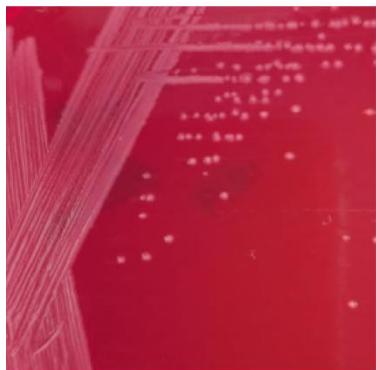


Annual Report

January 2023 to December 2023

Antimicrobial Resistance Research & Surveillance Network



Division of Descriptive Research

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List of acronyms

AFLP	Amplified fragment length polymorphism
AFST	Antifungal susceptibility testing
AMRSN	Antimicrobial Resistance Research & Surveillance Network
AMS	Antimicrobial Susceptibility
AST	Antimicrobial Susceptibility Testing
BAL	Bronchoalveolar lavage
BSI	Blood stream infections
CAM	COVID-19-associated mucormycosis
CARD	Comprehensive Antibiotic Resistance Database
CAUTI	Catheter associated urinary tract infections
CDS	Coding sequence regions
CGPS	Center for Genomic Pathogen Surveillance
CLABSI	Catheter associated blood stream infections
CLSI	Clinical & Laboratory Standards Institute
CoNS	Coagulase-negative Staphylococci
CRAB	Carbapenem-resistant <i>Acinetobacter baumannii</i>
CRE	Carbapenem resistant Enterobacterales
CSF	Cerebrospinal fluid
DI	Deep infections
DEC	Diarrheagenic <i>E coli</i>
DTR	Difficult to treat
ESBLs	Extended spectrum beta lactamases
GPC	Gram-positive cocci
GNB	Gram-negative bacteria
HAI	Hospital acquired Infections
HCAI	Health Care Associated infections
HCWs	Health care workers
ICU	Intensive care unit
IPC	Infection Prevention and Control
IV	Intravenous
OPD	Out-patient department
LOS	Length of stay
LRT	Lower Respiratory tract
MBL	Metallo-beta-lactamase
MFS	Major Facilitator superfamily
MIC	Minimum inhibitory concentration
MLST	Multi-locus sequence typing
MRSA	Methicillin-resistant <i>Staphylococcus aureus</i>
MSSA	Methicillin sensitive <i>Staphylococcus aureus</i>
NFGNB	Non fermenting Gram-negative bacilli
OXA	Oxacillinas
PBP2a	Penicillin binding protein 2a
PCV	Pnuemococcal Conjugate Vaccine
PMQR	Plasmid mediated quinolone resistance
QUAST	Quality assessment tool
RC	Regional centers
RGI	Resistance gene identifier

ROM	rhino-orbital mucormycosis
SCC <i>mec</i>	Staphylococcal cassette chromosome <i>mec</i>
SI	Superficial infections
SD	Standard deviation
SS	Sterile sites body fluids
ST	Sequence types
STR	Short tandem repeat
TMP-SMX	Trimethoprim sulfamethoxazole
TRF	Tandem repeat finder
UTI	Urinary Tract Infections
VAP	Ventilator Associated Pnuemonia
VRE	Vancomycin-resistant enterococci
VVE	Vancomycin Variable <i>Enterococcus</i>
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 Antimicrobial Resistance Research & Surveillance Network (AMRSN) since 2013. The data collected through the network provides trend and pattern of antimicrobial resistance among six key pathogenic groups in the country along with insights on key mechanisms of resistance prevalent in different pathogenic groups using genomics and whole genome sequencing (WGS). This is the seventh detailed report from the ICMR AMR surveillance network. 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.

This report also includes the interpretation of antibiograms from OPD/Ward/ICU which is crucial for assessing the impact of antimicrobial resistance and understanding its implications in clinical practice for empirical use of antibiotics. This further helps in identifying potential areas for interventions and improvements in antimicrobial stewardship practices.

Highlights of surveillance data 2023:

- This report presents data from January 1st, 2023 to December 31st, 2023. A total number of culture positive isolates studied during the year 2023 was **99,492**.
- Gram-negative bacilli remained the most commonly isolated pathogens from most clinically relevant samples like blood, urine, CSF and respiratory tract sample. Gram-positive pathogens were common in only pus/exudates sample.
- *Escherichia coli* was the most commonly isolated pathogen followed by the *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*.
- *E. coli* isolates demonstrated a decrease in susceptibility to most antibiotics, with piperacillin-tazobactam dropping from 56.8% in 2017 to 42.4% in 2023, amikacin from 79.2% in 2017 to 68.2% in 2023, and significant decline in susceptibility to carbapenems (81.4% in 2017 to 62.7% in 2023 for imipenem and 73.2% in 2017 to 66.0% in 2023 for meropenem).
- *Klebsiella pneumoniae* also showed reduced susceptibility, notably with piperacillin-tazobactam falling from 42.6% to 26.5%, carbapenems (imipenem from 58.5% to 35.6% and meropenem from 48% to 37.6%), fluoroquinolones (ciprofloxacin from 32% to 17.1%) over seven years.
- NDM-1 gene was the predominant β-lactamase gene in *E.coli* and was found to be present in 34% of the isolates, followed by OXA-1 in 18% of the isolates, OXA-48 in

14% and CTXM-15 in 12% of the isolates. SHV gene was the predominant β -lactamase gene in *Klebsiella pneumoniae* found in 50% of the isolates, followed by CTXM-15 in 34% and OXA-48 in 29% of the isolates.

- In *Acinetobacter baumannii*, there is no significant change in the susceptibility trends to all the tested antibiotics compared to last year. Resistance to carbapenems in *Acinetobacter baumannii* was recorded as 88.0% in the year 2023, limiting the availability of available treatment options. Susceptibility to minocycline was close to 72% to make it the most susceptible antibiotic after colistin for *A. baumannii*. Similar to previous years, blaOXA-23-like was the only predominant carbapenemase across all the centers contributing to 95% of carbapenem resistance. There was a significant increase in the proportion of dual carbapenemase co-producers (blaOXA-23 like with blaNDM like) from 56% in 2022 to 63% in 2023.
- It is important to notice that there was a gradual increase in carbapenem resistant *P. aeruginosa* from 26% in 2017 to 38.5% in 2023 (for imipenem) and from 31.3% in 2017 to 34.5% in 2023 (for meropenem). A significant increase in resistance rates for ciprofloxacin (26% in 2017 to 38.5% in 2023) and levofloxacin (31.3% in 2017 to 34.5% in 2023) has been observed in the last seven years.
- Over 50% of carbapenem resistant *Pseudomonas aeruginosa* isolates harbour class B type of β -lactamases (Metallo- β -lactamase), with NDM being the most common. For metallo beta-lactamase (MBL) producing *P. aeruginosa*, the treatment options are very limited. The combination of ceftazidime-avibactam plus aztreonam is less likely to provide an incremental benefit over aztreonam alone for MBL producing *P. aeruginosa* infections. Colistin or fosfomycin based combination strategy would be the best alternative for the treating MBL or DTR *P. aeruginosa* infection.
- Among the *Staphylococcus aureus* isolates, susceptibility to erythromycin, clindamycin, ciprofloxacin and co-trimoxazole was more evident in MSSA when compared to MRSA. 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 it being an important anti-TB drug, its use is not encouraged for *Staphylococcus aureus* infections.
- *E. faecalis* is usually the commonest species followed by *E. faecium*. However in 2021 and 2022, *E. faecium* predominated, which reversed in 2023, with *E. faecalis* dominating. Overall vancomycin resistance in enterococci was 17.5 % (2023) slightly higher than the rate in 2022 (16.7%). However, the rate was 5 times higher in *E. faecium* compared to *E. faecalis* (29.6% vs 5.8%).
- *Salmonella Typhi* isolates showed very good susceptibility to ceftriaxone (97.3% susceptible), cefixime (96 % susceptible), trimethoprim-sulfamethoxazole (97% susceptible) and azithromycin (96% susceptible) and very low susceptibility to fluoroquinolones (> 95% resistance). These findings emphasize the limited

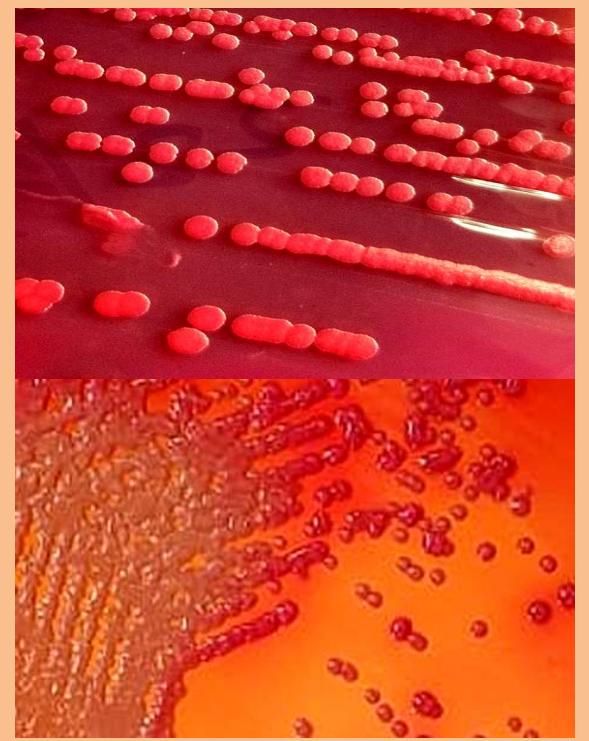
effectiveness of fluoroquinolones in treating infections caused by this pathogen in 2023.

- TMP-SMX and azithromycin remain very good oral options for 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.
- *Salmonella spp.*, followed by *Aeromonas spp.* and then Diarrhogenic *E. coli* were the common organisms isolated from stool samples. Antibiograms of stool isolates, exhibited, high rates of resistance to fluoroquinolones; more than 50% isolates of *Salmonella spp.*, and *Aeromonas spp.* were resistant to fluoroquinolones.
- The tested stool isolates of *Salmonella spp.*, and *Shigella* were susceptible to trimethoprim-sulfamethoxazole and azithromycin, respectively. Isolates of *Aeromonas spp.* showed relatively good susceptibility to tetracyclines and imipenem. Therefore, oral azithromycin, trimethoprim-sulfamethoxazole and doxycycline are good treatment choices for treating bacterial diarrhea for patients admitted in ward. Empirical use of ciprofloxacin or norfloxacin is not recommended for patients with diarrhea.
- As reported in previous years' reports, *C. tropicalis* and *C. albicans* were found to be leading cause of candidemia in the current year, followed by *C. glabrata*. Antifungal susceptibility profiling revealed, 90.8% fluconazole susceptibility in *C. albicans*, 92.5% in *C. tropicalis*, and 88.6% in *C. parapsilosis*. Resistance to echinocandins was low (<5%) for most of the species, making them the most suitable drugs for treatment.
- *Aspergillus spp.* isolates documented higher amphotericin B resistance in the current year compared to previous year in *Aspergillus flavus* (30.8% vs 12.17%) and *A. fumigatus* (51.13% vs 30.77%). The drug of choice, voriconazole, also depicted higher resistance in *A. fumigatus* compared to previous year (4.5% vs 1.1%).
- Among CLABSI causing pathogens, Gram-negative organisms (73.6%) were responsible for most CLABSI, followed by Gram-positive (17.6%) and fungal pathogens (8.8%).
- 80% of *Klebsiella pneumoniae* and 91% of *Acinetobacter baumannii* causing BSIs were imipenem resistant. Nearly 63% of *Staphylococcus aureus* and around 42.7% of *Enterococcus faecium* causing BSIs were respectively oxacillin and vancomycin-resistant. High prevalence of AMR in ICU underscores an urgent need to focus on infection control practices in ICU and other critical areas.

Key takeaways: Interpretations of common syndromic isolates and implications in clinical practice

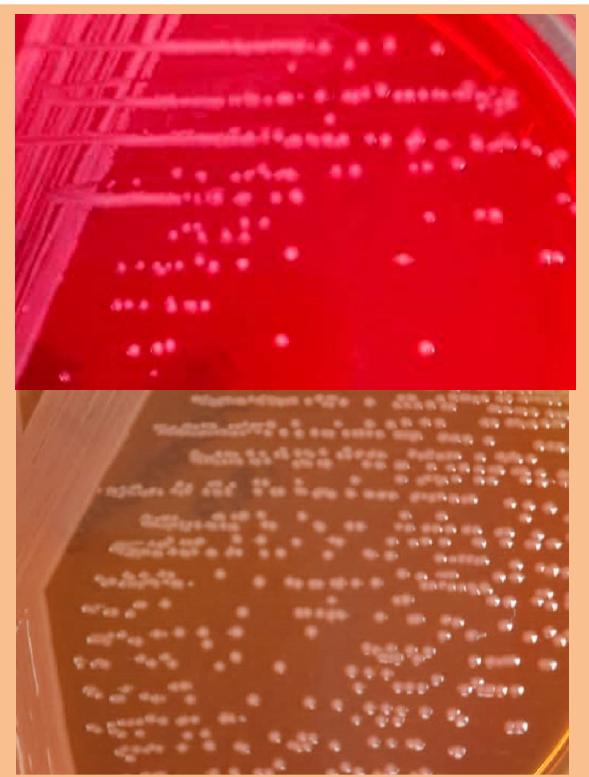
Urine

- *Escherichia coli* and *Klebsiella pneumoniae* are the most commonly isolated organisms from urine from OPD, wards and ICU.
- Fosfomycin (93.7% susceptible) and Nitrofurantoin (86.6% susceptible) showed very good susceptibility patterns in *E coli* urinary isolates particularly in OPD and ward patients. Hence, oral fosfomycin and oral nitrofurantoin may be used to treat cystitis.
- Amikacin (75% susceptible) and Ertapenem (79% susceptible) showed very good susceptibility patterns in *E coli* urinary isolates particularly in OPD and ward patients. Hence, IV Amikacin and IV Ertapenem may be used to treat upper UTI or patient presenting with fever and urinary symptoms.



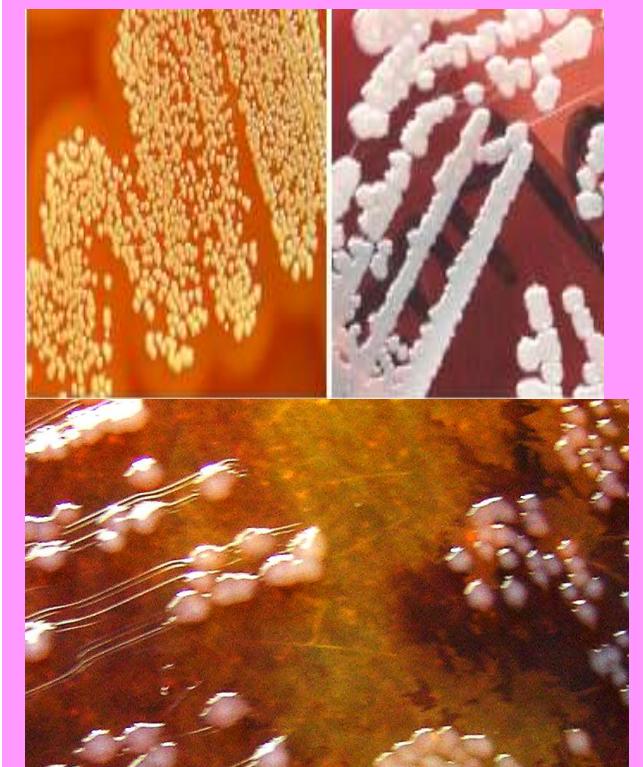
Stool

- *Salmonella spp.*, followed by *Aeromonas spp.* and Diarrhoeagenic *E. coli* were most commonly isolated from stool samples.
- Antibiograms of stool isolates, showed, high rates of resistance to fluoroquinolones; more than 50% isolates in *Salmonella spp.* Isolates of *Aeromonas spp.* showed relatively good susceptibility to tetracyclines and imipenem.
- The tested isolates of *Salmonella spp.*, and *Shigella* were susceptible to trimethoprim-sulfamethoxazole and azithromycin, respectively. for *Aeromonas spp.* tetracyclines and imipenem had fairly good susceptibility pattern
- Therefore, oral azithromycin, trimethoprim-sulfamethoxazole and doxycycline are good options to treat bacterial diarrhoea for patients admitted in ward. Most OPD patients with diarrhoea do-not require antibiotics as these infections are viral or self-limiting.



Pus

- *Staphylococcus aureus* was the most commonly isolated organism (> 30%) from pus samples of OPD patients, whereas *Escherichia coli* and *Klebsiella pneumoniae* were most commonly isolated from ward and ICU patients.
- Clindamycin (79% susceptible) and trimethoprim-sulfamethoxazole (72% susceptible) showed good susceptibility rates among *Staphylococcus aureus* isolates from OPD and ward.
- Hence oral clindamycin and oral trimethoprim-sulfamethoxazole remain very good therapeutic options for purulent skin-soft tissue infections in OPD and ward patients.
- It is also important to note that Gram-negative pathogens were more predominant in pus/exudates sent from ICU patients, so antibiotics targeting Gram-negative organisms should be also be used in patients admitted with skin-soft tissue infections.



Cerebrospinal fluid (CSF)

- Gram-negative isolates were more common among the isolated organisms from the CSF, indicating high representation of hospital acquired ventriculitis in the study population.
- *Acinetobacter baumannii* was the most commonly isolated organism followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*.
- Most of these isolates were resistant to carbapenems, cephalosporins and fluoroquinolones. Only colistin and minocycline showed promising susceptibility rates for *Acinetobacter baumannii* and *Klebsiella pneumoniae*.



Chapter 1. Summary of surveillance data

Total number of culture positive isolates studied during the year 2023 was **99,492**. Of these, **22,182** were from blood, **20,026** from urine, **19,360** superficial infections, **17,902** Lower Respiratory tract (LRT), **6826** Deep infections, **2969** Sterile sites (SS), **873** CSF, **773** Faeces and **8581** others. Majority of the isolates were from Enterobacterales except *Salmonella* and *Shigella* (46.3%) followed by Non fermenting Gram-negative bacilli (NFGNB) (25.0%), staphylococci (15.8%), enterococci (7.0%), fungi (2.8%), Typhoidal *Salmonella* (1.5%), Diarrheal bacterial pathogens (0.7%) and streptococci (0.6%) (**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 (74.2%), sterile body fluids (SS) (52.8%), deep infections (DI) (48.5%), others (46.8%), superficial infections (SI) (43.0%), LRT (36.1%), CSF (33.2%) and blood (32.5%). Non fermenting Gram-negative bacilli (NFGNB) group were the predominant isolates in the lower respiratory tract (56.0%), CSF (37.4%), superficial infections (SI) (25.0%), others (23.4%), deep infection (DI) (22.5%), sterile sites (SS) (21.4%), blood (16.9%) and urine (7.8%). *Staphylococci* constituted 32.2 % of the blood infections followed the superficial infections (SI) (23.0%), deep infection (DI) (21.3%) and CSF (15.7%). Enterococci group constituted 13.3% isolates from urine followed by sterile body fluid (12.3%), CSF (8.6%), blood (6.5%), superficial infections (6.0%), and deep infections (5.8%), and Typhoidal *Salmonella* group constituted 6.6% of the isolates from blood. *Yeast* group were significant isolates in the blood infection (4.7%) (**Table 1.1 and Figure 1.1**).

The distribution of top 10 isolates from different specimens is presented in **Table 1.2 and Figure 1.2**. *Escherichia coli* was most commonly isolated (23.2%) followed by the *Klebsiella pneumoniae* (16.3%), *Acinetobacter baumannii* (12.1%), *Pseudomonas aeruginosa* (11.8%), and *Staphylococcus aureus* (8.9%). Among these isolates, *Escherichia coli* was the most predominant isolate from the urine (50.1%), *K. pneumoniae* from the LRT (22.9%), *Acinetobacter baumannii* from LRT (31.1%), *Pseudomonas aeruginosa* from LRT (22.6%), *S. aureus* from SI (20.4%), *Enterococcus faecalis* and *Enterococcus faecium* from urine (7.9%), and (4.7%) respectively.

Table 1.1: Specimen wise distribution of major groups of organisms

Isolate	Culture positive																			
	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773		Others n=8581	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Enterobacteriales ex cept Salmonella and Shigella	46082 (46.3)	100	7216 (32.5)	15.7	14867 (74.2)	32.3	6464 (36.1)	14	8342 (43.0)	18.1	3312 (48.5)	7.2	290 (33.2)	0.6	1568 (52.8)	3.4	0 (0)	0	4023 (46.8)	8.7
NFGNB	24894 (25.0)	100	3767 (16.9)	15.1	1565 (7.8)	6.3	10035 (56.0)	40.3	5020 (25.9)	20.2	1536 (22.5)	6.2	327 (37.4)	1.3	636 (21.4)	2.6	0 (0)	0	2008 (23.4)	8.1
Staphylococci	15795 (15.8)	100	7144 (32.2)	45.2	298 (1.5)	1.9	933 (5.2)	5.9	4471 (23.0)	28.3	1458 (21.3)	9.2	137 (15.6)	0.9	228 (7.6)	1.4	0 (0)	0	1126 (13.1)	15795 (15.8)
Enterococci	6992 (7.03)	100	1437 (6.4)	20.6	2673 (13.3)	38.2	101 (0.5)	1.4	1166 (6.0)	16.7	399 (5.8)	5.7	75 (8.5)	1.1	366 (12.3)	5.2	0 (0)	0	775 (9.0)	11.1
Fungi	2792 (2.8)	100	1040 (4.7)	37.2	482 (2.4)	17.3	266 (1.5)	9.5	188 (0.9)	6.7	72 (1.0)	2.6	29 (3.3)	1	146 (4.9)	5.2	0 (0)	0	569 (6.6)	20.4
Diarrheal pathogens	759 (0.7)	100	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	759 (98.1)	100	0 (0)	0
Typhoidal Salmonella	1545 (1.5)	100	1470 (6.6)	95.1	0 (0)	0	2 (0.01)	0.1	17 (0.1)	1.1	13 (0.2)	0.8	4 (0.4)	0.3	5 (0.1)	0.3	14 (1.8)	0.9	20 (0.2)	1.3
Streptococci	634 (0.6)	100	108 (0.5)	17	141 (0.7)	22.2	101 (0.5)	15.9	156 (0.8)	24.6	36 (0.5)	5.7	11 (1.2)	1.7	20 (0.6)	3.2	0 (0)	0	61 (0.7)	9.6

Note:

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

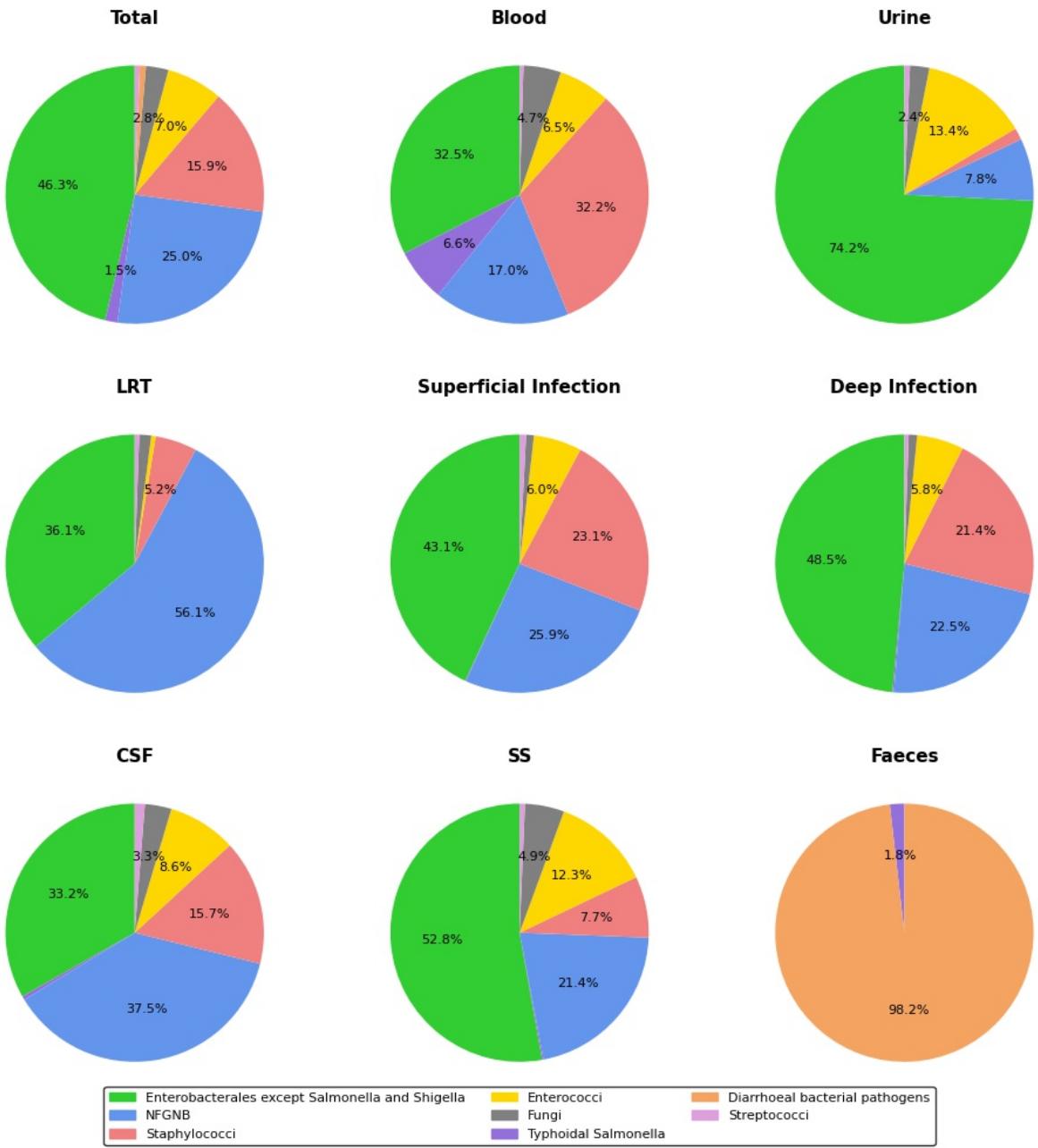


Figure 1.1: Specimen wise distribution of major groups of organisms

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

Organism	All Specimen	Blood	LRT	Superficial Infection	Deep Infection	SS	Faeces	Urine
<i>Escherichia coli</i>	23069 / 99492 (23.19%) R1	3244 / 22182 (14.62%) R1	1361 / 17902 (7.6%) R4	3636 / 19360 (18.78%) R2	1775 / 6826 (26%) R1	829 / 2969 (27.92%) R1	0 / 773 (0%)	10043 / 20026 (50.15%) R1
<i>Klebsiella pneumoniae</i>	16291 / 99492 (16.37%) R2	2909 / 22182 (13.11%) R2	4103 / 17902 (22.92%) R2	2816 / 19360 (14.55%) R4	944 / 6826 (13.8%) R3	515 / 2969 (17.35%) R2	0 / 773 (0%)	3496 / 20026 (17.46%) R2
<i>Acinetobacter baumannii</i>	11947 / 99492 (12.01%) R3	2130 / 22182 (9.6%) R3	5575 / 17902 (31.14%) R1	1914 / 19360 (9.89%) R5	646 / 6826 (9.46%) R5	333 / 2969 (11.22%) R3	0 / 773 (0%)	356 / 20026 (1.78%) R6
<i>Pseudomonas aeruginosa</i>	11757 / 99492 (11.82%) R4	1124 / 22182 (5.07%) R8	4062 / 17902 (22.69%) R3	3009 / 19360 (15.54%) R3	855 / 6826 (12.5%) R4	247 / 2969 (8.32%) R4	0 / 773 (0%)	1184 / 20026 (5.91%) R4
<i>Staphylococcus aureus</i>	8900 / 99492 (8.95%) R5	1472 / 22182 (6.64%) R6	803 / 17902 (4.49%) R5	3956 / 19360 (20.43%) R1	1330 / 6826 (19.48%) R2	158 / 2969 (5.32%) R6	0 / 773 (0%)	221 / 20026 (1.1%) R9
<i>Enterococcus faecalis</i>	3461 / 99492 (3.48%) R6	545 / 22182 (2.46%)	51 / 17902 (0.28%)	650 / 19360 (3.36%) R6	153 / 6826 (2.24%) R8	105 / 2969 (3.54%) R7	0 / 773 (0%)	1595 / 20026 (7.96%) R3
<i>Enterococcus faecium</i>	2746 / 99492 (2.76%) R7	731 / 22182 (3.3%)	24 / 17902 (0.13%)	377 / 19360 (1.95%) R9	159 / 6826 (2.33%) R9	163 / 2969 (5.49%) R5	0 / 773 (0%)	942 / 20026 (4.7%) R5
<i>Staphylococcus haemolyticus</i>	2262 / 99492 (2.27%) R8	1907 / 22182 (8.6%) R4	20 / 17902 (0.11%)	182 / 19360 (0.94%)	20 / 6826 (0.29%)	16 / 2969 (0.54%)	0 / 773 (0%)	26 / 20026 (0.13%)
<i>Staphylococcus epidermidis</i>	2056 / 99492 (2.07%) R9	1657 / 22182 (7.47%) R5	9 / 17902 (0.05%)	188 / 19360 (0.97%)	60 / 6826 (0.88%)	11 / 2969 (0.37%)	0 / 773 (0%)	12 / 20026 (0.06%)
<i>Enterobacter cloacae</i>	1708 / 99492 (1.72%) R10	402 / 22182 (1.81%)	204 / 17902 (1.14%) R7	513 / 19360 (2.65%) R8	169 / 6826 (2.48%) R7	64 / 2969 (2.16%) R9	0 / 773 (0%)	219 / 20026 (1.09%) R10

*R: ranks

Top 10 organisms for

-Blood include *Staphylococcus hominis*: 1275 / 22182 (5.75) **R7**; *Salmonella Typhi*: 1098 / 22182 (4.95) **R9**; *Staphylococcus* spp.: 734 / 22182 (3.31) **R10**

-LRT include *Stenotrophomonas maltophilia*: 358 / 17902(2) **R6**; *Klebsiella* spp.: 191 / 17902 (1.07) **R8**; *Proteus mirabilis*: 165 / 17902 (0.92) **R9**; *Serratia marcescens*: 161 / 17902(0.9) **R10**

-Superficial Infection include *Proteus mirabilis*: 630/19360 (3.25) **R7**; *Morganella morganii*: 201/19360(1.04) **R10**

-Deep Infection include *Proteus mirabilis*: 191 / 6826 (2.8) **R6**; *Enterococcus* spp.: 87 / 6826(1.27) **R10**

-SS include *Enterococcus* spp.: 98 / 2969 (3.3) **R8**; *Stenotrophomonas maltophilia*: 52 / 2969(1.75) **R10**

-Faeces include *Salmonella* spp. Faecal: 307 / 773 (39.72) **R1**; *Aeromonas* spp.: 181 / 773(23.42) **R2**; *Escherichia coli* Diarrheagenic: 85 / 773(11) **R3**; *Vibrio cholerae*: 62 / 773 (8.02) **R4**; *Shigella flexneri*: 48 / 773 (6.21) **R5**; *Shigella sonnei*: 34 / 773(4.4) **R6**; *Salmonella Typhimurium* Faecal: 17 / 773 (2.2) **R7**; *Salmonella* spp.: 11 / 773(1.42) **R8**; *Plesiomonas shigelloides*: 6 / 773(0.78) **R9**; *Shigella dysenteriae*: 5 / 773(0.65) **R10**

-Urine include *Proteus mirabilis*: 261 / 20026(1.3) **R7**; *Citrobacter koseri*: 256 / 20026(1.28) **R8**

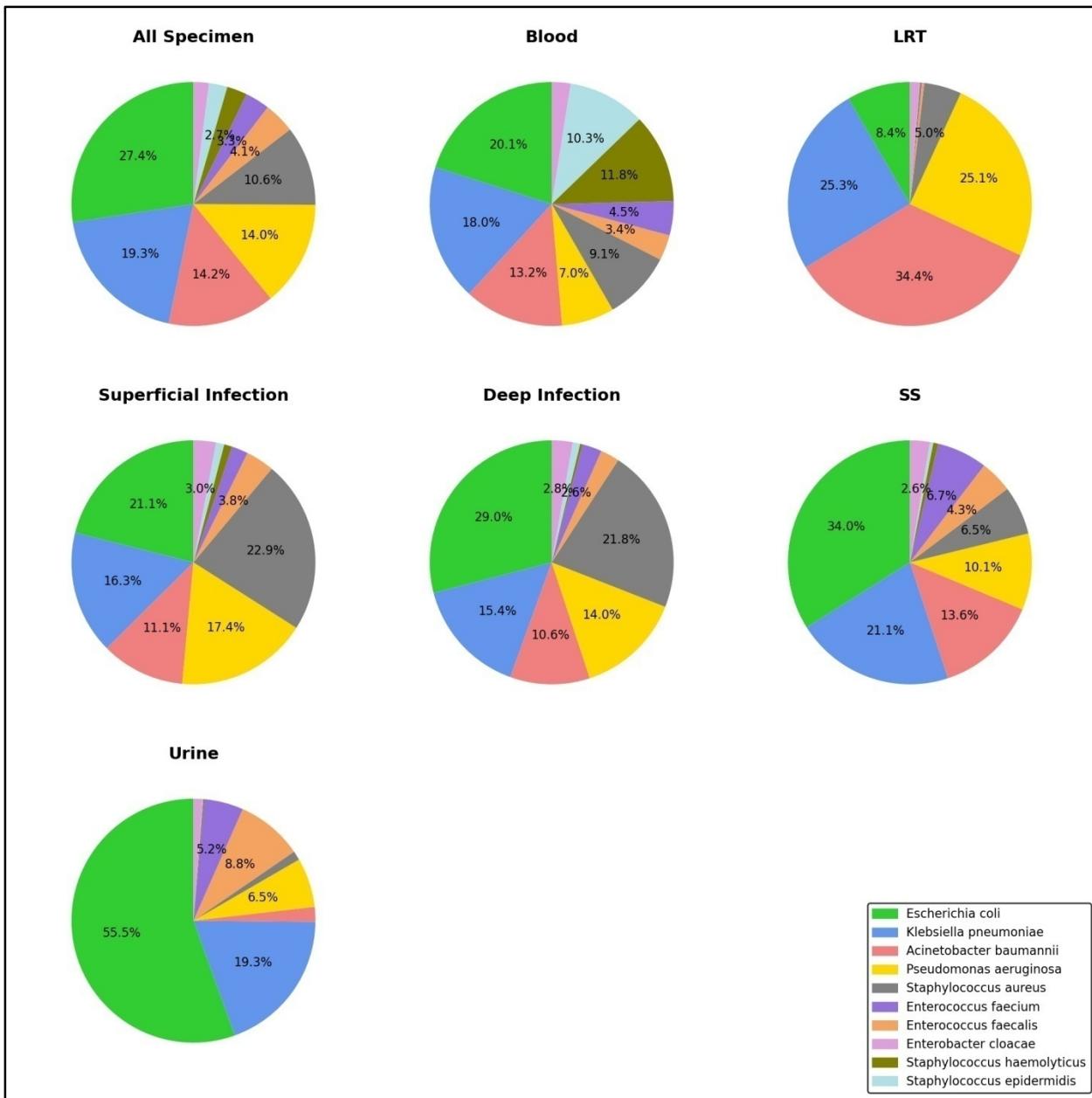


Figure 1.2: Isolation distribution of top 10 isolates from different specimens

The relative distribution of the various species isolated from patients in the out-patient department (OPD), admitted to the wards and intensive care unit (ICUs) are presented in **Table 1.3** and **Figures 1.3**. Top 5 isolates in descending order in OPD specimen were *E. coli*, *K. pneumoniae*, *S. aureus*, *P. aeruginosa*, and *Acinetobacter baumannii*; in wards *E. coli*, *K. pneumoniae*, *Acinetobacter baumannii*, *P. aeruginosa*, and *S. aureus*; and in ICU *Acinetobacter baumannii*, *K. pneumoniae*, *E. coli*, *P. aeruginosa* and *S. aureus*. *Enterococcus faecium* was common isolate from the ICU (3.4%) followed by ward and OPD; whereas, *E.*

faecalis was common isolate from the OPD (4.4%) followed by the wards and the ICU. (Table 1.3, Figure 1.3).

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

Organism	Total n(%)	OPD n(%)	Ward n(%)	ICU n(%)
<i>Escherichia coli</i>	23069 / 99492 (23.19%) R1	8863 / 28830 (30.74%) R1	11665 / 51279 (22.75%) R1	2541 / 19383 (13.11%) R3
<i>Klebsiella pneumoniae</i>	16291 / 99492 (16.37%) R2	3930 / 28830 (13.63%) R2	8314 / 51279 (16.21%) R2	4047 / 19383 (20.88%) R2
<i>Acinetobacter baumannii</i>	11947 / 99492 (12.01%) R3	1260 / 28830 (4.37%) R6	6086 / 51279 (11.87%) R3	4601 / 19383 (23.74%) R1
<i>Pseudomonas aeruginosa</i>	11757 / 99492 (11.82%) R4	3477 / 28830 (12.06%) R4	6062 / 51279 (11.82%) R4	2218 / 19383 (11.44%) R4
<i>Staphylococcus aureus</i>	8900 / 99492 (8.95%) R5	3504 / 28830 (12.15%) R3	4597 / 51279 (8.96%) R5	799 / 19383 (4.12%) R5
<i>Enterococcus faecalis</i>	3461 / 99492 (3.48%) R6	1272 / 28830 (4.41%) R5	1633 / 51279 (3.18%) R6	556 / 19383 (2.87%) R8
<i>Enterococcus faecium</i>	2746 / 99492 (2.76%) R7	460 / 28830 (1.6%) -	1631 / 51279 (3.18%) R7	655 / 19383 (3.38%) R6
<i>Staphylococcus haemolyticus</i>	2262 / 99492 (2.27%) R8	477 / 28830 (1.65%) -	1186 / 51279 (2.31%) R8	599 / 19383 (3.09%) R7
<i>Staphylococcus epidermidis</i>	2056 / 99492 (2.07%) R9	478 / 28830 (1.66%) R10	1108 / 51279 (2.16%) R9	470 / 19383 (2.42%) R9
<i>Enterobacter cloacae</i>	1708 / 99492 (1.72%) R10	521 / 28830 (1.81%) R9	929 / 51279 (1.81%) R10	258 / 19383 (1.33%) -

*R: ranks

- OPD includes *Salmonella Typhi* 688 / 28830 (2.39) **R7**; *Proteus mirabilis* 540 / 28830 (1.87) **R8**
- ICU includes *Stenotrophomonas maltophilia* 311 / 19383 (1.6) **R10**

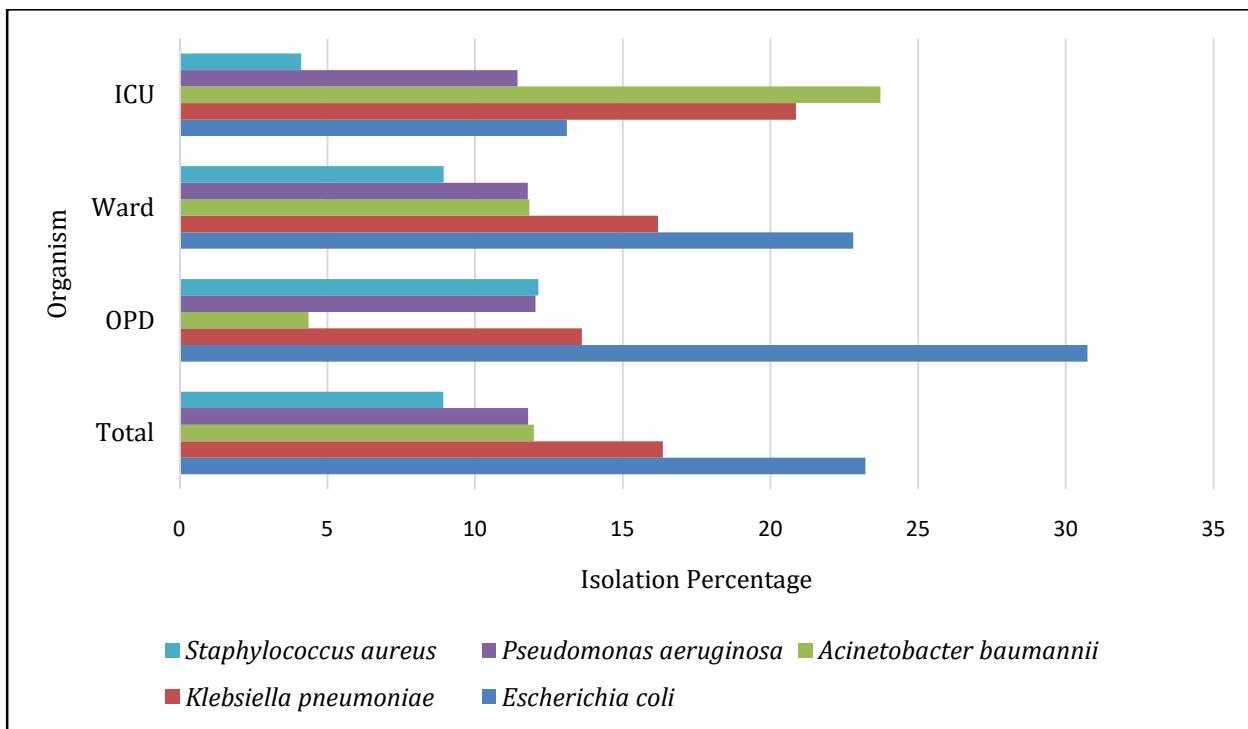


Figure 1.3: Distribution of top 5 isolates from all specimens across OPD, ward and ICU

Yearly isolation rates of top ten isolates from all samples showed a steady increase of *Klebsiella pneumoniae* from 14.7% in 2017 to 16.3% in 2023 (**Table 1.4, Figure 1.4**) and *A. baumannii* from 7.7% in 2017 to 12.0% in 2023 without much change in the isolation rates for the other species. Isolation rates for *Staphylococcus aureus* declined from 12.5% in 2017 to 8.9% in 2023.

