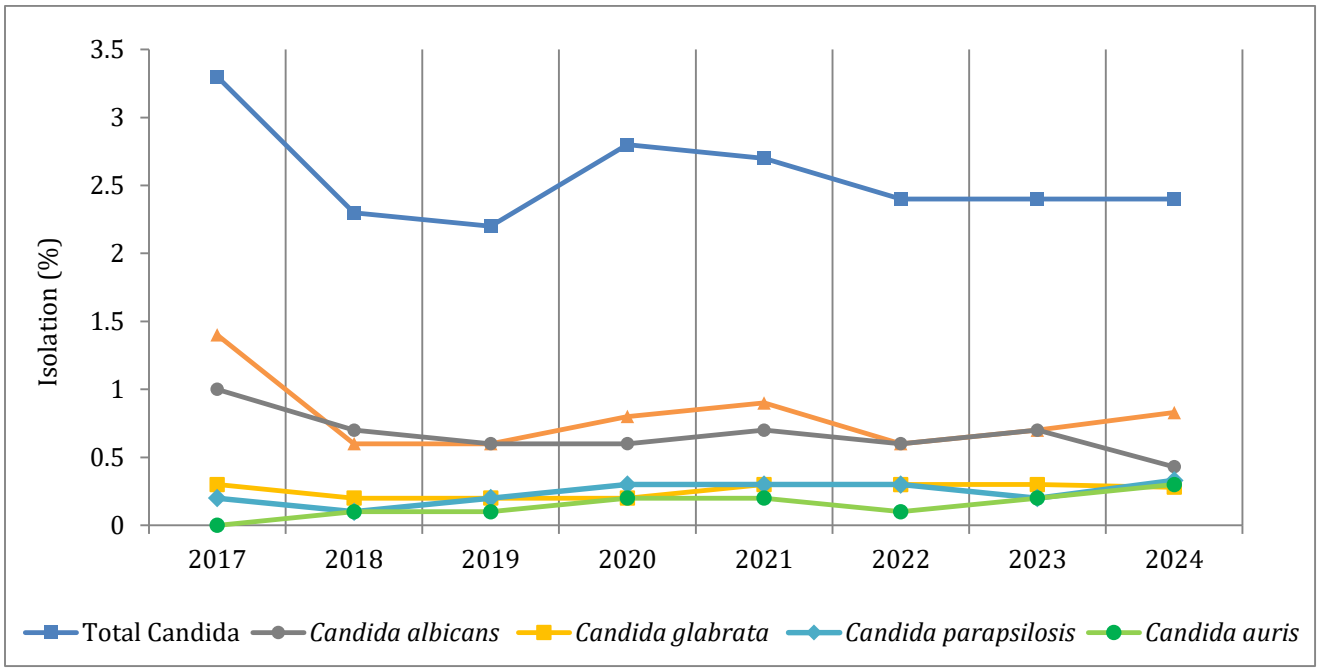


Figure 1.16: Yearly trends for isolation of *Candida* species isolated from all samples

Diarrheal pathogens

A total of 1086 diarrheal pathogen isolates were studied during the year 2024, which constituted 1.1% of total isolates **(Table 1.1)**. The predominant species among diarrheal pathogens isolated from the faeces sample was *Salmonella* spp. faecal (20.3%), followed by *Aeromonas* spp. (18.1%), diarrheagenic *Escherichia coli* (17.3%) and *Shigella sonnei* (8.9%) **(Table 1.24)**.

Table 1.24: Isolation rates of faecal isolates from faeces samples

Isolate	% Isolation from faecal isolates n(%)	% Isolation from total positive cultures n(%)
Salmonella spp. faecal	220 / 1086 (20.26)	220 / 99027 (0.22)
Aeromonas spp.	196 / 1086 (18.05)	256/ 99027 (0.25)
Diarrheagenic *Escherichia coli*	188 / 1086 (17.31)	188 / 99027 (0.19)
Shigella sonnei	97 / 1086 (8.93)	97 / 99027 (0.1)
Vibrio cholerae	91 / 1086 (8.38)	94 / 99027 (0.09)
Shigella flexneri	77 / 1086 (7.09)	77 / 99027 (0.07)
Shigella boydii	5 / 1086 (0.4)	5 /99027 (0.005)
Vibrio spp.	1/1086 (0.1)	1 /99027 (0.001)

Diarrheagenic pathogens were predominantly isolated from patients in OPD and wards **(Table 1.25** and **Figure 1.17)**. Diarrheagenic *Escherichia coli* was mainly isolated in OPD (30%), followed by the ward (8.97%), while *Vibrio cholerae* was predominant in the ICU (27.27%).

Table 1.25: Location-wise isolation pattern of the top 5 faecal isolates from faeces across OPD, Ward and ICU

Isolate	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Salmonella spp. faecal	220 / 1086 (20.26)	73 / 440 (16.59)	147 / 613 (23.98)	0 / 33 (0)
Aeromonas spp.	196 / 1086 (18.05)	96 / 440 (21.82)	100 / 613 (16.31)	0 / 33 (0)
Diarrheagenic *Escherichia coli*	188 / 1086 (17.31)	132 / 440 (30)	55 / 613 (8.97)	1 / 33 (3.03)
Shigella sonnei	97 / 1086 (8.93)	41 / 440 (9.32)	52 / 613 (8.48)	4 / 33 (12.12)
Vibrio cholerae	91 / 1086 (8.38)	8 / 440 (1.82)	74 / 613 (12.07)	9 / 33 (27.27)

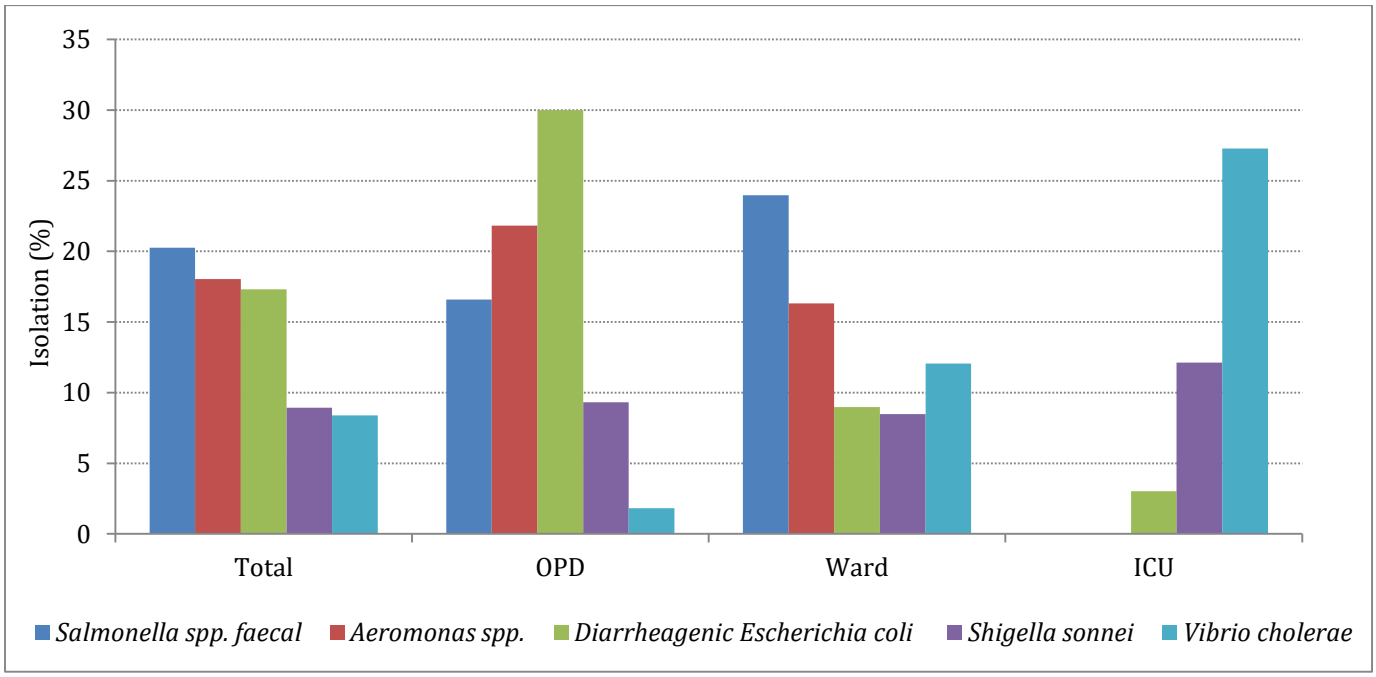


Figure 1.17: Location-wise isolation pattern of the top 5 faecal isolates from faeces across OPD, Ward and ICU

Yearly isolation trends showed a decline in isolation of *Salmonella* spp. faecal from 39.72% in 2023 to 20.26% in 2024. For *Aeromonas* spp., the isolation trend showed a steady decline from 26.1% in 2017 to 18.1% in 2024; however, an increase was observed in isolation rates of diarrheagenic *Escherichia coli* and *Shigella sonnei* in 2024 as compared to 2023. *V. cholerae* showed similar isolation percentages in 2023 and 2024. **(Table 1.26** and **Figure 1.18)**.

Table 1.26: Yearly isolation trends of the top 5 faecal isolates isolated from faeces

Isolate	Year-2017 n(%)	Year-2018 n(%)	Year-2019 n(%)	Year-2020 n(%)	Year-2021 n(%)	Year-2022 n(%)	Year-2023 n(%)	Year-2024 n(%)
Salmonella spp. faecal	20/501 (4)	39/621 (6.3)	60/1063 (5.6)	24/572 (4.2)	222/651 (34.1)	160/806 (34.1)	307 / 773 (39.72)	220 / 1086 (20.26)
Aeromonas spp.	131/ 501 (26.1)	114/ 621 (18.4)	170/10 63 (16)	77/ 572 (13.5)	179/ 651 (27.5)	164 / 806 (20.3)	181 / 773 (23.42)	196 / 1086 (18.05)
Diarrheagenic *Escherichia coli*	0/ 501 (0)	0/ 621 (0)	134/10 63 (12.6)	102/ 572 (17.8)	88/ 651 (13.5)	189 / 806 (23.4)	85 / 773 (10.99)	188 / 1086 (17.31)
Shigella sonnei	52 / 501 (10.4)	26/ 621 (4.2)	57/ 1063 (5.4)	14/ 572 (2.4)	41/ 651 (6.3)	39 / 806 (4.8)	15 / 773 (1.94)	97 / 1086 (8.93)
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 (8.02)	91 / 1086 (8.38)

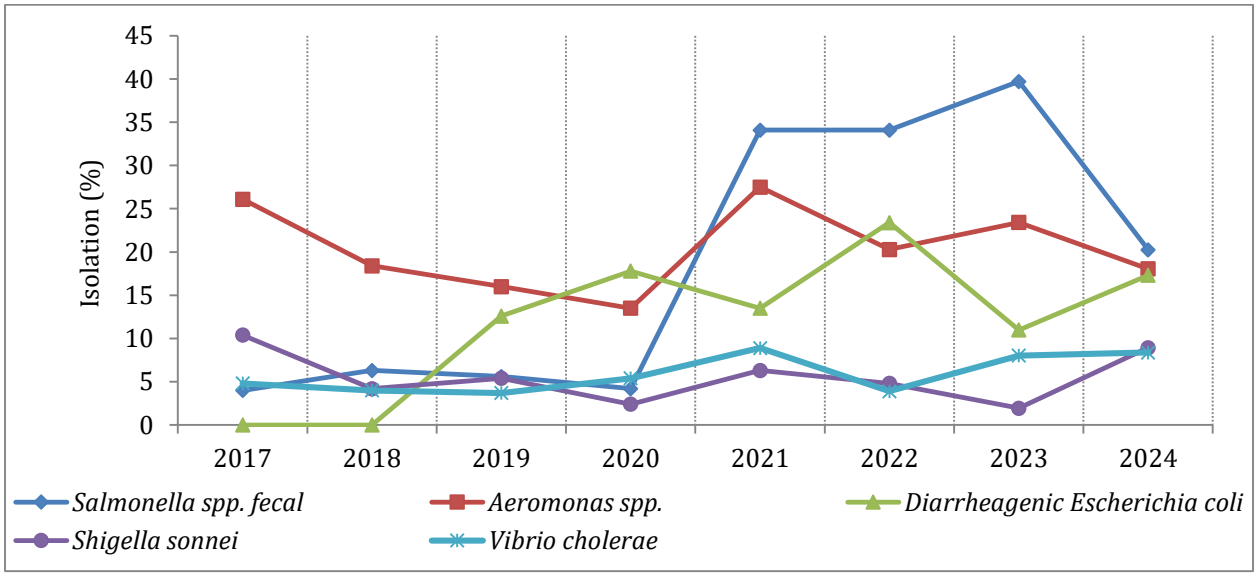


Figure 1.18: Yearly isolation trends of the top 5 faecal isolates isolated from faeces

Streptococcus species

The total number of *Streptococcus* isolates studied during the year 2024 was 534, of which 1.8% were isolated from the upper respiratory tract. The majority of the isolates were from *Streptococcus pneumoniae* (n=199), followed by *Streptococcus pyogenes* (n=193) *and Streptococcus agalactiae* (n=141) **(Table 1.27)**. Among clinical settings, *Streptococcus* isolates were common from OPD (0.7%), followed by ward and ICU **(Table 1.28** and **Figure 1.19)**.

Table 1.27: Sample-wise isolation pattern of *Streptococcus* species

Isolate	Total N=99027		Blood N=19027		Urine N=26562		LRT N=16327		SI N=13973		DI N=11858		CSF N=693		SS N=1994		Faeces N=1086	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Streptococcus	534 (0.5)	100	118 (0.6)	22.1	59 (0.2)	11	99 (0.6)	18.5	174 (1.2)	32.6	42 (0.4)	7.9	3 (0.4)	0.6	3 (0.2)	0.6	0 (0)	0
Streptococcus agalactiae	141 (0.1)	100	7 (0)	5	57 (0.2)	40.4	0 (0)	0	61 (0.4)	43.3	8 (0.1)	5.7	0 (0)	0	1 (0.1)	0.7	0 (0)	0
Streptococcus pneumoniae	199 (0.2)	100	74 (0.4)	37.2	2 (0)	1	96 (0.6)	48.2	11 (0.1)	5.5	4 (0)	2	3 (0.4)	1.5	2 (0.1)	1	0 (0)	0
Streptococcus pyogenes	193 (0.2)	100	36 (0.2)	18.7	0 (0)	0	3 (0)	1.6	102 (0.7)	52.8	30 (0.3)	15.5	0 (0)	0	0 (0)	0	0 (0)	0
Streptococcus viridans	1 (0)	-	1 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-

Table 1.28: Location-wise isolation pattern of *Streptococcus* isolated from all specimens across OPD, Ward and ICU

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
Streptococcus	534 / 99027 (0.54)	210 / 32729 (0.64)	259 / 48648 (0.53)	65 / 17650 (0.37)
Streptococcus agalactiae	141 / 99027 (0.14)	73 / 32729 (0.22)	63 / 48648 (0.13)	5 / 17650 (0.03)
Streptococcus pneumoniae	199 / 99027 (0.2)	66 / 32729 (0.2)	91 / 48648 (0.19)	42 / 17650 (0.24)
Streptococcus pyogenes	193 / 99027 (0.19)	71 / 32729 (0.22)	104 / 48648 (0.21)	18 / 17650 (0.1)
Streptococcus viridans	1 / 99027 (0)	0 / 32729 (0)	1 / 48648 (0)	0 / 17650 (0)

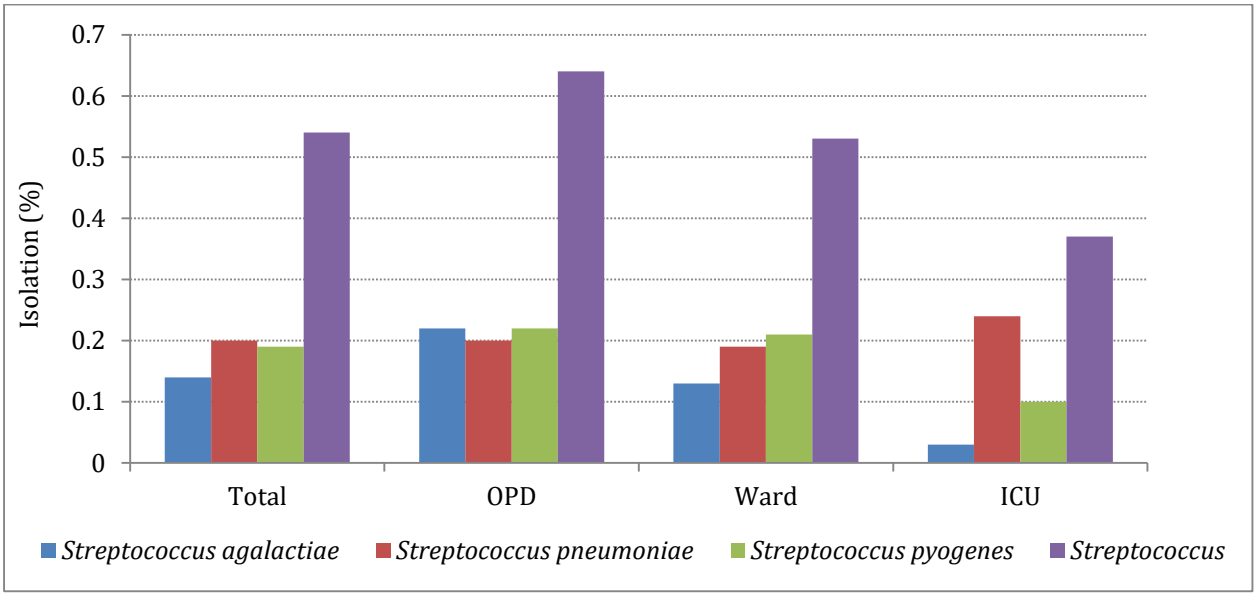


Figure 1.19: Location-wise isolation of *Streptococcus* species

Chapter 2. Enterobacterales

Significant clinical isolates belonging to various genera and species of Enterobacterales from all specimens (except urine and faeces) were tested for susceptibility to 10 antibiotics, including aminoglycosides (amikacin), cephalosporins (cefotaxime and ceftazidime), fluoroquinolones (ciprofloxacin and levofloxacin), beta-lactam and beta-lactamase inhibitor combination (piperacillin-tazobactam), carbapenems (imipenem, meropenem and ertapenem) and polymyxin (colistin).

The antimicrobial susceptibility profiles of Enterobacterales isolates shows extensive resistance among the major species, particularly *Escherichia coli* and *Klebsiella pneumoniae* **(Table 2.1)**. For *E. coli*, only 41.3% of isolates were susceptible to piperacillin-tazobactam, with even lower rates for third-generation cephalosporins such as cefotaxime (15.8%) and ceftazidime (27.5%), suggesting widespread extended-spectrum beta-lactamase (ESBL) production. Fluoroquinolone susceptibility was also very poor, with only 10.7% susceptible to ciprofloxacin and 15.8% to levofloxacin. Some activity was retained with carbapenems (57–63%), though resistance was still concerning. In contrast, high susceptibility was seen for amikacin (72.7%) and colistin (99.5%). *K. pneumoniae* showed an even more alarming resistance profile, as compared to *E. coli*, with only 26% susceptible to piperacillin-tazobactam, 20–24% to third-generation cephalosporins, and just 31–37% to carbapenems, highlighting a high prevalence of carbapenem-resistant strains. Fluoroquinolones were largely ineffective (20–25%), while amikacin susceptibility was limited to 40%. Colistin, however, remained highly effective, with 96.1% of isolates susceptible.

Other Enterobacterales species showed variable patterns. *Proteus mirabilis* retained higher susceptibility to most drugs, demonstrating 80% susceptibility to piperacillin-tazobactam and carbapenems (meropenem and ertapenem). Similarly, *Morganella morganii* and *Citrobacter koseri* demonstrated better responses to carbapenems (65–85%) and amikacin (>78%). *Proteus, Providencia* and *Morganella* spp. may have elevated minimum inhibitory concentrations (MICs) to imipenem by mechanisms other than by 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 (59–74%) and colistin (93-100%). In contrast, *Providencia stuartii* and *Providencia rettgeri* were highly resistant, with less than one-third of isolates susceptible to most agents, though amikacin (29–68%) retained partial activity.

Overall, the data reveal that *E. coli* and *K. pneumoniae* are the most resistant species, with severely compromised activity of cephalosporins, carbapenems, and fluoroquinolones, leaving colistin and, to some extent, amikacin as the most reliable therapeutic options. Other Enterobacterales species show a more favourable profile, but emerging resistance trends across the group underscore the urgent need for continued surveillance and antimicrobial stewardship.

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

AMA	*E. coli*	*K. pneumoniae*	*K. oxytoca*	*K. (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=12445	N=12517	N=352	N=62	N=132	N=1306	N=229	N=1417	N=374	N=102	N=126	N=459	N=454	N=186	N=88
Piperacillin-tazobactam	4818/11679 (41.3)	3024/11650 (26)	125/345 (36.2)	38/56 (67.9)	31/132 (23.5)	670/1213 (55.2)	82/199 (41.2)	1030/1258 (81.9)	204/338 (60.4)	36/92 (39.1)	59/122 (48.4)	205/291 (70.4)	330/394 (83.8)	59/135 (43.7)	36/68 (52.9)
Cefotaxime	1629/10279 (15.8)	2038/10032 (20.3)	103/319 (32.3)	30/44 (68.2)	56/132 (42.4)	445/1078 (41.3)	42/179 (23.5)	473/1140 (41.5)	173/319 (54.2)	32/83 (38.6)	41/116 (35.3)	183/346 (52.9)	170/352 (48.3)	26/140 (18.6)	23/62 (37.1)
Ceftazidime	1237/4500 (27.5)	1280/5404 (23.7)	84/262 (32.1)	2/6 (-)	58/123 (47.2)	209/465 (44.9)	32/100 (32)	167/391 (42.7)	93/187 (49.7)	25/51 (49)	11/24 (-)	67/123 (54.5)	78/121 (64.5)	8/63 (12.7)	10/19 (-)
Ertapenem	6457/10484 (61.6)	3762/10212 (36.8)	175/324 (54)	48/55 (87.3)	79/129 (61.2)	638/976 (65.4)	95/161 (59)	683/877 (77.9)	222/314 (70.7)	56/77 (72.7)	61/102 (59.8)	250/316 (79.1)	236/275 (85.8)	24/79 (30.4)	27/49 (55.1)
Imipenem	6715/11662 (57.6)	3634/11641 (31.2)	147/333 (44.1)	49/56 (87.5)	79/129 (61.2)	730/1221 (59.8)	104/198 (52.5)	331/1191 (27.8)	219/333 (65.8)	42/89 (47.2)	63/126 (50)	250/381 (65.6)	64/344 (18.6)	13/140 (9.3)	14/65 (21.5)
Meropenem	7594/12075 (62.9)	4283/12216 (35.1)	211/346 (61)	51/57 (89.5)	83/132 (62.9)	810/1252 (64.7)	123/206 (59.7)	966/1322 (73.1)	263/345 (76.2)	67/97 (69.1)	75/126 (59.5)	336/434 (77.4)	352/425 (82.8)	63/176 (35.8)	38/81 (46.9)
Colistin*	6046/6076 (99.5)	6834/7112 (96.1)	235/236 (99.6)	33/33 (100.0)	7/7 (-)	661/710 (93.1)	62/63 (98.4)	-	137/137 (100.0)	64/64 (100.0)	37/37 (100.0)	-	-	-	-
Amikacin	9045/12445 (72.7)	5006/12517 (40.0)	227/352 (64.5)	52/62 (83.9)	78/132 (59.1)	890/1306 (68.1)	151/229 (65.9)	743/1417 (52.4)	293/374 (78.3)	76/102 (74.5)	77/126 (61.1)	356/459 (77.6)	372/454 (81.9)	54/186 (29.0)	60/88 (68.2)
Ciprofloxacin	1320/12386 (10.7)	2506/12299 (20.4)	135/352 (38.4)	47/62 (75.8)	67/132 (50.8)	637/1298 (49.1)	105/226 (46.5)	414/1405 (29.5)	220/372 (59.1)	38/102 (37.3)	40/126 (31.7)	305/448 (68.1)	140/454 (30.8)	45/179 (25.1)	39/87 (44.8)
Levofloxacin	676/4269 (15.8)	1271/5118 (24.8)	88/253 (34.8)	5/6 (-)	66/122 (54.1)	206/381 (54.1)	54/86 (62.8)	105/400 (26.3)	95/185 (51.4)	20/38 (52.6)	11/15 (-)	83/133 (62.4)	34/103 (33)	11/65 (16.9)	7/16 (-)

* Colistin represents the percentage of intermediate susceptibility

Escherichia coli

Overall, of the total 12,445 *E. coli* isolates, 62.0% were from wards, 23.3% from OPDs, and 14.7% from ICUs **(Table 2.2)**. For piperacillin-tazobactam, the overall susceptibility rate was 41.3%, with OPD isolates showing higher susceptibility (48.7%) compared to ward (40.1%) and ICU (35%). Among carbapenems, meropenem exhibited the highest susceptibility at 62.9% overall, with 64.8% in OPD, 63.3% in wards, and 58.2% in ICU. Ertapenem and imipenem demonstrated slightly lower activity, with overall susceptibility rates of 61.6% and 57.6%, respectively, again indicating reduced activity in ICU isolates. Colistin remained highly effective, with near-universal susceptibility of 99.5% overall, ranging from 99.4% in the ward to 99.6% in OPD and ICU. Amikacin also retained good activity, with 72.7% overall susceptibility, highest in OPD (74.8%) and lowest in ICU (68.5%).

In contrast, third-generation cephalosporins and fluoroquinolones showed poor activity. Cefotaxime and ceftazidime susceptibility rates were 15.8% and 27.5% respectively, overall, with ICU isolates showing the lowest rates (13.5% and 18.9% respectively). Fluoroquinolones were largely ineffective, with overall susceptibility rates of 10.7% for ciprofloxacin and 15.8% for levofloxacin, both falling below 20% across all settings.

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=12445	OPD N=2904	Ward N=7717	ICU N=1824
	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	4818 / 11679 (41.3)	1310 / 2692 (48.7)	2872 / 7169 (40.1)	636 / 1818 (35)
Cefotaxime	1629 / 10279 (15.8)	491 / 2443 (20.1)	935 / 6330 (14.8)	203 / 1506 (13.5)
Ceftazidime	1237 / 4500 (27.5)	337 / 1150 (29.3)	774 / 2682 (28.9)	126 / 668 (18.9)
Ertapenem	6457 / 10484 (61.6)	1731 / 2540 (68.1)	3877 / 6382 (60.7)	849 / 1562 (54.4)
Imipenem	6715 / 11662 (57.6)	1575 / 2681 (58.7)	4175 / 7174 (58.2)	965 / 1807 (53.4)
Meropenem	7594 / 12075 (62.9)	1800 / 2776 (64.8)	4724 / 7460 (63.3)	1062 / 1824 (58.2)
Colistin*	6046 / 6076 (99.5)	1289 / 1294 (99.6)	3620 / 3641 (99.4)	1137 / 1141 (99.6)
Amikacin	9045 / 12445 (72.7)	2173 / 2904 (74.8)	5600 / 7717 (72.6)	1249 / 1824 (68.5)
Ciprofloxacin	1320 / 12386 (10.7)	378 / 2885 (13.1)	755 / 7650 (9.9)	179 / 1824 (9.8)
Levofloxacin	676 / 4269 (15.8)	177 / 1127 (15.7)	397 / 2525 (15.7)	102 / 617 (16.5)

*Colistin represents the percentage of intermediate 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 and infection control practices, especially for ICUs.

Klebsiella pneumoniae

Overall, of the total 12,517 *K. pneumoniae* isolates, 52.9% were from wards, 27.8% from ICUs, and 19.3% from OPDs **(Table 2.3)**. The resistance profile of *K. 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, with only 26% of the isolates susceptible. Third-generation cephalosporins showed similar activity, with cefotaxime susceptibility as low as 12.6% in ICU isolates and 20–32% in other settings, while ceftazidime susceptibility fell to under 9% in ICU isolates. Resistance to carbapenems was pronounced, with only 33–37% susceptibility in ward isolates and even lower rates in ICU (ertapenem 25.4%, imipenem 22%, and meropenem 24.2%). Even in OPD isolates, carbapenem susceptibility did not exceed 52.7% for ertapenem and remained below 50% for meropenem and imipenem, highlighting the heavy burden of carbapenem resistance. Among fluoroquinolones, ciprofloxacin and levofloxacin susceptibility was low in ICU isolates (nearly 13%) and 20–35% in other settings. Aminoglycoside resistance was notable, with amikacin susceptibility limited to 40% overall and falling to 28.2% among ICU isolates. Colistin remained the only consistently effective option, with susceptibility rates exceeding 94% across all locations, although its use is limited by concerns over toxicity.

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=12517 (S%)	OPD N=2415 (S%)	Ward N=6624 (S%)	ICU N=3478 (S%)
Piperacillin-tazobactam	3024 / 11650 (26)	851 / 2191 (38.8)	1558 / 6014 (25.9)	615 / 3445 (17.9)
Cefotaxime	2038 / 10032 (20.3)	634 / 1991 (31.8)	1049 / 5229 (20.1)	355 / 2812 (12.6)
Ceftazidime	1280 / 5404 (23.7)	364 / 1108 (32.9)	772 / 2673 (28.9)	144 / 1623 (8.9)
Ertapenem	3762 / 10212 (36.8)	1076 / 2040 (52.7)	1965 / 5332 (36.9)	721 / 2840 (25.4)
Imipenem	3634 / 11641 (31.2)	922 / 2172 (42.4)	1951 / 6010 (32.5)	761 / 3459 (22)
Meropenem	4283 / 12216 (35.1)	1119 / 2277 (49.1)	2314 / 6434 (36)	843 / 3477 (24.2)
Colistin*	6834 / 7112 (96.1)	1352 / 1369 (98.7)	3224 / 3351 (96.2)	2258 / 2392 (94.4)

Amikacin	5006 / 12517 (40.0)	1352 / 2415 (56)	2661 / 6624 (40.2)	981 / 3478 (28.2)
Ciprofloxacin	2506 / 12299 (20.4)	736 / 2355 (31.3)	1308 / 6438 (20.3)	458 / 3477 (13.2)
Levofloxacin	1271 / 5118 (24.8)	392 / 1108 (35.4)	695 / 2606 (26.7)	183 / 1399 (13.1)

* Colistin represents the percentage of intermediate susceptibility

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

Enterobacter cloacae

Overall, of the total 1,306 *E. cloacae* isolates, 25.9% were from OPD, 57.1% from wards, and 17.0% from ICU **(Table 2.4)**. *E. cloacae* demonstrated a decline in susceptibility among ICU isolates. Susceptibility to piperacillin-tazobactam was only 46.6% in the ICU. Resistance to third-generation cephalosporins was significant, with fewer than 40% of the ICU isolates susceptible to cefotaxime (35.1%) and ceftazidime (31%). Carbapenem resistance was also evident, with ertapenem, imipenem, and meropenem susceptibility ranging nearly 50% in ICU isolates. Among other agents, amikacin showed the highest retained activity, with an overall susceptibility rate of 68.1%, but lower in ICU isolates (52.3%). Resistance to fluoroquinolones was widespread, with ciprofloxacin susceptibility of 44.1% and levofloxacin susceptibility of 49.4% among ICU isolates. Overall, *E. cloacae* isolates showed good susceptibility to colistin **(Table 2.1)**.

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=1306 (S%)	OPD N=338 (S%)	Ward N=746 (S%)	ICU N=222 (S%)
Piperacillin-tazobactam	670 / 1213 (55.2)	210 / 308 (68.2)	358 / 686 (52.2)	102 / 219 (46.6)
Cefotaxime	445 / 1078 (41.3)	145 / 276 (52.5)	233 / 611 (38.1)	67 / 191 (35.1)
Ceftazidime	209 / 465 (44.9)	55 / 87 (63.2)	123 / 278 (44.2)	31 / 100 (31)
Ertapenem	638 / 976 (65.4)	207 / 259 (79.9)	349 / 560 (62.3)	82 / 157 (52.2)
Imipenem	730 / 1221 (59.8)	225 / 310 (72.6)	401 / 689 (58.2)	104 / 222 (46.8)
Meropenem	810 / 1252 (64.7)	248 / 311 (79.7)	449 / 718 (62.5)	113 / 222 (50.9)
Amikacin	890 / 1306 (68,1)	279 / 338 (82.5)	493 / 744 (66.3)	116 / 222 (52.3)
Ciprofloxacin	637 / 1298 (49.1)	195 / 335 (58.2)	342 / 738 (46.3)	98 / 222 (44.1)
Levofloxacin	206 / 381 (54.1)	38 / 68 (55.9)	129 / 234 (55.1)	39 / 79 (49.4)

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

Citrobacter koseri

Overall, of the total 374 *C. koseri* isolates, 28.9% were from OPD, 50.0% from wards, and 21.1% from ICU **(Table 2.5)**. These isolates showed comparatively lower resistance than other Enterobacterales, except for the ICU isolates, which demonstrated a high resistance rate. Piperacillin-tazobactam susceptibility was 60.4% overall, but only 44.9% of the ICU isolates were susceptible. Third-generation cephalosporins had reduced activity, with cefotaxime susceptibility 28.9% and ceftazidime 31.7% in ICU isolates. Carbapenems retained reasonable activity, though resistance was notable in ICU cases, whereas the ertapenem, imipenem, and meropenem susceptibility declined to 50.7%, 41%, and 54.4%, respectively. Among other agents, amikacin remained the most reliable option with 78.3% overall susceptibility. Fluoroquinolone resistance in the ICU isolates was also evident, with ciprofloxacin and levofloxacin susceptibility being less than 40%, i.e., 39.2% and 38.7% respectively.

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= 374 (S%)	OPD N= 108 (S%)	Ward N= 187 (S%)	ICU N=79 (S%)
Piperacillin-tazobactam	204 / 338 (60.4)	71 / 91 (78)	98 / 169 (58)	35 / 78 (44.9)
Cefotaxime	173 / 319 (54.2)	65 / 82 (79.3)	86 / 161 (53.4)	22 / 76 (28.9)
Ceftazidime	93 / 187 (49.7)	28 / 38 (73.7)	46 / 89 (51.7)	19 / 60 (31.7)
Ertapenem	222 / 314 (70.7)	74 / 83 (89.2)	111 / 158 (70.3)	37 / 73 (50.7)
Imipenem	219 / 333 (65.8)	73 / 90 (81.1)	114 / 165 (69.1)	32 / 78 (41)
Meropenem	263 / 345 (76.2)	83 / 92 (90.2)	135 / 172 (78.5)	43 / 79 (54.4)
Amikacin	293 / 374 (78.3)	96 / 108 (88.9)	146 / 187 (78.1)	48 / 79 (60.8)
Ciprofloxacin	220 / 372 (59.1)	79 / 105 (75.2)	108 / 186 (58.1)	31 / 79 (39.2)
Levofloxacin	95 / 185 (51.4)	31 / 38 (81.6)	39 / 84 (46.4)	24 / 62 (38.7)

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

Yearly susceptibility trends of different Enterobacterales

Analysis of surveillance data from 2017 to 2024 reveals a progressive decline in antimicrobial susceptibility across the major Enterobacterales species (*E. coli, K. pneumoniae, Enterobacter* spp., and *Citrobacter* spp.) **(Tables 2.6–2.9, Figures 2.1–2.4)**.

Escherichia coli

Over the last eight years (2017–2024), *E. coli* isolates demonstrated a steady decline in susceptibility across most antibiotics. Susceptibility to piperacillin-tazobactam fell from 56.8% in 2017 to 41.3% in 2024 **(Figure 2.1, Table 2.6)**. Third-generation cephalosporins remained largely ineffective, with cefotaxime susceptibility fluctuating between 14% and 18%, and ceftazidime susceptibility remaining below 30% throughout the period from 23.5% in 2017 to 27.5% in 2024. Carbapenem susceptibility showed a concerning decline. Imipenem susceptibility dropped from 81.4% in 2017 to 57.6% in 2024, while meropenem susceptibility decreased from 73.2% to 62.9% over the same period. Ertapenem susceptibility declined from 67.4% in 2017 to 61.6% in 2024. Amikacin continues as one of the more reliable treatment options. Fluoroquinolones showed persistently poor activity, with ciprofloxacin susceptibility decreasing from 19.2% in 2017 to 10.6% in 2024 and levofloxacin susceptibility remaining below 20% throughout.

In summary, a progressive decline in susceptibility to carbapenems and fluoroquinolones among *E. coli* has been seen over the last eight years, leaving amikacin as the most effective therapeutic option.

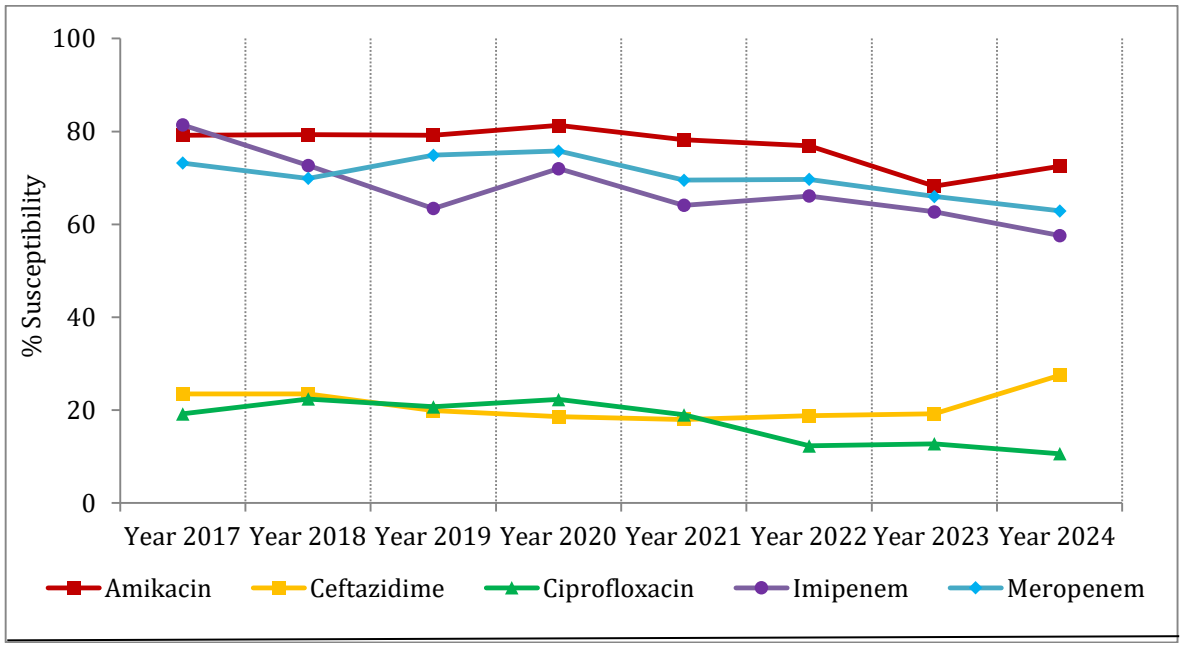


Figure 2.1: Yearly susceptibility trend of *E. coli* isolated from all samples (except faeces and urine)

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
	N=6282	N=9187	N=13133	N=8198	N=13533	N=14728	N=13026	N=12445
	(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)
Cefazolin	*0/8 (-)	*2/6 (-)	*0/1 (-)	*0/4 (-)	*0/1 (-)	5/22 (22.7)	8 / 18 (-)	21 / 94 (22.3)
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)
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)
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)
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)
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)
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)
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)
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)

Klebsiella pneumoniae

Over the last eight years (2017–2024), *K. pneumoniae* isolates documented a decline in susceptibility across most of the antibiotic classes **(Figure 2.2, Table 2.7)**. Susceptibility to piperacillin-tazobactam dropped from 42.6% in 2017 to 26.0% in 2024, and remained consistently below 30% for third-generation cephalosporins (cefotaxime fell from 21.8% in 2017 to 20.3% in 2024, and ceftazidime decreased from 27.6% to 23.7%). Among the carbapenems, imipenem susceptibility declined from 58.5% in 2017 to 31.2% in 2024, while meropenem dropped from 48.1% to 35.1%. Ertapenem showed a similar downward trend from 45.4% in 2017 to 36.8% in 2024. Amikacin retained better activity than β-lactams but still declined from 48.9% in 2017 to 39.9% in 2024. Fluoroquinolone susceptibility remained low throughout the period, with ciprofloxacin decreasing from 32% to 20.4% and levofloxacin from 28.3% to 24.8%.

In summary, *K. pneumoniae* has demonstrated a marked rise in resistance over the last eight years, particularly to carbapenems and β-lactam agents.

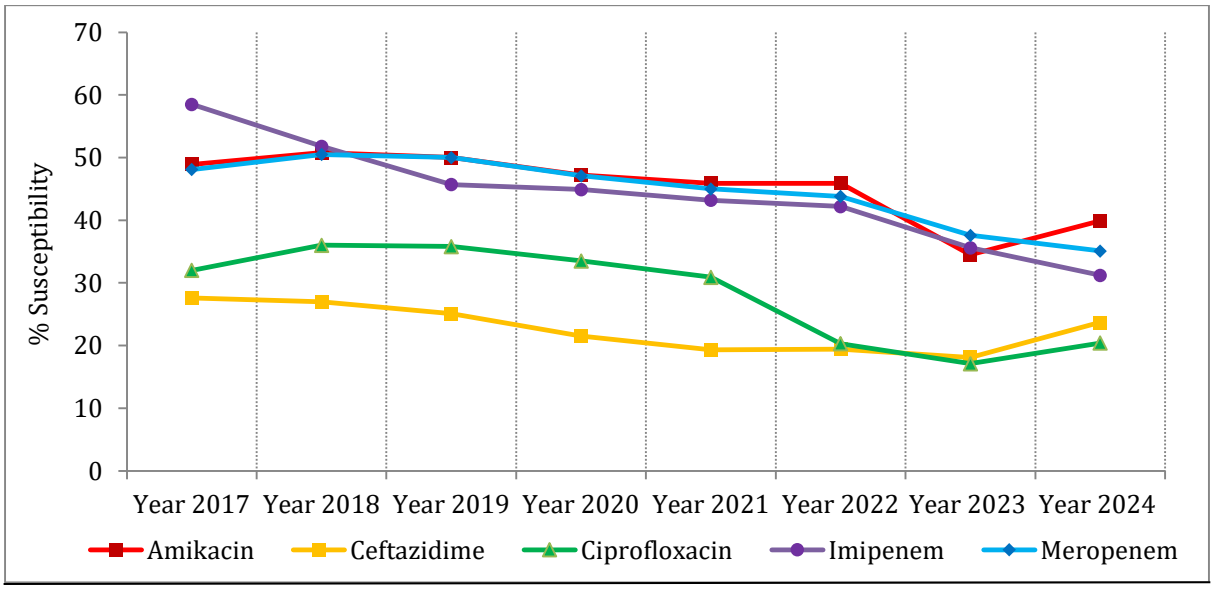


Figure 2.2: Yearly susceptibility trend of *K. pneumoniae* isolated from all samples (except faeces and urine)

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
	N=5389	N=8394	N=13381	N=8932	N=13633	N=15008	N=12795	N=12517
	(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)
Cefazolin	*0/3 (-)	*0/0 (-)	*0/1 (-)	*0/3 (-)	*1/3 (-)	5/16 (31.3)	*2 / 12 (-)	12 / 36 (33.3)
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)
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)
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)
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)
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)
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)
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)
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)

Enterobacter species

Over the last eight years (2017–2024), *Enterobacter* species showed fluctuating but overall declining susceptibility trends across multiple antibiotics **(Figure 2.3, Table 2.8)**. Piperacillin-tazobactam susceptibility remained around 61–66% until 2021 but declined sharply in recent years, reaching 41.2% in 2024. Resistance towards third-generation cephalosporins increased, with cefotaxime susceptibility declining from 28.4% in 2017 to 23.5% in 2024, and ceftazidime susceptibility decreasing from 35.8% to 32% over the same period. Carbapenems continued to be the most active agents against *Enterobacter* species; however, a progressive decline in susceptibility was observed over the period. Imipenem susceptibility decreased from 75.1% in 2017 to 52.5% in 2024, while meropenem declined from 69.9% to 59.7%. Ertapenem showed a comparable reduction, falling from 66% in 2017 to 59% in 2024. Amikacin remained the most effective non-carbapenem agent, though its activity also demonstrated a slight downward trend, with susceptibility decreasing from 69.3% in 2017 to 65.9% in 2024. Resistance to fluoroquinolones persisted at high levels throughout, with ciprofloxacin susceptibility declining from 53.1% in 2017 to 46.5% in 2024. Levofloxacin demonstrated fluctuating activity but remained suboptimal, with susceptibility of 62.8% in 2024.

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.

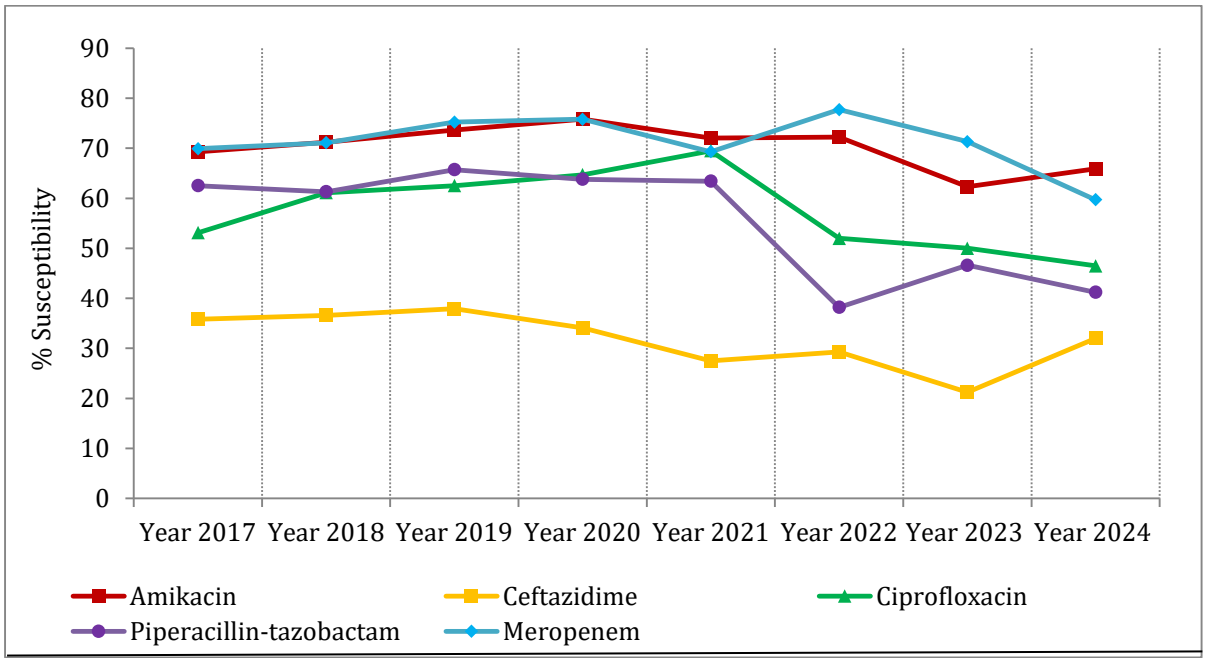


Figure 2.3: Yearly susceptibility trend of *Enterobacter* species isolated from all samples (except faeces and urine)

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
	N=1140	N=1600	N=2071	N=1287	N=393	N=324	N=194	N=229
	(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)
Cefazolin	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0 / 0 (-)	*0 / 0 (-)
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)
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)
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)
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)
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)
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)
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)
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)

Citrobacter species

Citrobacter species demonstrated variable but overall declining susceptibility across most antibiotics **(Figure 2.4, Table 2.9)**. Susceptibility to piperacillin-tazobactam reduced from 57.8% in 2017 to 48.4% in 2024. Third-generation cephalosporins showed consistently poor activity, with susceptibility to cefotaxime remaining low (30.7% in 2017 to 35.3% in 2024). Carbapenems retained moderate activity, though their susceptibility showed a gradual reduction over time. Imipenem susceptibility declined from 65.3% in 2017 to 50.0% in 2024, while susceptibility for meropenem decreased from 65.8% to 59.5%. Similarly, susceptibility for ertapenem decreased from 61.2% in 2017 to 59.8% in 2024. Amikacin remained the most reliable agent, although with a decline in susceptibility from 66.7% in 2017 to 61.1% in 2024. In contrast, fluoroquinolone resistance was sustained at high levels, with ciprofloxacin susceptibility declining from 46.8% in 2017 to 31.8% in 2024.

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 the narrowing of treatment options.

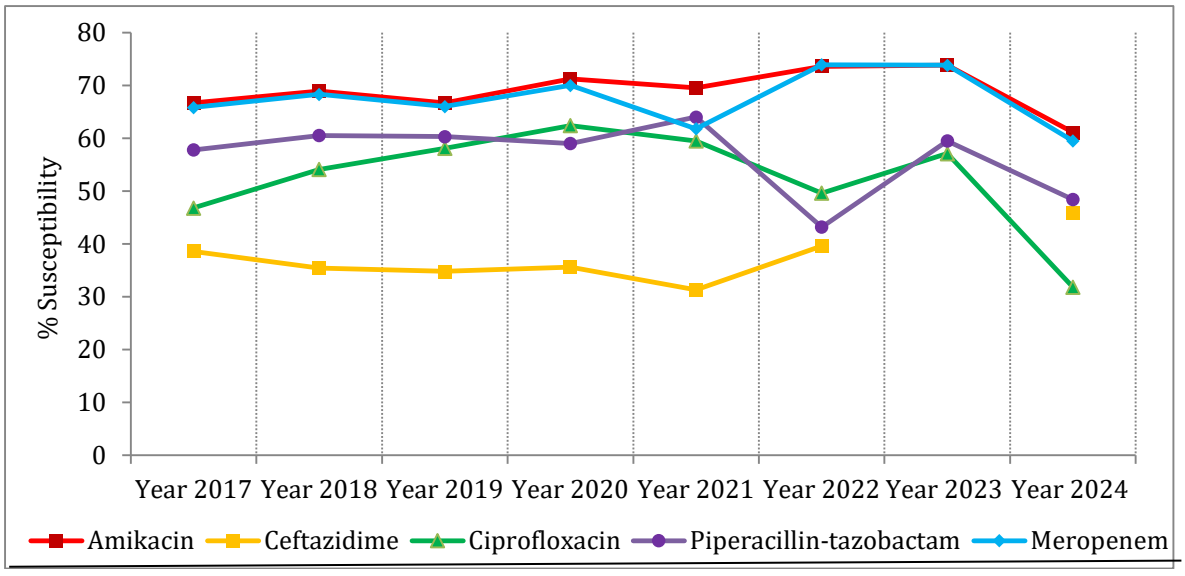


Figure 2.4: Yearly susceptibility trend of *Citrobacter* species isolated from all samples (except faeces and urine)

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
	N=321	N=613	N=796	N=447	N=136	N=139	N=77	N=126
	(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)
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)
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 (-)
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)
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)
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)
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)
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)
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 (41.6)	*11 / 15 (-)

Analysis of results from individual Regional Centres (RCs)

Twenty-one regional centres (RCs) from different parts of the country, representing both public and private sectors, contributed isolates for the surveillance. While overall susceptibility analysis included results from all centres 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 RCs, *E. coli* isolates demonstrated consistently low susceptibility to third-generation cephalosporins and fluoroquinolones, while moderate activity was retained with carbapenems and amikacin, and near-complete susceptibility persisted with colistin **(Table 2.10)**. Overall susceptibility was 41% to piperacillin-tazobactam, 16–28% to cephalosporins, 58–63% to carbapenems, 73% to amikacin, and <20% to fluoroquinolones. Most RCs mirrored this resistant profile, though RC3, RC8 and RC10 reported higher carbapenem susceptibility (~79–85%), and high amikacin (≥88%) susceptibility was reported in RC5 and RC8. In contrast, RC2, RC11, RC12, RC13, RC16, RC19 and RC21 showed markedly low susceptibility for multiple antimicrobial agents.

K. pneumoniae

K. pneumoniae isolates across RCs showed very low susceptibility, with national rates of 26% for piperacillin-tazobactam, 20–24% for cephalosporins, 31–37% for carbapenems, 40% for amikacin, and <25% for fluoroquinolones **(Table 2.11)**. Most RCs reported uniformly high resistance, but RC3, RC5, and RC10 demonstrated comparatively higher susceptibility for carbapenems (>60%) and aminoglycosides (53–69%). In contrast, RC6, RC11, RC12, RC13, RC16, RC17, RC19 and RC21 exhibited near-complete resistance across all drug classes.