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

Rank	Organism	Year-2017 (%)	Year-2018 (%)	Year-2019 (%)	Year-2020 (%)	Year-2021 (%)	Year-2022 (%)	Year-2023 (%)
1	<i>Escherichia coli</i>	10441 / 45714 22.8(%)	19459 / 75182 25.8(%)	30953 / 110268 28.0(%)	16921 / 68081 24.8(%)	23748 / 96650 24.5(%)	26550 / 107053 (24.8%)	23069 / 99492 (23.19%)
2	<i>Klebsiella pneumoniae</i>	6743 / 45714 14.7(%)	11136 / 75182 14.8(%)	18729 / 110268 16.9(%)	12173 / 68081 17.8(%)	17313 / 96650 17.9(%)	18847 / 107053 (17.6%)	16291 / 99492 (16.37%)
3	<i>Pseudomonas aeruginosa</i>	5695 / 45714 12.4(%)	8921 / 75182 11.8(%)	12650 / 110268 11.4(%)	8013 / 68081 11.7(%)	11704 / 96650 12.1(%)	13228 / 107053 (12.3%)	11757 / 99492 (11.82%)
4	<i>Acinetobacter baumannii</i>	3524 / 45714 7.7(%)	5446 / 75182 7.2(%)	8839 / 110268 8.0(%)	7301 / 68081 10.7(%)	12484 / 96650 12.9(%)	12158 / 107053 (11.3%)	11947 / 99492 (12.01%)
5	<i>Staphylococcus aureus</i>	5723 / 45714 12.5(%)	8874 / 75182 11.8(%)	12625 / 110268 11.4(%)	6562 / 68081 9.6(%)	8888 / 96650 9.2(%)	9415 / 107053 (8.7%)	8900 / 99492 (8.95%)
6	<i>Enterococcus faecalis</i>	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%)
7	<i>Enterococcus faecium</i>	181 / 7283 2.4(%)	937 / 45714 2.0(%)	1479 / 75182 1.9(%)	2742 / 110268 2.4(%)	2038 / 68081 2.9(%)	3006 / 107053 (2.8%)	2746 / 99492 (2.76%)
8	<i>Staphylococcus haemolyticus</i>	634 / 45714 1.4(%)	871 / 75182 1.1(%)	827 / 110267 0.7(%)	626 / 68081 0.9(%)	839 / 96658 0.8(%)	2373 / 107053 2.2(%)	2262 / 99492 (2.27%)
9	<i>Staphylococcus epidermidis</i>	579 / 45714 1.2(%)	912 / 75182 1.2(%)	730 / 110267 0.6(%)	397 / 68081 0.5(%)	596 / 96658 0.6(%)	1775 / 107053 1.6(%)	2056 / 99492 (2.07%)
10	<i>Enterobacter cloacae</i>	620 / 45714 1.36(%)	1098 / 75182 1.46(%)	1514 / 110268 1.37(%)	1080 / 68081 1.59(%)	1654 / 96836 1.71(%)	1780 / 109484 1.63(%)	1708 / 99492 (1.72%)

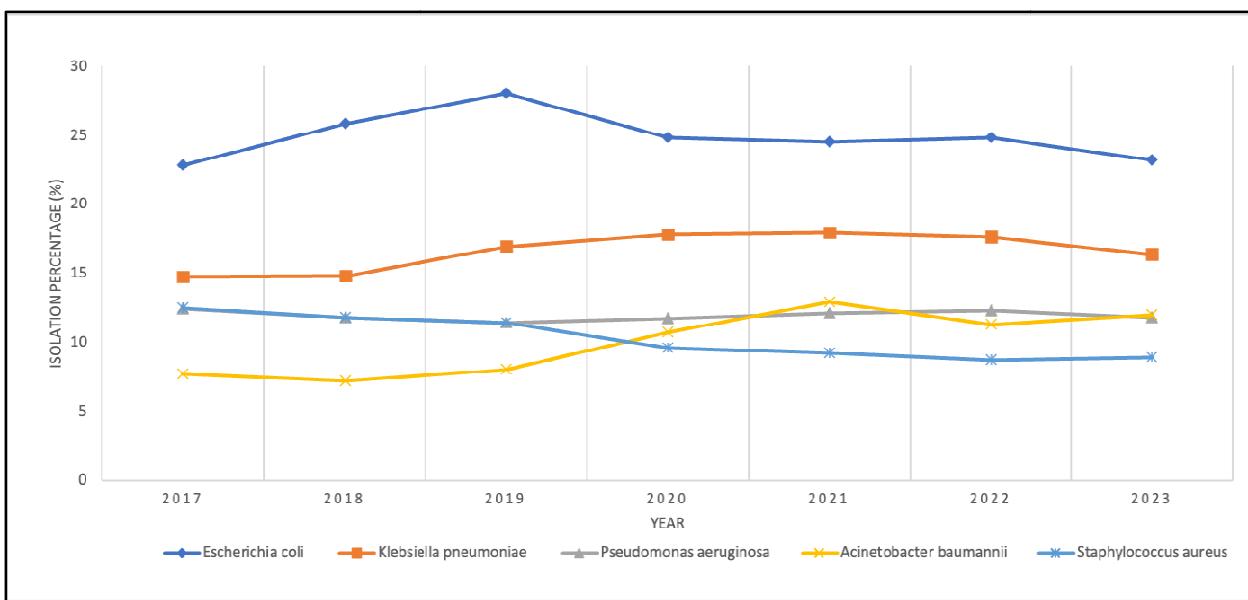


Figure 1.4: Yearly isolation trends of top 5 isolates from all samples

Enterobacterales

Of the overall isolates Enterobacterales (except *Salmonella* and *Shigella*) constituted a major group (46.3%) (Table 1.1). Out of a total of 99,492 culture positive isolates, specimen percentage wise distribution of major species within family Enterobacterales is shown in the **Table 1.5 and Figures 1.5**. *Escherichia coli* was the commonest species (23.2%) followed by *Klebsiella pneumoniae* (16.3%), *Enterobacter cloacae* (1.7%) and *Proteus mirabilis* (1.5%) (**Table 1.5**). *Escherichia coli* was the most predominant isolate from the urine (50.1%), sterile site (27.9%), Deep infections (26.0%), others (24.2%), superficial infection (18.7%), blood (14.6%) and CSF (11.3%). *Klebsiella pneumoniae* was the most predominant isolate in the lower respiratory tract (22.9%), CSF (17.7%), urine (17.4%), sterile sites (SS) (17.3%), others (15.7%), superficial infection (14.5%), deep infection (DI) (13.8%) and blood (13.1%). *Enterobacter cloacae* constituted 2.6% of superficial infections, 2.4 % of deep infections and both CSF and sterile site (1.5%). *Proteus mirabilis* was common in 3.2% of superficial infections, 2.8 % of deep and other specimens (2.1%). *Klebsiella* species constituted 1.5% of sterile site infections (SS).

Isolates from the regional centers (RC 17) had higher percentage isolate rate of *E. coli*, RC 15 had higher percentage isolate rate of *K. pneumoniae*. RC11 had higher percentage isolate rate of *Proteus mirabilis* and *Enterobacter cloacae* than the rest of RCs (**Table 1.6**).

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

Isolate	Culture positive																			
	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773		Others n=8581	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
<i>Escherichia coli</i>	23069 (23.2)	100	3244 (14.6)	14.1	10043 (50.1)	43.5	1361 (7.6)	5.9	3636 (18.7)	15.8	1775 (26)	7.7	99 (11.3)	0.4	829 (27.9)	3.6	0 (0)	0	2082 (24.26)	9
<i>Klebsiella pneumoniae</i>	16291 (16.37)	100	2909 (13.1)	17.9	3496 (17.4)	21.5	4103 (22.9)	25.2	2816 (14.5)	17.3	944 (13.8)	5.8	155 (17.7)	1	515 (17.3)	3.2	0 (0)	0	1353 (15.77)	8.3
<i>Enterobacter cloacae</i>	1708 (1.72)	100	402 (1.81)	23.5	219 (1.09)	12.8	204 (1.14)	11.9	513 (2.65)	30	169 (2.48)	9.9	19 (2.18)	1.1	64 (2.16)	3.7	0 (0)	0	118 (1.37)	6.9
<i>Proteus mirabilis</i>	1545 (1.55)	100	90 (0.41)	5.8	261 (1.3)	16.9	165 (0.92)	10.7	630 (3.25)	40.8	191 (2.8)	12. 4	2 (0.23)	0.1	28 (0.94)	1.8	0 (0)	0	178 (2.07)	11.5
<i>Citrobacter koseri</i>	661 (0.66)	100	54 (0.24)	8.2	256 (1.28)	38.7	86 (0.48)	13	166 (0.86)	25.1	35 (0.51)	5.3	3 (0.34)	0.5	13 (0.44)	2	0 (0)	0	48 (0.56)	7.3
<i>Morganella morganii</i>	511 (0.51)	100	33 (0.15)	6.5	117 (0.58)	22.9	22 (0.12)	4.3	201 (1.04)	39.3	74 (1.08)	14. 5	0 (0)	0	15 (0.51)	2.9	0 (0)	0	49 (0.57)	9.6
<i>Serratia marcescens</i>	509 (0.51)	100	161 (0.73)	31.6	68 (0.34)	13.4	161 (0.9)	31.6	58 (0.3)	11.4	23 (0.34)	4.5	2 (0.23)	0.4	14 (0.47)	2.8	0 (0)	0	22 (0.26)	4.3
<i>Klebsiella spp.</i>	422 (0.42)	100	101 (0.46)	23.9	32 (0.16)	7.6	191 (1.07)	45.3	21 (0.11)	5	12 (0.18)	2.8	3 (0.34)	0.7	46 (1.55)	10. 9	0 (0)	0	16 (0.19)	3.8
<i>Providencia stuartii</i>	168 (0.17)	100	20 (0.09)	11.9	17 (0.08)	10.1	37 (0.21)	22	54 (0.28)	32.1	13 (0.19)	7.7	0 (0)	0	2 (0.07)	1.2	0 (0)	0	25 (0.29)	14.9

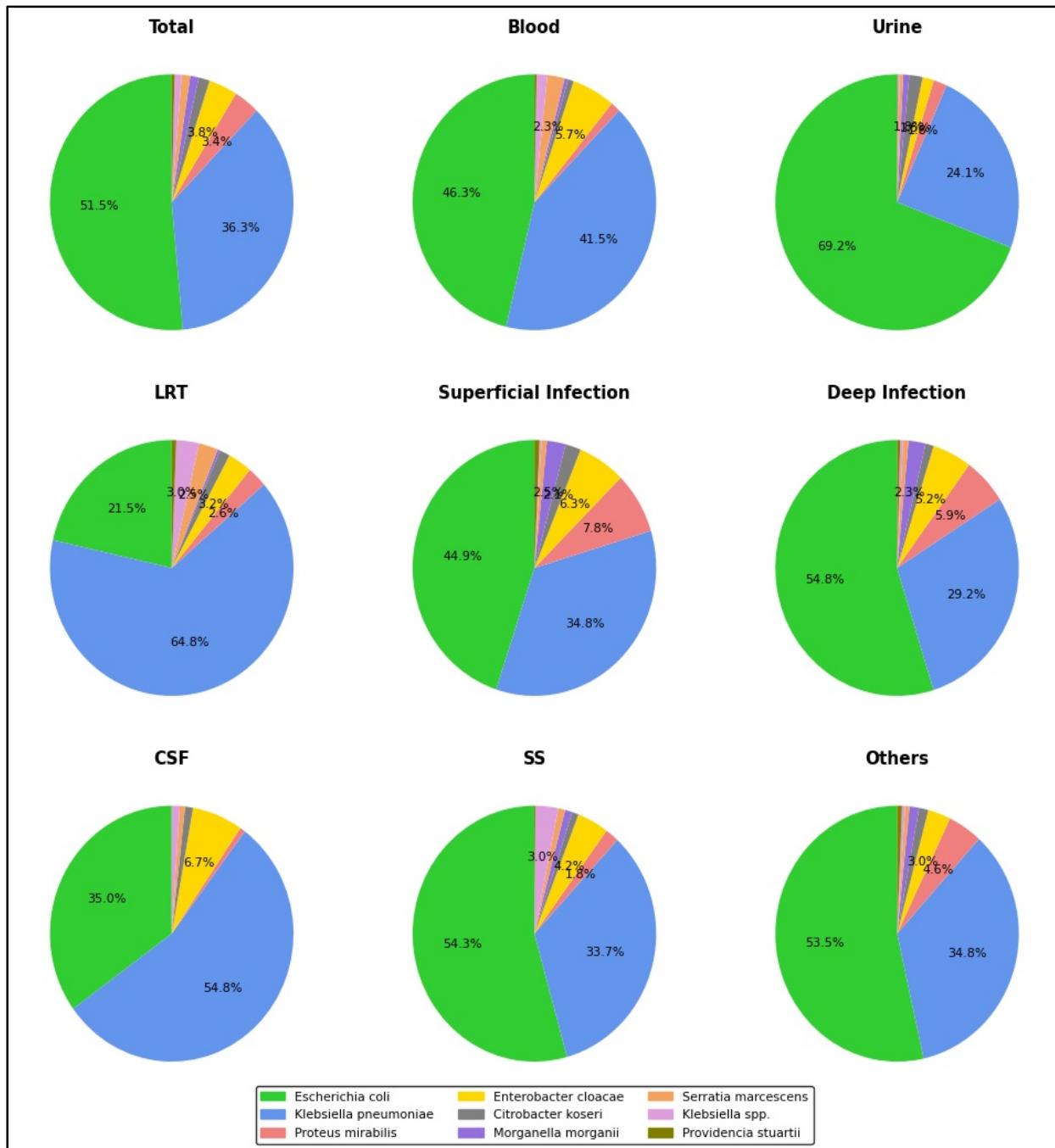


Figure 1.5: Specimen wise distribution of major species of Family Enterobacteriales except *Salmonella* and *Shigella*

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

Regional Centre	<i>Escherichia coli</i>	<i>Klebsiella pneumoniae</i>	<i>Proteus mirabilis</i>	<i>Enterobacter cloacae</i>	<i>Citrobacter koseri</i>	<i>Enterobacter spp.</i>	<i>Citrobacter spp.</i>	<i>Citrobacter freundii</i>	<i>Proteus vulgaris</i>
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	879/4335 (20.3)	802/4335 (18.5)	39/4335 (0.9)	99/4335 (2.3)	16/4335 (0.4)	3/4335 (0.1)	*0/0 (-)	7/4335 (0.2)	*0/0 (-)
RC2	2883/17084 (16.9)	1910/17084 (11.2)	168/17084 (1)	220/17084 (1.3)	11/17084 (0.1)	59/17084 (0.3)	13/17084 (0.1)	15/17084 (0.1)	*0/0 (-)
RC3	851/4317 (19.7)	231/4317 (5.4)	13/4317 (0.3)	*0/0 (-)	5/4317 (0.1)	73/4317 (1.7)	10/4317 (0.2)	*0/0 (-)	*0/0 (-)
RC4	3716/17183 (21.6)	2586/17183 (15)	441/17183 (2.6)	471/17183 (2.7)	153/17183 (0.9)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC5	804/2701 (29.8)	491/2701 (18.2)	39/2701 (1.4)	79/2701 (2.9)	31/2701 (1.1)	*0/0 (-)	9/2701 (0.3)	*0/0 (-)	8/2701 (0.3)
RC6	1157/5475 (21.1)	1160/5475 (21.2)	80/5475 (1.5)	71/5475 (1.3)	8/5475 (0.1)	*0/0 (-)	11/5475 (0.2)	8/5475 (0.1)	5/5475 (0.1)
RC7	409/1572 (26)	339/1572 (21.6)	40/1572 (2.5)	45/1572 (2.9)	6/1572 (0.4)	6/1572 (0.4)	*0/0 (-)	8/1572 (0.5)	2/1572 (0.1)
RC8	824/3057 (27)	703/3057 (23)	51/3057 (1.7)	79/3057 (2.6)	19/3057 (0.6)	12/3057 (0.4)	3/3057 (0.1)	8/3057 (0.3)	3/3057 (0.1)
RC9	1020/3623 (28.2)	670/3623 (18.5)	29/3623 (0.8)	16/3623 (0.4)	203/3623 (5.6)	*0/0 (-)	*0/0 (-)	4/3623 (0.1)	7/3623 (0.2)
RC10	1894/6686 (28.3)	1181/6686 (17.7)	174/6686 (2.6)	147/6686 (2.2)	124/6686 (1.9)	10/6686 (0.1)	24/6686 (0.4)	16/6686 (0.2)	11/6686 (0.2)
RC11	320/2894 (11.1)	609/2894 (21)	78/2894 (2.7)	133/2894 (4.6)	3/2894 (0.1)	*0/0 (-)	*0/0 (-)	6/2894 (0.2)	*0/0 (-)
RC12	605/1917 (31.6)	425/1917 (22.2)	*0/0 (-)	74/1917 (3.9)	*0/0 (-)	2/1917 (0.1)	1/1917 (0.1)	1/1917 (0.1)	*0/0 (-)
RC13	214/945 (22.6)	161/945 (17)	4/945 (0.4)	14/945 (1.5)	1/945 (0.1)	4/945 (0.4)	*0/0 (-)	1/945 (0.1)	1/945 (0.1)

RC14	1370/3501 (39.1)	615/3501 (17.6)	17/3501 (0.5)	127/3501 (3.6)	29/3501 (0.8)	*0/0 (-)	5/3501 (0.1)	6/3501 (0.2)	2/3501 (0.1)
RC15	370/1679 (22)	392/1679 (23.3)	41/1679 (2.4)	23/1679 (1.4)	*0/0 (-)	*0/0 (-)	1/1679 (0.1)	2/1679 (0.1)	*0/0 (-)
RC16	1716/5179 (33.1)	939/5179 (18.1)	91/5179 (1.8)	*0/0 (-)	36/5179 (0.7)	26/5179 (0.5)	5/5179 (0.1)	33/5179 (0.6)	58/5179 (1.1)
RC17	504/1266 (39.8)	205/1266 (16.2)	*0/0 (-)	29/1266 (2.3)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC18	120/491 (24.4)	111/491 (22.6)	7/491 (1.4)	6/491 (1.2)	3/491 (0.6)	*0/0 (-)	*0/0 (-)	2/491 (0.4)	3/491 (0.6)
RC19	1950/10107 (19.3)	1805/10107 (17.9)	161/10107 (1.6)	54/10107 (0.5)	8/10107 (0.1)	20/10107 (0.2)	*0/0 (-)	*0/0 (-)	14/10107 (0.1)
RC20	1170/3600 (32.5)	645/3600 (17.9)	54/3600 (1.5)	4/3600 (0.1)	5/3600 (0.1)	*0/0 (-)	6/3600 (0.2)	5/3600 (0.1)	14/3600 (0.4)
RC21	293/1108 (26.4)	311/1108 (28.1)	18/1108 (1.6)	13/1108 (1.2)	*0/0 (-)	1/1108 (0.1)	*0/0 (-)	4/1108 (0.4)	*0/0 (-)
Total National	23069/98719 (23.4)	16291/98719 (16.5)	1545/98719 (1.6)	1708/98719 (1.7)	661/98719 (0.7)	220/98719 (0.2)	90/98719 (0.1)	140/98719 (0.1)	135/98719 (0.1)

Typhoidal Salmonella

This distribution showed that isolates from the RC 6 had higher percentage isolation rate of *Salmonella Typhi* from blood (7.1%) than the rest of RCs (**Table 1.7**). *Salmonella Paratyphi A* isolation percentage was more in RC 4 (20.7) and in RC 6 (18.4%) as compared to other RCs. The relative distribution of Typhoidal *Salmonella* isolated from blood in the OPD, admitted to the wards and ICUs are presented in **Table 1.8 and Figures 1.6**. Typhoidal *Salmonella* was common isolate from the OPD (20.3%) followed by the wards and was least isolated from the ICU (Table 1.8). Among Typhoidal *Salmonella*, *Salmonella Typhi* had higher percentage isolation rate than *Salmonella Paratyphi A*. Yearly isolation trends showed declining in isolation rates of *Salmonella Typhi* from 2017 to 2022 from all over India but showed further increased in isolation rate in 2023 (**Table 1.9 & Figure 1.7**).

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

Regional Centre	Total Blood Isolates	Salmonella Typhi	Salmonella Paratyphi A
	n(%)	n(%)	n(%)
RC1	1049/22182 (4.7)	24/1049 (2.3)	82/1049 (7.8)
RC2	5848/22182 (26.4)	31/5848 (0.5)	107/5848 (1.8)
RC3	1969/22182 (8.9)	19/1969 (1)	408/1969 (20.7)
RC4	2328/22182 (10.5)	3/2328 (0.1)	11/2328 (0.5)
RC5	565/22182 (2.5)	4/565 (0.7)	32/565 (5.7)
RC6	1607/22182 (7.2)	114/1607 (7.1)	295/1607 (18.4)
RC7	214/22182 (1)	3/214 (1.4)	11/214 (5.1)
RC8	0/22182 (0)	*0/0 (-)	*0/0 (-)
RC9	700/22182 (3.2)	1/700 (0.1)	3/700 (0.4)
RC10	1058/22182 (4.8)	26/1058 (2.5)	74/1058 (7)
RC11	0/22182 (0)	*0/0 (-)	*0/0 (-)
RC12	388/22182 (1.7)	*0/0 (-)	23/388 (5.9)
RC13	189/22182 (0.9)	1/189 (0.5)	1/189 (0.5)

RC14	545/22182 (2.5)	6/545 (1.1)	31/545 (5.7)
RC15	0/22182 (0)	*0/0 (-)	*0/0 (-)
RC16	155/22182 (0.7)	*0/0 (-)	2/155 (1.3)
RC17	432/22182 (1.9)	*0/0 (-)	4/432 (0.9)
RC18	0/22182 (0)	*0/0 (-)	*0/0 (-)
RC19	0/22182 (0)	*0/0 (-)	*0/0 (-)
RC20	545/22182 (2.5)	6/545 (1.1)	14/545 (2.6)
RC21	299/22182 (1.3)	2/299 (0.7)	*0/0 (-)
Total National	22182	240/22182 (1.1)	1098/22182 (4.9)

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

	Total	OPD	Ward	ICU
Total Typhoidal Salmonella	1338/ 22182 (6.03%)	841/ 4125 (20.38%)	456/ 11443 (3.98%)	41/ 6614 (0.62%)
<i>Salmonella Typhi</i>	1098/ 22182 (4.95%)	679 / 4125 (16.46%)	382 / 11443 (3.34%)	37/ 6614 (0.56%)
<i>Salmonella Paratyphi A</i>	240/ 22182 (1.08%)	162 / 4125 (3.93%)	74 / 11443 (0.65%)	4 / 6614 (0.06%)

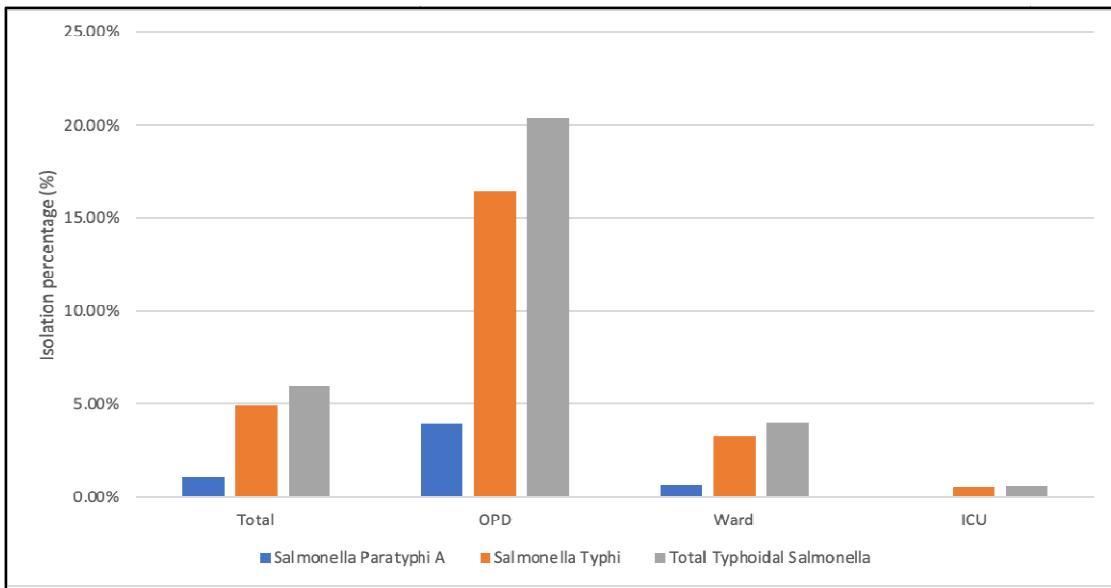


Figure 1.6: Location-wise Isolation pattern of Typhoidal Salmonella isolated from blood across OPD, Ward and ICU

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

Years	2017	2018	2019	2020	2021	2022	2023
	(%)	(%)	(%)	(%)	(%)	(%)	(%)
North	138/4272 (3.2%)	246/5248 (4.7%)	174/4533 (3.8%)	47/3479 (1.4%)	126/6498 (1.9%)	298/12206 (2.4%)	498/12083 (4%)
Central	0/0* (-)	12/110 (10.9%)	36/570 (6.3%)	14/448 (3.1%)	12/584 (2.1%)	51/882 (5.7%)	23/785 (2.9%)
East	0/171* (0%)	2/712 (0.3%)	4/1443 (0.3%)	1/935 (0.1%)	1/1746 (0.1%)	3/1568 (0.2%)	2/1147 (0.2%)
West	31/648 (4.8%)	116/2011 (5.8%)	164/2761 (5.9%)	41/2041 (2%)	41/2973 (1.4%)	61/3302 (1.8%)	47/1835 (2.6%)
South	176/4400 (4%)	204/6018 (3.4%)	350/8033 (4.4%)	103/6206 (1.7%)	113/7187 (1.6%)	171/6280 (2.7%)	528/6332 (8.3%)
National	345/9491 (3.6%)	580/14099 (4.1%)	728/17340 (4.2%)	206/13109 (1.6%)	293/18988 (1.5%)	584 / 24238 (2.41%)	1098/22182 (4.9%)

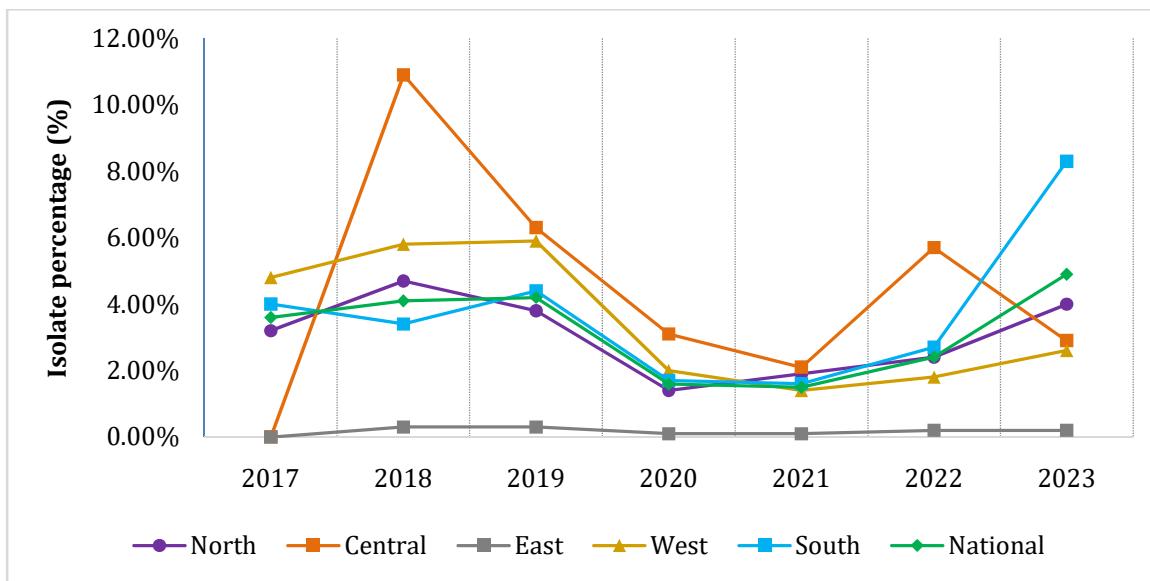


Figure 1.7: Yearly-isolation trends of *Salmonella Typhi* from blood across different regions

Non-fermenting Gram-negative bacteria

Non-fermenting Gram-negative bacteria (NFGNB) constituted 25.0% of the total isolates (26,352 out of 99492) (Table 1.1). Among the NFGNB, *Acinetobacter baumannii* (12.0%) was the commonest isolate followed by *Pseudomonas aeruginosa* (11.8%), *Stenotrophomonas maltophilia* and *Burkholderia cepacia* accounted for 1.0% and 0.2% of all isolates respectively. *Acinetobacter baumannii* was the predominant isolate from LRT (31.1%) and CSF (28.2%) followed by SS (11.2%) and blood (9.6%). *Pseudomonas aeruginosa* was grossly predominant in LRT (22.7%) followed by deep infections (12.5%), superficial infection (15.5%), and others (14.1%) (**Table 1.10**).

Regional center (RC) wise distribution showed that RC 11 had higher percentage isolate rate of *Acinetobacter baumannii* and RC 3 had higher percentage isolate rate of *Pseudomonas aeruginosa* than the rest of RCs (**Table 1.11**).

Table 1.10: Specimen-wise distribution of NFGNB

Isolate	Culture positive																			
	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773		Others n=8581	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
NFGNB	24894 (25)	100	3767 (17)	15.1	1565 (7.8)	6.3	10035 (56.1)	40.3	5020 (25.9)	20.2	1536 (22.5)	6.2	327 (37.5)	1.3	636 (21.4)	2.6	0 (0)	0	2008 (23.4)	8.1
<i>Acinetobacter baumannii</i>	11948 (12)	100	2130 (9.6)	17.8	356 (1.8)	3	5576 (31.1)	46.7	1914 (9.9)	16	646 (9.5)	5.4	246 (28.2)	2.1	333 (11.2)	2.8	0 (0)	0	747 (8.7)	6.3
<i>Pseudomonas aeruginosa</i>	11757 (11.8)	100	1124 (5.1)	9.6	1184 (5.9)	10.1	4062 (22.7)	34.5	3009 (15.5)	25.6	855 (12.5)	7.3	66 (7.6)	0.6	247 (8.3)	2.1	0 (0)	0	1210 (14.1)	10.3
<i>Stenotrophomonas maltophilia</i>	1011 (1)	100	390 (1.8)	38.6	20 (0.1)	2	358 (2)	35.4	92 (0.5)	9.1	35 (0.5)	3.5	14 (1.6)	1.4	52 (1.8)	5.1	0 (0)	0	50 (0.6)	4.9
<i>Burkholderia cepacia</i> complex	178 (0.2)	100	123 (0.6)	69.1	5 (0)	2.8	39 (0.2)	21.9	5 (0)	2.8	0 (0)	0	1 (0.1)	0.6	4 (0.1)	2.2	0 (0)	0	1 (0)	0.6

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

Regional Centre	Total Isolates	<i>Pseudomonas aeruginosa</i>	<i>Acinetobacter baumannii</i>	<i>Stenotrophomonas maltophilia</i>	<i>Burkholderia cepacia</i>
	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	4335 (4.4)	653/4335 (15.1)	555/4335 (12.8)	130/4335 (3)	*0/0 (-)
RC2	17084 (17.3)	1786/17084 (10.5)	3051/17084 (17.9)	291/17084 (1.7)	19/17084 (0.1)
RC3	4317 (4.4)	983/4317 (22.8)	626/4317 (14.5)	*0/0 (-)	*0/0 (-)
RC4	17183 (17.4)	2122/17183 (12.3)	1877/17183 (10.9)	250/17183 (1.5)	124/17183 (0.7)
RC5	2702 (2.7)	291/2702 (10.8)	67/2702 (2.5)	42/2702 (1.6)	6/2702 (0.2)
RC6	5475 (5.5)	723/5475 (13.2)	360/5475 (6.6)	89/5475 (1.6)	26/5475 (0.5)
RC7	1572 (1.6)	191/1572 (12.2)	95/1572 (6)	9/1572 (0.6)	1/1572 (0.1)
RC8	3057 (3.1)	428/3057 (14)	157/3057 (5.1)	34/3057 (1.1)	*0/0 (-)
RC9	3623 (3.7)	425/3623 (11.7)	536/3623 (14.8)	4/3623 (0.1)	*0/0 (-)
RC10	6686 (6.8)	708/6686 (10.6)	319/6686 (4.8)	41/6686 (0.6)	*0/0 (-)
RC11	2894 (2.9)	614/2894 (21.2)	754/2894 (26.1)	14/2894 (0.5)	*0/0 (-)
RC12	1917 (1.9)	285/1917 (14.9)	29/1917 (1.5)	3/1917 (0.2)	*0/0 (-)

RC13	945 (1.0)	99/945 (10.5)	160/945 (16.9)	4/945 (0.4)	*0/0 (-)
RC14	3501 (3.5)	317/3501 (9.1)	73/3501 (2.1)	*0/0 (-)	*0/0 (-)
RC15	1679 (1.7)	207/1679 (12.3)	287/1679 (17.1)	*0/0 (-)	*0/0 (-)
RC16	5179 (5.2)	344/5179 (6.6)	355/5179 (6.9)	*0/0 (-)	*0/0 (-)
RC17	1266 (1.3)	77/1266 (6.1)	135/1266 (10.7)	*0/0 (-)	*0/0 (-)
RC18	491 (0.5)	36/491 (7.3)	92/491 (18.7)	6/491 (1.2)	*0/0 (-)
RC19	10107 (10.2)	1011/10107 (10)	1819/10107 (18)	62/10107 (0.6)	*0/0 (-)
RC20	3600 (3.6)	345/3600 (9.6)	543/3600 (15.1)	*0/0 (-)	*0/0 (-)
RC21	1108 (1.1)	112/1108 (10.1)	58/1108 (5.2)	30/1108 (2.7)	2/1108 (0.2)
Total National	98719	11757/98719 (11.9)	11949/98719 (12.1)	1011/98719 (1)	178/98719 (0.2)

Among clinical settings, *A. baumannii* was predominant in ICU (23.7%), followed by ward (11.8%) and OPD (4.4%) respectively, while *P. aeruginosa* was predominantly isolated in all ward, ICU and OPD (11.4-12.0%) (**Table 1.12a and Figure 1.8**).

The trend analysis over the years 2017 – 2023 has shown an increasing isolation rates for *A. baumannii* from 7.7% to 12.0%. In contrast, isolation rates for *P. Aeruginosa* were found to be stable at 12.4% from 2017 to 2022, which decreased to 11.8% in 2023 (**Table 1.12b**). In case of *S. maltophilia*, no significant changes in the isolation rates of other pathogens such as *B. Cepacia* and *S. maltophilia* have been noted (**Figure 1.9**).

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

Organism	Total	OPD	Ward	ICU
<i>Acinetobacter baumannii</i>	11947 / 99492 (12.01%)	1260 / 28830 (4.37%)	6086 / 51279 (11.87%)	4601 / 19383 (23.74%)
<i>Pseudomonas aeruginosa</i>	11757 / 99492 (11.82%)	3477 / 28830 (12.06%)	6062 / 51279 (11.82%)	2218 / 19383 (11.44%)
<i>Stenotrophomonas maltophilia</i>	1011 / 99492 (1.02%)	163 / 28830 (0.57%)	537 / 51279 (1.05%)	311 / 19383 (1.6%)
<i>Burkholderiacepacia complex</i>	178 / 99492 (0.18%)	22 / 28830 (0.08%)	86 / 51279 (0.17%)	70 / 19383 (0.36%)

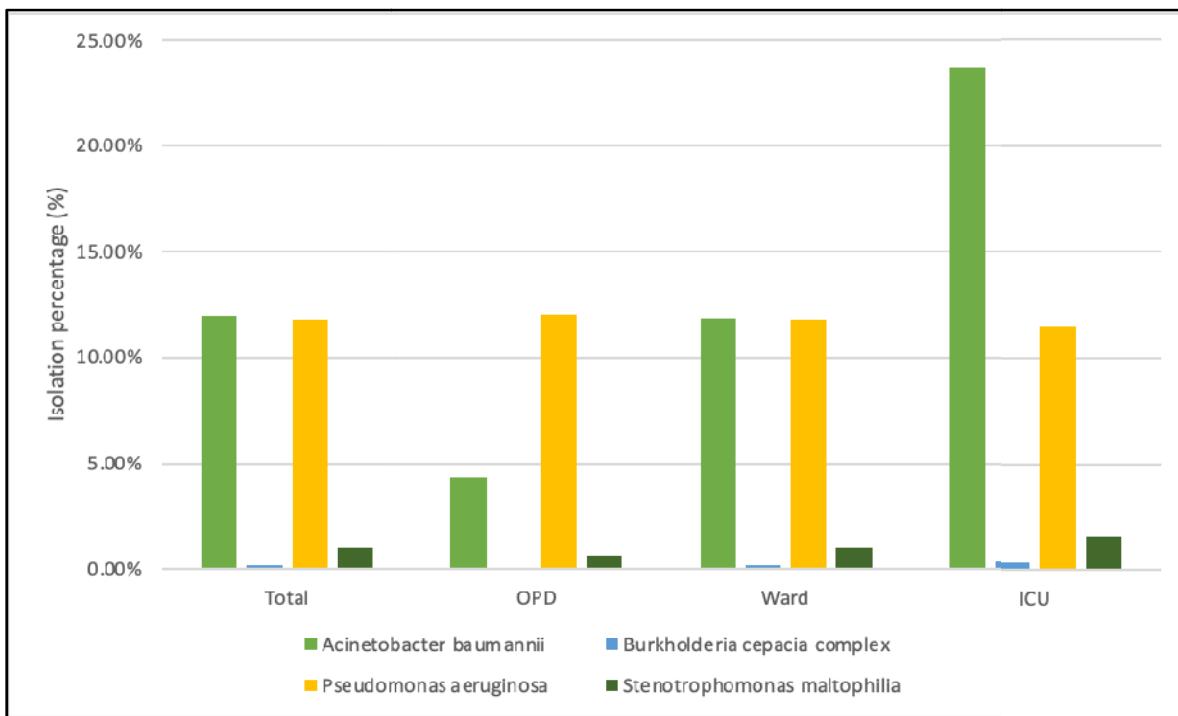


Figure 1.8: Location-wise isolation pattern of *A. baumannii*, *B. cepacia*, *P. aeruginosa*, and *S. maltophilia* isolated from all samples

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

Organism	Year-2017 (%)	Year-2018 (%)	Year-2019 (%)	Year-2020 (%)	Year-2021 (%)	Year-2022 (%)	Year-2023 (%)
<i>Acinetobacter baumannii</i>	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(%)
<i>Pseudomonas aeruginosa</i>	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(%)
<i>Stenotrophomonas maltophilia</i>	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(%)
<i>Burkholderia cepacia complex</i>	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(%)

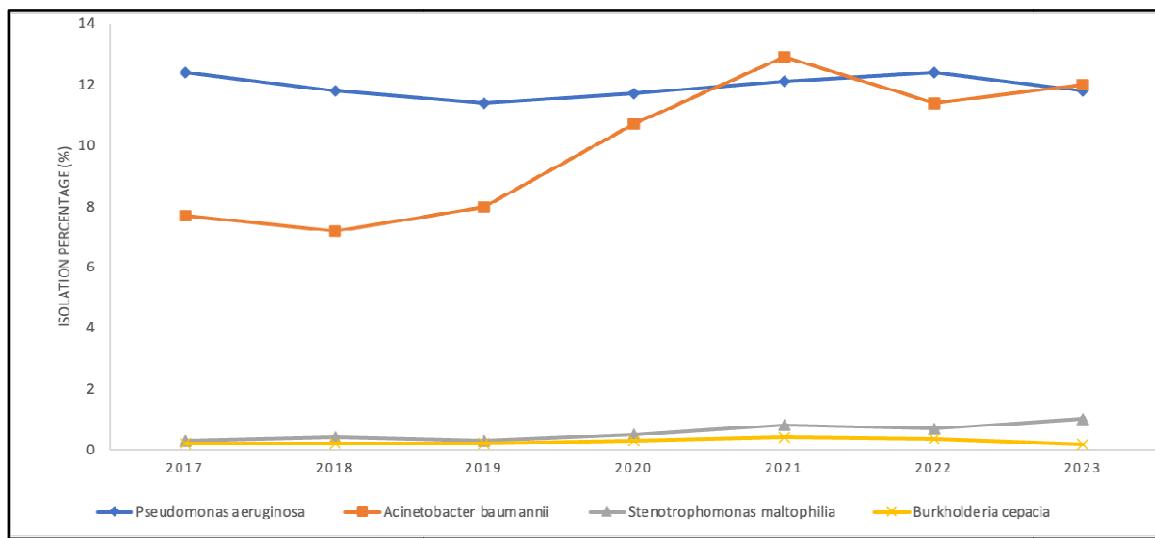


Figure 1.9: Yearly isolation trend of *P. aeruginosa*, *A. baumannii*, *S. maltophilia* and *B. cepacia* isolated from all samples

Staphylococci

Staphylococci constituted 15.8% of the total isolates (**Table 1.13**). *Staphylococcus aureus* was the predominant species in the superficial infections (20.4%) followed by deep infections (19.5%), others (10.8%), blood (6.6%) sterile body fluids (5.3%), LRT (4.5) and urine (1.1%) (**Table 1.13**). Coagulase-negative staphylococci (CoNS) were the predominant isolates in blood (25.6%) and CSF (11.6%) reflecting the high incidence of shunt infections and intra vascular device associated infections respectively. In blood and CSF, *Staphylococcus epidermidis* isolation rate was 7.5% and 3.6% 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 the deep infection (DI) 10.9% followed by isolation from superficial infections (SI) 9.5%, and 3.5% from blood. Methicillin sensitive *Staphylococcus aureus* (MSSA) were the predominant isolates from the superficial infection (SI) 11.0% followed by isolation from Deep infections (DI) (8.3%), 5.8% and 3.1% from others and blood respectively (**Figure 1.10**). Amongst the coagulase-negative staphylococci (CoNS), *S. haemolyticus* (32.8%) were the commonest species followed by *S. epidermidis* (29.8%) and *S. hominis* (20.4%) (**Table 1.13**).

Regional centre wise distribution showed the predominance of isolation of *Staphylococcus aureus* in RC14 (20.1%) with MRSA percentage isolation (7.7%). The least percentage isolation of *Staphylococcus aureus* and MRSA was found among RC 19 i.e., 2.8% and 1.6% respectively (**Table 1.14**).

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

Isolate	Culture positive																			
	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773		Others n=8581	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
No. culture positive	99492 (100)	100	22182 (100)	22.3	20026 (100)	20.1	17902 (100)	18	19360 (100)	19.5	6826 (100)	6.9	873 (100)	0.9	2969 (100)	3	773 (100)	0.8	8581 (100)	8.6
Total Staphylococcus	15795 (15.9)	100	7144 (32.2)	45.2	298 (1.5)	1.9	933 (5.2)	5.	4471 (23.1)	28.3	1458 (21.4)	9.2	137 (15.7)	0.9	228 (7.7)	1.4	0 (0)	0	1125 (13.1)	7.1
<i>Staphylococcus aureus</i>	8900 (8.9)	100	1472 (6.6)	16.5	221 (1.1)	2.5	803 (4.5)	9	3956 (20.4)	44.4	1330 (19.5)	14.9	36 (4.1)	0.4	158 (5.3)	1.8	0 (0)	0	923 (10.8)	10.4
MSSA	4539 (4.6)	100	699 (3.1)	15.4	128 (0.6)	2.8	424 (2.4)	9.	2117 (11.0)	46.6	565 (8.3)	12.4	19 (2.2)	0.4	86 (2.9)	1.9	0 (0)	0	501 (5.8)	11.0
MRSA	4311 (4.3)	100	773 (3.5)	17.9	93 (0.5)	2.2	371 (2.1)	8.	1833 (9.5)	42.5	743 (10.9)	17.2	17 (1.9)	0.4	72 (2.4)	1.7	0 (0)	0	408 (4.7)	9.5
CoNS	6895 (6.9)	100	5672 (25.6)	82.3	77 (0.4)	1.1	130 (0.7)	1.	515 (2.7)	7.5	128 (1.9)	1.9	101 (11.6)	1.5	70 (2.4)	1	0 (0)	0	202 (2.4)	2.9
<i>Staphylococcus haemolyticus</i>	2262 (2.3)	100	1907 (8.6)	84.3	26 (0.1)	1.1	20 (0.1)	0.	182 (0.9)	8	20 (0.3)	0.9	36 (4.1)	1.6	16 (0.5)	0.7	0 (0)	0	55 (0.6)	2.4
<i>Staphylococcus epidermidis</i>	2056 (2.1)	100	1657 (7.5)	80.6	12 (0.1)	0.6	9 (0.1)	0.	188 (1)	9.1	60 (0.9)	2.9	31 (3.6)	1.5	11 (0.4)	0.5	0 (0)	0	88 (1)	4.3
<i>Staphylococcus hominis</i>	1408 (1.4)	100	1275 (5.7)	90.6	6 (0)	0.4	6 (0)	0.	65 (0.3)	4.6	7 (0.1)	0.5	14 (1.6)	1	5 (0.2)	0.4	0 (0)	0	30 (0.3)	2.1
<i>Staphylococcus spp.</i>	1010 (1)	100	734 (3.3)	72.7	17 (0.1)	1.7	95 (0.5)	9.	53 (0.3)	5.2	32 (0.5)	3.2	17 (1.9)	1.7	36 (1.2)	3.6	0 (0)	0	26 (0.3)	2.6

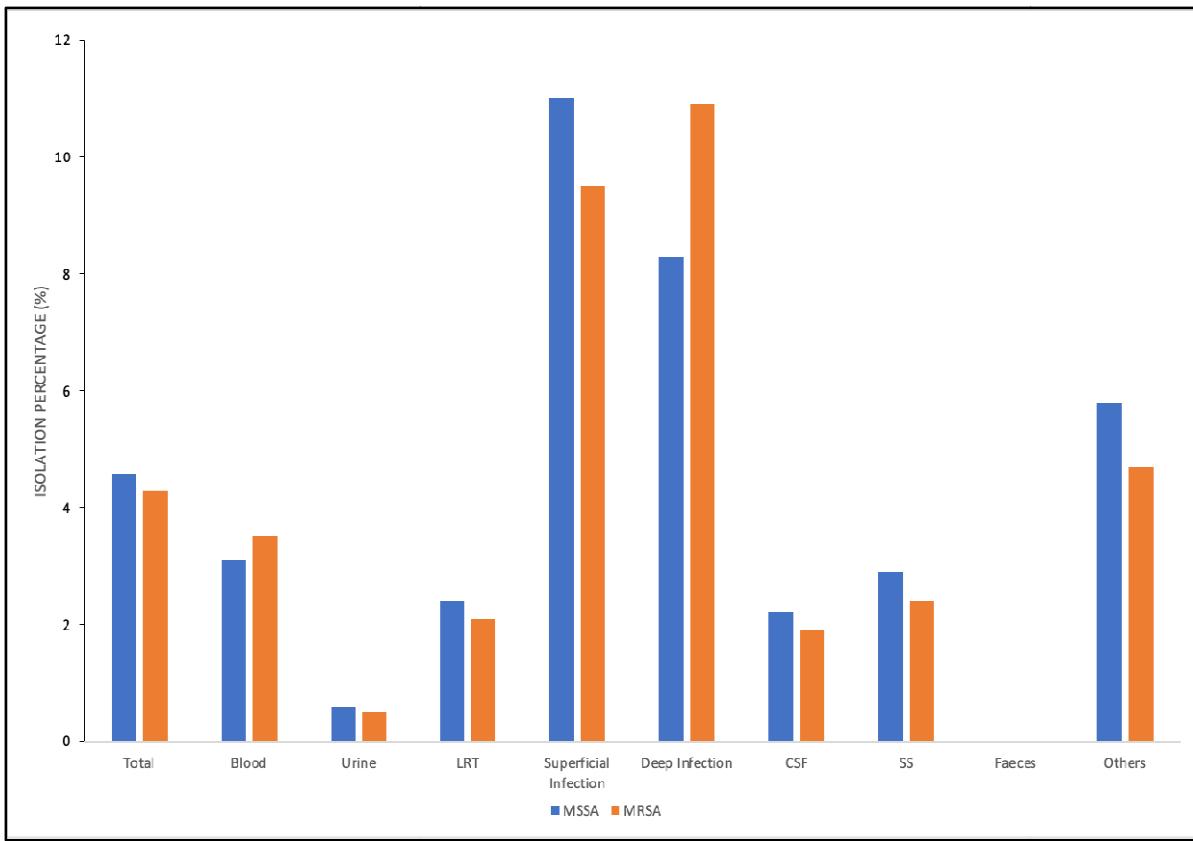


Figure 1.10: Specimen wise relative distributions of MSSA and MRSA

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

Regional Centre	Total Isolates	<i>S. aureus</i>	MRSA	MSSA	<i>S.haemolyticus</i>	<i>S.epidermidis</i>	<i>Staphylococcus hominis</i>	<i>S.lugdunensis</i>	<i>S.saprophyticus</i>	<i>Staphylococcus spp.</i>
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	4335 (4.4)	347/4335 (8)	223/4335 (5.1)	124/4335 (2.9)	156/4335 (3.6)	116/4335 (2.7)	111/4335 (2.6)	*0/0 (-)	*0/0 (-)	11/4335 (0.3)
RC2	17084 (17.3)	1693/17084 (9.9)	1120/17084 (6.6)	573/17084 (3.4)	750/17084 (4.4)	979/17084 (5.7)	580/17084 (3.4)	*0/0 (-)	*0/0 (-)	768/17084 (4.5)
RC3	4317 (4.4)	338/4317 (7.8)	149/4326 (3.4)	189/4326 (4.4)	47/4317 (1.1)	41/4317 (0.9)	46/4317 (1.1)	*0/0 (-)	*0/0 (-)	57/4317 (1.3)
RC4	17183 (17.4)	2134/17183 (12.4)	575/17183 (3.3)	1559/17183 (9.1)	137/17183 (0.8)	134/17183 (0.8)	24/17183 (0.1)	*0/0 (-)	10/17183 (0.1)	20/17183 (0.1)
RC5	2702 (2.7)	239/2702 (8.8)	99/2702 (3.7)	140/2702 (5.2)	11/2702 (0.4)	63/2702 (2.3)	27/2702 (1)	13/2702 (0.5)	4/2702 (0.1)	28/2702 (1)
RC6	5475 (5.5)	346/5475 (6.3)	200/5475 (3.7)	146/5475 (2.7)	88/5475 (1.6)	83/5475 (1.5)	21/5475 (0.4)	8/5475 (0.1)	9/5475 (0.2)	11/5475 (0.2)
RC7	1572 (1.6)	93/1572 (5.9)	49/1572 (3.1)	44/1572 (2.8)	21/1572 (1.3)	26/1572 (1.7)	5/1572 (0.3)	1/1572 (0.1)	1/1572 (0.1)	4/1572 (0.3)
RC8	3057 (3.1)	268/3057 (8.8)	93/3057 (3)	175/3057 (5.7)	8/3057 (0.3)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC9	3623 (3.7)	323/3623 (8.9)	165/3623 (4.6)	158/3623 (4.4)	*0/0 (-)	*0/0 (-)	*0/0 (-)	90/3623 (2.5)	*0/0 (-)	*0/0 (-)
RC10	6686 (6.8)	448/6686 (6.7)	141/6686 (2.1)	307/6712 (4.6)	9/6686 (0.1)	19/6686 (0.3)	6/6686 (0.1)	7/6686 (0.1)	*0/0 (-)	4/6686 (0.1)
RC11	2894 (2.9)	234/2894 (8.1)	172/2894 (5.9)	62/2894 (2.1)	5/2894 (0.2)	3/2894 (0.1)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC12	1917 (1.9)	214/1917 (11.2)	120/1917 (6.3)	94/1917 (4.9)	15/1917 (0.8)	8/1917 (0.4)	9/1917 (0.5)	1/1917 (0.1)	*0/0 (-)	*0/0 (-)
RC13	945 (1.0)	81/945 (8.6)	50/945 (5.3)	27/945 (2.9)	20/945 (2.1)	26/945 (2.8)	11/945 (1.2)	*0/0 (-)	*0/0 (-)	1/945 (0.1)
RC14	3501 (3.5)	702/3501 (20.1)	270/3501 (7.7)	432/3501 (12.3)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC15	1679 (1.7)	251/1679 (14.9)	141/1679 (8.4)	110/1679 (6.6)	16/1679 (1)	1/1679 (0.1)	7/1679 (0.4)	*0/0 (-)	*0/0 (-)	5/1679 (0.3)
RC16	5179 (5.2)	622/5179 (12)	456/5179 (8.8)	166/5179 (3.2)	*0/0 (-)	7/5179 (0.1)	3/5179 (0.1)	*0/0 (-)	*0/0 (-)	80/5179 (1.5)

RC17	1266 (1.3)	109/1266 (8.6)	51/1269 (4)	58/1269 (4.6)	8/1266 (0.6)	1/1266 (0.1)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC18	491 (0.5)	*0/0 (-)	0 (0)	0 (0)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)	*0/0 (-)
RC19	10107 (10.2)	281/10107 (2.8)	162/10107 (1.6)	119/10107 (1.2)	908/10107 (9)	459/10107 (4.5)	463/10107 (4.6)	*0/0 (-)	*0/0 (-)	6/10107 (0.1)
RC20	3600 (3.6)	106/3600 (2.9)	44/3600 (1.2)	16/3600 (0.4)	34/3600 (0.9)	69/3600 (1.9)	91/3600 (2.5)	*0/0 (-)	3/3600 (0.1)	8/3600 (0.2)
RC21	1108 (1.1)	71/1108 (6.4)	31/1108 (2.8)	40/1108 (3.6)	27/1108 (2.4)	20/1108 (1.8)	2/1108 (0.2)	*0/0 (-)	1/1108 (0.1)	6/1108 (0.5)
Total National	98719	8900/98719 (9)	4311/98719 (4.4)	4539/98719 (4.6)	2262/98719 (2.3)	2056/98719 (2.1)	1408/98719 (1.4)	130/98719 (0.1)	*0/0 (-)	1010/98719 (1)

Among clinical settings, *Staphylococcus aureus* was predominantly isolated in OPD (12.1%), followed by ward (8.9%) and ICU (4.1%), while the coagulase-negative staphylococci (CoNS) was predominant both in ICU (8.5%) and ward (7.9%) then OPD (5.6%) (**Table 1.15 and Figure 1.11**).