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

RC	Piperacillin-tazobactam (N=11679)	Cefotaxime (N=10279)	Ceftazidime (N=4500)	Ertapenem (N=10484)	Imipenem (N=11662)	Meropenem (N=12061)	Amikacin (N=12445)	Ciprofloxacin (N=12361)	Levofloxacin (N=4269)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	0 / 11 (-)	2 / 11 (-)	4 / 11 (-)	6 / 11 (-)	5 / 11 (-)	6 / 11 (-)	5 / 11 (-)	1 / 11 (-)	4 / 11 (-)
RC2	1491 / 3994 (37.3)	334 / 4022 (8.3)	130 / 382 (34.0)	1495 / 3047 (49.1)	1858 / 4040 (46.0)	2212 / 4041 (54.7)	2763 / 4041 (68.4)	270 / 4041 (6.7)	9 / 81 (11.1)
RC3	138 / 490 (28.2)	100 / 492 (20.3)	105 / 492 (21.3)	409 / 492 (83.1)	405 / 491 (82.5)	406 / 492 (82.5)	256 / 492 (52.0)	125 / 492 (25.4)	136 / 491 (27.7)
RC4	0 / 0 (-)	0 / 0 (-)	0 / 1 (-)	0 / 0 (-)	0 / 0 (-)	126 / 317 (39.7)	543 / 714 (76.1)	153 / 626 (24.4)	18 / 88 (20.5)
RC5	325 / 537 (60.5)	4 / 516 (0.8)	0 / 1 (-)	391 / 536 (72.9)	428 / 537 (79.7)	428 / 537 (79.7)	474 / 537 (88.3)	52 / 537 (9.7)	0 / 0 (-)
RC6	329 / 753 (43.7)	0 / 1 (-)	0 / 0 (-)	465 / 753 (61.8)	510 / 751 (67.9)	514 / 753 (68.3)	561 / 753 (74.5)	10 / 753 (1.3)	0 / 9 (-)
RC7	160 / 296 (54.1)	12 / 72 (16.7)	18 / 88 (20.5)	196 / 291 (67.4)	206 / 289 (71.3)	218 / 302 (72.2)	251 / 303 (82.8)	17 / 302 (5.6)	6 / 69 (8.7)
RC8	378 / 582 (64.9)	185 / 585 (31.6)	202 / 583 (34.6)	461 / 583 (79.1)	490 / 582 (84.2)	492 / 585 (84.1)	519 / 585 (88.7)	44 / 587 (7.5)	55 / 584 (9.4)
RC9	234 / 383 (61.1)	108 / 381 (28.3)	132 / 380 (34.7)	245 / 372 (65.9)	219 / 382 (57.3)	300 / 383 (78.3)	316 / 383 (82.5)	94 / 383 (24.5)	110 / 371 (29.6)
RC10	576 / 1040 (55.4)	326 / 1050 (31.0)	0 / 0 (-)	847 / 1050 (80.7)	893 / 1050 (85.0)	877 / 1050 (83.5)	731 / 1051 (69.6)	142 / 1051 (13.5)	0 / 0 (-)

RC11	88 / 317 (27.8)	37 / 317 (11.7)	46 / 317 (14.5)	111 / 248 (44.8)	156 / 318 (49.1)	165 / 318 (51.9)	207 / 317 (65.3)	40 / 317 (12.6)	43 / 316 (13.6)
RC12	61 / 181 (33.7)	6 / 112 (5.4)	34 / 172 (19.8)	103 / 179 (57.5)	97 / 180 (53.9)	107 / 181 (59.1)	114 / 181 (63.0)	10 / 181 (5.5)	20 / 176 (11.4)
RC13	9 / 56 (16.1)	0 / 33 (0)	2 / 17 (-)	0 / 3 (-)	18 / 56 (32.1)	21 / 59 (35.6)	16 / 59 (27.1)	4 / 59 (6.8)	0 / 17 (-)
RC14	345 / 622 (55.5)	121 / 622 (19.5)	0 / 0 (-)	436 / 620 (70.3)	482 / 621 (77.6)	479 / 622 (77.0)	526 / 622 (84.6)	46 / 622 (7.4)	1 / 2 (-)
RC16	53 / 548 (9.7)	50 / 547 (9.1)	67 / 548 (12.2)	232 / 546 (42.5)	123 / 482 (25.5)	328 / 549 (59.7)	397 / 549 (72.3)	83 / 549 (15.1)	123 / 547 (22.5)
RC17	94 / 400 (23.5)	22 / 56 (39.3)	13 / 62 (21.0)	236 / 395 (59.7)	260 / 400 (65.0)	260 / 401 (64.8)	309 / 401 (77.1)	86 / 401 (21.4)	23 / 66 (34.8)
RC18	7 / 19 (-)	5 / 18 (-)	0 / 0 (-)	0 / 0 (-)	12 / 18 (-)	13 / 19 (-)	13 / 19 (-)	3 / 19 (-)	0 / 0 (-)
RC19	208 / 584 (35.6)	38 / 584 (6.5)	69 / 584 (11.8)	253 / 584 (43.3)	1 / 584 (0.2)	14 / 584 (2.4)	375 / 584 (64.2)	26 / 584 (4.5)	7 / 583 (1.2)
RC20	283 / 699 (40.5)	273 / 697 (39.2)	404 / 695 (58.1)	541 / 699 (77.4)	467 / 699 (66.8)	553 / 699 (79.1)	586 / 699 (83.8)	100 / 699 (14.3)	106 / 697 (15.2)
RC21	39 / 167 (23.4)	6 / 163 (3.7)	11 / 167 (6.6)	30 / 75 (40.0)	85 / 171 (49.7)	75 / 172 (43.6)	83 / 172 (48.3)	14 / 172 (8.1)	15 / 161 (9.3)
Total	4818 / 11679 (41.3)	1629 / 10279 (15.8)	1237 / 4500 (27.5)	6457 / 10484 (61.6)	6715 / 11662 (57.6)	7594 / 12061 (62.9)	9045 / 12445 (72.7)	1320 / 12361 (10.7)	676 / 4269 (15.8)

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

RC	Piperacillin-tazobactam (N=11650)	Cefotaxime (N=10032)	Ceftazidime (N=5404)	Ertapenem (N=10212)	Imipenem (N=11641)	Meropenem (N=12189)	Amikacin (N=12517)	Ciprofloxacin (N=12271)	Levofloxacin (N=5113)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)	0 / 10 (-)
RC2	618 / 3283 (18.8)	298 / 3341 (8.9)	67 / 730 (9.2)	561 / 2276 (24.6)	688 / 3341 (20.6)	849 / 3341 (25.4)	1028 / 3341 (30.8)	378 / 3341 (11.3)	32 / 216 (14.8)
RC3	57 / 240 (23.8)	111 / 240 (46.3)	113 / 240 (47.1)	147 / 240 (61.3)	149 / 240 (62.1)	153 / 240 (63.8)	134 / 240 (55.8)	116 / 240 (48.3)	120 / 240 (50.0)
RC4	0 / 0 (-)	0 / 0 (-)	2 / 3 (-)	0 / 0 (-)	0 / 0 (-)	64 / 466 (13.7)	350 / 799 (43.8)	182 / 548 (33.2)	104 / 250 (41.6)
RC5	277 / 511 (54.2)	70 / 499 (14.0)	0 / 0 (-)	332 / 511 (65.0)	330 / 508 (65.0)	336 / 511 (65.8)	350 / 511 (68.5)	187 / 511 (36.6)	0 / 0 (-)
RC6	195 / 1006 (19.4)	0 / 1 (-)	0 / 10 (-)	260 / 1007 (25.8)	269 / 1007 (26.7)	280 / 1007 (27.8)	308 / 1007 (30.6)	102 / 1007 (10.1)	2 / 32 (6.3)
RC7	84 / 314 (26.8)	17 / 70 (24.3)	15 / 78 (19.2)	85 / 305 (27.9)	90 / 308 (29.2)	103 / 321 (32.1)	113 / 321 (35.2)	54 / 321 (16.8)	5 / 64 (7.8)
RC8	355 / 696 (51.0)	271 / 697 (38.9)	290 / 695 (41.7)	400 / 697 (57.4)	367 / 697 (52.7)	404 / 699 (57.8)	419 / 699 (59.9)	244 / 699 (34.9)	247 / 697 (35.4)
RC9	216 / 501 (43.1)	170 / 497 (34.2)	172 / 501 (34.3)	210 / 484 (43.4)	176 / 502 (35.1)	240 / 504 (47.6)	244 / 504 (48.4)	165 / 504 (32.7)	202 / 492 (41.1)
RC10	435 / 996 (43.7)	441 / 1000 (44.1)	3 / 5 (-)	618 / 1003 (61.6)	618 / 1004 (61.6)	619 / 1003 (61.7)	575 / 1005 (57.2)	383 / 1004 (38.1)	1 / 2 (-)

RC11	60 / 438 (13.7)	37 / 440 (8.4)	41 / 439 (9.3)	44 / 279 (15.8)	91 / 442 (20.6)	90 / 440 (20.5)	59 / 440 (13.4)	33 / 440 (7.5)	48 / 438 (11.0)
RC12	19 / 139 (13.7)	2 / 95 (2.1)	16 / 135 (11.9)	32 / 136 (23.5)	29 / 139 (20.9)	25 / 139 (18.0)	37 / 140 (26.4)	15 / 139 (10.8)	15 / 133 (11.3)
RC13	2 / 87 (2.3)	0 / 55 (0.0)	1 / 36 (2.8)	0 / 17 (-)	7 / 89 (7.9)	7 / 90 (7.8)	5 / 90 (5.6)	0 / 90 (0.0)	0 / 35 (0.0)
RC14	257 / 567 (45.3)	174 / 568 (30.6)	1 / 1 (-)	309 / 567 (54.5)	313 / 567 (55.2)	329 / 568 (57.9)	333 / 568 (58.6)	160 / 568 (28.2)	1 / 2 (-)
RC16	73 / 872 (8.4)	123 / 868 (14.2)	134 / 871 (15.4)	279 / 866 (32.2)	139 / 784 (17.7)	360 / 873 (41.2)	455 / 873 (52.1)	199 / 873 (22.8)	299 / 871 (34.3)
RC17	40 / 377 (10.6)	21 / 43 (48.8)	14 / 52 (26.9)	111 / 371 (29.9)	119 / 377 (31.6)	121 / 378 (32.0)	149 / 378 (39.4)	62 / 378 (16.4)	18 / 62 (29.0)
RC18	12 / 21 (-)	10 / 22 (-)	0 / 1 (-)	0 / 0 (-)	13 / 22 (-)	14 / 22 (-)	14 / 22 (-)	9 / 22 (-)	0 / 0 (-)
RC19	132 / 766 (17.2)	22 / 765 (2.9)	40 / 765 (5.2)	134 / 765 (17.5)	1 / 765 (0.1)	11 / 765 (1.4)	175 / 765 (22.9)	67 / 765 (8.8)	11 / 765 (1.4)
RC20	177 / 515 (34.4)	266 / 514 (51.8)	359 / 513 (70.0)	224 / 515 (43.5)	185 / 515 (35.9)	237 / 515 (46.0)	213 / 516 (41.3)	124 / 515 (24.1)	141 / 513 (27.5)
RC21	15 / 311 (4.8)	5 / 307 (1.6)	12 / 319 (3.8)	16 / 163 (9.8)	50 / 324 (15.4)	41 / 324 (12.7)	45 / 324 (13.9)	26 / 324 (8.0)	25 / 296 (8.4)
Total	3024 / 11650 (26.0)	2038 / 10032 (20.3)	1280 / 5404 (23.7)	3762 / 10212 (36.8)	3634 / 11641 (31.2)	4283 / 12189 (35.1)	5006 / 12517 (40.0)	2506 / 12271 (20.4)	1271 / 5113 (24.9)

Proteus mirabilis

Proteus mirabilis isolates showed high overall susceptibility to piperacillin-tazobactam (81.9%), ertapenem (77.9%), meropenem (72.2%), and amikacin (52%), whereas susceptibility to cephalosporins (41–43%), imipenem (27.9%), ciprofloxacin (29.1%), and levofloxacin (26.3%) was considerably lower **(Table 2.12)**. RC6, RC8 and RC10 reported unusually high susceptibility to carbapenems (>90%) and piperacillin-tazobactam (>90%). Fluoroquinolone resistance was widespread across RCs.

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

RC	Piperacillin-tazobactam (N=1257)	Cefotaxime (N=1140)	Ceftazidime (N=391)	Ertapenem (N=876)	Imipenem (N=1188)	Meropenem (N=1322)	Amikacin (N=1421)	Ciprofloxacin (N=1405)	Levofloxacin (N=400)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)
RC2	522 / 630 (82.9)	215 / 620 (34.7)	21 / 59 (35.6)	167 / 273 (61.2)	111 / 638 (17.4)	454 / 638 (71.2)	306 / 638 (48.0)	154 / 638 (24.1)	10 / 55 (18.2)
RC3	6 / 10 (-)	6 / 10 (-)	7 / 10 (-)	8 / 10 (-)	9 / 10 (-)	10 / 10 (-)	6 / 10 (-)	4 / 10 (-)	4 / 10 (-)
RC4	0 / 0 (-)	0 / 0 (0.0)	1 / 1 (-)	0 / 0 (-)	0 / 0 (-)	36 / 41 (87.8)	92 / 140 (65.7)	73 / 124 (58.9)	8 / 16 (-)
RC5	26 / 27 (-)	10 / 26 (-)	0 / 0 (-)	26 / 27 (-)	14 / 15 (-)	26 / 27 (-)	18 / 27 (-)	8 / 27 (-)	0 / 0 (-)
RC6	86 / 88 (97.7)	0 / 0 (0.0)	0 / 0 (-)	84 / 88 (95.5)	49 / 91 (53.8)	83 / 88 (94.3)	52 / 88 (59.1)	27 / 88 (30.7)	0 / 0 (-)
RC7	29 / 37 (78.4)	4 / 9 (-)	4 / 9 (-)	18 / 36 (50.0)	2 / 34 (5.9)	20 / 37 (54.1)	14 / 37 (37.8)	7 / 37 (18.9)	1 / 9 (-)
RC8	66 / 67 (98.5)	51 / 68 (75.0)	51 / 68 (75.0)	66 / 69 (95.7)	17 / 68 (25.0)	64 / 68 (94.1)	48 / 68 (70.6)	29 / 68 (42.6)	29 / 66 (43.9)

RC9	2 / 2 (-)	1 / 2 (-)	1 / 2 (-)	2 / 2 (-)	1 / 2 (-)	2 / 2 (-)	2 / 2 (-)	1 / 2 (-)	1 / 2 (-)
RC10	136 / 149 (91.3)	113 / 160 (70.6)	1 / 1 (-)	148 / 151 (98.0)	74 / 88 (84.1)	160 / 163 (98.2)	71 / 163 (43.6)	44 / 163 (27.0)	0 / 0 (-)
RC11	8 / 9 (-)	2 / 9 (-)	2 / 9 (-)	0 / 0 (-)	3 / 9 (-)	7 / 9 (-)	2 / 9 (-)	2 / 9 (-)	2 / 9 (-)
RC14	5 / 5 (-)	3 / 5 (-)	0 / 0 (-)	5 / 5 (-)	3 / 5 (-)	5 / 5 (-)	3 / 5 (-)	2 / 5 (-)	0 / 0 (-)
RC16	22 / 68 (32.4)	22 / 68 (32.4)	23 / 67 (34.3)	40 / 67 (59.7)	14 / 65 (21.5)	50 / 68 (73.5)	45 / 68 (66.2)	32 / 68 (47.1)	33 / 67 (49.3)
RC19	77 / 100 (77.0)	21 / 100 (21.0)	20 / 100 (20.0)	81 / 100 (81.0)	0 / 100 (-)	1 / 100 (1.0)	50 / 100 (50.0)	14 / 100 (14.0)	3 / 100 (3.0)
RC20	36 / 45 (80.0)	23 / 45 (51.1)	28 / 45 (62.2)	37 / 45 (82.2)	29 / 45 (64.4)	36 / 45 (80.0)	30 / 45 (66.7)	12 / 45 (26.7)	9 / 45 (20.0)
RC21	9 / 20 (-)	2 / 17 (-)	8 / 19 (-)	1 / 3 (-)	5 / 20 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	5 / 20 (-)
Total	1030 / 1257 (81.9)	473 / 1140 (41.5)	167 / 391 (42.7)	683 / 876 (77.9)	331 / 1188 (27.9)	954 / 1322 (72.2)	739 / 1421 (52.0)	409 / 1405 (29.1)	105 / 400 (26.3)

Enterobacter cloacae

Enterobacter cloacae isolate showed overall susceptibility of 55.2% to piperacillin-tazobactam, 41.3% to cefotaxime, 44.9% to ceftazidime, 65.4% to ertapenem, 59.8% to imipenem, 63.2% to meropenem, 66.3% to amikacin, 47.8% to ciprofloxacin, and 54.1% to levofloxacin. RC5, RC8, RC10, and RC14 demonstrated notably higher susceptibility to carbapenems (≥80%) and higher susceptibility to amikacin (≥80%) reported by RC5, RC7, RC8 and RC14, markedly above the national average **(Table 2.13)**. Fluoroquinolone resistance was widespread, but RC4, RC5, RC8 and RC14 reported higher susceptibility (65–75%).

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

RC	Piperacillin-tazobactam (N=1213)	Cefotaxime (N=1078)	Ceftazidime (N=464)	Ertapenem (N=976)	Imipenem (N=1221)	Meropenem (N=1251)	Amikacin (N=1306)	Ciprofloxacin (N=1297)	Levofloxacin (N=381)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC2	182 / 446 (40.8)	98 / 450 (21.8)	45 / 116 (38.8)	127 / 277 (45.8)	186 / 452 (41.2)	237 / 452 (52.4)	273 / 452 (60.4)	155 / 452 (34.3)	9 / 28 (-)
RC3	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	1 / 1 (-)	1 / 1 (-)	1 / 1 (-)	1 / 1 (-)	0 / 1 (-)	0 / 1 (-)
RC4	0 / 0 (-)	0 / 0 (-)	0 / 1 (-)	0 / 0 (-)	0 / 0 (-)	8 / 28 (-)	63 / 83 (75.9)	48 / 74 (64.9)	10 / 10 (-)
RC5	34 / 41 (82.9)	0 / 12 (-)	0 / 0 (-)	35 / 41 (85.4)	34 / 40 (85.0)	36 / 41 (87.8)	36 / 41 (87.8)	28 / 41 (68.3)	0 / 0 (-)
RC6	22 / 46 (47.8)	0 / 0 (-)	0 / 0 (-)	31 / 46 (67.4)	33 / 46 (71.7)	33 / 46 (71.7)	34 / 46 (73.9)	20 / 46 (43.5)	0 / 2 (-)
RC7	35 / 57 (61.4)	3 / 15 (-)	5 / 18 (-)	35 / 51 (68.6)	40 / 57 (70.2)	42 / 58 (72.4)	47 / 59 (79.7)	23 / 58 (39.7)	4 / 14 (-)

RC8	70 / 82 (85.4)	64 / 82 (78.0)	66 / 83 (79.5)	76 / 82 (92.7)	77 / 83 (92.8)	77 / 83 (92.8)	77 / 83 (92.8)	62 / 83 (74.7)	62 / 83 (74.7)
RC9	4 / 8 (-)	3 / 8 (-)	3 / 8 (-)	4 / 7 (-)	1 / 8 (-)	5 / 8 (-)	5 / 8 (-)	3 / 8 (-)	3 / 7 (-)
RC10	123 / 179 (68.7)	124 / 179 (69.3)	1 / 1 (-)	154 / 180 (85.6)	151 / 179 (84.4)	153 / 180 (85.0)	124 / 180 (68.9)	114 / 180 (63.3)	1 / 1 (-)
RC11	81 / 137 (59.1)	57 / 137 (41.6)	59 / 137 (43.1)	51 / 92 (55.4)	80 / 137 (58.4)	85 / 137 (62.0)	76 / 137 (55.5)	71 / 137 (51.8)	82 / 137 (59.9)
RC12	10 / 37 (27.0)	8 / 26 (-)	8 / 33 (24.2)	17 / 35 (48.6)	16 / 37 (43.2)	19 / 37 (51.4)	21 / 37 (56.8)	13 / 37 (35.1)	16 / 35 (45.7)
RC13	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 0 (-)	0 / 2 (-)	1 / 2 (-)	1 / 2 (-)	1 / 2 (-)	0 / 0 (-)
RC14	78 / 106 (73.6)	75 / 106 (70.8)	0 / 0 (-)	84 / 106 (79.2)	89 / 106 (84.0)	89 / 106 (84.0)	92 / 106 (86.8)	71 / 106 (67.0)	0 / 0 (-)
RC16	3 / 8 (-)	3 / 8 (-)	2 / 8 (-)	2 / 8 (-)	2 / 8 (-)	3 / 8 (-)	4 / 8 (-)	4 / 8 (-)	6 / 8 (-)
RC17	1 / 2 (-)	0 / 0 (-)	0 / 0 (-)	1 / 2 (-)	1 / 2 (-)	1 / 2 (-)	1 / 2 (-)	1 / 2 (-)	0 / 0 (-)
RC18	1 / 1 (-)	1 / 1 (-)	0 / 0 (-)	0 / 0 (-)	0 / 1 (-)	1 / 1 (-)	1 / 1 (-)	1 / 1 (-)	0 / 0 (-)
RC19	9 / 20 (-)	0 / 20 (-)	6 / 20 (-)	9 / 20 (-)	0 / 20 (-)	0 / 20 (-)	10 / 20 (-)	5 / 20 (-)	0 / 20 (-)
RC20	0 / 1 (-)	0 / 0 (-)	0 / 0 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 0 (-)
RC21	17 / 40 (42.5)	9 / 32 (28.1)	14 / 38 (36.8)	11 / 27 (-)	19 / 41 (46.3)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	13 / 35 (37.1)
Total	670 / 1213 (55.2)	445 / 1078 (41.3)	209 / 464 (44.9)	638 / 976 (65.4)	730 / 1221 (59.8)	791 / 1251 (63.2)	866 / 1306 (66.3)	620 / 1297 (47.8)	206 / 381 (54.1)

Species-wise susceptibility of Enterobacterales from urine

The antimicrobial susceptibility of Enterobacterales isolated from urine samples revealed marked variability across species **(Table 2.14)**, emphasizing the need for species-specific treatment strategies. *Escherichia coli* was the predominant uropathogen, accounting for 68% of the isolates, showing high susceptibility to fosfomycin (92.2%) and nitrofurantoin (80.8%), supporting their continued use as effective oral therapeutic options. However, resistance to commonly used oral agents such as cefazolin, ciprofloxacin, and levofloxacin was quite high, with susceptibility rates of 12.2%, 22.4%, and 22%, respectively. While resistance to piperacillin-tazobactam is high, moderate susceptibility can be observed for amikacin (75.8%) and carbapenems (ertapenem 76.9%, imipenem 68.8%, meropenem 73.0%). Similarly, the second most common isolate, *Klebsiella pneumoniae* (23.7%), exhibited substantially higher resistance across most antibiotics except fosfomycin, which presented susceptibility of more than 50% (59.2%). Also, *Klebsiella oxytoca* demonstrated relatively better susceptibility to only fosfomycin (59.4%), but resistance to third-generation cephalosporins and fluoroquinolones was still consistently high.

Among the less frequently isolated species, *Enterobacter cloacae* showed moderate susceptibility to carbapenems (ertapenem 74.2%, imipenem 68.5%, meropenem 67.8%) and amikacin (66.7%), though resistance to fluoroquinolones persisted. *Proteus mirabilis* was highly susceptible to piperacillin-tazobactam (74.9%), meropenem (81.5%), and fosfomycin (74.1%). *Citrobacter koseri* demonstrated high susceptibility to fosfomycin (90.8%) and nitrofurantoin (79.4%), while Citrobacter freundii retained moderate susceptibility to carbapenems and aminoglycosides. *Morganella morganii* displayed the highest susceptibility to carbapenems (ertapenem 84.4%, meropenem 86.8%), followed by piperacillin-tazobactam (81.6%) and cefotaxime (61.5%).

In summary, *E. coli* remains the leading uropathogen, documenting high resistance to cephalosporins and fluoroquinolones. Fosfomycin and nitrofurantoin remain highly effective oral options. In contrast, *K. pneumoniae* displays multidrug resistance with limited treatment choices, whereas *Enterobacter*, *Proteus*, *Citrobacter*, *Morganella*, and *Providencia* species exhibit variable susceptibility patterns. These findings underscore the importance of ongoing local surveillance and species-specific susceptibility data to guide effective management of urinary tract infections (UTIs).

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

AMA	*Escherichia coli* (N=13476)	*Klebsiella pneumoniae* (N=4875)	*Klebsiella oxytoca* (N=211)	*Klebsiella spp.* (N=9)	*Enterobacter cloacae* (N=318)	*Enterobacter spp.* (N=87)	*Proteus mirabilis* (N=383)	*Citrobacter koseri* (N=405)	*Citrobacter freundii* (N=51)	*Morganella morganii* (N=154)	*Providencia rettgeri* (N=33)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	5182 / 9269 (55.9)	1182 / 3499 (33.8)	35 / 185 (18.9)	3 / 9 (-)	136 / 218 (62.4)	11 / 27 (-)	221 / 295 (74.9)	218 / 262 (83.2)	14 / 41 (34.1)	80 / 98 (81.6)	7 / 29 (-)
Cefazolin	453 / 3727 (12.2)	169 / 1283 (13.2)	13 / 160 (8.1)	0 / 6 (-)	5 / 21 (-)	2 / 10 (-)	5 / 28 (17.9)	18 / 55 (32.7)	-	-	-
Cefotaxime	1913 / 7422 (25.8)	799 / 2764 (28.9)	46 / 178 (25.8)	5 / 9 (-)	97 / 184 (52.7)	4 / 17 (-)	133 / 233 (57.1)	187 / 244 (76.6)	13 / 34 (38.2)	48 / 78 (61.5)	3 / 23 (-)
Ceftazidime	1600 / 4722 (33.9)	468 / 1858 (25.2)	29 / 172 (16.9)	5 / 7 (-)	35 / 83 (42.2)	8 / 17 (-)	66 / 147 (44.9)	39 / 72 (54.2)	7 / 21 (-)	18 / 33 (54.5)	3 / 18 (-)
Ertapenem	6975 / 9066 (76.9)	1637 / 3305 (49.5)	84 / 184 (45.7)	4 / 9 (-)	147 / 198 (74.2)	17 / 26 (-)	216 / 275 (78.5)	236 / 261 (90.4)	24 / 41 (58.5)	76 / 90 (84.4)	8 / 29 (-)
Imipenem	5989 / 8708 (68.8)	1388 / 3244 (42.8)	47 / 170 (27.6)	2 / 9 (-)	139 / 203 (68.5)	11 / 19 (-)	112 / 243 (46.1)	227 / 257 (88.3)	18 / 35 (51.4)	26 / 58 (44.8)	3 / 23 (-)
Meropenem	7476 / 10241 (73)	1981 / 4078 (48.6)	110 / 193 (57)	5 / 9 (-)	162 / 239 (67.8)	20 / 42 (47.6)	251 / 308 (81.5)	246 / 268 (91.8)	27 / 43 (62.8)	92 / 106 (86.8)	14 / 31 (45.2)
Amikacin	10221 / 13476 (75.8)	2435 / 4871 (50.0)	129 / 211 (61.1)	3 / 9 (-)	212 / 318 (66.7)	52 / 87 (59.8)	236 / 383 (61.6)	356 / 405 (87.9)	38 / 51 (74.5)	121 / 154 (8.6)	10 / 33 (30.3)
Ciprofloxacin	3020 / 13476 (22.4)	1363 / 4850 (28.1)	73 / 211 (34.4)	3 / 9 (-)	180 / 318 (56.6)	47 / 87 (54)	119 / 383 (31.1)	344 / 405 (84.9)	24 / 51 (47.1)	71 / 159 (44.7)	6 / 33 (18.2)
Levofloxacin	951 / 4330 (22.0)	415 / 1656 (25.1)	60 / 168 (35.7)	2 / 7 (-)	17 / 67 (25.4)	6 / 12 (-)	38 / 133 (28.6)	34 / 65 (52.3)	7 / 18 (38.9)	8 / 25 (-)	4 / 13 (-)
Trimethoprim-sulfamethoxazole	4486 / 9094 (49.3)	1537 / 3417 (45.0)	102 / 182 (56)	4 / 8 (-)	150 / 208 (72.1)	17 / 27 (-)	117 / 288 (40.6)	233 / 260 (89.6)	24 / 39 (61.5)	60 / 96 (62.5)	6 / 29 (-)
Fosfomycin	6288 / 6821 (92.2)	1499 / 2530 (59.2)	104 / 175 (59.4)	5 / 8 (-)	73 / 107 (68.2)	16 / 23 (-)	149 / 201 (74.1)	108 / 119 (90.8)	21 / 26 (80.8)	-	6 / 21 (-)
Nitrofurantoin	8981 / 11119 (80.8)	736 / 3479 (21.2)	67 / 193 (34.7)	1 / 6 (-)	47 / 185 (25.4)	16 / 61 (26.2)	-	274 / 345 (79.4)	29 / 40 (72.5)	-	-

RC-wise Antimicrobial Susceptibility (AMS) Percentages of *Escherichia coli* from urine

Fosfomycin demonstrated the highest overall susceptibility among the tested antibiotics, with 92.2% of isolates remaining sensitive, followed by nitrofurantoin at 80.8%, reaffirming their value as effective oral options for treating UTIs. In contrast, cefotaxime, ciprofloxacin and cefazolin showed the least susceptibility with a sensitivity of less than 30%. Among carbapenems, meropenem and ertapenem maintained high susceptibility rates above 70%, while imipenem showed slightly reduced effectiveness at 68.8%. Notably, regional variation was observed across the reference centres (RCs), with RC6, RC8, RC9, RC10, RC14, and RC17 reporting higher susceptibility to carbapenems (exceeding 80%) and aminoglycosides (exceeding 75%), whereas RC12, RC16, RC19 and RC21 demonstrated high resistance across most antibiotic classes, including carbapenems. These findings highlight both the efficacy of specific agents, like fosfomycin, and the impact of regional resistance patterns on treatment decisions **(Table 2.15)**.

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

RC	Piperacillin-tazobactam (N=9269)	Cefazolin (N=3727)	Cefotaxime (N=7422)	Ertapenem (N=9066)	Imipenem (N=8708)	Meropenem (N=10241)	Amikacin (N=13476)	Ciprofloxacin (N=13476)	Levofloxacin (N=4330)	Trimethoprim-sulfamethoxazole (N=9094)	Fosfomycin (N=6821)	Nitrofurantoin (N=11119)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	12 / 66 (18.2)	18 / 66 (27.3)	0 / 66 (0.0)	21 / 66 (31.8)	23 / 66 (34.8)	25 / 66 (37.9)	30 / 66 (45.5)	4 / 66 (6.1)	21 / 66 (31.8)	18 / 66 (27.3)	46 / 66 (69.7)	52 / 66 (78.8)
RC4	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	232 / 890 (26.1)	2933 / 4165 (70.4)	1333 / 4160 (32.0)	0 / 0 (-)	0 / 0 (-)	128 / 131 (97.7)	3585 / 4111 (87.2)
RC5	249 / 401 (62.1)	0 / 0 (-)	1 / 400 (0.3)	304 / 399 (76.2)	331 / 401 (82.5)	328 / 401 (81.8)	358 / 401 (89.3)	37 / 401 (9.2)	0 / 0 (-)	207 / 401 (51.6)	76 / 84 (90.5)	257 / 375 (68.5)
RC6	606 / 937 (64.7)	0 / 0 (-)	0 / 0 (-)	759 / 938 (80.9)	780 / 936 (83.3)	775 / 938 (82.6)	770 / 938 (82.1)	40 / 938 (4.3)	0 / 5 (-)	383 / 934 (41.0)	924 / 937 (98.6)	803 / 922 (87.1)
RC7	335 / 502 (66.7)	55 / 110 (50.0)	30 / 118 (25.4)	378 / 472 (80.1)	72 / 123 (58.5)	461 / 513 (89.9)	372 / 513 (72.5)	89 / 516 (17.2)	10 / 105 (9.5)	246 / 505 (48.7)	476 / 486 (97.9)	317 / 407 (77.9)
RC8	304 / 411 (74.0)	0 / 0 (-)	139 / 414 (33.6)	355 / 411 (86.4)	370 / 412 (89.8)	371 / 413 (89.8)	350 / 413 (84.7)	38 / 414 (9.2)	53 / 413 (12.8)	208 / 412 (50.5)	410 / 411 (99.8)	0 / 0 (-)

RC9	495 / 614 (80.6)	169 / 603 (28.0)	264 / 619 (42.6)	508 / 613 (82.9)	444 / 620 (71.6)	542 / 621 (87.3)	526 / 621 (84.7)	216 / 621 (34.8)	247 / 610 (40.5)	360 / 612 (58.8)	559 / 592 (94.4)	521 / 598 (87.1)
RC10	1101 / 1576 (69.9)	0 / 0 (-)	528 / 1591 (33.2)	1401 / 1592 (88.0)	1437 / 1590 (90.4)	1428 / 1591 (89.8)	1216 / 1592 (76.4)	434 / 1592 (27.3)	0 / 1 (-)	843 / 1576 (53.5)	3 / 3 (-)	1306 / 1575 (82.9)
RC11	41 / 110 (37.3)	0 / 3 (-)	14 / 112 (12.5)	48 / 58 (82.8)	55 / 113 (48.7)	63 / 112 (56.3)	56 / 112 (50.0)	9 / 112 (8.0)	11 / 112 (9.8)	41 / 112 (36.6)	59 / 63 (93.7)	77 / 111 (69.4)
RC12	32 / 103 (31.1)	5 / 59 (8.5)	2 / 74 (2.7)	52 / 99 (52.5)	50 / 103 (48.5)	53 / 102 (52.0)	55 / 102 (53.9)	4 / 103 (3.9)	11 / 90 (12.2)	23 / 64 (35.9)	59 / 63 (93.7)	36 / 58 (62.1)
RC13	1 / 8 (-)	0 / 6 (-)	0 / 7 (-)	0 / 5 (-)	1 / 8 (-)	2 / 8 (-)	3 / 8 (-)	0 / 8 (-)	0 / 7 (-)	0 / 6 (-)	7 / 8 (-)	2 / 8 (-)
RC14	780 / 1088 (71.7)	2 / 2 (-)	302 / 1087 (27.8)	903 / 1087 (83.1)	939 / 1081 (86.9)	938 / 1089 (86.1)	954 / 1089 (87.6)	112 / 1089 (10.3)	0 / 0 (-)	597 / 1086 (55.0)	1075 / 1087 (98.9)	3 / 3 (-)
RC16	192 / 1622 (11.8)	112 / 1611 (7.0)	168 / 1625 (10.3)	864 / 1610 (53.7)	392 / 1376 (28.5)	1107 / 1627 (68.0)	1152 / 1627 (70.8)	322 / 1627 (19.8)	422 / 1624 (26.0)	808 / 1619 (49.9)	1500 / 1621 (92.5)	1141 / 1626 (70.2)
RC17	261 / 584 (44.7)	2 / 2 (-)	37 / 43 (86.0)	515 / 607 (84.8)	528 / 607 (87.0)	527 / 607 (86.8)	523 / 607 (86.2)	202 / 607 (33.3)	33 / 44 (75.0)	319 / 441 (72.3)	1 / 1 (-)	10 / 38 (26.3)
RC18	8 / 13 (-)	1 / 13 (-)	2 / 11 (-)	0 / 0 (-)	8 / 13 (-)	7 / 13 (-)	8 / 13 (-)	2 / 13 (-)	0 / 0 (-)	8 / 13 (-)	8 / 11 (-)	9 / 13 (-)
RC19	300 / 479 (62.6)	39 / 479 (8.1)	65 / 479 (13.6)	335 / 479 (69.9)	1 / 479 (0.2)	13 / 479 (2.7)	338 / 479 (70.6)	36 / 479 (7.5)	2 / 478 (0.4)	104 / 479 (21.7)	211 / 479 (44.1)	245 / 479 (51.1)
RC20	440 / 623 (70.6)	29 / 623 (4.7)	348 / 624 (55.8)	530 / 624 (84.9)	465 / 623 (74.6)	528 / 624 (84.6)	561 / 624 (89.9)	124 / 624 (19.9)	115 / 624 (18.4)	244 / 620 (39.4)	599 / 623 (96.1)	533 / 624 (85.4)
RC21	25 / 132 (18.9)	21 / 150 (14.0)	13 / 152 (8.6)	2 / 6 (-)	93 / 157 (59.2)	78 / 158 (49.4)	48 / 158 (30.4)	34 / 158 (21.5)	26 / 151 (17.2)	77 / 148 (52.0)	148 / 156 (94.9)	125 / 156 (80.1)
Total	5182 / 9269 (55.9)	453 / 3727 (12.2)	1913 / 7422 (25.8)	6975 / 9066 (76.9)	5989 / 8708 (68.8)	7476 / 10241 (73.0)	10221 / 13476 (75.8)	3020 / 13476 (22.4)	951 / 4330 (22.0)	4486 / 9094 (49.3)	6288 / 6821 (92.2)	8981 / 11119 (80.8)

RC-wise Antimicrobial Susceptibility (AMS) Percentages of *Klebsiella pneumoniae* from urine

K. pneumoniae isolates from urine demonstrated generally low susceptibility (≤50%) across most antibiotics **(Table 2.16)**. Cefazolin (13.2%), nitrofurantoin (21.2%), levofloxacin (25.1%), ciprofloxacin (28.1%), and cefotaxime (28.9%) were the least susceptible drugs. Marked inter-centre variation was noted: RC10, RC14 and RC17 reported higher carbapenem susceptibility (>65%) compared to the national average, whereas RC6, RC11 and RC19 showed near-complete resistance across most antibiotic classes. Fluoroquinolone and nitrofurantoin resistance was widespread. These findings underscore the regional disparities in resistance and the growing challenge posed by highly resistant *K. pneumoniae* strains in UTIs.

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

RC	Piperacillin-tazobactam (N=3499)	Cefazolin (N=1283)	Cefotaxime (N=2764)	Ertapenem (N=3305)	Imipenem (N=3244)	Meropenem (N=4078)	Amikacin (N=4871)	Ciprofloxacin (N=4850)	Levofloxacin (N=1656)	Nitrofurantoin (N=3479)	Trimethoprim-sulfamethoxazole (N=3417)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC1	2 / 43 (4.7)	3 / 43 (7.0)	0 / 43 (0.0)	4 / 43 (9.3)	5 / 43 (11.6)	6 / 43 (14.0)	6 / 43 (14.0)	0 / 43 (0.0)	4 / 43 (9.3)	11 / 43 (25.6)	5 / 43 (11.6)
RC4	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	132 / 561 (23.5)	569 / 1381 (41.2)	449 / 1358 (33.1)	0 / 0 (-)	158 / 797 (19.8)	0 / 0 (-)
RC5	78 / 199 (39.2)	0 / 0 (-)	24 / 198 (12.1)	89 / 199 (44.7)	92 / 196 (46.9)	94 / 199 (47.2)	101 / 199 (50.8)	47 / 199 (23.6)	0 / 1 (-)	24 / 189 (12.7)	80 / 199 (40.2)
RC6	107 / 396 (27.0)	0 / 0 (-)	0 / 0 (-)	142 / 396 (35.9)	155 / 396 (39.1)	158 / 396 (39.9)	156 / 396 (39.4)	49 / 396 (12.4)	0 / 3 (-)	55 / 383 (14.4)	119 / 396 (30.1)
RC7	91 / 244 (37.3)	9 / 28 (-)	13 / 40 (32.5)	117 / 208 (56.3)	17 / 45 (37.8)	212 / 247 (85.8)	128 / 247 (51.8)	63 / 248 (25.4)	3 / 30 (-)	24 / 189 (12.7)	108 / 239 (45.2)
RC8	66 / 201 (32.8)	0 / 0 (-)	46 / 200 (23.0)	94 / 201 (46.8)	90 / 201 (44.8)	99 / 202 (49.0)	100 / 202 (49.5)	40 / 202 (19.8)	40 / 202 (19.8)	0 / 0 (-)	85 / 201 (42.3)

RC9	97 / 151 (64.2)	53 / 142 (37.3)	79 / 150 (52.7)	87 / 146 (59.6)	78 / 151 (51.7)	98 / 151 (64.9)	88 / 151 (58.3)	68 / 151 (45.0)	77 / 145 (53.1)	64 / 149 (43.0)	91 / 147 (61.9)
RC10	279 / 578 (48.3)	0 / 0 (-)	248 / 582 (42.6)	375 / 582 (64.4)	396 / 583 (67.9)	396 / 583 (67.9)	388 / 582 (66.7)	223 / 582 (38.3)	0 / 1 (-)	105 / 571 (18.4)	328 / 573 (57.2)
RC11	14 / 113 (12.4)	0 / 0 (-)	9 / 113 (8.0)	17 / 26 (-)	24 / 113 (21.2)	23 / 113 (20.4)	18 / 113 (15.9)	8 / 113 (7.1)	11 / 113 (9.7)	17 / 109 (15.6)	21 / 109 (19.3)
RC12	6 / 55 (10.9)	2 / 21 (-)	2 / 39 (5.1)	8 / 55 (14.5)	11 / 55 (20.0)	9 / 55 (16.4)	10 / 55 (18.2)	4 / 55 (7.3)	2 / 49 (4.1)	4 / 20 (-)	6 / 22 (-)
RC13	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 0 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)	0 / 1 (-)
RC14	177 / 333 (53.2)	0 / 0 (-)	152 / 334 (45.5)	221 / 333 (66.4)	223 / 334 (66.8)	236 / 334 (70.7)	239 / 334 (71.6)	132 / 334 (39.5)	0 / 0 (-)	1 / 2 (-)	205 / 334 (61.4)
RC16	48 / 615 (7.8)	56 / 617 (9.1)	96 / 618 (15.5)	210 / 611 (34.4)	85 / 537 (15.8)	292 / 620 (47.1)	337 / 620 (54.4)	147 / 620 (23.7)	188 / 617 (30.5)	148 / 620 (23.9)	288 / 617 (46.7)
RC17	70 / 151 (46.4)	6 / 6 (-)	11 / 18 (-)	113 / 156 (72.4)	112 / 156 (71.8)	117 / 156 (75.0)	124 / 156 (79.5)	66 / 156 (42.3)	13 / 21 (-)	1 / 12 (-)	72 / 114 (63.2)
RC18	1 / 2 (-)	1 / 2 (-)	1 / 2 (-)	0 / 0 (-)	1 / 2 (-)	1 / 2 (-)	2 / 2 (-)	1 / 2 (-)	0 / 0 (-)	1 / 2 (-)	1 / 2 (-)
RC19	64 / 194 (33.0)	13 / 194 (6.7)	14 / 194 (7.2)	80 / 194 (41.2)	0 / 194 (0.0)	3 / 194 (1.5)	83 / 194 (42.8)	19 / 194 (9.8)	2 / 194 (1.0)	50 / 194 (25.8)	29 / 194 (14.9)
RC20	72 / 152 (47.4)	12 / 152 (7.9)	94 / 152 (61.8)	78 / 152 (51.3)	70 / 152 (46.1)	83 / 152 (54.6)	70 / 152 (46.1)	38 / 152 (25.0)	49 / 152 (32.2)	52 / 152 (34.2)	56 / 152 (36.8)
RC21	10 / 71 (14.1)	14 / 77 (18.2)	10 / 80 (12.5)	2 / 3 (-)	29 / 85 (34.1)	27 / 85 (31.8)	31 / 85 (36.5)	25 / 85 (29.4)	26 / 84 (31.0)	24 / 78 (30.8)	43 / 74 (58.1)
Total	1182 / 3499 (33.8)	169 / 1283 (13.2)	799 / 2764 (28.9)	1637 / 3305 (49.5)	1388 / 3244 (42.8)	1981 / 4078 (48.6)	2435 / 4871 (50.0)	1363 / 4850 (28.1)	415 / 1656 (25.1)	736 / 3479 (21.2)	1537 / 3417 (45.0)

Yearly susceptibility trends of different Enterobacterales from urine samples

Over the eight-year period from 2017 to 2024, *E. coli* and *K. pneumoniae* urinary isolates demonstrated a consistent decline in susceptibility for the majority of the antibiotic classes, highlighting a concerning trend in antimicrobial resistance **(Tables 2.17-2.18, Figures 2.5-2.6)**. In *E. coli*, susceptibility to piperacillin-tazobactam dropped notably from 73.7% in 2017 to 55.9% in 2024, while third-generation cephalosporins remained largely ineffective throughout, with cefotaxime ranging from 24.5% to 25.8% and cefazolin consistently below 30% **(Figure 2.17, Figure 2.5)**. Although carbapenems retained relatively good activity, their efficacy had significantly declined - imipenem susceptibility fell from 88.3% to 68.8%, and meropenem from 80.8% to 73.4% over the same period. Amikacin susceptibility, although higher, dropped from 84.0% to 73.0%. Fluoroquinolone resistance persisted, with ciprofloxacin at 22.4% and levofloxacin at 22.0% in 2024. Despite these declining trends, fosfomycin (92.2%) and nitrofurantoin (80.8%) retained the highest susceptibility, reinforcing their value as reliable oral therapeutic options for UTIs caused by *E. coli*.

In *K. pneumoniae*, antimicrobial resistance was even more pronounced than in *E. coli*. Susceptibility to piperacillin-tazobactam declined from 52.5% in 2017 to 33.8% in 2024, while cefazolin and cefotaxime remained consistently low (13.2% and 28.9%, respectively) in 2024 **(Figure 2.18, Figure 2.6)**. Carbapenem susceptibility decreased substantially, with imipenem falling from 70.8% in 2017 to 42.8% in 2024 and meropenem from 56.3% to 48.6%. Amikacin decreased from 56.9% to 50.0% over the same period. Among fluoroquinolones, ciprofloxacin showed decreased susceptibility at 25.1% and levofloxacin at 21.0% in 2024. Trimethoprim-sulfamethoxazole (TMP-SMX) showed moderate susceptibility (45.0%), while nitrofurantoin remained ineffective (21.2%).

In summary, *E. coli* demonstrated a relatively higher susceptibility than *K. pneumoniae* for most antibiotics; however, both species showed a decline in carbapenem and aminoglycoside sensitivity. Fosfomycin and nitrofurantoin remain the most reliable oral options for *E. coli*, whereas *K. pneumoniae* exhibited high resistance across nearly all agents, underscoring the urgent need for strengthened antimicrobial stewardship and infection control measures in UTIs.

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%)
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)
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)
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)
Ceftazidime	*1/10 (-)	*0/2 (-)	*0/3 (-)	*1/2 (-)	*1/2 (-)	701 / 3222 (21.8)	727 / 3289 (22.1)	1600 / 4722 (33.9)
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)
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)
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)
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)
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)
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)
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)
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)
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)

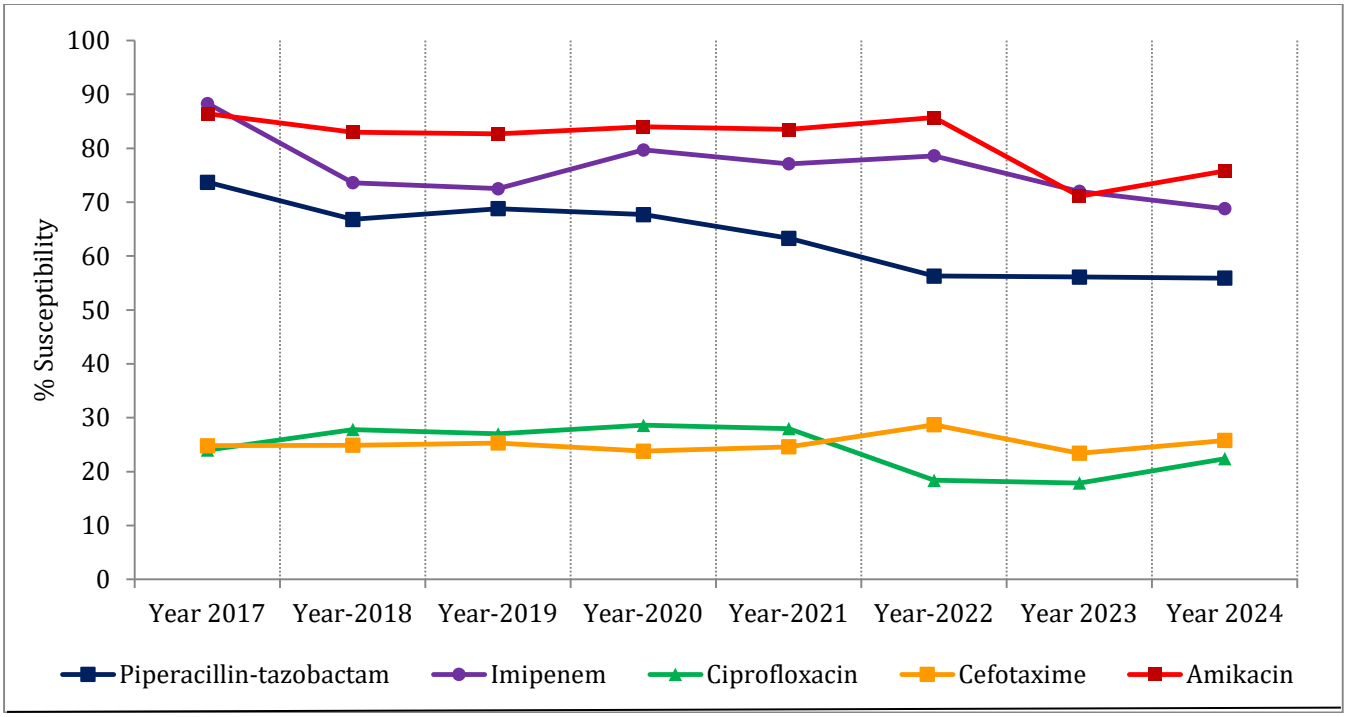


Figure 2.5: Yearly susceptibility trends of *E. coli* isolated from urine

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
	N=1336	N=2626	N=5027	N=2860	N=3583	N=3825	N=3496	N=4875
	(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)
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)
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)
Ceftazidime	*2/10 (-)	*0/1 (-)	*0/2 (-)	*0/3 (-)	*1/10 (-)	281 / 1202 (23.4)	214 / 1193 (17.9)	468 / 1858 (25.2)
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)
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)
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)
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)
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)
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)
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)
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)

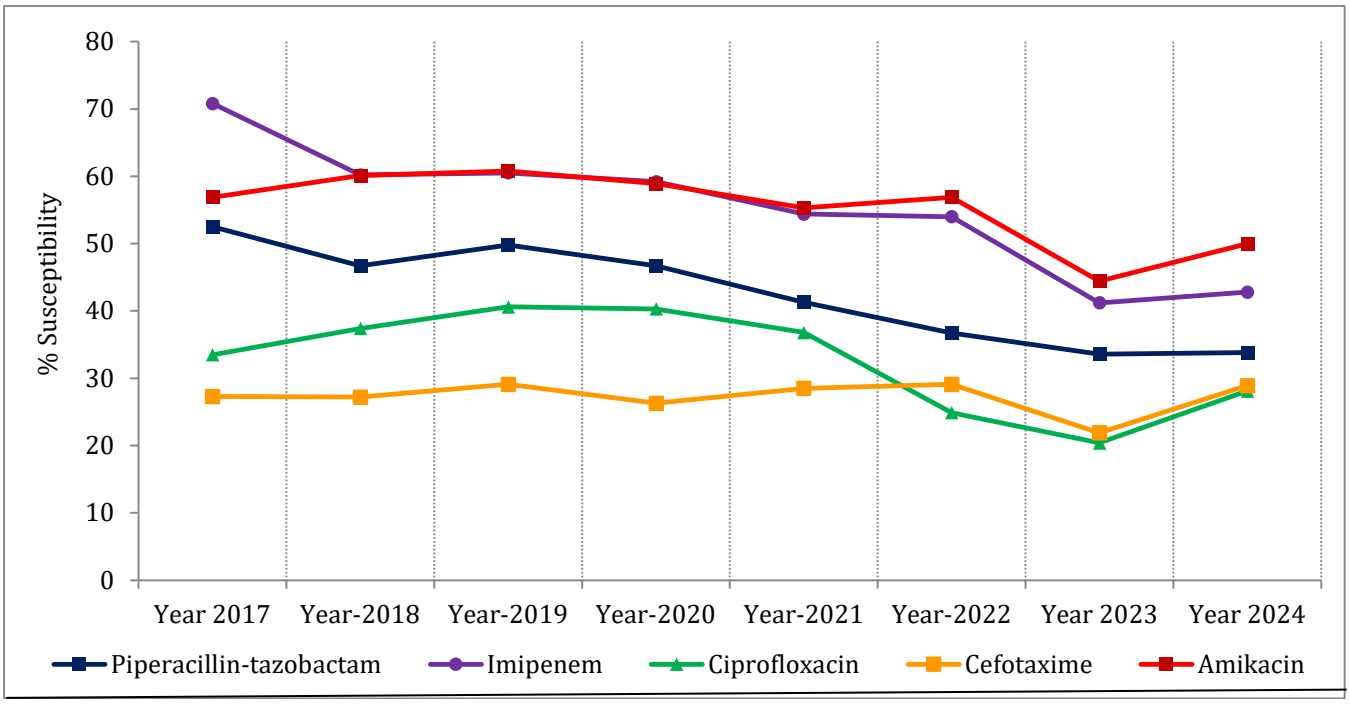


Figure 2.6: Yearly susceptibility trend of *K. pneumoniae* isolated from urine

Relative susceptibilities of carbapenem-susceptible and carbapenem-resistant isolates of *E. coli* and *K. pneumoniae*

The comparison between carbapenem-resistant (CR) versus carbapenem-susceptible (CS) isolates highlights marked differences in susceptibility patterns for *E. coli* and *K. pneumoniae* **(Tables 2.19–2.20)**. In *E. coli*, CR isolates (N=5313) demonstrated extensive multidrug resistance, with only 10.8% susceptible to piperacillin-tazobactam, 7.9–17.6% to carbapenems, and 56.3% to amikacin, while fluoroquinolone susceptibility was almost negligible (3.5–7.1%). In contrast, CS isolates (N=6753) retained higher susceptibility to carbapenems (>96%), amikacin (84.2%), and piperacillin-tazobactam (64.8%), though resistance to third-generation cephalosporins and fluoroquinolones persisted (susceptibility 14.9–23.1%). Among *K. pneumoniae*, the difference was more marked. CR isolates (N=8343) showed extremely low susceptibility across all agents, ≤10% for β-lactams and carbapenems, 15.1% for amikacin, and ≤7.1% for fluoroquinolones. In contrast, CS *K. pneumoniae* isolates (N=3850) exhibited high susceptibility to carbapenems (93.6–98.7%) and amikacin (89.9%), though susceptibility to cephalosporins (52.6–65.8%) and fluoroquinolones (53.0–64.3%) remained moderate. Overall, the data underscore the critical therapeutic challenges posed by CR *E. coli* and *K. pneumoniae*, both of which display extensive multidrug resistance and limited treatment options. Even among CS strains, resistance to cephalosporins and fluoroquinolones remains a concern, further emphasizing the need for robust antimicrobial stewardship, targeted therapy, and enhanced infection control measures.