Trend analysis over the years 2017 – 2023 have shown a steady decline in the isolation rates of *Staphylococcus aureus* from 12.5% to 8.9% in 2017 to 2023 respectively (**Table 1.16 and Figure 1.12**).

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

Organism	Total	OPD	Ward	ICU
Total staphylococci	15795 / 99492 (15.88%)	5059 / 28830 (17.55%)	8383 / 51279 (16.35%)	2353 / 19383 (12.14%)
<i>Staphylococcus aureus</i>	8900/99492 (8.9)	3504/28830 (12.1)	4597/51279 (8.9)	799/19383 (4.1)
MSSA	4539/99492 (4.6)	2003/28830 (6.9)	2148/51279 (4.2)	388/19383 (2)
MRSA	4311/99492 (4.3)	1478/28830 (5.1)	2427/51279 (4.7)	406/19383 (2.1)
CoNS	7314/99492 (7.3)	1608/28830 (5.6)	4050/51279 (7.9)	1656/19383 (8.5)

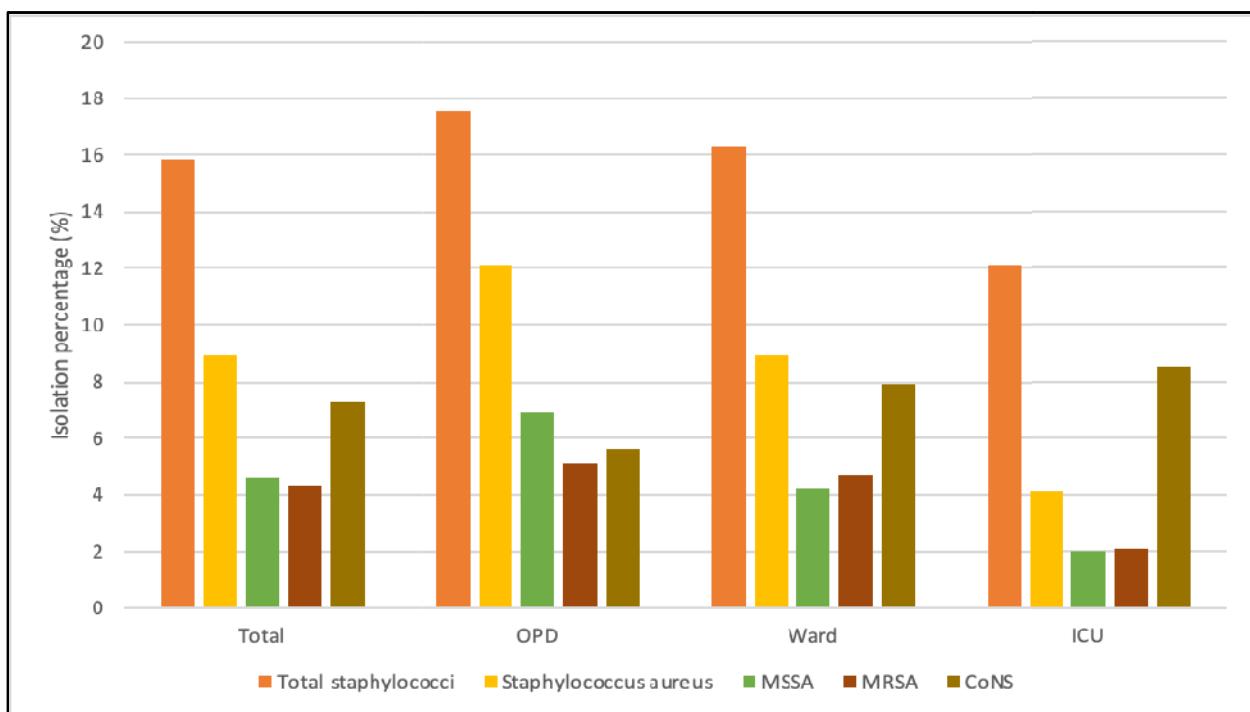


Figure 1.11: Location-wise isolation pattern of *Staphylococcus aureus*, CoNS, MRSA, MSSA isolated from all samples

Table 1.16: Yearly isolation trend of *Staphylococcus* species

Bacteria	Year-2017 (%)	Year-2018 (%)	Year-2019 (%)	Year-2020 (%)	Year-2021 (%)	Year-2022 (%)	Year-2023 (%)
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 (15.88%)
<i>S. aureus</i>	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)
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)
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)
<i>CoNS</i>	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)
<i>S. haemolyticus</i>	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)
<i>S. epidermidis</i>	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)
<i>S. hominis</i>	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)
<i>Staphylococcus spp.</i>	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)

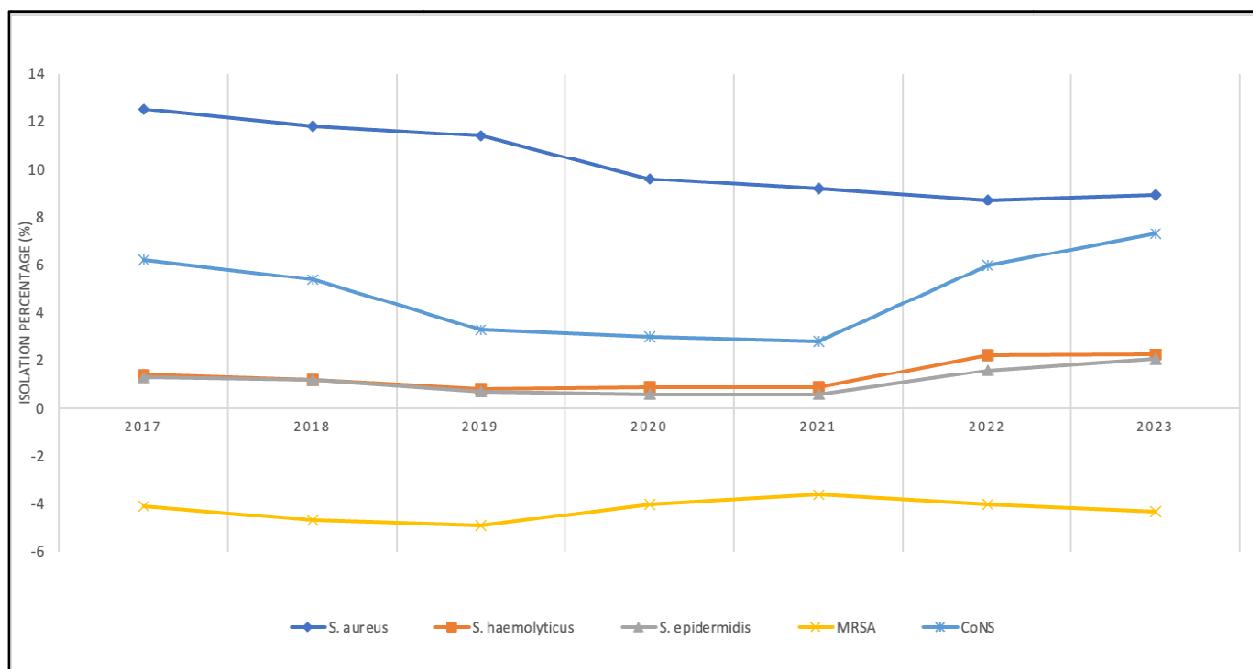


Figure 1.12: Yearly isolation trends of *Staphylococcus* species

Enterococci

Enterococci constituted overall 7.0% of all the isolates (**Table 1.17**). Among the *Enterococcus* species, *E. faecalis* and *E. faecium* accounted for 88.6% of all the total isolates, both *E. faecalis* (49.4%) and *E. faecium* (39.2%) were the predominant species. *E. faecalis* was more frequent in the urine (8.0%) and SI (3.4%) while *E. faecium* was relatively more frequent in the SS (5.5%) and urine (4.7 %) (**Table 1.17 and Figure 1.13**). Among clinical settings, *E. faecalis* was predominantly isolated in OPD (4.4%), followed by ward (3.1%) and ICU (2.8%), while *E. faecium* was predominant in ICU (3.3%) and ward (3.1) and then OPD (1.6%) (**Table 1.18**) Regional centre wise distribution showed the predominance of isolation of *E. faecalis* in RC10 (7.3%) and *E. faecium* in RC18 (8.6%) (**Table 1.19**). The trend analysis over the years have shown a stable trend in the isolation rates of *E. faecium* from 2.0% to 2.7% in 2017 to 2023 and in *E. faecalis* from 2.2% to 3.5% in 2017 to 2023 respectively (**Table 1.20 and Figure 1.14**).

Table 1.17: Specimen wise distribution of *Enterococcus* species

	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773		
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	
Enterococci	6992 (7)	100	1437 (6.5)	20.6	2673 (13.3)	38.	101 (0.6)	1.4	1166 (6)	16.7	399 (5.8)	5.7	75 (8.6)	1.1	366 (12.3)	5.2	0 (0)	0	0
<i>Enterococcus faecalis</i>	3461 (3.5)	100	545 (2.5)	15.7	1595	46.	51 (0.3)	1.5	650 (3.4)	18.8	153 (2.2)	4.4	29 (3.3)	0.8	105 (3.5)	3	0 (0)	0	0
<i>Enterococcus faecium</i>	2746 (2.8)	100	731 (3.3)	26.6	942	34.	24 (0.1)	0.9	377 (1.9)	13.7	159 (2.3)	5.8	33 (3.8)	1.2	163 (5.5)	5.9	0 (0)	0	0
<i>Enterococcus spp.</i>	785 (0.8)	100	161 (0.7)	20.5	136	17.	26 (0.1)	3.3	139 (0.7)	17.7	87 (1.3)	11.	13 (1.5)	1.7	98 (3.3)	12.	0 (0)	0	0

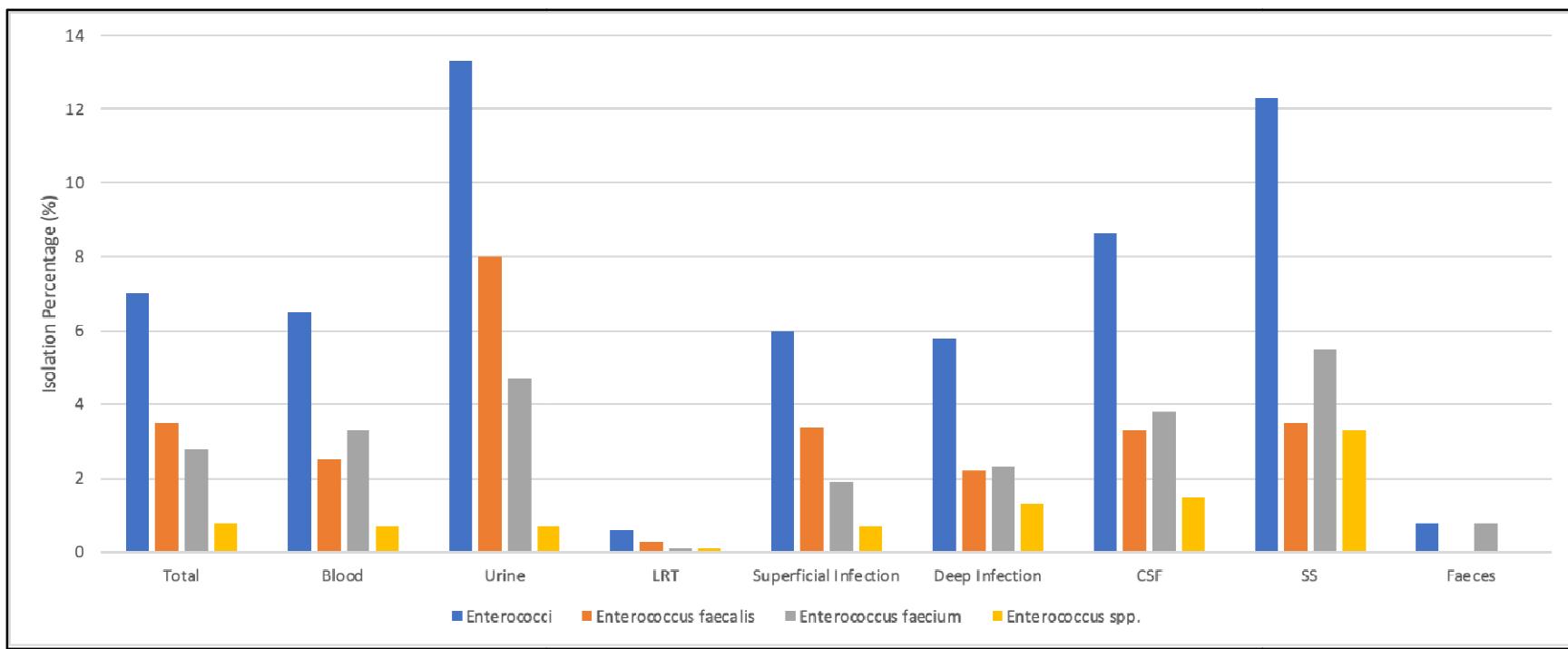


Figure 1.13: Specimen wise distribution of *Enterococcus* species

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

Organism	Total	OPD	Ward	ICU
<i>Enterococcus faecalis</i>	3461 / 99492 (3.48%)	1272 / 28830 (4.41%)	1633 / 51279 (3.18%)	556 / 19383 (2.87%)
<i>Enterococcus faecium</i>	2746 / 99492 (2.76%)	460 / 28830 (1.6%)	1631 / 51279 (3.18%)	655 / 19383 (3.38%)
<i>Enterococcus</i> spp.	785 / 99492 (0.79%)	160 / 28830 (0.55%)	506 / 51279 (0.99%)	119 / 19383 (0.61%)

Table 1.19: Isolates percentages across Regional Centres of *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus* spp. from All Specimen (Except faeces)

Regional Centre	Total Isolates n(%)	<i>Enterococcus faecalis</i> n(%)	<i>Enterococcus faecium</i> n(%)	<i>Enterococcus</i> spp. n(%)
RC1	4335 (4.4)	74/4335 (1.7)	179/4335 (4.1)	7/4335 (0.2)
RC2	17084 (17.3)	117/17084 (0.7)	423/17084 (2.5)	272/17084 (1.6)
RC3	4317 (4.4)	54/4317 (1.3)	53/4317 (1.2)	81/4317 (1.9)
RC4	17183 (17.4)	833/17183 (4.8)	538/17183 (3.1)	113/17183 (0.7)
RC5	2702 (2.7)	54/2701 (2)	64/2701 (2.4)	18/2701 (0.7)
RC6	5475 (5.5)	100/5475 (1.8)	242/5475 (4.4)	17/5475 (0.3)
RC7	1572 (1.6)	68/1572 (4.3)	55/1572 (3.5)	6/1572 (0.4)
RC8	3057 (3.1)	59/3057 (1.9)	88/3057 (2.9)	35/3057 (1.1)
RC9	3623 (3.7)	180/3623 (5)	74/3623 (2)	*0/0 (-)
RC10	6686 (6.8)	489/6686 (7.3)	245/6686 (3.7)	58/6686 (0.9)
RC11	2894 (2.9)	22/2894 (0.8)	45/2894 (1.6)	*0/0 (-)
RC12	1917 (1.9)	44/1917 (2.3)	77/1917 (4)	*0/0 (-)
RC13	945 (1.0)	43/945 (4.6)	47/945 (5)	1/945 (0.1)
RC14	3501 (3.5)	2/3501 (0.1)	5/3501 (0.1)	*0/0 (-)
RC15	1679 (1.7)	23/1679 (1.4)	32/1679 (1.9)	*0/0 (-)
RC16	5179 (5.2)	269/5179 (5.2)	135/5179 (2.6)	144/5179 (2.8)
RC17	1266 (1.3)	66/1266 (5.2)	20/1266 (1.6)	1/1266 (0.1)
RC18	491 (0.5)	24/491 (4.9)	42/491 (8.6)	*0/0 (-)
RC19	10107 (10.2)	752/10107 (7.4)	166/10107 (1.6)	14/10107 (0.1)
RC20	3600 (3.6)	168/3600 (4.7)	153/3600 (4.3)	13/3600 (0.4)
RC21	1108 (1.1)	20/1108 (1.8)	63/1108 (5.7)	4/1108 (0.4)
Total	98719	3461/98719 (3.5)	2746/98719 (2.8)	785/98719 (0.8)

Table 1.20: Yearly isolation trend of *Enterococcus* species

Bacteria	Year-2017 (%)	Year-2018 (%)	Year-2019 (%)	Year-2020 (%)	Year-2021 (%)	Year-2022 (%)	Year-2023 (%)
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)
<i>Enterococcus faecium</i>	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%)
<i>Enterococcus faecalis</i>	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%)
<i>Enterococcus</i> 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%)

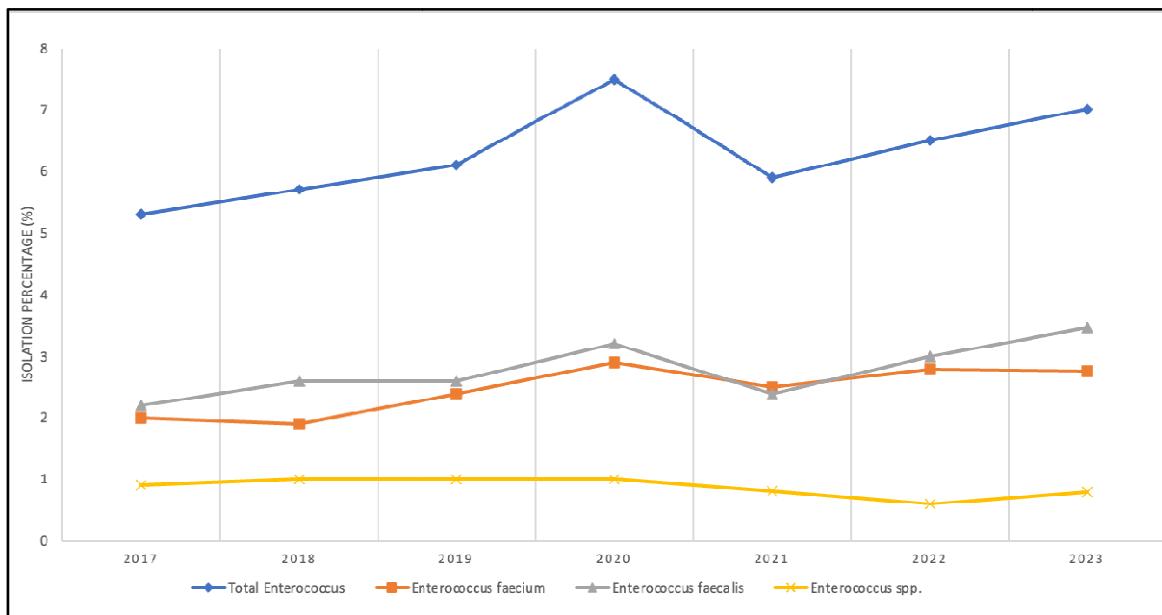


Figure 1.14: Yearly isolation trends of *Enterococcus* species

Fungal species

Total number of yeast isolates studied during the year 2023 was 2792, of those 37.2% (1040) were isolated from blood. Majority of the isolates were from *Candida albicans* (n=746) followed by *Candida tropicalis* (n=706) (**Table 1.21**). In the distribution of fungi species in different specimens, *Candida albicans* was the predominant isolates in the sterile sites (1.6%) followed by CSF (1.0%) and *C. tropicalis* was the predominant isolates in the blood (1.4%) followed by sterile sites (1.1%) (**Table 1.21**). Among clinical settings, in ICUs, *C. tropicalis* and were common isolates from the ICU (1.07%) and *C. albicans* from the ward (0.87%) (**Table 1.22 and Figure 1.15**). Among *Aspergillus* species, *A. flavus* was the predominant isolate followed by *A. fumigatus* (**Table 1.23**).

Yearly isolation trend showed that there is a steady decline in isolation of *C. tropicalis* from 1.4% in 2017 to 0.7% in 2023. Similarly, yearly isolation trend of *Candida albicans* showed a decline from 1.0% in 2017 to 0.7 in 2023. Both *C. auris* and *C. parapsilosis* isolates showed a stable trend from 2017 to 2023 (**Table 1.24 & Figure 1.16**).

Table 1.21: Candida species isolated from different sample types except faeces

Isolate	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773		
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	
Fungal isolates	2792 (2.81)	100	1040 (4.56)	37.2	482 (2.40)	17.3	266 (1.48)	9.5	188 (0.97)	6.7	72 (1.11)	2.6	29 (3.32)	1	146 (4.92)	5.2	0 (0)	0	0
<i>Candida albicans</i>	746 (0.75)	100	171 (0.77)	22.9	136 (0.68)	18.2	16 (0.08)	2.1	53 (0.27)	7.1	18 (0.26)	2.4	9 (1.03)	1.2	48 (1.62)	6.4	0 (0)	0	0
<i>Candida tropicalis</i>	706 (0.71)	100	313 (1.41)	44.3	156 (0.78)	22.1	7 (0.03)	1	79 (0.41)	11. 2	21 (0.31)	3	1 (0.11)	0.1	34 (1.15)	4.8	0 (0)	0	0
<i>Candida glabrata</i>	316 (0.32)	100	115 (0.52)	36.4	74 (0.37)	23.4	0 (0)	0	21 (0.11)	6.6	13 (0.19)	4.1	0 (0)	0	21 (0.71)	6.6	0 (0)	0	0
<i>Candida auris</i>	240 (0.24)	100	154 (0.69)	64.2	56 (0.28)	23.3	0 (0)	0	11 (0.56)	4.6	2 (0.02)	0.8	4 (0.45)	1.7	5 (0.17)	2.1	0 (0)	0	0
<i>Candida parapsilosis</i>	202 (0.20)	100	166 (0.75)	82.2	9 (0.04)	4.5	1 (0)	0.5	2 (0.01)	1	0 (0)	0	2 (0.23)	1	7 (0.24)	3.5	0 (0)	0	0
<i>Candida krusei</i>	63 (0.06)	100	27 (0.12)	42.9	7 (0.03)	11.1	2 (0)	3.2	2 (0.01)	3.2	3 (0.04)	4.8	0 (0)	0	11 (0.37)	17. 5	0 (0)	0	0

<i>Candida kefyr</i>	24 (0.02)	100	5 (0.02)	20.8	6 (0.03)	25	3 (0.02)	12. 5	1 (0)	4.2	2 (0.02)	8.3	0 (0)	0	3 (0.10)	12. 5	0 (0)	0
<i>Candida pelliculosa</i>	23 (0.02)	100	21 (0.09)	91.3	0 (0)	0	0 (0)	0	0 (0)	0	0 (0)	0	1 (0.11)	4.3	0 (0)	0	0 (0)	0
<i>Candida lusitanae</i>	9 (0.01)	-	3 (0.01)	-	1 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	2 (0.06)	-	0 (0)	-
<i>Candida utilis</i>	5 (0.01)	-	4 (0.01)	-	1 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-	0 (0)	-
Candida	2394 (2.41)	100	1022 (4.60)	42.7	453 (2.26)	18.9	29 (0.16)	1.2	172 (0.88)	7.2	59 (0.86)	2.5	17 (1.94)	0.7	135 (4.55)	5.6	0 (0)	0

Notes:

1. Percentages are out of 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. Superficial Infection includes: SST (Skin & Soft Tissue), Pus/exudate, Wound swab, Superficial Biopsy and Superficial Tissue.
6. 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 1.22: Candida species isolated from all samples across OPD, Ward and ICUs

Organism	Total	OPD	Ward	ICU
<i>Candida albicans</i>	746 / 99492 (0.75%) R1	155 / 28830 (0.54%) R1	448 / 51279 (0.87%) R1	143 / 19383 (0.74%) R2
<i>Candida tropicalis</i>	705 / 99492 (0.71%) R2	78 / 28830 (0.27%) R2	419 / 51279 (0.82%) R2	208 / 19383 (1.07%) R1
<i>Candida glabrata</i>	316 / 99492 (0.32%) R3	48 / 28830 (0.17%) R3	202 / 51279 (0.39%) R3	66 / 19383 (0.34%) R4
<i>Candida auris</i>	240 / 99492 (0.24%) R4	29 / 28830 (0.1%) R5	132 / 51279 (0.26%) R4	79 / 19383 (0.41%) R3
<i>Candida parapsilosis</i>	202 / 99492 (0.2%) R5	39 / 28830 (0.14%) R4	106 / 51279 (0.21%) R5	57 / 19383 (0.29%) R5
<i>Candida krusei</i>	62 / 99492 (0.06%) R6	8 / 28830 (0.03%) R6	36 / 51279 (0.07%) R6	18 / 19383 (0.09%) R6
<i>Candida kefyr</i>	24 / 99492 (0.02%) R7	6 / 28830 (0.02%) R7	12 / 51279 (0.02%) R8	6 / 19383 (0.03%) R8
<i>Candida pelliculosa</i>	23 / 99492 (0.02%) R8	1 / 28830 (0%) R9	15 / 51279 (0.03%) R7	7 / 19383 (0.04%) R7
<i>Candida lusitaniae</i>	9 / 99492 (0.01%) R9	2 / 28830 (0.01%) R8	6 / 51279 (0.01%) R9	1 / 19383 (0.01%) R10
<i>Candida utilis</i>	5 / 99492 (0.01%) R10	0 / 28830 (0%) R10	2 / 51279 (0%) R10	3 / 19383 (0.02%) R9

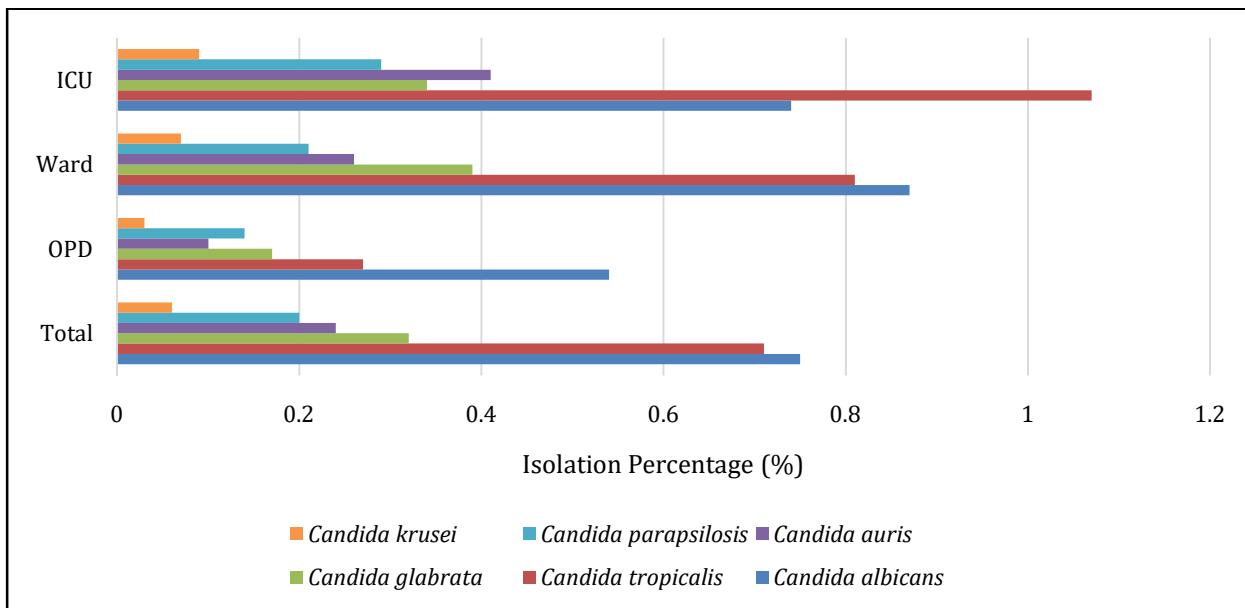


Figure 1.15: Location-wise pattern of *Candida* species isolated from all samples across OPD, Wards and ICUs

Table 1.23: Isolation patterns of *Aspergillus* species from all specimens

Organism	Total n=99492
<i>Aspergillus flavus</i>	250 / 99492 (0.25%)
<i>Aspergillus fumigatus</i>	178 / 99492 (0.17%)
<i>Aspergillus nidulans</i>	2 / 99492 (0%)
<i>Aspergillus niger</i>	22 / 99492 (0.02%)
<i>Aspergillus terreus</i>	17 / 99492 (0.02%)

Table 1.24: Yearly trends for isolation of *Candida* species isolated from all samples

Fungal species	Year-2017 (%)	Year-2018 (%)	Year-2019 (%)	Year-2020 (%)	Year-2021 (%)	Year-2022 (%)	Year-2023 (%)
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)
<i>Candida tropicalis</i>	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)
<i>Candida albicans</i>	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)
<i>Candida glabrata</i>	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)
<i>Candida parapsilosis</i>	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)
<i>Candida auris</i>	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)

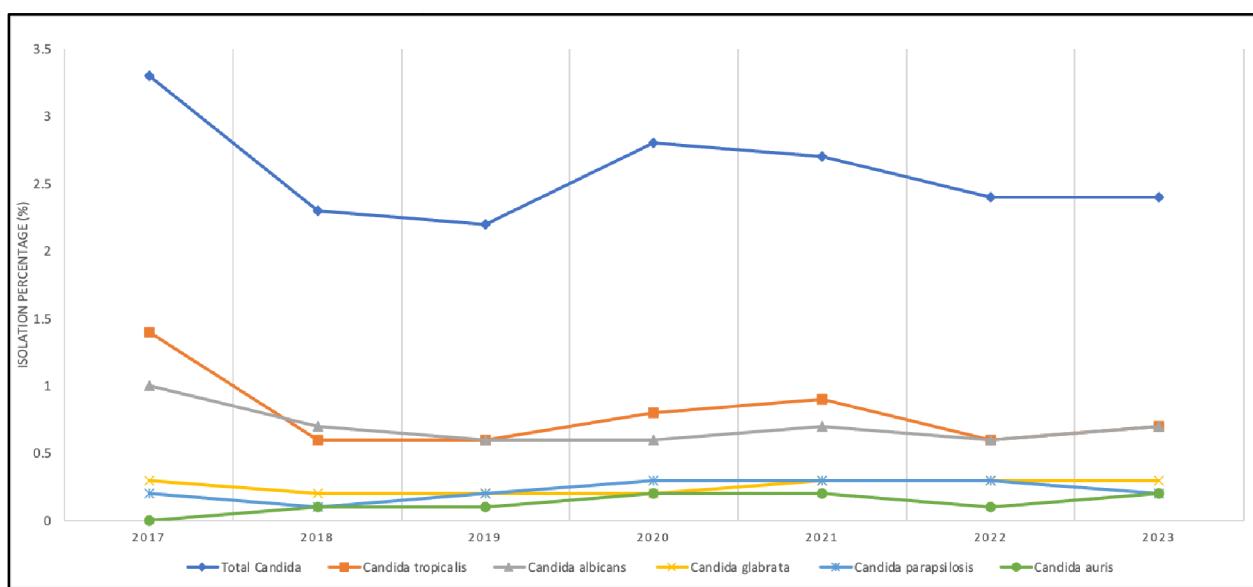


Figure 1.16: Yearly trends for isolation of *Candida* species isolated from all samples

Diarrheal pathogens

A total of 759 diarrheal pathogen isolates were studied during the year 2023 which constituted 0.76% of total isolates (Table 1.1). The predominant species among diarrheal pathogens isolated from faeces sample identified was Non Typhoidal Salmonella (38.9%), followed by *Aeromonas spp* (28.0%), *Escherichia coli Diarrheagenic* (9.9%), *Shigella* (10.1%) and *Vibrio cholerae* (7.2%) (**Table 1.25**). From non-faecal specimens, *Aeromonas spp* was isolated (n=63) and constituted 0.06% of total cultures (**Table 1.26**).

Table 1.25: Isolation rates of faecal isolates from faeces samples

Isolates	% Isolation from faecal isolates (n= 871)	% Isolation from total positive cultures (n=99492)
Non Typhoidal Salmonella	339/871 (38.9%)	339/99492 (0.34%)
Salmonella Typhimurium Faecal	21 / 871 (2.4%)	21 / 99492 (0.02%)
<i>Aeromonas spp.</i>	244 / 871 (28%)	244 / 99492 (0.24%)
<i>Escherichia coli</i> diarrheagenic	86 / 871 (9.9%)	86 / 99492 (0.09%)
<i>Shigella flexneri</i>	50 / 871 (5.7%)	50 / 99492 (0.05%)
<i>Shigella sonnei</i>	34 / 871 (3.9%)	34 / 99492 (0.03%)
<i>Shigella boydii</i>	4 / 871 (0.5%)	4 / 99492 (0%)
<i>Vibrio cholerae</i>	63 / 871 (7.2%)	63 / 99492 (0.06%)
Vibrio spp	5 / 871 (0.6%)	5 / 99492 (0.01%)

Table 1.26: Isolation rates of Diarrheagenic pathogens from non-faecal specimens

Organism	Isolation Percentage from all samples except faeces
<i>Aeromonas spp.</i>	63 / 98719 (0.06%)
<i>Escherichia coli Diarrheagenic</i>	1 / 98719 (0%)
<i>Shigella boydii</i>	0 / 98719 (0%)
<i>Shigella dysenteriae</i>	0 / 98719 (0%)
<i>Shigella flexneri</i>	2 / 98719 (0%)
<i>Shigella sonnei</i>	0 / 98719 (0%)
<i>Shigella spp.</i>	0 / 98719 (0%)
<i>Vibrio cholerae</i>	1 / 98719 (0%)
<i>Vibrio parahaemolyticus</i>	0 / 98719 (0%)
<i>Vibrio spp.</i>	0 / 98719 (0%)

Diarrheagenic pathogens were predominantly isolated from patients in OPD and wards (**Table 1.27**). *Escherichia coli* Diarrheagenic was mainly isolated in OPD (20.2%) followed by ward (5.03%), while the *Aeromonas spp* was predominant in OPD (24.8%) followed by ward (22.5%), and ICU (20%) (**Table 1.27 and Figure 1.17**). *Shigella flexneri* was predominant in OPD and *Vibrio cholerae* in ward. The isolation trend over the period of seven years (2017– 2023) showed a decreasing trend in the isolation of *Aeromonas spp.* from 2017 to 2022 but showed a slight increase in isolation rate in 2023 whereas, the isolation trend of Non Typhoidal Salmonella showed an decreasing trend from last year (**Table 1.28 and Figure 1.18**). The isolation trend of *Vibrio spp* showed an increasing trend from 2017 (4.8%) to 2023 (8.0%).

Table 1.27: Location-wise Isolation pattern of top 5 faecal isolates isolated from faeces across OPD, Ward and ICU

	Total	OPD	Ward	ICU
<i>Aeromonas spp.</i>	181 / 773 (23.42%)	76 / 306 (24.84%)	103 / 457 (22.54%)	2 / 10 (20%)
<i>Escherichia coli Diarrhoeagenic</i>	85 / 773 (11%)	62 / 306 (20.26%)	23 / 457 (5.03%)	0 / 10 (0%)
<i>Salmonella spp. Faecal</i>	307 / 773 (39.72%)	96 / 306 (31.37%)	210 / 457 (45.95%)	1 / 10 (10%)
<i>Shigella flexneri</i>	48 / 773 (6.21%)	23 / 306 (7.52%)	25 / 457 (5.47%)	0 / 10 (0%)
<i>Vibrio cholerae</i>	62 / 773 (8.02%)	11 / 306 (3.59%)	49 / 457 (10.72%)	2 / 10 (20%)

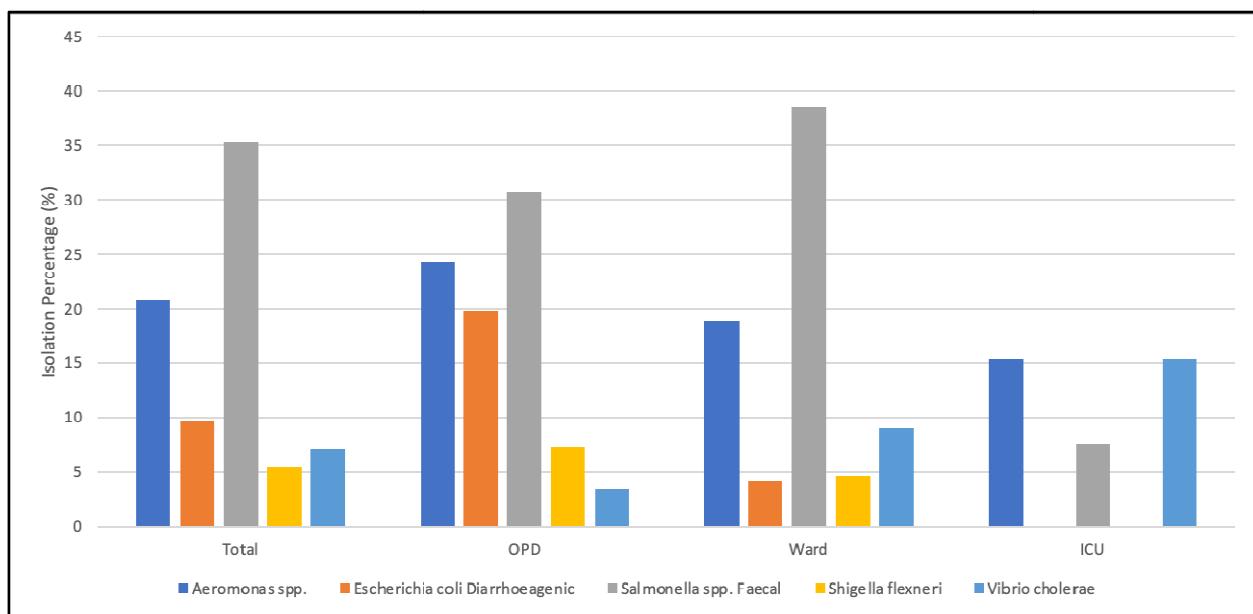


Figure 1.17: Location-wise Isolation pattern of top 5 faecal isolates isolated from faeces across OPD, Ward and ICU

Table 1.28: Yearly Isolation trends of top 5 faecal isolates isolated from faeces

Bacteria	Year-2017 (%)	Year-2018 (%)	Year-2019 (%)	Year-2020 (%)	Year-2021 (%)	Year-2022 (%)	Year-2023 (%)
<i>Escherichia coli</i> Diarrheagenic	0/501 (0)	0/621 (0)	134/1063 (12.6)	102/572 (17.8)	88/651 (13.5)	189 / 806 23.4(%)	85 / 773 (11%)
<i>Aeromonas</i> spp.	131/501 (26.1)	114/621 (18.4)	170/1063 (16.0)	77/572 (13.5)	179/651 (27.5)	164 / 806 20.3(%)	181 / 773 (23.42%)
<i>Shigella flexneri</i>	89/501 (17.8)	47/621 (7.6)	95/1063 (8.9)	55/572 (9.6)	37/651 (5.7)	51 / 806 (6.3%)	48 / 773 (6.21%)
<i>Vibrio cholerae</i>	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%)
Non Typhoidal Salmonella	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%)

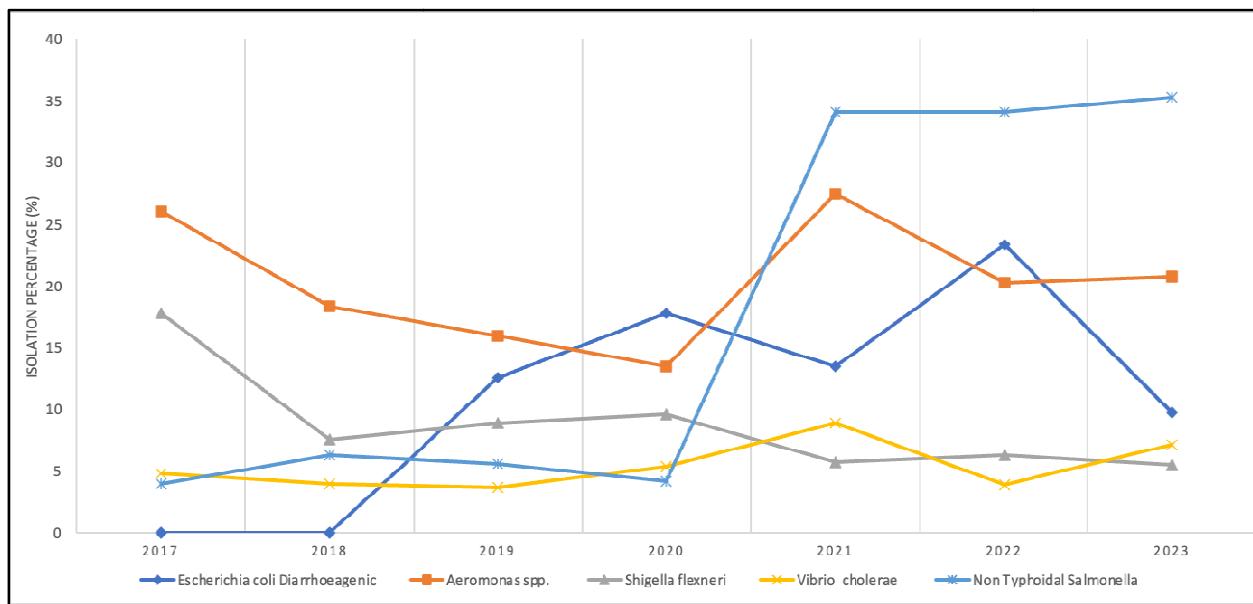


Figure 1.18: Yearly Isolation trends of top 5 faecal isolates isolated from faeces

***Streptococcus* species**

Total number of *Streptococcus* isolates studied during the year 2023 was 634, of those 1.8% were isolated from the upper respiratory tract. Majority of the isolates were from *Streptococcus agalactiae* (n=183) followed by *Streptococcus pyogenes* (n=156) and *Streptococcus pneumoniae* (n=144) (**Table 1.29**). Among clinical settings, *Streptococcus* isolates were common isolates from the OPD (0.7%) followed by ward and ICU (**Table 1.30 and Figure 1.19**).