Table 2.19: Susceptibility pattern of carbapenem-resistant (CR) and susceptible (CS) *E. coli* isolates from all specimens (except faeces and urine)

AMA	CR N=5313 (S%)	CS N=6753 (S%)
Piperacillin-tazobactam	548 / 5092 (10.8)	4270 / 6586 (64.8)
Cefotaxime	214 / 4585 (4.7)	1415 / 5694 (24.9)
Ceftazidime	238 / 2054 (11.6)	1003 / 2451 (40.9)
Ertapenem	668 / 4511 (14.8)	5789 / 5972 (96.9)
Imipenem	402 / 5094 (7.9)	6313 / 6566 (96.1)
Meropenem	933 / 5313 (17.6)	6656 / 6753 (98.6)
Amikacin	2989 / 5313 (56.3)	5683 / 6753 (84.2)
Ciprofloxacin	185 / 5298 (3.5)	1008 / 6743 (14.9)
Levofloxacin	136 / 1928 (7.1)	525 / 2275 (23.1)
Trimethoprim-sulfamethoxazole	116 / 605 (19.2)	878 / 1635 (53.7)
Nitrofurantoin	28 / 52 (53.8)	51 / 67 (76.1)

Table 2.20: Susceptibility pattern of carbapenem-resistant and susceptible *K. pneumoniae* isolates from all specimens (except faeces and urine)

AMA	CR N=8343 (S%)	CS N=3850 (S%)
Piperacillin-tazobactam	335 / 7893 (4.2)	2689 / 3755 (71.6)
Cefotaxime	290 / 6709 (4.3)	1748 / 3323 (52.6)
Ceftazidime	297 / 3914 (7.6)	986 / 1499 (65.8)
Ertapenem	373 / 6746 (5.5)	3389 / 3465 (97.8)
Imipenem	152 / 7916 (1.9)	3482 / 3721 (93.6)
Meropenem	483 / 8343 (5.8)	3798 / 3849 (98.7)
Amikacin	1258 / 8343 (15.1)	3461 / 3849 (89.9)
Ciprofloxacin	321 / 8240 (3.9)	2032 / 3835 (53.0)
Levofloxacin	251 / 3555 (7.1)	919 / 1429 (64.3)

Molecular characterisation of *E. coli* isolates

Three hundred eleven (311) *E. coli* isolates were subjected to four multiplex PCRs and two monoplex PCRs for OXA-48 and NDM. Overall, TEM (29.58%) was the most common, followed by IMP (27.97%), VIM (19.29%), NDM-1 (14.47%), OXA1 (12.86), OXA-48 (11.90%), CTXM-1 (9.65%), SHV (6.43%), CIT (5.79%), CTXM-9 & MOX each (4.82%), KPC (1.29%), CTXM-2 (1.23%), and ACC & DHA (0.96%) (**Figure 2.7)**.

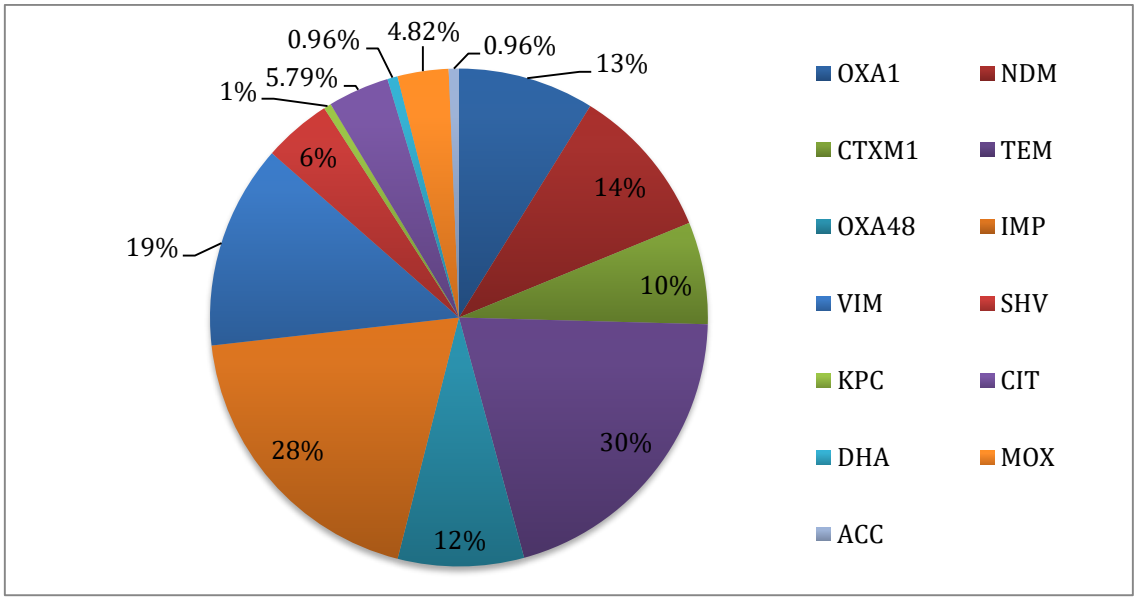


Figure 2.7: Percentage positivity of AMR-associated genetic determinants in *E. coli* (2024)

RC-wise analysis **(Figure 2.8** and **Table 2.21**) showed that the isolates from RC2 displayed maximum positivity for TEM (78%), followed by NDM-1 (47%), IMP (42%), VIM (19%), OXA-1 (17%), OXA-48 (6%), and KPC (3%). The majority of RC3 isolates were positive for IMP (52%), NDM-1 (48%), VIM (39%), TEM & OXA1 (26%), CTXM-9 (22%), SHV (17%) and the remaining genes showed presence less than 10%. Similarly, the RC5 isolates were majorly positive for OXA-48 (73%), VIM (45%) and IMP (36%). RC6 isolates showed OXA-48 (33%), VIM (18%), TEM & IMP (15%), OXA1 (12%) and other genes at less than 10%. RC8 isolates showed OXA1 (27%), TEM (24%), IMP & CIT (16%), CTXM-9 (13%), OXA-48 & SHV (11%), and NDM & KPC (4%). The RC9 isolates were positive for TEM (36%), IMP (24%), VIM (21%), NDM-1 (15%), OXA-48 & SHV (12%), and MOX, DHA & CIT (6%). In RC10, IMP was (32%), TEM, VIM & MOX (27%) and CIT was detected in 5% of isolates. From RC13, only one strain of *E. coli* was revived, and only SHV was detected. RC14 isolates were positive for IMP (32%), TEM (29%), OXA1 (15%), VIM 12%, CTXM-2 (9%), NDM & SHV were 6%, and others were less than 5%. In RC16 isolates, CTXM1 (56%) was the most common gene, followed by IMP (44%), VIM (41%), MOX & CIT (22% each), TEM & CTXM-9 (11%), and others were less than 5%. In RC17 samples, TEM 26%, OXA-1 (20%), CTXM-1 (17%), OXA-48 (14%), NDM (11%), VIM 9% and others were less than 5%. RC21 samples showed IMP (45%), CTXM-1 (27%), TEM & NDM (18%), OXA-48 & VIM (9%).

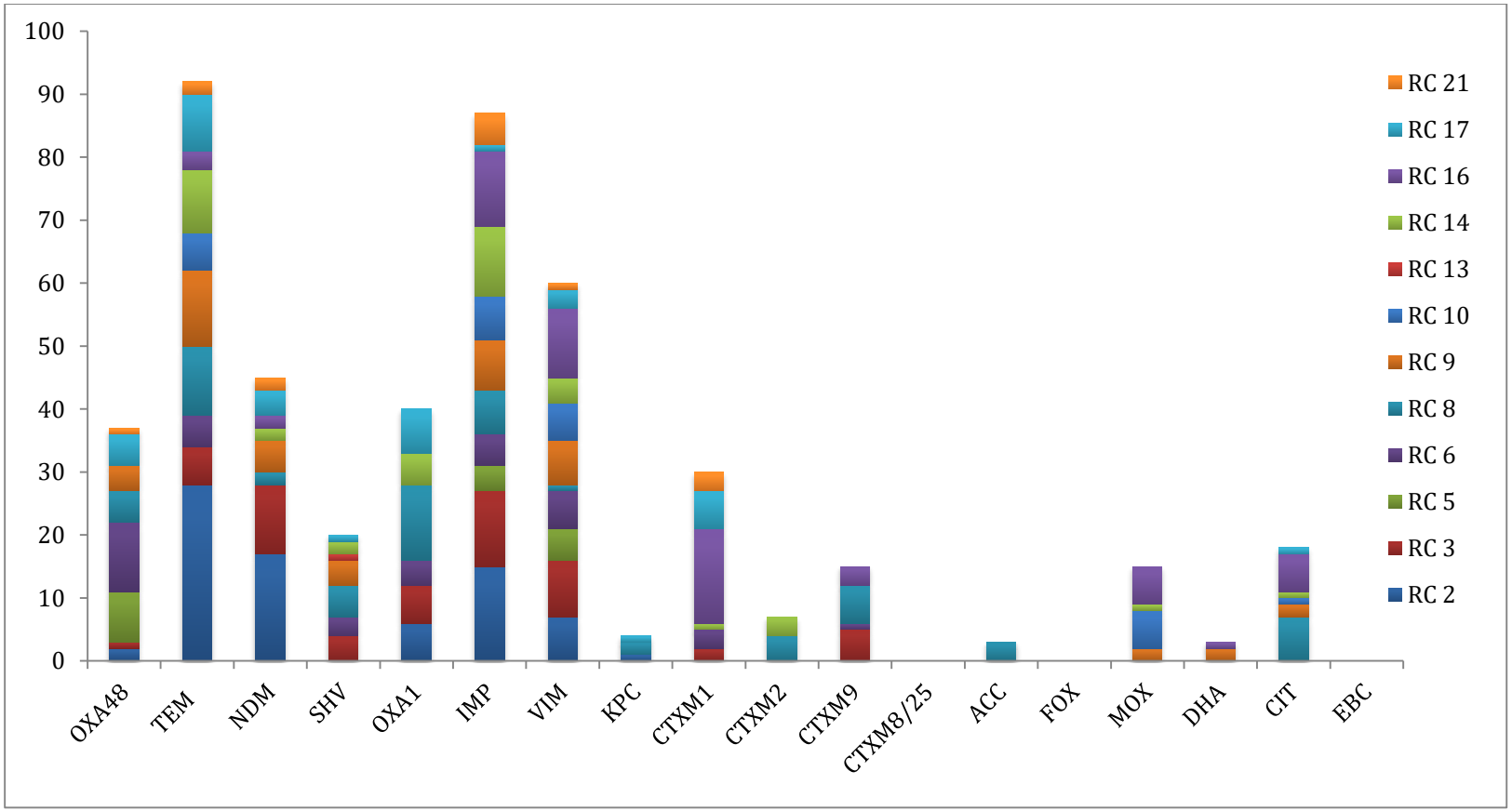


Figure 2.8: Various resistance genes in *E. coli* isolates from different regional centres across India (2024)

The stacked bar graph in **Figure 2.8** represents the prevalence of resistant genes in *E. coli* isolates received from the regional centres (RC = 12) in the year 2024. Each colour on the bar graph represents a different regional centre (data table below).

CENTRE	OXA48	TEM	NDM	SHV	OXA1	IMP	VIM	KPC	CTXM1	CTXM2	CTXM9	CTXM8/25	ACC	FOX	MOX	DHA	CIT	EBC
RC2 (N=36)	2	28	17	0	6	15	7	1	0	0	0	0	0	0	0	0	0	0
RC3 (N=23)	1	6	11	4	6	12	9	0	2	0	5	0	0	0	0	0	0	0
RC5 (N=11)	8	0	0	0	0	4	5	0	0	0	0	0	0	0	0	0	0	0
RC6 (N=33)	11	5	0	3	4	5	6	0	3	0	1	0	0	0	0	0	0	0
RC8 (N=45)	5	11	2	5	12	7	1	2	0	4	6	0	3	0	0	0	7	0
RC9 (N=33)	4	12	5	4	0	8	7	0	0	0	0	0	0	0	2	2	2	0
RC10 (N=22)	0	6	0	0	0	7	6	0	0	0	0	0	0	0	6	0	1	0
RC13 (N=1)	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RC14 (N=34)	0	10	2	2	5	11	4	0	1	3	0	0	0	0	1	0	1	0
RC16 (N=27)	0	3	2	0	0	12	11	0	15	0	3	0	0	0	6	1	6	0
RC17 (N=35)	5	9	4	1	7	1	3	1	6	0	0	0	0	0	0	0	1	0
RC21 (N=11)	1	2	2	0	0	5	1	0	3	0	0	0	0	0	0	0	0	0

Table 2.21: Percentage positivity of resistant genes in *E. coli* from each centre

CENTRE	OXA48	TEM	NDM	SHV	OXA1	IMP	VIM	KPC	CTXM1	CTXM2	CTXM9	CTXM8/25	ACC	FOX	MOX	DHA	CIT	EBC
RC2 (N=36)	6%	78%	47%	0	17%	42%	19%	3%	0	0	0	0	0	0	0	0	0	0
RC3 (N=23)	4%	26%	48%	17%	26%	52%	39%	0	9%	0	22%	0	0	0	0	0	0	0
RC5 (N=11)	73%	0	0	0	0	36%	45%	0	0	0	0	0	0	0	0	0	0	0
RC6 (N=33)	33%	15%	0	9%	12%	15%	18%	0	9%	0	3%	0	0	0	0	0	0	0
RC8 (N=45)	11%	24%	4%	11%	27%	16%	2%	4%	0	9%	13%	0	7%	0	0	0	16%	0
RC9 (N=33)	12%	36%	15%	12%	0	24%	21%	0	0	0	0	0	0	0	6%	6%	6%	0
RC10 (N=22)	0	27%	0	0	0	32%	27%	0	0	0	0	0	0	0	27%	0	5%	0
RC13 (N=1)	0	0	0	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RC14 (N=34)	0	29%	6%	6%	15%	32%	12%	0	3%	9%	0	0	0	0	3%	0	3%	0
RC16 (N=27)	0	11%	7%	0	0	44%	41%	0	56%	0	11%	0	0	0	22%	4%	22%	0
RC17 (N=35)	14%	26%	11%	3%	20%	3%	9%	3%	17%	0	0	0	0	0	0	0	3%	0
RC21 (N=11)	9%	18%	18%	0	0	45%	9%	0	27%	0	0	0	0	0	0	0	0	0

Molecular characterisation of *K. pneumoniae* isolates

Three hundred nine (309) *K. pneumoniae* isolates were subjected to four multiplex PCRs and two monoplex PCRs for OXA-48 and NDM. Overall, the TEM gene was the predominant one present in 33.66% of the isolates, followed by OXA-48 in 25.57%, SHV in 22.98% NDM-1 & OXA1 each in 14.89%, VIM in 13.77%, CTXM1 in 8.41%, KPC in 6.47%, IMP 5.83%, MOX in 2.59%, CIT in 1.94% and CTXM-9 in 1.29% (**Figure 2.9).**

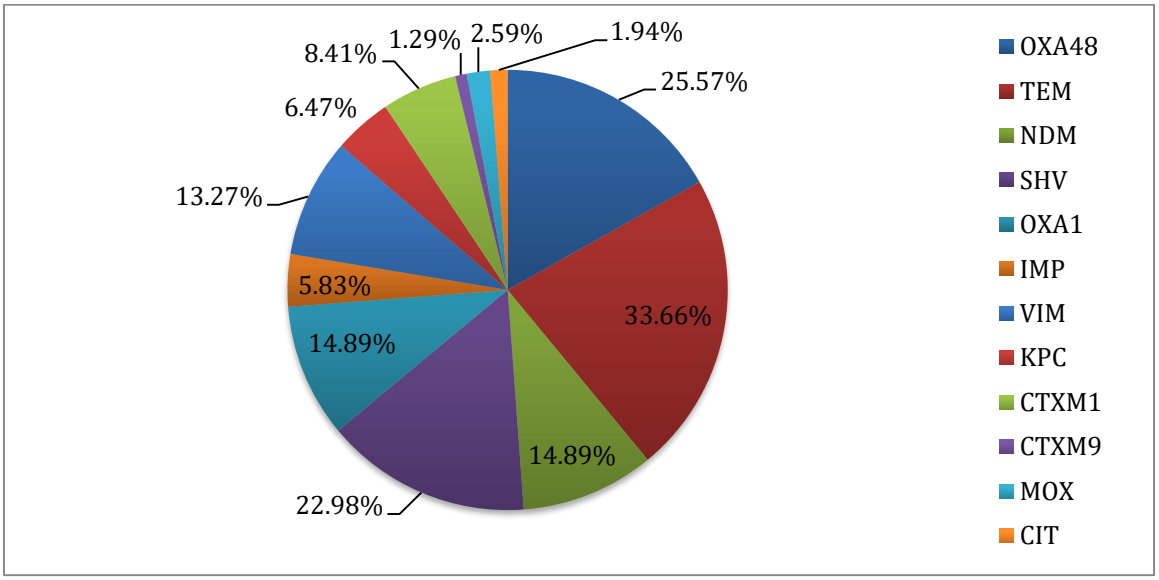


Figure 2.9: Percentage positivity of AMR-associated genetic determinants in *K. pneumoniae* (2024)

RC-wise analysis (**Figure 2.10** and **Table 2.22**) showed that RC2 isolates displayed maximum positivity for SHV (45%), followed by NDM (40%), TEM (38%), OXA-48 (28%), OXA1 (23%), VIM (10%), IMP (5%) and KPC & MOX (3%). In the RC3 samples, NDM showed the highest prevalence at 75%, followed by TEM (41%), CTXM-1 (18%), OXA-48, IMP & VIM (14%) and CTXM-9 (5%). In RC5 isolates, OXA-48 (75%) was the predominant gene, followed by VIM (63%) and KPC (13%). RC6 samples exhibited prevalence of TEM (39%), OXA-48 (31%), VIM (17%), OXA1 & KPC (14%), NDM (11%), SHV & CTXM1 (8%) and CTXM-9 (3%). The RC8 isolates were positive for SHV (43%), TEM & OXA1 (18%), OXA-48, MOX & CIT (15%), NDM, IMP & CTXM-1 (8%), and KPC (3%). The RC9 samples showed a prevalence of OXA-48 (60%), OXA1 (34%), SHV & TEM (23%), and IMP & KPC (3%). RC10 isolates were positive for VIM (11%) and MOX (5%). Within RC13 isolates, TEM (83%), NDM (33%), and CTXM-1 (50%) were detected. RC14 samples exhibited prevalence of TEM (44%), NDM (18%), OXA1 & VIM (15%), SHV (12%), KPC & CTXM-1 (6%) and OXA-48 & IMP (3%). In RC16 samples, TEM (80%), CTXM-1 (60%), OXA-48 (53%), VIM (40%), SHV (33%), KPC (27%), NDM (20%), IMP (13%) and CTXM-9 (7%) were detected. RC17 isolates showed TEM (33%), OXA1, OXA-48 & SHV (17%), NDM, VIM & KPC (8%) and IMP & CTXM-9 (3%) prevalence. In RC21, SHV (56%), TEM (39%), OXA-48 (33%), IMP & VIM each (28%), NDM (17%), KPC & CTXM1 each (11%), and OXA1 (6%) were observed.

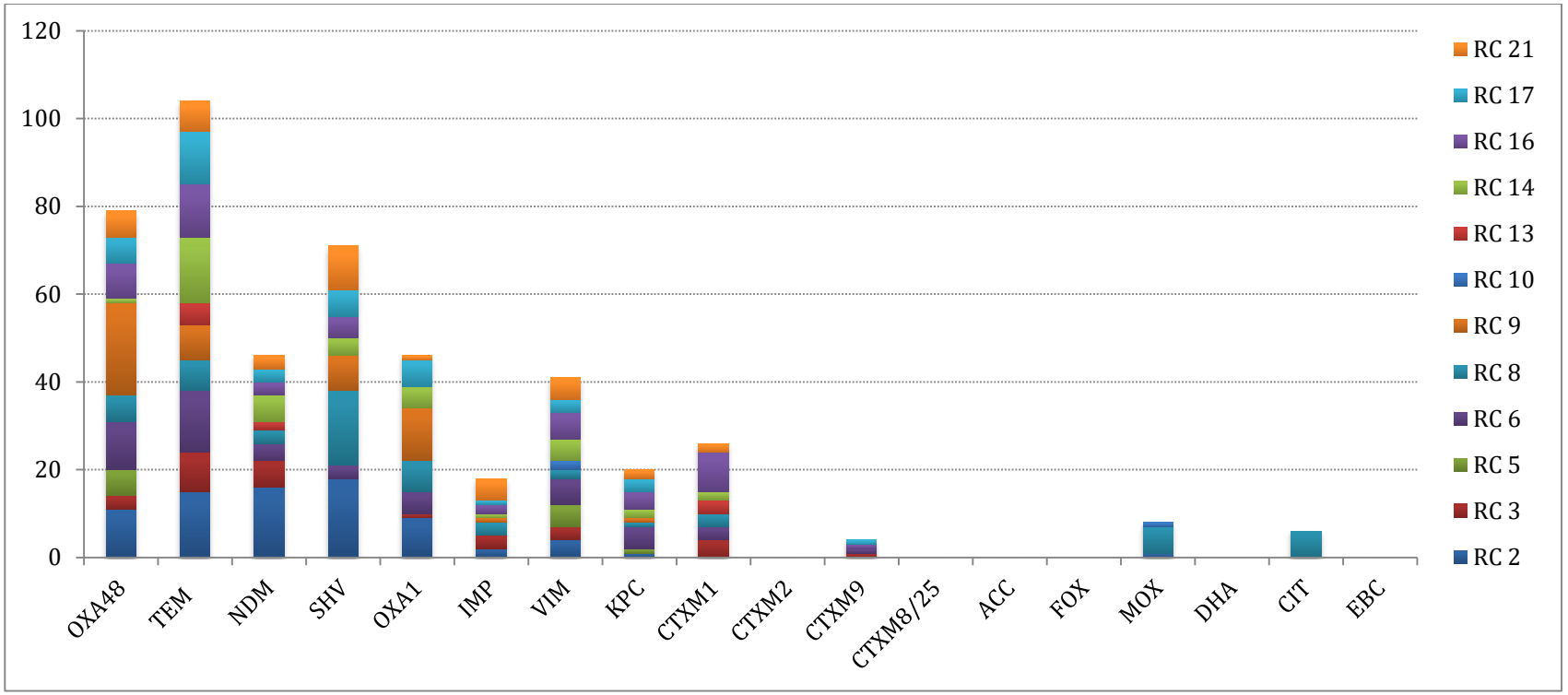


Figure 2.10: Various resistance genes in *K. pneumoniae* isolates from different regional centres across India (2024)

The stacked bar graph in **Figure 2.10** represents the prevalence of resistant genes in *K. pneumoniae* isolates received from the regional centres (RC = 12) in the year 2024. Each colour on the bar graph represents a different regional centre (data table below).

CENTRE	OXA48	TEM	NDM	SHV	OXA1	IMP	VIM	KPC	CTXM1	CTXM2	CTXM9	CTXM8/25	ACC	FOX	MOX	DHA	CIT	EBC
RC2 (N=40)	11	15	16	18	9	2	4	1	0	0	0	0	0	0	1	0	0	0
RC3 (N=22)	3	9	6	0	1	3	3	0	4	0	1	0	0	0	0	0	0	0
RC5 (N=8)	6	0	0	0	0	0	5	1	0	0	0	0	0	0	0	0	0	0
RC6 (N=36)	11	14	4	3	5	0	6	5	3	0	1	0	0	0	0	0	0	0
RC8 (N=40)	6	7	3	17	7	3	2	1	3	0	0	0	0	0	6	0	6	0
RC9 (N=35)	21	8	0	8	12	1	0	1	0	0	0	0	0	0	0	0	0	0
RC10 (N=19)	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0
RC13 (N=6)	0	5	2	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
RC14 (N=34)	1	15	6	4	5	1	5	2	2	0	0	0	0	0	0	0	0	0
RC16 (N=15)	8	12	3	5	0	2	6	4	9	0	1	0	0	0	0	0	0	0
RC17 (N=36)	6	12	3	6	6	1	3	3	0	0	1	0	0	0	0	0	0	0
RC21 (N=18)	6	7	3	10	1	5	5	2	2	0	0	0	0	0	0	0	0	0

Table 2.22: Percentage positivity of resistant genes in *K. pneumoniae* from each centre

CENTRE	OXA48	TEM	NDM	SHV	OXA1	IMP	VIM	KPC	CTXM1	CTXM2	CTXM9	CTXM8/25	ACC	FOX	MOX	DHA	CIT	EBC
RC2 (N=40)	28%	38%	40%	45%	23%	5%	10%	3%	0	0	0	0	0	0	3%	0	0	0
RC3 (N=22)	14%	41%	75%	0	5%	14%	14%	0	18%	0	5%	0	0	0	0	0	0	0
RC5 (N=8)	75%	0	0	0	0	0	63%	13%	0	0	0	0	0	0	0	0	0	0
RC6 (N=36)	31%	39%	11%	8%	14%	0	17%	14%	8%	0	3%	0	0	0	0	0	0	0
RC8 (N=40)	15%	18%	8%	43%	18%	8%	5%	3%	8%	0	0	0	0	0	15%	0	15%	0
RC9 (N=35)	60%	23%	0	23%	34%	3%	0	3%	0	0	0	0	0	0	0	0	0	0
RC10 (N=19)	0	0	0	0	0	0	11%	0	0	0	0	0	0	0	5%	0	0	0
RC13 (N=6)	0	83%	33%	0	0	0	0	0	50%	0	0	0	0	0	0	0	0	0
RC14 (N=34)	3%	44%	18%	12%	15%	3%	15%	6%	6%	0	0	0	0	0	0	0	0	0
RC16 (N=15)	53%	80%	20%	33%	0	13%	40%	27%	60%	0	7%	0	0	0	0	0	0	0
RC17 (N=36)	17%	33%	8%	17%	17%	3%	8%	8%	0	0	3%	0	0	0	0	0	0	0
RC21 (N=18)	33%	39%	17%	56%	6%	28%	28%	11%	11%	0	0	0	0	0	0	0	0	0

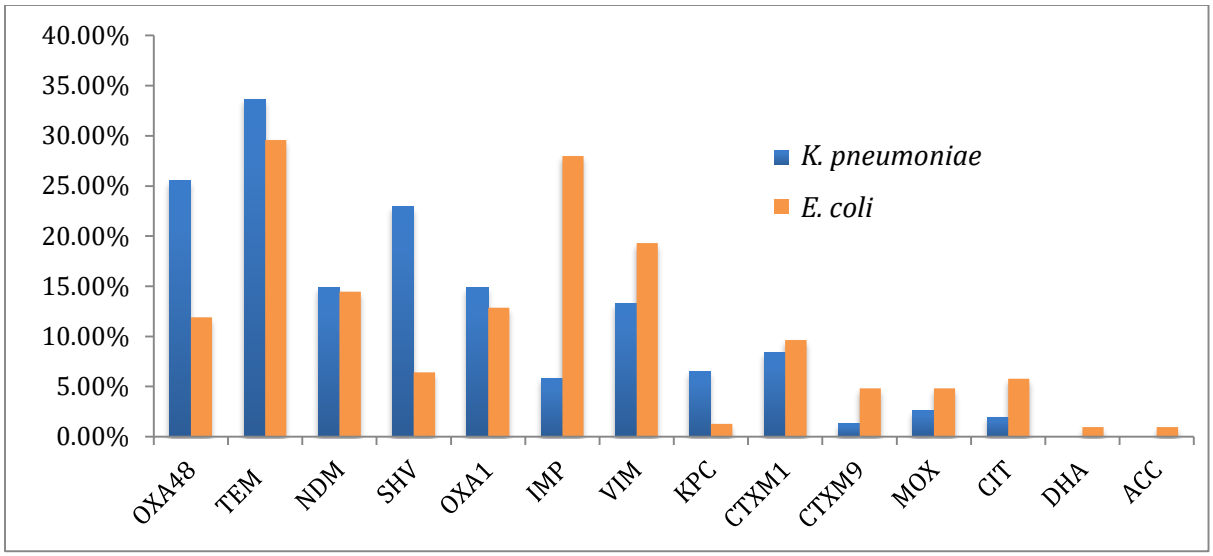


Figure 2.11: Comparison of resistance genes present in *E. coli* and *K. pneumoniae* isolates from regional centres across India (2024)

As seen in **Figure 2.11,** a comparison between *E. coli* (n= 11) and *K. pneumoniae* (n=309) isolates received from RCs (n= 2) in 2024 revealed a higher prevalence of resistance genes in *Klebsiella* isolates than *E. coli*.

Clinical relevance

The increasing prevalence of carbapenem-resistant Enterobacterales (CREs) in healthcare-associated infections has made these infections more difficult to treat and has contributed to higher mortality. As in previous years, *E. coli* and *K. pneumoniae* remain the most frequently isolated and clinically important species, exhibiting marked resistance to multiple antimicrobial classes. The situation is further compounded by the fact that carbapenemase genes are commonly located on mobile genetic elements, which facilitate horizontal transfer of resistance within Enterobacterales and to other Gram-negative organisms. As a result, the potential for rapid and widespread dissemination of resistance continues to grow.

Over the last two decades, the carbapenem use has increased manifold, and the same is reflected in declining imipenem susceptibility of *E. coli* from 81% in 2017 to 58% in 2024, while meropenem susceptibility has dropped from 73% to 63% over the same period. *K. pneumoniae* shows an even more profound decline, with 2024 susceptibility rates of 31% for imipenem, 35% for meropenem, and 25% for ertapenem in certain ICU settings. These values fall well below the thresholds required for empirical therapy, especially in critically ill patients, and point to the widespread dissemination of carbapenemase-producing strains across multiple regions. ICU isolates consistently exhibited lower

susceptibility than those from wards and outpatient settings, highlighting the intense antibiotic selection pressure in critical care units and the potential for intra-hospital transmission of resistant clones.

The declining efficacy of carbapenems has driven increased reliance on colistin, a last-resort antimicrobial agent. This trend is concerning given colistin's known toxicity and the emerging resistance, despite its preserved *in vitro* sensitivity, with *E. coli* showing 99.5% susceptibility and *K. pneumoniae* 96.1% in 2024. Although these figures appear reassuring, notable rates of colistin resistance have already been reported in some *K. pneumoniae* isolates from ICUs, underscoring the urgency of restricting its use. As a salvage therapy, colistin should not be considered a cornerstone of treatment and must be reserved for situations where no safer or more effective alternatives exist.

Cefotaxime and ceftazidime continue to demonstrate markedly reduced efficacy against *E. coli*, with susceptibilities falling to 15–28%, while ciprofloxacin activity has declined to below 11%. These trends clearly indicate that cephalosporins and fluoroquinolones can no longer be considered viable empiric options for this species. The situation for *K. pneumoniae* is even more concerning. Third-generation cephalosporins remain active in fewer than 10% of isolates, and ciprofloxacin susceptibility is similarly low. Even piperacillin-tazobactam, which was previously used as a step-down agent, demonstrated poor coverage, highlighting the diminishing role of beta-lactam–beta-lactamase inhibitor combinations in current practice.

Aminoglycosides continue to show partial utility. Amikacin retained 73% activity against *E. coli*, offering a possible option for combination therapy in bloodstream infections (BSI). However, its effectiveness against *K. pneumoniae* was substantially lower, with only 40% overall susceptibility and as low as 28% in ICU isolates. These findings emphasize an increasingly narrowing therapeutic window, with aminoglycosides functioning only as partially reliable agents and their use limited by toxicity concerns and the need for therapeutic drug monitoring.

Other Enterobacterales species demonstrated more variable susceptibility patterns. *Proteus mirabilis*, *Morganella morganii,* and *Citrobacter koseri* generally retained higher levels of susceptibility across multiple antimicrobial classes, particularly when compared with *E. coli* and *K. pneumoniae*. However, resistance in these species was not insignificant, and in ICU isolates demonstrated less favourable susceptibility profiles. Notably, these organisms may still act as reservoirs of resistance determinants and therefore, must be monitored closely.

Urinary isolates of *E. coli* and *K. pneumoniae* also demonstrated a progressive decline in susceptibility to most antibiotics over the eight-year period (2017-2024), reflecting the broader trend of increasing antimicrobial resistance. *E. coli* maintained comparatively higher resistance, with susceptibilities to piperacillin-tazobactam falling from 73.7% to

55.9%, carbapenems moderately declining (imipenem 88.3% to 68.8%, meropenem 80.6% to 73.0%), and fluoroquinolones remaining largely ineffective. Fosfomycin (92.2%) and nitrofurantoin (80.8%) continued to serve as reliable oral options.

In contrast, *K. pneumoniae* exhibited far more profound resistance. Piperacillin-tazobactam susceptibility fell to 33.8%, carbapenems to 42.8–49.5%, and amikacin to 50.0%, while nitrofurantoin and most other agents were largely ineffective. Overall, *K. pneumoniae* represents a higher-risk urinary pathogen, emphasizing the need for strengthened antimicrobial stewardship and rigorous infection-control measures in the management of UTIs.

From a stewardship and infection control standpoint, these findings demand urgent, coordinated action. The markedly reduced susceptibility in ICU isolates compared to OPD and ward isolates further underscores the need for empiric treatment guidelines tailored to high-risk settings, alongside stringent infection-control practices to prevent cross-transmission of carbapenem-resistant Enterobacterales.

In conclusion, the 2024 Enterobacterales data highlight the persistence and continued progression of multidrug resistance, with *E. coli* and *K. pneumoniae* posing the most significant clinical challenges. Strengthening the surveillance systems, antimicrobial stewardship, rapid diagnostic capabilities, and infection-control measures are essential to mitigate the impact of these increasingly resistant pathogens.

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

A total of 22,831 non-fermenting Gram-negative bacteria (NFGNB) isolates were collected from various clinical settings in India. Among these, *Pseudomonas aeruginosa* represented the largest proportion with 11,419 isolates (50.0%), followed by *Acinetobacter baumannii* with 10,351 isolates (45.3%), *Stenotrophomonas maltophilia* with 726 isolates (3.2%), and *Burkholderia cepacia* with 334 isolates (1.5%). Surveillance data from 2017–2024 reveal high resistance to carbapenems, cephalosporins, and fluoroquinolones in *A. baumannii* and *P. aeruginosa*. However, colistin and minocycline remain largely effective. *S. maltophilia* shows stable susceptibility to minocycline and trimethoprim-sulfamethoxazole (TMP-SMX), while *B. cepacia* maintains sensitivity against ceftazidime, meropenem, and co-trimoxazole. Overall, these findings highlight an evolving resistance landscape, emphasizing the need for continued antimicrobial stewardship and the development of novel therapeutic approaches.

Pseudomonas aeruginosa

In 2024, a total of 11,419 *P. aeruginosa* isolates were collected from multiple centres across India, including OPD (N=3,781), ward (N=5,673), and ICU (N=1,965) settings. Location-wise analysis **(Table 3.1)** revealed that colistin remained the most active agent with 97.7% susceptibility across all clinical areas, followed by amikacin (73.3%) and gentamicin (69.8%). Among β-lactams, piperacillin-tazobactam exhibited 69.3% susceptibility, cefepime 67.5%, and ceftazidime 64.2%. Carbapenems exhibited lower activity, with meropenem at 62% and imipenem at 56.9%. OPD isolates generally demonstrated higher susceptibility compared to ward and ICU isolates, with ICU isolates showing the lowest susceptibility to most agents, including imipenem (43%) and levofloxacin (40.4%). Sample-wise analysis **(Table 3.2)** indicated that lower respiratory tract (LRT) specimens had higher susceptibility to most antimicrobials, while blood and urine isolates showed reduced susceptibility. Colistin consistently maintained high intermediate susceptibility (>97%) across all sample types. Fluoroquinolones, particularly levofloxacin (54%) and ciprofloxacin (57%), showed relatively lower activity. Temporal analysis over the last eight years **(Table 3.3, Figure 3.1)** revealed mostly stable susceptibility patterns for most antibiotics, though a gradual decline in carbapenem susceptibility emphasizes the ongoing challenge of multidrug resistance in *P. aeruginosa* across Indian healthcare settings.

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

AMA	Total N=11419 (S%)	OPD N=3781 (S%)	Ward N=5673 (S%)	ICU N=1965 (S%)
Piperacillin-tazobactam	7242/10443 (69.3)	2706 / 3389 (79.8)	3399 / 5092 (66.8)	1137 / 1965 (57.9)
Cefepime	6964/10317 (67.5)	2588 / 3352 (77.2)	3354 / 5033 (66.6)	1022 / 1932 (52.9)
Ceftazidime	7306/11381 (64.2)	2775 / 3753 (73.9)	3502 / 5627 (62.2)	1007 / 1965 (51.2)
Imipenem	5944/10443 (56.9)	2219 / 3387 (65.5)	2880 / 5091 (56.6)	845 / 1965 (43)
Meropenem	6730/10857 (62)	2480 / 3491 (71)	3299 / 5380 (61.3)	942 / 1965 (47.9)
Colistin*	5281/5408 (97.7)	1535 / 1559 (98.5)	2489 / 2561 (97.2)	1257 / 1288 (97.6)
Amikacin	7017/9578 (73.3)	2641 / 3282 (80.5)	3577 / 4934 (72.5)	772 / 1329 (58.1)
Gentamicin	2373/3399 (69.8)	977 / 1272 (76.8)	1094 / 1589 (68.8)	302 / 538 (56.1)
Tobramycin	3099/4522 (68.5)	1262 / 1585 (79.6)	1370 / 1988 (68.9)	467 / 949 (49.2)
Ciprofloxacin	6397/11222 (57)	2288 / 3711 (61.7)	3159 / 5518 (57.2)	935 / 1965 (47.6)
Levofloxacin	4537/8407 (54)	1604 / 2727 (58.8)	2340 / 4220 (55.5)	587 / 1454 (40.4)
Polymixin B	0/223 (0)	0 / 20 (-)	0 / 112 (0)	0 / 91 (0)

*Colistin represents the percentage of intermediate susceptibility

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

AMA	Blood N=1026 (S%)	LRT N=3858 (S%)	SI N=2032 (S%)	DI N=1678 (S%)	CSF N=64 (S%)	Urine N=1534 (S%)
Piperacillin-tazobactam	665/1020 (65.2)	2800/3720 (75.3)	1276/1824 (70)	1158/1668 (69.4)	35/63 (55.6)	667/1175 (56.8)
Cefepime	695/1011 (68.7)	2685/3677 (73)	1163/1800 (64.6)	1140/1659 (68.7)	35/63 (55.6)	592/1140 (51.9)
Ceftazidime	681/1025 (66.4)	2778/3858 (72)	1254/2032 (61.7)	1071/1678 (63.8)	33/64 (51.6)	707/1486 (47.6)
Imipenem	634/1020 (62.2)	2332/3720 (62.7)	1035/1824 (56.7)	844/1668 (50.6)	25/63 (39.7)	533/1175 (45.4)
Meropenem	683/1022 (66.8)	2556/3734 (68.5)	1264/1931 (65.5)	964/1671 (57.7)	26/63 (41.3)	609/1335 (45.6)
Colistin*	717/742 (96.6)	1506/1521 (99)	1103/1131 (97.5)	587/611 (96.1)	31/35 (88.6)	951/973 (97.7)
Amikacin	634/826 (76.8)	2465/3049 (80.8)	1152/1595 (72.2)	1054/1452 (72.6)	36/60 (60)	887/1505 (58.9)
Levofloxacin	470/717 (65.6)	2063/3276 (63)	716/1451 (49.3)	526/1112 (47.3)	25/54 (46.3)	343/921 (37.2)

*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
	N=5687	N=8880	N=12634	N=7839	N=11622	N=13228	N=11757	N=11419
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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)
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)
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)
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)
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)
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)
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)
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)
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)
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)
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)

*Colistin represents percentage intermediate susceptibility

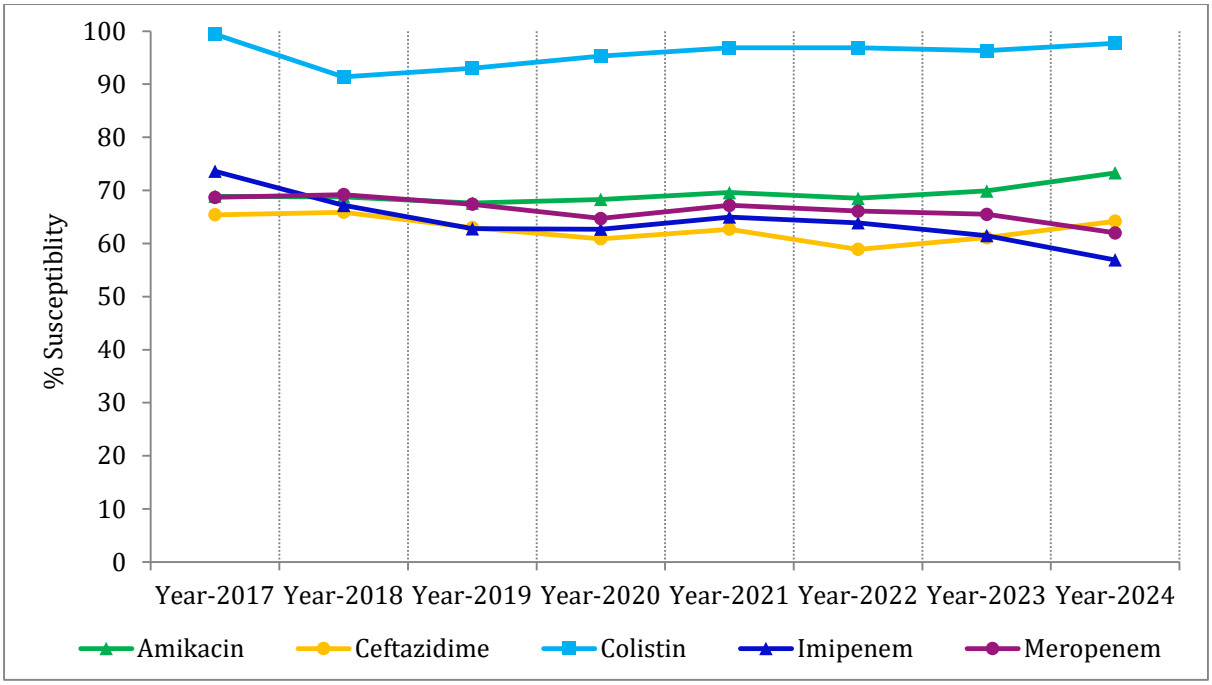


Figure 3.1: Yearly susceptibility trend of *Pseudomonas aeruginosa* isolated from all samples

Acinetobacter baumannii

In 2024, a total of 10,351 *A. baumannii* isolates were collected from multiple centres across India, including outpatient (N=1,341), ward (N=4,901), and ICU (N=4,109) settings. Location-wise analysis **(Table 3.4)** revealed that colistin retained the highest activity, with 97.4% overall susceptibility, followed by minocycline (70.2%). Other antibiotics, such as piperacillin-tazobactam (11.7%), cefepime (8.9%), ceftazidime (10.4%), carbapenems like meropenem (9%) and imipenem (8.4%), and amikacin (15.8%), demonstrated markedly lower susceptibility. OPD isolates showed relatively higher susceptibility compared to ward and ICU isolates, while ICU isolates consistently displayed the lowest susceptibility across most agents. Sample-wise analysis **(Table 3.5)** indicated that colistin remained highly effective (>95% intermediate susceptibility) across blood, respiratory, superficial, deep infection, CSF, and urine specimens. Minocycline retained good activity across sample types, while most β-lactams, carbapenems, and fluoroquinolones demonstrated limited efficacy, especially in LRT and deep infection samples. Temporal analysis over the past eight years **(Table 3.6, Figure 3.2)** demonstrated persistently low susceptibility to most antibiotics, except for colistin and minocycline, which maintained high effectiveness. This underscores the ongoing challenge of multidrug resistance 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=10351 (S%)	OPD N=1341 (S%)	Ward N=4901 (S%)	ICU N=4109 (S%)
Piperacillin-tazobactam	1148/9852 (11.7)	372 / 1264 (29.4)	501 / 4480 (11.2)	275 / 4109 (6.7)
Cefepime	869/9741 (8.9)	269 / 1255 (21.4)	438 / 4415 (9.9)	162 / 4072 (4)
Ceftazidime	1081/10351 (10.4)	254 / 1340 (19)	591 / 4899 (12.1)	235 / 4108 (5.7)
Imipenem	826/9852 (8.4)	208 / 1264 (16.5)	455 / 4480 (10.2)	163 / 4109 (4)
Meropenem	924/10304 (9)	256 / 1323 (19.3)	481 / 4857 (9.9)	187 / 4108 (4.6)
Colistin*	5194/5331 (97.4)	757/765 (99.1)	1927/1997 (69.5)	2510/2569 (97.7)
Amikacin	1638/10351 (15.8)	389 / 1341 (29)	860 / 4901 (17.5)	386 / 4108 (9.4)
Minocycline	5873/8368 (70.2)	933 / 1135 (82.2)	2546 / 3731 (68.2)	2384 / 3491 (68.3)
Levofloxacin	830/6809 (12.2)	188 / 918 (20.5)	451 / 3138 (14.4)	189 / 2750 (6.9)

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

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

AMA	Blood N=2142 (S%)	LRT N=4804 (S%)	SI N=1112 (S%)	DI N=940 (S%)	CSF N=225 (S%)	Urine N=289 (S%)
Piperacillin-tazobactam	265/2139 (12.4)	459/4701 (9.8)	145/957 (15.2)	59/933 (6.3)	32/211 (15.2)	107/289 (37)
Cefepime	213/2121 (10)	335/4666 (7.2)	92/929 (9.9)	61/923 (6.6)	27/206 (13.1)	65/277 (23.5)
Ceftazidime	199/2142 (9.3)	518/4804 (10.8)	107/1112 (9.6)	61/940 (6.5)	25/225 (11.1)	64/289 (22.1)
Imipenem	178/2139 (8.3)	303/4701 (6.4)	100/957 (10.4)	86/933 (9.2)	21/211 (10)	66/289 (22.8)
Meropenem	208/2142 (9.7)	342/4790 (7.1)	108/1097 (9.8)	65/939 (6.9)	22/224 (9.8)	92/289 (31.8)
Colistin*	1672/1736 (96.3)	1943/1975 (98.4)	637/648 (98.3)	311/326 (95.4)	102/110 (92.7)	220/224 (98.2)
Amikacin	402/2142 (18.8)	591/4804 (12.3)	208/1112 (18.7)	98/940 (10.4)	36/225 (16)	124/289 (42.9)
Minocycline	1374/1775 (77.4)	2532/3907 (64.8)	686/959 (71.5)	497/626 (79.4)	157/193 (81.3)	177/261 (67.8)
Levofloxacin	212/1125 (18.8)	332/3831 (8.7)	90/695 (12.9)	25/302 (8.3)	11/106 (10.4)	92/250 (36.8)

*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 N=3359 (S%)	Year-2018 N=4549 (S%)	Year-2019 N= 8531 (S%)	Year-2020 N=6849 (S%)	Year-2021 N= 12393 (S%)	Year-2022 N= 12142 (S%)	Year-2023 N= 11948 (S%)	Year-2024 N= 10351 (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)
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)
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)
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)
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)
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)
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)
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)
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)

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

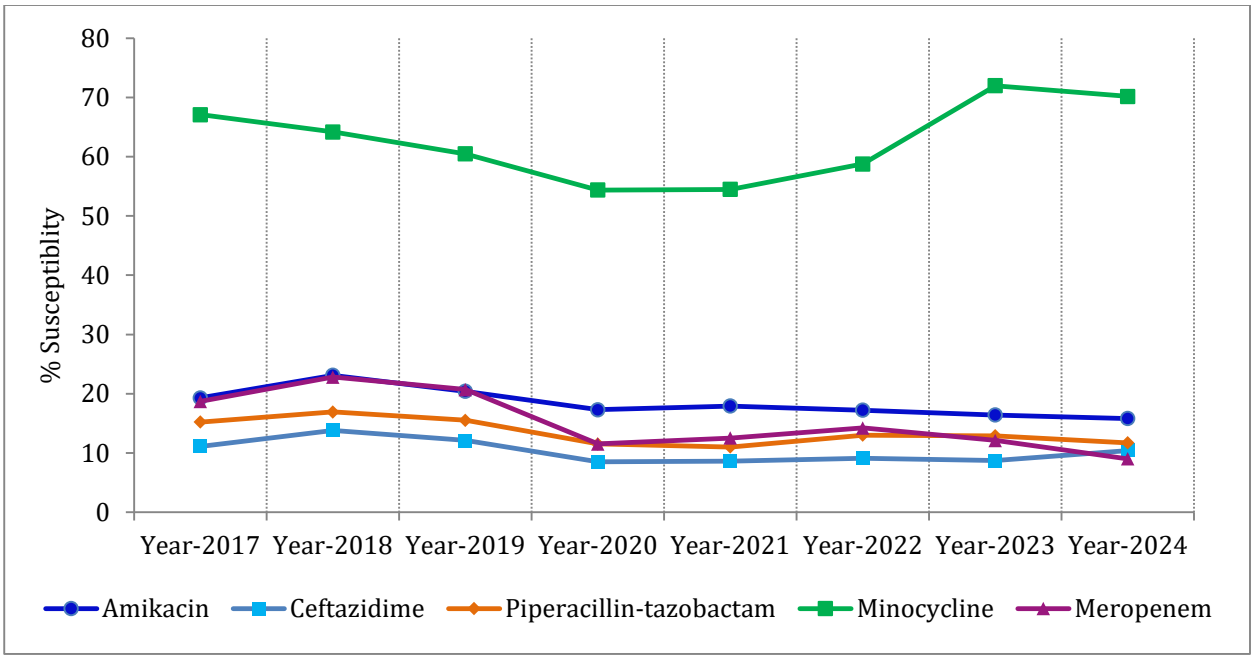


Figure 3.2: Yearly susceptibility trend of *A. baumannii* isolated from all samples (except faeces)

Stenotrophomonas maltophilia

In 2024, a total of 726 *S. maltophilia* isolates were collected across OPD (N=120), ward (N=350), and ICU (N=256) settings. Location-wise analysis **(Table 3.7)** revealed that minocycline had the highest overall susceptibility at 95.5%, followed by levofloxacin (88.6%) and TMP-SMX (87.4%). Ceftazidime showed moderate activity (58.3%), while ticarcillin-clavulanic acid and chloramphenicol exhibited negligible or variable effectiveness. Sample-wise distribution **(Table 3.8)** confirmed these patterns, with minocycline maintaining excellent activity across blood, respiratory, superficial, deep infection, and urine specimens (94–98%). Levofloxacin and TMP-SMX showed moderate effectiveness, whereas ceftazidime and chloramphenicol had limited efficacy across most sample types. Temporal analysis over eight years **(Table 3.9, Figure 3.3)** demonstrated that susceptibility to minocycline has remained consistently high (>95%) since 2017, while levofloxacin and TMP-SMX have maintained stable moderate activity. Overall, minocycline remains the most reliable therapeutic option for *S. maltophilia* infections in Indian healthcare settings, while other antibiotics show variable and often limited effectiveness.