Table 1.29: Sample-wise Isolation pattern of *Streptococcus* species

Isolate	Total n=99492		Blood n=22182		Urine n=20026		LRT n=17902		Superficial Infection n=19360		Deep Infection n=6826		CSF n=873		SS n=2969		Faeces n=773	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
No. culture positive	99675 (100)	100	22219 (100)	22.3	20030 (100)	20.1	17907 (100)	18	19365 (100)	19.4	6832 (100)	6.9	873 (100)	0.9	2979 (100)	3	871 (100)	0.9
<i>Streptococcus</i>	634 (0.6)	100	108 (0.5)	17	141 (0.7)	22.2	101 (0.6)	15.9	156 (0.8)	24.6	36 (0.5)	5.7	11 (1.3)	1.7	20 (0.7)	3.2	0 (0)	0
<i>Streptococcus agalactiae</i>	269 (0.3)	100	16 (0.1)	5.9	141 (0.7)	52.4	2 (0)	0.7	63 (0.3)	23.4	15 (0.2)	5.6	0 (0)	0	4 (0.1)	1.5	0 (0)	0
<i>Streptococcus pneumoniae</i>	208 (0.2)	100	70 (0.3)	33.7	0 (0)	0	95 (0.5)	45.7	5 (0)	2.4	2 (0)	1	11 (1.3)	5.3	15 (0.5)	7.2	0 (0)	0
<i>Streptococcus pyogenes</i>	129 (0.1)	100	13 (0.1)	10.1	0 (0)	0	2 (0)	1.6	88 (0.5)	68.2	18 (0.3)	14	0 (0)	0	1 (0)	0.8	0 (0)	0
<i>Streptococcus viridans</i>	28 (0)	100	9 (0)	32.1	0 (0)	0	2 (0)	7.1	0 (0)	0	1 (0)	3.6	0 (0)	0	0 (0)	0	0 (0)	0

Table 1.30: Location-wise Isolation pattern of *Streptococcus* isolated from all specimens across OPD, Ward and ICU

Organism	Total	OPD	Ward	ICU
<i>Streptococcus agalactiae</i>	269 / 99492 (0.27%)	171 / 28830 (0.59%)	83 / 51279 (0.16%)	15 / 19383 (0.08%)
<i>Streptococcus pneumoniae</i>	208 / 99492 (0.21%)	62 / 28830 (0.22%)	93 / 51279 (0.18%)	53 / 19383 (0.27%)
<i>Streptococcus pyogenes</i>	129 / 99492 (0.13%)	62 / 28830 (0.22%)	49 / 51279 (0.1%)	18 / 19383 (0.09%)
<i>Streptococcus viridans</i>	28 / 99492 (0.03%)	21 / 28830 (0.07%)	4 / 51279 (0.01%)	3 / 19383 (0.02%)
<i>Streptococcus</i>	634 / 99492 (0.64%)	316 / 28830 (1.1%)	229 / 51279 (0.45%)	89 / 19383 (0.46%)

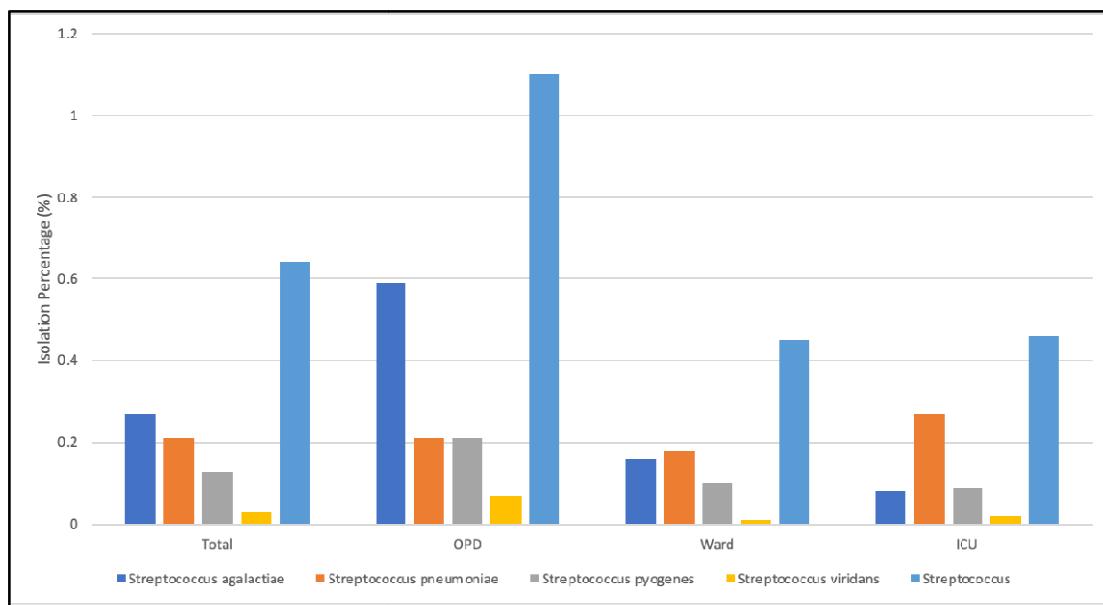


Figure 1.19: Location wise isolation of *Streptococcus* species

Chapter 2. Analysis of common syndromic isolates, their susceptibilities and implications in clinical practice

This chapter includes the interpretation of antibiograms from OPD/Ward/ICU which is crucial for assessing the impact of antimicrobial resistance and its implications in clinical practice for empirical use of antibiotics. This further helps in identifying potential areas for interventions and improvements in antibiotic stewardship practices.

Section A: Location wise distribution of isolates

Distribution of isolates from total samples

The distribution of top 5 isolates from OPD, ICU and ward from all specimens is presented in **Table 2.1**. Among OPD, *Escherichia coli* was most commonly isolated (30.74%) followed by the *Klebsiella pneumoniae* (13.63%), *Staphylococcus aureus* (12.15%), *Pseudomonas aeruginosa* (12.06%), and *Enterococcus faecalis* (4.41%). Among ward, again *Escherichia coli* was most commonly isolated (22.75%) followed by *Klebsiella pneumoniae* (16.21%), and *A. baumannii* (11.87%). In ICU, *A. baumannii* was most commonly isolated (23.74%) followed by *Klebsiella pneumoniae* (20.88%) and *E. coli* (13.11%).

Table 2.1: Top 5 isolates from all specimens

OPD		Ward		ICU	
Organisms	Isolation rate	Organisms	Isolation rate	Organisms	Isolation rate
<i>Escherichia coli</i>	8863 / 28830 (30.74)	<i>Escherichia coli</i>	11665 / 51279 (22.75)	<i>Acinetobacter baumannii</i>	4601 / 19383 (23.74)
<i>Klebsiella pneumoniae</i>	3930 / 28830 (13.63)	<i>Klebsiella pneumoniae</i>	8314 / 51279 (16.21)	<i>Klebsiella pneumoniae</i>	4047 / 19383 (20.88)
<i>Staphylococcus aureus</i>	3504 / 28830 (12.15)	<i>Acinetobacter baumannii</i>	6086 / 51279 (11.87)	<i>Escherichia coli</i>	2541 / 19383 (13.11)
<i>Pseudomonas aeruginosa</i>	3477 / 28830 (12.06)	<i>Pseudomonas aeruginosa</i>	6062 / 51279 (11.82)	<i>Pseudomonas aeruginosa</i>	2218 / 19383 (11.44)
<i>Enterococcus faecalis</i>	1272 / 28830 (4.41)	<i>Staphylococcus aureus</i>	4597 / 51279 (8.96)	<i>Staphylococcus aureus</i>	799 / 19383 (4.12)

Distribution of isolates from blood

Among blood specimen, *Salmonella Typhi* was the most predominant isolate from OPD (16.46%) followed by *Escherichia coli* (15.39%) and *Staphylococcus haemolyticus* (8.63%). *Escherichia coli* (16.46%) was the most predominant isolate from ward followed by *K. pneumoniae* and *Staphylococcus haemolyticus*, whereas *K. pneumoniae* (18.29%) was most common from ICU, followed by *Acinetobacter baumannii* and *Escherichia coli* (**Table 2.2**).

Table 2.2: Top 5 isolates from blood

OPD		Ward		ICU	
Organisms	Isolation rate	Organisms	Isolation rate	Organisms	Isolation rate
<i>Salmonella Typhi</i>	679 / 4125 (16.46)	<i>Escherichia coli</i>	1883 / 11443 (16.46)	<i>Klebsiella pneumoniae</i>	1210 / 6614 (18.29)
<i>Escherichia coli</i>	635 / 4125 (15.39)	<i>Klebsiella pneumoniae</i>	1388 / 11443 (12.13)	<i>Acinetobacter baumannii</i>	1040 / 6614 (15.72)
<i>Staphylococcus haemolyticus</i>	356 / 4125 (8.63)	<i>Staphylococcus haemolyticus</i>	987 / 11443 (8.63)	<i>Escherichia coli</i>	726 / 6614 (10.98)
<i>Staphylococcus hominis</i>	348 / 4125 (8.44)	<i>Acinetobacter baumannii</i>	918 / 11443 (8.01)	<i>Staphylococcus haemolyticus</i>	564 / 6614 (8.53)
<i>Klebsiella pneumoniae</i>	311 / 4125 (7.54)	<i>Staphylococcus epidermidis</i>	917 / 11443 (8.01)	<i>Staphylococcus epidermidis</i>	434 / 6614 (6.56)

Distribution of isolates from urine

Among urinary specimens, *Escherichia coli* was the most common organism isolated from OPD, Wards and ICU, followed by *K. pneumoniae* and *Enterococcus species* in all three places (**Table 2.3**).

Table 2.3: Top 5 isolates from urine

OPD		Ward		ICU	
Organisms	Isolation rate	Organisms	Isolation rate	Organisms	Isolation rate
<i>Escherichia coli</i>	6022 / 10303 (58.45)	<i>Escherichia coli</i>	3411 / 7908 (43.13)	<i>Escherichia coli</i>	610 / 1815 (33.61)
<i>Klebsiella pneumoniae</i>	1627 / 10303 (15.79)	<i>Klebsiella pneumoniae</i>	1495 / 7908 (18.9)	<i>Klebsiella pneumoniae</i>	374 / 1815 (20.61)
<i>Enterococcus faecalis</i>	755 / 10303 (7.33)	<i>Enterococcus faecalis</i>	663 / 7908 (8.38)	<i>Enterococcus faecium</i>	183 / 1815 (10.08)
<i>Pseudomonas aeruginosa</i>	476 / 10303 (4.62)	<i>Enterococcus faecium</i>	542 / 7908 (6.85)	<i>Enterococcus faecalis</i>	177 / 1815 (9.75)
<i>Enterococcus faecium</i>	217 / 10303 (2.11)	<i>Pseudomonas aeruginosa</i>	537 / 7908 (6.79)	<i>Pseudomonas aeruginosa</i>	171 / 1815 (9.42)

Distribution of isolates from pus/exudates

Staphylococcus aureus was the most common organism isolated from pus/exudate samples sent from OPD followed by *Escherichia coli* and *Pseudomonas aeruginosa*. From wards, *Escherichia coli*, was most common followed by *K. pneumoniae*. From ICUs, *E. coli*

was most common followed by *K. pneumoniae* and *Pseudomonas aeruginosa* and *A.baumannii* (**Table 2.4**).

Table 2.4: Top 5 isolates from pus/exudates

OPD		Ward		ICU	
Organisms	Isolation rate	Organisms	Isolation rate	Organisms	Isolation rate
<i>Staphylococcus aureus</i>	1119 / 3582 (31.24)	<i>Escherichia coli</i>	1005 / 4018 (25.01)	<i>Escherichia coli</i>	248 / 1009 (24.58)
<i>Escherichia coli</i>	618 / 3582 (17.25)	<i>Klebsiella pneumoniae</i>	716 / 4018 (17.82)	<i>Klebsiella pneumoniae</i>	230 / 1009 (22.79)
<i>Pseudomonas aeruginosa</i>	554 / 3582 (15.47)	<i>Staphylococcus aureus</i>	713 / 4018 (17.75)	<i>Pseudomonas aeruginosa</i>	122 / 1009 (12.09)
<i>Klebsiella pneumoniae</i>	450 / 3582 (12.56)	<i>Pseudomonas aeruginosa</i>	450 / 4018 (11.2)	<i>Acinetobacter baumannii</i>	122 / 1009 (12.09)
<i>Acinetobacter baumannii</i>	144 / 3582 (4.02)	<i>Acinetobacter baumannii</i>	296 / 4018 (7.37)	<i>Staphylococcus aureus</i>	87 / 1009 (8.62)

Distribution of isolates from CSF

Gram-negative isolates were more common among the isolated organisms from the CSF, indicating high representation of hospital acquired ventriculitis in the study population. *Acinetobacter baumannii* was the most common organism followed by *Klebsiella pneumoniae* and *E. coli* (**Table 2.5**).

Table 2.5: Top 5 isolates from CSF from all locations

Organisms	Isolation rate
<i>Acinetobacter baumannii</i>	246 / 873 (28.18)
<i>Klebsiella pneumoniae</i>	155 / 873 (17.75)
<i>Escherichia coli</i>	99 / 873 (11.34)
<i>Staphylococcus aureus</i>	36 / 873 (4.12)
<i>Pseudomonas aeruginosa</i>	66 / 873 (7.56)

Distribution of isolates from faeces

Salmonella spp. Faecal was the most common organism isolated from stool specimen from OPDs followed by *Aeromonas* and Diarrheagenic *Escherichia coli*. *Salmonella spp.* and *Aeromonas* were also the most common from wards (**Table 2.6**).

Table 2.6: Top 5 isolates from faeces

OPD		Ward	
Organisms	Isolation rate	Organisms	Isolation rate
<i>Salmonella spp.</i> <i>Faecal</i>	96 / 306 (31.37)	<i>Salmonella spp.</i> <i>Faecal</i>	210 / 457 (45.95)
<i>Aeromonas spp.</i>	76 / 306 (24.84)	<i>Aeromonas spp.</i>	103 / 457 (22.54)
<i>Escherichia coli</i> <i>Diarrheagenic</i>	62 / 306 (20.26)	<i>Vibrio cholerae</i>	49 / 457 (10.72)
<i>Shigella flexneri</i>	23 / 306 (7.52)	<i>Shigella flexneri</i>	25 / 457 (5.47)
<i>Shigella sonnei</i>	19 / 306 (6.21)	<i>Escherichia coli</i> <i>Diarrheagenic</i>	23 / 457 (5.03)

Section B: Specimen wise antibiograms**AMR patterns from various specimens**

- Resistance to 3rd Gen cephalosporins was very high among Gram-negative isolates (*Escherichia coli*, *Klebsiella pneumoniae* and *Acinetobacter baumannii*) from all the three locations with exception of *P. aeruginosa*, in which susceptibility to ceftazidime was close to 60% in OPD isolates and close to 20% in ICU isolates.
- Amikacin showed good susceptibility rates among *E. coli* and *P. aeruginosa* isolates (close to 70%), but its susceptibility rates remained poor in *Klebsiella pneumoniae* and *Acinetobacter baumannii*.
- Acinetobacter baumannii* isolates, showed good susceptibility rates only to minocycline (>75%) and colistin (>95%).
- For carbapenems, *E. coli* and *P. aeruginosa* isolates were fairly susceptible but carbapenem resistance rates were very high for *Klebsiella pneumoniae* and *Acinetobacter baumannii* even among OPD isolates.
- MRSA rates were close to 50% among ICU isolates whereas the same was close to 35% among OPD isolates. The isolates showed high susceptibility to antibiotics such as TMP-SMX and clindamycin, with vancomycin and linezolid demonstrating near 100% susceptibility.
- Salmonella Typhi isolates showed very good susceptibility to Ceftriaxone (97.3% susceptible), Cefixime (96 % susceptible), trimethoprim-sulfamethoxazole (97% susceptible) and azithromycin (96% susceptible) and showed very poor susceptibility (> 95% resistance) to Fluoroquinolones.
- Salmonella spp., followed by *Aeromonas spp.* and then Diarrhoeagenic *E. coli* were the common organisms in stool sample. Antibiograms of stool samples, showed, high rates of resistance to fluoroquinolones; more than 50% isolates of Salmonella spp., and *Aeromonas spp.* were resistant to fluoroquinolones. Among the tested isolates, trimethoprim-sulfamethoxazole and azithromycin showed

good susceptible rates to *Salmonella spp.*, and *Shigella* respectively. *Aeromonas spp.* displayed good susceptibility to tetracyclines and imipenem.

The antimicrobial susceptibility of top most pathogens identified from different specimens are depicted in tables (**Table 2.7- 2.23**).

Blood

Table 2.7: Susceptibility percentages of *E. coli* isolates from blood

AMA	<i>Escherichia coli</i>		
	OPD n=635	Ward n=1883	ICU n=726
Amikacin	277 / 367 (75.5%)	768 / 1120 (68.6%)	291 / 447 (65.1%)
Ceftriaxone	70 / 235 (29.8%)	147 / 713 (20.6%)	63 / 329 (19.1%)
Ciprofloxacin	62 / 369 (16.8%)	170 / 1111 (15.3%)	64 / 445 (14.4%)
Colistin	166 / 168 (98.8%)	482 / 482 (100.0%)	239 / 240 (99.6%)
Ertapenem	232 / 302 (76.8%)	673 / 929 (72.4%)	245 / 398 (61.6%)
Fosfomycin	30 / 31 (96.8%)	71 / 73 (97.3%)	30 / 30 (100%)
Imipenem	273 / 361 (75.6%)	775 / 1088 (71.2%)	241 / 431 (55.9%)
Levofloxacin	35 / 183 (19.1%)	104 / 511 (20.4%)	27 / 195 (13.8%)
Meropenem	283 / 364 (77.7%)	800 / 1104 (72.5%)	265 / 443 (59.8%)
Minocycline	186 / 211 (88.2%)	503 / 618 (81.4%)	217 / 242 (89.7%)
Piperacillin-tazobactam	207 / 364 (56.9%)	537 / 1111 (48.3%)	215 / 443 (48.5%)
Trimethoprim-sulfamethoxazole	29 / 68 (42.6%)	102 / 201 (50.7%)	52 / 101 (51.5%)

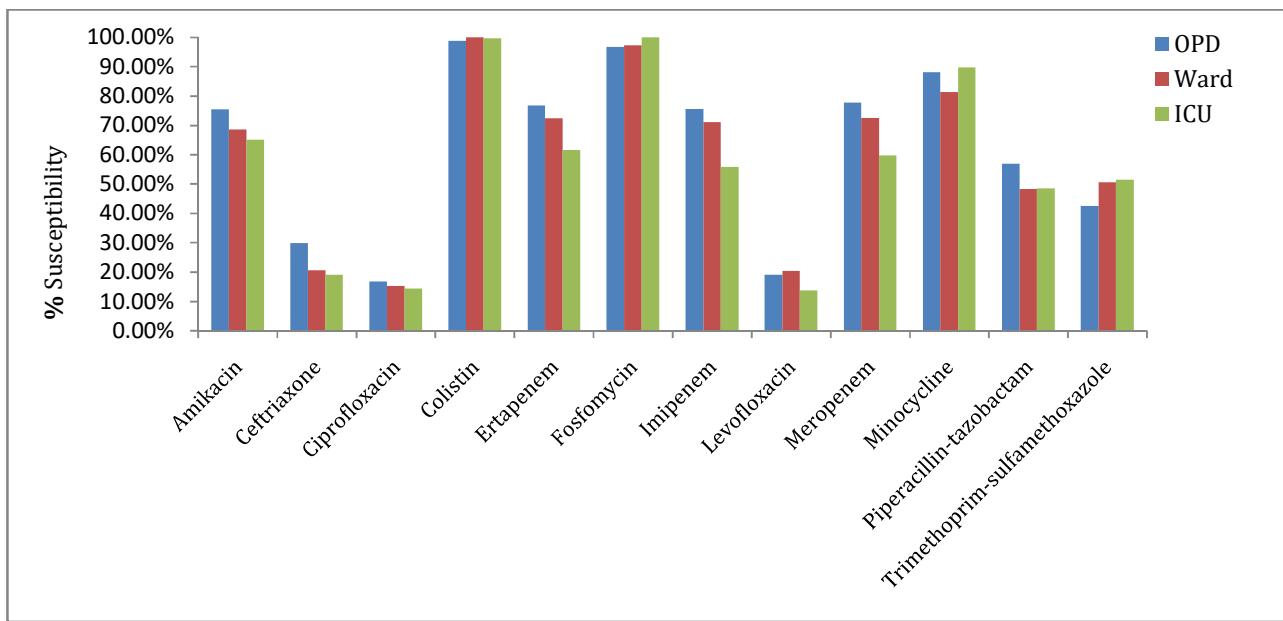


Figure 2.1: Susceptibility pattern of *E. coli* from blood samples

Table 2.8: % Susceptibility of *Klebsiella pneumoniae* isolates from blood

AMA	<i>Klebsiella pneumoniae</i>		
	OPD n=311	Ward n=1388	ICU n=1210
Amikacin	84 / 199 (42.2%)	290 / 814 (35.6%)	224 / 734 (30.5%)
Ceftriaxone	37 / 162 (22.8%)	114 / 668 (17.1%)	90 / 604 (14.9%)
Ciprofloxacin	44 / 198 (22.2%)	143 / 814 (17.6%)	103 / 729 (14.1%)
Colistin	129 / 130 (99.2%)	485 / 507 (95.7%)	486 / 505 (96.2%)
Ertapenem	78 / 157 (49.7%)	196 / 604 (32.5%)	171 / 595 (28.7%)
Fosfomycin	9 / 14 (64.3%)	44 / 63 (69.8%)	39 / 75 (52%)
Imipenem	74 / 195 (37.9%)	252 / 798 (31.6%)	169 / 717 (23.6%)
Levofloxacin	31 / 104 (29.8%)	74 / 388 (19.1%)	55 / 363 (15.2%)
Meropenem	78 / 196 (39.8%)	262 / 810 (32.3%)	186 / 730 (25.5%)
Minocycline	97 / 125 (77.6%)	340 / 509 (66.8%)	343 / 481 (71.3%)
Piperacillin-tazobactam	67 / 201 (33.3%)	189 / 814 (23.2%)	160 / 730 (21.9%)
Trimethoprim-sulfamethoxazole	11 / 32 (34.4%)	61 / 142 (43%)	72 / 194 (37.1%)

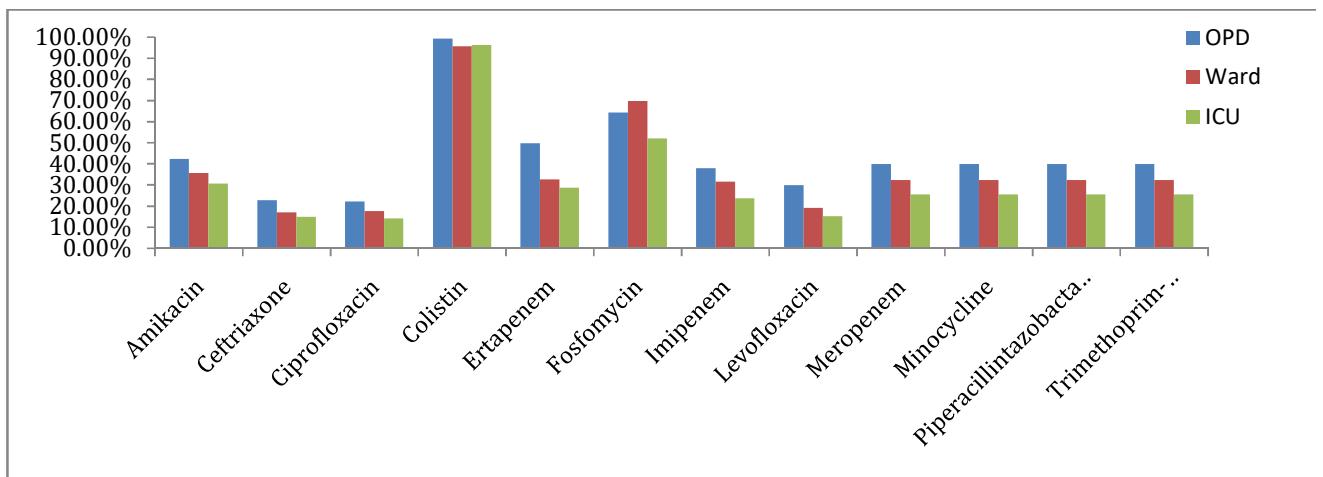


Figure 2.2: Susceptibility pattern of *Klebsiella pneumoniae* from blood samples

Table 2.9: % Susceptibility of *Acinetobacter baumannii* isolates from blood

AMA	<i>Acinetobacter baumannii</i>		
	OPD n=173	Ward n=918	ICU n=1040
Amikacin	32 / 84 (38.1%)	136 / 554 (24.5%)	131 / 632 (20.7%)
Cefepime	24 / 84 (28.6%)	90 / 551 (16.3%)	79 / 629 (12.6%)
Ceftazidime	21 / 84 (25%)	73 / 554 (13.2%)	58 / 633 (9.2%)
Colistin	58 / 58 (100%)	409 / 421 (97.1%)	455 / 469 (97%)
Imipenem	20 / 84 (23.8%)	76 / 554 (13.7%)	62 / 633 (9.8%)
Levofloxacin	15 / 49 (30.6%)	58 / 345 (16.8%)	70 / 437 (16%)
Meropenem	20 / 84 (23.8%)	93 / 554 (16.8%)	73 / 632 (11.6%)
Minocycline	52 / 79 (65.8%)	349 / 498 (70.1%)	445 / 566 (78.6%)
Piperacillintazobactam	25 / 84 (29.8%)	90 / 554 (16.2%)	91 / 634 (14.4%)

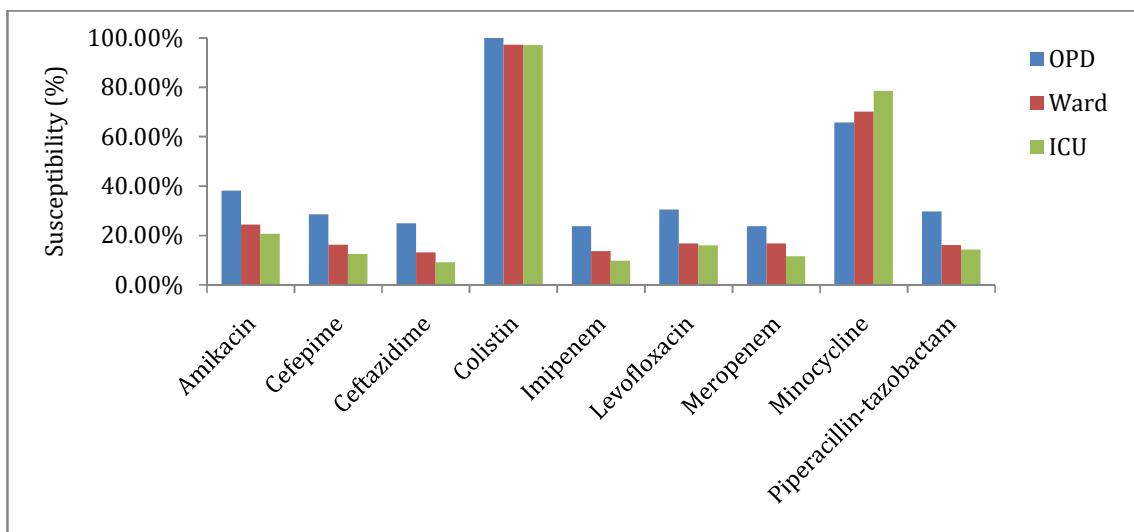


Figure 2.3: Susceptibility pattern of *Acinetobacter baumannii* from blood samples

Table 2.10: % Susceptibility of *Salmonella Typhi* isolates from blood

AMA	Salmonella Typhi	
	OPD n=679	Ward n=382
Ampicillin	414 / 425 (97.4%)	190 / 193 (98.4%)
Azithromycin	420 / 436 (96.3%)	203 / 204 (99.5%)
Cefixime	380 / 395 (96.2%)	160 / 164 (97.6%)
Cefotaxime	209 / 216 (96.8%)	113 / 121 (93.4%)
Ceftriaxone	427 / 439 (97.3%)	198 / 205 (96.6%)
Chloramphenicol	406 / 414 (98.1%)	175 / 178 (98.3%)
Ciprofloxacin	8 / 446 (1.8%)	6 / 211 (2.8%)
Levofloxacin	10 / 45 (22.2%)	0 / 7 (-)
Trimethoprim-sulfamethoxazole	423 / 436 (97%)	195 / 201 (97%)

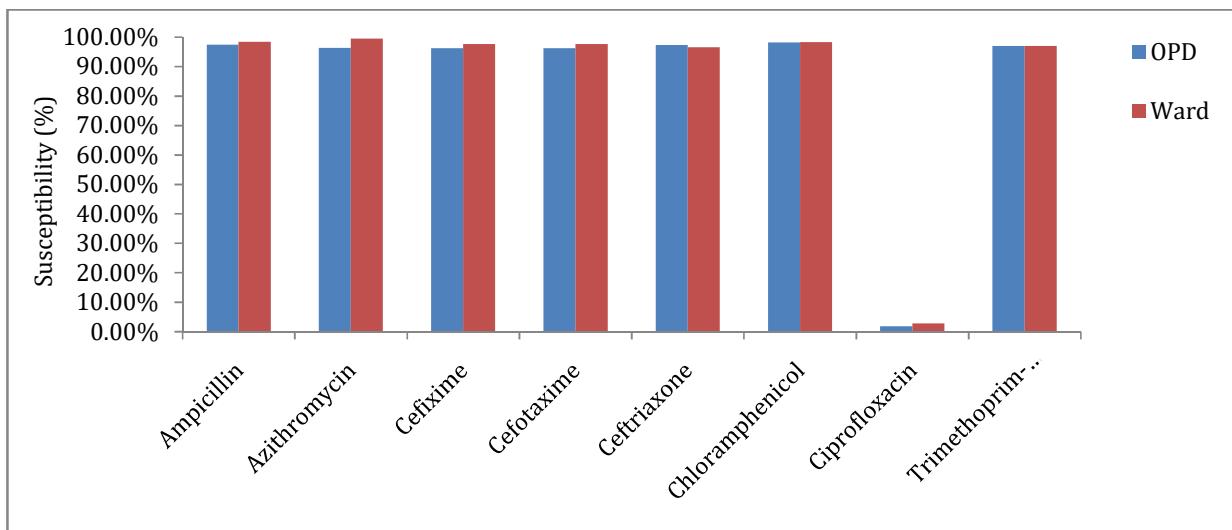


Figure 2.4: Susceptibility pattern of *Salmonella Typhi* from blood samples

Urine

Table 2.11: % Susceptibility of *E. coli* isolates from urine

AMA	<i>Escherichia coli</i>		
	OPD n=6022	Ward n=3411	ICU n=610
Amikacin	2541 / 3378 (75.2%)	1361 / 2059 (66.1%)	261 / 421 (62%)
Cefazolin	156 / 1413 (11%)	85 / 829 (10.3%)	14 / 204 (6.9%)
Ceftriaxone	766 / 2645 (29%)	294 / 1554 (18.9%)	67 / 354 (18.9%)
Ciprofloxacin	676 / 3378 (20%)	309 / 2059 (15%)	65 / 421 (15.4%)
Colistin	1945 / 1970 (99.7%)	967 / 978 (99.6%)	305 / 305 (99.6%)
Ertapenem	2322 / 2929 (79.3%)	1097 / 1667 (65.8%)	220 / 376 (58.5%)
Fosfomycin	2011 / 2147 (93.7%)	1261 / 1325 (95.2%)	205 / 239 (85.8%)
Imipenem	2451 / 3206 (76.5%)	1403 / 2023 (69.4%)	201 / 401 (50.1%)
Levofloxacin	318 / 1549 (20.5%)	183 / 985 (18.6%)	16 / 218 (7.3%)
Meropenem	2762 / 3379 (81.7%)	1525 / 2059 (74.1%)	239 / 421 (56.8%)
Minocycline	1356 / 1729 (78.4%)	695 / 915 (76%)	190 / 237 (80.2%)
Nitrofurantoin	2504 / 2891 (86.6%)	1453 / 1702 (85.4%)	332 / 406 (81.8%)
Piperacillin-tazobactam	2059 / 3371 (61.1%)	1016 / 2055 (49.4%)	202 / 419 (48.2%)
Trimethoprim-sulfamethoxazole	1146 / 2911 (39.4)	734 / 1662 (44.2)	154 / 381 (40.4)

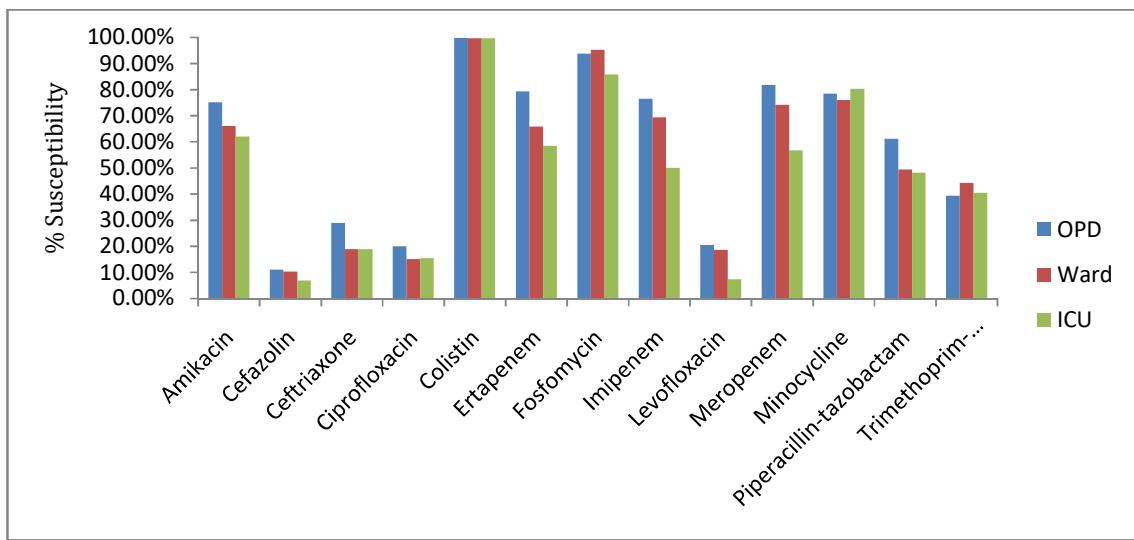


Figure 2.5: Susceptibility pattern of *E. coli* from urine

Table 2.12: % Susceptibility of *Klebsiella pneumoniae* isolates from urine

	<i>Klebsiella pneumoniae</i>		
	OPD n=1627	Ward n=1495	ICU n=374
Amikacin	456 / 855 (53.3%)	341 / 901 (37.8%)	93 / 250 (37.2%)
Cefazolin	39 / 364 (10.7%)	27 / 354 (7.6%)	6 / 106 (5.7%)
Ceftriaxone	238 / 587 (40.5%)	154 / 587 (26.2%)	33 / 206 (16%)
Ciprofloxacin	240 / 854 (28.1%)	139 / 901 (15.4%)	31 / 250 (12.4%)
Colistin	535 / 554 (97.3%)	450 / 484 (96.1%)	170 / 173 (94.4%)
Ertapenem	418 / 748 (55.9%)	260 / 749 (34.7%)	66 / 215 (30.7%)
Fosfomycin	341 / 551 (61.9%)	343 / 570 (60.2%)	64 / 127 (50.4%)
Imipenem	408 / 809 (50.4%)	331 / 881 (37.6%)	57 / 241 (23.7%)
Levofloxacin	80 / 434 (18.4%)	70 / 514 (13.6%)	9 / 130 (6.9%)
Meropenem	476 / 854 (55.7%)	361 / 902 (40%)	66 / 250 (26.4%)
Minocycline	318 / 433 (73.4%)	231 / 381 (60.6%)	87 / 120 (72.5%)
Nitrofurantoin	328 / 720 (45.6%)	218 / 705 (30.9%)	61 / 230 (26.5%)
Piperacillin-tazobactam	378 / 852 (44.4%)	237 / 897 (26.4%)	56 / 249 (22.5%)
Trimethoprim-sulfamethoxazole	364 / 748 (48.7%)	259 / 749 (34.6%)	66 / 225 (29.3%)

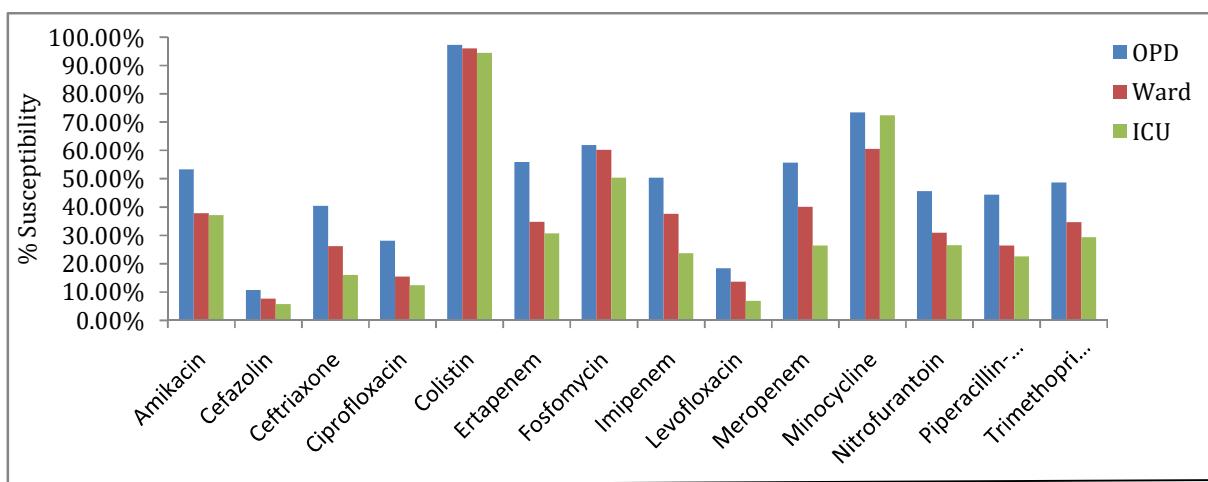


Figure 2.6: Susceptibility pattern of *Klebsiella pneumoniae* from urine

Table 2.13: % Susceptibility of *Pseudomonas aeruginosa* isolates from urine

	<i>Pseudomonas aeruginosa</i>		
	OPD n=476	Ward n=537	ICU n=171
Amikacin	177 / 258 (68.6%)	160 / 327 (48.9%)	38 / 117 (32.5%)
Cefepime	158 / 249 (63.5%)	138 / 321 (43%)	30 / 117 (25.6%)
Ceftazidime	154 / 259 (59.5%)	124 / 330 (37.6%)	25 / 118 (21.2%)
Ciprofloxacin	117 / 259 (45.2%)	119 / 330 (36.1%)	21 / 118 (17.8%)
Colistin	195 / 198 (95.4%)	237 / 246 (95.8%)	97 / 102 (97.3%)
Gentamicin	127 / 210 (60.5%)	117 / 252 (46.4%)	18 / 80 (22.5%)
Imipenem	159 / 259 (61.4%)	146 / 330 (44.2%)	23 / 118 (19.5%)
Levofloxacin	71 / 200 (35.5%)	85 / 282 (30.1%)	7 / 97 (7.2%)
Meropenem	176 / 259 (68%)	153 / 330 (46.4%)	28 / 118 (23.7%)
Piperacillin-tazobactam	200 / 259 (77.2%)	185 / 330 (56.1%)	52 / 118 (44.1%)
Tobramycin	76 / 135 (56.3%)	70 / 166 (42.2%)	13 / 77 (16.9%)

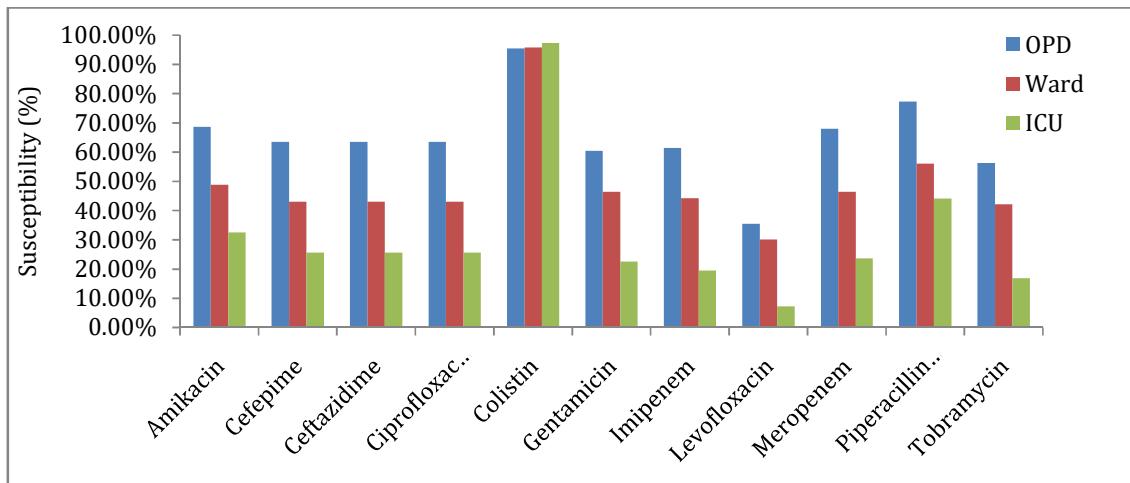


Figure 2.7: Susceptibility pattern of *Pseudomonas aeruginosa* from urine

Table 2.14: % Susceptibility of *Enterococcus faecalis* isolates from urine

	<i>Enterococcus faecalis</i>		
	OPD n=755	Ward n=663	ICU n=177
Ampicillin	573 / 739 (77.5)	376 / 630 (59.7)	70 / 174 (40.2)
Ciprofloxacin	89 / 724 (12.3)	71 / 636 (11.2)	14 / 172 (8.1)
Fosfomycin	398 / 529 (75.2)	408 / 533 (76.5)	114 / 145 (78.6)
Gentamicin_HL	301 / 606 (49.7)	262 / 600 (43.7)	40 / 157 (25.5)
Linezolid	729 / 755 (96.6)	636 / 663 (95.9)	172 / 177 (97.2)
Nitrofurantoin	628 / 723 (86.9)	481 / 632 (76.1)	111 / 176 (63.1)
Penicillin	293 / 613 (47.8)	184 / 505 (36.4)	35 / 156 (22.4)
Teicoplanin	675 / 727 (92.8)	596 / 647 (92.1)	154 / 175 (88)
Vancomycin	726 / 755 (96.2)	619 / 663 (93.4)	166 / 177 (93.8)