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

AMA	Total N=726 (S%)	Ward N=350 (S%)	ICU N=256 (S%)	OPD N=120 (S%)
Ticarcillin-clavulanic acid	*1 / 4 (-)	*1 / 2 (-)	*0 / 2 (-)	*0 / 0 (-)
Ceftazidime	21 / 36 (58.3)	*7 / 10 (-)	*8 / 14 (-)	*6 / 12 (-)
Minocycline	693 / 726 (95.5)	338 / 350 (96.6)	241 / 256 (94.1)	114 / 120 (95)
Levofloxacin	642 / 725 (88.6)	311 / 349 (89.1)	225 / 256 (87.9)	106 / 120 (88.3)
Trimethoprim-sulfamethoxazole	501 / 573 (87.4)	222 / 253 (87.7)	200 / 234 (85.5)	79 / 86 (91.9)
Chloramphenicol	27 / 50 (54)	*12 / 24 (-)	*7 / 9 (-)	*8 / 17 (-)

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

AMA	All Specimens (except faeces)	Blood	LRT	SI	DI	Urine
	N=724 (S%)	N=173 (S%)	N=306 (S%)	N=53 (S%)	N=63 (S%)	N=*21 (S%)
Ticarcillin-clavulanic acid	*1/4 (-)	*1/2 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
Ceftazidime	2 / 36 (5.6)	*0 / 15 (-)	*2 / 12 (-)	*0 / 2 (-)	*0 / 2 (-)	*0 / 2 (-)
Minocycline	698/731 (95.5)	167/173 (96.5)	289/306 (94.4)	55/56 (98.2)	61/63 (96.8)	*20/21 (-)
Levofloxacin	646/730 (88.5)	166/173 (96)	263/306 (85.9)	51/56 (91.1)	54/63 (85.7)	*19/21 (-)
Trimethoprim-sulfamethoxazole	501/573 (87.4)	151/169 (89.3)	247/287 (86.1)	30/32 (93.8)	20/21 (-)	*15/15 (-)
Chloramphenicol	27/50 (54)	*1/3 (-)	*0/0 (-)	*2/6 (-)	*12/24 (-)	*0/0 (-)

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
	N=157	N=310	N=374	N=360	N=766	N=827	N=1011	N=726
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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 (-)
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)
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)
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)
Chloramphenicol	*0/0 (-)	*1/2 (-)	*3/3 (-)	*8/9 (-)	*2/2 (-)	*4/5 (-)	21/35 (60)	27 / 50 (54)

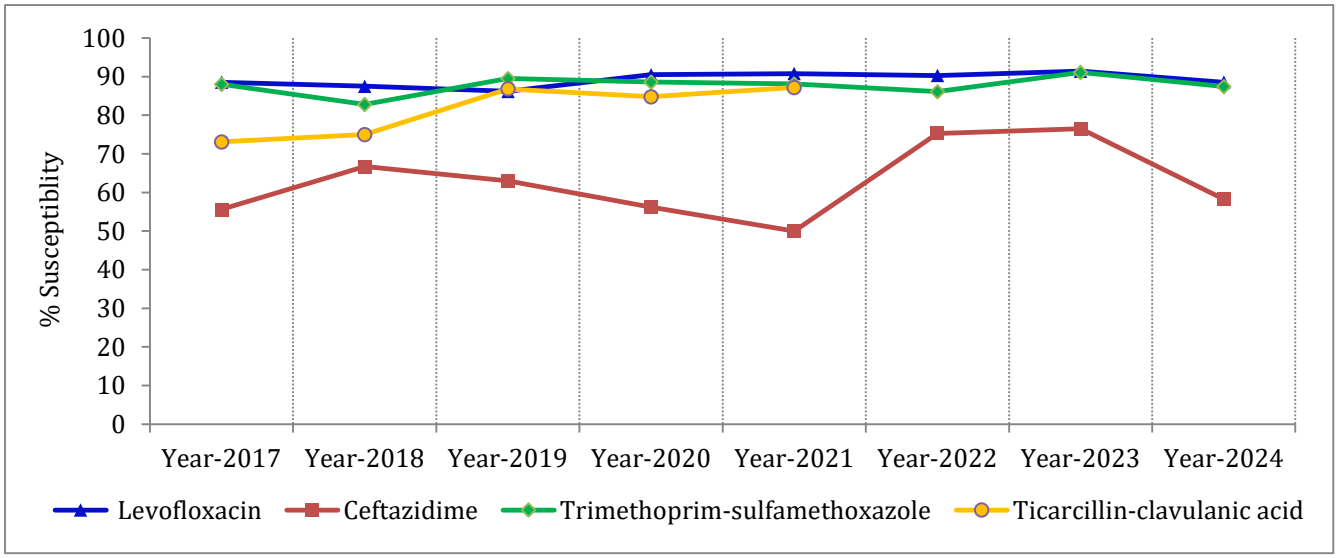


Figure 3.3: Yearly susceptibility trend of *Stenotrophomonas maltophilia* isolated from all samples

Burkholderia cepacia

In 2024, a total of 334 *Burkholderia cepacia* isolates were collected across OPD (N=33), ward (N=116), and ICU (N=185) settings. Location-wise susceptibility **(Table 3.10)** revealed that ceftazidime (91.6%) and meropenem (89.8%) remained the most active antimicrobials, followed by TMP-SMX (87.4%) and minocycline (71.3%). Levofloxacin showed moderate activity (51.5%), while ticarcillin-clavulanic acid and chloramphenicol demonstrated minimal effectiveness. Sample-wise analysis **(Table 3.11)** confirmed these trends across blood, lower respiratory tract, superficial and deep infections, and sterile site specimens, with ceftazidime and meropenem maintaining high efficacy (89–94%) and minocycline and TMP-SMX showing good activity. Temporal analysis over the past eight years **(Table 3.12, Figure 3.4)** showed consistent high susceptibility of ceftazidime and meropenem since 2017, while minocycline displayed a slight decline in activity over the years. Overall, ceftazidime, meropenem, and TMP-SMX remain the preferred therapeutic options for *B. cepacia* infections in Indian clinical settings in 2024.

Table 3.10: Location-wise susceptibility percentages of *Burkholderia cepacia* isolated from all samples across OPD, Ward and ICU

AMA	Total N=334 (S%)	OPD N=33 (S%)	Ward N=116 (S%)	ICU N=185 (S%)
Ticarcillin-clavulanic acid	*2 / 11 (-)	*0 / 0 (-)	*0 / 1 (-)	*2 / 10 (-)
Ceftazidime	306 / 334 (91.6)	30 / 33 (90.9)	105 / 116 (90.5)	171 / 185 (92.4)
Meropenem	300 / 334 (89.8)	32 / 33 (97.0)	100 / 116 (86.2)	168 / 185 (90.8)
Minocycline	238 / 334 (71.3)	23 / 33 (69.7)	83 / 116 (71.6)	132 / 185 (71.4)
Levofloxacin	172 / 334 (51.5)	19 / 33 (57.6)	52 / 116 (44.8)	101 / 185 (54.6)
Trimethoprim-sulfamethoxazole	285 / 326 (87.4)	26 / 33 (78.8)	90 / 108 (83.3)	169 / 185 (91.4)
Chloramphenicol	*13 / 26 (-)	*4 / 7 (-)	*3 / 6 (-)	*6 / 13 (-)

Table 3.11: Sample-wise susceptibility percentages of *Burkholderia cepacia complex*

AMA	All Specimens	Blood	LRT	SI	DI	SS
	N=334	N=190	N=63	N=*15	N=*18	N=*13
Ticarcillin-clavulanic acid	2 / 11 (-)	1 / 7 (-)	0 / 2 (-)	0 / 0 (-)	0 / 0 (-)	1 / 1 (-)
Ceftazidime	306 / 334 (91.6)	175 / 190 (92.1)	59 / 63 (93.7)	11 / 15 (-)	13 / 18 (-)	11 / 13 (-)
Meropenem	300 / 334 (89.8)	171 / 190 (90.0)	56 / 63 (88.9)	12 / 15 (-)	17 / 18 (-)	12 / 13 (-)
Minocycline	238 / 334 (71.3)	140 / 190 (73.7)	42 / 63 (66.7)	6 / 15 (-)	14 / 18 (-)	8 / 13 (-)
Levofloxacin	172 / 334 (51.5)	105 / 190 (55.3)	25 / 63 (39.7)	5 / 15 (-)	12 / 18 (-)	7 / 13 (-)
Trimethoprim-sulfamethoxazole	285 / 326 (87.4)	168 / 190 (88.4)	54 / 61 (88.5)	11 / 15 (-)	17 / 18 (-)	9 / 12 (-)
Chloramphenicol	13 / 26 (-)	5 / 10 (-)	2 / 2 (-)	0 / 0 (-)	4 / 8 (-)	1 / 3 (-)

Table 3.12: Yearly susceptibility trend of *Burkholderia cepacia* isolated from all samples

AMA	Year-2017 N=112	Year-2018 N=197	Year-2019 N=181	Year-2020 N=200	Year-2021 N=247	Year-2022 N=114	Year-2023 N=178	Year-2024 N=334
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Ticarcillin-clavulanic acid	*0/9 (-)	4/51 (7.8)	36/103 (35)	36/80 (45)	13/58 (22.4)	*1/1 (-)	*2/3 (-)	*2/11 (-)
Ceftazidime	73/101 (72.3)	137/192 (71.4)	156/178 (87.6)	172/198 (86.9)	180/237 (75.9)	102/113 (90.1)	91/103 (88.3)	306 / 334 (91.6)
Meropenem	83/111 (74.8)	140/171 (81.9)	161/181 (89)	166/198 (83.8)	199/241 (82.6)	84/116 (72.4)	91/105 (86.7)	300/334 (89.8)
Minocycline	89/104 (85.6)	146/185 (78.9)	133/174 (76.4)	163/191 (85.3)	191/225 (84.9)	90/117 (76.9)	81/109 (74.3)	238/334 (71.3)
Levofloxacin	*4/13 (-)	34/66 (51.5)	70/124 (56.5)	81/125 (64.8)	49/90 (54.4)	27 / 68 (39.7)	77/102 (75.5)	172/334 (51.5)
Trimethoprim-sulfamethoxazole	84/109 (77.1)	179/192 (93.2)	164/177 (92.7)	174/200 (87)	193/234 (82.5)	98/115 (85.2)	99/102 (97.1)	285/326 (87.4)
Chloramphenicol	*0/0 (-)	*1/1 (-)	*3/3 (-)	*4/4 (-)	*3/3 (-)	*1/1 (-)	*5/11 (-)	*13/26 (-)

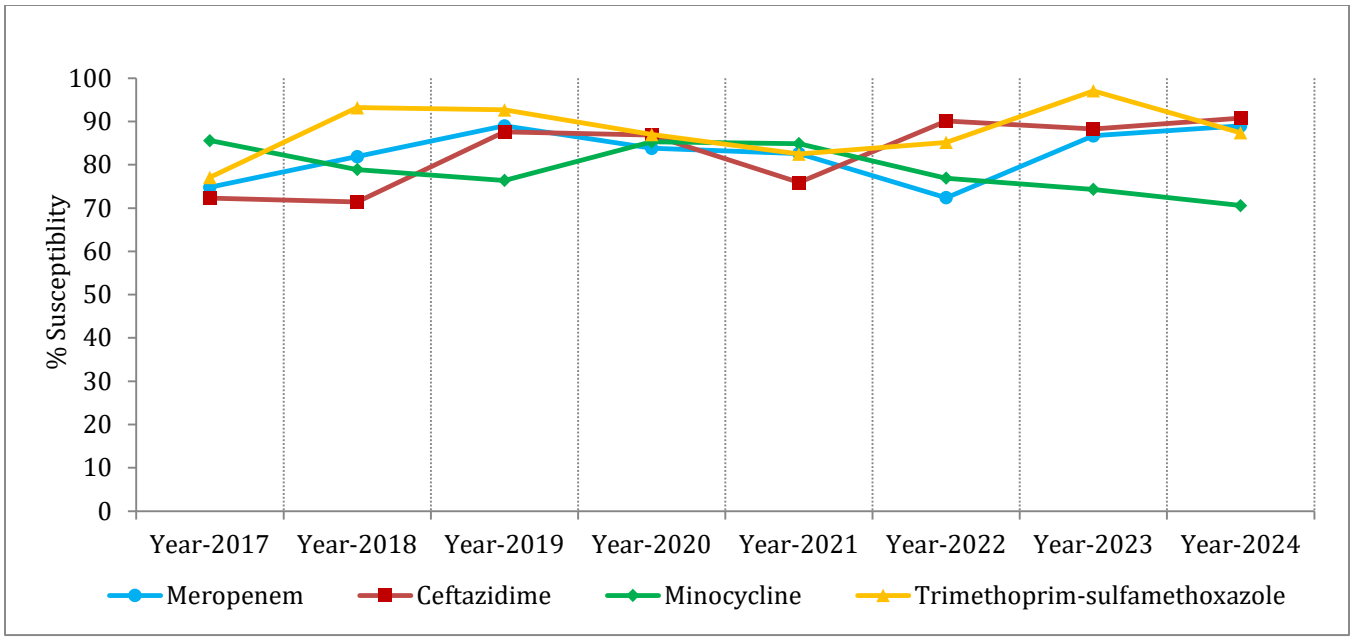


Figure 3.4: Yearly susceptibility trend of *Burkholderia cepacia* isolated from all samples

Molecular mechanism of resistance

Pseudomonas aeruginosa

In this multicentre surveillance analysis, a total of 276 revived *Pseudomonas aeruginosa* isolates collected from 12 Indian centres during 2024 were analyzed for carbapenem resistance and underlying molecular mechanisms (**Table 3.13**). Out of these, 67 isolates (24.3%) were carbapenem-resistant (CR), while 209 isolates (75.7%) remained susceptible (CS). PCR-based molecular screening revealed that metallo-β-lactamases (MβL) were the most common resistance determinants, with NDM detected in 27 isolates (10%) and VIM in 10 isolates (4%). Co-production of MβL with extended-spectrum β-lactamases (VEB) was identified in 10 isolates (3.6%), of which 8 isolates had NDM (3%) and 2 isolates were with VIM (0.7%). Among Class A carbapenemases, KPC and GES were each detected in only one isolate (0.36%), with a few co-producers carrying both KPC along with VEB and/or GES. Class D carbapenemases were rarely observed, with a single OXA-48-like isolate (0.36%) reported. Notably, 222 isolates (80.4%) were PCR-negative for all the screened carbapenemase genes, suggesting that alternate mechanisms, such as efflux pump overexpression, AmpC β-lactamase hyper-production, or porin loss, likely played a major role in conferring carbapenem resistance. Overall, the molecular profile of carbapenem resistance in *P. aeruginosa* across Indian centres in 2024 was predominantly driven by MβL genes, particularly NDM and VIM, while classical KPC, GES, and OXA-type carbapenemases remained uncommon.

Table 3.13: Molecular characterization of carbapenem-resistant *Pseudomonas aeruginosa* isolates collected across India during the year 2024

Centre	Total (Revived tested)	CR	CS	ESBL			Class A Carbapenemase		Class B carbapenemase (MβL's)					Co-producers (n)	PCR Negative
				SHV	TEM	VEB	KPC	GES	SPM	IMP	VIM	NDM	OXA-48 LIKE		
RC5	35(24)	-	24	-	-	-	-	-	-	-	-	-	-	-	24
RC6	60(29)	7	22	-	-	-	-	-	-	-	1	3	-	NDM + VEB (1)	24
RC8	23(17)	4	13	-	-	1		1				2	-	KPC + GES (1)	12
RC9	75(58)	3	55	-	-	-	-	-	-	-	4	3	1	-	50
RC10	32(25)	11	14	-	-	-	-	-	-	-	-	8	-	-	17
RC12	15 (13)	-	13	-	-	-	-	-	-	-	-	-	-	-	13
RC13	16(16)	10	6	-	-	-	-	-	-	-	1	4	-	NDM + VEB (1)	10
RC14	31(28)	6	22	-	-	-	-	-	-	-	-	-	-	-	28
RC16	29(26)	14	12	-	-	-	-	-	-	-	1	3	-	KPC + VEB (3)	19
RC17	30(26)	8	18	-	-	-	-	-	-	-	-	3	-	VIM + VEB (2), NDM + VEB (6)	15
RC21	7(4)	1	3	-	-	-	-	-	-	-	-	1	-	-	3
RC20	45(10)	3	7	-	-	-	-	-	-	-	3	-	-	-	7
TOTAL (12 Centres)	**398 (276)**	**67**	**209**			**1**		**1**			**10**	**27**	**1**	**14**	**222**

Acinetobacter baumannii

A total of 202 *Acinetobacter baumannii* isolates, revived from 11 centres across India, were tested for carbapenem resistance (**Table 3.14)**. Of these, 174 isolates (86.1%) were carbapenem-resistant (CRAB), while 28 (13.9%) were carbapenem-susceptible. Molecular characterization revealed that resistance was primarily driven by Class D carbapenemases, with blaOXA-23 detected in 76 isolates (38%). The most concerning finding was the high frequency of co-producers, with 78 isolates carrying both blaOXA-23 and blaNDM (36%), and a smaller subset carrying blaOXA-23 with blaTEM (2%). This dual carriage of OXA- and NDM-type enzymes represents a critical step in the evolution of CRAB, as it confers resistance to nearly all β-lactams and undermines treatment efficacy. Other carbapenemase classes, including Class A (KPC, GES), Class B (IMP, VIM, SIM), and alternative OXAs (OXA-24, OXA-58), were notably absent, except for sporadic detections of TEM in 6 isolates as a co-producer (2.9%) and OXA-58 in 1 isolate (0.49%). Approximately 44 isolates (21.8%) remained PCR-negative, suggesting the role of additional mechanisms such as efflux pumps, AmpC overexpression, or porin loss. Overall, the multicentre data show that Indian CRAB isolates are overwhelmingly driven by blaOXA-23, with a rapidly expanding integration of blaNDM, often in co-carriage, which significantly amplifies their resistance potential.

Table 3.14: Molecular characterization of carbapenem-resistant *A. baumannii* collected across India during the year 2024

Centre	Total (Revived tested)	CR	CS	ESBL				Class A		Class B carbapenemase (MβLs)				Class D carbapenemase			Co-producers	PCR Negative
				SHV	TEM	VEB	PER	KPC	GES	IMP	VIM	NDM	SIM	OXA-23	OXA-24	OXA-58		
RC5	34 (15)	7	8	-	-	-	-	-	-	-	-	1	-	1	-	-	OXA-23 + NDM (4)	9
RC6	60 (26)	24	2	-	-	-	-	-	-	-	-	-	-	13	-	-	OXA-23 + NDM (10)	3
RC8	12 (5)	4	1	-	-	-	-	-	-	-	-	-	-	2	-	-	OXA-23 + TEM (1), OXA-23 + NDM + TEM (1)	1
RC9	75 (45)	40	5	-	-	-	-	-	-	-	-	2	-	15	-	-	OXA-23 + TEM (3), OXA-23 + NDM (21)	4
RC10	35 (22)	18	4	-	-	-	-	-	-	-	-	-	-	6	-	-	OXA-23 + NDM (13)	3
RC13	34 (13)	13	-	-	-	-	-	-	-	-	-	-	-	11	-	-	OXA-23 + NDM (2)	-
RC14	41(29)	29	-	-	-	-	-	-	-	-	-	-	-	12	-	1	OXA-23 + TEM (1), OXA-23 + NDM (4)	11
RC16	30 (21)	14	7	-	-	-	-	-	-	-	-	-	-	8	-	-	OXA-23 + NDM (5)	8
RC17	31 (20)	19	1	-	-	-	-	-	-	-	-	-	-	7	-	-	OXA-23 + NDM (8)	5
RC20	45 (6)	6	-	-	-	-	-	-	-	-	-	-	-	1	-	-	OXA-23 + NDM (5)	-
RC21	62 (0)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TOTAL (11 Centres)	**459 (202)**	**174**	**28**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**3**	**-**	**76**	**-**	**1**	**78**	**44**

Clinical relevance and treatment guidelines

Pseudomonas aeruginosa

This data highlights the clinical relevance of carbapenem resistance in *Pseudomonas aeruginosa* across Indian centres, with nearly one in four isolates exhibiting resistance in 2024. The predominance of metallo-β-lactamase (MβL)-producing strains, particularly those carrying VIM and NDM genes, is concerning, as these enzymes render conventional β-lactam–β-lactamase inhibitor (BL–BLI) combinations, including Ceftazidime–avibactam, ineffective. Notably, around 80% of resistant isolates were PCR-negative for known carbapenemase genes, suggesting that alternative mechanisms, such as AmpC overexpression, efflux pump upregulation, and porin loss, remain widespread contributors to resistance. The occurrence of co-producers, including MβL with ESBLs such as VEB or Class A carbapenemases (KPC, GES), further complicates treatment decisions, since single-agent therapies are unlikely to achieve adequate efficacy. Current international guidelines (IDSA/ESCMID 2024–25) recommend tailoring therapy based on molecular profile. For non-MβL-resistant isolates, ceftolozane/tazobactam or cefiderocol are preferred, with high-dose extended-infusion meropenem as an option in select cases. For MβL producers, cefiderocol remains effective, and a combination of aztreonam with ceftazidime/avibactam provides an effective strategy, particularly for co-producers. Class A carbapenemase producers are best treated with ceftazidime/avibactam, meropenem/vaborbactam, or imipenem/relebactam, while OXA-48-like producers, though rare, remain susceptible to ceftazidime/avibactam. Colistin or polymyxin B, preferably in combination with fosfomycin, should be reserved as salvage therapy. Overall, the molecular landscape underscores the urgent need for routine molecular diagnostics and antimicrobial stewardship to guide rational therapy and preserve the efficacy of novel BL–BLI agents in improving patient outcomes.

Acinetobacter baumannii

The high prevalence of carbapenem-resistant *A. baumannii* across Indian centres poses a major therapeutic challenge, especially with the predominance of OXA-23 producers and the widespread emergence of OXA-23–NDM co-producers. Clinically, isolates with OXA-23 alone may still be partially responsive to certain therapies, but treatment failures remain frequent. In contrast, co-producers of OXA-23 and NDM are virtually untreatable with conventional β-lactam–β-lactamase inhibitor (BL–BLI) combinations such as ceftazidime/avibactam, leaving very few treatment options. Based on current IDSA/ESCMID 2024–25 guidelines, cefiderocol remains the most reliable therapy against both OXA- and NDM-producing *A. baumannii*, while sulbactam/durlobactam provides excellent activity against OXA-type carbapenemases but is ineffective against NDM carriers. Combination regimens involving colistin or polymixins B with tigecycline

or high-dose ampicillin–sulbactam may be used as salvage approaches in resource-limited settings, though efficacy is inconsistent and toxicity is high. The presence of 22% PCR-negative isolates highlights the clinical relevance of alternative resistance mechanisms, which may explain partial susceptibility to carbapenems under optimized dosing strategies. In conclusion, the multicentre data from India emphasize the urgent need for routine molecular surveillance, incorporation of novel agents such as cefiderocol and sulbactam–durlobactam into treatment protocols, and strengthened antimicrobial stewardship practices to improve patient outcomes and contain the further spread of multidrug-resistant *A. baumannii*.

Stenotrophomonas maltophilia

For *S. maltophilia* infections, minocycline should be considered the first-line treatment, particularly for serious bloodstream or respiratory tract infections. TMP-SMX and levofloxacin may be considered as second-line or step-down therapy, depending on the site of infection, severity, and patient tolerance. Combination therapy is generally not indicated, except in cases of severe sepsis or when resistance to first-line agents is suspected. Continuous monitoring of susceptibility patterns is warranted, as *S. maltophilia* has a propensity to develop resistance under antibiotic pressure.

The eight-year temporal analysis shows stable efficacy of minocycline (>95% susceptibility since 2017), reinforcing its role as a cornerstone of treatment guidelines. These findings support the recommendation that empirical therapy for suspected *S. maltophilia* infections in Indian healthcare settings should prioritize minocycline, with levofloxacin or TMP-SMX used as alternative agents based on susceptibility results.

Burkholderia cepacia

From a clinical management perspective, ceftazidime and meropenem should be considered first-line treatment choices for severe *B. cepacia* infections, either as monotherapy or in combination in critically ill patients. TMP-SMX remains a reliable oral option for step-down therapy. Levofloxacin and minocycline may be reserved for cases where susceptibility is confirmed, though their declining or limited efficacy restricts broad use. Regular surveillance is crucial, as *B. cepacia* has an inherent ability to acquire resistance, and inappropriate therapy can lead to poor outcomes in high-risk patients.

Chapter 4. Typhoidal Salmonella

In 2024, a total of 841 *Salmonella* typhi and 346 *Salmonella* Paratyphi A isolates were collected across the network. Data from the North, Central, East, West, and South regions reveal significant fluctuations in isolation rates over time. These variations underscore the necessity for region-specific public health strategies tailored to local epidemiological patterns. Such targeted approaches are crucial for effective typhoid fever control and the prevention of antimicrobial resistance spread.

Salmonella Typhi and *Salmonella* Paratyphi A isolated from blood samples **(Table 4.1)** showed high susceptibility to first-line antibiotics, including ampicillin, chloramphenicol, and TMP-SMX and to third-generation cephalosporins, such as ceftriaxone and cefixime. Additionally, *S.* Typhi demonstrated 99.5% susceptibility to azithromycin. In contrast, ciprofloxacin resistance was 98-99%.

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

AMA	Blood	
	***Salmonella* Typhi N=841 (S%)**	***Salmonella* Paratyphi A N=346 (S%)**
Ampicillin	748 / 767 (97.5)	319 / 324 (98.5)
Azithromycin*	837 / 841 (99.5)	0 / 0 (-)
Cefixime	614 / 627 (97.9)	275 / 281 (97.9)
Cefotaxime	824 / 841 (98)	46 / 49 (93.9)
Ceftriaxone	824 / 841 (98)	342 / 346 (98.8)
Chloramphenicol	578 / 592 (97.6)	265 / 266 (99.6)
Ciprofloxacin	11 / 841 (1.3)	4 / 346 (1.2)
Levofloxacin	1 / 22 (-)	0 / 5 (-)
Ofloxacin	1 / 8 (-)	0 / 0 (-)
Trimethoprim-sulfamethoxazole	812 / 831 (97.7)	342 / 343 (99.7)

*Azithromycin sensitivity cut-off values are not given in CLSI for *Salmonella* Paratyphi A

Salmonella Typhi

Salmonella Typhi isolates across India showed high susceptibility to first-line antibiotics (ampicillin, chloramphenicol, TMP-SMX) and third-generation cephalosporins (ceftriaxone, cefixime) **(Table 4.2).**

In the South region, ampicillin exhibited a susceptibility rate of 98.6% (276/280), while in the North region, it was 98.4% (441/448), with a national average of 97.5% (748/767). Chloramphenicol demonstrated a susceptibility rate of 97.6% (578/592) across India, with 100% susceptibility in the South (155/155) and 98.2% in the North (333/339). Azithromycin also showed high effectiveness, with susceptibility rates ranging from 99% to 100% across regions. However, regional variations exist. North and South India exhibited the highest susceptibility for ceftriaxone, azithromycin, and first-line drugs, all exceeding 98%. In contrast, West, Central, and East India showed relatively lower susceptibility, particularly for ceftriaxone (94.2%, 56.3%, and 66.7%, respectively) and ampicillin (75–86%). Azithromycin and TMP-SMX remained effective across all regions. Fluoroquinolone resistance was widespread nationally, with very low susceptibility to ciprofloxacin in all the regions. These findings underscore the importance of region-specific treatment strategies and the need for ongoing antimicrobial surveillance to monitor resistance patterns and inform treatment protocols.

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

AMA	National (N=841) (S%)	North (N=451) (S%)	South (N=281) (S%)	West (N=86) (S%)	Central (N=14) (S%)	East (N=9) (S%)
Ceftriaxone	824 / 841 (97.7)	449 / 451 (99.6)	279 / 281 (99.3)	81 / 86 (94.2)	9 / 14 (56.3)	6 / 9 (66.7)
Azithromycin	837 / 841 (99.5)	450 / 451 (99.8)	278 / 281 (98.9)	86 / 86 (100.0)	14 / 14 (100.0)	9 / 9 (100.0)
Cefixime	614 / 627 (97.9)	442 / 449 (98.4)	151 / 155 (97.4)	13 / 14 (92.9)	2 / 2 (100.0)	6 / 7 (85.7)
Ampicillin	748 / 767 (97.5)	441 / 448 (98.4)	276 / 280 (98.6)	12 / 16 (75.0)	12 / 14 (85.7)	7 / 9 (77.8)
Chloramphenicol	578 / 592 (97.6)	333 / 339 (98.2)	155 / 155 (100.0)	70 / 75 (93.3)	13 / 14 (92.9)	7 / 9 (77.8)
Trimethoprim-sulfamethoxazole	812 / 831 (97.7)	442 / 450 (98.2)	267 / 272 (98.2)	80 / 86 (93.0)	14 / 14 (100.0)	9 / 9 (100.0)
Pefloxacin	12 / 47 (25.5)	0 / 0 (-)	1 / 33 (3.0)	9 / 12 (75.0)	1 / 1 (-)	1 / 1 (-)
Levofloxacin	1 / 22 (-)	0 / 0 (-)	1 / 3 (-)	0 / 2 (-)	0 / 12 (0.0)	0 / 5 (-)
Ciprofloxacin	11 / 841 (1.3)	7 / 451 (1.6)	3 / 281 (1.1)	1 / 86 (1.2)	0 / 14 (0.0)	0 / 9 (-)

Table 4.3 and **Figure 4.1** reflect yearly susceptibility trends of *S.* Typhi isolated from blood between 2017 and 2024. Throughout this period, *S.* Typhi demonstrated consistently high susceptibility to most first-line antibiotics and third-generation cephalosporins, whereas fluoroquinolones remained largely ineffective. Ampicillin susceptibility steadily improved rising from 91.9% (305/332) in 2017 to 97.5% (748/767) in 2024, indicating a recovery in its therapeutic effectiveness, indicating its regained effectiveness. Ceftriaxone remained a strong treatment option, maintaining high susceptibility from 98.5% (329/334) in 2017 to 98% (824/841) in 2024, despite a noticeable decline in 2022 to 93.8% (534/569). Similarly, Cefixime remained highly effective, with susceptibility rates ranging from 99.1% (221/223) in 2017 to 97.9% (614/627) in 2024, with a temporary dip to 94.5% (416/440) in 2022. Azithromycin showed a steady increase in effectiveness, improving from 95.7% (266/278) in 2017 to 99.5% (837/841) in 2024.

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

AMA	Year-2017 N=345 (S%)	Year-2018 N=580 (S%)	Year-2019 N=728 (S%)	Year-2020 N=206 (S%)	Year-2021 N=293 (S%)	Year - 2022 N=584 (S%)	Year-2023 N=1098 (S%)	Year-2024 N=841 (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)
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)
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)
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)
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)
Levofloxacin	*0/3 (-)	*5/18 (-)	3/35 (8.6)	*4/12 (-)	9/30 (30)	7 / 108 (6.4)	10 / 55 (18.2)	*1 / 22 (-)
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)
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)

In contrast, ciprofloxacin susceptibility was consistently low and continued to decline from 11.6% (35/302) in 2017 to just 1.3% (11/841) in 2024, indicating widespread resistance. Other first-line antibiotics showed renewed effectiveness. TMP-SMX maintained high susceptibility, increasing from 94.4% (322/341) in 2017 to 97.7% (812/831) in 2024. Chloramphenicol also remained effective, with susceptibility improving from 96% (267/278) in 2017 to 97.6% (578/592) in 2024, peaking at 98.2% (597/608) in 2023.

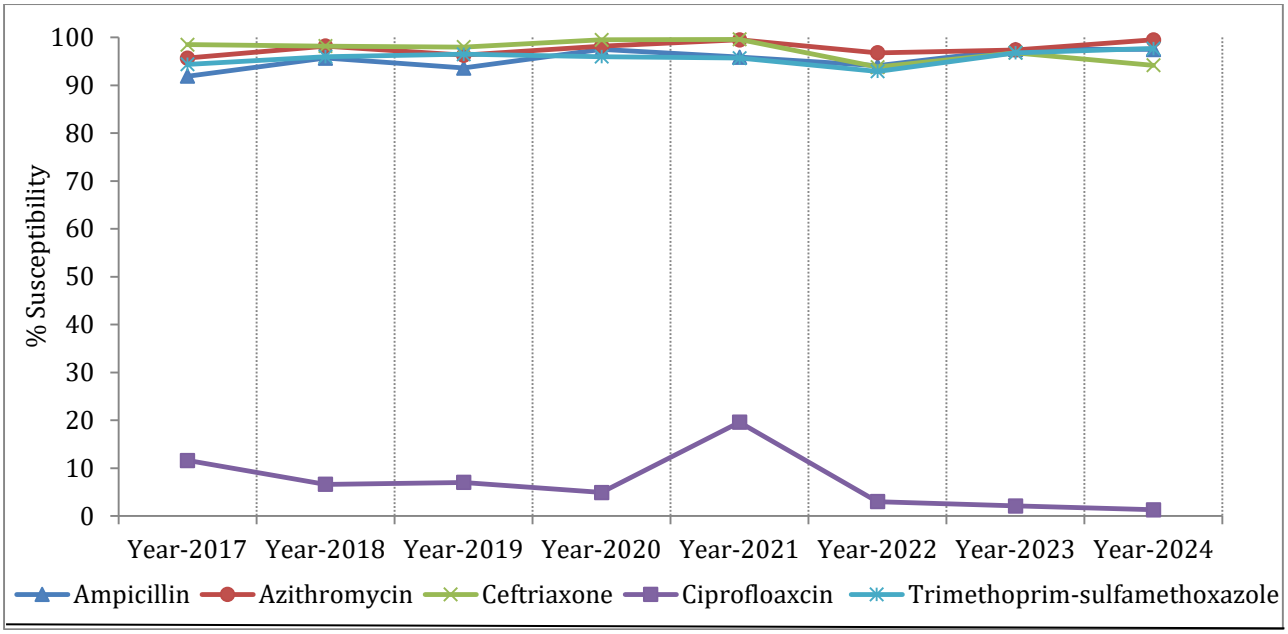
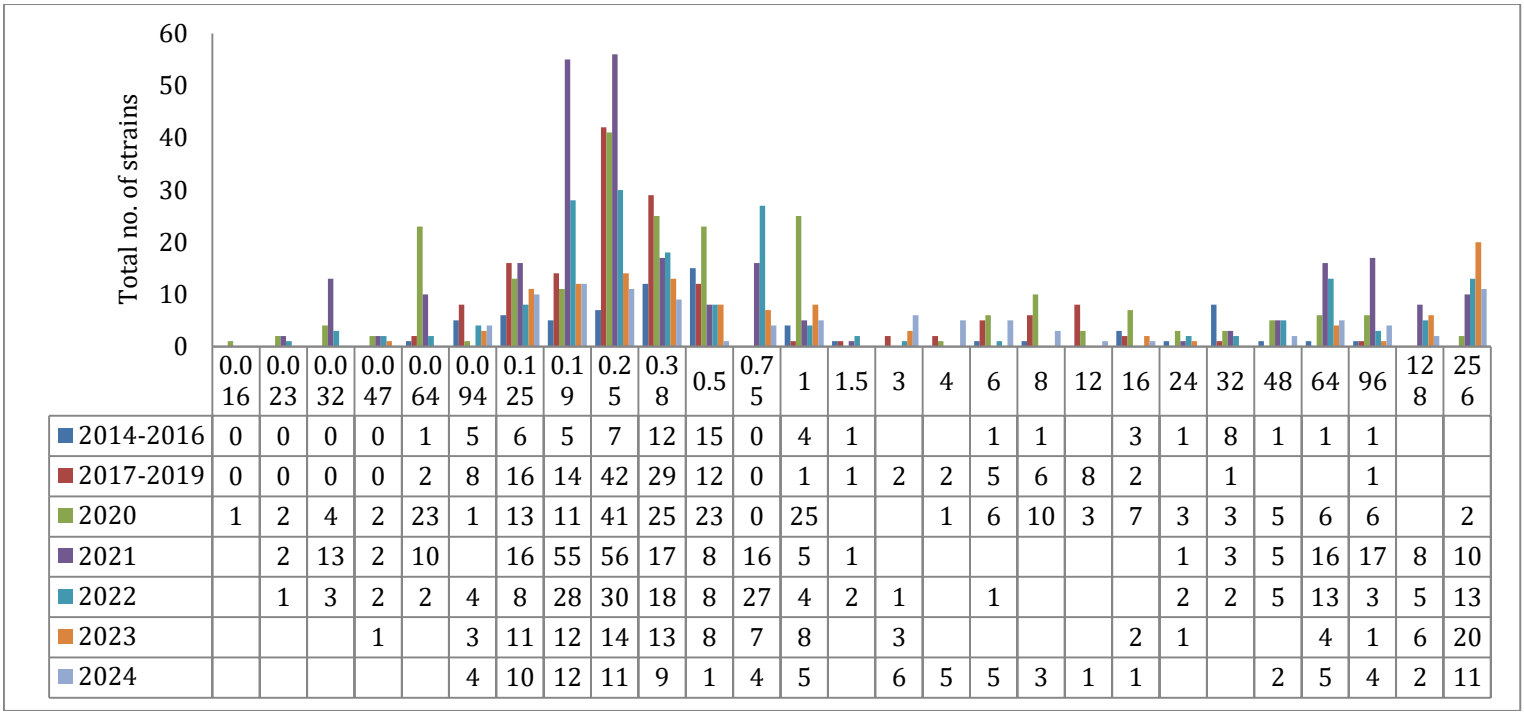


Figure 4.1: Yearly susceptibility trends of *S.* Typhi from blood

In summary, ceftriaxone, cefixime, and azithromycin remain the most reliable treatment options for typhoid fever in India. The resurgence in susceptibility to ampicillin, TMP-SMX, and chloramphenicol suggests these agents may be reconsidered for therapeutic use. However, fluoroquinolones, particularly ciprofloxacin, is consistently ineffective and no longer suitable for empirical therapy. The emergence of cephalosporin resistance and XDR strains reinforces the critical need for continuous antimicrobial surveillance to detect evolving resistance trends and support informed treatment decisions.

Ciprofloxacin MIC trends in *Salmonella* Typhi:

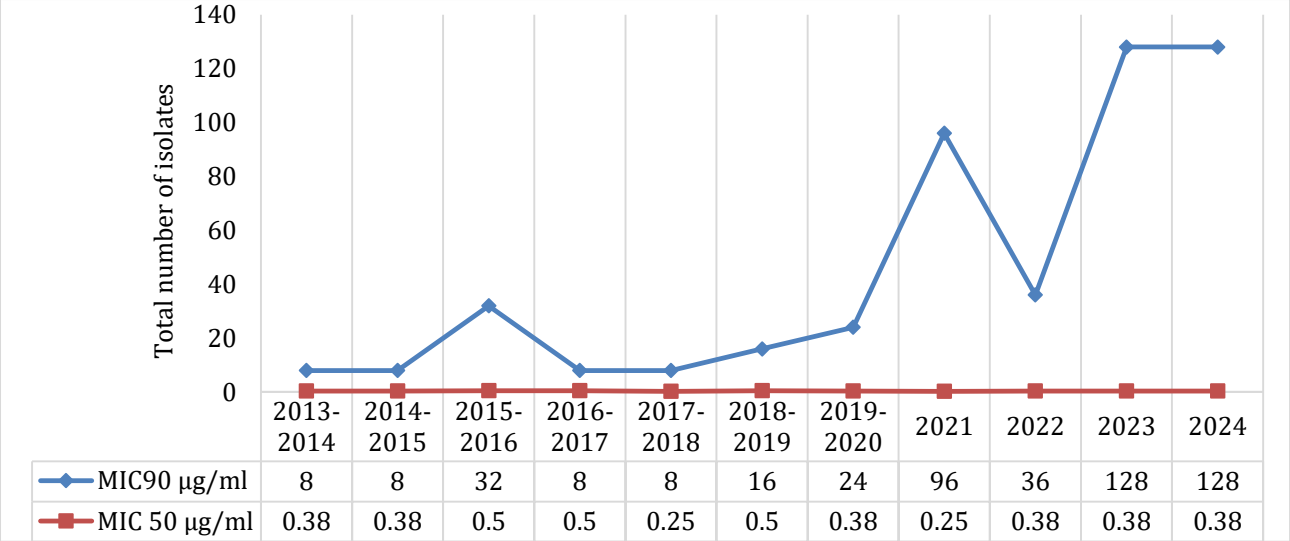
To understand evolving resistance trends and their clinical implications, it is important to examine the MIC distribution of ciprofloxacin in *Salmonella* Typhi. Even within the susceptible range, a gradual shift toward higher MIC values can signal emerging resistance. Such shifts are often associated with delayed clinical recovery and increased risk of treatment failure. Therefore, monitoring the complete MIC distribution enables the early detection of low-level resistance, which may be missed when results are reported solely as “susceptible” or “resistant.”.



	0.016	0.023	0.032	0.047	0.064	0.094	0.125	0.19	0.25	0.38	0.5	0.75	1	1.5	3	4	6	8	12	16	24	32	48	64	96	128	256
2014-2016	0	0	0	0	1	5	6	5	7	12	15	0	4	1			1	1		3	1	8	1	1	1		
2017-2019	0	0	0	0	2	8	16	14	42	29	12	0	1	1	2	2	5	6	8	2		1			1		
2020	1	2	4	2	23	1	13	11	41	25	23	0	25			1	6	10	3	7	3	3	5	6	6		2
2021		2	13	2	10		16	55	56	17	8	16	5	1							1	3	5	16	17	8	10
2022		1	3	2	2	4	8	28	30	18	8	27	4	2	1		1				2	2	5	13	3	5	13
2023				1		3	11	12	14	13	8	7	8		3					2	1			4	1	6	20
2024						4	10	12	11	9	1	4	5		6	5	5	3	1	1			2	5	4	2	11

Figure 4.2a: Ciprofloxacin MIC trends in Salmonella Typhi from pan-India over a period of ten years

The MIC distribution of *Salmonella* isolates (**Figure 4.2a**) reveals notable shifts before and after the COVID-19 period. During the pre-COVID years (2014–2019), most isolates clustered within lower MIC ranges, particularly 0.12–0.25 µg/mL, with only occasional higher values observed. This pattern reflected overall high susceptibility and a relatively narrow MIC distribution. However, in post-COVID (2020–2024), the distribution broadened considerably. While the peak remained around 0.12–0.25 µg/mL, a gradual rightward shift became apparent, with increasing numbers of isolates exhibiting higher MICs. From 2022 onwards, isolates with MICs ≥32 µg/mL became more common, and by 2023–2024, strains with extremely high MICs, up to 256 µg/mL, were detected. This trend marks the emergence and expansion of high-level ciprofloxacin resistance and indicates a more heterogeneous susceptibility profile compared to the relatively uniform distribution seen in the pre-COVID years.



	2013-2014	2014-2015	2015-2016	2016-2017	2017-2018	2018-2019	2019-2020	2021	2022	2023	2024
MIC90 µg/ml	8	8	32	8	8	16	24	96	36	128	128
MIC 50 µg/ml	0.38	0.38	0.5	0.5	0.25	0.5	0.38	0.25	0.38	0.38	0.38

Figure 4.2b: Comparison of MIC50 and MIC90 of *S.* Typhi for ciprofloxacin over a period of ten years

Analysis of MIC50 and MIC90 values by dividing the timeline into pre-COVID (2013–2019) and post-COVID (2020–2024) periods **(Figure 4.2b)** reveals a distinct pattern. During the pre-COVID years, both MIC50 and MIC90 values remained low and stable, indicating consistent susceptibility to ciprofloxacin. In the post-COVID period, however, MIC90 values increased notably, signaling the emergence of higher-level resistance among *S.* Typhi isolates. In contrast, MIC50 remained relatively unchanged, suggesting that while the majority of isolates remain susceptible, a growing minority is developing significant resistance—reflected in the upward shift of MIC90.

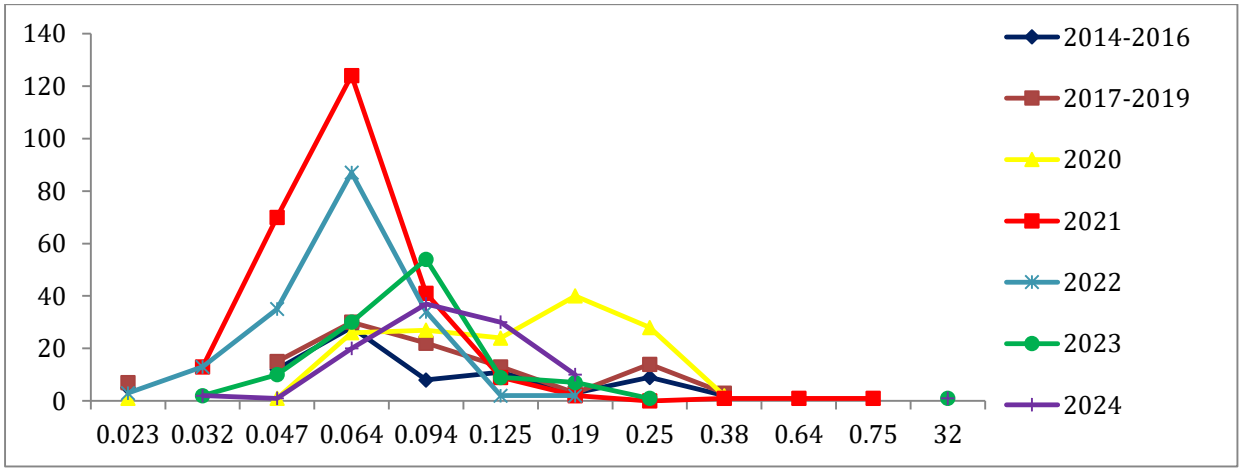
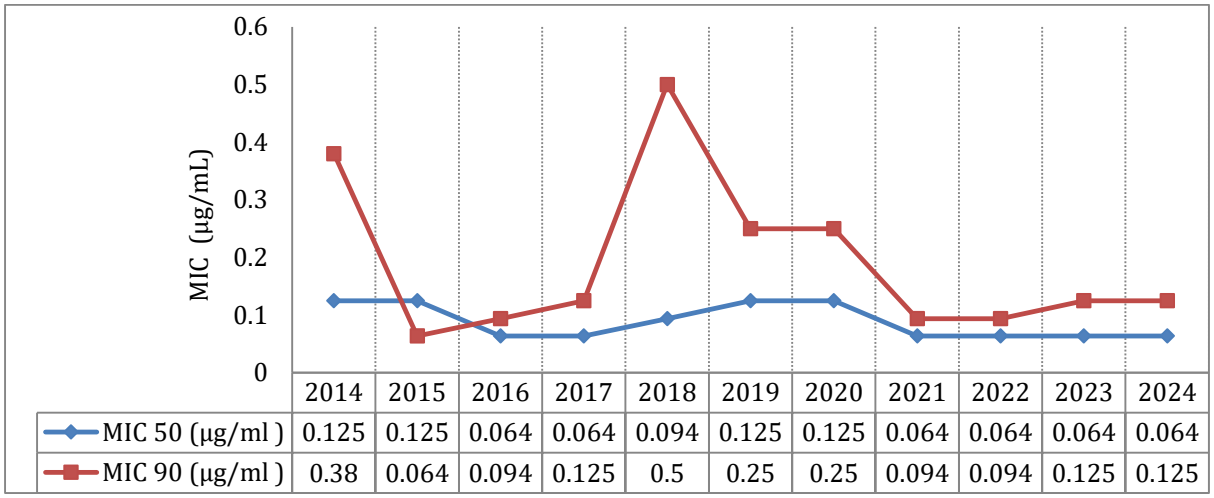


Figure 4.3a: MIC trend for Ceftriaxone in *S.* Typhi from pan-India over a period of ten years

The MIC trend for ceftriaxone in *Salmonella* Typhi across India over the past decade shows a clear divergence between the pre-COVID and post-COVID periods **(Figure 4.3a)**. During the pre-COVID years (2014–2016 and 2017–2019), MIC values remained low and stable, with peaks around 0.047 to 0.094 µg/mL. However, the post-COVID period (2020–2024) reveals a shift in this pattern. Beginning in 2020, MIC values began

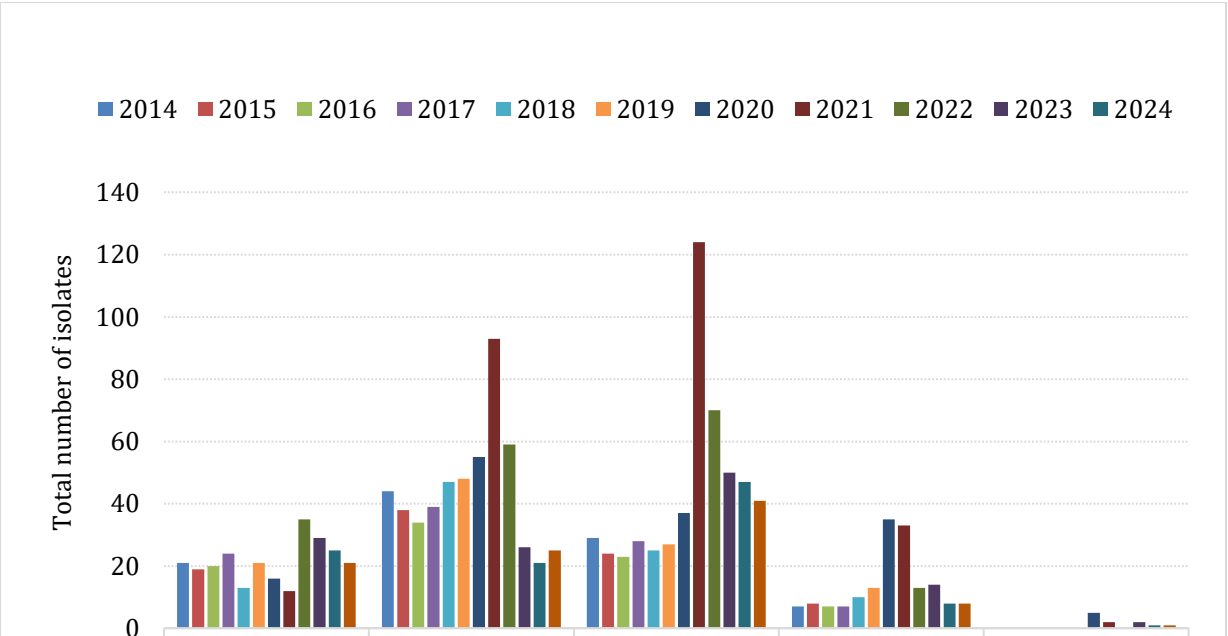
to rise, with a noticeable spike in 2021, particularly at 0.064 µg/mL and 0.047 µg/mL, levels that remained consistent through 2022 and 2023, but were higher than those seen in the pre-COVID years. A notable change in the post-COVID period is the emergence of isolates with higher MIC values, including 0.19 µg/mL and 0.25 µg/mL—ranges not observed before 2020. Most significantly, isolates with MICs as high as 32 µg/mL were detected in 2023 and 2024, marking the first appearance of such high-level ceftriaxone resistance during the surveillance period.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
MIC 50 (µg/ml)	0.125	0.125	0.064	0.064	0.094	0.125	0.125	0.064	0.064	0.064	0.064
MIC 90 (µg/ml)	0.38	0.064	0.094	0.125	0.5	0.25	0.25	0.094	0.094	0.125	0.125

Figure 4.3b: Comparison of MIC50 and MIC90 of *S.* Typhi for Ceftriaxone over a period of ten years

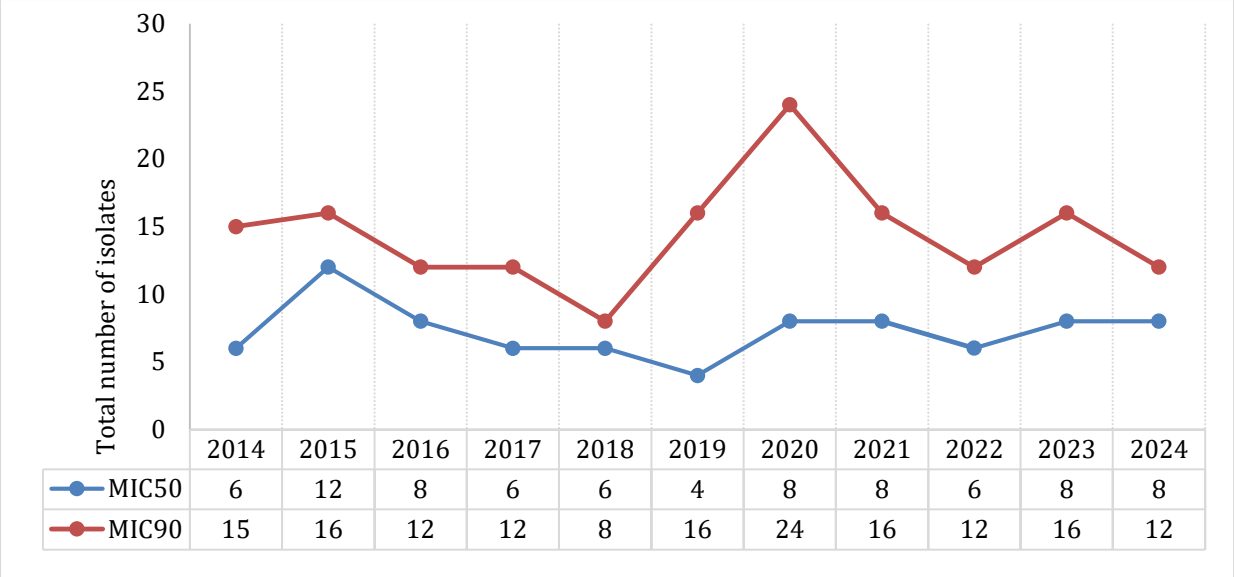
The MIC50 for ceftriaxone in *S.* Typhi remained stable throughout both the pre- and post-COVID years, consistently ranging between 0.064–0.125 µg/mL **(Figure 4.3b)**. In contrast, MIC90 values exhibited greater fluctuation during the pre-COVID years, with notable peaks in 2014 and 2018, followed by a subsequent decline. In the post-COVID period, MIC90 levels were lower than these earlier peaks but stabilized at slightly elevated levels, ranging from 0.094 to 0.125 µg/mL. Overall, the data indicate that while MIC50 remained unchanged, MIC90 became more stable in the post-COVID period, albeit at a modestly higher range. Notably, a small number of ceftriaxone-resistant and extensively drug-resistant (XDR) *S.* Typhi isolates have been reported recently, underscoring the importance of continued surveillance.