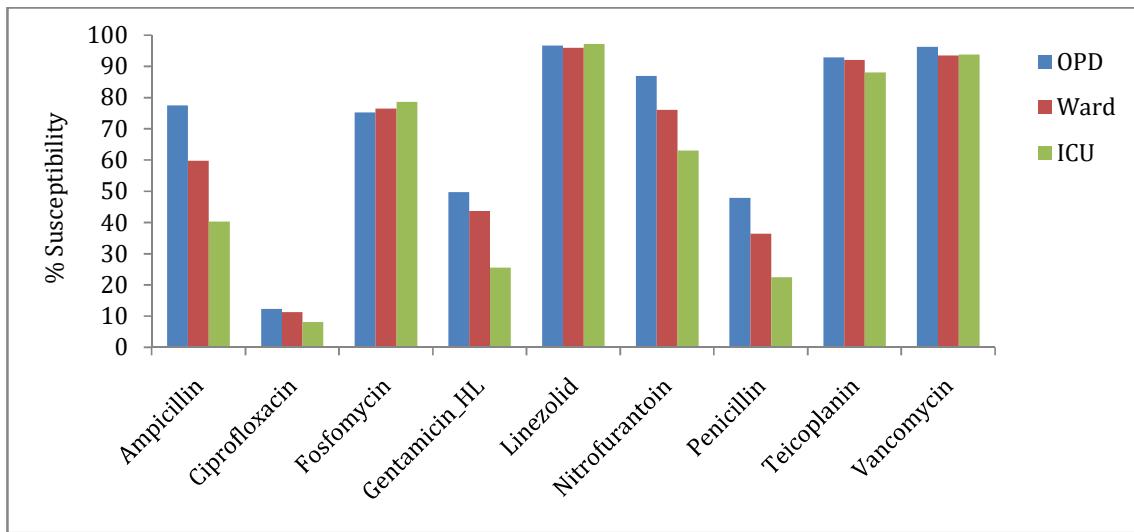


Figure 2.8: Susceptibility pattern of *Enterococcus faecalis* from urine

Table 2.15: % Susceptibility of *Enterococcus faecium* isolates from urine

	<i>Enterococcus faecium</i>		
	OPD n=217	Ward n=542	ICU n=183
Ampicillin	71 / 208 (34.1)	63 / 512 (12.3)	11 / 180 (6.1)
Ciprofloxacin	18 / 196 (9.2)	16 / 491 (3.3)	5 / 174 (2.9)
Fosfomycin	0 / 3 (-)	0 / 3 (-)	0 / 1 (-)
Gentamicin_HL	97 / 185 (52.4)	183 / 484 (37.8)	40 / 132 (30.3)
Linezolid	198 / 217 (91.2)	498 / 542 (91.9)	172 / 183 (94)
Nitrofurantoin	94 / 193 (48.7)	168 / 467 (36)	48 / 164 (29.3)
Penicillin	37 / 160 (23.1)	33 / 358 (9.2)	7 / 128 (5.5)
Teicoplanin	167 / 205 (81.5)	393 / 521 (75.4)	107 / 182 (58.8)
Vancomycin	181 / 217 (83.4)	402 / 542 (74.2)	105 / 183 (57.4)

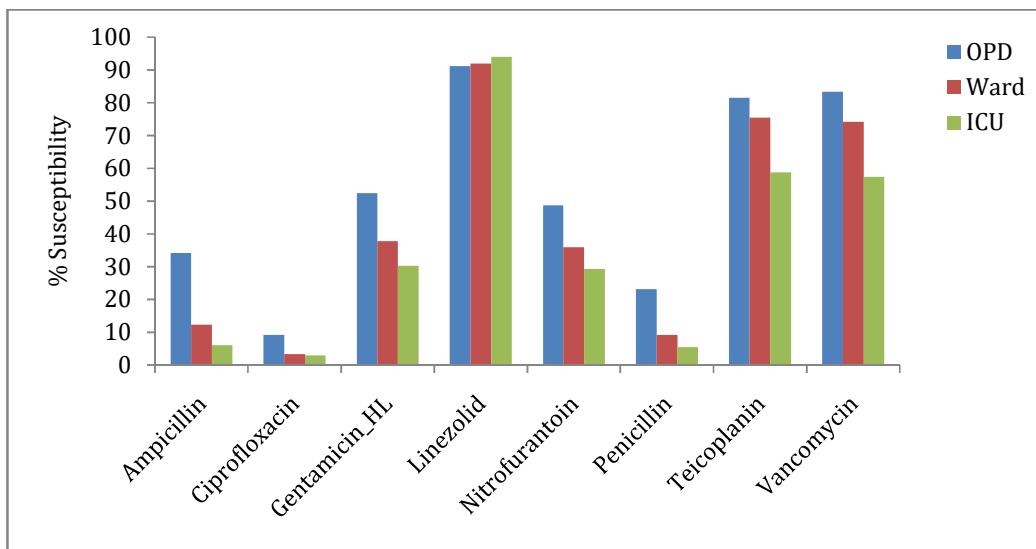


Figure 2.9: Susceptibility pattern of *Enterococcus faecium* from urine

Pus/Exudates

Table 2.16: % Susceptibility of *E.coli* isolates from pus/exudates

	<i>Escherichia coli</i>		
	OPD n=618	Ward n=1005	ICU n=248
Amikacin	221 / 352 (62.8%)	385 / 634 (60.7%)	96 / 160 (60%)
Ceftriaxone	51 / 223 (22.9%)	79 / 398 (19.8%)	16 / 131 (12.2%)
Ciprofloxacin	49 / 352 (13.9%)	71 / 634 (11.2%)	8 / 160 (5.0%)
Colistin	192 / 194 (99)	366 / 370 (98.9)	117 / 177 (100)
Ertapenem	197 / 312 (63.1%)	310 / 565 (54.9%)	67 / 155 (43.2%)
Fosfomycin	12 / 12 (-)	10 / 11 (-)	2 / 2 (-)
Imipenem	205 / 348 (58.9%)	370 / 625 (59.2%)	51 / 157 (32.5%)
Levofloxacin	51 / 238 (21.4%)	73 / 419 (17.4%)	11 / 134 (8.2%)
Meropenem	231 / 352 (65.6%)	414 / 634 (65.3%)	68 / 160 (42.5%)
Minocycline	156 / 169 (92.3%)	282 / 330 (85.5%)	108 / 121 (89.3%)
Nitrofurantoin	0 / 0 (-)	3 / 4 (-)	0 / 0 (-)
Piperacillin-tazobactam	171 / 352 (48.6%)	248 / 632 (39.2%)	55 / 160 (34.4%)
Trimethoprim-sulfamethoxazole	24 / 42 (57.1%)	42 / 78 (53.8%)	8 / 17 (-)

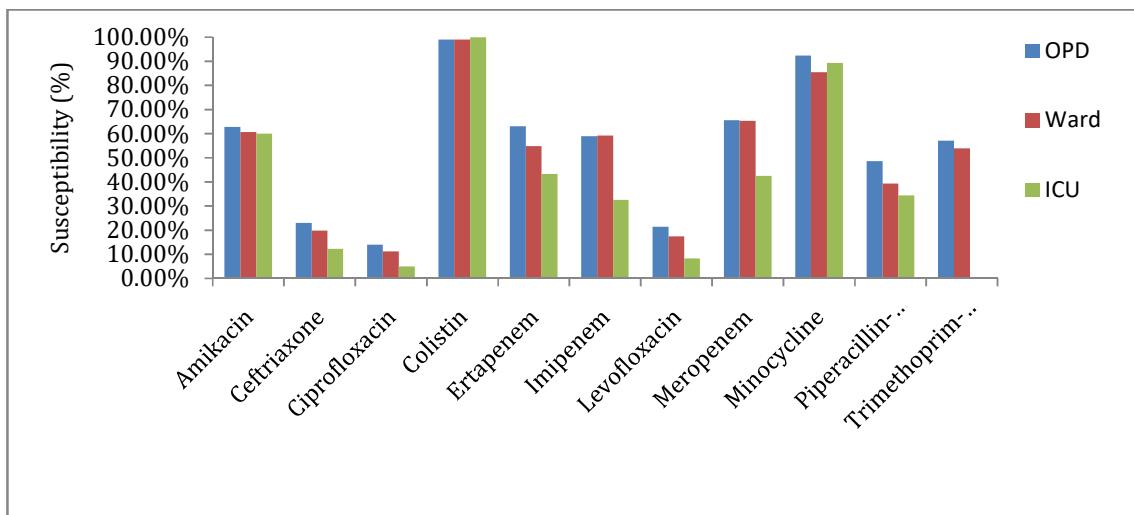


Figure 2.10: Susceptibility pattern of *E. coli* from pus/exudates samples

Table 2.17: % Susceptibility of *S. aureus* isolates from pus/exudates

	<i>Staphylococcus aureus</i>		
	OPD n=1119	Ward n=713	ICU n=87
Cefoxitin	328 / 665 (49.3%)	198 / 442 (44.8%)	35 / 66 (53%)
Ciprofloxacin	95 / 680 (14%)	70 / 458 (15.3%)	8 / 66 (12.1%)
Clindamycin	520 / 679 (76.6%)	367 / 458 (80.1%)	41 / 67 (61.2%)
Daptomycin	186 / 200 (93%)	108 / 116 (93.1%)	4 / 6 (-)
Erythromycin	249 / 676 (36.8%)	170 / 459 (37%)	21 / 66 (31.8%)
Linezolid	661 / 678 (97.5%)	449 / 457 (98.2%)	63 / 66 (95.5%)
Oxacillin	90 / 157 (57.3%)	57 / 131 (43.5%)	3 / 12 (-)
Teicoplanin	256 / 256 (100%)	171 / 171 (100%)	18 / 18 (-)
Tetracycline	513 / 642 (79.9%)	350 / 423 (82.7%)	31 / 59 (52.5%)
Tigecycline	148 / 148 (100%)	111 / 111 (100%)	8 / 8 (-)
Trimethoprim-sulfamethoxazole	520 / 679 (76.6%)	351 / 458 (76.6%)	46 / 66 (69.7%)
Vancomycin	677 / 677 (100%)	457 / 457 (100%)	66 / 66 (100%)

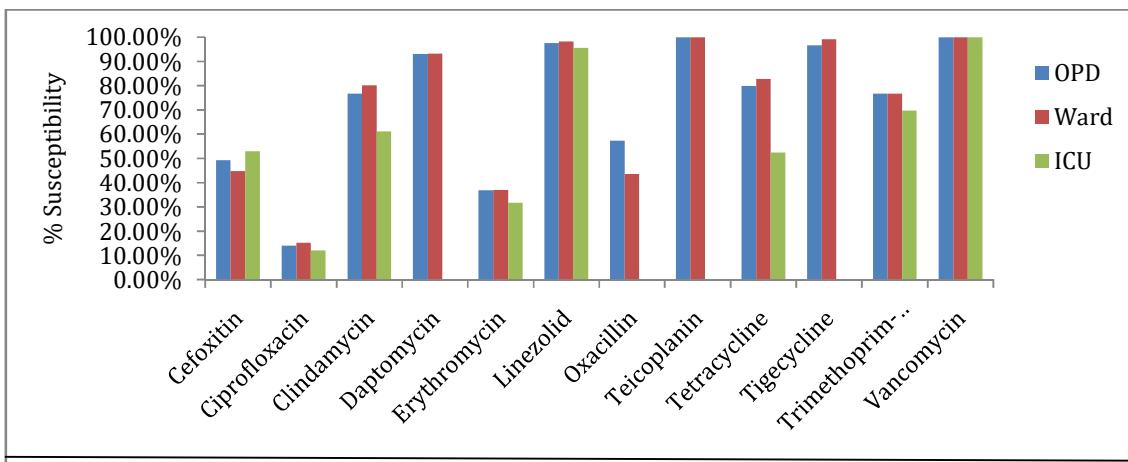


Figure 2.11: Susceptibility pattern of *S. aureus* from pus/exudates samples

Table 2.18 % Susceptibility of *K. pneumoniae* isolates from pus/exudates

	<i>Klebsiella pneumoniae</i>		
	OPD n=450	Ward n=716	ICU n=230
Amikacin	108 / 244 (44.3%)	170 / 484 (35.1%)	36 / 149 (24.2%)
Ceftriaxone	59 / 157 (37.6%)	95 / 289 (32.9%)	11 / 119 (9.2%)
Ciprofloxacin	54 / 244 (22.1%)	92 / 483 (19%)	10 / 148 (6.8%)
Colistin	146 / 150 (97.3%)	284 / 287 (98.9%)	119 / 120 (99.2%)
Ertapenem	95 / 207 (45.9%)	125 / 415 (30.1%)	33 / 139 (23.7%)
Fosfomycin	15 / 20 (-)	6 / 17 (-)	2 / 6 (-)
Imipenem	105 / 239 (43.9%)	160 / 470 (34%)	19 / 147 (12.9%)
Levofloxacin	30 / 151 (19.9%)	39 / 317 (12.3%)	2 / 111 (1.8%)
Meropenem	116 / 244 (47.5%)	182 / 483 (37.7%)	28 / 148 (18.9%)
Minocycline	113 / 136 (83.1%)	200 / 261 (76.6%)	98 / 109 (89.9%)
Piperacillin-tazobactam	86 / 242 (35.5%)	128 / 483 (26.5%)	23 / 148 (15.5%)
Trimethoprim-sulfamethoxazole	22 / 42 (52.4%)	39 / 59 (66.1%)	6 / 19 (-)

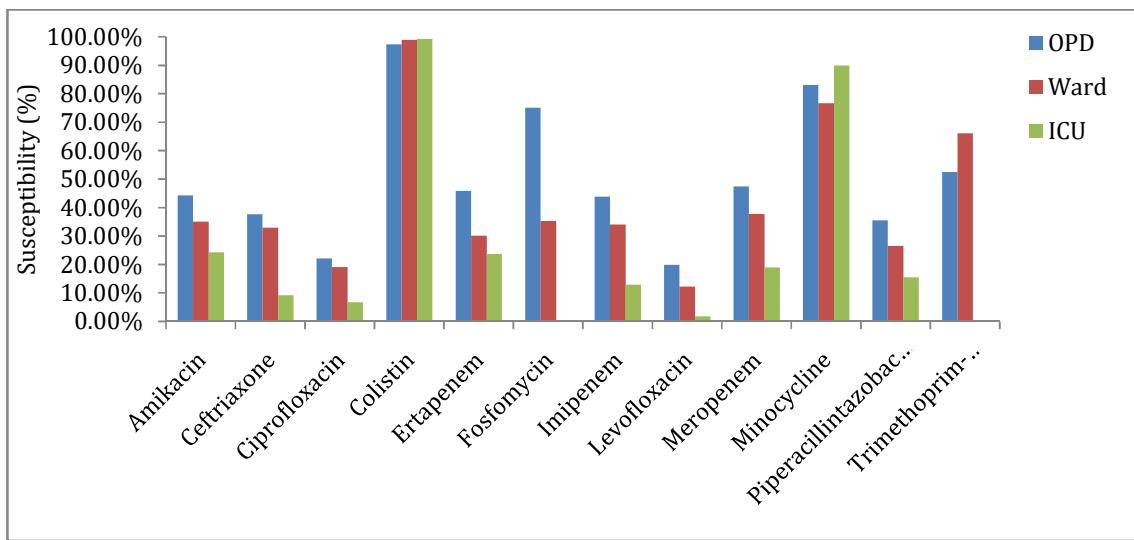


Figure 2.12: Susceptibility pattern of *Klebsiella pneumoniae* from pus/exudates samples

Table 2.19: % Susceptibility of *A. baumannii* isolates from pus/exudates

	<i>Acinetobacter baumannii</i>		
	OPD n=144	Ward n=296	ICU n=122
Amikacin	16 / 83 (19.3%)	42 / 204 (20.6%)	10 / 91 (11%)
Cefepime	22 / 83 (26.5%)	29 / 204 (14.2%)	2 / 91 (2.2%)
Ceftazidime	16 / 83 (19.3%)	18 / 204 (8.8%)	2 / 91 (2.2%)
Colistin	76 / 76 (100%)	160 / 160 (100%)	82 / 82 (100%)
Imipenem	17 / 83 (20.5%)	25 / 204 (12.3%)	2 / 91 (2.2%)
Levofloxacin	9 / 81 (11.1%)	38 / 201 (18.9%)	5 / 90 (5.6%)
Meropenem	15 / 83 (18.1%)	34 / 204 (16.7%)	3 / 91 (3.3%)
Minocycline	61 / 81 (75.3%)	149 / 195 (76.4%)	81 / 90 (90%)
Piperacillin-tazobactam	25 / 83 (30.1%)	30 / 204 (14.7%)	8 / 91 (8.8%)

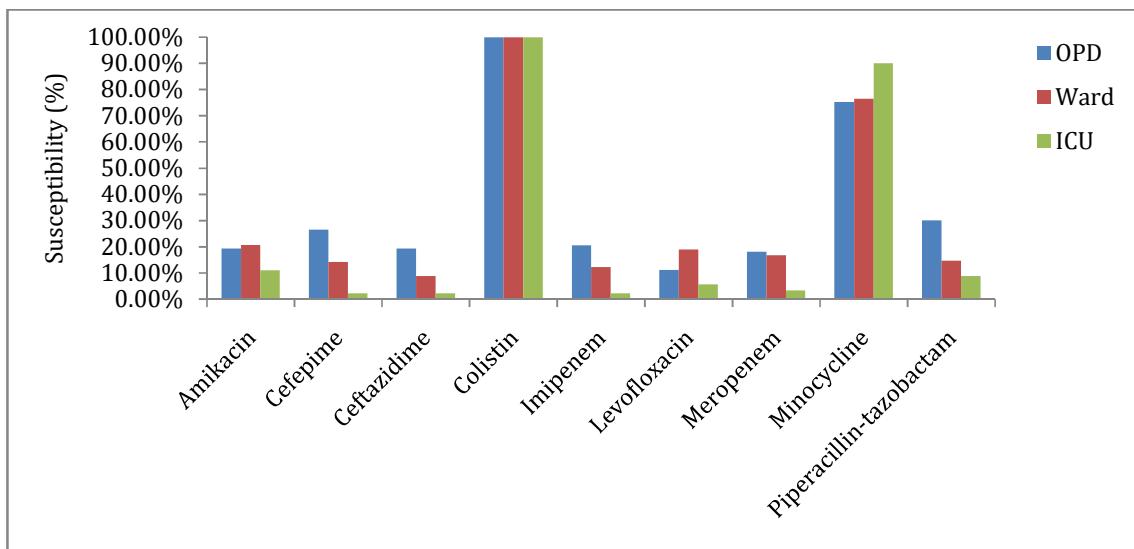


Figure 2.13: Susceptibility pattern of *A. baumannii* from pus/exudates samples

Table 2.20: % Susceptibility of *P. aeruginosa* isolates from pus/exudates

	<i>Pseudomonas aeruginosa</i>		
	OPD n=554	Ward n=450	ICU n=121
Amikacin	220 / 303 (72.6%)	202 / 274 (73.7%)	45 / 76 (59.2%)
Cefepime	194 / 284 (68.3%)	162 / 277 (58.5%)	37 / 79 (46.8%)
Ceftazidime	214 / 312 (68.6%)	159 / 283 (56.2%)	37 / 79 (46.8%)
Ciprofloxacin	153 / 312 (49%)	128 / 283 (45.2%)	24 / 79 (30.4%)
Colistin	237 / 248 (95.6%)	202 / 204 (99%)	60 / 62 (96.8%)
Gentamicin	163 / 255 (63.9%)	167 / 238 (70.2%)	36 / 69 (52.2%)
Imipenem	205 / 312 (65.7%)	169 / 283 (59.7%)	22 / 80 (27.5%)
Levofloxacin	136 / 292 (46.6%)	111 / 269 (41.3%)	14 / 76 (18.4%)
Meropenem	229 / 312 (73.4%)	201 / 283 (71%)	39 / 79 (49.4%)
Piperacillin-tazobactam	252 / 312 (80.8%)	197 / 283 (69.6%)	46 / 79 (58.2%)
Tobramycin	134 / 197 (68%)	155 / 211 (73.5%)	37 / 68 (54.4%)

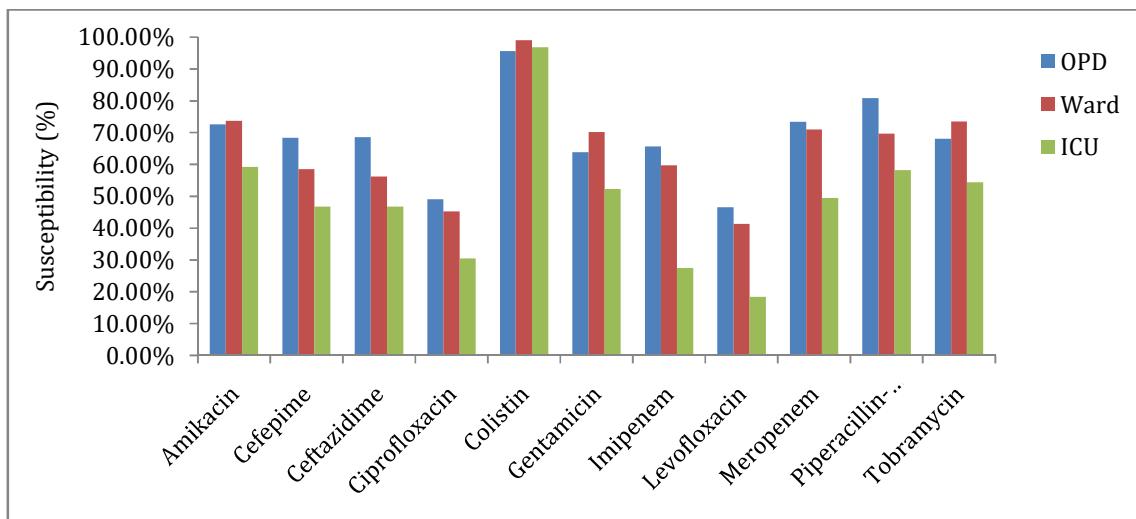


Figure 2.14: Susceptibility pattern of *P. aeruginosa* from pus/exudates samples

Faecal samples

Table 2.21: % Susceptibility of *Salmonella* spp faecal isolates from faecal samples

	Salmonella spp. Faecal	
	OPD n=96	Ward n=210
Ampicillin	35 / 39 (89.7%)	66 / 92 (71.7%)
Chloramphenicol	38 / 38 (100%)	91 / 92 (98.9%)
Ciprofloxacin	14 / 40 (35%)	38 / 92 (41.3%)
Trimethoprim-sulfamethoxazole	29 / 36 (80.6%)	80 / 88 (90.9%)

Table 2.22: % Susceptibility of *Aeromonas* spp. isolates from faecal samples

	<i>Aeromonas</i> spp.	
	OPD n=76	Ward n=103
Ciprofloxacin	8 / 30 (26.7%)	10 / 54 (18.5%)
Imipenem	16 / 30 (53.3%)	36 / 51 (70.6%)
Meropenem	28 / 30 (93.3%)	45 / 51 (88.2%)
Tetracycline	23 / 30 (76.7%)	42 / 54 (77.8%)

Table 2.23: % Susceptibility of *Shigella flexneri* isolates from faecal specimen

AMA	<i>Shigella flexneri</i>	
	OPD n=23	Ward n=25
Ampicillin	2 / 10	2 / 15
Azithromycin	7 / 9	13 / 15
Cefixime	7 / 10	9 / 15
Ciprofloxacin	0 / 10	0 / 15
Nalidixic acid	0 / 2	0 / 3
Trimethoprim-sulfamethoxazole	7 / 10	12 / 14

Chapter 3. 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). Susceptibility was tested following CLSI guidelines using disc diffusion or automated systems, except colistin, where a micro-broth dilution test was used.

The percentage of susceptibilities of different species to the antibiotics is presented in **Table 3.1**. 100% colistin susceptibility was seen in species (recommended for testing by CLSI) such as *Citrobacter koseri*, *Klebsiella oxytoca*, and *Klebsiella (Enterobacter) aerogenes* followed by *Escherichia coli* (99.3%). *K. pneumoniae* and *Enterobacter cloacae* showed 96.2% and 93.3% susceptibility, respectively. Higher susceptibility was observed for piperacillin-tazobactam in *P. mirabilis* (84.1%) and *M. morganii* (80.8%), whereas *K. pneumoniae* (26.5%) showed the lowest susceptibility. High level of resistance to third-generation cephalosporins was observed. The susceptibility of cefotaxime was comparatively higher for *M. morganii* (54.7%) and *Citrobacter koseri* (52.5%), whereas the susceptibility was very low for *Escherichia coli* (14.9%), *K. pneumoniae* (17.5%) and *Enterobacter* spp (13.1%). Carbapenem resistance was also relatively high among Enterobacterales. Among these organisms, *M. morganii* (85.6%) and *C. koseri* (79%) showed the highest susceptibility towards meropenem, but susceptibility was low for *K. pneumoniae* (37.7%). Similarly, a relatively higher susceptibility to imipenem was seen in *Citrobacter koseri* (67.6%) and *Klebsiella (Enterobacter) aerogenes* (71.4%), as compared to lower rates in *K. pneumoniae* (35.6%). Among aminoglycosides, ciprofloxacin, and levofloxacin, *K. pneumonia* had the lowest susceptibility. *E. coli* and other Enterobacterales remained relatively more susceptible to amikacin. However, *E. coli* had poor susceptibility to fluoroquinolones (ciprofloxacin 12.8% and levofloxacin 16.2%).

Colistin had highest sensitivity, followed by carbapenems (ertapenem, imipenem, meropenem), while piperacillin-tazobactam and cefotaxime exhibited lower susceptibility rates. Aminoglycosides (amikacin) and fluoroquinolones (ciprofloxacin, levofloxacin) showed variable susceptibilities depending on the bacterial species.

Table 3.1: Species-wise Susceptibility of Enterobacterales isolated from all specimens except urine and faeces

AMA	<i>Escherichia coli</i>	<i>K. pneumoniae</i>	<i>K. oxytoca</i>	<i>Klebsiella (Enterobacter) aerogenes</i>	<i>Klebsiella spp.</i>	<i>Enterobacter cloacae</i>	<i>Enterobacter spp.</i>	<i>Proteus mirabilis</i>	<i>Citrobacter koseri</i>	<i>Citrobacter freundii</i>	<i>Citrobacter spp.</i>	<i>Serratia marcescens</i>	<i>Morganella morganii</i>	<i>Providencia stuartii</i>	<i>Providencia rettgeri</i>
	n=13026	n=12795	n=250	n=57	n=390	n=1489	n=194	n=1284	n=405	n=91	n=77	n=441	n=394	n=151	n=68
	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)
Piperacillin-tazobactam	3205 / 7559 (42.4%)	1939 / 7312 (26.5%)	48 / 131 (36.6%)	21 / 49 (42.9%)	50 / 182 (27.5%)	495 / 783 (63.2%)	56 / 120 (46.7%)	555 / 660 (84.1%)	144 / 226 (63.7%)	25 / 52 (48.1%)	25 / 42 (59.5%)	115 / 220 (52.3%)	185 / 229 (80.8%)	24 / 51 (47.1%)	19 / 36 (52.8%)
Cefotaxime	1021 / 6833 (14.9%)	1119 / 6479 (17.3%)	33 / 120 (27.5%)	12 / 42 (28.6%)	84 / 180 (46.7%)	307 / 679 (45.2%)	13 / 99 (13.1%)	261 / 586 (44.5%)	117 / 223 (52.5%)	13 / 45 (28.9%)	16 / 34 (47.1%)	63 / 216 (29.2%)	110 / 201 (54.7%)	17 / 50 (34%)	9 / 31 (29%)
Ceftazidime	935 / 4859 (19.2%)	915 / 5063 (18.1%)	37 / 115 (32.2%)	12 / 32 (37.5%)	69 / 158 (43.7%)	241 / 512 (47.1%)	24 / 113 (21.2%)	233 / 519 (44.9%)	84 / 172 (48.8%)	10 / 36 (27.8%)	5 (-)	84 / 197 (42.6%)	83 / 153 (54.2%)	12 / 41 (29.3%)	10 / 31 (32.3%)
Ertapenem	3364 / 5625 (59.8%)	1803 / 5275 (34.2%)	48 / 98 (49%)	21 / 32 (65.6%)	119 / 182 (65.4%)	368 / 501 (73.5%)	60 / 79 (75.9%)	282 / 348 (81%)	127 / 187 (67.9%)	26 / 34 (76.5%)	29 / 36 (80.6%)	113 / 156 (72.4%)	112 / 131 (85.5%)	10 / 14 (-)	13 / 23 (-)
Imipenem	4686 / 7472 (62.7%)	2568 / 7211 (35.6%)	58 / 124 (46.8%)	35 / 49 (71.4%)	106 / 176 (60.2%)	558 / 772 (72.3%)	83 / 122 (68%)	411 / 635 (64.7%)	140 / 207 (67.6%)	32 / 50 (64%)	26 / 37 (70.3%)	155 / 242 (64%)	122 / 204 (59.8%)	23 / 48 (47.9%)	19 / 35 (54.3%)
Meropenem	5006 / 7582 (66%)	2764 / 7335 (37.7%)	68 / 132 (51.5%)	40 / 49 (81.6%)	125 / 184 (67.9%)	580 / 779 (74.5%)	87 / 122 (71.3%)	528 / 668 (79%)	165 / 226 (73%)	36 / 52 (69.2%)	31 / 42 (73.8%)	195 / 274 (71.2%)	196 / 229 (85.6%)	33 / 51 (64.7%)	21 / 36 (58.3%)
Colistin*	3806 / 3832 (99.3%)	4048 / 4206 (96.2%)	69 / 69 (100.0)	19 / 19 (-)	46 / 50 (92.0)	305 / 327 (93.3)	305 / 327 (93.3)	305 / 327 (93.3)	58 / 58 (100.0)	29 / 30 (-)	27 / 28 (-)	-	-	-	-
Amikacin	5196 / 7611 (68.3%)	2539 / 7357 (34.5%)	64 / 132 (48.5%)	35 / 49 (71.4%)	104 / 184 (56.5%)	517 / 783 (66%)	76 / 122 (62.3%)	349 / 668 (52.2%)	159 / 226 (70.4%)	36 / 52 (69.2%)	31 / 42 (73.8%)	182 / 277 (65.7%)	165 / 229 (72.1%)	27 / 51 (52.9%)	21 / 36 (58.3%)
Ciprofloxacin	969 / 7597 (12.8%)	1258 / 7341 (17.1%)	43 / 132 (32.6%)	23 / 49 (46.9%)	92 / 184 (50%)	386 / 784 (49.2%)	61 / 122 (50%)	181 / 666 (27.2%)	139 / 226 (61.5%)	19 / 52 (36.5%)	24 / 42 (57.1%)	136 / 274 (49.6%)	70 / 229 (30.6%)	16 / 51 (31.4%)	12 / 36 (33.3%)
Levofloxacin	567 / 3500 (16.2%)	647 / 3709 (17.4%)	28 / 101 (27.7%)	15 / 35 (42.9%)	73 / 157 (46.5%)	135 / 273 (49.5%)	43 / 69 (62.3%)	72 / 331 (21.8%)	62 / 134 (46.3%)	9 / 27 (-)	5 / 12 (-)	58 / 121 (47.9%)	30 / 76 (39.5%)	1 / 15 (-)	4 / 23 (-)

* Colistin represents the percentage of Intermediate susceptibility

Escherichia coli

Out of a total of 13,026 *E. coli* isolates, 21.8% were from outpatient (OPD), 63.3% were from various wards, and 14.8% were from Intensive Care Units (ICU) (**Table 3.2**). For piperacillin-tazobactam, the overall susceptibility was 42.4%, with OPD showing higher susceptibility (51.4%) compared to the ward (40.1%) and ICU (39.4%). Among carbapenems, meropenem exhibited the highest susceptibility, 66% overall, 72.6% OPD, 66.4% ward, and 55.6% ICU. Colistin demonstrated near-universal effectiveness with a total susceptibility of 99.3%, 99.1% in OPD, 99.3% in Ward, and 99.7% in ICU. *E.coli* showed poor susceptibility to cefotaxime, ceftazidime, ciprofloxacin, and levofloxacin, with less than 20% overall susceptibility.

In summary, the OPD isolates showed the highest antibiotic susceptibilities while the isolates from the ICU showed the lowest susceptibilities across most antibiotics tested. Isolates from the wards demonstrated higher susceptibility than those from the ICU, but lower susceptibility compared to isolates from the OPD.

Table 3.2 Location-wise susceptible percentages of *Escherichia coli* isolated from all specimens except urine and faeces across OPD, ward, and ICU

AMA	Total n=13026	OPD n=2841	Ward n=8254	ICU n=1931
	(S %)	(S %)	(S %)	(S %)
Piperacillin-tazobactam	3205 / 7559 (42.4)	818 / 1590 (51.4%)	1936 / 4824 (40.1%)	451 / 1145 (39.4%)
Cefotaxime	1021 / 6833 (14.9)	278 / 1444 (19.3%)	607 / 4335 (14%)	136 / 1054 (12.9%)
Ceftazidime	935 / 4859 (19.2)	280 / 1052 (26.6%)	561 / 3080 (18.2%)	94 / 727 (12.9%)
Ertapenem	3364 / 5625 (59.8)	830 / 1227 (67.6%)	2026 / 3437 (58.9%)	508 / 961 (52.9%)
Imipenem	4686 / 7472 (62.7)	1070 / 1568 (68.2%)	3051 / 4781 (63.8%)	565 / 1123 (50.3%)
Meropenem	5006 / 7582 (66.0)	1155 / 1592 (72.6%)	3213 / 4842 (66.4%)	638 / 1148 (55.6%)
Colistin*	3806 / 3832 (99.3)	775 / 782 (99.1)	2385 / 2402 (99.3)	646 / 648 (99.7)
Amikacin	5196 / 7611 (68.3)	1121 / 1595 (70.3%)	3360 / 4863 (69.1%)	715 / 1153 (62%)
Ciprofloxacin	969 / 7597 (12.8)	266 / 1597 (16.7%)	569 / 4850 (11.7%)	134 / 1150 (11.7%)
Levofloxacin	567 / 3500 (16.2)	143 / 715 (20%)	354 / 2209 (16%)	70 / 576 (12.2%)

*Colistin represents the percentage of Intermediate susceptibility

Klebsiella pneumoniae

A total of 12,795 *K. pneumoniae* isolates from OPD (18%), ward (53.3%), and ICU (28.7%) were tested for antibiotics including piperacillin-tazobactam, cefotaxime,

ceftazidime, ertapenem, imipenem, meropenem, colistin, amikacin, ciprofloxacin, and levofloxacin (**Table 3.3**). Cefotaxime, ceftazidime, ciprofloxacin, and levofloxacin had an overall susceptibility of less than 20%. Colistin showed an overall susceptibility of 96.2%, lowest in the ICU isolates. Among carbapenems, overall susceptibility was approximately 35%, lowest in ICU isolates (average of 23.5%).

Generally, the OPD category had the highest susceptibilities, while the ICU category showed the lowest susceptibilities for most antibiotics tested. Isolates from the wards showed higher susceptibility than the ICU isolates, but lower susceptibility compared to isolates from the OPD.

Table 3.3: Comparison of Susceptibility of *Klebsiella pneumoniae* isolated from OPD, ward, and ICU isolated from all samples (except faeces and urine)

AMA	Total n=12795	OPD n=2303	Ward n=6819	ICU n=3673
	(S %)	(S %)	(S %)	(S %)
Piperacillin-tazobactam	1939 / 7312 (26.5)	524 / 1194 (43.9%)	1022 / 3919 (26.1%)	393 / 2199 (17.9%)
Cefotaxime	1119 / 6479 (17.3)	370 / 1104 (33.5%)	560 / 3495 (16%)	189 / 1880 (10.1%)
Ceftazidime	915 / 5063 (18.1)	337 / 882 (38.2%)	449 / 2734 (16.4%)	129 / 1447 (8.9%)
Ertapenem	1803 / 5275 (34.2)	466 / 841 (55.4%)	909 / 2667 (34.1%)	428 / 1767 (24.2%)
Imipenem	2568 / 7211 (35.6)	632 / 1157 (54.6%)	1449 / 3878 (37.4%)	487 / 2176 (22.4%)
Meropenem	2764 / 7335 (37.7)	694 / 1195 (58.1%)	1544 / 3935 (39.2%)	526 / 2205 (23.9%)
Colistin*	4048 / 4206 (96.2)	564 / 573 (98.4)	2065 / 2147 (96.2)	1419 / 1486 (95.5)
Amikacin	2539 / 7357 (34.5)	626 / 1198 (52.3%)	1360 / 3947 (34.5%)	553 / 2212 (25%)
Ciprofloxacin	1258 / 7341 (17.1)	383 / 1197 (32%)	648 / 3940 (16.4%)	227 / 2204 (10.3%)
Levofloxacin	647 / 3709 (17.4)	198 / 596 (33.2%)	330 / 1934 (17.1%)	119 / 1179 (10.1%)

* Colistin represents the percentage of Intermediate susceptibility

Enterobacter cloacae

For *Enterobacter cloacae*, a total of 1,489 bacterial isolates were tested for antibiotics, including piperacillin-tazobactam, cefotaxime, ceftazidime, ertapenem, imipenem, meropenem, amikacin, ciprofloxacin, and levofloxacin. The breakup of the isolates was as follows: OPD (27.3%), ward (56.2%), and ICU (16.4%). Carbapenems (meropenem, ertapenem, and imipenem) were the most effective antibiotics, especially in the OPD setting, where 87.4% of strains were susceptible to carbapenems. The isolates from the ICU showed the lowest susceptibilities across most antibiotics tested (**Table 3.4**).

Table 3.4: Comparison of Susceptibility of *Enterobacter cloacae* isolated from OPD, ward, and ICU isolated from all samples (except faeces and urine)

AMA	Total n=1489	OPD n=407	Ward n=837	ICU n=245
	(S %)	(S %)	(S %)	(S %)
Piperacillin-tazobactam	495 / 783 (63.2)	166 / 213 (77.9%)	257 / 435 (59.1%)	72 / 135 (53.3%)
Cefotaxime	307 / 679 (45.2)	123 / 190 (64.7%)	141 / 375 (37.6%)	43 / 114 (37.7%)
Ceftazidime	241 / 512 (47.1)	94 / 133 (70.7%)	121 / 299 (40.5%)	26 / 80 (32.5%)
Ertapenem	368 / 501 (73.5)	110 / 132 (83.3%)	202 / 275 (73.5%)	56 / 94 (59.6%)
Imipenem	558 / 772 (72.3)	184 / 208 (88.5%)	301 / 430 (70%)	73 / 134 (54.5%)
Meropenem	580 / 779 (74.5)	192 / 212 (90.6%)	308 / 432 (71.3%)	80 / 135 (59.3%)
Amikacin	517 / 783 (66.0)	149 / 212 (70.3%)	286 / 436 (65.6%)	82 / 135 (60.7%)
Ciprofloxacin	386 / 784 (49.2)	147 / 213 (69%)	192 / 436 (44%)	47 / 135 (34.8%)
Levofloxacin	135 / 273 (49.5)	35 / 59 (59.3%)	82 / 160 (51.3%)	18 / 54 (33.3%)

Citrobacter koserii

A total of 405 *C. koserii* isolates were screened for various antibiotics. These isolates were from OPD (33.3%), ward (42%), and ICU (24.6%). Carbapenems and amikacin were the most susceptible antibiotics in all the isolates (**Table 3.5**).

Table 3.5: Comparison of Susceptibility of *Citrobacter koserii* isolated from OPD, ward, and ICU from all samples (except faeces and urine)

AMA	Total n= 405	OPD n= 135	Ward n=170	ICU n=100
	(S %)	(S %)	(S %)	(S %)
Piperacillin-tazobactam	144 / 226 (63.7)	59 / 75 (78.7%)	54 / 83 (65.1%)	31 / 68 (45.6%)
Cefotaxime	117 / 223 (52.5)	54 / 73 (74%)	43 / 82 (52.4%)	20 / 68 (29.4%)
Ceftazidime	84 / 172 (48.8)	35 / 51 (68.6%)	33 / 64 (51.6%)	16 / 57 (28.1%)
Ertapenem	127 / 187 (67.9)	50 / 54 (92.6%)	44 / 65 (67.7%)	33 / 68 (48.5%)
Imipenem	140 / 207 (67.6)	58 / 67 (86.6%)	52 / 74 (70.3%)	30 / 66 (45.5%)
Meropenem	165 / 226 (73.0)	69 / 75 (92%)	63 / 83 (75.9%)	33 / 68 (48.5%)
Amikacin	159 / 226 (70.4)	64 / 75 (85.3%)	57 / 83 (68.7%)	38 / 68 (55.9%)
Ciprofloxacin	139 / 226 (61.5)	60 / 75 (80%)	53 / 83 (63.9%)	26 / 68 (38.2%)
Levofloxacin	62 / 134 (46.3)	19 / 29 (65.5%)	26 / 48 (54.2%)	17 / 57 (29.8%)

Yearly susceptibility trends of different Enterobacterales

Over the last seven years (2017-2023), the susceptibility trends for *E. coli*, *Klebsiella pneumoniae*, *Enterobacter* species, and *Citrobacter* species isolated from non-fecal and non-urine samples show a general decline in antibiotic susceptibilities. *E. coli* demonstrated a decrease in susceptibility across most antibiotics, with piperacillin-tazobactam dropping from 56.8% in 2017 to 42.4% in 2023, amikacin from 79.2% in the year 2017 to 68.2% in 2023, and significant decline in susceptibility for carbapenems (81.4% to 62.7% for imipenem and 73.2% to 66.0% for meropenem) (**Table 3.6 and Figure 3.1**). *Klebsiella pneumoniae* also showed reduced susceptibility, notably with piperacillin-tazobactam falling from 42.6% to 26.5%, carbapenems (imipenem from 58.5% to 35.6% and meropenem from 48% to 37.6%), fluoroquinolones (ciprofloxacin from 32% to 17.1%) over seven years (**Table 3.7 and Figure 3.2**). *Enterobacter* species exhibited variable trends but, overall, a decreasing pattern, particularly with piperacillin-tazobactam (from 62.5% to 42.6%) and cefotaxime (from 28.4% to 13.1%) (**Table 3.8 and Figure 3.3**). *Citrobacter* species maintained relatively higher susceptibility rates for some antibiotics but still showed declines, particularly in levofloxacin (from 51.2% to 41.6%) (**Table 3.9 and Figure 3.4**).