Time Period	3µg/ml	6µg/ml	12µg/ml	24µg/ml	32µg/ml
2014	21	44	29	7	
2015	19	38	24	8	
2016	20	34	23	7	
2017	24	39	28	7	
2018	13	47	25	10	
2019	21	48	27	13	
2020	16	55	37	35	5
2021	12	93	124	33	2
2022	35	59	70	13	
2023	29	26	50	14	2
2024	25	21	47	8	1

Figure 4.4a: Azithromycin MIC trend in *S.* Typhi over a period of ten years from pan-India

Antimicrobial susceptibility testing (AST) data for azithromycin between 2014 and 2019 showed that most *S.* Typhi isolates had MIC values ranging from 3 µg/mL to 12 µg/mL (**Figure 4.4a**), with a peak around 6 µg/mL. In contrast, during 2020–2024, the MIC distribution broadened significantly, spanning 3 µg/mL to 24 µg/mL, with some isolates exhibiting MICs of 32 µg/mL or higher, indicating a clear trend toward higher resistance. Phenotypic analysis of isolates initially showing an MIC of 32 µg/mL revealed that all reverted to susceptibility by the second or third subculture. Hybrid sequencing of representative isolates confirmed the absence of known resistance-associated mutations. This behavior suggests the presence of transient or heteroresistance, which disappears upon subculture without selective antibiotic pressure. These findings underscore the importance of interpreting elevated MIC values cautiously, particularly when they are not reproducible on repeat testing.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
MIC50	6	12	8	6	6	4	8	8	6	8	8
MIC90	15	16	12	12	8	16	24	16	12	16	12

Figure 4.4b: Comparison of MIC50 and MIC90 of *S.* Typhi for Azithromycin over a period of ten years

From 2014 to 2019, MIC50 for azithromycin remained stable at 6 µg/mL, with a peak of 12 µg/mL in 2015. During the 2020–2024 period, MIC50 increased to 8 µg/mL. Meanwhile, MIC90 values fluctuated between 12 µg/mL and 16 µg/mL, reaching a peak of 24 µg/mL in 2024 **(Figure 4.4b)**. Although no consistent upward trend in MIC values was evident overall, these variations highlight the importance of continuous surveillance.

Salmonella Paratyphi A

AST of *Salmonella* Paratyphi A from 2017–2024 demonstrated persistent and widespread fluoroquinolone resistance, while most other antibiotics—including cephalosporins and traditional first-line drugs—maintained high effectiveness **(Table 4.4** and **Figure 4.5)**.

Ampicillin maintained strong activity against *S.* Paratyphi A, with susceptibility rates of 95% (38/40) in 2017, increasing to 97.6% (122/125) in 2018, dipping slightly to 90.6% (125/138) in 2019, and rebounding to 98.5% (319/324) in 2024. Ceftriaxone consistently demonstrated high effectiveness, ranging from 95% (38/40) in 2017 to 98.8% (342/346) in 2024, including perfect susceptibility in 2020 (47/47) and 2021 (57/57). Cefixime also showed excellent activity overall, with susceptibility rates of 96.3% (26/27) in 2017 and 100% (105/105) in 2018, experiencing a temporary decline to 90% (72/80) in 2022, then recovering to 97.9% (275/281) in 2024.

In contrast, ciprofloxacin susceptibility remained consistently low, decreasing from 10% (4/40) in 2017 to just 1.2% (4/346) in 2024. Traditional first-line antibiotics continued to show strong susceptibility, with TMP-SMX exhibiting 100% susceptibility

in 2017 and 2018, and 99.7% in 2024. Similarly, chloramphenicol maintained full susceptibility at 100% from 2017 to 2019, and 99.6% in 2024.

Table 4.4: Yearly susceptibility trends of *S.* Paratyphi A from blood

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year - 2021	Year-2022	Year-2023	Year-2024
	N=41	N=125	N=147	N=52	N=58	N=118	N=240	N=346
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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)
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)
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)
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)
Levofloxacin	*0/2 (-)	*0/5 (-)	0/25 (0)	*0/9 (-)	*0/8 (-)	*1 / 6 (-)	4 / 19 (21.1)	*0 / 5 (-)
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)
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)

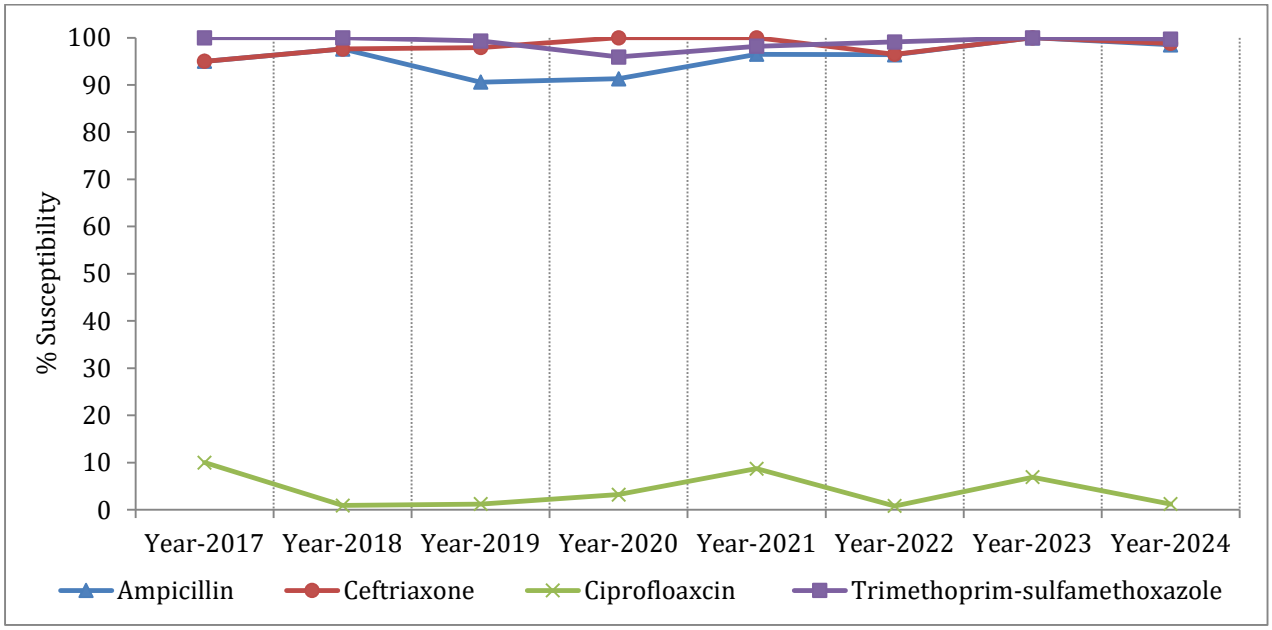
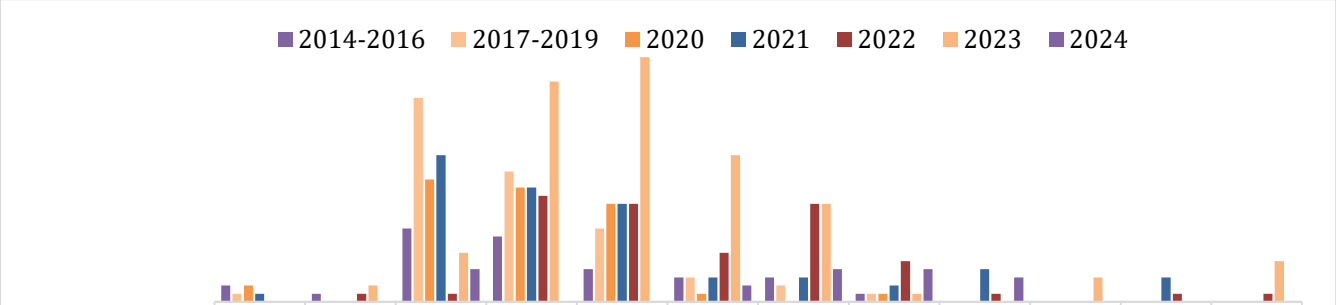


Figure 4.5: Yearly susceptibility trends of *S.* Paratyphi A from blood

Among *S.* Paratyphi A isolates, the majority exhibited intermediate ciprofloxacin MICs ranging from 0.125–0.5 µg/mL **(Figure 4.6a)**. However, a notable shift occurred between 2021–2023, with the emergence of isolates showing significantly higher MICs in the range of 128 to 256 µg/mL—indicative of high-level resistance. Interestingly, in 2024, no isolates with MICs above 64 µg/mL were detected, suggesting a possible decline or stabilization in high-level resistance.

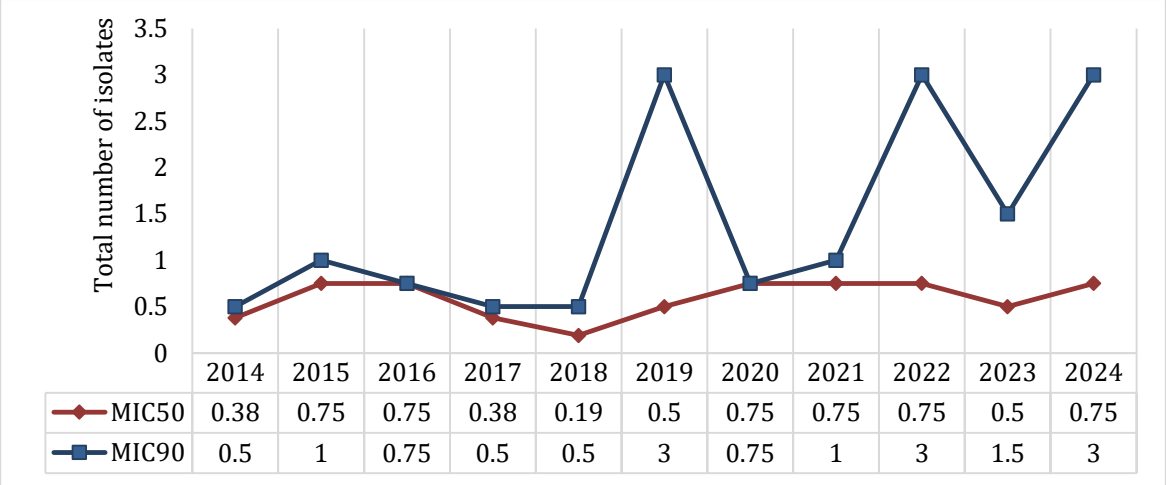


	0.032	0.064	0.125	0.25	0.5	1	2	8	64	96	128	256
2014-2016	2	1	9	8	4	3	3	1	0	0	0	0
2017-2019	1	0	25	16	9	3	2	1	0	0	0	0
2020	2	0	15	14	12	1	0	1	0	0	0	0
2021	1	0	18	14	12	3	3	2	4	0	3	0
2022	0	1	1	13	12	6	12	5	1	0	1	1
2023	0	2	6	27	30	18	12	1	0	3	0	5
2024	0	0	4			2	4	4	3			

Figure 4.6a: Ciprofloxacin MIC trends in *S.* Paratyphi A from pan-India over a period of ten years

Analysis of pre- and post-COVID trends in *Salmonella* isolates revealed that, prior to 2020, most isolates exhibited intermediate ciprofloxacin MICs ranging from 0.125 to 0.5 µg/mL, indicating moderate susceptibility. However, during the post-COVID period (2021–2023), the emergence of isolates displaying high-level resistance was observed, with MICs ranging from 128 to 256 µg/mL. In 2024, no isolates with MICs above 64 µg/mL were detected, suggesting a partial decline in high-level ciprofloxacin resistance.

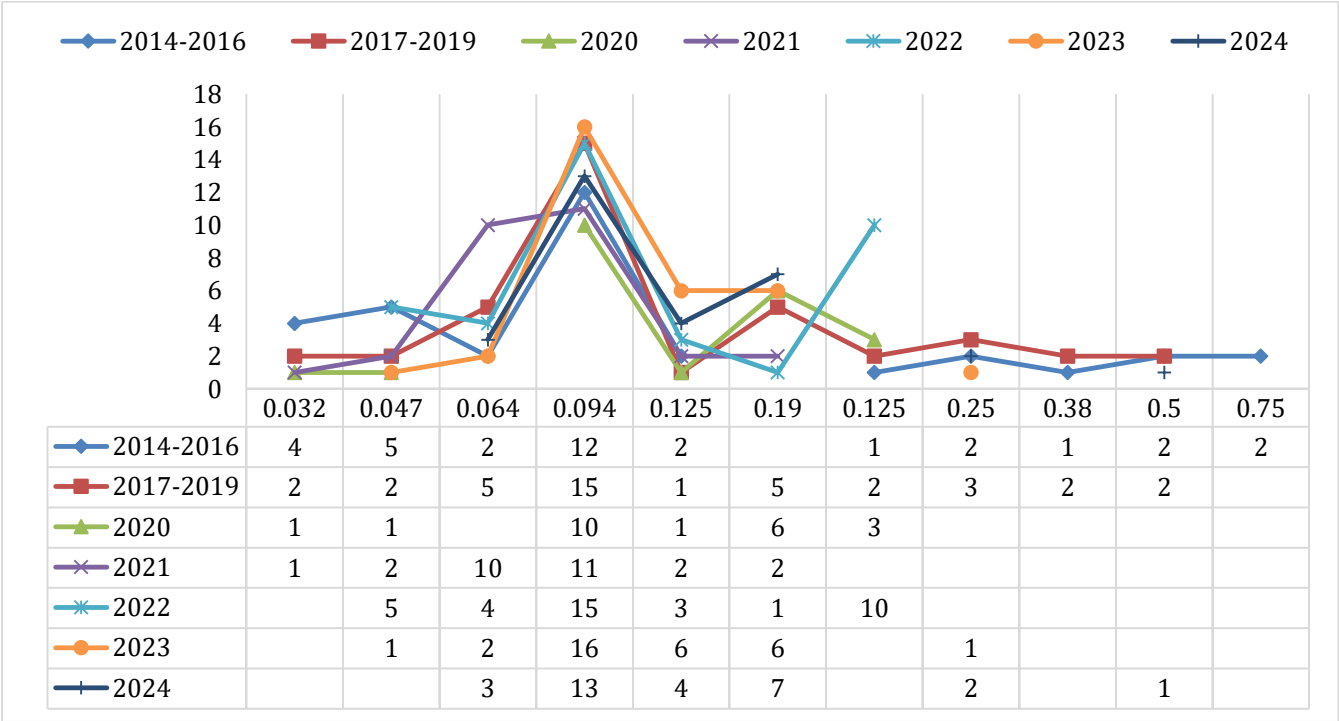
In *S.* Paratyphi A, both MIC50 and MIC90 values for ciprofloxacin have increased over time. MIC50 rose from 0.38 µg/mL to 0.75 µg/mL, while MIC90 increased from 0.5 µg/mL to 3 µg/mL by 2024 **(Figure 4.6b)**. Overall, fluoroquinolone resistance remains more pronounced in *S.* Typhi compared to *S.* Paratyphi A.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
MIC50	0.38	0.75	0.75	0.38	0.19	0.5	0.75	0.75	0.75	0.5	0.75
MIC90	0.5	1	0.75	0.5	0.5	3	0.75	1	3	1.5	3

Figure 4.6b: Ciprofloxacin MIC50 and MIC90 trends in *S.* Paratyphi A from pan-India over a period of ten years

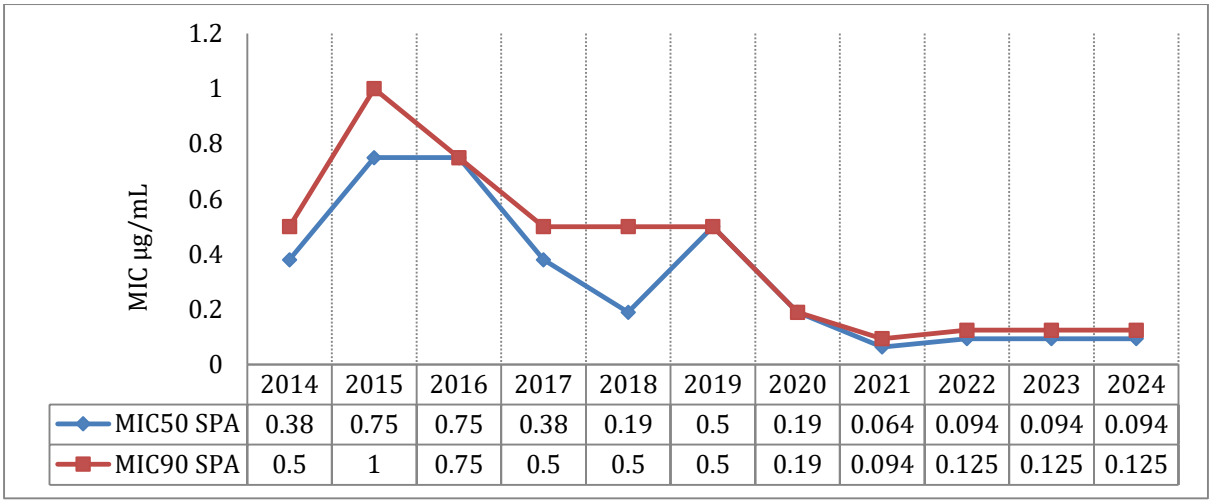
For ceftriaxone, creeping MIC values among *S.* Paratyphi A isolates ranged from 0.032 to 0.75 µg/mL **(Figure 4.7a)**, with the majority clustering between 0.064 and 0.125 µg/mL, most commonly at 0.094 µg/mL. Importantly, none of the *S.* Paratyphi A isolates exhibited ceftriaxone resistance.



	0.032	0.047	0.064	0.094	0.125	0.19	0.125	0.25	0.38	0.5	0.75
2014-2016	4	5	2	12	2		1	2	1	2	2
2017-2019	2	2	5	15	1	5	2	3	2	2	
2020	1	1		10	1	6	3				
2021	1	2	10	11	2	2					
2022		5	4	15	3	1	10				
2023		1	2	16	6	6		1			
2024			3	13	4	7		2		1	

Figure 4.7a: Ceftriaxone creeping MIC in *S.* Paratyphi A from pan-India over a period of ten years

MIC50 and MIC90 for ceftriaxone in *S.* Paratyphi A showed a fluctuating pattern over time. MIC50 ranged from 0.38 µg/mL during 2014 to 0.094 µg/mL in 2024, while MIC90 ranged from 0.5 µg/mL to 0.125 µg/mL in 2024 **(Figure 4.7b)**.



	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024
MIC50 SPA	0.38	0.75	0.75	0.38	0.19	0.5	0.19	0.064	0.094	0.094	0.094
MIC90 SPA	0.5	1	0.75	0.5	0.5	0.5	0.19	0.094	0.125	0.125	0.125

Figure 4.7b: Ceftriaxone MIC50 and MIC90 trends in *S.* Paratyphi A from pan-India over a period of ten years

Clinical relevance and treatment guidance:

The findings presented here have important clinical implications for the management of enteric fever in India. Data from the ICMR-AMRSN network (2017–2024) reveal fluctuating *S.* Typhi isolation trends across different regions, emphasizing the need for region-specific public health strategies. Both *S.* Typhi and *S.* Paratyphi A demonstrated high susceptibility to first-line antibiotics—ampicillin, cotrimoxazole, and chloramphenicol—as well as third-generation cephalosporins (ceftriaxone and cefixime). Notably, *S.* Typhi showed 99.5% susceptibility to azithromycin, supporting its continued use as an effective oral agent for uncomplicated typhoid fever. In contrast, fluoroquinolone resistance was widespread, with consistently low susceptibility to ciprofloxacin. These findings underscore the urgent need for rational antibiotic use, improved diagnostic capacity, strengthened WASH (Water, Sanitation, and Hygiene) interventions, and broader vaccine deployment to reduce disease burden and curb the spread of resistant strains.

The transient elevation of azithromycin MICs in *S.* Typhi, which reverted to susceptibility upon subculture and showed no detectable resistance-associated genetic mutations, suggests a phenomenon of heteroresistance rather than stable resistance. This underscores the importance of repeat testing and cautious interpretation of atypical MIC results to avoid misclassification of resistance. Accurate interpretation is essential to guide appropriate therapy and prevent unnecessary modifications to treatment guidelines.

Overall, the trends highlight the sustained efficacy of ceftriaxone, cefixime, and azithromycin for treatment, while emphasizing the critical need for ongoing surveillance, careful interpretation of elevated MICs, and rational antibiotic use to prevent the emergence and spread of resistant and XDR strains.

Chapter 5. Diarrheal pathogens

The number of diarrheal pathogens studied in 2024 was slightly higher compared to previous years. However, stool samples accounted for only 1% of the total isolates, indicating limited representation of the actual burden of bacterial diarrheal pathogens. The dataset encompassed *Aeromonas* spp., *Shigella* spp. (both *S. sonnei* and *S. flexneri*), *Vibrio cholerae* and diarrheagenic *Escherichia coli* (DEC), revealing both persistent susceptibilities and concerning trends of multidrug resistance across several commonly used antibiotics.

Aeromonas spp.

Among the *Aeromonas* species isolated from faecal samples (n = 196), the highest levels of susceptibility were observed with meropenem (87.8%) and tetracycline (82%), confirming these antibiotics as the most effective therapeutic agents against these isolates. Imipenem demonstrated moderate activity, with 61.9% of isolates susceptible **(Table 5.1)**. This slightly reduced effectiveness compared to meropenem may be attributed to differences in resistance mechanisms. In contrast, fluoroquinolone resistance was widespread, with only 10.2% of isolates susceptible to ciprofloxacin. This highlights the diminished efficacy of this antibiotic class, likely due to mutations in quinolone resistance–determining regions and plasmid-mediated resistance determinants.

Table 5.1: Susceptibility pattern of *Aeromonas spp.*

AMA	Faeces N=196 (S%)
Cefixime	*0 / 1 (-)
Ciprofloxacin	20 / 196 (10.2)
Imipenem	117 / 189 (61.9)
Meropenem	166 / 189 (87.8)
Tetracycline	159 / 194 (82)

Trends from 2017 to 2024 reveal that carbapenems (both meropenem and imipenem) and tetracycline have consistently exhibited superior efficacy against *Aeromonas* isolates. Meropenem susceptibility peaked at 89% in some years and remained above 54% throughout the surveillance period. Imipenem susceptibility, while improving, generally ranged from 44%–64%, reflecting moderate effectiveness. Tetracycline susceptibility

remained consistently high (75–86%), with no significant decline, highlighting its continued relevance in empirical therapy. In contrast, ciprofloxacin susceptibility fluctuated but generally remained low, around 10%, with only transient increases. This persistent low activity highlights the ongoing challenges in managing *Aeromonas* infections with fluoroquinolones (**Table 5.2)**.

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
	N=131	N=114	N=170	N=77	N=179	N=164	N=181	N=196
	(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 (-)
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)
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)
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)
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)

Collectively, these data emphasize that meropenem and tetracycline remain reliable mainstays for treating *Aeromonas*-associated diarrhea, whereas resistance to fluoroquinolones is notably high. The continued decline in ciprofloxacin effectiveness, from around 20% in select earlier years to just 10.2% in 2024, underscores the growing impact of molecular resistance determinants and highlights the critical need for continued resistance surveillance **(Figure 5.1).**

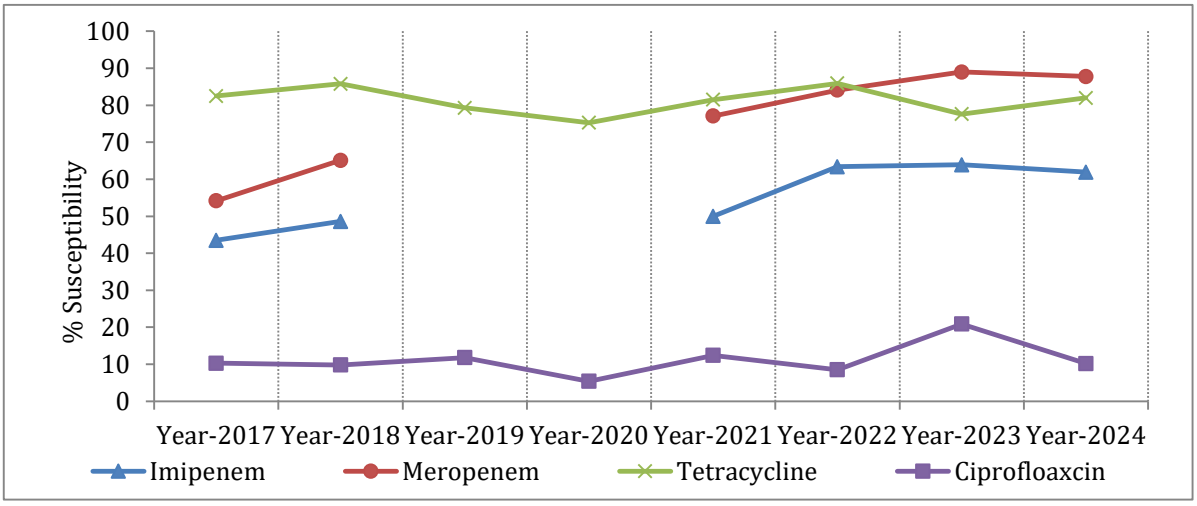


Figure 5.1: Yearly susceptibility trends of *Aeromonas* spp.

Shigella spp.

Shigella species isolated from faecal samples in 2024 exhibited marked heterogeneity in antimicrobial susceptibility profiles, with notable differences between *Shigella sonnei* and *Shigella flexneri.* For *S. sonnei*, high susceptibility levels were observed for cefixime (86.2%), ampicillin (82.5%), and azithromycin (76.8%). In contrast, *S. flexneri* demonstrated much lower susceptibility to ampicillin (27.3%), although cefixime (74.7%) and azithromycin (84.4%) remained relatively effective (**Table 5.3)**. Both species exhibited low levels of susceptibility to ciprofloxacin, with only 3.1% of *S. sonnei* and 6.5% of *S. flexneri* isolates remaining sensitive, highlighting entrenched fluoroquinolone resistance across *Shigella* species. Susceptibility to TMP-SMX was moderate (51.6% in *S. sonnei* and 53.5% in *S. flexneri*), reflecting its limited current therapeutic value.

Table 5.3: Susceptibility pattern of *Shigella* species

AMA	All specimens	
	Shigella sonnei **N=97 (S%)**	***Shigella flexneri*** **N=77 (S%)**
Ampicillin	80 / 97 (82.5)	21 / 77 (27.3)
Azithromycin	53 / 69 (76.8)	27 / 32 (84.4)
Cefixime	81 / 94 (86.2)	56 / 75 (74.7)
Ciprofloxacin	3 / 96 (3.1)	5 / 77 (6.5)
Nalidixic acid	*0 / 17 (-)	*1 / 18 (-)
Trimethoprim-sulfamethoxazole	49 / 95 (51.6)	38 / 71 (53.5)

Year-wise analysis of *S. sonnei* isolates reveals both persistence and gradual shifts in antimicrobial susceptibility over the eight-year period (**Table 5.4)**. Cefixime maintained high efficacy throughout, with susceptibility consistently above 80% and peaking above 90% between 2017 and 2019. Although ampicillin susceptibility fluctuated, it ultimately improved to 82.5% in 2024. TMP-SMX displayed a notable upward trend in susceptibility, increasing steadily from 7.7% in 2017 to 51.6% in 2024, suggesting a potential decline in resistance determinants. Overall, the longitudinal data highlight a stable susceptibility profile for cefixime, partial recovery in ampicillin effectiveness, and a gradual improvement in TMP-SMX susceptibility (**Figure 5.2)**.

Table 5.4: 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%)
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)
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)
Nalidixic acid	*0/8 (-)	*0/1 (-)	*0/8 (-)	*0/0 (-)	*0/7 (-)	*0 / 4 (-)	*0/1 (-)	*0 / 17 (-)
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)

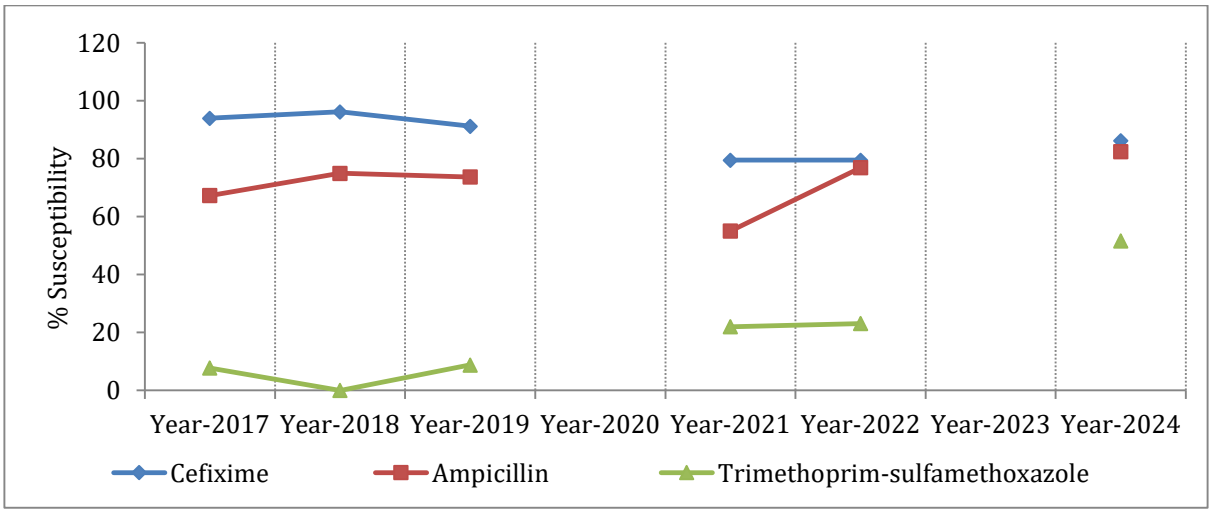


Figure 5.2: Yearly susceptibility trends of *Shigella sonnei*

Compared to *S. sonnei*, *S. flexneri* exhibited a more challenging resistance profile, particularly against traditional first-line antimicrobials. Ampicillin susceptibility remained consistently low throughout the surveillance period, rarely exceeding 30% and dropping to a low of 11.8% in 2022 **(Table 5.5)**. Cefixime maintained moderate to high activity, with susceptibility ranging between 67.6% and 88.2% over the years, suggesting stable efficacy of third-generation cephalosporins. However, a slight decline in recent years may suggest the emergence of plasmid-mediated resistance determinants. TMP-SMX demonstrated a gradual improvement in susceptibility, increasing from 9.7% in 2017 to 53.5% in 2024, possibly reflecting reduced selective pressure from declining TMP-SMX usage in clinical settings.

Table 5.5: 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=37 (S%)	Year-2023 N=25 (S%)	Year-2024 N=77 (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)
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)
Nalidixic acid	0/24 (0)	*0/15 (-)	2/35 (5.7)	*2/13 (-)	*0/8 (-)	*0 / 8 (-)	*0/5 (-)	*1 / 18 (-)
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)

Overall, the longitudinal analysis highlights the persistent resistant phenotype of *S. flexneri*, characterized by sustained resistance to ampicillin and fluoroquinolones, alongside partial recovery of TMP-SMX susceptibility and relatively stable cefixime efficacy. These findings emphasize the necessity for continuous surveillance and molecular monitoring to track the emergence and evolution of cephalosporin and macrolide resistance determinants in circulating *S. flexneri* strains **(Figure 5.3)**.

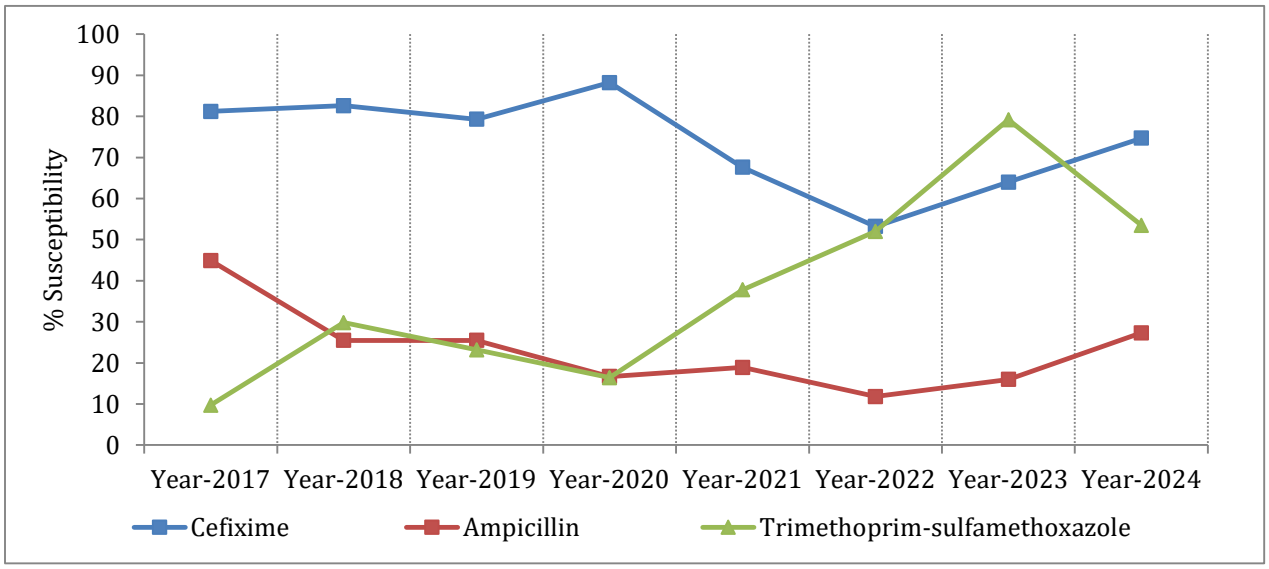


Figure 5.3: Yearly susceptibility trends of *Shigella flexneri*

Vibrio cholerae

The antimicrobial susceptibility profile of *Vibrio cholerae* isolates (n = 94) recovered from faecal specimens in 2024 demonstrated sustained high sensitivity to tetracycline, with 97.5% of isolates remaining susceptible (79/81) **(Table 5.6)**. Ampicillin exhibited moderate activity, with 79.8% susceptibility (71/89), suggesting partial retention of efficacy; however, emerging resistance necessitates cautious clinical use and periodic susceptibility verification. In contrast, TMP-SMX performed poorly, with only 23.7% of isolates susceptible (22/93), reflecting widespread resistance and limited therapeutic relevance.

Table 5.6: Susceptibility pattern of *Vibrio cholerae*

AMA	*Vibrio cholerae* N=94 (S%)
Ampicillin	71 / 89 (79.8)
Nalidixic acid	*1 / 1 (-)
Tetracycline	79 / 81 (97.5)
Trimethoprim-sulfamethoxazole	22 / 93 (23.7)

Year-wise trend analysis from 2017 through 2024 revealed overall stability in tetracycline susceptibility, ranging between 90.5% and 100%, underscoring its sustained effectiveness. Ampicillin susceptibility fluctuated during the surveillance period, dropping to 39.3% in 2020 before rebounding to 86.3% in 2021, with an overall average of approximately 70–80% susceptibility (**Table 5.7)**.

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%)
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)
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)
Nalidixic acid	*1/8 (-)	*0/4 (-)	*0/5 (-)	*1/1 (-)	*0/0 (-)	*0 / 1 (-)	*0/0 (-)	*1 / 1 (-)
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)

In contrast, TMP-SMX susceptibility remained consistently low (<50% in most years), declining to 17.2% in 2021 and recovering modestly thereafter, a pattern likely driven by the stable carriage of plasmid-mediated resistance determinants (**Figure 5.4)**.

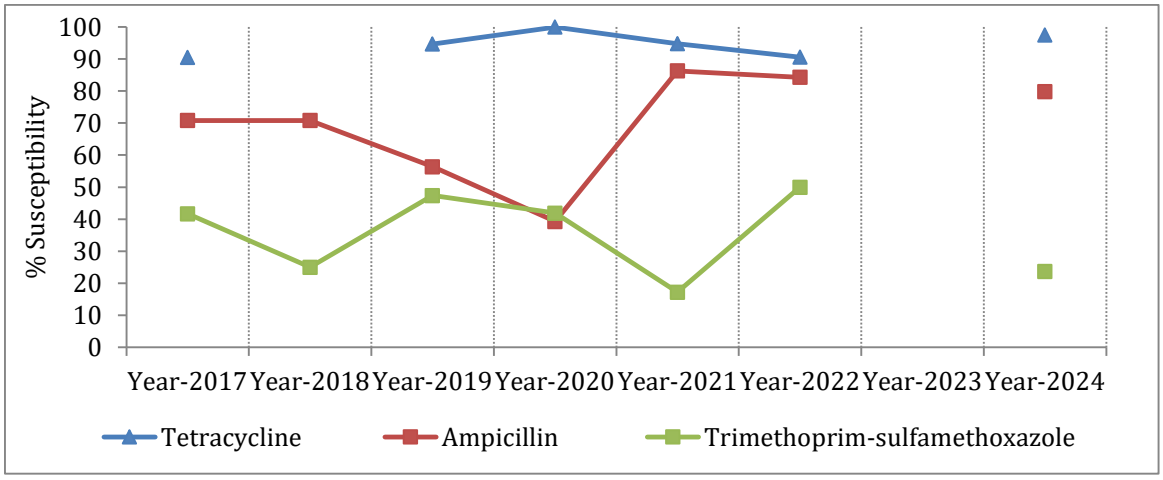


Figure 5.4: Yearly susceptibility trends of *Vibrio cholerae*

Overall, the data reinforce tetracycline as the most reliable therapeutic agent for cholera, while highlighting fluctuating ampicillin susceptibility and persistent resistance to older, low-cost antimicrobials such as TMP-SMX. These findings underscore the importance of continued antimicrobial resistance surveillance, especially during outbreak seasons, to enable timely detection of resistance trends and to inform effective empirical therapy.

Diarrheagenic *Escherichia coli* (DEC)

Diarrheagenic *Escherichia coli* (DEC) isolates (n = 188) exhibited widespread resistance to multiple first-line and commonly prescribed antibiotics. Only 11.7% (22/188) of isolates were susceptible to ampicillin, and 6.4% (12/188) to cefixime (**Table 5.8**). Nalidixic acid susceptibility was modest, with 17% (32/188) of isolates remaining sensitive, while TMP-SMX retained the highest relative efficacy, with 68.6% (129/188) of isolates susceptible.

Table 5.8: Susceptibility pattern of DEC

AMA	Diarrheagenic *Escherichia coli* N=188 (S%)
Ampicillin	22 / 188 (11.7)
Azithromycin	*0 / 0 (-)
Cefixime	12 / 188 (6.4)
Ciprofloxacin	0 / 158 (0)
Nalidixic acid	32 / 188 (17)
Trimethoprim-sulfamethoxazole	129 / 188 (68.6)

Yearly susceptibility trends from 2019 through 2024 reveal persistent and concerning resistance patterns. Ampicillin susceptibility remained consistently low, fluctuating between 0% and 11.7%, with the lowest levels observed in 2021 (0%) and 2020 (1%) (**Table 5.9** and **Figure 5.5)**, and an increase to 11.7% in 2024. Cefixime showed a similar trend, with susceptibility declining to 3.2% in 2022 and 3.0% in 2023, with a slight increase to 6.4% in 2024, confirming extensive resistance to extended-spectrum cephalosporins. Nalidixic acid susceptibility was variable but low throughout the surveillance period, ranging from 8% to 17%, indicating widespread quinolone resistance. In contrast, TMP-SMX exhibited moderate and somewhat fluctuating activity. Susceptibility ranged from 21.2% to 36.4% between 2019 and 2023, but notably increased to 68.6% in 2024, possibly reflecting either reduced selective pressure from decreased clinical use or strain replacement phenomena within the DEC population.

Table 5.9: Yearly susceptibility trend of DEC

AMA	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024
	N=134	N=102	N=88	N=189	N=33	N=188
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Ampicillin	6/132 (4.5)	1/102 (1)	0/87 (0)	6 / 189 (3.2)	1/33 (3)	22 / 188 (11.7)
Cefixime	17/129 (13.2)	11/100 (11)	12/87 (13.8)	6 / 189 (3.2)	1/33 (3)	12 / 188 (6.4)
Nalidixic acid	14/122 (11.5)	11/98 (11.2)	7/87 (8)	15 / 164 (9.1)	5/32 (15.6)	32 / 188 (17)
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)

Overall, the findings reveal the prevalence of multidrug resistance among DEC isolates, with particularly high resistance to ampicillin and cefixime. These results underscore the urgent need for revision of empirical treatment strategies for diarrheal illnesses. Continuous monitoring of susceptibility trends and guided antibiotic stewardship remain crucial to mitigate the impact of multidrug-resistant DEC strains in diarrheal disease management.

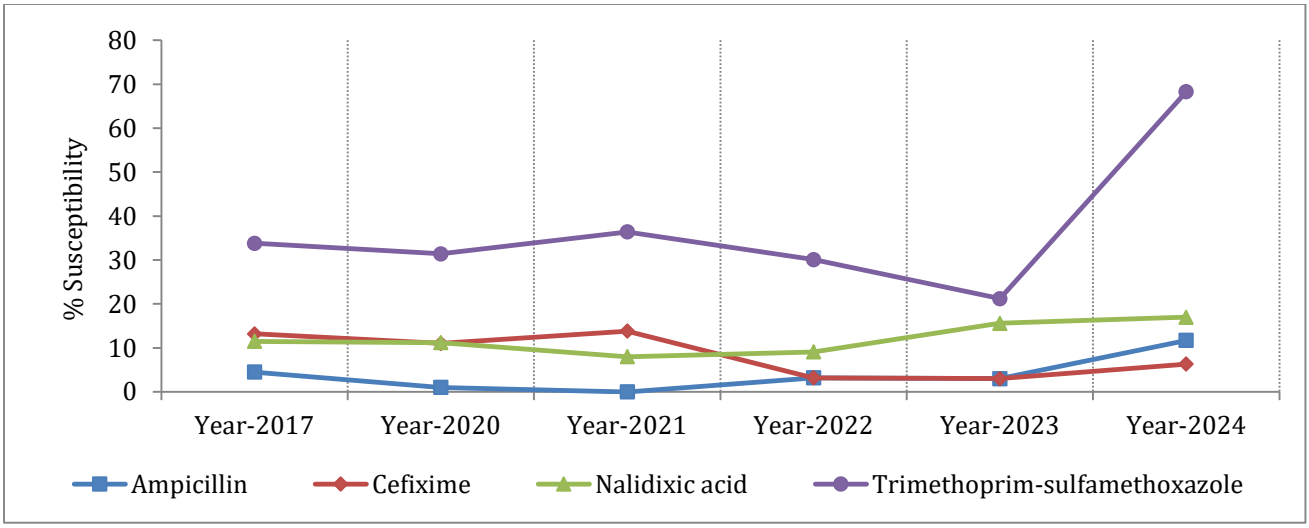


Figure 5.5: Yearly susceptibility trend of DEC

Summary

Collectively, the surveillance data suggest that tetracycline and meropenem remain among the most reliably effective antimicrobial agents for their respective organisms, particularly *V. cholerae* and *Aeromonas* spp. Third-generation cephalosporins (e.g., cefixime) and macrolides (azithromycin) maintain varying degrees of effectiveness against *Shigella* species. In contrast, fluoroquinolones and older agents such as TMP-SMX show entrenched or variable resistance across taxa. The findings underscore the need for ongoing, organism-specific susceptibility monitoring, integration of molecular resistance surveillance, and stewardship-driven updates to empirical therapy guidelines.

Molecular biology

A total of 27 diarrheal isolates were received at the nodal centre from various regional centres during the surveillance period. Of these, 22 isolates were identified as diarrheagenic *Escherichia coli*, two as *Shigella flexneri*, two as *Shigella sonnei*, and one as *Vibrio cholerae*. All isolates were successfully revived and subjected to PCR-based screening for the detection and characterization of antimicrobial resistance (AMR) genes.

Among the 22 diarrheagenic *E. coli* isolates, 19 (86.4%) exhibited resistance to ampicillin, all of which harboured the *bla*$_{TEM}$ gene. Resistance to third-generation cephalosporins (cefixime) was observed in 15 of 22 isolates (68.2%), associated with the presence of the *bla*$_{OXA}$ gene. Additionally, 5 isolates (22.7%) were resistant to TMP-SMX, associated with the carriage of *dfrA* and *sul* resistance determinants.

All four *Shigella* isolates (two *S. flexneri* and two *S. sonnei*) demonstrated resistance to both ampicillin and cefixime. However, PCR screening did not detect bla$_{TEM}$ or *bla*$_{CTX-M}$ genes, suggesting resistance may be mediated by alternative β-lactamase genes not included in

the current PCR panel or through non-enzymatic mechanisms such as porin loss or efflux pump overexpression. Resistance to TMP-SMX in these isolates corresponded with the presence of *dfrA* and *sul* genes.

The single *Vibrio cholerae* isolate was susceptible to all tested first-line antimicrobials. PCR analysis confirmed the absence of common AMR genes, indicating that standard treatments remain effective against this strain.

Clinical relevance and treatment guidelines:

General recommendations:

- Empirical therapy should be guided by local susceptibility patterns and clinical severity; de-escalation to narrow-spectrum agents should follow once culture/AST or molecular results are available.
- Avoid routine empirical use of fluoroquinolones for enteric pathogens in this setting because of very low susceptibility across *Shigella*, *Aeromonas*, and diarrheagenic *E. coli* (DEC).
- Ensure close liaison between clinicians and microbiology teams for timely specimen collection prior to antibiotic administration, rapid AST reporting, and prompt modification of therapy.

Pathogen-specific guidance:

***Aeromonas* spp.:** Meropenem demonstrated the highest activity, and tetracyclines remain effective; however, reserve carbapenems for severe or invasive infections and use tetracycline for non-severe, susceptibility-confirmed cases where appropriate. Avoid empirical use of ciprofloxacin.

***Shigella* spp.:** For empiric therapy of moderate-to-severe dysentery, consider cefixime or azithromycin given good current activity, particularly against *S. sonnei.* Given species-specific differences, targeted therapy is advised once species and AST are available. TMP-SMX may be considered when local susceptibility for the isolate is confirmed. Avoid quinolones as first-line empiric agents.

***Vibrio cholerae*:** Tetracycline (or doxycycline) remains the preferred empirical oral agent given sustained high susceptibility (~97.5%). Ampicillin may be considered in select cases where susceptibility is confirmed; TMP-SMX should generally be avoided empirically because of low activity.

Diarrheagenic *E. coli* (DEC): High resistance to ampicillin and cefixime preclude their empirical use. TMP-SMX may be considered only if susceptibility is confirmed; otherwise, therapy should be individualized based on AST results and clinical severity.

Chapter 6. Staphylococci and Enterococci

A total of 8515 *S. aureus*, 4574 coagulase-negative *Staphylococcus* (CoNS) and 6044 enterococcal isolates collected across India were analysed in the year 2024. The total number of enterococcal isolates available for analysis in 2024 was significantly higher than in 2023.

S. aureus

A total of 8515 isolates of *S. aureus* were reported from various centres across India. The proportion of methicillin-resistant *S. aureus* (MRSA) in 2024 was higher than the rates reported in 2023. MRSA identification was carried out using susceptibility testing to cefoxitin (4690 isolates) and/or oxacillin (5930 isolates). The overall proportion of MRSA was 52.4% based on cefoxitin testing and 47.9% based on oxacillin testing. A discrepancy in MRSA detection rates between the two methods of oxacillin MIC and cefoxitin DD/MIC was observed, likely due to the differing number of isolates tested with each method and the possibility that not all isolates were subjected to both tests. According to CLSI guidelines, an isolate of *S. aureus* can be identified as MRSA using either cefoxitin and /or oxacillin. In some cases, only one of the two methods yields a positive result; for example, *mec*C isolates may be cefoxitin-sensitive but oxacillin-resistant.

When comparing susceptibility, methicillin-sensitive *S. aureus* (MSSA) isolates showed higher susceptibility to tetracycline, clindamycin, co-trimoxazole, erythromycin, and ciprofloxacin compared to MRSA. Anti-MRSA antibiotics such as vancomycin, teicoplanin and tigecycline demonstrated excellent *in vitro* activity, showing 100% effectiveness against MRSA isolates. Resistance to linezolid was observed in MRSA, MSSA, and CoNS isolates, with rates of 3.4%, 1.5%, and 1.9%, respectively **(Table 6.1)**.