Table 3.6: 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
	Total n=6282	Total n=9187	Total n=13133	Total n=8198	Total n=13533	Total n=14728	Total n=13026
Piperacillin-tazobactam	3424/6030 (56.8)	4857/8961 (54.2)	6620/12121 (54.6)	4211/7890 (53.4)	6126/12935 (47.4)	5170 / 14729 (35.10)	3205 / 7559 (42.4)
Cefazolin	*0/8	*2/6	*0/1	*0/4	*0/1	5/22 (22.7)	8 / 18 (-)
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 (14.94)
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)
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)
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)
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)
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)
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)
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)

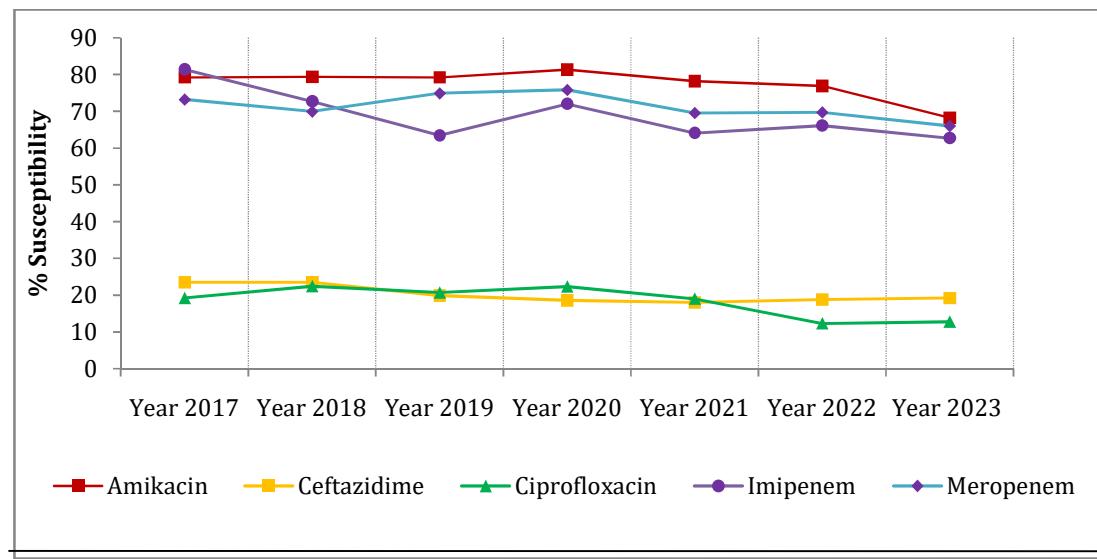


Figure 3.1: Yearly susceptibility trend of *E. coli* isolated from all samples (except faeces and urine)

Table 3.7: Yearly susceptibility trend of *Klebsiella pneumoniae* isolated from all samples (except faeces and urine)

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Total n=5389	Total n=8394	Total n=13381	Total n=8932	Total n=13633	Total n=15008	Total n=12795	
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 (26.52)
Cefazolin	*0/3	*0/0	*0/1	*0/3	*1/3	5/16 (31.3)	2 / 12 (-)
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 (17.27)
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 (18.07)
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)
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)
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)
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 (34.51)
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)
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 (17.44)

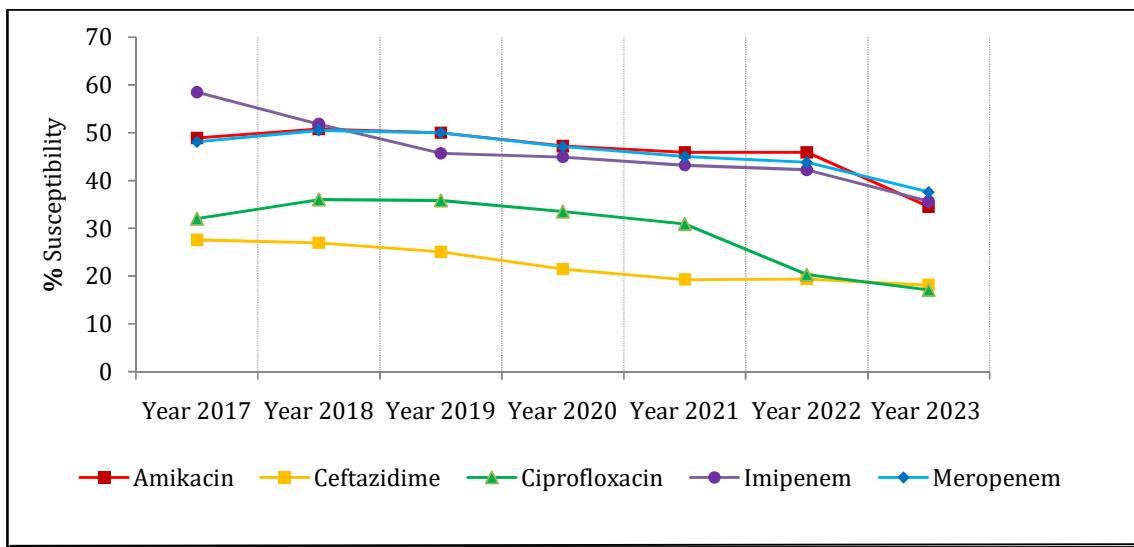


Figure 3.2: Yearly susceptibility trend of *Klebsiella pneumoniae* isolated from all samples (except faeces and urine)

Table 3.8: 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
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
	Total n=1140	Total n=1600	Total n=2071	Total n=1287	Total n=393	Total n=324	Total n=194
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)
Cefazolin	*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)
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)
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)
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)
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)
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)
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)
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)

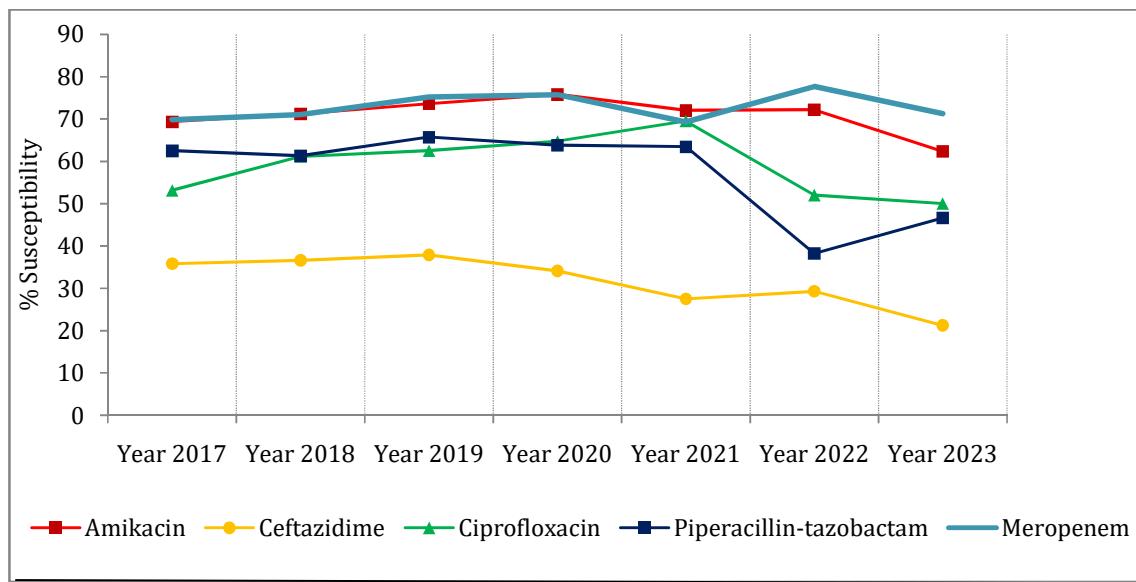


Figure 3.3: Yearly susceptibility trend of *Enterobacter* species isolated from all samples (except faeces and urine)

Table 3.9: 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
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
	Total n=321	Total n=613	Total n=796	Total n=447	Total n=136	Total n=139	Total n=77
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)
Cefazolin	*0/0	*0/0	*0/0	*0/0	*0/0	*0/0	0 / 0
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)
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 (-)
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)
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)
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)
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)
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)
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)

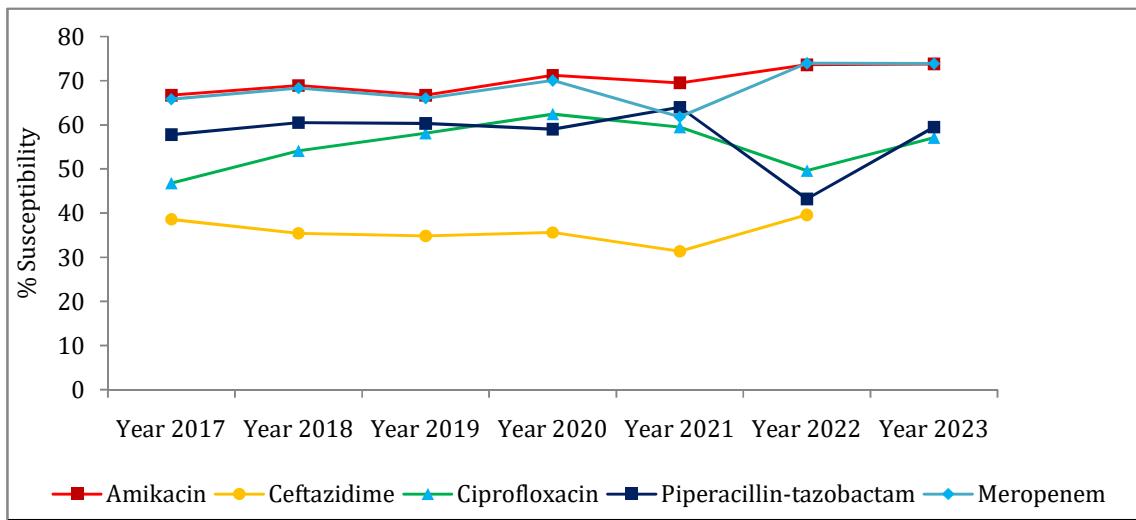


Figure 3.4: Yearly susceptibility trend of *Citrobacter* species isolated from all samples (except faeces and urine)

Analysis of results from individual Regional Centers (RCs)

Twenty-one regional centers (RCs) from various parts of the country, both public and private sectors, participated in the surveillance. The results of all centers for the designated organisms and antibiotics were used for overall susceptibility, but only those drug-pathogen combinations where the number tested was 30 or more were used for RC-wise analyses. The susceptibility profiles showed considerable variation between the RCs.

Escherichia coli

The overall susceptibility to piperacillin-tazobactam was 42.4%, with eight RCs showing more than 50% susceptibility. The overall susceptibility of cefotaxime, ceftazidime, ciprofloxacin, and levofloxacin was below 20%. Among carbapenems, meropenems showed the maximum susceptibility of 66%, followed by imipenem (62.7%) and ertapenem (59.8%). Amikacin retained a relatively higher susceptibility (68.3%) (**Table 3.10**).

K. pneumoniae

The overall susceptibility to piperacillin-tazobactam was 26.5%, with only RC14 showing a susceptibility of 50%. The overall susceptibility of cefotaxime, ceftazidime, ciprofloxacin, and levofloxacin was below 20%. Among carbapenems, meropenems showed the maximum susceptibility of 37.7%, followed by imipenem (35.6%) and ertapenem (34.2%) (**Table 3.11**).

Table 3.10: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Escherichia coli* from Total (Except Faeces & Urine)

RC	Piperacillin-tazobactam (n=12815)	Cefotaxime (n=11805)	Ceftazidime (n=7768)	Ertapenem (n=9563)	Imipenem (n=12855)	Meropenem (n=13016)	Amikacin (n=13016)	Ciprofloxacin (n=13016)	Levofloxacin (n=5696)
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	136 / 391 (34.8)	42 / 391 (10.7)	69 / 391 (17.6)	163 / 391 (41.7)	190 / 391 (48.6)	201 / 391 (51.4)	249 / 391 (63.7)	25 / 391 (6.4)	88 / 391 (22.5)
RC2	556 / 1553 (35.8)	65 / 1222 (5.3)	96 / 549 (17.5)	458 / 961 (47.7)	771 / 1578 (48.9)	861 / 1574 (54.7)	1163 / 1578 (73.7)	130 / 1575 (8.3)	10 / 127 (7.9)
RC3	182 / 502 (36.3)	136 / 504 (27.0)	148 / 504 (29.4)	422 / 504 (83.7)	425 / 504 (84.3)	424 / 504 (84.1)	318 / 504 (63.1)	138 / 504 (27.4)	149 / 504 (29.6)
RC4	521 / 988 (52.7)	207 / 977 (21.2)	232 / 959 (24.2)	133 / 204 (65.2)	694 / 978 (71.0)	694 / 979 (70.9)	580 / 1004 (57.8)	229 / 993 (23.1)	0 / 0 (-)
RC5	173 / 306 (56.5)	0 / 275 (0.0)	1 / 23 (-)	216 / 306 (70.6)	255 / 306 (83.3)	243 / 306 (79.4)	271 / 306 (88.6)	28 / 306 (9.2)	0 / 1 (-)
RC6	113 / 237 (47.7)	1 / 13 (-)	2 / 3 (-)	156 / 236 (66.1)	166 / 237 (70.0)	162 / 237 (68.4)	174 / 237 (73.4)	2 / 237 (0.8)	1 / 4 (-)
RC7	62 / 111 (55.9)	4 / 44 (9.1)	18 / 34 (52.9)	79 / 100 (79.0)	85 / 109 (78.0)	93 / 115 (80.9)	87 / 115 (75.7)	11 / 115 (9.6)	2 / 20 (-)
RC8	163 / 264 (61.7)	68 / 255 (26.7)	87 / 263 (33.1)	195 / 256 (76.2)	215 / 264 (81.4)	210 / 264 (79.5)	232 / 264 (87.9)	23 / 264 (8.7)	26 / 262 (9.9)
RC9	116 / 203 (57.1)	49 / 203 (24.1)	69 / 203 (34.0)	133 / 203 (65.5)	126 / 203 (62.1)	156 / 203 (76.8)	133 / 203 (65.5)	39 / 203 (19.2)	55 / 203 (27.1)
RC10	246 / 403 (61.0)	111 / 403 (27.5)	0 / 0 (-)	335 / 403 (83.1)	261 / 322 (81.1)	336 / 403 (83.4)	353 / 403 (87.6)	66 / 403 (16.4)	0 / 0 (-)

RC11	28 / 111 (25.2)	10 / 110 (9.1)	14 / 110 (12.7)	40 / 94 (42.6)	52 / 111 (46.8)	52 / 111 (46.8)	57 / 111 (51.4)	8 / 111 (7.2)	11 / 110 (10.0)
RC12	38 / 182 (20.9)	2 / 151 (1.3)	13 / 176 (7.4)	80 / 178 (44.9)	87 / 180 (48.3)	90 / 182 (49.5)	95 / 182 (52.2)	2 / 182 (1.1)	6 / 163 (3.7)
RC13	49 / 108 (45.4)	58 / 108 (53.7)	1 / 11 (-)	23 / 35 (65.7)	86 / 109 (78.9)	91 / 109 (83.5)	81 / 109 (74.3)	5 / 109 (4.6)	6 / 77 (7.8)
RC14	231 / 380 (60.8)	68 / 380 (17.9)	0 / 0 (-)	287 / 380 (75.5)	323 / 380 (85.0)	321 / 380 (84.5)	329 / 380 (86.6)	18 / 380 (4.7)	0 / 0 (-)
RC15	135 / 309 (43.7)	27 / 310 (8.7)	31 / 287 (10.8)	3 / 3 (-)	301 / 310 (97.1)	300 / 310 (96.8)	270 / 310 (87.1)	13 / 310 (4.2)	37 / 305 (12.1)
RC16	15 / 198 (7.6)	6 / 199 (3.0)	12 / 199 (6.0)	95 / 199 (47.7)	80 / 199 (40.2)	135 / 199 (67.8)	50 / 199 (25.1)	23 / 199 (11.6)	40 / 199 (20.1)
RC17	111 / 151 (73.5)	119 / 148 (80.4)	6 / 7 (-)	117 / 152 (77.0)	120 / 152 (78.9)	119 / 152 (78.3)	125 / 152 (82.2)	113 / 152 (74.3)	0 / 0 (-)
RC18	15 / 45 (33.3)	4 / 45 (8.9)	4 / 45 (8.9)	19 / 45 (42.2)	24 / 45 (53.3)	23 / 45 (51.1)	26 / 45 (57.8)	16 / 45 (35.6)	18 / 45 (40.0)
RC19	267 / 818 (32.6)	29 / 818 (3.5)	116 / 819 (14.2)	333 / 819 (40.7)	267 / 819 (32.6)	322 / 819 (39.3)	392 / 819 (47.9)	57 / 819 (7.0)	82 / 819 (10.0)
RC20	45 / 256 (17.6)	12 / 242 (5.0)	12 / 238 (5.0)	72 / 151 (47.7)	136 / 232 (58.6)	154 / 256 (60.2)	207 / 256 (80.9)	22 / 256 (8.6)	33 / 231 (14.3)
RC21	3 / 43 (7.0)	3 / 35 (8.6)	4 / 38 (10.5)	5 / 5 (-)	22 / 43 (51.2)	19 / 43 (44.2)	4 / 43 (9.3)	1 / 43 (2.3)	3 / 39 (7.7)
Total	3205 / 7559 (42.4)	1021 / 6833 (14.9)	935 / 4859 (19.2)	3364 / 5625 (59.8)	4686 / 7472 (62.7)	5006 / 7582 (66.0)	5196 / 7611 (68.3)	969 / 7597 (12.8)	567 / 3500 (16.2)

Table 3.11: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *K. pneumoniae* from total (Except faeces & urine)

RC	Piperacillin-tazobactam (n=12577)	Cefotaxime (n=11306)	Ceftazidime (n=8073)	Ertapenem (n=9072)	Imipenem (n=12631)	Meropenem (n=12779)	Amikacin (n=12779)	Ciprofloxacin (n=12779)	Levofloxacin (n=6001)
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	77 / 362 (21.3)	42 / 362 (11.6)	49 / 362 (13.5)	92 / 362 (25.4)	103 / 362 (28.5)	99 / 362 (27.3)	103 / 362 (28.5)	48 / 362 (13.3)	72 / 362 (19.9)
RC2	174 / 837 (20.8)	45 / 573 (7.9)	68 / 431 (15.8)	88 / 354 (24.9)	181 / 854 (21.2)	208 / 854 (24.4)	267 / 859 (31.1)	85 / 854 (10.0)	6 / 75 (8.0)
RC3	36 / 143 (25.2)	58 / 143 (40.6)	60 / 143 (42.0)	79 / 143 (55.2)	80 / 143 (55.9)	81 / 143 (56.6)	69 / 143 (48.3)	61 / 143 (42.7)	62 / 143 (43.4)
RC4	427 / 1076 (39.7)	317 / 1064 (29.8)	371 / 1037 (35.8)	48 / 167 (28.7)	578 / 1065 (54.3)	578 / 1066 (54.2)	366 / 1080 (33.9)	294 / 1071 (27.5)	0 / 1 (-)
RC5	148 / 282 (52.5)	23 / 255 (9.0)	4 / 23 (-)	181 / 283 (64.0)	186 / 283 (65.7)	186 / 283 (65.7)	203 / 283 (71.7)	92 / 283 (32.5)	0 / 0 (-)
RC6	78 / 413 (18.9)	2 / 26 (-)	0 / 4 (-)	98 / 411 (23.8)	105 / 413 (25.4)	104 / 413 (25.2)	115 / 413 (27.8)	39 / 413 (9.4)	0 / 6 (-)
RC7	34 / 138 (24.6)	5 / 52 (9.6)	14 / 40 (35.0)	38 / 115 (33.0)	39 / 138 (28.3)	41 / 142 (28.9)	55 / 143 (38.5)	24 / 142 (16.9)	1 / 16 (0)
RC8	84 / 279 (30.1)	64 / 274 (23.4)	74 / 279 (26.5)	96 / 275 (34.9)	102 / 279 (36.6)	105 / 279 (37.6)	109 / 279 (39.1)	59 / 279 (21.1)	57 / 277 (20.6)
RC9	93 / 251 (37.1)	66 / 249 (26.5)	73 / 250 (29.2)	95 / 251 (37.8)	85 / 251 (33.9)	101 / 251 (40.2)	102 / 251 (40.6)	58 / 251 (23.1)	91 / 250 (36.4)
RC10	188 / 474 (39.7)	169 / 475 (35.6)	0 / 1 (-)	264 / 476 (55.5)	169 / 373 (45.3)	269 / 476 (56.5)	268 / 476 (56.3)	142 / 476 (29.8)	0 / 0 (-)
RC11	20 / 287 (7.0)	19 / 287 (6.6)	24 / 287 (8.4)	25 / 222 (11.3)	47 / 289 (16.3)	47 / 289 (16.3)	33 / 290 (11.4)	15 / 289 (5.2)	23 / 282 (8.2)

RC12	24 / 187 (12.8)	6 / 157 (3.8)	17 / 178 (9.6)	27 / 179 (15.1)	29 / 188 (15.4)	31 / 188 (16.5)	36 / 189 (19.0)	11 / 188 (5.9)	19 / 166 (11.4)
RC13	12 / 78 (15.4)	18 / 81 (22.2)	2 / 12 (-)	5 / 27 (-)	25 / 81 (30.9)	28 / 81 (34.6)	23 / 81 (28.4)	3 / 81 (3.7)	8 / 52 (15.4)
RC14	134 / 268 (50.0)	104 / 268 (38.8)	0 / 1 (-)	166 / 267 (62.2)	171 / 268 (63.8)	173 / 268 (64.6)	166 / 268 (61.9)	80 / 268 (29.9)	0 / 0 (-)
RC15	75 / 376 (19.9)	29 / 376 (7.7)	25 / 316 (7.9)	9 / 27 (-)	194 / 377 (51.5)	188 / 377 (49.9)	110 / 377 (29.2)	27 / 377 (7.2)	50 / 374 (13.4)
RC16	9 / 218 (4.1)	6 / 218 (2.8)	13 / 217 (6.0)	86 / 218 (39.4)	56 / 218 (25.7)	103 / 218 (47.2)	53 / 218 (24.3)	30 / 218 (13.8)	54 / 216 (25.0)
RC17	54 / 141 (38.3)	66 / 139 (47.5)	5 / 7 (-)	63 / 141 (44.7)	64 / 141 (45.4)	63 / 141 (44.7)	74 / 141 (52.5)	63 / 141 (44.7)	0 / 0 (-)
RC18	41 / 91 (45.1)	25 / 91 (27.5)	13 / 91 (14.3)	53 / 91 (58.2)	54 / 91 (59.3)	56 / 91 (61.5)	51 / 91 (56.0)	41 / 91 (45.1)	50 / 91 (54.9)
RC19	219 / 1131 (19.4)	28 / 1131 (2.5)	86 / 1132 (7.6)	270 / 1132 (23.9)	235 / 1132 (20.8)	246 / 1132 (21.7)	281 / 1132 (24.8)	56 / 1132 (4.9)	105 / 1132 (9.3)
RC20	11 / 206 (5.3)	15 / 190 (7.9)	14 / 185 (7.6)	19 / 126 (15.1)	40 / 191 (20.9)	42 / 207 (20.3)	54 / 207 (26.1)	23 / 207 (11.1)	29 / 195 (14.9)
RC21	1 / 74 (1.4)	12 / 68 (17.6)	3 / 67 (4.5)	1 / 8 (-)	25 / 74 (33.8)	15 / 74 (20.3)	1 / 74 (1.4)	7 / 75 (9.3)	20 / 71 (28.2)
Total	1939 / 7312 (26.5)	1119 / 6479 (17.3)	915 / 5063 (18.1)	1803 / 5275 (34.2)	2568 / 7211 (35.6)	2764 / 7335 (37.7)	2539 / 7357 (34.5)	1258 / 7341 (17.1)	647 / 3709 (17.4)

Proteus mirabilis

The overall susceptibility to piperacillin-tazobactam was 84.1%. The overall susceptibility of ciprofloxacin and levofloxacin was below 30%. Among carbapenems, ertapenem (81%) showed the maximum susceptibility, followed by meropenem (79%) and imipenem (64.7%) (**Table 3.12**).

Table 3.12: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Proteus mirabilis* from Total (Except Faeces & Urine)

RC	Piperacillin-tazobactam (n=1237)	Cefotaxime (n=1154)	Ceftazidime (n=897)	Ertapenem (n=594)	Imipenem (n=1234)	Meropenem (n=1284)	Amikacin (n=1284)	Ciprofloxacin (n=1284)	Levofloxacin (n=588)
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	15 / 18 (-)	4 / 18 (-)	4 / 18 (-)	7 / 18 (-)	11 / 18 (-)	13 / 18 (-)	8 / 18 (-)	4 / 18 (-)	5 / 18 (-)
RC2	52 / 68 (76.5)	2 / 30 (6.7)	13 / 56 (23.2)	2 / 15 (-)	17 / 71 (23.9)	37 / 70 (52.9)	39 / 71 (54.9)	8 / 70 (11.4)	4 / 37 (10.8)
RC3	6 / 7 (-)	4 / 7 (-)	4 / 7 (-)	6 / 7 (-)	6 / 7 (-)	6 / 7 (-)	5 / 7 (-)	2 / 7 (-)	2 / 7 (-)
RC4	157 / 175 (89.7)	102 / 175 (58.3)	106 / 172 (61.6)	1 / 4 (-)	164 / 178 (92.1)	164 / 177 (92.7)	75 / 176 (42.6)	81 / 175 (46.3)	0 / 0 (-)
RC5	16 / 16 (-)	10 / 15 (-)	0 / 0 (-)	16 / 16 (-)	16 / 16 (-)	16 / 16 (-)	11 / 16 (-)	7 / 16 (-)	0 / 0 (-)
RC6	17 / 20 (-)	0 / 0 (-)	0 / 0 (-)	19 / 21 (-)	14 / 21 (-)	19 / 21 (-)	13 / 21 (-)	10 / 21 (-)	0 / 0 (-)
RC7	12 / 17 (-)	1 / 6 (-)	2 / 7 (-)	4 / 9 (-)	0 / 17 (-)	7 / 18 (-)	7 / 18 (-)	1 / 18 (-)	0 / 6 (-)
RC8	16 / 16 (-)	11 / 15 (-)	14 / 17 (-)	14 / 15 (-)	8 / 17 (-)	16 / 17 (-)	15 / 17 (-)	7 / 17 (-)	6 / 17 (-)

RC9	8 / 12 (-)	6 / 12 (-)	7 / 12 (-)	9 / 12 (-)	6 / 12 (-)	9 / 12 (-)	5 / 12 (-)	3 / 12 (-)	3 / 12 (-)
RC10	73 / 73 (100.0)	53 / 73 (72.6)	0 / 0 (-)	73 / 73 (100.0)	40 / 44 (90.9)	73 / 73 (100.0)	57 / 73 (78.1)	26 / 73 (35.6)	0 / 0 (-)
RC11	19 / 23 (-)	8 / 22 (-)	9 / 23 (-)	1 / 1 (-)	8 / 23 (-)	18 / 23 (-)	10 / 23 (-)	2 / 23 (-)	6 / 23 (-)
RC12	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)
RC13	2 / 2 (-)	3 / 3 (-)	1 / 1 (-)	1 / 1 (-)	3 / 3 (-)	3 / 3 (-)	2 / 3 (-)	0 / 3 (-)	1 / 2 (-)
RC14	4 / 4 (-)	2 / 4 (-)	0 / 0 (-)	4 / 4 (-)	2 / 4 (-)	4 / 4 (-)	2 / 4 (-)	0 / 4 (-)	0 / 0 (-)
RC15	40 / 41 (97.6)	20 / 41 (48.8)	21 / 40 (52.5)	0 / 0 (-)	41 / 41 (100.0)	41 / 41 (100.0)	37 / 41 (90.2)	4 / 41 (9.8)	13 / 41 (31.7)
RC16	7 / 12 (-)	4 / 12 (-)	4 / 12 (-)	7 / 12 (-)	6 / 12 (-)	11 / 12 (-)	4 / 12 (-)	7 / 12 (-)	7 / 12 (-)
RC17	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)	0 / 0 (-)
RC18	4 / 7 (-)	2 / 7 (-)	2 / 7 (-)	6 / 7 (-)	4 / 7 (-)	7 / 7 (-)	6 / 7 (-)	0 / 7 (-)	0 / 7 (-)
RC19	97 / 124 (78.2)	23 / 124 (18.5)	39 / 124 (31.5)	104 / 124 (83.9)	53 / 124 (42.7)	63 / 124 (50.8)	45 / 124 (36.3)	16 / 124 (12.9)	16 / 124 (12.9)
RC20	8 / 19 (-)	5 / 18 (-)	6 / 17 (-)	8 / 9 (-)	9 / 14 (-)	16 / 19 (-)	7 / 19 (-)	2 / 19 (-)	7 / 19 (-)
RC21	2 / 6 (-)	1 / 4 (-)	1 / 6 (-)	0 / 0 (-)	3 / 6 (-)	5 / 6 (-)	1 / 6 (-)	1 / 6 (-)	2 / 6 (-)
Total	555 / 660 (84.1)	261 / 586 (44.5)	233 / 519 (44.9)	282 / 348 (81.0)	411 / 635 (64.7)	528 / 668 (79.0)	349 / 668 (52.2)	181 / 666 (27.2)	72 / 331 (21.8)

Enterobacter cloacae

The overall susceptibility to piperacillin-tazobactam was 63.2%. The carbapenems showed maximum susceptibility (nearly 70%), followed by amikacin (66%). The overall susceptibility of cefotaxime, ceftazidime, ciprofloxacin, and levofloxacin was almost 50% (**Table 3.13**).

Table 3.13: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Enterobacter cloacae* from Total (Except Faeces & Urine)

RC	Piperacillin-tazobactam (n=1466)	Cefotaxime (n=1312)	Ceftazidime (n=905)	Ertapenem (n=877)	Imipenem (n=1470)	Meropenem (n=1489)	Amikacin (n=1489)	Ciprofloxacin (n=1489)	Levofloxacin (n=499)
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	44 / 64 (68.8)	30 / 64 (46.9)	32 / 64 (50.0)	44 / 64 (68.8)	44 / 64 (68.8)	49 / 64 (76.6)	40 / 64 (62.5)	23 / 64 (35.9)	33 / 64 (51.6)
RC2	44 / 67 (65.7)	1 / 50 (2.0)	24 / 51 (47.1)	7 / 8 (-)	37 / 68 (54.4)	43 / 68 (63.2)	55 / 68 (80.9)	25 / 68 (36.8)	4 / 6 (-)
RC3	0 / 2	0 / 2	0 / 2	2 / 2	2 / 2	2 / 2	0 / 2	2 / 2	2 / 2
RC4	120 / 196 (61.2)	89 / 190 (46.8)	104 / 189 (55.0)	31 / 37 (83.8)	150 / 190 (78.9)	150 / 190 (78.9)	97 / 194 (50.0)	103 / 196 (52.6)	0 / 0 (-)
RC5	37 / 49 (75.5)	0 / 15 (-)	1 / 4 (-)	41 / 49 (83.7)	43 / 49 (87.8)	43 / 49 (87.8)	43 / 49 (87.8)	30 / 49 (61.2)	0 / 0 (-)
RC6	13 / 23 (-)	0 / 1 (-)	0 / 0 (-)	14 / 23 (-)	16 / 23 (-)	16 / 23 (-)	16 / 23 (-)	6 / 23 (-)	0 / 1 (-)
RC7	9 / 16 (-)	1 / 5 (-)	2 / 3 (-)	11 / 16 (-)	11 / 16 (-)	11 / 16 (-)	11 / 16 (-)	10 / 16 (-)	0 / 2 (-)

RC8	30 / 37 (81.1)	25 / 35 (71.4)	28 / 36 (77.8)	33 / 35 (94.3)	35 / 37 (94.6)	35 / 37 (94.6)	37 / 37 (100.0)	26 / 37 (70.3)	26 / 37 (70.3)
RC9	6 / 8	6 / 8	6 / 8	6 / 8	4 / 8	6 / 8	4 / 8	6 / 8	6 / 8
RC10	56 / 73 (76.7)	57 / 73 (78.1)	0 / 0 (0)	61 / 73 (83.6)	56 / 67 (83.6)	62 / 73 (84.9)	61 / 73 (83.6)	60 / 73 (82.2)	0 / 0 (-)
RC11	16 / 56 (28.6)	10 / 55 (18.2)	11 / 55 (20.0)	10 / 29 (-)	17 / 56 (30.4)	20 / 57 (35.1)	19 / 57 (33.3)	11 / 56 (19.6)	15 / 52 (28.8)
RC12	11 / 35 (31.4)	5 / 28 (-)	12 / 34 (35.3)	18 / 35 (51.4)	20 / 35 (57.1)	20 / 35 (57.1)	19 / 35 (54.3)	18 / 35 (51.4)	18 / 34 (52.9)
RC13	7 / 12 (-)	1 / 12 (-)	1 / 4 (-)	2 / 3 (-)	9 / 12 (-)	10 / 12 (-)	3 / 12 (-)	3 / 12 (-)	4 / 8 (-)
RC14	55 / 68 (80.9)	50 / 68 (73.5)	0 / 0 (-)	61 / 68 (89.7)	64 / 68 (94.1)	62 / 68 (91.2)	66 / 68 (97.1)	38 / 68 (55.9)	0 / 0 (-)
RC15	21 / 23 (-)	13 / 23 (-)	14 / 23 (-)	0 / 0 (-)	22 / 23 (-)	23 / 23 (-)	21 / 23 (-)	4 / 23 (-)	14 / 23 (-)
RC16	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
RC17	12 / 16	13 / 16	1 / 3	15 / 16	12 / 16	12 / 16	12 / 16	11 / 16	0 / 0
RC18	2 / 5 (-)	0 / 5 (-)	0 / 5 (-)	1 / 5 (-)	3 / 5 (-)	3 / 5 (-)	2 / 5 (-)	2 / 5 (-)	2 / 5 (-)
RC19	9 / 28 (-)	5 / 28 (-)	5 / 28 (-)	9 / 28 (-)	9 / 28 (-)	9 / 28 (-)	8 / 28 (-)	5 / 28 (-)	10 / 28 (-)
RC20	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
RC21	3 / 5 (60.0)	1 / 1	0 / 3	2 / 2	4 / 5	4 / 5	3 / 5	3 / 5	1 / 3
Total	495 / 783 (63.2)	307 / 679 (45.2)	241 / 512 (47.1)	368 / 501 (73.5)	558 / 772 (72.3)	580 / 779 (74.5)	517 / 783 (66.0)	386 / 784 (49.2)	135 / 273 (49.5)

Species-wise susceptibility of Enterobacterales from urine

The antimicrobial susceptibility of various Enterobacterales species (14727) isolated from urine samples shows significant variability (**Figure 3.14**). *Escherichia coli* was the maximally isolated species (68%) from the urine samples. It showed high susceptibility to fosfomycin (93.7%) and nitrofurantoin (85.8%). Resistance to oral antibiotics like cefazolin, ciprofloxacin, and levofloxacin was very high. They were the least effective antibiotics, with susceptibilities of 10.4%, 7.9%, and 18.8% for cefazolin, ciprofloxacin, and levofloxacin, respectively. *Klebsiella pneumoniae* showed less susceptibility to almost all antibiotics except fosfomycin (59.9%). The organism showed a relatively better susceptibility to amikacin (44.4%) and the least susceptibility to cefazolin (8.7%). *Klebsiella oxytoca* demonstrated similar resistance patterns except for higher susceptibility to fosfomycin (74.7%) and nitrofurantoin (66.7%). *Enterobacter cloacae* showed a relatively higher susceptibility to carbapenem (imipenem, 73.7%; meropenem, 70.9%) and amikacin (72.6%). *Proteus mirabilis* was highly susceptible to piperacillin-tazobactam (80.7%), meropenem (79.5%), and fosfomycin (76.3%). *Citrobacter koseri* showed high susceptibility to fosfomycin (91.5%) and nitrofurantoin (77.0%). *Morganella morganii* demonstrated high susceptibility towards carbapenems (ertapenem-82.1%), followed by piperacillin-tazobactam (73.2%) and ceftazidime (68.1%).

This analysis highlights that *Escherichia coli*, the commonest uropathogen, has become resistant to third-generation cephalosporins, fluoroquinolones, and amikacin and developed resistance to other clinically relevant antimicrobials like piperacillin-tazobactam and ertapenem. Nitrofurantoin and fosfomycin are two oral antimicrobials having the best in-vitro susceptibility. *Klebsiella pneumoniae*, the second most common organism (23.7%), exhibited higher level of resistance, necessitating careful selection of antibiotics based on susceptibility profiles to manage urinary tract infections effectively.

Table 3.14: Species-wise Susceptibility of Enterobacterales isolated from urine

AMA	<i>Escherichia coli</i> n=10042	<i>Klebsiella pneumoniae</i> n=3496	<i>Klebsiella oxytoca</i> n=195	<i>Klebsiella spp.</i> n=32	<i>Enterobacter cloacae</i> n=219	<i>Enterobacter spp.</i> n=26	<i>Proteus mirabilis</i> n=261	<i>Citrobacter koseri</i> n=256	<i>Citrobacter freundii</i> n=49	<i>Morganella morganii</i> n=117	<i>Providencia rettgeri</i> n=34
Piperacillin-tazobactam	3277 / 5845 (56.1)	671 / 1998 (33.6)	20 / 82 (24.4)	7 / 19 (36.8)	70 / 117 (59.8)	2 / 11 (-)	121 / 150 (80.7)	106 / 143 (74.1)	11 / 24 (-)	56 / 76 (73.7)	7 / 18 (-)
Cefazolin	255 / 2446 (10.4)	72 / 824 (8.7)	4 / 65 (6.2)	0 / 11 (-)	3 / 30 (10.0)	0 / 7 (-)	3 / 48 (6.3)	6 / 59 (10.2)	1 / 9 (-)	1 / 22 (-)	0 / 5 (-)
Cefotaxime	1253 / 5356 (23.4)	390 / 1782 (21.9)	12 / 78 (15.4)	7 / 19 (36.8)	47 / 105 (44.8)	1 / 10 (-)	62 / 130 (47.7)	79 / 139 (56.8)	8 / 21 (-)	36 / 69 (52.2)	5 / 18 (-)
Ceftazidime	727 / 3289 (22.1)	214 / 1193 (17.9)	12 / 70 (17.1)	0 / 11 (-)	27 / 55 (49.1)	0 / 8 (-)	35 / 88 (39.8)	44 / 82 (53.7)	5 / 16 (-)	32 / 47 (68.1)	2 / 11 (-)
Ertapenem	3639 / 4972 (73.2)	744 / 1712 (43.5)	28 / 78 (35.9)	11 / 19 (-)	71 / 103 (68.9)	4 / 11 (-)	97 / 123 (78.9)	100 / 128 (78.1)	15 / 24 (-)	55 / 67 (82.1)	6 / 18 (-)
Imipenem	4055 / 5630 (72.0)	796 / 1931 (41.2)	29 / 82 (35.4)	5 / 15 (-)	84 / 114 (73.7)	2 / 10 (-)	75 / 133 (56.4)	89 / 123 (72.4)	13 / 24 (-)	37 / 64 (57.8)	3 / 17 (-)
Meropenem	4526 / 5859 (77.2)	903 / 2006 (45.0)	40 / 82 (48.8)	12 / 19 (-)	83 / 117 (70.9)	4 / 11 (-)	120 / 151 (79.5)	124 / 144 (86.1)	15 / 24 (-)	67 / 78 (85.9)	5 / 18 (-)
Amikacin	4163 / 5858 (71.1)	890 / 2006 (44.4)	38 / 83 (45.8)	12 / 19 (-)	85 / 117 (72.6)	3 / 11 (-)	83 / 151 (55.0)	104 / 144 (72.2)	14 / 24 (-)	62 / 78 (79.5)	7 / 18 (-)
Ciprofloxacin	1050 / 5858 (17.9)	410 / 2005 (20.4)	19 / 82 (23.2)	6 / 19 (-)	65 / 117 (55.6)	2 / 11 (-)	42 / 151 (27.8)	99 / 144 (68.8)	7 / 24 (-)	33 / 78 (42.3)	5 / 18 (-)
Levofloxacin	517 / 2752 (18.8)	159 / 1078 (14.7)	12 / 69 (17.4)	3 / 11 (-)	19 / 40 (47.5)	1 / 8 (-)	20 / 74 (27.0)	36 / 67 (53.7)	6 / 16 (-)	13 / 35 (37.1)	2 / 12 (-)
Trimethoprim-sulfamethoxazole	2334 / 4954 (47.1)	689 / 1722 (40.0)	33 / 75 (44.0)	11 / 19 (-)	64 / 103 (62.1)	1 / 8 (-)	48 / 130 (36.9)	92 / 125 (73.6)	14 / 23 (-)	36 / 65 (55.4)	7 / 16 (-)
Fosfomycin	3477 / 3711 (93.7)	748 / 1248 (59.9)	56 / 75 (74.7)	5 / 12 (-)	34 / 63 (54.0)	5 / 7 (-)	58 / 76 (76.3)	75 / 82 (91.5)	18 / 18 (-)	10 / 36 (27.8)	5 / 12 (-)
Nitrofurantoin	4289 / 4999 (85.8)	607 / 1655 (36.7)	48 / 72 (66.7)	4 / 18 (-)	47 / 85 (55.3)	5 / 9 (-)	5 / 68 (7.4)	97 / 126 (77.0)	16 / 18 (-)	4 / 32 (12.5)	0 / 7 (-)

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

Fosfomycin had the highest overall susceptibility (93.7%), followed by nitrofurantoin (85.8%). Ciprofloxacin and cefazolin were the least susceptible drugs, with a sensitivity of less than 30%. The carbapenems showed susceptibility of more than 70%. There was a great deal of variation among the different centres (**Table 3.15**).

Table 3.15: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Escherichia coli* from urine

RC	Piperacillin-tazobactam n=9922	Cefazolin n=4275	Cefotaxime n=9106	Ertapenem n=7976	Imipenem n=9683	Meropenem n=10042	Amikacin n=10042	Ciprofloxacin n=10042	Levofloxacin n=4770	Trimethoprim-sulfamethoxazole n=8030	Fosfomycin n=6356	Nitrofurantoin n=8654
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	110 / 294 (37.4)	78 / 282 (27.7)	49 / 294 (16.7)	134 / 294 (45.6)	146 / 294 (49.7)	158 / 294 (53.7)	157 / 294 (53.4)	43 / 294 (14.6)	91 / 294 (31.0)	90 / 280 (32.1)	263 / 282 (93.3)	229 / 282 (81.2)
RC4	440 / 613 (71.8)	0 / 0 (-)	166 / 615 (27.0)	0 / 0 (-)	523 / 615 (85.0)	523 / 615 (85.0)	413 / 615 (67.2)	171 / 615 (27.8)	1 / 1 (-)	1 / 1 (-)	0 / 0 (-)	565 / 600 (94.2)
RC5	231 / 344 (67.2)	0 / 0 (-)	2 / 315 (0.6)	288 / 342 (84.2)	312 / 344 (90.7)	310 / 344 (90.1)	318 / 344 (92.4)	23 / 344 (6.7)	3 / 3 (-)	187 / 341 (54.8)	90 / 92 (97.8)	277 / 328 (84.5)
RC6	189 / 323 (58.5)	0 / 0 (-)	1 / 9 (-)	243 / 323 (75.2)	258 / 324 (79.6)	255 / 324 (78.7)	244 / 323 (75.5)	11 / 323 (3.4)	0 / 1 (-)	106 / 322 (32.9)	317 / 323 (98.1)	266 / 317 (83.9)
RC7	113 / 184 (61.4)	19 / 37 (51.4)	4 / 79 (5.1)	135 / 171 (78.9)	140 / 183 (76.5)	149 / 191 (78.0)	136 / 191 (71.2)	20 / 191 (10.5)	0 / 26 (-)	62 / 172 (36.0)	37 / 40 (92.5)	117 / 145 (80.7)
RC8	121 / 184 (65.8)	0 / 0 (-)	41 / 184 (22.3)	145 / 184 (78.8)	157 / 184 (85.3)	155 / 184 (84.2)	158 / 184 (85.9)	6 / 184 (3.3)	12 / 184 (6.5)	98 / 184 (53.3)	183 / 184 (99.5)	0 / 0 (-)
RC9	247 / 309 (79.9)	49 / 309 (15.9)	130 / 309 (42.1)	266 / 309 (86.1)	252 / 309 (81.6)	285 / 309 (92.2)	238 / 309 (77.0)	102 / 309 (33.0)	137 / 309 (44.3)	123 / 308 (39.9)	296 / 307 (96.4)	294 / 309 (95.1)
RC10	502 / 706 (71.1)	0 / 0 (0)	212 / 707 (30.0)	616 / 706 (87.3)	444 / 516 (86.0)	626 / 707 (88.5)	617 / 707 (87.3)	158 / 707 (22.3)	0 / 0 (0)	367 / 708 (51.8)	0 / 0 (0)	619 / 703 (88.1)
RC11	22 / 44 (50.0)	0 / 0 (0)	5 / 44 (11.4)	22 / 24 (-)	23 / 44 (52.3)	24 / 44 (54.5)	18 / 44 (40.9)	4 / 44 (9.1)	4 / 43 (9.3)	9 / 44 (20.5)	41 / 43 (95.3)	32 / 44 (72.7)

RC12	71 / 174 (40.8)	24 / 170 (14.1)	11 / 148 (7.4)	115 / 173 (66.5)	120 / 175 (68.6)	119 / 175 (68.0)	111 / 175 (63.4)	5 / 175 (2.9)	24 / 141 (17.0)	75 / 167 (44.9)	165 / 166 (99.4)	139 / 167 (83.2)
RC13	43 / 84 (51.2)	1 / 1 (-)	61 / 83 (73.5)	53 / 69 (76.8)	75 / 84 (89.3)	84 / 84 (100.0)	69 / 84 (82.1)	10 / 84 (11.9)	14 / 81 (17.3)	2 / 6 (-)	78 / 78 (100.0)	75 / 81 (92.6)
RC14	450 / 560 (80.4)	1 / 1 (-)	167 / 559 (29.9)	514 / 559 (91.9)	526 / 560 (93.9)	526 / 560 (93.9)	505 / 560 (90.2)	48 / 560 (8.6)	0 / 0 (0)	313 / 560 (55.9)	554 / 559 (99.1)	0 / 0 (0)
RC15	28 / 49 (57.1)	7 / 49 (14.3)	9 / 45 (20.0)	0 / 0 (0)	46 / 49 (93.9)	48 / 49 (98.0)	38 / 49 (77.6)	6 / 49 (12.2)	5 / 45 (11.1)	30 / 49 (61.2)	13 / 15 (-)	43 / 49 (87.8)
RC16	40 / 626 (6.4)	8 / 625 (1.3)	12 / 626 (1.9)	317 / 626 (50.6)	237 / 626 (37.9)	428 / 626 (68.4)	189 / 626 (30.2)	58 / 626 (9.3)	101 / 626 (16.1)	289 / 625 (46.2)	578 / 626 (92.3)	512 / 626 (81.8)
RC17	311 / 352 (88.4)	11 / 11 (-)	325 / 348 (93.4)	284 / 352 (80.7)	315 / 352 (89.5)	317 / 352 (90.1)	334 / 352 (94.9)	307 / 352 (87.2)	0 / 0 (0)	284 / 311 (91.3)	0 / 0 (0)	321 / 351 (91.5)
RC18	30 / 75 (40.0)	3 / 75 (4.0)	14 / 75 (18.7)	46 / 75 (61.3)	49 / 75 (65.3)	53 / 75 (70.7)	44 / 75 (58.7)	20 / 75 (26.7)	17 / 75 (22.7)	32 / 75 (42.7)	72 / 75 (96.0)	65 / 75 (86.7)
RC19	256 / 634 (40.4)	52 / 635 (8.2)	20 / 632 (3.2)	383 / 635 (60.3)	232 / 635 (36.5)	249 / 635 (39.2)	356 / 635 (56.1)	28 / 635 (4.4)	61 / 635 (9.6)	217 / 634 (34.2)	534 / 635 (84.1)	518 / 635 (81.6)
RC20	73 / 237 (30.8)	2 / 207 (1.0)	20 / 233 (8.6)	76 / 128 (59.4)	164 / 207 (79.2)	188 / 237 (79.3)	215 / 237 (90.7)	24 / 237 (10.1)	33 / 234 (14.1)	31 / 119 (26.1)	216 / 234 (92.3)	193 / 233 (82.8)
Total	3277 / 5845 (56.1)	255 / 2446 (10.4)	1253 / 5356 (23.4)	3639 / 4972 (73.2)	4055 / 5630 (72.0)	4526 / 5859 (77.2)	4163 / 5858 (71.1)	1050 / 5858 (17.9)	517 / 2752 (18.8)	2334 / 4954 (47.1)	3477 / 3711 (93.7)	4289 / 4999 (85.8)

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

Cumulatively, *K. pneumoniae* isolates showed less than 50% susceptibility to all the drugs tested. The carbapenems showed a susceptibility of nearly 45%, followed by amikacin (44.4%). Cefazolin, ciprofloxacin, and levofloxacin were the least susceptible drugs. There was a lot of variation among the different centers (**Table 316**).