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

AMA	All Specimens			
	S. aureus N=8515 (S%)	MSSA N=4262 (S%)	MRSA N=4253 (S%)	CoNS N=4574 (S%)
Cefoxitin	2233 / 4690 (47.6)	2183/2183 (100)	0/2505 (0)	423 / 1780 (23.8)
Oxacillin	3088 / 5930 (52.1)	3002/3002 (100)	0/2908 (0)	633 / 3032 (20.9)
Vancomycin	7968 / 7968 (100)	3896 /3896 (100)	4072/4072 (100)	4574 / 4574 100%)
Teicoplanin	3377 / 3377 (100)	1751/1751 (100)	1626/1626 (100)	1178 / 1178 (100)
Erythromycin	2976 / 8293 (35.9)	1908/4119 (46.3)	1059/4153 (25.5)	328 / 2444 (13.4)

Tetracycline	3765 / 4241 (88.8)	1765/1920 (91.9)	2000/2321 (86.2)	802 / 1902 (42.2)
Tigecycline	2846/ 2846 (100)	1306/1306 (100)	1540/1540 (100)	-
Ciprofloxacin	1474 / 8036 (18.3)	1021/3933 (26)	452/4101 (11)	1323 / 4574 (28.9)
Clindamycin	6013 / 8270 (72.7)	3330/4122 (80.8)	2670/4132 (64.6)	1474 / 4574 (32.2)
Trimethoprim-sulfamethoxazole	6118 / 7968 (76.8)	3102/3896 (79.6)	3016/4072 (74.1)	2279 / 4574 (49.8)
Linezolid	7961 / 8169 (97.5)	3882/3942 (98.5)	4069/4212 (96.6)	4487/4574 (98.1)

Table 6.2 presents the susceptibility pattern of *S. aureus* and CoNS across various hospital locations. As expected, the overall MRSA rates among *S. aureus* were lowest in the OPD isolates, compared to ward and ICU isolates, although the difference was not significant. Susceptibility to most antibiotics was lowest in ICU isolates and highest in OPD isolates of *S. aureus,* including MRSA and CoNS. However, for *S. aureus*, susceptibility to ciprofloxacin and clindamycin was slightly higher in ICU isolates than in OPD isolates, although this difference was not significant. Linezolid resistance rates observed in MRSA, MSSA and CoNS isolates were consistent with those reported in 2023. Notably, no resistance to teicoplanin was detected in MRSA, MSSA, or CoNS isolates.

Table 6.2: Location-wise susceptibility of *S. aureus*, MSSA, MRSA and CoNS from all samples

AMA	*Staphylococcus aureus*				MSSA				MRSA				CoNS			
	Total N=8515	OPD N=3779	Ward N=3942	ICU N=794	Total N=4262	OPD N=2002	Ward N=1910	ICU N=350	Total N=4253	OPD N=1777	Ward N=2032	ICU N=444	Total N=4574	OPD N=1066	Ward N=2330	ICU N=1178
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	2233/4690 (47.6)	1036/2090 (49.6)	960/2081 (46.1)	237/519 (45.7)	2183/2183 (100)	1023/1023 (100)	933/933 (100)	227/227 (100)	0/2505 (0)	0/1067 (0)	0/1146 (0)	0/292 (0)	423/1780 (23.8)	239/779 (30.7)	105/574 (18.3)	79/427 (18.5)
Oxacillin	3088/5930 (52.1)	1419/2509 (56.6)	1458/2913 (50.1)	211/508 (41.5)	3002/3002 (100)	1390/1390 (100)	1412/1412 (100)	200/200 (100)	0/2908 (0)	0/1116 (0)	0/1484 (0)	0/308 (0)	633/3032 (20.9)	88/302 (29.1)	410/1890 (21.7)	135/840 (16.1)
Vancomycin	7968/7968 (100)	3496/3496 (100)	3678/3678 (100)	794/794 (100)	3896/3896 (100)	1808/1808 (100)	1738/1738 (100)	350/350 (100)	4072/4072 (100)	1688/1688 (100)	1940/1940 (100)	444/444 (100)	4574/4574 (100)	1066/1066 (100)	2330/2330 (100)	1178/1178 (100)
Teicoplanin	3377/3377 (100)	1372/1372 (100)	1571/1571 (100)	434/434 (100)	1751/1751 (100)	769/769 (100)	777/777 (100)	205/205 (100)	1626/1626 (100)	603/603 (100)	794/794 (100)	229/229 (100)	1178/1178 (100)	127/127 (100)	709/709 (100)	342/342 (100)
Erythromycin	2976/8293 (35.9)	1279/3648 (35.1)	1436/3862 (37.2)	261/783 (33.3)	1908/4119 (46.3)	853/1914 ((44.6)	891/1860 (47.9)	164/345 (47.5)	1059/4153 (25.5)	425/1732 (24.5)	537/1983 (27.1)	97/438 (22.1)	328/2444 (13.4)	131/797 (16.4)	136/1046 (13.0)	61/601 (10.1)
Tetracycline	3765/4241 (88.8)	1599/1857 (86.1)	1823/1967 (92.7)	343/417 (82.3)	1765/1920 (91.9)	783/881 (88.9)	834/877 (95.1)	148/162 (91.4)	2000/2321 (86.2)	816/976 (83.6)	989/1090 (90.7)	195/255 (76.5)	802/1902 (42.2)	213/783 (27.2)	411/664 (61.9)	178/455 (39.1)
Tigecycline	2846/2846 (100)	1305/1305 (100)	1346/1346 (100)	195/195 (100)	1306/1306 (100)	612/612 (100)	603/603 (100)	91/91 (100)	1540/1540 (100)	693/693 (100)	743/743 (100)	104/104 (100)	-	-	-	-
Ciprofloxacin	1474/8036 (18.3)	615/3531 (17.4)	743/3711 (20)	116/794 (14.6)	1022/3937 (26)	445/1831 (24.3)	488/1756 (27.8)	89/350 (25.4)	454/4104 (11.1)	171/1703 (10)	256/1957 (13.1)	27/444 (6.1)	1323/4574 (28.9)	373/1066 (35)	682/2330 (29.2)	268/1178 (22.8)
Clindamycin	6013/8270 (72.7)	2617/3644 (71.8)	2847/3841 (74.1)	549/785 (69.9)	3330/4122 (80.8)	1517/1921 (79.0)	1535/1855 (82.7)	278/346 (80.3)	2670/4132 (64.6)	1099/1721.0 (63.9)	1300/1972 (65.9)	271/439 (61.7)	1474/4574 (32.2)	369/1066 (34.6)	818/2330 (35.1)	287/1178 (24.4)

Trimethoprim - sulfamethoxazole	6118/7968 (76.8)	2689/3496 (76.9)	2867/3678 (77.9)	562/794 (70.8)	3102/3896 (79.6)	1414/1808 (78.2)	1413/1738.0 (81.3)	275/350 (78.6)	3016/4072 (74.1)	1275/1688.0 (75.5)	1454/1940 (74.9)	287/444 (64.6)	2279/4574 (49.8)	467/1066 (43.8)	1242/2330 (53.3)	570/1179 (48.3)
Linezolid	7961/8169 (97.5)	3489/3586 (97.3)	3698/3789 (97.6)	774/794 (97.5)	3882/3942 (98.5)	1802/1826 (98.7)	1733/1766 (98.1)	347/350 (99.1)	4069/4212 (96.6)	1686/1758.0 (95.9)	1956/2010 (97.3)	427/444 (96.2)	4487/4574 (98.1)	1045/1066 (98.0)	2288/2330 (98.2)	1154/1178 (98.0)

Regional Centre-wise analysis

As shown in **Table 6.3**, there were significant differences in MRSA rates observed between the various RCs. Based on cefoxitin test results, the highest MRSA rates were observed from RC5 and RC20, while the lowest MRSA rates were observed from RC4 and RC7. Ciprofloxacin susceptibility was extremely low across all the centres. The susceptibility rates of other antibiotics varied widely between the centres for many of the antibiotics. Linezolid resistance was highest among isolates from RC16 and RC3.

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

RC/ AMA	Cefoxitin (N=4475)	Oxacillin (N=5780)	Vancomycin (N=7745)	Teicoplanin (N=3238)	Erythromycin (N=8128)	Tetracycline (N=4078)	Tigecycline (N=2712)	Ciprofloxacin (N=7745)	Clindamycin (N=8081)	Trimethoprim - sulfamethoxazole (N=7745)	Linezolid (N=7939)
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
RC2	0/0 (-)	1514/2962 (51.1)	2962/2962 (100.0)	76/76 (100.0)	1051/2914 (36.1)	0/1 (-)	0/0 (-)	410/2962 (13.8)	1782/2962 (60.2)	2231/2962 (75.3)	2962/2962 (100.0)
RC3	95/153 (62.1)	0/0 (-)	153/153 (100.0)	0/0 (-)	72/154 (46.8)	138/142 (97.2)	0/0 (-)	152/153 (99.3)	103/144 (71.5)	149/153 (97.4)	131/153 (85.6)
RC4	44/46 (95.7)	345/505 (68.3)	46/46 (100.0)	6/6 (-)	275/503 (54.7)	44/46 (95.7)	2/2 (-)	40/46 (87.0)	360/417 (86.3)	45/46 (97.8)	239/240 (99.6)
RC5	19/170 (11.2)	20/167 (12.0)	170/170 (100.0)	170/170 (100.0)	45/170 (26.5)	140/158 (88.6)	0/0 (-)	5/170 (2.9)	155/170 (91.2)	118/170 (69.4)	168/170 (98.8)
RC6	165/396 (41.7)	15/28 (-)	399/399 (100.0)	399/399 (100.0)	124/398 (31.2)	329/383 (85.9)	3/3 (-)	15/399 (3.8)	256/397 (64.5)	181/399 (45.4)	388/401 (96.8)
RC7	44/52 (84.6)	78/185 (42.2)	202/202 (100.0)	174/174 (100.0)	54/199 (27.1)	165/195 (84.6)	182/182 (100.0)	16/203 (7.9)	160/199 (80.4)	116/202 (57.4)	200/203 (98.5)
RC8	202/312 (64.7)	209/316 (66.1)	316/316 (100.0)	316/316 (100.0)	120/309 (38.8)	289/316 (91.5)	316/316 (100.0)	67/316 (21.2)	308/316 (97.5)	237/316 (75.0)	316/316 (100.0)
RC9	173/337 (51.3)	0/0 (-)	337/337 (100.0)	0/0 (-)	109/329 (33.1)	317/334 (94.9)	2/2 (-)	47/337 (13.9)	284/324 (87.7)	311/337 (92.3)	307/337 (91.1)

RC10	392/639 (61.3)	38/212 (17.9)	648/648 (100.0)	623/623 (100.0)	259/648 (40.0)	0/0 (-)	0/0 (-)	118/648 (18.2)	508/648 (78.4)	549/648 (84.7)	648/648 (100.0)
RC11	65/175 (37.1)	66/175 (37.7)	177/177 (100.0)	177/177 (100.0)	71/175 (40.6)	159/177 (89.8)	0/0 (-)	14/177 (7.9)	160/177 (90.4)	105/177 (59.3)	177/177 (100.0)
RC12	40/86 (46.5)	37/80 (46.3)	86/86 (100.0)	84/84 (100.0)	45/83 (54.2)	81/86 (94.2)	84/84 (100.0)	6/86 (7.0)	73/85 (85.9)	34/86 (39.5)	78/88 (88.6)
RC13	0/3 (-)	0/0 (-)	3/3 (-)	0/0 (-)	1/3 (-)	1/3 (-)	1/2 (-)	1/3 (-)	1/3 (-)	2/3 (-)	2/3 (-)
RC14	429/795 (54.0)	442/796 (55.5)	796/796 (100.0)	796/796 (100.0)	309/796 (38.8)	796/796 (100.0)	796/796 (100.0)	174/796 (21.9)	767/796 (96.4)	665/796 (83.5)	796/796 (100.0)
RC16	139/538 (25.8)	0/0 (-)	538/538 (100.0)	0/0 (-)	101/538 (18.8)	460/529 (87.0)	534/534 (100.0)	160/538 (29.7)	319/538 (59.3)	445/538 (82.7)	439/538 (81.6)
RC17	124/157 (79.0)	195/231 (84.4)	293/293 (100.0)	291/291 (100.0)	130/293 (44.4)	288/293 (98.3)	290/290 (100.0)	63/293 (21.5)	178/288 (61.8)	267/293 (91.1)	293/293 (100.0)
RC19	69/163 (42.3)	0/0 (-)	163/163 (100.0)	0/0 (-)	44/163 (27.0)	17/163 (10.4)	45/45 (100.0)	25/163 (15.3)	63/163 (38.7)	87/163 (53.4)	161/163 (98.8)
RC20	75/338 (22.2)	3/8 (-)	338/338 (100.0)	8/8 (-)	79/338 (23.4)	303/338 (89.6)	338/338 (100.0)	46/338 (13.6)	297/338 (87.9)	309/338 (91.4)	322/338 (95.3)
RC21	43/117 (36.8)	52/115 (45.2)	118/118 (100.0)	118/118 (100.0)	26/118 (22.0)	103/118 (87.3)	118/118 (100.0)	22/118 (18.6)	107/118 (90.7)	97/118 (82.2)	118/118 (100.0)
Total	2118/4475 (47.3)	3014/5780 (52.2)	7745/7745 (100.0)	3238/3238 (100.0)	2915/8128 (35.9)	3630/4078 (89)	2712/2712 (100.0)	1381/7745 (17.8)	5881/8081 (72.8)	5948/7745 (76.8)	7745/7939 (97.6)

MRSA rates steadily increased over the 8 years of surveillance from 33% in 2017 to nearly 53% in 2024. 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. There was only a marginal decrease in the susceptibility rates to erythromycin. Overall susceptibility rates to erythromycin, clindamycin, ciprofloxacin, and co-trimoxazole were more evident in MSSA when compared to MRSA **(Table 6.4** and **Figure 6.1)**.

Most of the *S. aureus* isolates were obtained from superficial infections, followed by bloodstream and deep infections. MRSA rates differed based on the source of isolation, with isolates from superficial and deep infection demonstrating the highest rates (around 55%) while those from blood showed the lowest rates (45%) **(Tables 6.5-6.7)**.

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
	N=5708	N=8644	N=12320	N=6281	N=8827	N=9415	N=8900	N=8515
	(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 (47.61)
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 (52.03)
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)
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)
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 (35.86)
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 (88.78)
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)
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 (18.33)
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 (72.68)
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 (76.78)
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 (97.45)

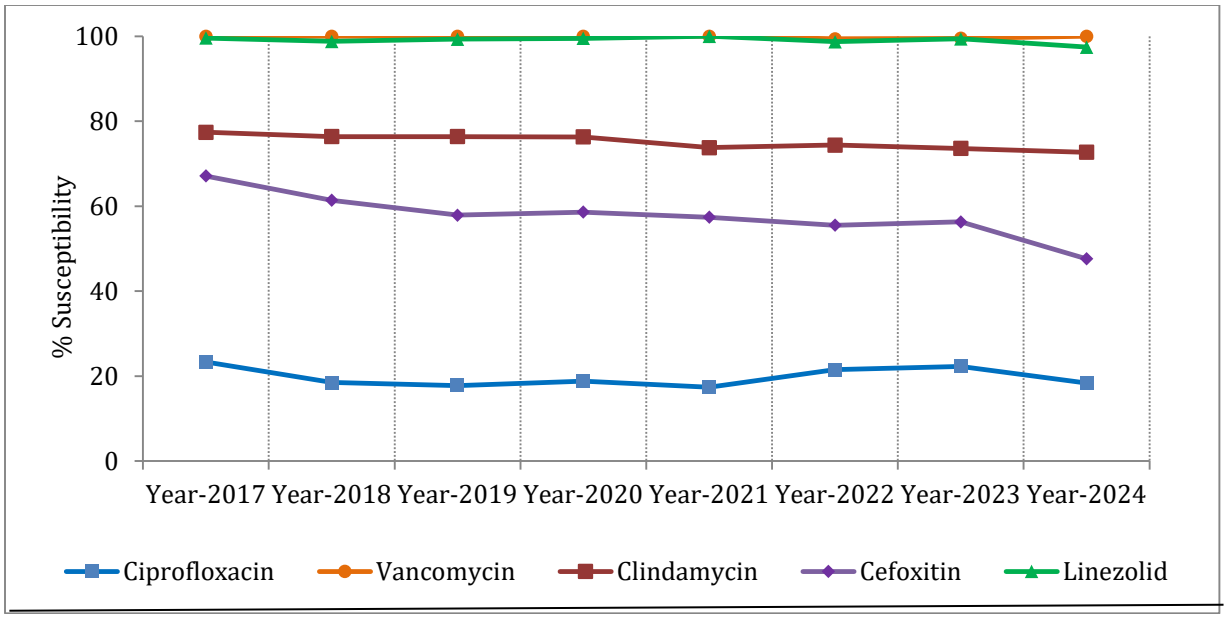


Figure 6.1: Year-wise susceptibility trends of *S. aureus* from all samples

Table 6.5: Susceptibility percentages of staphylococci isolated from blood

AMA	Blood			
	S. aureus N=1067 (S%)	MSSA N=559 (S%)	MRSA N=508 (S%)	CoNS N=3897 (S%)
Cefoxitin	388/706 (55)	378/378 (100.0)	0/328 (0.0)	323/1326 (24.4)
Oxacillin	367/698 (52.6)	351/351 (100.0)	0/347 (0)	579/2740 (21.1)
Vancomycin	1065/1065 (100)	557/557 (100)	508/508 (100)	3897/3897 (100)
Teicoplanin	581/581 (100)	316/316 (100)	265/265 (100)	901/901 (100)
Erythromycin	415/1063 (39)	278/556 (50.0)	137/506 (27.1)	252/1929 (13.1)
Tetracycline	561/639 (87.8)	314/340 (92.4)	247/299 (82.6)	503/1412 (35.6)
Tigecycline	360/360 (100)	213/213 (100)	147/147 (100)	-
Ciprofloxacin	247/1065 (23.2)	197/557 (35.4)	50/508 (9.8)	1111/3897 (28.5)
Clindamycin	784/1061 (73.9)	458/554 (82.7)	326/506 (64.4)	1220/3897 (31.3)
Trimethoprim-sulfamethoxazole	765/1065 (71.8)	444/557 (79.7)	321/508 (63.2)	1907/3897 (48.9)
Linezolid	1033/1067 (96.8)	542/557 (97.3)	491/508 (96.7)	3843/3897 (98.6)

Table 6.6: Susceptibility percentages of staphylococci isolated from Superficial Infections

AMA	Superficial Infections			
	S. aureus **N=2850 (S%)**	**MSSA N=1364 (S%)**	**MRSA N=1486 (S%)**	**CoNS N=263 (S%)**
Cefoxitin	993/2142 (46.4)	967/967 (100.0)	0/1174 (0)	53/239 (22.2)
Oxacillin	853/1674 (51)	814/814 (100.0)	0/852 (0)	6/40 (15.0)
Vancomycin	2620/2620 (100)	1196/1196 (100)	1424/1424 (100)	263/263 (100)
Teicoplanin	1428/1428 (100)	714/714 (100)	714/714 (100)	89/89 (100)
Erythromycin	1015/2846 (35.7)	669/1359 (49.2)	342/1479 (23.1)	31/261 (11.9)
Tetracycline	1757/1969 (89.2)	780/855 (91.2)	977/1114 (87.7)	133/242 (55.0)
Tigecycline	1429/1429 (100)	608/608 (100)	821/821 (100)	-
Ciprofloxacin	449/2620 (17.1)	312/1198 (26.0)	139/1426 (9.7)	71/263 (27.0)
Clindamycin	2160/2809 (76.9)	1152/1345 (85.7)	1003/1458 (68.8)	95/263 (36.1)
Trimethoprim-sulfamethoxazole	2052/2620 (78.3)	984/1196 (82.3)	1068/1424 (75.0)	118/263 (44.9)
Linezolid	2603/2719 (95.7)	1203/1227 (98.0)	1395/1486 (93.9)	247/263 (93.9)

Table 6.7: Susceptibility percentages of staphylococci isolated from Deep Infections

AMA	Deep Infections			
	S. aureus **N=2438 (S%)**	**MSSA N=1223 (S%)**	**MRSA N=1215 (S%)**	**CoNS N=53 (S%)**
Cefoxitin	330/713 (46.3)	328/328 (100.0)	0/385 (0)	9/26 (34.6)
Oxacillin	1078/2107 (51.2)	1067/1067 (100.0)	0/1039 (0)	5/37 (13.5)
Vancomycin	2409/2409 (100.0)	1203/1203 (100.0)	1206/1206 (99.8)	53/53 (100.0)
Teicoplanin	630/630 (100.0)	339/339 (100.0)	291/291 (100.0)	37/37 (100.0)
Erythromycin	850/2415 (35.2)	526/1207 (43.6)	323/1207 (26.8)	9/29 (31.0)
Tetracycline	574/626 (91.7)	270/287 (94.1)	304/339 (89.7)	15/24 (62.5)
Tigecycline	367/367 (100.0)	187/187 (100.0)	180/180 (100.0)	-
Ciprofloxacin	332/2409 (13.8)	206/1204 (17.1)	126/1206 (10.4)	15/53 (28.3)
Clindamycin	1647/2432 (67.7)	925/1219 (75.9)	721/1212 (59.5)	24/53 (45.3)
Trimethoprim-sulfamethoxazole	1815/2409 (75.3)	894/1203 (74.3)	921/1206 (76.4)	32/53 (60.4)
Linezolid	2414/2422 (99.7)	1202/1205 (99.8)	1211/1215 (99.7)	53/53 (100.0)

As shown in **Table 6.8** and **Figure 6.2**, there was not much variation in the susceptibility of MSSA isolates to different antibiotics over the years studied. Susceptibility to ciprofloxacin remained extremely low, while susceptibility to erythromycin was moderate. In contrast, susceptibility to clindamycin and tetracycline remained consistently high, with little to no change observed over time.

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
	N=3819	N=5135	N=7029	N=3655	N=5273	N=5050	N=4539	N=4262
	(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)
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)
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)
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)
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)
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)
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)
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)
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)
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)
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)

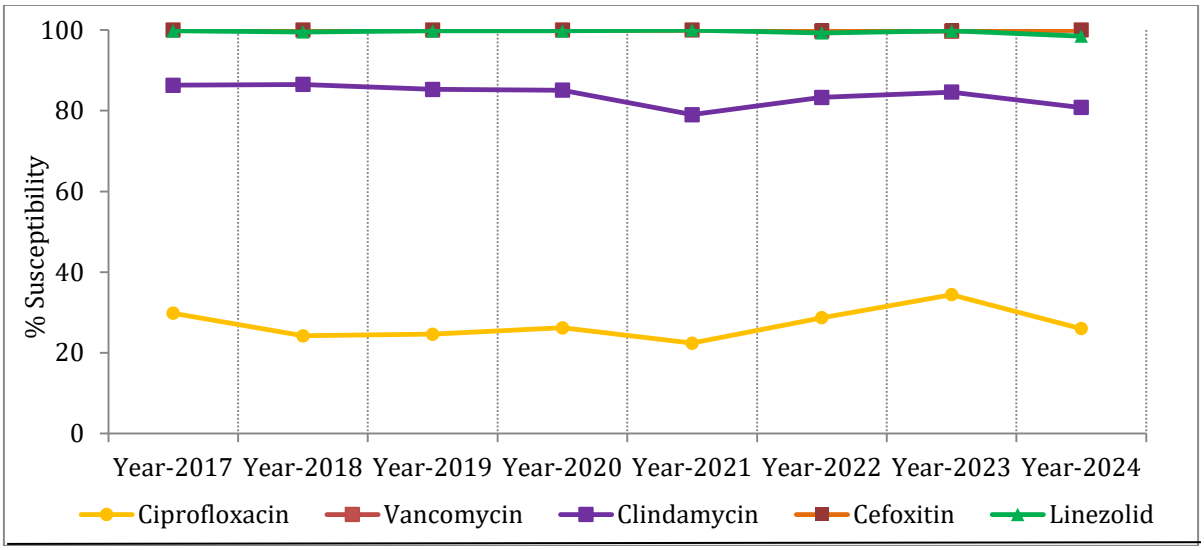


Figure 6.2: Year-wise susceptibility trends of MSSA from all samples

Similar to MSSA, MRSA susceptibility rates to various antibiotics showed little variation over the years, except for TMP-SMX, which demonstrated a slight increase in susceptibility in 2024 compared to previous years (**Table 6.9** and **Figure 6.3**). Fortunately, anti-MRSA antibiotics such as vancomycin, tigecycline, and linezolid continued to exhibit excellent activity.

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
	N=1870	N=3445	N=5185	N=2582	N=3423	N=4266	N=4311	N=4253
	(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)
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)
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)
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)
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)
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)
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)
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)
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)

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)
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)

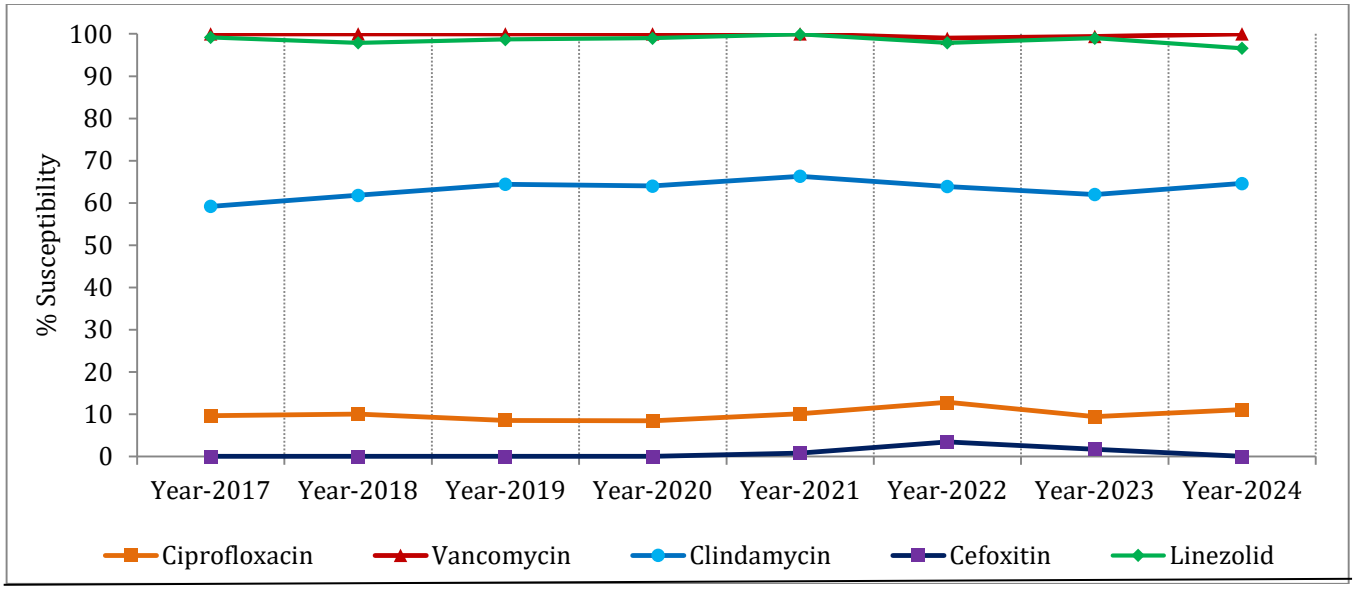


Figure 6.3: Year-wise susceptibility trends of MRSA from all samples

Coagulase-negative *Staphylococcus*

The most commonly identified CoNS species were *S. haemolyticus, S. epidermidis, S. hominis, S. lugdunensis* and *S. saprophyticus*. Cefoxitin resistance was highest in *S. haemolyticus*, followed by *S. hominis* and *S. epidermidis*. 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,* but were slightly increased in *S. haemolyticus* (0.7 to 2.6%) **(Table 6.10)**.

Table 6.10: Susceptibility percentages of CoNS isolated from all specimens

AMA	All Specimens					
	S. haemolyticus **N=1572 (S%)**	***S. epidermidis*** **N=1269 (S%)**	***S. hominis*** **N=1241 (S%)**	***Staphylococcus* spp.** **N=425 (S%)**	***S. lugdunensis*** **N=20 (S%)**	***S. saprophyticus*** **N=43 (S%)**
Cefoxitin	119/607 (19.6)	89/443 (20.1)	140/438 (31.96)	45/244 (18.4)	18/20 (-)	12/28 (42.9)
Vancomycin	1572/1572 (100)	1269/1269 (100)	1241/1241 (100)	425/425 (100)	20/20 (-)	43/43 (100)
Teicoplanin	462/462 (100)	407/407 (100)	180/180 (100)	75/75 (100)	17/17 (-)	34/34 (100)
Erythromycin	66/881 (7.5)	90/652 (13.8)	89/572 (15.6)	68/284 (23.9)	8/19 (-)	6/32 (18.8)
Tetracycline	220/684 (32.2)	250/460 (54.4)	117/478 (24.5)	184/239 (76.99)	4/4 (-)	25/33 (75.8)
Ciprofloxacin	242/1572 (15.4)	474/1269 (37.4)	381/1241 (30.7)	175/425 (41.2)	18/20 (-)	33/43 (76.7)
Clindamycin	297/1572 (18.9)	442/1269 (34.8)	519/1241 (41.8)	185/425 (43.5)	12/20 (-)	18/43 (41.9)
Linezolid	1531/1572 (97.4)	1263/1269 (99.5)	1233/1241 (99.4)	394/425 (92.7)	20/20 (-)	42/43 (97.7)
Trimethoprim-sulfamethoxazole	690/1572 (43.9)	692/1269 (54.5)	572/1241 (46.1)	270/425 (63.5)	19/20 (-)	35/43 (81.4)

As shown in **Table 6.11** and **Figure 6.4**, the rate of methicillin resistance among CoNS remained relatively stable throughout the surveillance period, ranging from 67% in 2017 to nearly 80% in the following years. Erythromycin susceptibility showed a significant decline, dropping from 27.7% in 2017 to 13.4% in 2024. Similar trends were observed for tetracycline (87% in 2017 to 42% in 2024) and clindamycin (58% in 2017 to 32% in 2024). However, susceptibility to higher antibiotics such as vancomycin, tigecycline, and linezolid remained excellent throughout the surveillance period.

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

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023	Year-2024
	N=2830	N=4016	N=3571	N=2018	N=2655	N=6333	N=6895	N=4574
	(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)
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)
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)
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)
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)
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)
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)
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)
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)

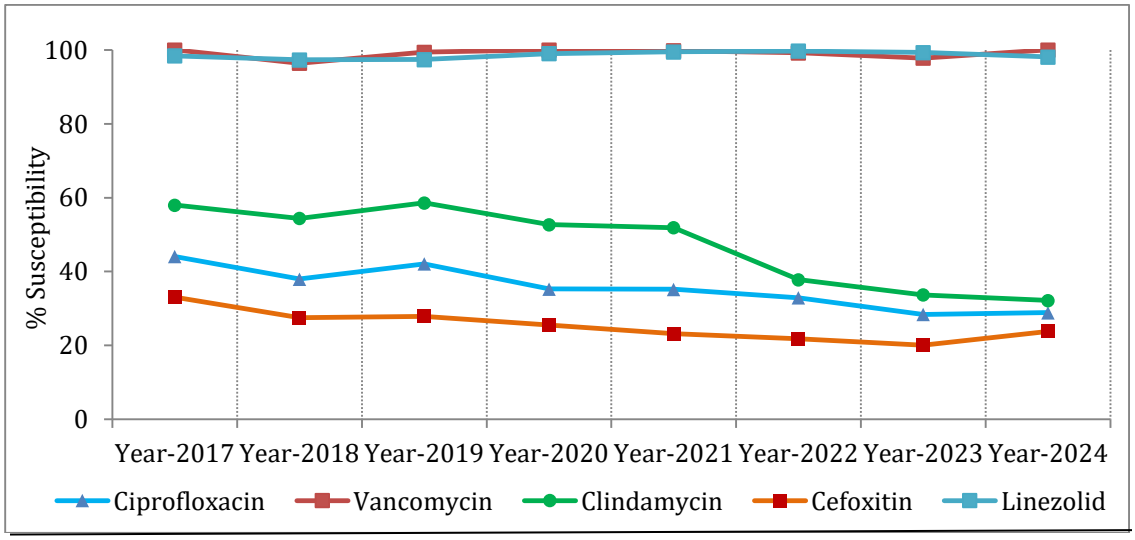


Figure 6.4: Year-wise susceptibility trends of CoNS from all samples

Enterococci

E. faecalis is typically the most common species, followed by *E. faecium*. However, in 2024, *E. faecium* emerged as 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 22%, a slight increase from 17.5% in 2023. Notably, the vancomycin resistance rate in *E. faecium* was 10 times higher than in *E. faecalis* (34.2% vs. 3.4%). Isolates from blood (for both species) appear to be more resistant when compared to those from superficial infections. Although the numbers are too small for statistical significance, vancomycin resistance among CSF isolates was much higher than the overall rate **(Table 6.12)**.

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=1180 (S%)	*E. faecium* N=1630 (S%)	*E. faecalis* N=276 (S%)	*E. faecium* N=603 (S%)	*E. faecalis* N=378 (S%)	*E. faecium* N=233 (S%)	*E. faecalis* N=188 (S%)	*E. faecium* N=293 (S%)	*E. faecalis* N=*7 (S%)	*E. faecium* N=*12 (S%)
Ampicillin	932/1100 (84.7)	310/1463 (21.2)	208/256 (81.3)	142/527 (26.9)	309/370 (83.5)	38/231 (16.5)	153/164 (93.3)	46/281 (16.4)	0/6 (-)	*6/11 (-)
Vancomycin	977/1011 (96.6)	1006/1529 (65.8)	258/276 (93.5)	343/603 (56.9)	278/282 (98.6)	159/213 (74.6)	176/183 (96.2)	187/288 (64.9)	0/7 (-)	*8/10 (-)
Teicoplanin	936/990 (94.5)	1011/1511 (66.9)	241/264 (91.3)	343/597 (57.5)	267/280 (95.4)	156/211 (73.9)	171/178 (96.1)	194/285 (68.1)	0/7 (-)	*9/10 (-)
Gentamicin HL	480/839 (57.2)	486/1362 (35.7)	136/249 (54.6)	159/506 (31.4)	135/256 (52.7)	79/195 (40.5)	92/165 (55.8)	90/270 (33.3)	0/6 (-)	*7/10 (-)
Linezolid	1142/1164 (98.1)	1479/1630 (90.7)	264/276 (95.7)	519/603 (86.1)	362/367 (98.6)	219/233 (93.99)	188/188 (100)	267/293 (91.1)	0/7 (-)	*12/12 (-)

As presented in **Table 6.13**, the susceptibility to all the antibiotics was higher among *E. faecalis* isolates as compared to *E. faecium*. The difference was particularly marked for ampicillin and nitrofurantoin. Linezolid resistance was encountered more frequently among *E. faecium* isolates.

Table 6.13: Susceptibility patterns of enterococci from urine

AMA	Urine	
	Enterococcus faecalis **N=1862** **(S%)**	***Enterococcus faecium*** **N=1372** **(S%)**
Ampicillin	1303/1808 (72.1)	156/1311 (11.9)
Vancomycin	1297/1344 (96.5)	777/995 (78.1)
Teicoplanin	1215/1291 (94.1)	712/930 (76.6)
Ciprofloxacin	375/1840 (20.4)	65/1310 (5)
Nitrofurantoin	1556/1770 (87.9)	436/1255 (34.7)
Linezolid	1336/1367 (97.7)	1110/1209 (91.8)

As expected, most antibiotics showed lower susceptibility rates among ICU isolates when compared to ward isolates for both *Enterococcus faecalis* and *Enterococcus faecium*. However, in the case of *E. faecalis*, susceptibility rates for fosfomycin were slightly higher in ICU isolates than in ward isolates **(Table 6.14)**.

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

AMA	*Enterococcus faecalis*				*Enterococcus faecium*			
	Total N=3042	OPD N=1345	Ward N=1394	ICU N=303	Total N=3002	OPD N=569	Ward N=1791	ICU N=639
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Ampicillin	2204/2874 (76.69)	1015/1284 (79)	975/1297 (75.2)	214/292 (73.3)	464/2756 (16.84)	112/540 (20.7)	281/1605 (17.5)	71/611 (11.6)
Vancomycin	2274/2370 (95.95)	1033/1066 (96.9)	954/992 (96.2)	287/312 (92)	1783/2538 (70.25)	347/447 (77.6)	1080/1443 (74.8)	356/639 (55.7)
Teicoplanin	2151/2281 (94.3)	965/1029 (93.8)	913/955 (95.6)	273/297 (91.9)	1723/2442 (70.56)	330/433 (76.2)	1041/1380 (75.4)	352/629 (56)
Gentamicin HL	964/1694 (56.91)	380/664 (57.2)	460/787 (58.4)	124/243 (51)	807/2106 (38.32)	161/367 (43.9)	509/1222 (41.7)	137/517 (26.5)
Ciprofloxacin	397/1951 (20.35)	211/1019 (20.7)	179/836 (21.4)	7/95 (7.4)	75/1429 (5.25)	25/363 (6.9)	44/865 (5.1)	6/201 (3)
Nitrofurantoin	1600/1816 (88.11)	847/948 (89.3)	693/781 (88.7)	59/86 (68.6)	431/1252 (34.42)	137/343 (39.9)	265/772 (34.3)	29/137 (21.2)
Fosfomycin	322/714 (45.1)	163/357 (45.7)	132/303 (43.6)	27/54 (50)	-	-	-	-
Linezolid	2473/2526 (97.9)	1098/1113 (98.7)	1083/1110 (97.6)	292/303 (96.4)	2575/2832 (90.93)	469/511 (91.8)	1567/1682 (93.2)	539/639 (84.4)

Enterococcus faecalis

The year-wise susceptibility rates of *E. faecalis* from 2017 to 2024 are depicted in **Table 6.15 and Figure 6.5**. The susceptibility rates showed a slight increase for almost all the antibiotics in 2024 when compared to 2023. Compared to the index year of 2017, there was a significant reduction in susceptibility to fosfomycin from 2017 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
	N=1034	N=2014	N=2895	N=2101	N=2373	N=3240	N=3461	N=3042
	(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)
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)
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)
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)
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)
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)
Fosfomycin	209/222 (94.1)	469/536 (87.5)	669/706 (94.8)	483/498 (97)	478/524 (91.2)	722/916 (78.8)	945/1247 (75.8)	322/714 (45.1)
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)

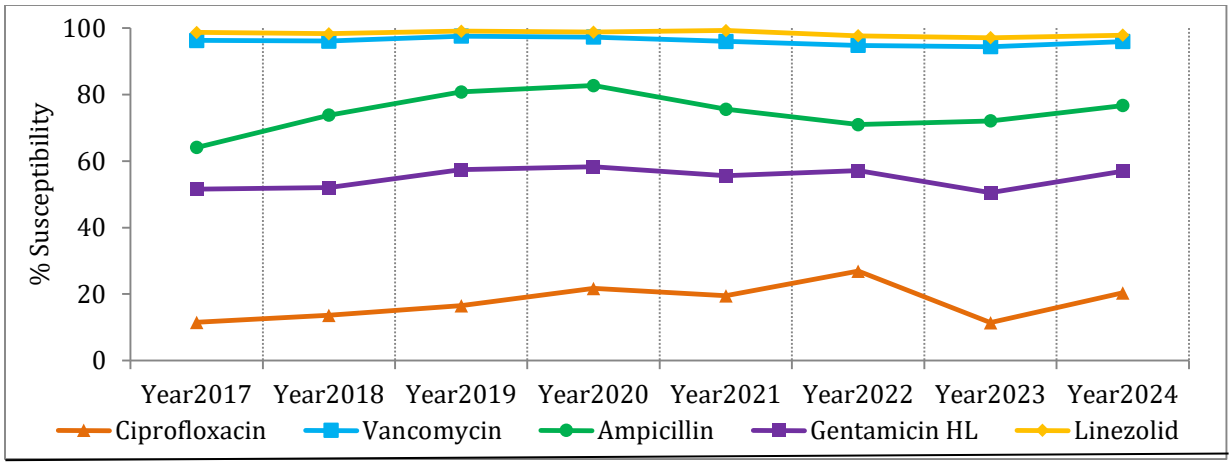


Figure 6.5: Year-wise susceptibility trends of *Enterococcus faecalis* from all samples

In *E. faecalis,* the susceptibility rates to vancomycin ranged from 82.9% to 100% across RCs (**Table 6.16**). Significant differences were observed between the various RCs, with the highest Vancomycin-resistant *Enterococci* (VRE) rate in the isolates from RC19. Susceptibility to linezolid was high (>90%) in most centres. Susceptibility to ampicillin ranged from 39.7% to 100%, while susceptibility to high-level gentamicin ranged from 20.6% to 90.9%.

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

RC/ Antibiotics	Ampicillin (N=1100) (S%)	Vancomycin (N=1011) (S%)	Teicoplanin (N=990) (S%)	Gentamicin HL (N=842) (S%)	Linezolid (N=1164) (S%)
RC2	63/76 (82.9)	65/76 (85.5)	64/71 (90.1)	46/76 (60.5)	76/76 (100.0)
RC3	19/21 (-)	20/21 (-)	20/21 (-)	12/21 (-)	18/21 (-)
RC4	175/187 (93.6)	11/11 (-)	11/11 (-)	4/13 (-)	164/164 (100.0)
RC5	1/1 (-)	1/1 (-)	0/0 (-)	0/0 (-)	1/1 (-)
RC6	68/72 (94.4)	75/80 (93.8)	75/80 (93.8)	24/73 (32.9)	75/80 (93.8)
RC7	28/34 (82.4)	39/43 (90.7)	36/43 (83.7)	9/11 (-)	43/43 (100.0)
RC8	0/0 (-)	48/48 (100.0)	48/48 (100.0)	27/47 (57.4)	48/48 (100.0)
RC9	52/79 (65.8)	79/81 (97.5)	76/79 (96.2)	48/81 (59.3)	73/81 (90.1)
RC10	331/331 (100.0)	330/331 (99.7)	331/331 (100.0)	153/258 (59.3)	331/331 (100.0)
RC11	30/32 (93.8)	32/33 (97.0)	32/33 (97.0)	7/12 (-)	33/33 (100.0)
RC12	6/9 (-)	7/10 (-)	8/9 (-)	0/0 (-)	6/9 (-)
RC13	4/6 (-)	6/7 (-)	7/7 (-)	4/5 (-)	7/7 (-)
RC14	11/12 (-)	12/12 (-)	12/12 (-)	4/12 (-)	12/12 (-)
RC16	29/67 (43.3)	67/67 (100.0)	64/67 (95.5)	46/67 (68.7)	66/67 (98.5)
RC17	55/56 (98.2)	70/71 (98.6)	68/70 (97.1)	40/44 (90.9)	70/70 (100.0)
RC18	7/13 (-)	11/13 (-)	0/0 (-)	12/13 (-)	12/13 (-)
RC19	25/63 (39.7)	63/76 (82.9)	43/63 (68.3)	13/63 (20.6)	63/63 (100.0)
RC20	23/33 (69.7)	31/34 (91.2)	31/34 (91.2)	26/32 (81.3)	34/34 (100.0)
RC21	5/8 (-)	10/11 (-)	10/11 (-)	5/11 (-)	10/11 (-)
Total	932/1100 (84.7)	977/1011 (96.6)	936/990 (94.5)	480/842 (57.0)	1142/1164 (98.1)

Enterococcus faecium

The trends in antibiotic susceptibility rates in *E. faecium* from 2017-2024 are depicted in **Table 6.17 and Figure 6.6**. Lower susceptibility trends were observed for all antibiotics in 2024 isolates when compared to 2023, except for high-level gentamicin and ciprofloxacin.

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

AMA	Year-2017 N=937 (S%)	Year-2018 N=1476 (S%)	Year-2019 N=2700 (S%)	Year-2020 N=1994 (S%)	Year-2021 N=2422 (S%)	Year-2022 N=2998 (S%)	Year-2023 N=2746 (S%)	Year-2024 N=3002 (S%)
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)
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)
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)
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)
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)
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)
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)

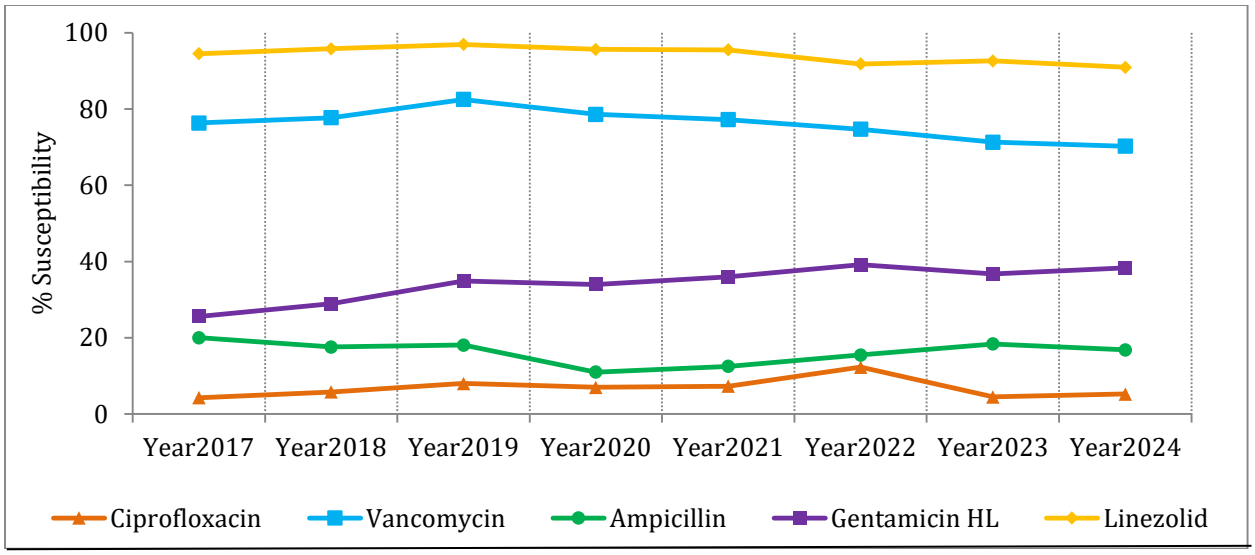


Figure 6.6: Year-wise susceptibility trends of *Enterococcus faecium* from all samples

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

RC/ Antibiotics	Ampicillin (N=1464)	Vancomycin (N=1526)	Teicoplanin (N=1508)	Gentamicin_HL (N=1365)	Linezolid (N=1632)
	(S%)	(S%)	(S%)	(S%)	(S%)
R2	81/453 (17.9)	265/453 (58.5)	279/446 (62.6)	136/452 (30.1)	452/453 (99.8)
R3	6/36 (16.7)	23/36 (63.9)	25/36 (69.4)	21/36 (58.3)	28/36 (77.8)
R4	21/113 (18.6)	4/6 (-)	4/6 (-)	2/8 (-)	112/112 (100.0)
R6	13/215 (6.0)	102/224 (45.5)	103/223 (46.2)	39/213 (18.3)	154/224 (68.8)
R7	15/15 (-)	16/24 (-)	16/24 (-)	1/2 (-)	22/24 (-)
R8	0/0 (-)	55/87 (63.2)	57/86 (66.3)	24/86 (27.9)	76/87 (87.4)
R9	20/43 (46.5)	40/43 (93.0)	37/41 (90.2)	25/43 (58.1)	41/43 (95.3)
R10	17/201 (8.5)	131/203 (64.5)	134/203 (66.0)	74/198 (37.4)	177/203 (87.2)
R11	4/42 (9.5)	26/42 (61.9)	26/42 (61.9)	4/17 (-)	38/42 (90.5)
R12	2/19 (-)	10/18 (-)	11/18 (-)	0/0 (-)	11/19 (-)
R13	2/18 (-)	15/19 (-)	12/17 (-)	4/11 (-)	19/19 (-)
R14	1/15 (-)	9/15 (-)	11/15 (-)	3/15 (-)	13/15 (-)
R16	4/59 (6.8)	58/59 (98.3)	55/59 (93.2)	35/59 (59.3)	58/59 (98.3)
R17	97/98 (99.0)	147/156 (94.2)	144/153 (94.1)	66/77 (85.7)	152/153 (99.3)
R18	1/5 (-)	5/5 (-)	0/0 (-)	3/5 (-)	5/5 (-)
R19	11/43 (25.6)	43/53 (81.1)	34/43 (79.1)	11/43 (25.6)	42/43 (97.7)
R20	8/49 (16.3)	39/50 (78.0)	45/50 (90.0)	28/48 (58.3)	50/50 (100.0)
R21	7/39 (17.9)	16/47 (34.0)	16/47 (34.0)	9/46 (19.6)	27/47 (57.4)
Total	310/1464 (21.2)	1004/1526 (65.8)	1009/1508 (66.9)	485/1365 (35.5)	1477/1632 (90.5)

As presented in **Table 6.18**, in *E. faecium,* the susceptibility rates of vancomycin (34% to 98.3%) and teicoplanin ranged from 34% to 94%, from most of the RCs. There were significant differences in VRE observed between the various RCs, with the highest rate in the isolates from RC21 and RC6, while the lowest VRE rates were observed from RC17 and RC16. Susceptibility to linezolid was high in most of the centres in the range between 57.4% to 100%. Unusually high resistance to linezolid was observed in isolates from RC6 and RC21.

Clinical relevance and treatment guidance

The rising proportion of MRSA and VRE among blood isolates is concerning. While vancomycin susceptibility remains high among MRSA isolates, the emergence 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 consider alternate drugs if the MIC value is close to the break point, as such isolates are likely to be hVISA. Given that daptomycin susceptibility remains near 100% for MRSA, it could serve as an alternative to vancomycin and linezolid for infections, excluding those of the respiratory tract. This may also reduce the selection pressure on antimicrobial resistance genes exerted by these agents. Ultimately, the decision to initiate empirical vancomycin treatment for serious *S. aureus* infections should be based on the local MRSA prevalence at the institution.

In centres with high MRSA rates, vancomycin or linezolid may be used as empirical therapy, with de-escalation based on susceptibility results. Conversely, 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, tetracyclines and or clindamycin remain viable options due to their consistently high susceptibility rates. The new antibiotic, Levonadifloxacin, appears to be a very effective antibiotic against MRSA, as no resistance has been identified in isolates tested till date. According to available literature, levonadifloxacin appears to be highly effective 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, this is not the case for CoNS. Often dismissed as colonizers, CoNS, particularly *S. haemolyticus,* are being increasingly recognized as opportunistic pathogens, particularly *S. haemolyticus*. Importantly, these isolates frequently exhibit multidrug resistance, with resistance genes carried on mobile elements, raising the risk of resistance transfer. When there is a strong suspicion of CoNS as pathogens, it may be prudent to use vancomycin or linezolid, given the extremely high resistance rates to beta-lactams.

The number of *E. faecium* isolates was almost equal to *E. faecalis* across most centres of India, which is concerning since *E. faecium* tends to be far more drug-resistant. For serious infections such as meningitis or bacteraemia, linezolid may be tried as empirical therapy, with de-escalation if indicated. In centres reporting linezolid resistance among enterococci, daptomycin may be considered an alternative. Additionally, the identification of *Enterococcus* species beyond *faecalis* and *faecium* is clinically important, as some of these species are intrinsically resistant to glycopeptides. Therefore, precise speciation of enterococci is of clinical significance and is not just an academic exercise but has clear clinical relevance for guiding antibiotic use.

Chapter 7. Fungal pathogens

A total of 2729 fungal isolates were studied during the year 2024. The antifungal susceptibility testing (AFST) of various *Candida* species (including *C. tropicalis*, *C. albicans*, *C. glabrata*, *C. parapsilosis*, *C. auris* and *C. krusei*) isolated from all specimens revealed fluconazole susceptibility rates of 87.9% for *C. albicans*, 92.2% for *C. tropicalis*, 91.9% for *C. glabrata,* 80.2% for *C. parapsilosis* and 40.8% for *C. auris*. Voriconazole susceptibility was 93.8% for *C. krusei*, 85.2% for *C. albicans,* 86.3% for *C. tropicalis,* 83.6% for *C. parapsilosis,* 62.6% for *C. glabrata* and 11.8% for *C. auris*.

C. auris demonstrated notable resistance to echinocandins, with up to 9.7% resistance to anidulafungin and caspofungin, and 1.9% resistance to micafungin **(Table 7.1)**. In contrast, *C. parapsilosis,* which is generally reported as less susceptible to echinocandins, exhibited high susceptibility to echinocandins (caspofungin-99.4%, anidulafungin-95.6% and micafungin–99.6%) **(Table 7.1)**. However, up to 12% of *C. tropicalis* isolates were resistant to anidulafungin, which is of concern. *C. glabrata* also exhibited around 10% resistance to at least one of the echinocandins, micafungin.

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

AMA		*C. tropicalis* N=822	*C. albicans* N=429	*C. parapsilosis* N=329	*C. auris* N=293	*C. glabrata* N=277	*C. krusei* N=48
Anidulafungin	S	359/506 (70.9)	217/245 (88.6)	171/179 (95.6)	224/248 (90.3)	145/160 (90.7)	34/35 (97.1)
	I	84/506 (16.6)	10/245 (4.1)	4/179 (2.2)	-	4/160 (2.5)	-
	R	63/506 (12.5)	18/245 (7.3)	4/179 (2.2)	24/248 (9.7)	11/160 (6.8)	1/35 (2.9)
Caspofungin	S	802/819 (97.9)	418/428 (97.8)	327/329 (99.4)	262/290 (90.4)	226/274 (82.5)	35/48 (72.9)
	I	10/819 (1.3)	5/428 (1.1)	-	-	25/274 (9.2)	10/48 (20.8)
	R	7/819 (0.8)	5/428 (1.1)	4/329 (1.2)	28/262 (9.6)	23/274 (8.3)	3/48 (6.3)
Micafungin	S	609/624 (97.6)	375/389 (96.5)	275/276 (99.6)	210/214 (98.1)	225/264 (85.3)	44/46 (95.7)
	I	8/624 (1.3)	8/389 (2.0)	-	-	15/264 (5.7)	-
	R	7/624 (1.1)	6/389 (1.5)	1/276 (0.4)	4/214 (1.9)	24/264 (9.0)	2/46 (4.3)
Fluconazole	S	758/822 (92.2)	377/429 (87.9)	264/329 (80.2)	118/289 (40.8)	228/248 (91.9)	7/41 (17.1)
	SDD	23/822 (2.8)	4/429 (0.9)	12/329 (3.6)	-	12/248 (4.8)	3/41 (7.3)
	R	51/822 (6.2)	48/429 (11.2)	57/329 (17.3)	171/289 (59.2)	8/248 (3.3)	31/41 (75.6)
Voriconazole	S	714/822	359/422	275/329	31/264	155/248	45/48

		(86.3)	(85.2)	(83.6)	(11.8)	(62.6)	(93.8)
	I	74/822 (9.0)	45/422 (10.6)	41/329 (12.5)	-	77/248 (31.0)	3/48 (6.2)
	R	40/822 (4.9)	18/422 (4.2)	15/329 (4.6)	233/264 (88.2)	16/248 (6.4)	-

The rising resistance rates among these *Candida* species, particularly *C. auris,* with a fluconazole susceptibility of 40.8% and voriconazole susceptibility of 11.8%, are a significant health concern. *Candida* species isolated from urine demonstrated higher antifungal susceptibility compared to those isolated from blood **(Tables 7.2** and **7.3)**. The continued decline in antifungal susceptibility among major *Candida* species, including *C. albicans*, *C. tropicalis*, *C. parapsilosis*, and *C. glabrata*, is a growing concern that warrants close and ongoing surveillance. This trend presents substantial challenges to clinical management and highlights the urgent need for robust antifungal stewardship programs, routine susceptibility testing, and the development of novel therapeutic strategies to address emerging resistance.

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

AMA		*C. tropicalis* N=533	*C. albicans* N=148	*C. parapsilosis* N=278	*C. auris* N=182	*C. glabrata* N=117	*C. krusei* N=24
Anidulafungin	S	216/352 (61.4)	69/94 (73.4)	143/149 (96.0)	126/146 (86.3)	62/69 (89.9)	*17/18 (94.5)
	I	77/352 (21.8)	8/94 (8.5)	2/149 (1.3)	-	3/69 (4.3)	-
	R	59/352 (16.8)	17/94 (18.1)	4/149 (2.7)	20/146 (13.7)	4/69 (5.8)	1/18 (5.5)
Caspofungin	S	517/530 (97.6)	140/147 (95.2)	277/278 (99.6)	161/179 (89.9)	94/116 (81)	16/24 (66.7)
	I	9/530 (1.7)	3/147 (2.0)	-	-	13/116 (11.3)	7/24 (28.0)
	R	4/530 (0.7)	4/147 (2.8)	4/281 (1.4)	18/179 (10.1)	9/116 (7.7)	2/24 (8.3)
Micafungin	S	326/338 (96.6)	104/110 (94.6)	224/225 (99.6)	103/106 (97.2)	94/111 (84.7)	22/23 (95.7)
	I	7/338 (2.0)	3/110 (2.7)	-	-	7/111 (6.3)	-
	R	5/338 (1.4)	3/110 (2.7)	1/225 (0.4)	3/106 (2.8)	10/111 (9.0)	1/23 (4.3)
Fluconazole	S	499/533 (93.6)	142/146 (97.3)	222/278 (79.9)	90/180 (50)	91/98 (92.9)	5/22 (22.8)
	SDD	11/533 (2.1)	1/146 (0.6)	7/278 (2.5)	-	5/98 (5.1)	3/22 (13.6)
	R	33/533 (6.2)	3/146 (2.1)	53/278 (19.1)	90/180 (50)	2/98 (2.0)	14/22 (63.6)
Voriconazole	S	472/533 (88.6)	131/143 (91.7)	232/278 (83.5)	27/169 (16.0)	82/112 (73.3)	23/24 (95.8)
	I	40/533 (7.5)	8/143 (5.5)	37/278 (13.3)	-	26/112 (23.2)	1/24 (4.2)
	R	28/533 (5.3)	4/143 (2.8)	12/278 (4.3)	142/169 (84.0)	4/112 (3.5)	-

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

AMA		*C. tropicalis* N=163	*C. albicans* N=149	*C. glabrata* N=88	*C. auris* N=65	*C. parapsilosis* N=22
Anidulafungin	S	67/75 (89.4)	76/77 (98.7)	43/49 (87.8)	56/57 (98.2)	*10/10 (100)
	I	7/75 (9.3)	1/77 (1.3)	-	-	-
	R	1/75 (1.3)	-	6/49 (12.2)	1/57 (1.8)	-
Caspofungin	S	162/163 (99.4)	149/149 (100)	73/86 (84.9)	57/65 (87.6)	22/22 (100)
	I	-	-	3/86 (3.5)	-	-
	R	1/163 (0.6)	-	10/86 (11.6)	8/65 (12.4)	-
Micafungin	S	159/160 (99.4)	145/148 (98)	67/82 (81.7)	63/64 (98.4)	22/22 (100)
	I	-	3/148 (2)	5/82 (6.1)	-	-
	R	1/160 (0.6)	-	10/82 (12.2)	1/64 (0.6)	-
Fluconazole	S	143/163 (87.7)	122/149 (81.9)	74/83 (89.2)	12/64 (18.7)	18/22 (81.8)
	SDD	8/163 (4.9)	2/149 (1.3)	4/83 (4.8)	-	1/22 (4.6)
	R	12/163 (7.4)	25/149 (16.8)	5/83 (6.0)	52/65 (81.3)	3/22 (13.6)
Voriconazole	S	136/160 (85)	120/146 (82.2)	36/70 (51.5)	1/50 (2)	19/21 (90.6)
	I	16/160 (10)	19/146 (13.0)	26/70 (37.1)	9/50 (18)	1/21 (4.7)
	R	8/160 (5)	7/146 (4.8)	8/70 (11.4)	40/50 (80)	1/21 (4.7)

* Less than 20 samples

The antifungal susceptibility testing (AFST) profile of *Aspergillus* species isolated from all specimens is presented in **Table 7.4**. *A. flavus* and *A. fumigatus* were the most frequently isolated moulds from clinical samples. Resistance to amphotericin B was observed in 23.1% of *A. flavus* isolates and 33.3% of *A. fumigatus* isolates.

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

AMA	*Aspergillus flavus* (N=186) (S%)	*Aspergillus fumigatus* (N=111) **(S%)**
Amphotericin B	143/186 (76.9)	74/111 (66.7)
Caspofungin	182/186 (97.8)	111/111 (100)
Itraconazole	174/186 (93.5)	106/111 (95.5)
Posaconazole	165/186 (88.7)	-/111 (-)
Voriconazole	186/186 (100)	111/111 (100)

Characterization of the resistance mechanism

Carbon substrates promote stress resistance and drug tolerance in clinical isolates of *Candida tropicalis*

Candida tropicalis is a human pathogen and one of the most prevalent non-*Candida albicans Candida* (NCAC) species responsible for invasive infections. Azole antifungal resistance in *C. tropicalis* has been gradually increasing alongside the rise in infection rates. The pathogenic success of *C. tropicalis* largely depends on its ability to adapt to the host microenvironment. Key to this adaptability are cellular metabolism and physiological status, which determine the pathogen's capacity to counteract various stresses within the host. However, there is limited understanding of how carbon substrate metabolism influences stress adaptation and azole resistance in *C. tropicalis*. The impact of glucose, fructose, and sucrose as sole carbon sources on fluconazole resistance and the pathogen's ability to withstand osmotic (NaCl) and oxidative (H_2O_2) stress in clinical *C. tropicalis* isolates was assessed. The findings confirmed that the abundance of carbon substrates enhances drug resistance and improves tolerance to osmotic and oxidative stress in *C. tropicalis*. Notably, both azole-resistant and susceptible isolates exhibited similar stress adaptation phenotypes, suggesting that their ability to become successful pathogens is not solely dependent on drug susceptibility.

The growth of the ATCC750 strain was assessed in media supplemented with varying concentrations of different carbon sources, along with different fluconazole concentrations (1, 2, 4, and 8 µg/mL). It was observed that, at each fluconazole

concentration tested, cells were able to overcome drug suppression up to two to three times higher than their original MIC (2 µg/mL) as the concentration of carbon supplements increased **(Figure 7.1)**.

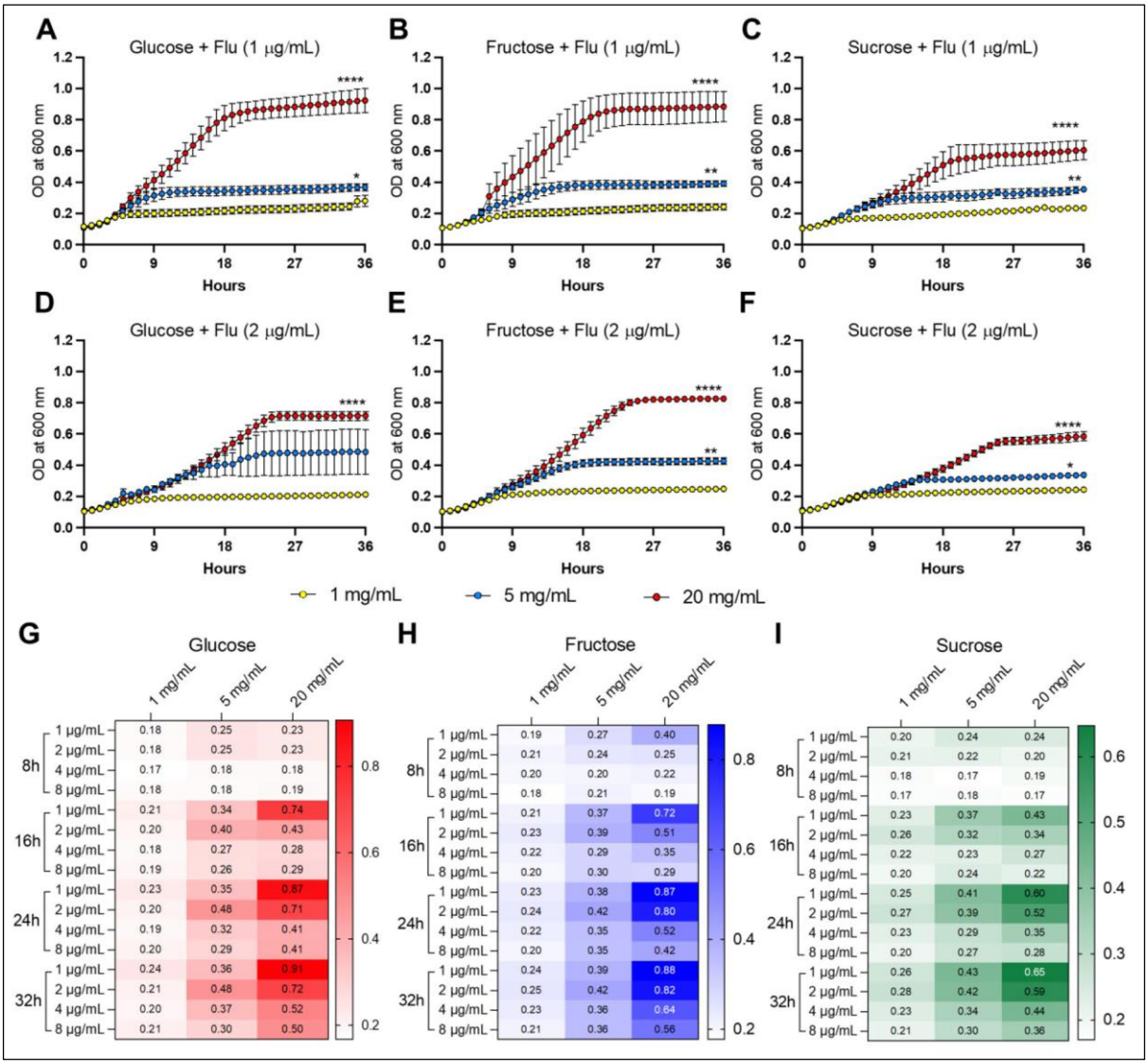


Figure 7.1: Sugar metabolism can enhance fluconazole tolerance in *C. tropicalis*. ATCC750 standard strain was grown in the presence of different concentrations of carbon substrates and fluconazole: Glucose + Fluconazole (A and D), Fructose + Fluconazole (B and E), Sucrose + Fluconazole (C and F). Growth was kinetically measured in each hour by obtaining OD600. All experiments were repeated in biological triplicate and shown as mean ± SEM. Significance was assessed using One-way ANOVA *, $p < 0.05$; **, $p < 0.01$; ****, $p < 0.0001$; ns, not significant. Heat Map representing growth as OD600 in the presence of different concentrations of glucose + fluconazole (G), fructose + fluconazole (H) and sucrose + fluconazole (I) at 8, 16, 24, and 32 h. All experiments were repeated in biological triplicate and shown as mean OD.

Clinical relevance and treatment guidance:

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, while *C. glabrata* is less frequently isolated, ranking as the fifth most commonly identified yeast species. Increasing antifungal resistance is a growing concern. The rising number of isolates exhibiting intermediate or full resistance to anidulafungin, particularly in *C. tropicalis*, is concerning. However, these findings may not fully reflect the true resistance patterns, and further verification is needed. In addition to the concerning anidulafungin resistance in *C. tropicalis*, echinocandin resistance in other species remains relatively low (<3.6%). Echinocandins continue to be the first-line of drugs for treating *Candida* infections. Resistance to voriconazole has remained consistent with levels observed in the previous year, with no significant changes in the resistance pattern. In *C. auris,* resistance to echinocandins was observed in up to 10% of isolates, while 59.2% and 88.2% of isolates showed resistance to fluconazole and voriconazole, respectively. In comparison to last year, caspofungin susceptibility has either increased or remained comparable across the five most commonly isolated species, i.e. *C. tropicalis* (97.9% vs. 92.2%), *C. albicans* (97.8% vs. 92.1%), *C. glabrata* (82.5% vs. 72.2%), *C. parapsilosis* (99.4% vs 99.2%) and *C. auris* (90.4% vs. 75.2%). Increased susceptibility to amphotericin B was observed in *Aspergillus flavus* (76.9% vs 69.2%) and *Aspergillus fumigatus* (66.7% vs. 48.9%). All *A. flavus* and *A. fumigatus* isolates were susceptible to voriconazole, positioning voriconazole as the preferred treatment for these infections.

Echinocandins and fluconazole continue to be the most effective treatment options for *Candida* infections. Given their antifungal susceptibility profiles, echinocandins are particularly suitable for treating *C. auris* infections. The declining susceptibility of *C. tropicalis* isolates to anidulafungin suggests that the remaining two echinocandins, along with azoles, may be more appropriate for treating infections caused by *C. tropicalis*. Moderate resistance levels in *C. albicans* indicate that echinocandins or azoles can be used for treatment, depending on the patient's clinical condition. For *Aspergillus* infections, voriconazole remains the drug of choice.

Chapter 8. Streptococcus pneumoniae

Serotype distribution and antimicrobial susceptibility profile of invasive and non-invasive *S. pneumoniae* in India for the year 2024

As part of the national reference laboratory, *S. pneumoniae* isolates were received from various hospitals within India. The invasive isolates included *S. pneumoniae* isolated from sterile specimens such as CSF, blood and body fluids. The non-invasive isolates included *S. pneumoniae* isolated from respiratory specimen (sputum, BAL and other respiratory specimens).

Serotype Distribution:

A total of 136 invasive (children below the age of 5 years, n= 46, adults and children above 5 years of age, n=90) and 148 non-invasive (children below the age of 5 years, n= 15; adults and children above 5 years of age, n= 133) *S. pneumoniae* isolated in the year 2024 were included in the analysis. The majority of the invasive isolates were from blood (n=107), followed by CSF (n=11) and sterile fluids (n=18). The serotype distribution among the invasive and non-invasive isolates of *S. pneumoniae* is depicted in **Figure 8.1** and **Table 8.1**. PCV13 serotypes were the predominant ones, with serotypes 19F, 19A, 14, 3, 1, and 5 being the major ones among the invasive isolates. Whereas, among the non-invasive isolates, serotypes 19F, 3, 35B, 23B, and 15B/C were the major serotypes.

Serotype percentage covered by Pneumosil (PCV10 Sii) was 50% for children less than 5 years (n=61) and 35% for those above 5 years of age (n=223), respectively **(Table 8.2)**. Among the serotypes not included in the Pneumosil (PCV10Sii), serotype 4 constitutes 0.3% (n=1/284), serotype 3 constitutes 9.8% (n=28/284), and serotype 18C constitutes 3.5% (10/284) of the total isolates. The majority of serotype 3 was observed among the adults (8%, n=23/284) and was isolated from the non-invasive infections. Overall, the predominant other non-Pneumosil serotypes were serotype 23A, 35B, 15B/C, 11A, and 23B.

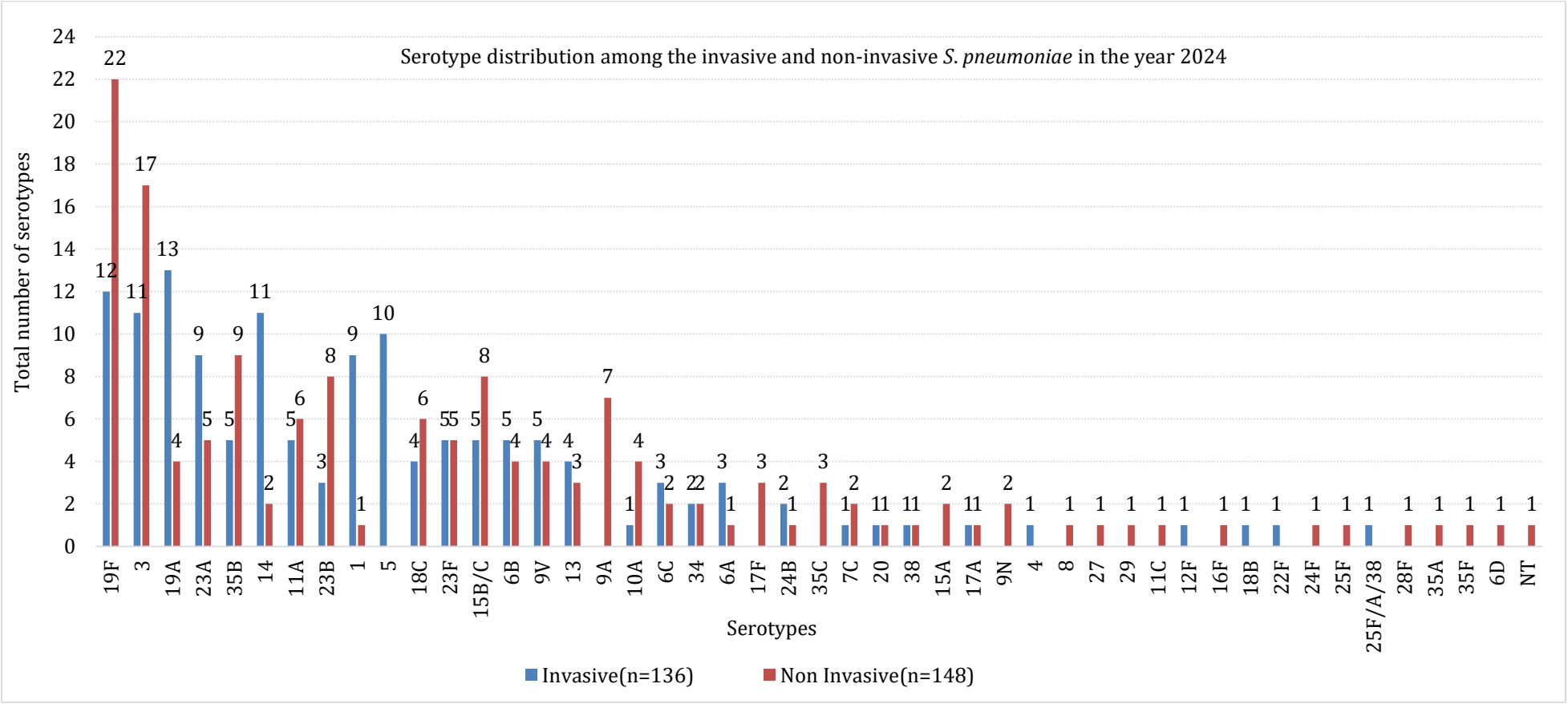


Figure 8.1: **The serotype distribution of invasive (N=136) and non-invasive (N=148) isolates of *S. pneumoniae* (NT indicates non-typeable)**

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

Serotypes	Invasive (N=136)	Non-Invasive (N=148)	Total (N=284)
19F	12	22	34
3	11	17	28
19A	13	4	17
23A	9	5	14
35B	5	9	14
14	11	2	13
11A	5	6	11
23B	3	8	11
1	9	1	10
5	10	0	10
18C	4	6	10
23F	5	5	10
15B/C	5	8	13
6B	5	4	9
9V	5	4	9
13	4	3	7
9A	0	7	7
10A	1	4	5
6C	3	2	5
34	2	2	4
6A	3	1	4
17F	0	3	3
24B	2	1	3
35C	0	3	3
7C	1	2	3
20	1	1	2
38	1	1	2
15A	0	2	2
17A	1	1	2
9N	0	2	2
25F	1	1	2

One isolate each of serotypes 4, 12F, 18B, and 22F in invasive infections and serotypes 8, 27, 29, 11C, 16F, 24F, 25F, 28F, 35A, 35F, 6D and NT in non-invasive infections were seen.

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

Serotypes	<5 Years (N=61)	>5 years (N=223)
19F	5	29
3	5	23
35B	0	14
1	0	10
15B/15C	3	10
5	1	9
19A	8	9
23A	5	9
23B	2	9
14	5	8
11A	3	8
23F	2	8
13	1	6
18C	4	6
6B	3	6
9A	1	6
9V	3	6
6C	0	5
10A	1	4
34	1	3
17F	0	3
35C	0	3
7C	0	3
20	0	2
15A	0	2
17A	0	2
25F	0	2
9N	0	2
24B	2	1
6A	3	1
38	2	0
18B	1	0
Grand Total	61	223

One isolate each of serotypes 4, 8, 27, 29, 11C, 12F, 16F, 22F, 24F, 28F, 35A, 35F, 6D and NT were seen.

Antimicrobial Susceptibility Profile

The penicillin and cefotaxime antimicrobial susceptibility percentage of invasive *S. pneumoniae* isolates (N=61) was 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.

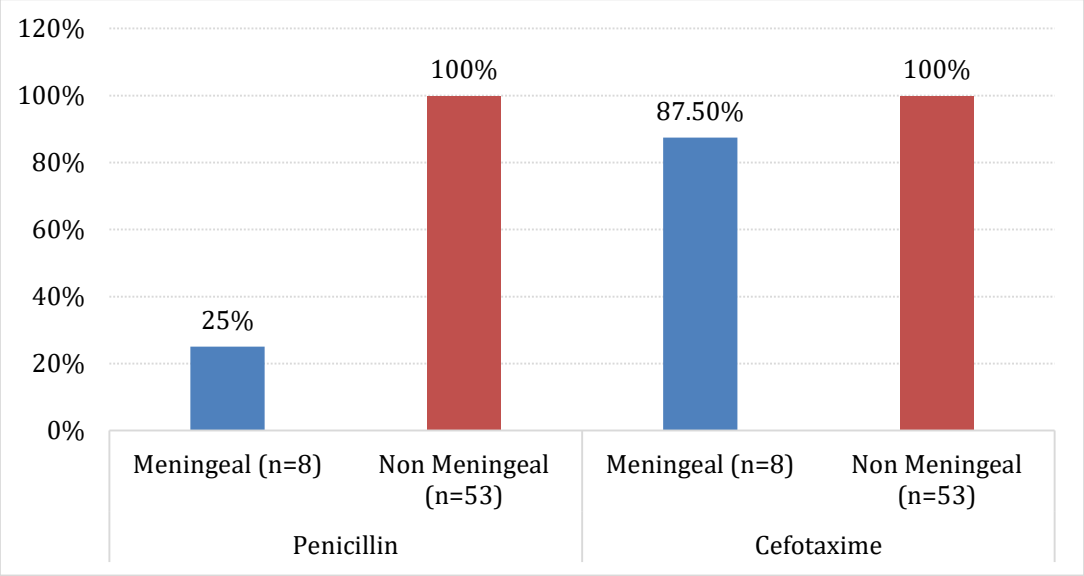


Figure 8.2: **Penicillin and cefotaxime antimicrobial susceptibility of invasive isolates of *S. pneumoniae*.** Due to the limited number of isolates fulfilling the meningeal criteria, the results should be interpreted with caution.

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

Organism	Penicillin		Cefotaxime	
	Meningeal (N=8)	Non-Meningeal (N =53)	Meningeal (N =8)	Non-Meningeal (N =53)
	(S%)	(S%)	(S%)	(S%)
S. pneumoniae	2/8 (25%)	53/53 (100%)	7/8 (87.5%)	53/53 (100%)

The antimicrobial susceptibility profile for antibiotics other than penicillin and cefotaxime, for invasive *S. pneumoniae* isolates, is given in **Figure 8.3**.

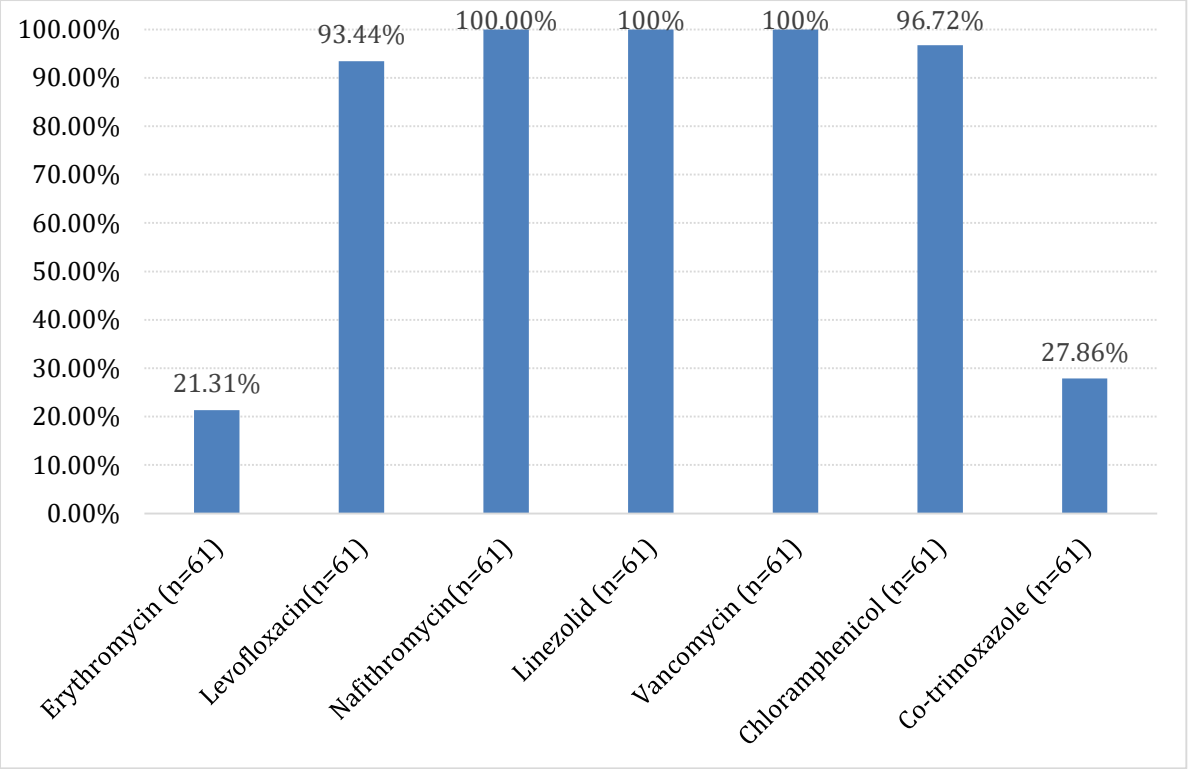


Figure 8.3: **Antimicrobial susceptibility profile of invasive *S. pneumoniae* isolates for antibiotics other than penicillin and cefotaxime**

The antimicrobial susceptibility profile of non-invasive *S. pneumoniae* isolates is depicted in **Figure 8.4**.

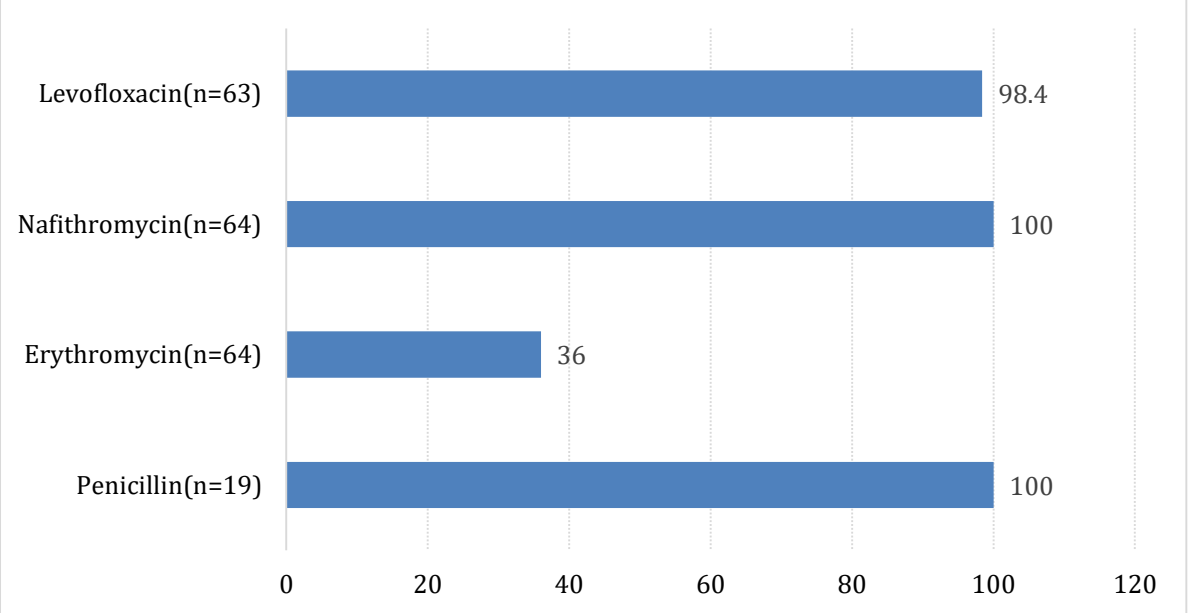


Figure 8.4: Antimicrobial susceptibility profile of non-invasive *S. pneumoniae* isolates

Summary

Pneumosil (PCV10Sii) percentage serotype coverage is 50% among children under 5 years of age. Among the non-vaccine serotypes, serotypes 3 and 18C constitute 14.7% among the children and 13.4% in individuals older than 5 years. In adults, serotype 3 was a major cause of non-invasive infections. Compared to the year 2023, serotypes 23B, 15B/15C and 35B have become predominant, along with serotype 11A. The new higher valent vaccine, PCV20, provides a serotype coverage of 67.2% in children less than 5 years of age. Continued monitoring of serotypes 3 and 18C is important, as they are prevalent in both invasive and non-invasive isolates. Antimicrobial susceptibility to penicillin and cefotaxime in meningeal isolates is gradually decreasing. Similarly, the decrease in erythromycin susceptibility is alarming in both invasive and non-invasive isolates.

Chapter 9. Healthcare-Associated Infections

During the period from January 2024 to December 2024, a total of 146 intensive care units (ICUs) from the 42 centres reported HAI rates to our centralized database. Medical and Neonatal ICUs accounted for 28.1% and 14.4% of the total ICUs in our network, respectively. The methodology, standard operating procedures (SOPs) and training modules for healthcare-associated infection (HAI) surveillance are provided on the website www.haisindia.com.

The cumulative patient days for the network for this period were 7,51,764. A total of 2,38,356 central line days and 4,32,767 urinary catheter days were reported during this period. A total of 3,668 episodes of BSIs and 1,659 episodes of UTIs were reported, accounting for the total BSI rate to be 4.9 per 1,000 patient days and the total UTI rate to be 2.2 per 1,000 patient days. An associated fatal outcome (14-day outcome) was reported in 36.6% of BSIs and 20.4% of UTI cases. However, this is not attributable to BSI or UTI mortality, since other predisposing factors, underlying critical illness and other infections also contribute to patients' mortality in the ICUs. A total of 1,10,244 patient days and 40,318 ventilator days were reported. A total of 310 VAP events were reported, giving a VAP rate of 7.6/1,000 ventilator days.

Gram-negative bacteria (GNB) accounted for 72.1% of all BSI cases, while 10.2% were due to fungal pathogens. For UTI, GNB accounted for 61.2% of cases. *Klebsiella* spp. (36.1%) was the most common GNB and *Enterococcus* spp. (9.3%) was the most common Gram-positive cocci (GPC) causing BSIs. 80% of *Klebsiella pneumoniae* and 91.5% of *Acinetobacter baumannii* causing BSIs were imipenem-resistant. Nearly 63% of *Staphylococcus aureus* and around 12.7% of *Enterococcus faecium* causing BSIs were respectively oxacillin and vancomycin-resistant. A total of 429 organisms were recovered from the events of VAP, of which *Acinetobacter* spp. was the most common.

The focus of this network has been on the generation of quality-assured HAI data and assessing the impact of infection prevention and control on the rates of HAIs. The network hospitals reported AMR according to their own running systems (manual/automated). Not all hospitals used the same set of antimicrobials. Moreover, speciation was not done uniformly by all hospitals; several of the organisms were identified only to the genus level. Efforts will be made to strengthen and homogenize AMR reporting across the network and to ensure that the HAI-causing strains are also made part of the Quality Assurance work of ICMR so that AMR data is quality assured.

The AMR-HAI burden is an important metric, considering the fact that ICUs are the hotbeds for AMR infections, which may cause adverse outcomes. ICU-based surveillance, coupled with infection prevention and control (IPC), will help in the reduction of overall AMR in individual hospitals.

This HAI surveillance work is primarily ICU-based, considering the high rate of device utilization in the ICUs. The most common ICUs represented in this network are Medical,

Trauma, Pediatric Medical and Surgical ICUs. The distribution of ICUs is shown in **Table 9.1**.

Table 9.1: Distribution of ICUs in the network

Name of ICU	Number (%)
Medical ICU	41 (28.1)
Trauma ICU	15 (10.3)
Pediatric Medical ICU	13 (8.9)
Surgical ICU	12 (8.2)
Neurosurgical ICU	4 (2.7)
Medical/Surgical ICU	9 (6.2)
Neonatal ICU	21 (14.4)
High Dependency Unit	3 (2.1)
Pediatric Medical/Surgical ICU	8 (5.5)
Gastrointestinal ICU	3 (2.1)
Anesthesia ICU	3 (2.1)
Cardiothoracic Surgical ICU	3 (2.1)
Respiratory ICU	3 (2.1)
Neurologic ICU	2 (1.4)
Cardiac ICU	2 (1.4)
Oncologic Medical ICU	2 (1.4)
Oncologic Surgical ICU	2 (1.4)
Total	**146**

The distribution of organisms from blood and urine cultures is shown in **Table 9.2**. *Enterobacterales* were the most common, followed by NFGNBs.

Table 9.2: Specimen-wise distribution of major groups of organisms isolated from BSIs and UTIs

Isolate	Culture Positive					
	Total (N = 5864)		Blood (N = 4104)		Urine (N = 1760)	
	n	%	n	%	n	%
Enterobacterales	2,332	39.8	1,519	37	813	46.2
NFGNB	1,637	27.9	1,376	33.5	371	21.1
Enterococci	665	11.3	380	9.3	285	16.2
***Candida* spp.**	782	13.3	411	10	371	21.1
Staphylococci	352	6	331	8.1	21	1.2
Others	96	1.6	87	2.1	9	0.5

The denominators for the calculation of HAI rates during this period are shown in **Table 9.3**.

Table 9.3: Denominator data for calculation of HAI rates

Indicator	2021	2022	2023	2024
Patient days	4,72,959	3,12,310	5,97,777	7,51,764
Central line days	1,50,744	1,03,079	1,91,083	2,38,356
Urinary catheter days	2,64,344	1,67,272	3,33,850	4,32,767

Network Level BSI data

A total of 3,668 cases of BSIs were reported by the network. The distribution (types) of BSI cases is shown in **Table 9.4**.

Table 9.4: Types of BSI cases

Type of BSI cases	No. of BSI cases (%)
Central line-associated bloodstream infections (CLABSI)	1,836 (50.1)
Non-CLABSI	1,306 (35.6)
Secondary BSI	526 (14.3)
Total	**3,668**

The total BSI rate in our network was 4.9/1,000 patient days, with the CLABSI rate being 7.7/ 1,000 central line days. The rates of BSIs, Primary BSIs, CLABSIs and Secondary BSIs are shown in **Table 9.5**. The trend of BSI rates in the surveillance network for four years (2021-2024) is depicted in **Figure 9.1**.

Table 9.5: BSI rates

Indicator	Rates
Total BSI rate (per 1,000 patient days)	4.9
Primary BSI rate (per 1,000 patient days)	4.2
CLABSI rate (per 1,000 central line days)	7.7
Secondary BSI rate (per 1,000 patient days)	0.7

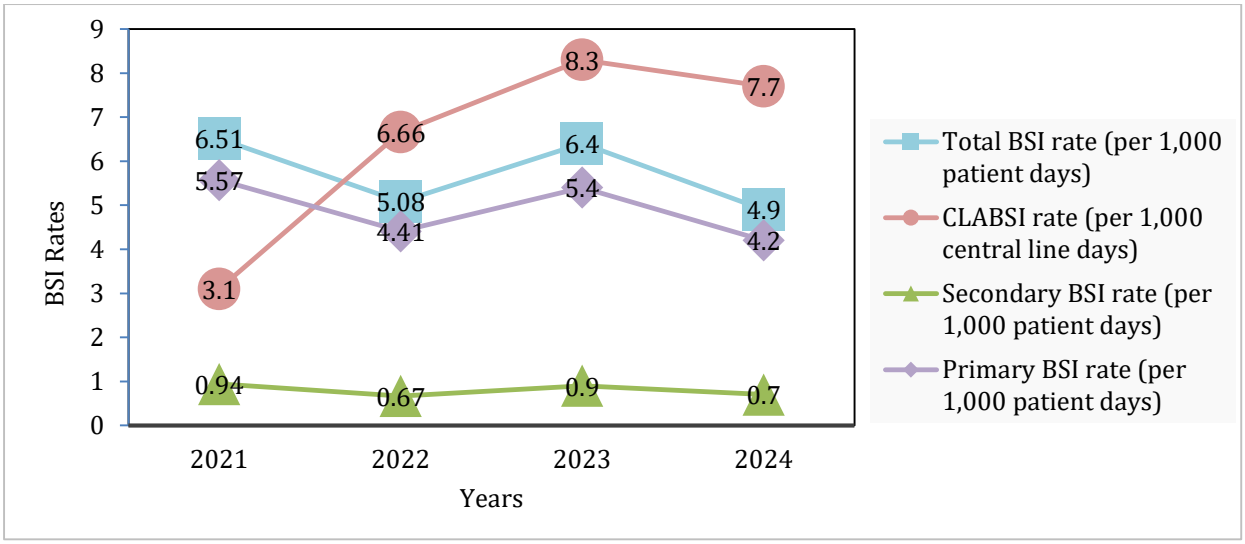


Figure 9.1: Trends of BSI rates in the surveillance network of Indian hospitals over four years (2021-2024)

The rates of total BSIs were compared against different types of ICUs since the morbidity of patients varies with the different types of ICUs. **Table 9.6** compares the rates of BSIs across the different ICU types in our network.

Table 9.6: Distribution of BSI cases by ICUs

Types of ICUs	No. of BSI cases (%)	Total BSI rate (per 1,000 patient days)
Neonatal ICU	814 (22.5)	4.5
Medical ICU	1105 (28.8)	4.9
Medical/Surgical ICU	386 (10.7)	6.5
Trauma ICU	467 (13.1)	4.6
Surgical ICU	219(6.4)	8.9
Pediatric ICU	158 (4.3)	4.1
Gastrointestinal ICU	106 (3.2)	11.0
Anaesthesia ICU	105 (2.7)	7.7
High Dependency Unit	48 (1.3)	3.1
Pediatric Medical/Surgical ICU	60 (1.5)	2.0
Neuro Surgery ICU	60 (1.5)	3.2
Respiratory ICU	28 (0.9)	4.8
Neurologic ICU	11 (0.3)	2.4
Oncologic Medical ICU	17 (0.5)	5.3
Oncologic Surgical ICU	58 (1.5)	9.2
Cardiothoracic ICU	12 (0.3)	2.9
Cardiac ICU	14 (0.3)	1.4
Total	**3,668**	**4.9**

Of the 3,668 cases of BSIs, males accounted for 62.6%, as shown in **Table 9.7**. However, no interpretation can be made from this data. It may reflect a higher admission rate in the ICUs.

Table 9.7: Distribution of BSI cases by gender and age

Gender	No. of BSI cases (%)
Males	2,296 (62.6)
Females	1,372 (37.4)
Total	**3,668**

	Median (Years)	Range (Years)
Age of males	34	0–95
Age of females	30	0–93

The duration of stay in the ICUs and the duration between ICU admission and the development of BSI are presented in **Table 9.8**. The duration of ICU stay is a risk factor for the development of HAIs. Some patients had a very prolonged ICU stay, and invariably, the BSI cases were found more in patients who had a longer ICU stay, across all ICU types. The 14-day mortality in cases of BSIs was 36.6%. This may not be the actual attributable mortality, since severe primary illness or other underlying co-morbidities may be contributing to the fatal outcome. Nearly 10% of BSI cases were discharged in 14 days. **Table 9.9** shows the short-term outcomes of BSI cases.

Table 9.8: Median and range of ICU stay for BSI cases

	Median (Days)	Range (Days)
Duration of stay in the unit	15	3-335
Duration between date of admission and date of event	9	3-276

Table 9.9: Outcomes of BSIs

14-day outcome	No. of BSI cases (%)
Died	1,344 (36.6)
Still in surveillance unit	1,004 (27.4)
Transferred to other ward/unit within same hospital	729 (19.9)
Discharged	353 (9.6)
LAMA	205 (5.6)
Transferred to other hospitals	29 (0.8)
Unknown	4 (0.1)
Total	**3,668**

A total of 4,104 pathogens were isolated from the BSI cases. Gram-negative organisms predominated as the cause of BSIs in our network, as shown in **Table 9.10, Figure 9.2**.

Table 9.10: Distribution of organisms causing BSIs

S. No.	Type of organism	Number (%)
1	Gram-negative organisms	2,960 (72.1)
2	Gram-positive organisms	727 (17.7)
3	Fungal pathogens	417 (10.2)
Total		**4,104**

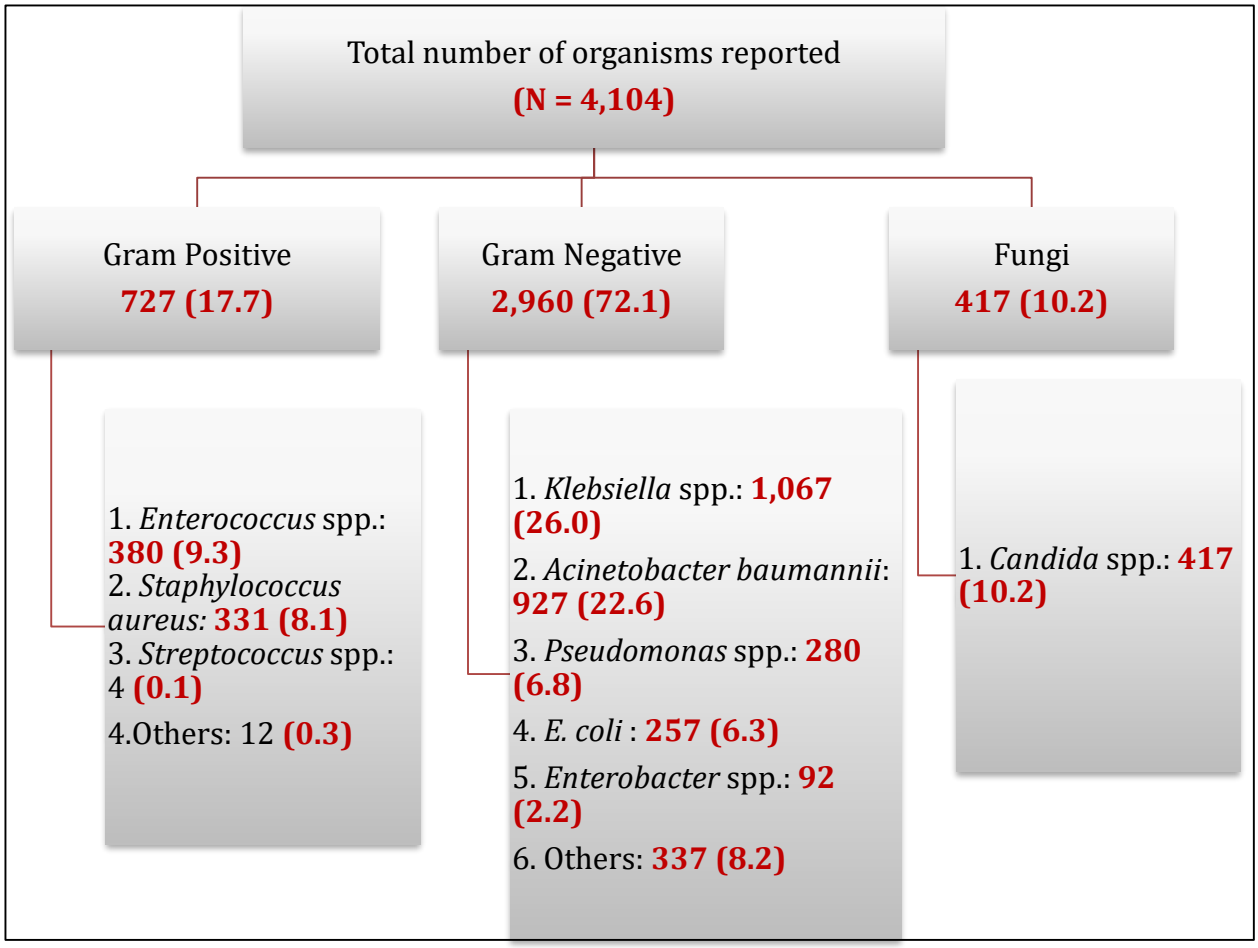


Figure 9.2: Distribution of organisms causing BSIs

The genus-level distribution in Gram-negative and Gram-positive organisms and species distribution of *Candida* causing overall BSIs is shown in **Tables 9.11-9.13**. *Enterococcus* spp. was the most common Gram-positive organism; *Klebsiella* spp. was the most common Gram-negative organism, and *C. tropicalis* was the most common fungal pathogen.

Table 9.11: Distribution of Gram-positive organisms causing BSIs (total BSIs)

S. No.	Organism	Number (%)
1	*Enterococcus* spp.	380 (9.3)
2	*Staphylococcus aureus*	331 (8.1)
3	*Streptococcus* spp.	4 (0.1)
4	Others	12 (0.3)
Total Gram-positive organisms		**727 (17.7)**

Table 9.12: Distribution of Gram-negative organisms causing BSI (Genus level)

S. No.	Organism	Number (%)
1	*Klebsiella* spp.	1067 (26.0)
2	*Acinetobacter* spp.	927 (22.6)
3	*Escherichia coli*	257 (6.3)
4	*Pseudomonas* spp.	280 (6.8)
5	*Burkholderia* spp.	82 (2.0)
6	*Enterobacter* spp.	92 (2.2)
7	*Stenotrophomonas* spp.	79 (1.9)
8	*Serratia* spp.	52 (1.3)
9	*Elizabethkingia* spp.	26 (0.6)
10	*Proteus* spp.	13 (0.3)
11	*Citrobacter* spp.	15 (0.4)
12	*Ralstonia* spp.	2 (0.1)
13	*Chryseobacterium* spp.	5 (0.1)
14	*Achromobacter* spp.	8 (0.2)
15	Others	55 (1.3)
Total Gram-negative organisms		**2,960 (72.1)**

Table 9.13: Distribution of *Candida* species causing BSIs

S. No.	Organism	Number (%)
1	*Candida tropicalis*	152 (3.7)
2	*Candida parapsilosis*	55 (1.3)
3	*Candida albicans*	40 (1.0)
4	*Candida auris*	56 (1.4)
5	*Candida* spp.	37 (0.9)
6	*Candida glabrata*	23 (0.6)
7	*Candida krusei*	5 (0.1)
8	*Candida utilis*	15 (0.4)
9	*Candida guilliermondii*	9 (0.2)
10	*Candida pelliculosa*	8 (0.2)
11	*Candida rugosa*	4 (0.1)
12	Others	11 (0.3)
Total		**417 (10.2)**

Central line-associated bloodstream infections (CLABSIs) data

The denominator in cases of CLABSI is taken as the central line days. The risk of developing CLABSIs varies with the position of the central lines. **Table 9.14** shows the locations of central lines in our surveillance data. Even in CLABSIs, Gram-negative pathogens predominated over Gram-positive pathogens **(Table 9.15)**. A high proportion of CLABSIs were caused by *Candida* species in our network. The distribution of Gram-positive, Gram-negative and *Candida* species causing CLABSIs is shown in **Tables 9.16-9.18**.

Table 9.14: Location of central lines

Location of central line*	No. of CLABSI cases (%)
Jugular	1,438 (57.5)
Subclavian	540 (21.6)
Umbilical	215 (8.6)
Brachial	46 (1.8)
Femoral	220 (8.8)
Other	43 (1.7)
Total	**2,502**

*Multiple central lines possible in a single patient

Table 9.15: Distribution of organisms causing CLABSIs

S. No.	Type of Organism	Number (%)
1	Gram-positive organisms	324 (17.7)
2	Gram-negative organisms	1,306 (71.1)
3	Fungal pathogens	206 (11.2)
	Total organisms	**1,836**

Table 9.16: Distribution of Gram-positive organisms causing CLABSIs

S. No.	Organism	Number (%)
1	*Enterococcus* spp.	190 (10.3)
2	*Staphylococcus aureus*	126 (6.9)
3	Others	8 (0.4)
	Total Gram-positive organisms	**324 (17.7)**

Table 9.17: Distribution of Gram-negative organisms causing CLABSIs (Genus level)

S. No.	Organism	Number (%)
1	*Klebsiella* spp.	448 (24.4)
2	*Acinetobacter* spp.	406 (22.1)
3	*Pseudomonas* spp.	114 (6.2)
4	*Escherichia coli*	111 (6.1)
5	*Burkholderia* spp.	49 (2.7)
6	*Enterobacter* spp.	45 (2.5)
7	*Stenotrophomonas* spp.	42 (2.3)
8	*Serratia* spp.	25 (1.4)
9	*Elizabethkingia* spp.	17 (0.9)
10	*Ralstonia* spp.	1 (0.1)
11	*Achromobacter* spp.	4 (0.2)
12	*Chryseobacterium* spp.	4 (0.2)
13	Others	40 (2.2)
Total Gram-negative organisms		**1,306 (71.1)**

Table 9.18: Distribution of *Candida* species causing CLABSIs

S. No.	Organism	Number (%)
1	*Candida tropicalis*	62 (3.4)
2	*Candida parapsilosis*	32 (1.7)
3	*Candida albicans*	19 (1.0)
4	*Candida auris*	30 (1.6)
5	*Candida* spp.	25 (1.4)
6	*Candida glabrata*	12 (0.7)
7	*Candida guilliermondii*	7 (0.4)
8	*Candida pelliculosa*	5 (0.3)
9	Others	14 (0.8)
Total		**206 (11.2)**

Data of Primary Non-CLABSIs

Non-CLABSI primary BSIs are the BSI cases for which no secondary sources are traced and that do not have a central line in place for ≥ two calendar days. The organism distribution of non-CLABSI Primary BSIs is shown in **Tables 9.19-9.22**.