Table 3.16: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Klebsiella pneumoniae* from urine

RC	Piperacillin-tazobactam (n=3431)	Cefazolin (n=1489)	Cefotaxime (n=3084)	Ertapenem (n=2839)	Imipenem (n=3389)	Meropenem (n=3496)	Amikacin (n=3496)	Ciprofloxacin (n=3496)	Levofloxacin (n=1889)	Nitrofurantoin (n=2717)	Trimethoprim-sulfamethoxazole (n=2891)
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
RC1	33 / 224 (14.7)	22 / 194 (11.3)	19 / 224 (8.5)	37 / 224 (16.5)	41 / 224 (18.3)	47 / 224 (21.0)	42 / 224 (18.8)	16 / 224 (7.1)	28 / 224 (12.5)	55 / 196 (28.1)	28 / 196 (14.3)
RC4	78 / 148 (52.7)	0 / 0 (0)	56 / 150 (37.3)	0 / 0 (0)	100 / 150 (66.7)	100 / 150 (66.7)	66 / 150 (44.0)	58 / 150 (38.7)	0 / 0 (0)	88 / 112 (78.6)	1 / 1 (-)
RC5	59 / 116 (50.9)	0 / 0 (0)	9 / 112 (8.0)	75 / 114 (65.8)	78 / 116 (67.2)	77 / 116 (66.4)	85 / 116 (73.3)	27 / 116 (23.3)	0 / 0 (0)	45 / 111 (40.5)	69 / 116 (59.5)
RC6	47 / 139 (33.8)	0 / 0 (0)	1 / 2 (-)	56 / 139 (40.3)	57 / 139 (41.0)	60 / 139 (43.2)	61 / 139 (43.9)	25 / 139 (18.0)	1 / 1 (-0)	34 / 138 (24.6)	56 / 139 (40.3)
RC7	31 / 99 (31.3)	3 / 13 (-)	4 / 46 (8.7)	36 / 91 (39.6)	42 / 99 (42.4)	45 / 102 (44.1)	52 / 102 (51.0)	27 / 102 (26.5)	0 / 6 (-)	7 / 62 (11.3)	30 / 77 (39.0)
RC8	27 / 119 (22.7)	0 / 0 (0)	23 / 116 (19.8)	40 / 114 (35.1)	47 / 119 (39.5)	44 / 119 (37.0)	43 / 119 (36.1)	19 / 119 (16.0)	18 / 119 (15.1)	0 / 0 (0)	46 / 119 (38.7)

RC9	23 / 44 (52.3)	4 / 44 (9.1)	16 / 44 (36.4)	22 / 44 (50.0)	22 / 44 (50.0)	25 / 44 (56.8)	24 / 44 (54.5)	13 / 44 (29.5)	19 / 44 (43.2)	23 / 44 (52.3)	14 / 44 (31.8)
RC10	106 / 236 (44.9)	0 / 0 (0)	91 / 235 (38.7)	132 / 236 (55.9)	80 / 169 (47.3)	135 / 237 (57.0)	149 / 236 (63.1)	79 / 236 (33.5)	0 / 0 (0)	46 / 236 (19.5)	118 / 236 (50.0)
RC11	12 / 66 (18.2)	0 / 0 (0)	9 / 66 (13.6)	6 / 13 (-)	14 / 66 (21.2)	18 / 66 (27.3)	12 / 66 (18.2)	4 / 66 (6.1)	6 / 66 (9.1)	10 / 64 (15.6)	11 / 65 (16.9)
RC12	25 / 81 (30.9)	17 / 77 (22.1)	12 / 68 (17.6)	25 / 79 (31.6)	27 / 81 (33.3)	24 / 81 (29.6)	28 / 82 (34.1)	18 / 81 (22.2)	15 / 63 (23.8)	27 / 75 (36.0)	24 / 74 (32.4)
RC13	11 / 50 (22.0)	0 / 1 (-)	15 / 50 (30.0)	16 / 41 (39.0)	24 / 51 (47.1)	24 / 51 (47.1)	18 / 51 (35.3)	4 / 51 (7.8)	6 / 50 (12.0)	10 / 48 (20.8)	1 / 9 (-)
RC14	72 / 105 (68.6)	0 / 0 (0)	62 / 105 (59.0)	91 / 104 (87.5)	95 / 105 (90.5)	97 / 105 (92.4)	91 / 105 (86.7)	49 / 105 (46.7)	0 / 0 (0)	0 / 0 (0)	80 / 105 (76.2)
RC15	5 / 9 (-)	1 / 9 (-)	2 / 9 (-)	0 / 0 (0)	7 / 9 (-)	7 / 9 (-)	7 / 9 (-)	0 / 9 (-)	5 / 9 (-)	3 / 9 (-)	5 / 9 (-)
RC16	5 / 128 (3.9)	5 / 127 (3.9)	3 / 128 (2.3)	51 / 128 (39.8)	32 / 128 (25.0)	60 / 128 (46.9)	29 / 128 (22.7)	9 / 128 (7.0)	22 / 128 (17.2)	42 / 128 (32.8)	58 / 128 (45.3)
RC17	41 / 64 (64.1)	2 / 2 (-)	47 / 64 (73.4)	40 / 64 (62.5)	42 / 64 (65.6)	41 / 64 (64.1)	51 / 64 (79.7)	41 / 64 (64.1)	0 / 0 (0)	42 / 64 (65.6)	41 / 60 (68.3)
RC18	6 / 20 (-)	0 / 20 (-)	1 / 20 (-)	5 / 20 (-)	8 / 20 (-)	8 / 20 (-)	9 / 20 (-)	4 / 20 (-)	6 / 20 (-)	9 / 20 (-)	13 / 20 (-)
RC19	84 / 272 (30.9)	18 / 272 (6.6)	10 / 269 (3.7)	106 / 272 (39.0)	46 / 272 (16.9)	59 / 272 (21.7)	98 / 272 (36.0)	8 / 272 (2.9)	12 / 272 (4.4)	150 / 272 (55.1)	80 / 271 (29.5)
RC20	6 / 49 (12.2)	0 / 42 (0.0)	7 / 50 (14.0)	6 / 28 (-)	17 / 46 (37.0)	21 / 50 (42.0)	23 / 50 (46.0)	6 / 50 (12.0)	13 / 47 (27.7)	13 / 47 (27.7)	4 / 29 (13.8)
Total	671 / 1998 (33.6)	72 / 824 (8.7)	390 / 1782 (21.9)	744 / 1712 (43.5)	796 / 1931 (41.2)	903 / 2006 (45.0)	890 / 2006 (44.4)	410 / 2005 (20.4)	159 / 1078 (14.7)	607 / 1655 (36.7)	689 / 1722 (40.0)

Yearly susceptibility trends of different Enterobacterales from urine samples

Over the last seven years (2017-2023), the susceptibility trends for *E. coli* and *Klebsiella pneumoniae* isolated from urine samples show a general decline in antibiotic susceptibility. *Escherichia coli* demonstrated a decrease in susceptibility across most antibiotics with piperacillin-tazobactam dropping from 73.7% in 2017 to 56.1% in 2023, cefazolin from 23.7% in the year 2017 to 10.4% in 2023, and significant decline in susceptibility for carbapenems (88.3% to 72% for imipenem and 80% to 77.2% for meropenem) and amikacin (86.4% to 71.1%) (**Table 3.17 and Figure 3.5**).

Klebsiella pneumoniae also documented reduced susceptibility, notably with piperacillin-tazobactam falling from 52.5% to 46.7%, carbapenems (imipenem from 70.8% to 41.2% and meropenem from 56.9% to 44.4%), fluoroquinolones (ciprofloxacin from 33.5% to 20.4%) over seven years (**Table 3.18 and Figure 3.6**).

Table 3.17: Yearly susceptibility trend of *E. coli* isolated from urine

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
	Total n=4087	Total n=9972	Total n=17291	Total n=8201	Total n=10096	Total n=11781	Total n=10042
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)
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)
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)
Ceftazidime	*1/10	*0/2	*0/3	*1/2	*1/2 (-)	701 / 3222 (21.8)	727 / 3289 (22.1)
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)
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)
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)
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)
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)
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)
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)
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)
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)

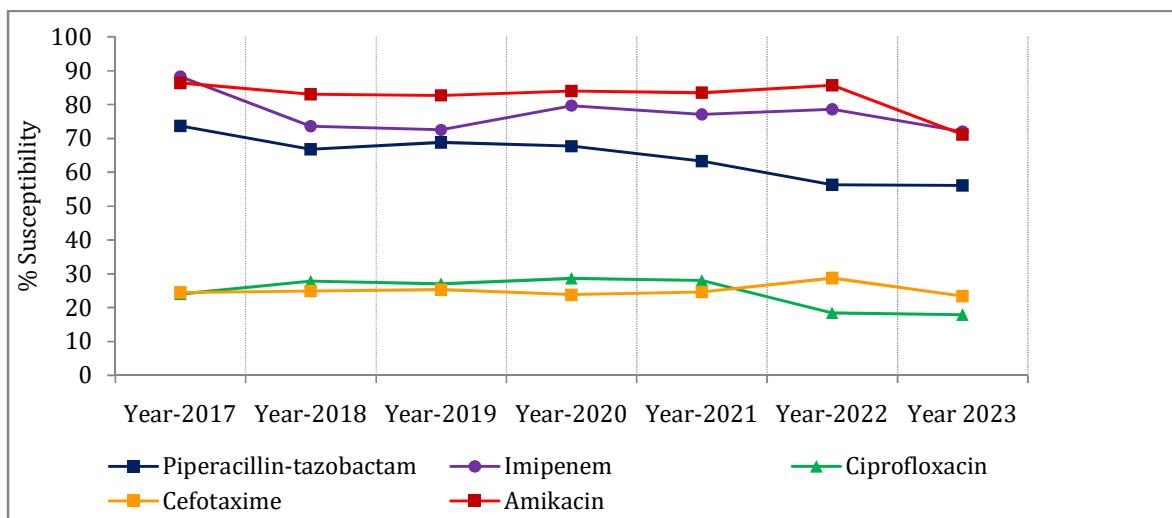


Figure 3.5: Yearly susceptibility trend of *E. coli* isolated from urine

Table 3.18: Yearly susceptibility trend of *Klebsiella pneumoniae* isolated from urine

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
	Total n=1336	Total n=2626	Total n=5027	Total n=2860	Total n=3583	Total n=3825	Total n=3496
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)
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)
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)
Ceftazidime	*2/10	*0/1	*0/2	*0/3	*1/10	281 / 1202 (23.4)	214 / 1193 (17.9)
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)
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)
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)
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)
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)
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)
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)
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)

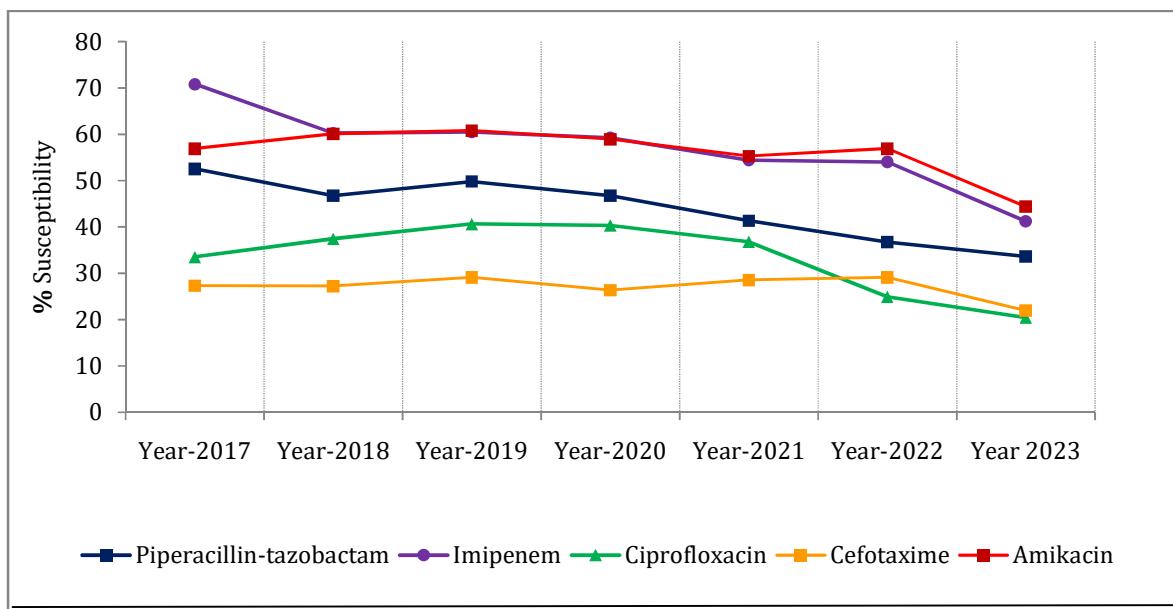


Figure 3.6: Yearly susceptibility trend of *Klebsiella pneumoniae* isolated from urine

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

Carbapenem-susceptible isolates were more susceptible to all the antibiotics tested than carbapenem-resistant (resistant to at least one of the tested carbapenems) isolates (**Table 3.19 and 3.20**). The difference was more marked in *K. pneumoniae* than *E. coli*, indicating that carbapenem-resistant *K. pneumoniae* isolates were more resistant to all the antibiotics than carbapenem-resistant *E. coli* isolates.

In *E. coli*, the differences in susceptibility were high for Piperacillin-tazobactam, carbapenems, and amikacin (range of differences 40-89%) and moderate for other antibiotics (range of differences 13-39%). In *K. pneumoniae*, the differences were high for all the antibiotics tested (range of differences 29-92%).

Table 3.19: Susceptibility pattern of carbapenem-resistant and susceptible records for *E. coli* isolated from all (except faeces and urine) specimens

AMA	CR n=5236	CS n=7780
Piperacillin-tazobactam	473 / 5177 (9.1)	5032 / 7665 (65.6)
Cefotaxime	174 / 4714 (3.7)	1583 / 7093 (22.3)
Ceftazidime	151 / 3226 (4.7)	1381 / 4544 (30.4)
Ertapenem	462 / 4144 (11.1)	5211 / 5422 (96.1)
Imipenem	467 / 5227 (8.9)	7396 / 7636 (96.9)
Meropenem	750 / 5242 (14.3)	7671 / 7780 (98.6)
Amikacin	2994 / 5659 (52.9)	6337 / 7837 (80.9)
Ciprofloxacin	137 / 5237 (2.6)	1478 / 7803 (18.9)
Levofloxacin	113 / 2501 (4.5)	798 / 3196 (25.0)
Trimethoprim-sulfamethoxazole	93 / 443 (21.0)	822 / 1545 (53.2)
Nitrofurantoin	22 / 39 (56.4)	67 / 77 (87.0)

Table 3.20: Susceptibility pattern of carbapenem-resistant and susceptible records for *Klebsiella pneumoniae* isolated from all (except faeces and urine) specimens

AMA	CR n=7999	CS n=4780
Piperacillin-tazobactam	347 / 7904 (4.4)	3199 / 4694 (68.2)
Cefotaxime	189 / 6898 (2.7)	1890 / 4410 (42.9)
Ceftazidime	144 / 5306 (2.7)	1428 / 2770 (51.6)
Ertapenem	298 / 6043 (4.9)	2890 / 3030 (95.4)
Imipenem	264 / 7971 (3.3)	4385 / 4662 (94.1)
Meropenem	421 / 8002 (5.3)	4664 / 4780 (97.6)
Amikacin	967 / 8020 (12.1)	3649 / 4803 (76.0)
Ciprofloxacin	164 / 8002 (2.0)	2105 / 4791 (43.9)
Levofloxacin	211 / 4275 (4.9)	958 / 1726 (55.5)

Molecular characterization of *E. coli* isolates

Five hundred sixty-nine (569) *E. coli* isolates were subjected to four multiplex PCRs and three monoplex PCRs for OXA-48, CTXM-15, and NDM. Overall, NDM-1 (34%) was the most common, followed by OXA-1 (18%), OXA-48 (14%), CTXM-15 (12%), TEM (10%), SHV (6%), IMP (12%), CTXM-1 and IMP (4% each), VIM (3%) and KPC (1%) (**Figures 3.7, Table 3.21 and Figure 3.8**). The *E. coli* isolates received from RC1 were majorly positive for NDM-1 (37%); the remaining genes showed less than 10% presence. The isolates from RC2 also showed maximum positivity for NDM-1 (30%), followed by OXA-1 (27%), OXA-48 (23%), CTXM-15 (13%), CTXM-1 (10%), and TEM, SHV, IMP, VIM, KPC, CIT, and EBC less than 10%. Most RC3 isolates were positive for NDM (21%), and the remaining genes showed less than 10% presence. Similarly, the RC4 isolates were majorly positive for NDM-1 (76%), followed by CTXM-15 and SHV (22% each), OXA-48 (17%) and OXA-1 (15%). RC5 isolates showed only NDM (16%) and other genes at less than 10%. RC6 isolates showed OXA-48 (29%), followed by SHV (21%) and CTXM-1 (19%). The RC8 isolates were positive for NDM-1 (55%), OXA-48 (41%), OXA-1 (28%), and CTXM-15 (24%).

In RC9, VIM was detected in 24% of isolates, NDM-1 and TEM in 18%, and OXA-48, IMP, and DHA in 12% of the isolates. RC10 showed high positivity for CTXM-15 and TEM (20%), followed by OXA-1 (17%) and NDM (15%). RC12 isolates were maximally positive for NDM-1 (73%), followed by OXA-1 (46%), OXA-48 (27%), CTXM-15 (19%), and IMP (12%). The RC13 isolates showed positivity for NDM (43%), OXA-1 and IMP (36% each), CTXM-1 and OXA-48 (21% each), FOX (14%), and rest genes showed lesser prevalence (less than 10%). In RC14 isolates, CTXM-15 (29%) was the most common, followed by TEM and OXA-1 (27% each) and NDM (22%). In RC15 samples, OXA-1 (33%), IMP, and NDM (22%) had the highest prevalence. Among the RC16 samples, the NDM-1 resistance gene was found in 29% of cases, while CTXM-15, TEM, and OXA-1 resistance genes were present in 15% of isolates and OXA-48 in 12% of the isolates. In the RC17 samples, NDM and VIM had the highest prevalence at 40% each, followed by IMP and FOX at 33% each. The predominant resistance genes in RC18 samples were NDM-1 (80%), followed by CTXM-15 and SHV at 13% each. RC19 samples showed a higher prevalence of NDM-1 (73%), followed by OXA-1 (45%), OXA-48 (36%), and IMP (18%). RC20 isolates showed the presence of TEM, NDM-1, and OXA-1 at 25% each. The RC21 isolates had a higher prevalence of CTXM-15 (38%), followed by TEM, NDM-1, OXA-1, and VIM (27% each).

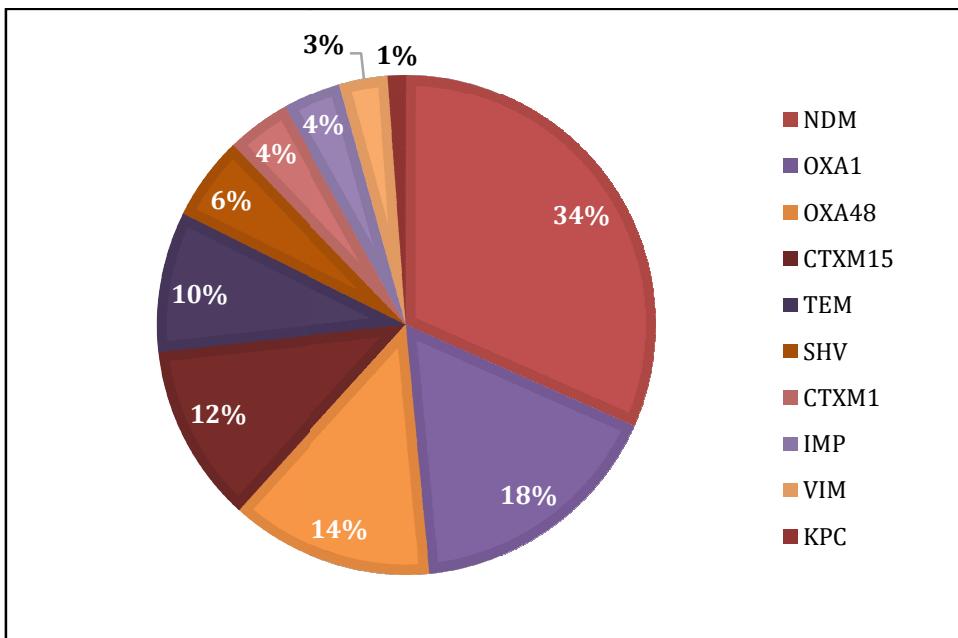


Figure 3.7: Percentage positivity of AMR-associated genetic determinants in *E. coli*

In *E. coli* isolates, the NDM-1 gene was the predominant gene present in 34% of the isolates, followed by OXA-1 in 18% of the isolates and OXA-48 in 14% and CTXM-15 in 12% of the isolates. The genes encoding for AmpC β-lactamases were the least prevalent.

Table 3.21: Percentage positivity of resistant genes in *E. coli* from each centre

Regional Centers	Antimicrobial Resistance Genes									
	CTXM15	OXA48	TEM	ND M	SHV	OXA1	IMP	VIM	KPC	CTXM1
RC1	2%	2%	2%	37%	0%	0%	0%	0%	0%	0%
RC2	13%	23%	8%	30%	5%	27%	3%	3%	2%	10%
RC3	0%	2%	2%	21%	2%	9%	0%	0%	0%	2%
RC4	22%	17%	10%	76%	22%	15%	0%	2%	5%	2%
RC5	4%	0%	8%	16%	8%	8%	0%	0%	0%	4%
RC6	2%	29%	0%	7%	21%	0%	0%	0%	0%	19%
RC8	24%	41%	3%	55%	7%	28%	0%	0%	7%	0%
RC9	0%	12%	18%	18%	0%	6%	12%	24%	6%	6%
RC10	20%	5%	20%	15%	2%	17%	0%	0%	0%	0%
RC12	19%	27%	8%	73%	4%	46%	12%	0%	4%	4%
RC13	0%	21%	0%	43%	0%	36%	36%	7%	0%	21%
RC14	29%	13%	27%	22%	7%	27%	0%	0%	0%	4%
RC15	6%	11%	0%	22%	0%	33%	22%	11%	0%	0%
RC16	15%	12%	15%	29%	0%	15%	0%	0%	0%	0%
RC17	0%	7%	0%	40%	0%	20%	33%	40%	0%	7%
RC18	13%	0%	0%	80%	13%	0%	0%	0%	0%	0%
RC19	0%	36%	0%	73%	0%	45%	18%	0%	0%	0%
RC20	0%	0%	25%	25%	0%	25%	0%	0%	0%	0%

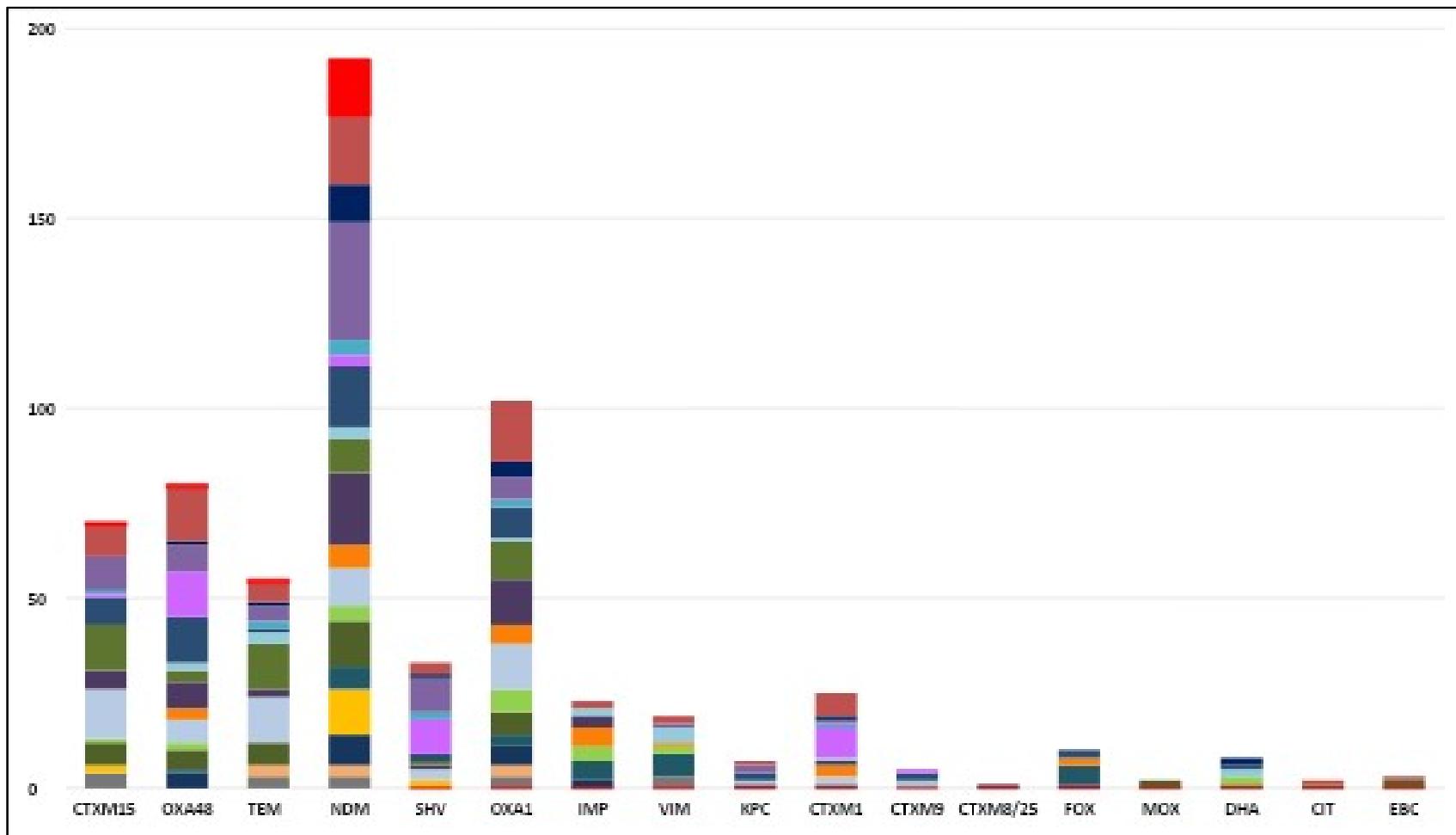


Figure 3.8: Various resistance genes found in *E. coli* isolates from different regional centers across India

The stacked bar graph represents the prevalence of resistant genes in *E. coli* isolates received from the regional centers (RC = 19) in 2023. Each color on the bar graph represents a different regional center.

Molecular characterization of *K. pneumoniae* isolates

Five hundred and forty (540) *K. pneumoniae* isolates were subjected to four multiplex PCRs and three monoplex PCRs for OXA-48, CTXM-15, and NDM. Overall, the SHV gene was the predominant present in 50% of the isolates, followed by CTXM-15 in 34%, OXA-48 in 29%, OXA-1, and CTXM-1 in 22% each, NDM and TEM in 19% each, IMP and KPC in 5% each, VIM and FOX in 6% each of the isolates (**Figures 3.9, Table 3.22 and Figure 3.10**). Among the RC1 isolates, the most prevalent resistance genes were NDM (39%), followed by TEM (32%), SHV (22%), OXA-48 (15%), and CTXM-15 (17%). The isolates from RC2 showed maximum positivity for OXA-48 (40%), followed by NDM (23%), SHV (15%) and IMP (13%). In the RC3 samples, SHV had the highest prevalence at 49%, followed by OXA-48 (29%), NDM, and OXA-1 (22%), whereas the rest genes were less than 10%. The RC4 isolates were majorly positive for CTXM-15 and OXA-48 (43% each), followed by NDM (38%) and OXA-1 (26%). Within RC5 isolates, SHV (67%) was the predominant resistance gene, followed by CTXM-15 (56%) and OXA-48 (39%). RC6 samples also exhibited high prevalence for SHV (31%) and CTXM-15 (19%). The RC8 isolates were positive for SHV (66%), followed by OXA-48 (45%), CTXM-15 (31%), OXA-1 (24%), TEM and NDM (21% each).

The RC9 samples showed a high prevalence of SHV (55%), NDM (41%), and CTXM-15 (38%). The RC10 isolates were positive for NDM (51%), OXA-48 (43%), and SHV (38%). The RC12 isolates showed maximum positivity for NDM (75%), SHV (71%), OXA-48 (54%), and CTXM-15 (42%). Within RC13 isolates, CTXM-15, OXA-48, TEM, and CTXM-1 (57%) were the most prevalent resistance genes. RC14 samples exhibited high prevalence of SHV and NDM (49%) and OXA-48 (45%). Among the RC15 isolates, OXA-48 (80%), SHV (60%), and OXA-1 (40%) were the most common resistance genes. In RC16 samples, SHV (47%) and TEM (32%) were prevalent, followed by OXA-1 (29%) and CTXM-15 (26%). RC17 isolates showed a significant proportion of isolates positive for IMP (67%), followed by SHV (33%). Other resistant marker genes were less than 20%. RC18 samples showed varying prevalence for different resistance genes, with NDM (87%), SHV (47%), and CTXM-15 (20%) being notable. Others like VIM, KPC, and OXA-1 were detected at lower levels (lesser than 15%) or were absent. Within RC19 isolates, 50% of the isolates were positive for OXA-48, SHV, and IMP, followed by NDM (43%). In RC21, 53% of the isolates showed the presence of OXA-1, followed by SHV in 42% of the isolates and NDM in 37%.

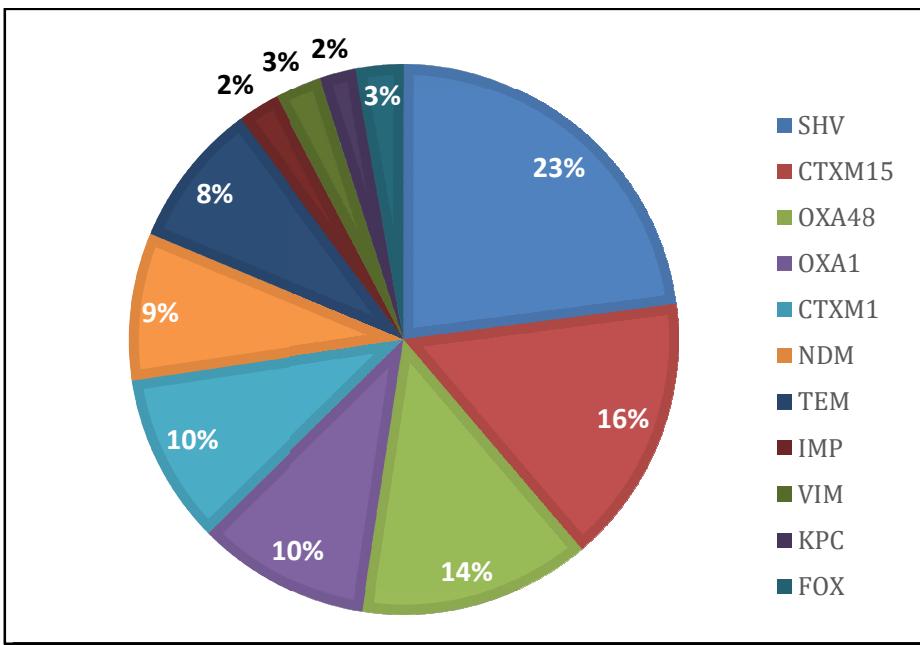


Figure 3.9: Percentage positivity of AMR-associated genetic determinants in *K. pneumoniae*

In *K. pneumoniae* isolates, the SHV gene was the predominant gene in 50% of the isolates, followed by CTXM-15 in 34% and OXA-48 in 29% of the isolates. The genes encoding for AmpC β-lactamases were the least prevalent.

Table 3.22: Percentage positivity of resistant genes in *K. pneumoniae* from each centre

Regional Centers	Antimicrobial Resistance Genes									
	CTXM15	OXA48	TEM	NDM	SHV	OXA1	IMP	VIM	KPC	CTXM1
RC1	17%	15%	32%	39%	22%	7%	0%	2%	0%	12%
RC2	5%	40%	5%	23%	15%	10%	13%	0%	0%	7%
RC3	4%	29%	2%	22%	49%	22%	0%	0%	0%	14%
RC4	43%	43%	7%	38%	24%	26%	2%	5%	0%	0%
RC5	56%	39%	6%	22%	67%	28%	0%	0%	11%	6%
RC6	19%	5%	2%	12%	31%	5%	0%	0%	0%	10%
RC8	31%	45%	21%	21%	66%	24%	0%	7%	0%	0%
RC9	38%	0%	17%	41%	55%	31%	7%	7%	17%	28%
RC10	17%	43%	23%	51%	38%	9%	0%	0%	0%	0%
RC12	42%	54%	8%	75%	71%	29%	8%	4%	4%	8%
RC13	57%	57%	57%	43%	0%	0%	14%	14%	0%	57%
RC14	22%	45%	31%	49%	49%	33%	0%	0%	0%	6%
RC15	0%	80%	0%	0%	60%	40%	0%	0%	0%	20%
RC16	26%	15%	32%	24%	47%	29%	0%	0%	0%	3%
RC17	0%	0%	17%	17%	33%	17%	67%	0%	0%	17%
RC18	20%	0%	0%	87%	47%	13%	0%	0%	0%	0%
RC19	0%	50%	7%	43%	50%	7%	50%	0%	0%	0%
RC20	0%	25%	25%	13%	13%	0%	0%	0%	0%	0%

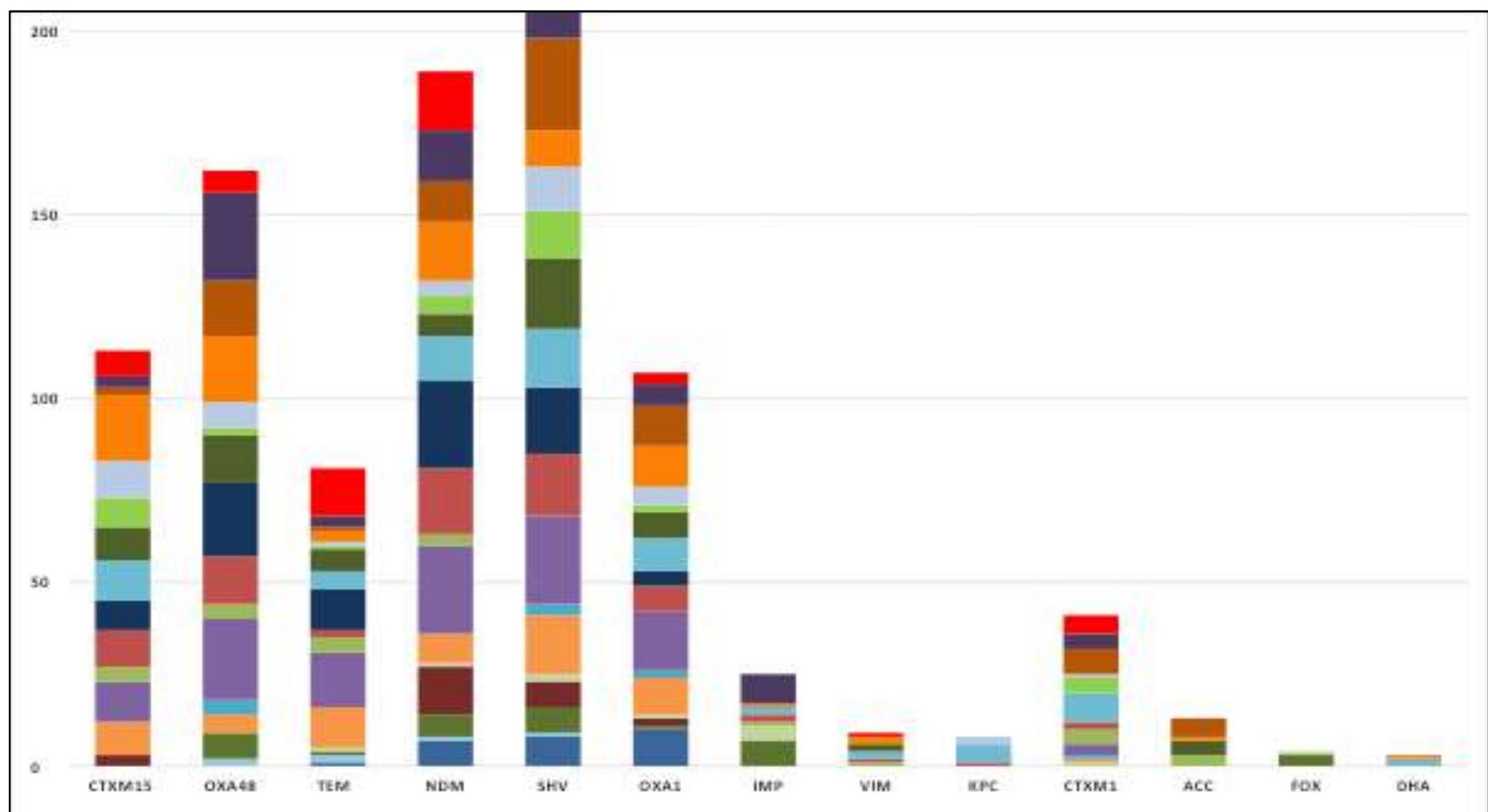


Figure 3.10: Various resistance genes found in *K. pneumoniae* isolates from different regional centers across India

The comparison between the *E. coli* (n= 569) and *K. pneumoniae* (n= 540) isolates received from regional centers (n = 19) in 2023 revealed the presence of resistance genes in *Klebsiella* isolates than *E. coli* (**Figure 3.11**).

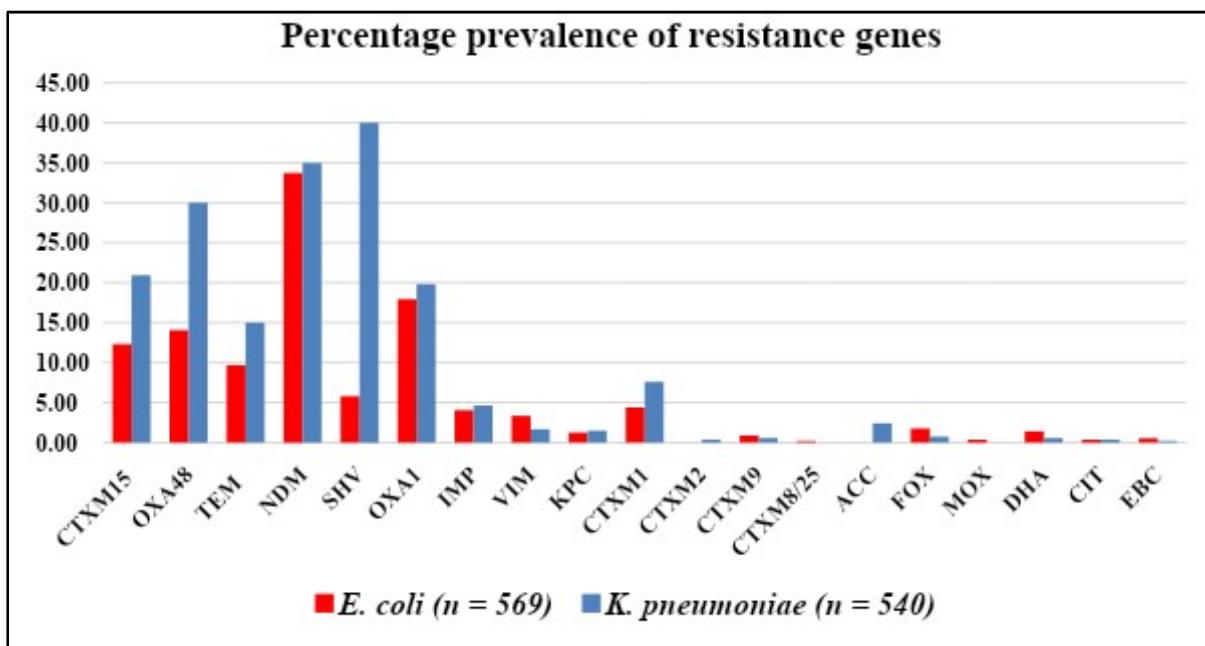


Figure 3.11: Comparison of resistance genes in *E. coli* and *K. pneumoniae* isolates from regional centers across India

Clinical relevance

We observed a significant decrease in antimicrobial susceptibilities to different agents, especially during and after the COVID-19 pandemic. Antibiotic overuse and misuse are the biggest drivers of AMR. Various species' relative isolation frequency and susceptibility trends are essential in deciding empiric hospital antibiotic policies. Trends of change in susceptibility indicate the behaviour of organisms over time and alert us to take appropriate preventive measures. The decrease in susceptibility to piperacillin-tazobactam, carbapenems, and colistin is concerning, especially coinciding with the overuse of antibiotics during the COVID-19 pandemic. Carbapenem-resistant Enterobacteriales (CREs) are a severe cause of healthcare-associated infections, are challenging to treat, and cause high mortality rates. Because carbapenemase genes are often located on mobile genetic elements, transfer of resistance among/across Enterobacteriales or other gram-negative organisms is enhanced, resulting in the potential

for widespread transmission. Carbapenem resistance also leads to the use of colistin, which is a last-resort antimicrobial agent.

The resistance of an organism to an antibiotic is a direct outcome of the organism's isolation frequency and the selection pressure of the antibiotic load used to treat it. Over the last two decades, the use of carbapenems has increased many folds, and the same is reflected in imipenem susceptibility of *E. coli* dropping steadily from 81% in 2017 to 63% in 2023 and that of *Klebsiella pneumoniae* dropping steadily from 59% in 2017 to 36% in 2023. Carbapenem (meropenem) resistance was very high in *Klebsiella pneumoniae* (62.3%), *P. rettgeri* (41.7%), and *K. oxytoca* (48.5%), with an overall all-species susceptibility of 60%. Carbapenems have been the mainstay in empiric therapy in tertiary care ICU settings. Though there was good susceptibility in *M. morganii* (86%), *P. mirabilis* (79%), and *K. aerogenes* (82%), the efficacy of this drug as an empiric therapy protocol should depend on the relative distribution of the various species in a particular set up. This also demands regular surveillance of carbapenem-resistant Enterobacterales by molecular detection of multiple genes. Ceftazidime-avibactam has excellent in-vitro activity against many ESBL, AmpC, KPC, and OXA-48-producing Enterobacterales. Cefiderocol is another antimicrobial comparable to or superior to ceftazidime-avibactam.

Colistin had highest overall susceptibility of nearly 96%, with most species tested except *Klebsiella* species (92%) and *Enterobacter* species (93%). With increasing use over the last five years, colistin resistance is emerging, and the recent removal by CLSI of the susceptible category from colistin indicates that there are strains of organisms without any detectable resistance mechanism (wild strains) that may not respond to therapy with this drug. Systemic treatment with colistin has also been mentioned as inadequate for treating respiratory tract infections. The fact that, in tertiary care facilities, many isolates from hospital-acquired and ventilator-associated pneumonia is carbapenem-resistant. Therefore, if colistin therapy is required, it should be supplemented with nebulized colistin administered through inhalation. The removal of the susceptible category from colistin also indicates that, in all situations, therapy with colistin may have unpredictable outcomes and, therefore, should be highly restricted. Colistin-resistant organisms need combinatorial treatment. These agents include colistin with tigecycline, meropenem, gentamicin, or fosfomycin.

Piperacillin-tazobactam susceptibility overall was quite low at 52%. Although *Proteus mirabilis* (84%), *M. morganii* (81%), and *Citrobacter koseri* (64%) showed reasonable susceptibility, susceptibility was low in commonly isolated species like *Klebsiella pneumoniae* (26.5%) and *E. coli* (42.4%). It, therefore, should be used only when an isolate is tested susceptible.

Third-generation cephalosporins and fluoroquinolones have susceptibilities far below the level to consider them appropriate for use in severe patients. Extensive use and abuse of these two groups over the last three decades have resulted in a high prevalence of extended-spectrum beta-lactamases and carbapenemases against oxyimino-cephalosporins and multiple mutations in organisms against fluoroquinolones making them nearly unusable as empiric therapy in seriously ill patients in tertiary care practices. Amongst the urinary isolates, fosfomycin showed the highest susceptibility (93%) in *E. coli*, the most familiar species and the one for which CLSI recommends it. The urinary isolates showed

marginally better susceptibility than non-urinary isolates to most antibiotics, and this fact, combined with the concentration of urine on many antibiotics, should be considered while treating such infections. The differences in susceptibility of various organisms isolated from patients in OPD, indoor wards, and ICU practices indicate the extent of antibiotic use in these areas and the consequent selection pressure. While OPD patients are usually put on oral antibiotics, indoor patients are frequently on parenteral antibiotics. ICU patients are generally exposed to the highest and broad-spectrum antibiotics, often multiple.

In conclusion, continuous surveillance of antimicrobial susceptibilities is crucial for tailoring empiric antibiotic therapy, optimizing patient outcomes, and controlling the spread of resistance. The dynamic nature of resistance patterns requires ongoing monitoring and adaptive strategies to maintain the efficacy of current antibiotics. Therefore, implementing robust antimicrobial stewardship programs, routine susceptibility testing, and developing new therapeutics are essential to address the growing threat of antimicrobial resistance in clinical settings.