Table 9.19: Distribution of organisms causing Non-CLABSI Primary BSIs

S. No.	Type of Organism	Number (%)
1	Gram-positive organisms	299 (22.9)
2	Gram-negative organisms	889 (68.1)
3	Fungi	118 (9.0)
Total		**1,306**

Table 9.20: Distribution of Gram-positive organisms causing Non-CLABSI Primary BSIs

S. No.	Organism	Number (%)
1	*Staphylococcus aureus*	165 (12.6)
2	*Enterococcus* spp.	128 (9.8)
3	Others	6 (0.5)
Total Gram-positive organisms		**299**

Table 9.21: Distribution of Gram-negative organisms causing Non-CLABSI Primary BSIs (Genus level)

S. No.	Organism	Number (%)
1	*Klebsiella* spp.	325 (24.9)
2	*Acinetobacter* spp.	267 (20.4)
3	*Escherichia coli*	96 (7.4)
4	*Pseudomonas* spp.	77 (5.9)
5	*Enterobacter* spp.	37 (2.8)
6	*Burkholderia* spp.	19 (1.5)
7	*Stenotrophomonas* spp.	24 (1.8)
8	*Citrobacter* spp.	3 (0.2)
9	*Serratia* spp.	20 (1.5)
10	Others	24 (1.8)
Total Gram-negative organisms		**889**

Table 9.22: Distribution of *Candida* species causing Non-CLABSI Primary BSIs

S. No.	Organism	Number (%)
1	*Candida tropicalis*	56 (4.3)
2	*Candida albicans*	10 (0.8)
3	*Candida parapsilosis*	12 (0.9)
4	*Candida glabrata*	6 (0.5)
5	*Candida* spp.	8 (0.6)
6	*Candida utilis*	11 (0.8)
7	*Candida auris*	9 (0.7)
8	*Candida guilliermondii*	1 (0.1)
9	*Candida krusei*	1 (0.1)
10	*Candida haemulonii*	1 (0.1)
11	*Candida pelliculosa*	1 (0.1)
12	*Candida rugosa*	2 (0.2)
Total *Candida* sp.		**118**

Data of Secondary BSIs

Secondary BSIs are those cases in which the source of infection is found at some other body site and bacteremia is secondary to the primary source. The organism distribution in cases of secondary BSIs is shown in **Tables 9.23-9.26**.

Table 9.23: Distribution of organisms causing Secondary BSI

S. No.	Organism	Number (%)
1	Gram-positive organisms	33 (6.3)
2	Gram-negative organisms	469 (89.1)
3	*Candida* spp.	24 (4.6)
Total		**526**

Table 9.24: Distribution of Gram-positive organisms causing Secondary BSI

S. No.	Organism	Number (%)
1	*Staphylococcus* spp.	20 (3.8)
2	*Enterococcus* spp.	13 (2.5)
Total Gram-positive organisms		**33 (6.3)**

Table 9.25: Distribution of Gram-negative organisms causing Secondary BSIs (Genus level)

S. No.	Organism	Number (%)
1	*Acinetobacter* spp.	183 (34.8)
2	*Klebsiella* spp.	182 (34.6)
3	*Pseudomonas* spp.	47 (8.9)
4	*Escherichia coli*	34 (6.5)
5	Others	23 (4.4)
Total Gram-negative organisms		**469 (89.1)**

Table 9.26: Distribution of *Candida* species causing Secondary BSIs

S. No.	Organism	Number (%)
1	*Candida tropicalis*	8 (1.5)
2	*Candida auris*	3 (0.6)
3	*Candida glabrata*	1 (0.3)
4	*Candida albicans*	7 (1.3)
5	*Candida* spp.	5 (1.0)
Total		**24 (4.6)**

AMS profile in isolates causing BSIs

A high rate of resistance was seen against third-generation cephalosporins, carbapenems, fluoroquinolones and aminoglycosides in *K. pneumoniae, E. coli* and *A. baumannii* causing BSIs. The rate of resistance in *P. aeruginosa* was lower compared to these. Minocycline and Tigecycline appear to be promising alternatives in *Klebsiella* and *Acinetobacter* spp. **(Table 9.27)**. Almost 40% strains of *Enterococcus faecium* causing BSIs were vancomycin-resistant **(Table 9.28),** and nearly 66% strains of *Staphylococcus aureus* were resistant to oxacillin **(Table 9.29)**.

Table 9.27: Antimicrobial susceptibility (AMS) pattern for Gram-negative organisms causing BSIs in HAI surveillance network (2024)

AMA	*K. pneumoniae* (N = 947)	*E. coli* (N = 257)	*A. baumannii* (N = 583)	*P. aeruginosa* (N = 193)
	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)
Amoxicillin-Clavulanate	29/334 (8.7)	22/106 (20.8)	-	-
Amikacin	217/889 (24.4)	143/245 (58.4)	74/561 (13.2)	53/104 (51.0)
Ampicillin	1/93 (1.1)	3/85 (3.5)	-	-
Cefazolin	13/332 (3.9)	1/73 (1.4)	-	-
Cefepime	113/832 (13.6)	53/225 (23.6)	31/401 (7.7)	73/164 (44.5)
Cefotaxime	36/391 (9.2)	15/129 (11.6)	7/165 (4.2)	-

Ceftazidime	23/267 (8.6)	10/70 (14.3)	39/546 (7.1)	87/177 (49.2)
Ceftriaxone	51/697 (7.3)	28/182 (15.4)	8/227 (3.5)	-
Ciprofloxacin	163/886 (18.4)	33/234 (14.1)	55/540 (10.2)	75/176 (42.6)
Colistin	508/535 (94.9)	88/89 (98.9)	402/406 (99.0)	77/82 (93.9)
Ertapenem	96/576 (16.7)	46/138 (33.3)	0/10 (0.0)	-
Gentamicin	250/810 (30.9)	119/232 (51.3)	75/485 (15.5)	25/51 (49.0)
Imipenem	196/876 (22.4)	101/233 (43.4)	49/547 (9.0)	68/175 (38.9)
Levofloxacin	131/457 (28.7)	29/121 (24.0)	57/361 (15.8)	47/130 (36.2)
Meropenem	201/873 (23.0)	98/222 (44.1)	52/544 (9.6)	64/168 (38.1)
Minocycline	77/156 (49.4)	31/49 (63.3)	325/470 (69.2)	-
Netilmicin	15/67 (22.4)	11/15 (73.3)	25/65 (38.5)	25/57 (38.6)
Piperacillin	-	-	5/78 (6.4)	7/24 (29.2)
Tetracycline	126/250 (50.4)	18/52 (34.6)	30/80 (37.5)	-
Tigecycline	111/140 (79.3)	21/25 (84.0)	25/33 (75.8)	-
Tobramycin	87/305 (28.5)	23/48 (47.9)	63/262 (24.1)	48/103 (46.6)

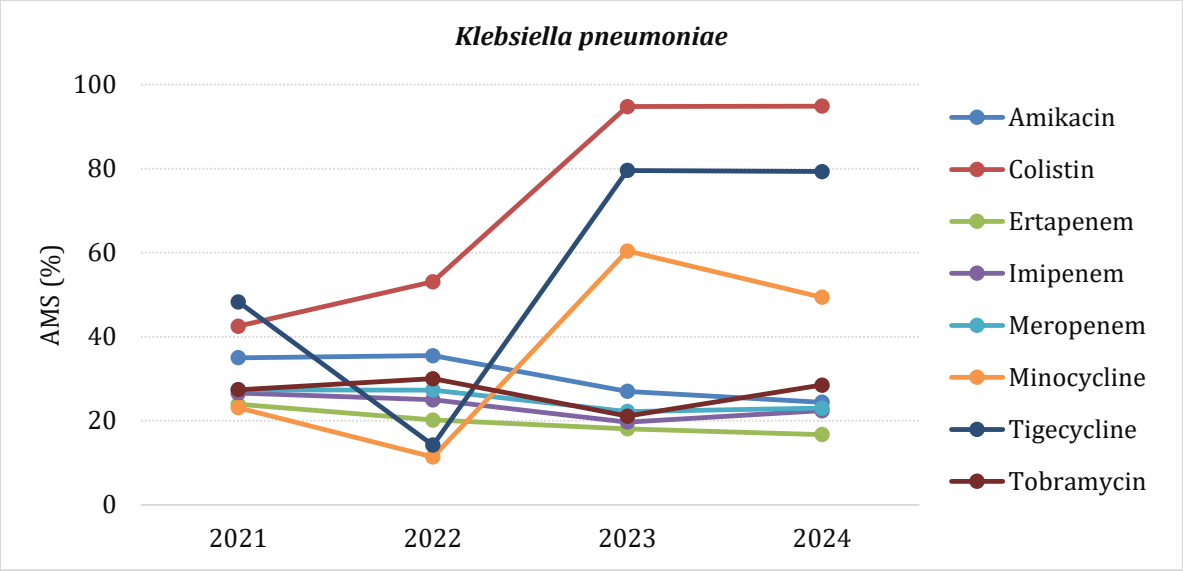
Table 9.28: AMS pattern for *Enterococcus* species causing BSI (2024)

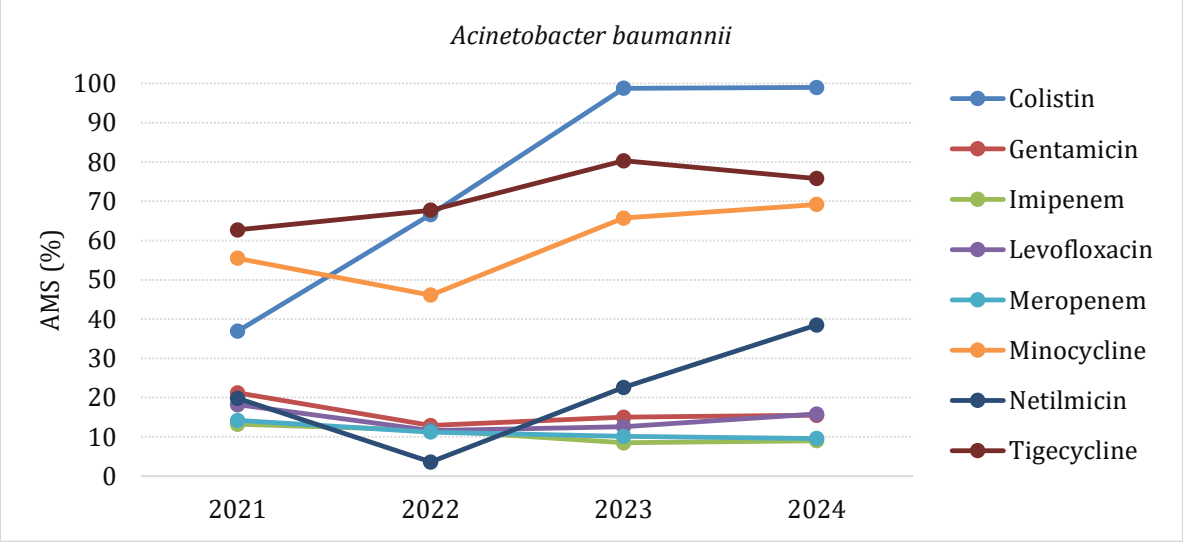
AMA	*Enterococcus faecalis* (N = 89)	*Enterococcus faecium* (N = 207)	*Enterococcus* spp. (N = 81)
	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)
Ampicillin	35/76 (46.1)	10/133 (7.5)	15/65 (23.1)
Ciprofloxacin	23/65 (35.4)	7/138 (5.1)	11/56 (19.6)
Gentamicin	-	-	-
Linezolid	48/52 (92.3)	145/168 (86.3)	73/76 (96.1)
Teicoplanin	60/63 (95.2)	98/167 (58.7)	24/31 (77.4)
Vancomycin	77/88 (87.5)	119/203 (58.6)	62/71 (87.3)
Tetracycline	10/31 (32.3)	10/76 (13.2)	5/23 (21.7)

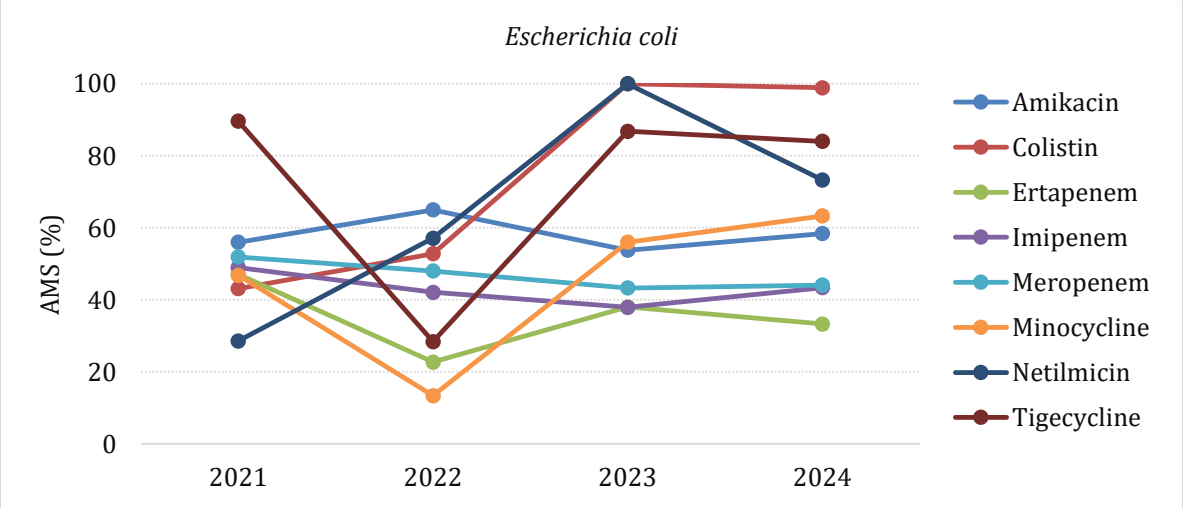
Table 9.29: AMS pattern for *Staphylococcus aureus* causing BSIs (2024)

AMA	*Staphylococcus aureus* (N = 219) Sensitive/Tested (S%)
Erythromycin	52/202 (25.7)
Ciprofloxacin	61/194 (31.4)
Oxacillin	27/80 (33.8)
Clindamycin	87/200 (43.5)
Trimethoprim/Sulfamethoxazole	106/165 (64.2)
Tetracycline	38/51 (74.5)
Teicoplanin	45/46 (97.8)
Linezolid	182/185 (98.4)
Vancomycin	96/ 96 (100)

The AMS profiles of organisms causing BSIs over four years (2021-2024) are shown in **Figures 9.3 and 9.4**.







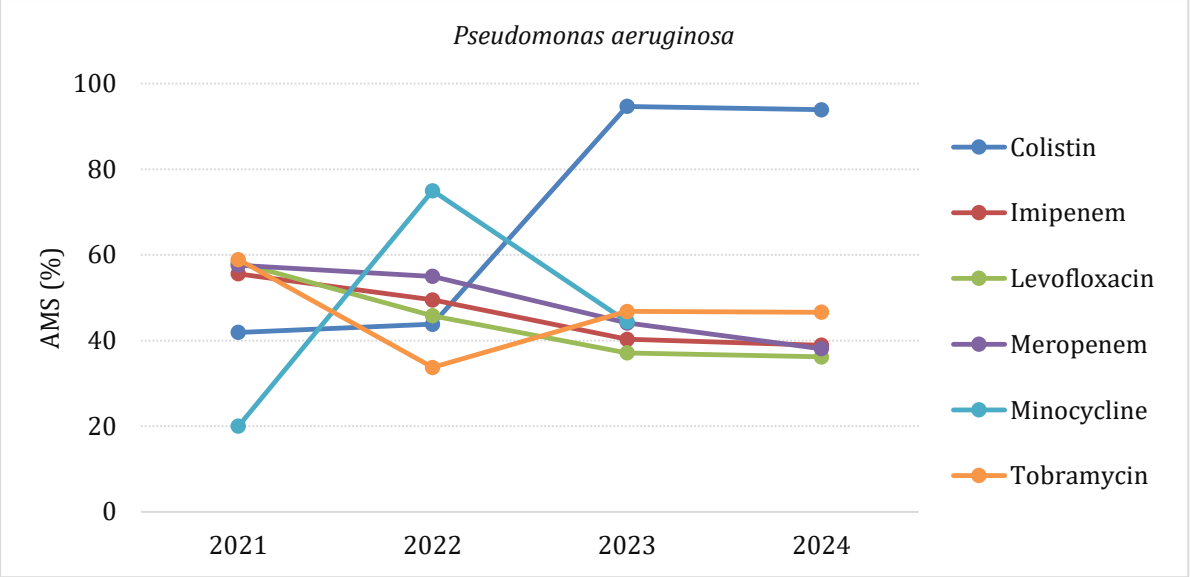
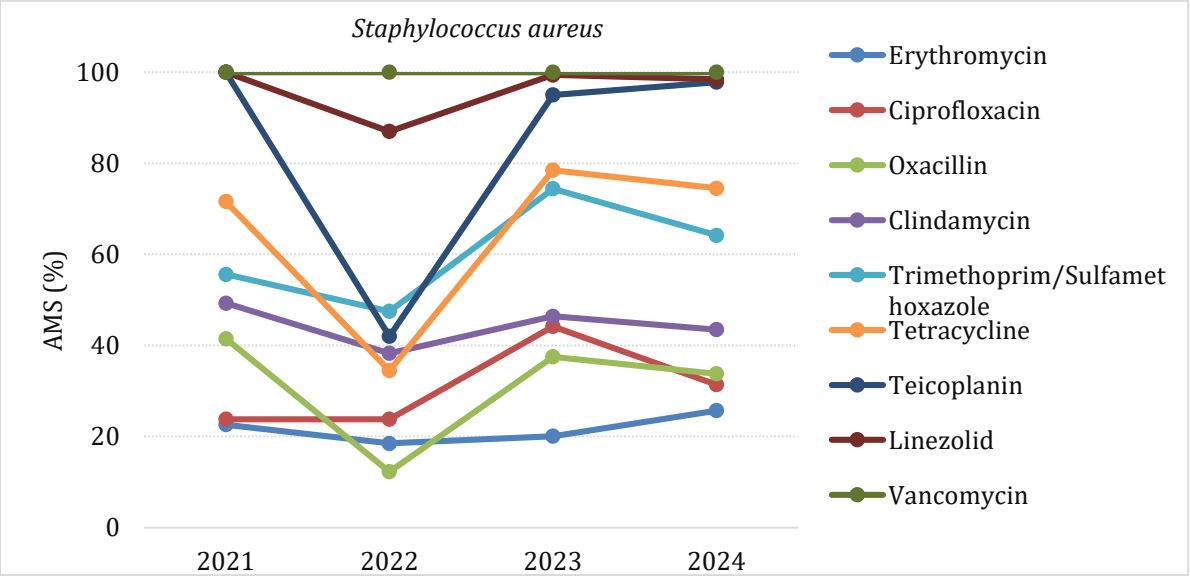


Figure 9.3: AMS profile of Gram-negative organisms (*Klebsiella pneumoniae, Acinetobacter baumannii, Escherichia coli* and *Pseudomonas aeruginosa*) in the surveillance network over four years (2021-2024)



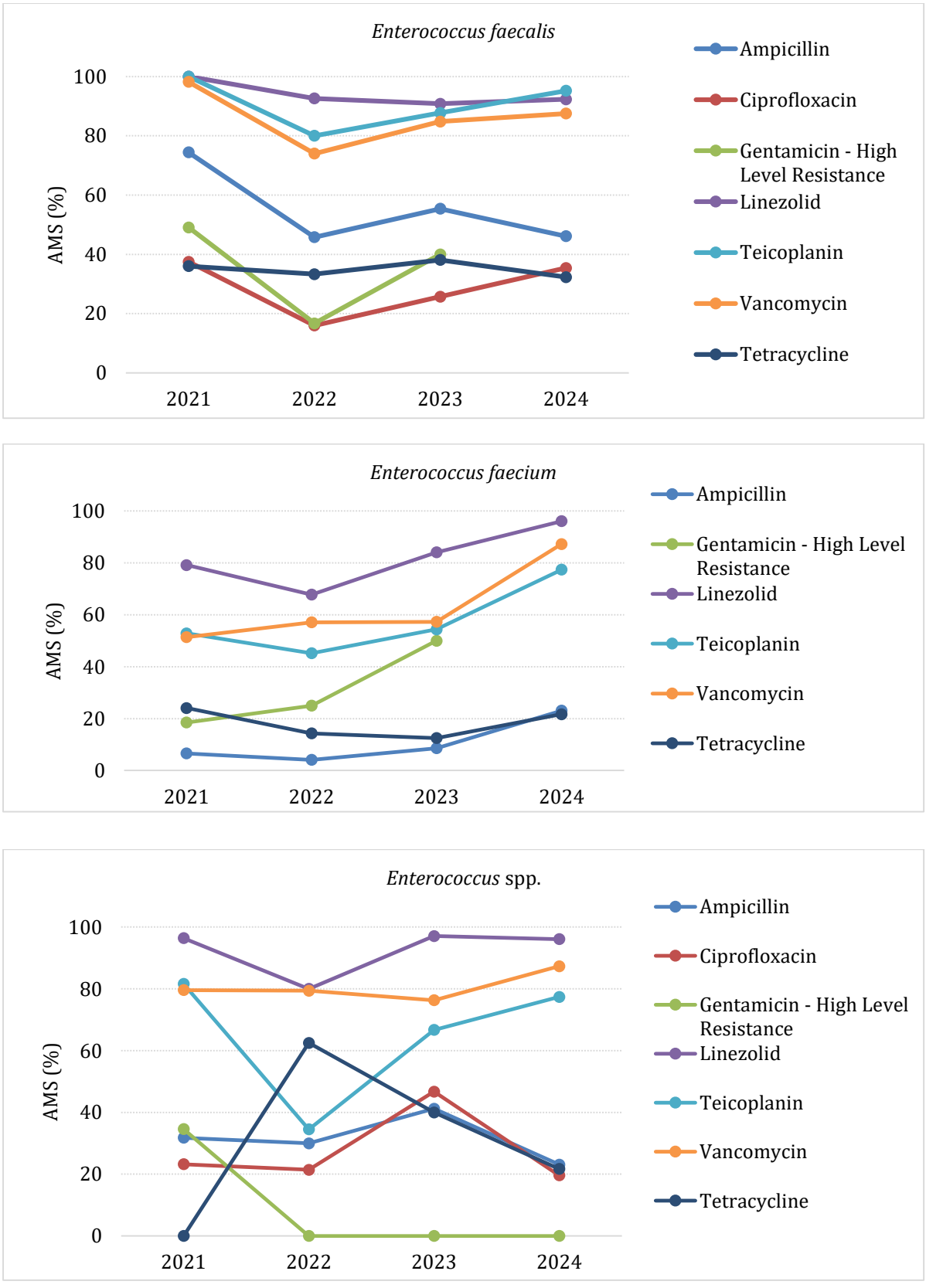


Figure 9.4: AMS profile of Gram-positive organisms (*Staphylococcus aureus, Enterococcus faecalis, Enterococcus faecium* and *Enterococcus* spp.) in the surveillance network over four years (2021-2024)

Urinary Tract Infections (UTI)

A total of 1,659 cases of UTIs were reported. The distribution and profile of UTIs are shown in **Table 9.30**. The catheter-associated UTI (CAUTI) rate was 3.3/1,000 urinary catheter days, as shown in **Table 9.31**. The rates of total UTIs were compared against different types of ICUs since the morbidity of patients varies with the different types of ICUs. The trend of UTI rates in the surveillance network for four years (2021-2024) is shown in **Figure 9.5**.

Table 9.30: Type of UTI cases

Type of UTI cases	No. of UTI cases (%)
CAUTI (catheter-associated UTIs)	1,412 (85.1)
Non-CAUTI	247 (14.9)
Total	**1,659**

Table 9.31: UTI rates

S. No.	Indicator	Rates
1	UTI incidence rate (per 1,000 patient days)	**2.2**
2	CAUTI rate (per 1,000 urinary catheter days)	**3.3**

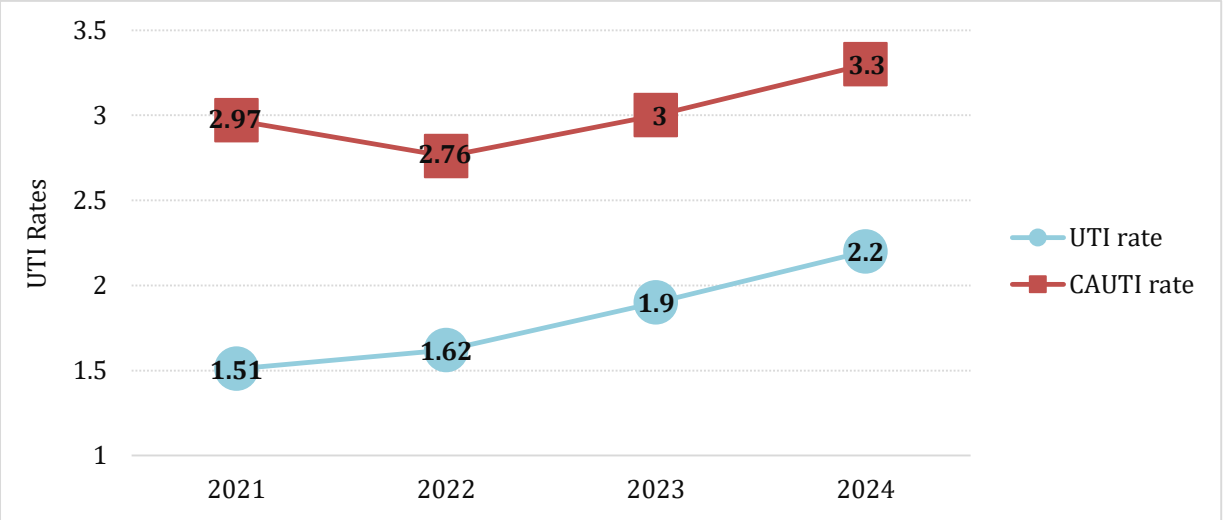


Figure 9.5: Trend of UTI rates in the surveillance network of Indian hospitals over four years (2021-2024)

Table 9.32 compares the rates of UTIs across the different ICU types in our network.

Table 9.32: Distribution of UTI cases by ICUs

Type of ICUs	No. of UTI cases (%)	UTI rate (per 1,000 patient days)
Medical ICU	887 (53.5)	3.9
Medical/Surgical ICU	119 (7.2)	2.0
Trauma ICU	201 (12.1)	2.0
Surgical ICU	108 (6.5)	4.4
Anaesthesia	102 (6.2)	7.5
High Dependency Unit	47 (2.8)	3.0
Neuro Surgery ICU	39 (2.4)	2.1
Gastrointestinal ICU	20 (1.2)	2.1
Pediatric ICU	31 (1.9)	0.8
Neurologic ICU	6 (0.4)	1.3
Neonatal ICU	35 (2.1)	0.2
Oncologic Surgical ICU	13 (0.8)	2.1
Pediatric Medical/Surgical ICU	23 (1.4)	0.8
Oncologic Medical ICU	15 (0.9)	4.7
Respiratory ICU	8 (0.5)	1.4
Cardiothoracic ICU	3 (0.2)	0.7
Cardiac ICU	2 (0.1)	0.2
Total	**1,659**	**2.2**

Of the 1,659 UTI cases, females accounted for 52.8% of the cases, as shown in **Table 9.33.**

Table 9.33: Distribution of UTI cases by gender and age

Gender	No. of UTI cases (%)
Males	783 (47.2)
Females	876 (52.8)
Total	**1,659**

	Median	Range (Days)
Age of males	45	0 – 96
Age of females	44	0 – 92

Table 9.34 shows the duration of stay in the ICUs and the duration between ICU admission and the development of UTI. The duration of ICU stay is a risk factor for the development of HAIs. Some patients had a very prolonged ICU stay, and the UTI cases were found more in patients who had a longer ICU stay, across all ICU types. The 14-day mortality in cases of UTI was 20.4%. This may not be the actual attributable mortality,

since severe primary illness or other underlying co-morbidities may be contributing to the fatal outcome. 16.0% of UTI cases were discharged at 14 days.

Table 9.34: Duration between ICU admission and development of UTI

	Median	Range
Duration of stay in the unit	16	3–217
Duration between date of admission and date of event	8	3–374

Table 9.35 shows the short-term outcomes of UTI cases.

Table 9.35: Outcome of UTI cases

14-day outcome	No. of UTI cases (%)
Died	339 (20.4)
Discharged	265 (16.0)
LAMA	82 (4.9)
Still in surveillance unit	334 (26.2)
Transferred to another hospital	17(1.0)
Transferred to another ward/unit within the hospital	522 (31.5)
Unknown	0 (0.0)
Total	**1,659**

A total of 1,760 pathogens were isolated from the UTI cases. Gram-negative organisms predominated as the cause of UTIs in our network, as shown in **Tables 9.36-9.38**.

Table 9.36: Distribution of organisms causing UTI

S. No.	Organism	Number (%)
1	Gram-negative organisms	1,077 (61.2)
2	Gram-positive organisms	306 (17.4)
3	Fungal pathogens ∞	377 (21.4)
Total		**1,760**

∞ *In this surveillance network, Candida* sp. *was also included in order to understand the epidemiology and significance of Candiduria.*

Table 9.37: Distribution of organisms causing UTI (Genus level)

S. No.	Organism	Number (%)
1	*Candida* spp.	371 (21.1)
2	*Escherichia coli*	390 (22.2)
3	*Enterococcus* spp.	285 (16.2)
4	*Klebsiella* spp.	341 (19.4)
5	*Pseudomonas* spp.	171 (9.7)
6	*Acinetobacter* spp.	86 (4.9)

7	*Providencia* spp.	11 (0.6)
8	*Proteus* spp.	23 (1.3)
9	*Enterobacter* spp.	26 (1.5)
10	*Stenotrophomonas* spp.	3 (0.2)
11	*Staphylococcus aureus*	21 (1.2)
12	*Morganella morganii*	9 (0.5)
13	*Myroides* spp.	2 (0.1)
14	*Citrobacter* spp.	11 (0.6)
15	*Trichosporon* spp.	5 (0.3)
16	*Serratia* spp.	2 (0.1)
17	Others	2 (0.1)
18	*Burkholderia* spp.	1 (0.1)
	Total	**1,760**

Table 9.38: Distribution of organisms (species-level) causing UTI

S. No.	Organism	Number (%)
1	*Escherichia coli*	390 (22.2)
2	*Klebsiella pneumoniae*	266 (15.1)
3	*Enterococcus faecium*	120 (6.8)
4	*Pseudomonas aeruginosa*	133 (7.6)
5	*Candida albicans*	97 (5.5)
6	*Candida tropicalis*	95(5.4)
7	*Candida* spp.	113 (6.4)
8	*Enterococcus* spp.	104 (5.9)
9	*Acinetobacter baumannii*	60 (3.4)
10	*Enterococcus faecalis*	61 (3.5)
11	*Providencia rettgeri*	8 (0.5)
12	*Proteus mirabilis*	19 (1.1)
13	*Candida parapsilosis*	5 (0.3)
14	*Candida glabrata*	21 (1.2)
15	*Candida auris*	12 (0.7)
16	*Klebsiella* spp.	44 (2.5)
17	Others	212 (12.0)
	Total	**1,760**

AMS profile of organisms causing UTI

A high resistance rate was seen against third-generation cephalosporins, carbapenems, fluoroquinolones, colistin, and aminoglycosides in *K. pneumoniae, E. coli*, *A. baumannii* and *P. aeruginosa* causing UTIs; nearly 30% of *Enterococcus faecium* isolates were vancomycin-resistant **(Tables 9.39-9.41)**.

Table 9.39: AMS pattern for Gram-negative organisms causing UTIs (2024)

AMA	Organism			
	K. pneumoniae (N=266)	*E. coli* (N=390)	*A. baumannii* (N=60)	*P. aeruginosa* (N=133)
	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)
Amikacin	75/248 (30.2)	221/361 (61.2)	5/58 (8.6)	42/112 (37.5)
Ampicillin	1/43 (2.3)	5/162 (3.1)	-	-
Cefazolin	7/111 (6.3)	15/168 (8.9)	-	-
Cefepime	32/193 (16.8)	78/289 (27.0)	8/39 (20.5)	26/107 (24.3)
Cefotaxime	12/152 (7.9)	33/260 (12.7)	1/27 (3.7)	-
Ceftazidime	4/94 (4.3)	12/111 (10.8)	6/51 (11.8)	33/124 (26.6)
Ceftriaxone	17/171 (9.9)	28/219 (12.8)	0/26 (0.0)	-
Ciprofloxacin	39/243 (16.1)	47/346 (13.6)	8/55 (14.6)	32/124 (25.8)
Colistin	85/95 (89.5)	117/118 (99.1)	24/26 (92.3)	45/45 (100.0)
Ertapenem	29/136 (21.3)	84/176 (47.7)	-	-
Gentamicin	67/239 (28.0)	167/343 (48.7)	4/55 (7.3)	18/41 (43.9)
Imipenem	78/251 (31.1)	191/348 (54.9)	9/57 (15.8)	30/125 (24.0)
Levofloxacin	17/128 (13.3)	18/134 (13.4)	4/33 (12.1)	21/84 (25.0)
Meropenem	74/227 (32.6)	184/326 (56.4)	11/51 (21.6)	28/114 (24.6)
Minocycline	23/56 (41.1)	48/66 (72.7)	31/46 (67.4)	-
Netilmicin	-	-	-	9/46 (19.6)
Piperacillin	-	-	0/16 (0.0)	6/25 (24.0)
Piperacillin/ Tazobactam	49/234 (21.0)	141/335 (42.1)	11/58 (19.0)	54/124 (43.6)
Tetracycline	37/104 (35.6)	31/111 (27.9)	8/30 (26.7)	-
Tigecycline	10/15 (66.7)	17/17 (100.0)	-	-
Tobramycin	6/26 (23.1)	12/29 (41.4)	1/17 (5.9)	12/62 (19.4)
Amoxicillin/ Clavulanate	21/135 (15.6)	49/217 (22.6)	-	-

Table 9.40: AMS pattern for *Enterococcus* species causing UTI (2024)

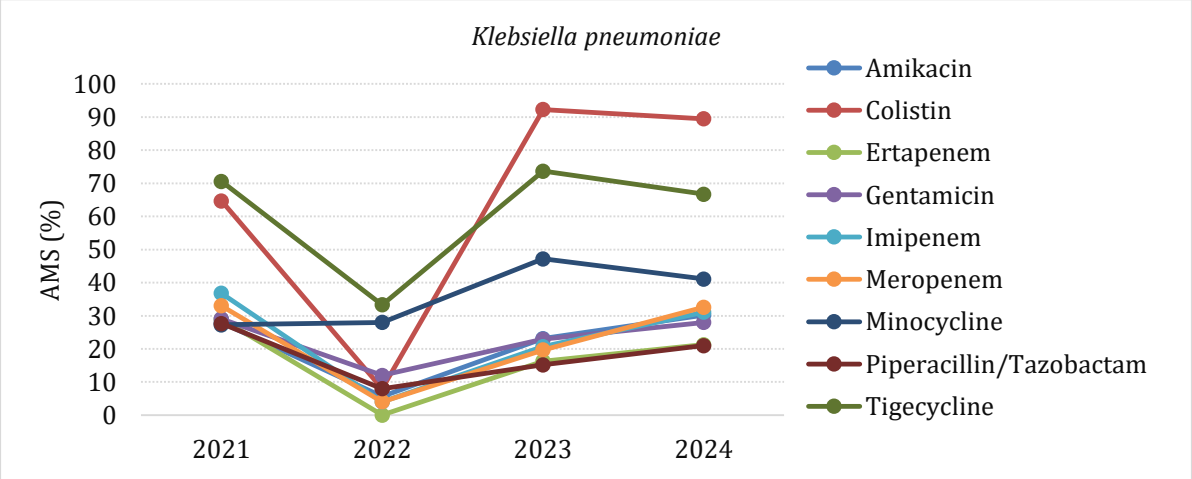
AMA	*Enterococcus faecalis* (N=61)	*Enterococcus faecium* (N=120)	*Enterococcus* spp. (N=104)
	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)
Ampicillin	17/53 (32.1)	11/92 (12.0)	12/77 (15.6)
Ciprofloxacin	4/57 (7.0)	5/106 (4.7)	7/82 (8.5)
Linezolid	1/5 (20.0)	81/86 (94.2)	83/90 (92.2)
Nitrofurantoin	32/51 (62.8)	39/101 (38.6)	45/81 (55.6)
Teicoplanin	23/34 (67.7)	46/65 (70.8)	25/36 (69.4)
Tetracycline	3/37 (8.1)	14/60 (23.3)	14/44 (31/8)
Vancomycin	37/54 (68.5)	75/109 (68.8)	18/98 (81.6)
Fosfomycin	22/43 (51.2)	11/23 (47.8)	15/27 (55.6)

Table 9.41: AMS pattern for *Staphylococcus aureus* causing UTI (2024)

AMA	*Staphylococcus aureus* (N=14) ∞
	Sensitive/Tested (S%)
Clindamycin	6/10 (16.0)
Erythromycin	1/7 (14.3)
Linezolid	13/13 (100.0)
Rifampicin	-
Teicoplanin	4/4 (100.0)
Tetracycline	1/3 (33.3)
Tigecycline	-
Trimethoprim/Sulfamethoxazole	6/9 (66.7)
Vancomycin	5/5 (100.0)

∞ *numbers too low*

The AMS profiles of organisms causing UTIs over four years (2021 – 2024) are shown in **Figures 9.6 and 9.7**.



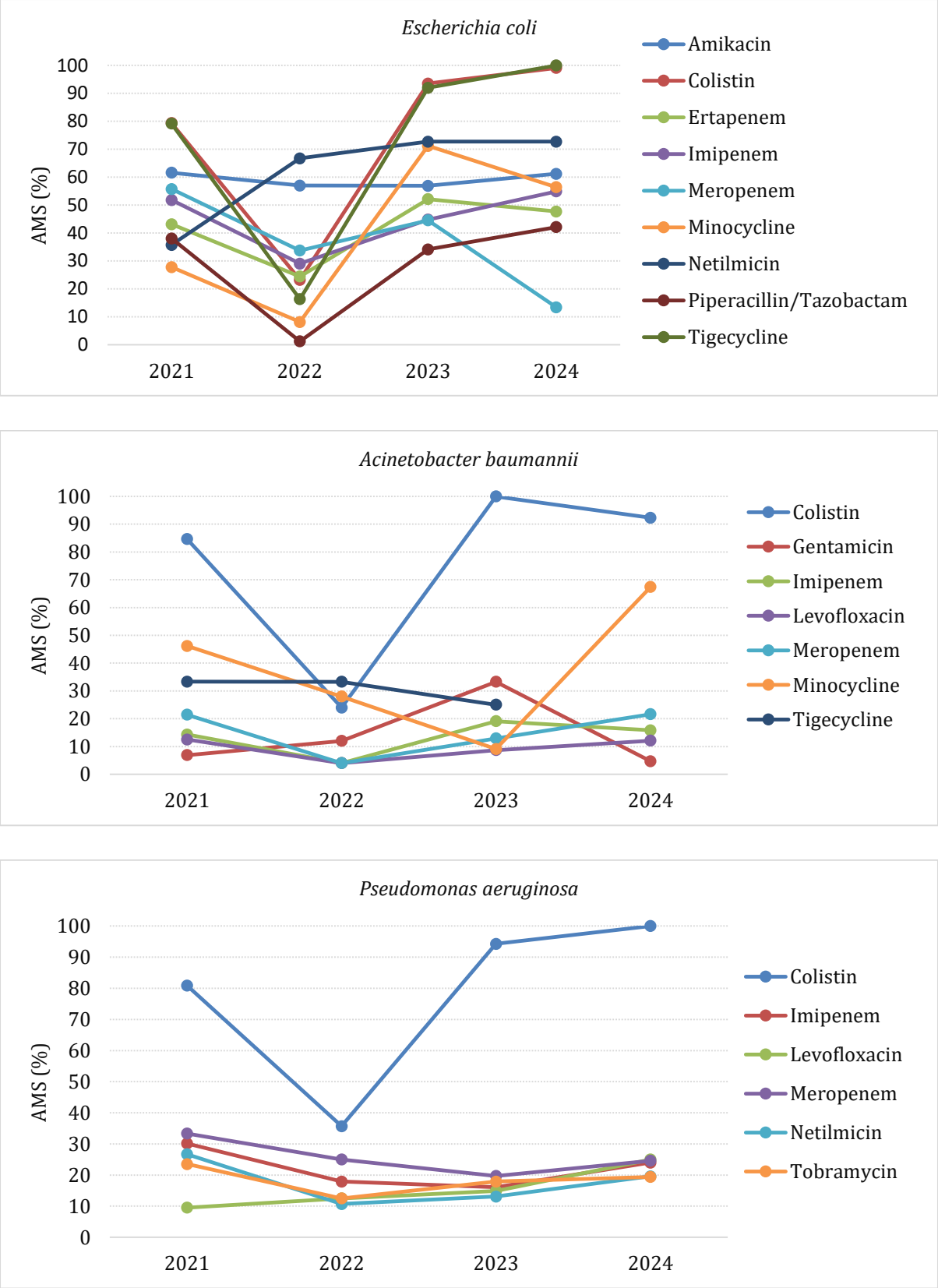
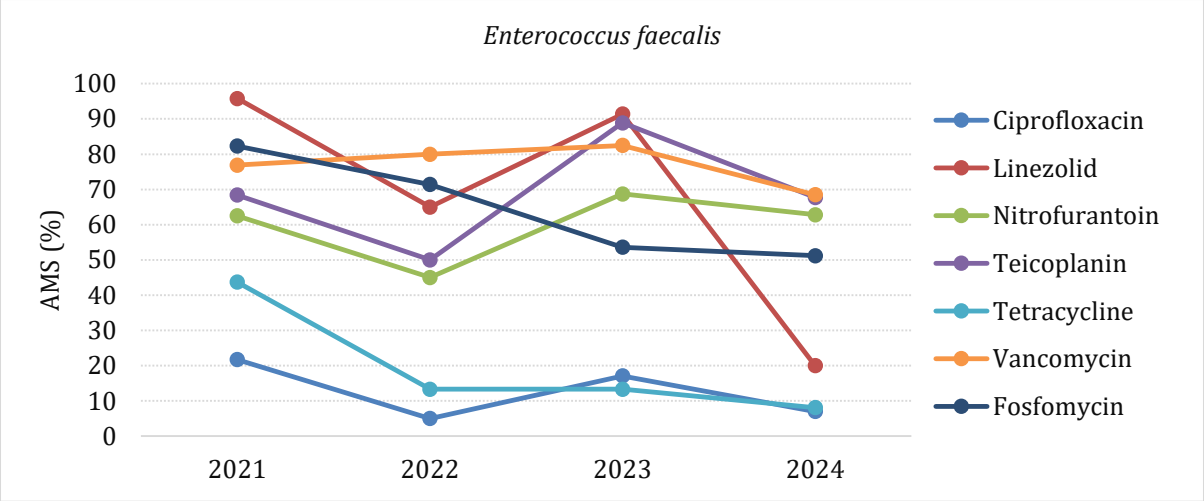
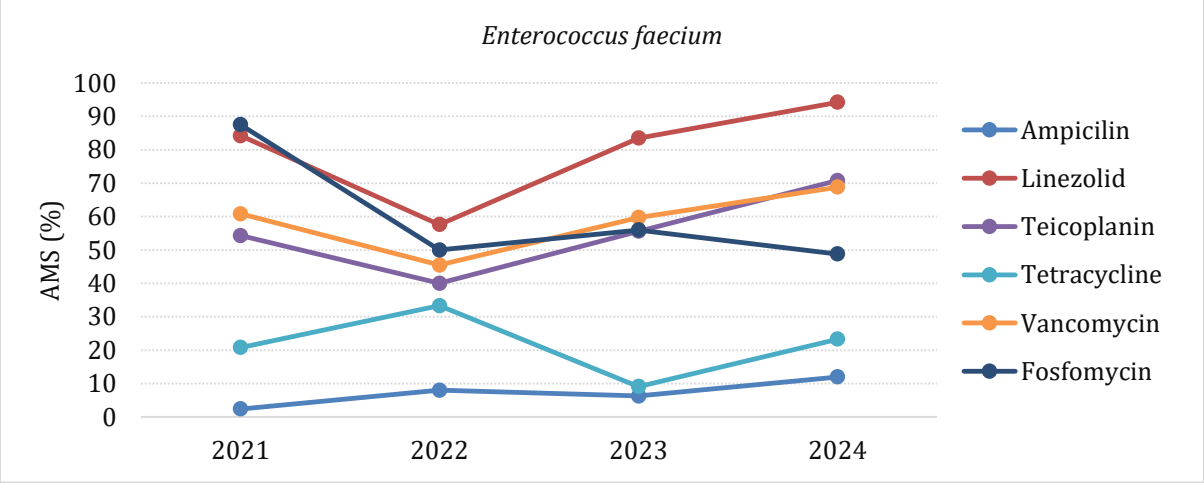


Figure 9.6: AMS profile of Gram-negative organisms (*Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii* and *Pseudomonas aeruginosa*) in the surveillance network over four years (2021-2024)





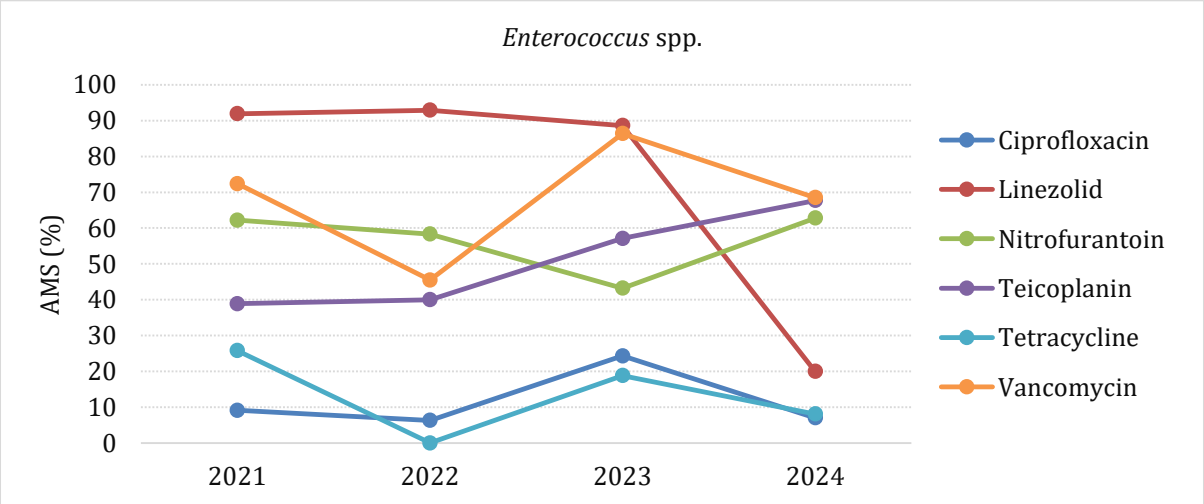


Figure 9.7: AMS profile of Gram-positive organisms (*Enterococcus faecalis, Enterococcus faecium* and *Enterococcus* spp.) in the surveillance network over four years (2021-2024)

Ventilator-Associated Pneumonia

Surveillance for VAP was started towards the end of 2021 using tailor-made definitions for Indian ICUs. The definitions are being validated against the currently used global criteria for ventilator-associated events. The data below shows the VAP events reported by the hospitals in the network **(Tables 9.42-9.44)**.

A total of 328 VAP events were reported from January 2024 to December 2024, giving a VAP rate of 7.17/1,000 ventilator days. A total of 499 organisms were recovered, of which *Acinetobacter* spp. was the most common (43.8%).

Table 9.42: Demographic details of VAP patients under HAI surveillance network (2024)

S. No.	Features	No. of patients (%) (N=328)
1.	**Gender** ▪ Male ▪ Female	 208 (63.4) 120 (36.6)
2.	**Age: median (range)** ▪ <=18 ▪ >18	40 (0 – 88) years 56 (17.1) 272 (83)
3.	**Time to infection** ▪ Within 7 days ▪ 8 – 14 days ▪ 15 - 21 days ▪ 21+ days	 165(50.3) 102(31.1) 35 (10.7) 26 (7.9)
4.	**Outcome** **14-day Outcome** ▪ Still in a surveillance unit ▪ Died ▪ Transferred to another ward/unit within the hospital ▪ Discharged ▪ LAMA ▪ Transferred to other hospitals ▪ Unknown **Final Outcome** ▪ Died ▪ Discharged ▪ LAMA ▪ Transferred to other Hospital ▪ Unknown	 124 (37.8) 114 (34.7) 52 (15.8) 26 (7.9) 10 (3.0) 1 (0.3) 1 (0.3) 151(46) 91 (27.7) 18 (5.5) 1 (0.3) 67(20.4)

Table 9.43: Distribution of organisms isolated from VAP patients (2024)

Organism	Count	Percent
Acinetobacter spp.	219	43.8
Pseudomonas spp.	91	18.2
Klebsiella spp.	86	17.2
Providencia stuartii	23	4.6
Stenotrophomonas maltophilia	17	3.4
Escherichia coli	15	3.0
Staphylococcus aureus	9	1.8
Proteus spp.	7	1.4
Serratia marcescens	5	1.0
Elizabethkingia spp.	5	1.0
Burkholderia cepaciae	4	0.8
Citrobacter spp.	1	0.2
Others	17	3.4
Total	**499**	

Table 9.44: AMS pattern for Gram-negative organisms isolated from VAP patients (2024)

AMA	Enterobacterales (N = 130)	*A. baumannii* (N = 219)	*P. aeruginosa* (N = 82)
	Sensitive/Tested (S%)	Sensitive/Tested (S%)	Sensitive/Tested (S%)
Amoxicillin-Clavulanate	14/78 (18.0)	2/81 (2.5)	9/19 (47.4)
Amikacin	32/125 (25.6)	7/215 (3.2)	40/57 (70.2)
Ampicillin	14/78 (18.0)	2/81 (2.5)	9/19 (47.4)
Cefazolin	9/53 (17.0)	2/81 (2.5)	9/19 (47.4)
Cefepime	12/116 (10.3)	9/201(4.5)	41/80 (51.3)
Cefotaxime	9/50 (18.0)	0/51(0)	9/19 (47.4)
Ceftazidime	8/71 (11.3)	10/198 (5.0)	43/81 (53.1)
Ceftriaxone	8/75 (10.7)	2/81(2.5)	9/19 (47.4)
Ciprofloxacin	11/129 (8.5)	3/211 (1.4)	33/78 (42.3)
Colistin	59/90 (65.6)	143/145 (98.6)	34/35 (97.1)
Gentamicin	32/123 (26.0)	10/200 (5)	9/15 (60.0)
Imipenem	27/130 (20.8)	4/215 (1.9)	24/82 (29.3)
Levofloxacin	11/74 (14.9)	10/179 (5.6)	27/64 (42.2)
Meropenem	25/127 (19.7)	4/213 (1.9)	26/81 (32.1)
Minocycline	21/59 (35.6)	99/173 (57.2)	9/19 (47.4)
Netilmicin	14/78 (18.0)	5/37 (13.5)	4/16 (25.0)
Piperacillin	14/78 (18.0)	0/24 (0)	9/19 (47.4)
Tetracycline	14/60 (23.3)	15/52 (28.8)	9/19 (47.4)
Tigecycline	16/48 (33.3)	2/81(2.5)	9/19 (47.4)
Tobramycin	14/78 (18.0)	18/90 (20)	34/56 (60.7)

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