Chapter 4. Non fermenting Gram Negative Bacteria (NFGNB)

Among non-fermenting gram negative bacilli, *Acinetobacter baumannii* (50%) was most common followed by *Pseudomonas aeruginosa* (47%), *Stenotrophomonas maltophilia* (4%) and *Burkholderia cepacia* (0.7%). *A. baumannii* and *P. aeruginosa* causes serious healthcare associated infections such as pneumonia, bloodstream infections and postoperative wound infections. Further, carbapenem resistant *A. baumannii* and *P. aeruginosa* with difficult-to-treat resistance are designated as priority pathogens by the World Health Organisation, to which new antimicrobials are urgently needed. Whilst, *S. maltophilia* and *B. cepacia* are the opportunistic pathogens in causing invasive infections. A significant increase in the trend of the isolation of *A. baumannii* (7% in 2017 vs 46% in 2022 vs 50% in 2023), *P. aeruginosa* (9.5% in 2017 vs 50% in 2022 vs 47% in 2023), and *S. maltophilia* (6% in 2017 vs 3% in 2022 vs 4% in 2023) were seen. However, no significant difference in the trend of isolation of these pathogens was noticed in the last two years for all pathogens.

Acinetobacter baumannii

Isolation rate of *A. baumannii* was found to be higher in wards and ICUs, compared to OPD settings (**Table 4.1**), indicates the adaption of pathogen to hospital settings with increased resistance to various antibiotics. Overall, all the tested showed limited activity against *A. baumannii* isolates with <20% susceptibility except minocycline and the pattern of susceptibility was almost similar, irrespective of the location and clinical source of the isolation (**Table 4.1 and Table 4.2**). Nearly, 88% of the isolates were resistant to carbapenems that left with limited treatment options. No significant change in the trend of susceptibility was observed between 2017 and 2023 (**Table 4.3 and Figure 4.1**). Overall, 72% of the tested isolates were found to be susceptible to minocycline and there is no significant change in the trend of susceptibility was seen between 2017 and 2023.

Table 4.1: Location-wise susceptible percentage of *A. baumannii* isolated from all samples except faeces across OPD, Ward and ICU

AMA	Total n=11948 (S %)	OPD n=1260 (S %)	Ward n=6086 (S %)	ICU n=4601 (S %)
	(S%)	(S%)	(S%)	(S%)
Piperacillin-tazobactam	936/7260 (12.9)	193/621 (31.1)	474/3654 (13)	269/2985 (9)
Cefepime	808/7240 (11.2)	175/618 (28.3)	435/3644 (11.9)	198/2978 (6.6)
Ceftazidime	635/7260 (8.7)	143/621 (23)	344/3654 (9.4)	148/2985 (5)
Imipenem	745/7260 (10.3)	167/621 (26.9)	418/3654 (11.4)	160/2985 (5.4)
Meropenem	877/7260 (12.1)	176/621 (28.3)	491/3654 (13.4)	210/2985 (7)
Colistin*	4914/4970 (98.9)	384/385 (99.7)	2385/2416 (98.7)	2145/2169 (98.9)
Amikacin	1194/7260 (16.4)	208/621 (33.5)	629/3654 (17.2)	357/2985 (12)
Minocycline	4018/5579 (72)	404/563 (71.8)	1770/2581 (68.6)	1844/2435 (75.7)
Levofloxacin	749/6221 (12)	138/548 (25.2)	407/3119 (13)	204/2554 (8)

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

Table 4.2: Sample-wise susceptible percentage of *A. baumannii*

AMA	Blood	LRT	Superficial infection	Deep infection	CSF	Urine
	n=1270	n=3519	n=1080	n=334	n=156	n=228
Piperacillin-tazobactam	206/1270 (16.2)	356/3519 (10.1)	140/1080 (13)	33/334 (9.9)	22/156 (14.1)	68/228 (29.8)
Cefepime	193/1264 (15.3)	279/3515 (7.9)	126/1077 (11.7)	33/332 (9.9)	22/155 (14.2)	51/227 (22.5)
Ceftazidime	152/1270 (12)	223/3519 (6.3)	98/1080 (9.1)	29/334 (8.7)	17/156 (10.9)	41/228 (18)
Imipenem	158/1270 (12.4)	259/3519 (7.4)	117/1080 (10.8)	32/334 (9.6)	19/156 (12.2)	57/228 (25)
Meropenem	186/1270 (14.6)	312/3519 (8.9)	136/1080 (12.6)	35/334 (10.5)	21/156 (13.5)	68/228 (29.8)
Colistin*	922/948 (97.3)	2430/2441 (99.5)	606/611 (99.2)	246/255 (96.5)	127/127 (100)	181/182 (99.5)
Amikacin	299/1270 (23.5)	379/3519 (10.8)	204/1080 (18.9)	51/334 (15.3)	34/156 (21.8)	83/228 (36.4)
Minocycline	846/1136 (74.5)	1753/2633 (66.6)	702/876 (80.1)	120/148 (81.1)	90/111 (81.1)	158/203 (77.8)
Levofloxacin	143/831 (17.2)	292/3202 (9.1)	123/1003 (12.3)	21/257 (8.2)	25/127 (19.7)	50/210 (23.8)

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

Table 4.3: Yearly susceptibility trend of *A. baumannii* isolated from all samples except faeces

AMA	Year -2017 Total=3359	Year -2018 Total=4549	Year -2019 Total=8531	Year -2020 Total=6849	Year -2021 Total=12393	Year -2022 Total=12142	Year -2023 Total=11948
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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)
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)
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)
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)
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)
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)
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)
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)
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)

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

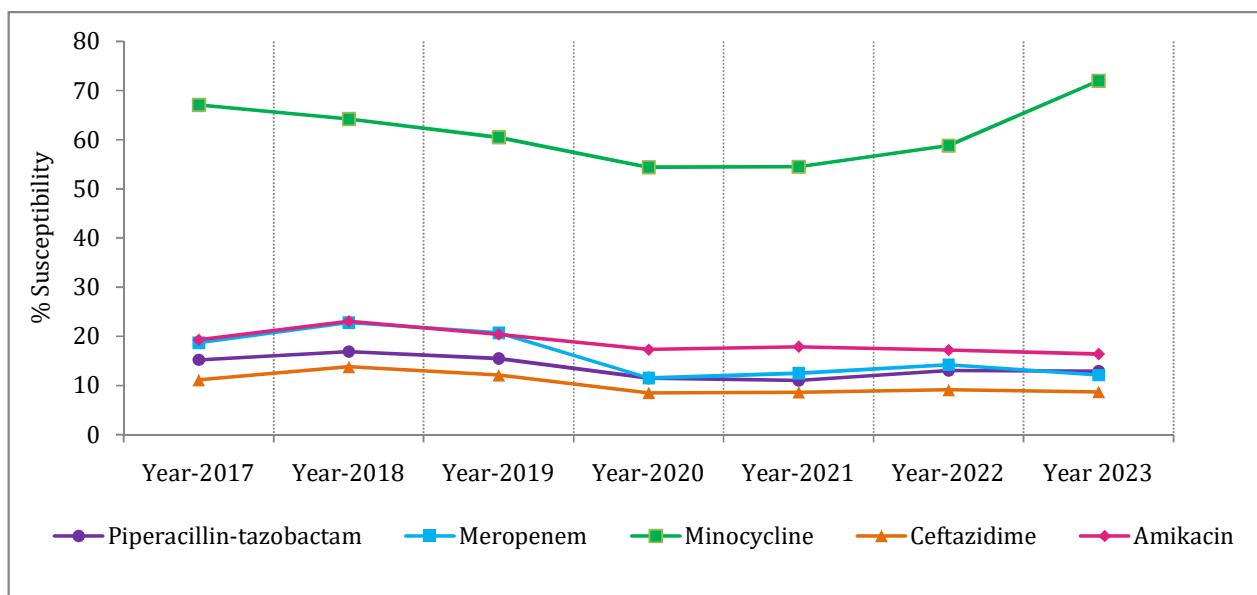


Figure 4.1: Yearly susceptibility trend of *A. baumannii* isolated from all samples except faeces

Pseudomonas aeruginosa

Hospital-acquired infections with *P. aeruginosa* especially in critically ill and immunocompromised patients are a major concern. *P. aeruginosa* causes high morbidity and mortality, and remains difficult to treat because of its extensive and emerging antibiotic-resistance mechanisms. It is the second most common cause of ventilator-associated pneumonia and fourth leading cause of hospital-associated infections (HAIs). Alarmingly, the emergence of multidrug-resistant strains of *P. aeruginosa* is increasing and there are very few treatments options. The resistance to antibiotics among *P. aeruginosa* strains is a result of the de novo emergence of resistance after exposure to antibiotics, patient to patient transfer of resistant bacteria and cross-resistance, which can result in multiple-drug-resistant (MDR) *P. aeruginosa* strains.

The rate of isolation of *P. aeruginosa* is higher in wards compared to OPD followed by ICU (**Table 4.4**). *P. aeruginosa* isolated from ward/ICU were found to more drug resistant than those that were isolated from OPD, which represent the increasing prevalence of MDR in *P. aeruginosa* in hospital settings (**Table 4.4**). The percentage of susceptibility to anti-pseudomonal cephalosporin such as ceftazidime (58.9% vs 46.5%) and cefepime (62.9% vs 47.5%) was higher in those *P. aeruginosa* that were isolated from wards, compared to ICU. Susceptibility to piperacillin/tazobactam was lower in ICU settings (57.6%) compared to wards (65.2%). Overall, 35% of *P. aeruginosa* isolates were resistant to carbapenems and the proportion was higher in ICU population (53%) compared to wards (35%) and OPD (19%). Susceptibility to amikacin and tobramycin was more than 50% and less than 50% to fluroquinolones (levofloxacin and ciprofloxacin) (**Table 4.4**).

No significant difference in the susceptibility was noticed for those *P. aeruginosa* isolates from blood, lower respiratory tract and superficial infection sample (**Table 4.5**). Among these isolates, >60% susceptibility was noticed for all the tested antibiotics except levofloxacin. In deep seated infections, <60% susceptibility was seen for piperacillin/tazobactam, ceftazidime, cefepime, and levofloxacin (**Table 4.5**). Among CSF samples, lower susceptibility rate of 52.5% to ceftazidime, 55% to cefepime, and 38.2% to levofloxacin has been noticed. Among urinary isolates <50% susceptibility was noticed for ceftazidime, cefepime imipenem and levofloxacin.

Among the isolated *P. aeruginosa*, there was no change in the trend of susceptibility to anti-pseudomonal cephalosporins such as ceftazidime and cefepime and piperacillin/tazobactam, was observed (**Table 4.6 and Figure 4.2**). It is important to notice that there was a gradual increase in carbapenem resistant *P. aeruginosa* from 26% in 2017 to 38.5% in 2023 (for imipenem) and from 31.3% in 2017 to 34.5% in 2023 (for meropenem). A significant increase in resistance rates for ciprofloxacin (26% in 2017 to 38.5% in 2023) and levofloxacin (31.3% in 2017 to 34.5% in 2023) was seen.

Table 4.4: Location-wise susceptible percentage of *Pseudomonas aeruginosa* isolated from all samples (except faeces) across OPD, Ward and ICU

AMA	Total n=11757	OPD n=3477	Ward n=6062	ICU n=2218
	(S %)	(S %)	(S %)	(S %)
Piperacillin-tazobactam	4483/6525 (68.7)	1458/1730 (84.3)	2251/3451 (65.2)	774/1344 (57.6)
Cefepime	4057/6380 (63.6)	1301/1674 (77.7)	2132/3392 (62.9)	624/1314 (47.5)
Ceftazidime	3988/6525 (61.1)	1329/1730 (76.8)	2034/3451 (58.9)	625/1344 (46.5)
Imipenem	4010/6525 (61.5)	1321/1730 (76.4)	2123/3451 (61.5)	566/1344 (42.1)
Meropenem	4275/6525 (65.5)	1399/1730 (80.9)	2242/3451 (65)	634/1344 (47.2)
Colistin*	2923/3037 (96.3)	805/825 (97.6)	1351/1407 (96.0)	767/805 (95.3)
Amikacin	4334/6202 (69.9)	1322/1638 (80.7)	2280/3309 (68.9)	732/1255 (58.3)
Gentamicin	2844/4398 (64.7)	899/1207 (74.5)	1490/2303 (64.7)	455/888 (51.2)
Tobramycin	2523/3957 (63.8)	871/1126 (77.4)	1235/1977 (62.5)	417/854 (48.8)
Ciprofloxacin	3313/6525 (50.8)	1072/1730 (62)	1724/3451 (50)	517/1344 (38.5)
Levofloxacin	2769/5771 (48)	907/1505 (60.3)	1503/3097 (48.5)	359/1169 (30.7)
Polymixin B	0/29 (0)	*0/3 (-)	0/21 (0)	*0/5 (-)

*Colistin represents the percentage intermediate susceptible

Table 4.5: Sample-wise susceptible percentage of *Pseudomonas aeruginosa*

AMA	Blood	LRT	Superficial Infection	Deep Infection	CSF	Urine
	n=583	n=2262	n=1663	n=399	n=40	n=707
Piperacillin-tazobactam	395/583 (67.8)	1664/2262 (73.6)	1140/1663 (68.6)	234/399 (58.6)	27/40 (67.5)	437/707 (61.8)
Cefepime	372/576 (64.6)	1551/2215 (70)	986/1619 (60.9)	232/391 (59.3)	22/40 (55)	326/687 (47.5)
Ceftazidime	365/583 (62.6)	1538/2262 (68)	1003/1663 (60.3)	233/399 (58.4)	21/40 (52.5)	303/707 (42.9)
Imipenem	361/583 (61.9)	1473/2262 (65.1)	1029/1663 (61.9)	232/399 (58.1)	24/40 (60)	328/707 (46.4)
Meropenem	379/583 (65)	1558/2262 (68.9)	1125/1663 (67.6)	241/399 (60.4)	25/40 (62.5)	357/707 (50.5)
Colistin*	312/322 (96.9)	895/918 (97.5)	708/749 (94.5)	242/256 (94.5)	*18/18 (-)	529/546 (96.9)
Amikacin	383/556 (68.9)	1628/2156 (75.5)	1087/1560 (69.7)	235/353 (66.6)	26/40 (65)	375/702 (53.4)
Levofloxacin	230/448 (51.3)	1171/2099 (55.8)	721/1534 (47)	118/290 (40.7)	13/34 (38.2)	163/579 (28.2)

*Colistin represents percentage Intermediate susceptibility

Table 4.6: 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
	Total n=5687	Total n=8880	Total n=12634	Total n=7839	Total n=11622	Total n=13228	Total n=11757
	(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)	9017/113156 (68.5)	4483/6525 (68.7)
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)
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)
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)
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)
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)
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)
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)
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)
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)
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)

*Colistin represents percentage Intermediate susceptibility

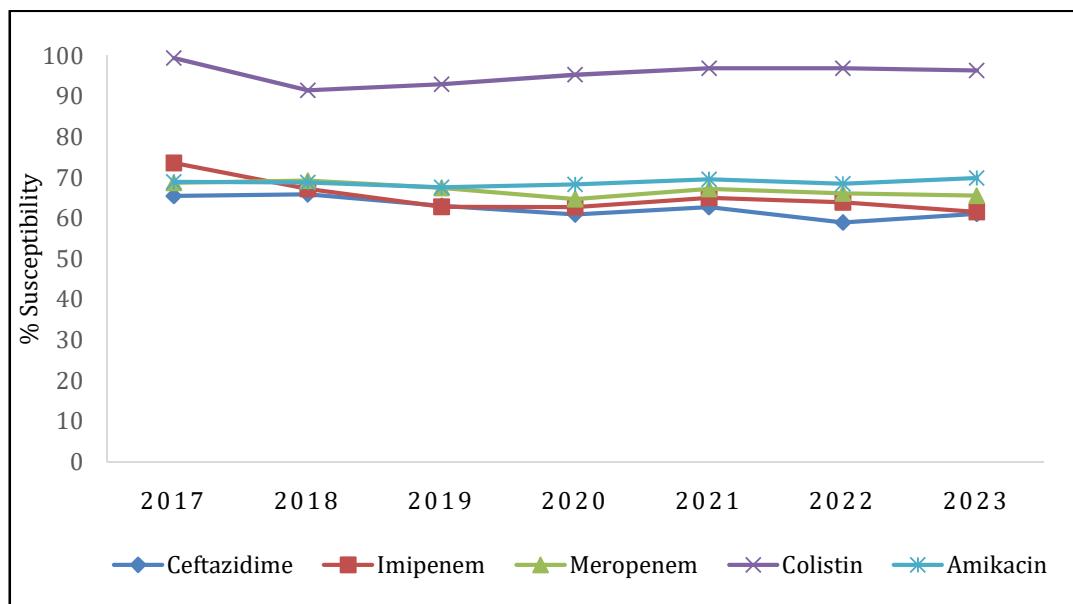


Figure 4.2: Yearly susceptibility trend of *Pseudomonas aeruginosa* isolated from all samples

Stenotrophomonas maltophilia

S. maltophilia was frequently isolated from wards and ICU compared to OPD (**Table 4.7**). No significant change in the susceptibility pattern was seen, irrespective of the location and sample of isolation (**Table 4.7 and Table 4.8**). Overall, *S. maltophilia* were highly susceptible to levofloxacin (91.4 %) and trimethoprim-sulfamethoxazole (91.4 %) (**Table 4.7**). However, *S. maltophilia* isolated from ICU were comparatively less susceptible to levofloxacin and trimethoprim-sulfamethoxazole than those that were isolated from wards. There is no significant change in the trend of susceptibility was noticed between 2017 and 2023 (**Table 4.9 and Figure 4.3**).

Table 4.7: Location-wise susceptible percentage of *Stenotrophomonas maltophilia* isolated from all samples across OPD, Ward and ICU

AMA	Total n=1011	Ward n=537	ICU n=311	OPD n=163
Ticarcillin-clavulanic acid	*1/2 (-)	1 / 1 (100)	0 / 1 (0)	0 / 0 (0)
Ceftazidime	173/226 (76.5)	86 / 116 (74.1)	43 / 62 (69.4)	44 / 48 (91.7)
Minocycline	516/533 (96.8)	278 / 289 (96.2)	155 / 159 (97.5)	83 / 85 (97.6)
Levofloxacin	487/533 (91.4)	274 / 292 (93.8)	137 / 160 (85.6)	76 / 85 (88.4)
Trimethoprim-sulfamethoxazole	379/416 (91.1)	195 / 212 (92)	116 / 129 (89.9)	68 / 75 (90.7)
Chloramphenicol	21/35 (60)	16 / 25 (64)	5 / 9 (55.6)	0 / 1 (0)

Table 4.8: Sample-wise susceptible percentage of *Stenotrophomonas maltophilia*

AMA	All Specimens (except faeces)	Blood	LRT	Superficial Infection	Deep Infection	Urine
	n=1011	n=390	n=358	n=92	n=35	n=20
Ticarcillin-clavulanic acid	*1/2 (-)	*0/1 (-)	*0/0 (-)	*1/1 (-)	*0/0 (-)	*0/0 (-)
Ceftazidime	173/226 (76.5)	115/146 (78.8)	42/55 (76.4)	*3/4 (-)	*3/3 (-)	*0/2 (-)
Minocycline	516/533 (96.8)	216/220 (98.2)	186/192 (96.9)	35/35 (100)	*13/13 (-)	*9/10 (-)
Levofloxacin	487/533 (91.4)	206/220 (93.6)	181/192 (94.3)	32/35 (91.4)	*11/13 (-)	*6/10 (-)
Trimethoprim-sulfamethoxazole	379/416 (91.1)	151/161 (93.8)	131/144 (91)	34/35 (97.1)	*11/13 (-)	*8/10 (-)
Chloramphenicol	21/35 (60)	*8/17 (-)	*9/12 (-)	*0/1 (-)	*0/0 (-)	*0/0 (-)

Table 4.9: 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
	Total n=157	Total n=310	Total n=374	Total n=360	Total n=766	Total n=827	Total n=1011
	(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 (-)
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)
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)
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)
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)
Chloramphenicol	*0/0 (-)	*1/2 (-)	*3/3 (-)	*8/9 (-)	*2/2 (-)	*4/5 (-)	21/35 (60)

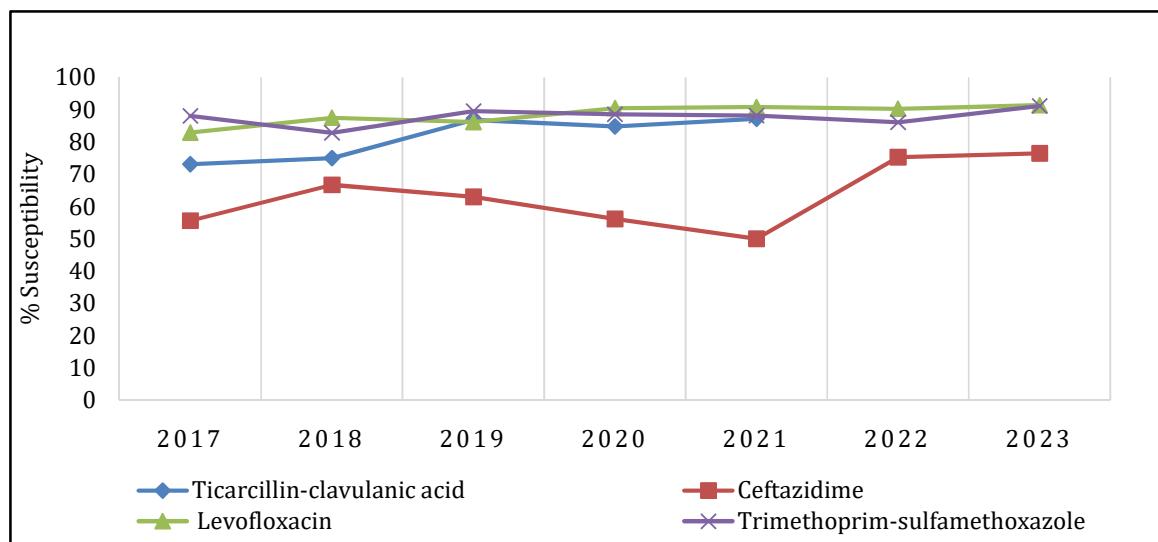


Figure 4.3: Yearly susceptibility trend of *Stenotrophomonas maltophilia* isolated from all samples

Burkholderia cepacia

Burkholderia cepacia is an important opportunistic pathogen and are intrinsically resistant to multiple classes of antibiotics, including aminoglycosides and polymyxins. Among the tested antibiotics, higher rate susceptibility has been noticed for trimethoprim-sulfamethoxazole (97.1%) followed by meropenem (86.7%), and ceftazidime (88.3%). In addition, >70% of the tested isolates were susceptible to minocycline and levofloxacin (**Table 4.10**). There is no significant difference in the susceptibility profile of *B. cepacia* was seen between wards and ICU, except levofloxacin (**Table 4.10**). Among the specimen source, there is no significant change in the proportion of isolates that were susceptible to the tested antibiotics (**Table 4.11**). There is no notable change in the trend of susceptibility was seen in *B. cepacia* during 2017 to 2023 (**Table 4.12 and Figure 4.4**), except minocycline (85.6% in 2017 vs 74.3% in 2023).

Table 4.10: Location-wise susceptible percentage of *Burkholderia cepacia* isolated from all samples across OPD, Ward and ICU

AMA	Total n=178	OPD n=22	Ward n=86	ICU n=70
Ticarcillin-clavulanic acid	2 / 3 (-)	0 / 0 (0%)	1 / 2 (50%)	1 / 1 (100%)
Ceftazidime	91 / 103 (88.3%)	9 / 9 (100%)	46 / 52 (88.5%)	36 / 42 (85.7%)
Meropenem	91 / 105 (86.7%)	9 / 9 (100%)	45 / 54 (83.3%)	37 / 42 (88.1%)
Minocycline	81 / 109 (74.3%)	7 / 9 (77.8%)	43 / 56 (76.8%)	31 / 44 (70.5%)
Levofloxacin	77 / 102 (75.5%)	6 / 9 (66.7%)	42 / 52 (80.8%)	29 / 41 (70.7%)
Trimethoprim-sulfamethoxazole	99 / 102 (97.1%)	9 / 9 (100%)	51 / 52 (98.1%)	39 / 41 (95.1%)
Chloramphenicol	5 / 11 (-)	1 / 1 (100%)	3 / 7 (42.9%)	1 / 3 (33.3%)

Table 4.11: Sample-wise susceptible percentage of *Burkholderia cepacia complex*

AMA	All Specimens	Blood	LRT	Superficial Infection	Deep Infection	SS
	n=178	n=123	n=39	n=5*	n=0	n=4*
Ticarcillin-clavulanic acid	2 / 3	1 / 2	1 / 1	0 / 0	0 / 0	0 / 0
Ceftazidime	91 / 103 (88.3%)	64 / 68 (94.1%)	22 / 27 (81.5%)	2 / 2 (-)	0 / 0 (-)	2 / 2 (-)
Meropenem	91 / 105 (86.7%)	64 / 69 (92.8%)	20 / 28 (71.4%)	2 / 2 (-)	0 / 0 (-)	2 / 2 (-)
Minocycline	81 / 109 (74.3%)	58 / 74 (78.4%)	20 / 27 (74.1%)	2 / 2 (-)	0 / 0 (-)	1 / 2 (-)
Levofloxacin	77 / 102 (75.5%)	60 / 68 (88.2%)	13 / 26 (50%)	2 / 2 (-)	0 / 0 (-)	1 / 2 (-)
Trimethoprim-sulfamethoxazole	99 / 102 (97.1%)	68 / 68 (100%)	25 / 26 (96.2%)	2 / 2 (-)	0 / 0 (-)	2 / 2 (-)
Chloramphenicol	5 / 11	2 / 6	2 / 3	1 / 1	0 / 0	0 / 1

Table 4.12: 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
	(S%)						
Ticarcillin-clavulanic acid	*0/9 (-)	4/51 (7.8)	36/103 (35)	36/80 (45)	13/58 (22.4)	*1/1 (-)	2 / 3 (-)
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%)
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%)
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%)
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%)
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%)
Chloramphenicol	*0/0 (-)	*1/1 (-)	*3/3 (-)	*4/4 (-)	*3/3 (-)	*1/1 (-)	5 / 11 (-)

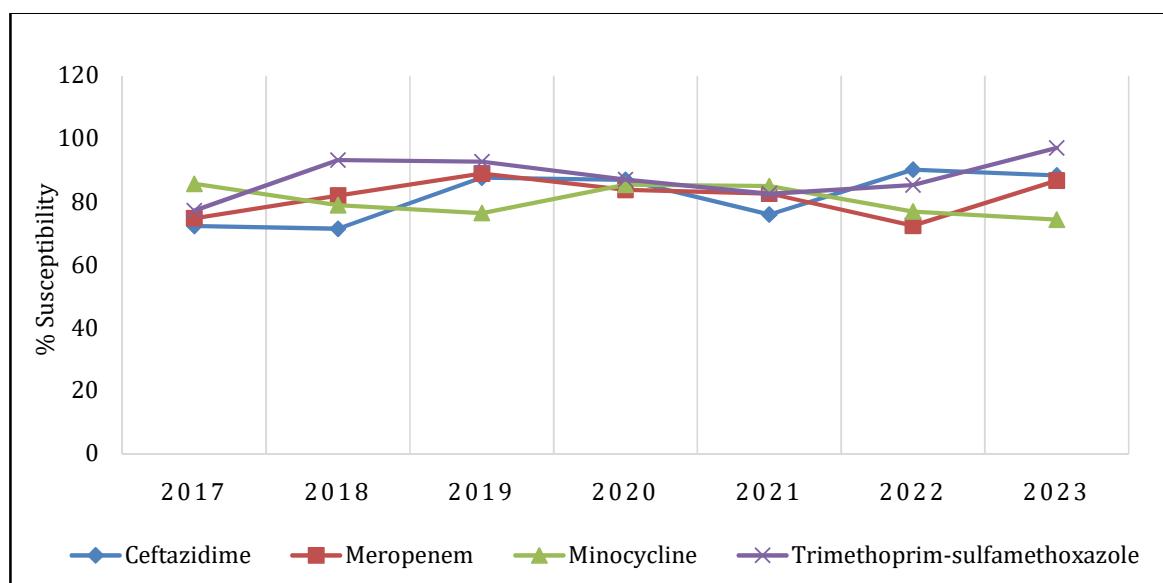


Figure 4.4: Yearly susceptibility trend of *Burkholderia cepacia* isolated from all samples

Molecular mechanism of resistance

Characterization of resistance mechanism in A. baumannii

A total of 646 isolates received from various regional centers, of them 473 were revived and subjected to PCR for characterization of antimicrobial resistance genes (**Table 4.13**). All the isolates harbored the blaOXA-51 like gene, which is intrinsically present in *A. baumannii* isolates. Molecular gene profile of all the tested *A. baumannii* isolates is given in Table 3.14. As expected, blaOXA-23 like was the predominant carbapenemase across all the centers contributing to 95% of the carbapenem resistance. Co-producers of OXA-23 with ESBLs and/or NDM was observed across all the centers (**Table 4.13**). Of which, the majority of the isolates 63% (n=268) had dual carbapenemases of blaOXA-23 like with blaNDM like. The combination of blaOXA-23 with blaPER in 8% (n=33) and blaOXA-23 with blaTEM in 18% (n=76) was noted. The antimicrobial resistance gene profile was found to be consistent across all the centers with blaOXA-23 like being the predominant carbapenemase and sporadic presence of blaOXA-58 like were observed. There was a significant increase in the proportion of dual carbapenemase co-producers (blaOXA-23 like with blaNDM like) from 56% in 2022 to 63% in 2023.

Table 4.13: Molecular characterization of carbapenem resistant *A. baumannii* collected across India during the year 2023

Centres	Total (Revived)	CR	CS	ESBL				Class A carbapenemase		Class B carbapenemase (M β Ls)				Class D carbapenemase			Co-producers	PCR Neg
				SHV	TEM	VEB	PER	KPC	GES	IMP	VIM	NDM	SIM	OXA-23	OXA-24	OXA-58		
RC 3	61(61)	61	-	-	22	-	-	-	-	-	-	36	-	46	-	-	OXA23&NDM=41 OXA23,NDM&TEM=4 OXA23&TEM=22	-
RC 20	30(18)	17	1	-	4	-	3	-	-	-	-	7	-	18	-	-	OXA23&NDM=7 OXA23&PER=3 OXA23&TEM=4 OXA23,NDM&TEM=2 OXA23,NDM&PER=2 OXA51 Carbapenem Susceptible=1	-
RC 16	28(19)	19	-	-	-	-	-	-	-	-	-	12	-	19	-	-	OXA23&NDM=12	-
RC 10	39(30)	27	3	-	4	-	2	-	-	-	-	19	-	25	-	-	OXA23&NDM=18 OXA23,NDM&TEM=2 OXA23,& TEM=4 OXA51 Carbapenem Susceptible=3	5
RC1, RC12, RC 13	81(59)	59	-	-	10	-	10	-	-	-	-	23	-	59	-	-	OXA23&NDM=23 OXA23&PER=8 OXA23,NDM,,PER=4 OXA23&TEM=8	-

																OXA 23,NDM,TEM=4	
RC 21	15(12)	10	2	-	1	-	1	-	-	-	-	2	-	9	-	OXA23&NDM=1 OXA 23,NDM,TEM=1 OXA 23,TEM=1 OXA23&PER=1 OXA51 Carbapenem Susceptible=2	3
RC 15	18(17)	17	-	-	1	-	-	-	-	-	-	5	-	16	-	OXA23&NDM=4 OXA 23,TEM=1 OXA 23,NDM,TEM=1 OXA51 Carbapenem Susceptible=1	1
RC 9	45(29)	27	2	-	2	-	-	-	-	-	-	13	-	25	-	OXA23&NDM=13 OXA23& TEM=2 OXA51 Carbapenem Susceptible=2	4
RC 14	47(40)	40	-	-	5	-	-	-	-	-	-	31	-	38	-	OXA23&NDM=38 OXA23& TEM=4 OXA23,NDM, TEM=3	-
RC 17	49(30)	19	11	-	4	-	-	-	-	-	-	18	-	19	-	OXA23&NDM=18 OXA23& TEM=4 OXA23,NDM, TEM=3	-
RC 19	15(11)	11	-	-	1	-	-	-	-	-	-	9	-	11	-	OXA23&NDM=9 OXA 23,TEM=1	-
RC 4	44(39)	19	20	-	5	-	2	-	-	-	-	13	-	19	-	OXA23&NDM=13 OXA 23,TEM=5 OXA23&PER=2 OXA23,NDM, TEM=5 OXA23,NDM, PER=1 OXA51 Carbapenem Susceptible=20	-

RC 6	45(41)	40	1	-	4	-	13	-	-	-	-	13	-	40	-	1	OXA23&NDM=13 OXA23,NDM,TEM=1 OXA23,NDM,,PER=3 OXA23&PER=13 OXA23,TEM=4 OXA51 Carbapenem Susceptible=1	1
RC 2	76(25)	24	1	-	13	-	4	-	-	-	-	9	-	24	-	-	OXA23,NDM,TEM=6 OXA23,NDM=9 OXA23,TEM=12 OXA23,PER=4 OXA23,TEM, PER=1	-
RC 5	28(22)	19	3	-	1	-	1	-	-	-	-	14	-	19	-	-	OXA23&NDM=14 OXA23,PER=1 OXA23,TEM=1 OXA51 Carbapenem Susceptible=3	3
RC 8	25(20)	19	1	-	2	-	1	-	-	-	-	9	-	19	-	-	OXA23&NDM=9 OXA23,TEM=2 OXA23,NDM,TEM=1 OXA23,PER=1 OXA51 Carbapenem Susceptible=1	1
TOTAL	646(473)	428	45	-	79	-	37	-	-	-	-	23 3		406	-	-	428	18

Characterization of resistance mechanism in *P. aeruginosa*

A total of 631 *P. aeruginosa* isolates recovered from various clinical specimens were received at the reference laboratory. Of them 533 isolates were retrieved and available for further molecular testing (**Table 4.14**). Of the 533 isolates, 188 were identified as carbapenem resistant and were screened for the presence of beta lactamases by molecular methods (ESBLs and carbapenemases). Among ESBLs, only *bla_{VEB}* was identified in six isolates. None of the isolates had *blaTEM*, *blaSHV* and *blaPER* as seen previously. Among the carbapenemases, *blaNDM* was found as the most common metallo beta lactamase (carbapenemase), followed by *blaVIM* and *blaDIM* was identified in two isolates (**Table 4.14**).

Interestingly, dual carbapenemase producers (VIM and NDM) were identified in three isolates. Trend analysis over the last two years highlights that NDM producing *P. aeruginosa* continues to be predominant different geographical location in India.

Table 4.14: Molecular characterization of carbapenem resistant *P. aeruginosa* collected across India during the year 2023

CENTER	Total (Revived tested)	CR	CS	ESBL				Class A Carbapenemase		Class B Metallo beta-lactamase				Co-producers (n)	PCR Negative	
				SHV	TEM	VEB	PER	KPC	GES	IMP	VIM	NDM	DIM			
RC 3	60 (60)	60	-	-	-	-	-	-	-	-	5	53	2	-	-	
RC 14	28 (28)	6	22	-	-	-	1	-	-	-	1	3	-	-	23	
RC 8	35 (34)	13	21	-	-	-	1	-	-	1	-	-	8	-	24	
RC 6	45 (42)	13	29	-	-	-	2	-	-	-	-	-	6	-	34	
RC 17	47 (15)	-	15	-	-	-	-	-	-	-	-	-	-	-	15	
RC 1	74 (68)	33	35	-	-	-	1	-	-	-	-	-	21	-	VEB & NDM (4)	42
RC 16	28 (28)	4	24	-	-	-	-	-	-	-	-	-	1	-	VIM & NDM (1)	26
RC 2	76 (44)	2	42	-	-	-	-	-	-	-	-	-	-	-	-	44
RC 10	43 (42)	12	30	-	-	-	-	-	-	-	-	-	-	-	-	42
RC 21	14 (14)	4	10	-	-	-	1	-	-	-	-	1	2	-	-	10
RC 18	15 (15)	-	15	-	-	-	-	-	-	-	-	-	-	-	-	15
RC 9	45 (42)	3	39	-	-	-	-	-	-	-	-	-	2	-	-	40
RC 15	18 (12)	2	10	-	-	-	-	-	-	-	1	-	-	-	-	11
RC 5	12 (11)	1	10	-	-	-	-	-	-	-	-	1	-	-	-	10
RC 4	45 (40)	15	25	-	-	-	-	-	-	-	-	-	4	-	VIM & NDM (1)	35
RC 20	46 (38)	20	18	-	-	-	-	-	-	-	-	7	2	-	VIM & NDM (1) VEB & NDM (2) VEB & VIM (2)	24
TOTAL (16 Centres)	631 (533)	188	345	-	-	-	6	-	-	1	-	15	103	2	11	395

Clinical relevance and treatment guidelines

Acinetobacter baumannii

Management of carbapenem resistant *A. baumannii* (CRAB) infections is difficult and associated with 40% mortality, irrespective of the treatment options. The production of OXA carbapenemases (eg, OXA-24/40, OXA-23) mediates resistance to all beta-lactams. CRAB isolates may also produce metallo-β-lactamases and additional serine carbapenemases (*A. baumannii*-derived cephalosporinases), further limiting the utility of common beta-lactam agents. Sulbactam resistance is not completely understood but appears to be driven primarily via mutations targeting PBPs (ie, PBP1a/1b and PBP3). The use of high-dose ampicillin-sulbactam (total daily dose of 6–9 g of the sulbactam component) in combination with at least one other agent is suggested for the treatment of CRAB infections. Additional agents that can be considered as components of combination regimens for the treatment of CRAB infections include polymyxin B, minocycline, tigecycline, or cefiderocol. Fosfomycin and rifampin are not suggested as components of combination therapy.

The preferred treatment options are ampicillin-sulbactam with tigecycline for pneumonia and complicated intra-abdominal infection, ampicillin-sulbactam with polymyxin B for bloodstream infection, ampicillin-sulbactam with colistin for urinary tract infections. It is suggested to reserve the addition of a third agent for patients with delayed clinical responses or recurrent infections. As with any treatment regimen selected, timely source control and close monitoring for clinical response and toxicity are required.

Pseudomonas aeruginosa

In 2018, the Infectious Disease Society of America (IDSA), introduced the concept of difficult to treat resistance (DTR) *P. aeruginosa*. In this guidance document, DTR is defined as *P. aeruginosa* exhibiting non susceptibility to all of the following: piperacillintazobactam, ceftazidime, cefepime, aztreonam, meropenem, imipenem-cilastatin, ciprofloxacin, and levofloxacin. MDR- *P.aeruginosa* or DTR-*P.aeruginosa* generally evolve as a result of an interplay of multiple complex resistance mechanisms, including decreased expression of outer membrane porins (OprD), increased production of or amino acid substitutions within *Pseudomonas*-derived cephalosporinase (PDC) enzymes (commonly referred to as pseudomonal AmpC enzymes), upregulation of efflux pumps (eg, MexAB-OprM), and mutations in PBP targets.

Among carbapenem resistant *P. aeruginosa*, there are carbapenemase and non-carbapenemase (carbapenem resistance due to porin loss and overexpression of efflux) producers. In India, majority of the proportion of carbapenem resistant *P. aeruginosa* are carbapenemase producers, mainly metallo beta-lactamase producers. Ceftazidime/avibactam and ceftolozane/tazobactam (at present not available in India)

are considered as the treatment options for non-carbapenemase producing, carbapenem resistant *P. aeruginosa*. However, growing evidence shows that resistance to ceftazidime/avibactam and ceftolozane/tazobactam are widely reported among non-carbapenemase producing, carbapenem resistant *P. aeruginosa* due to the combined mutations in ampC regulators (ampD/R), oprD, efflux and PBP3.

For metallo beta-lactamase (MBL) producing *P. aeruginosa*, the treatment options are very limited and generally remain susceptible to cefiderocol (at present not available in India). The combination of ceftazidime-avibactam plus appears less likely to provide an incremental benefit over aztreonam alone for MBL producing *P. aeruginosa* infections. Colistin or fosfomycin based combination strategy would be the best alternative for the treating MBL or DTR *P. aeruginosa* infection.

Stenotrophomonas maltophilia

Stenotrophomonas maltophilia is an emerged opportunistic pathogen causing life-threatening invasive infections with mortality ranging from 21%–69% in patients with bacteremia. It is intrinsically resistant to beta-lactams, carbapenems, monobactams (aztreonam), aminoglycosides, and fosfomycin, thus making first-line antibiotics, in particular beta-lactams, ineffective. Importantly, *S. maltophilia* produces chromosomally inducible beta-lactamases including class B metallo beta-lactamase, L1 and class A serine β-lactamase, L2. Similar to other MBLs, L1 hydrolyses all beta-lactam antibiotics except aztreonam. In contrast, beta-lactamase L2 is a narrow-spectrum cephalosporinase that can hydrolyze cephalosporins and monobactam, resulting in the appearance of a discordant ceftazidime-susceptible and carbapenem-resistant phenotype. Furthermore, ceftazidime's activity against *S. maltophilia* is expected to be low, regardless of its susceptibility, due to the presence of L2 beta-lactamase. Trimethoprim-sulfamethoxazole (TMP-SMZ) has long been considered a workhorse for treating *S. maltophilia* infections. Levofloxacin is the preferred alternative to TMP-SMZ, but it carries the risk of drug interactions and QTc prolongation. Alternatively, minocycline has emerged as a reasonable treatment option for *S. maltophilia* infections.

Burkholderia cepacia complex

Infections due to *B. cepacia* complex can be challenging to treat, as it is intrinsically resistant to a number of commonly used antibiotics. *B. cepacia* often is susceptible to trimethoprim-sulfamethoxazole, meropenem, minocycline, and tigecycline. Ceftazidime-avibactam has shown activity against multidrug-resistant *B. cepacia* complex strains and was found to be useful in persistent bacteremia.

Chapter 5. Typhoidal Salmonella

Typhoid fever is a serious illness that requires prompt diagnosis and appropriate antibiotic treatment to prevent complications. This infectious disease leads to substantial morbidity and mortality worldwide. With an estimated 11–20 million cases and 128,000–161,000 deaths annually, the emergence and spread of antimicrobial-resistant *Salmonella* Typhi has a significant impact on global health and is associated with a high disease burden, higher rates of hospitalisation, mortality, and higher healthcare costs. Increasing antimicrobial resistance significantly complicates the treatment of typhoid fever, necessitating accurate diagnosis, timely treatment, and continuous surveillance. Understanding and addressing the historical and current trends in antibiotic resistance are crucial for managing this disease. The geographical distribution of typhoid fever reflects a complex interplay of factors including sanitation, water quality, healthcare infrastructure, population density, and climate. Additionally, limited AMR data and insufficient microbiology lab capabilities for culture-based infection detection add to the challenges.

Understanding the history of antibiotic resistance reveals that the introduction of any new antibiotics has led to a gradual acquisition of resistance. Initially, multidrug-resistant strains (resistant to chloramphenicol, ampicillin, and co-trimoxazole) emerged, leading to fluoroquinolones being designated as the first-line drugs. Treatment options for fluoroquinolone- and multidrug-resistant typhoid fever now include azithromycin and third-generation cephalosporins. Nevertheless, these therapeutic options have been severely restricted due to recent outbreaks of extensively drug-resistant (XDR) pathogens in Asian countries. The emergence of these extensively drug-resistant typhoidal *Salmonellae* poses a global threat. So it's more important than ever to address this issue because travel has eliminated geographical boundaries and spreads drug-resistant isolates. Overall, *Salmonella* Typhi, commonly referred to as *S. Typhi*, is the primary cause of typhoid fever in India, followed by *Salmonella* Paratyphi A (*S. Paratyphi A*).

To analyze the yearly isolation trends of *S. Typhi* across India since 2017, we examined data from the North, Central, East, West, and South regions. In 2017, the highest isolation rate was recorded in West India, accounting for 4.8% of the cases. However, in 2018, there was a notable shift, with Central India experiencing the highest isolation rate, which increased significantly to 10.9%. In 2019, the maximum isolation of *S. Typhi* was once again observed in West India, but the rate had slightly increased to 5.9%. The year 2020, which coincided with the COVID-19 pandemic, saw the highest isolations of *S. Typhi* reported from West India, constituting 6.2% of the cases. This period may have been influenced by various factors related to the pandemic, impacting disease prevalence. In 2021, Central India experienced the highest isolation rate of *S. Typhi* at

2.5%, marking a shift from the previous years' trends. Finally, in 2022, the maximum isolation was recorded in North India, indicating a change in the distribution pattern once again. In 2023, nationally total isolation was 76.4%.

A total of 1338 typhoidal *Salmonellae* cases were reported across India in 2023 (**Table 5.1**). Among them, 1098 cases were positive for *Salmonella Typhi*, while 240 cases were positive for *Salmonella Paratyphi A*. The antimicrobial susceptibility results for *Salmonella Typhi* revealed that 97.5% of isolates were susceptible to ampicillin, 97% were susceptible to trimethoprim-sulfamethoxazole, and 98% were susceptible to chloramphenicol. Additionally, 3rd generation cephalosporins exhibited a susceptibility rate of 96% in 2023, whereas fluoroquinolones showed a susceptibility rate of only 2%. Azithromycin, on the other hand, exhibited a susceptibility rate of 97.4% during the same period. Both *S. Typhi* and *S. Paratyphi A* exhibit high susceptibility rates to ampicillin, ceftriaxone, and trimethoprim-sulfamethoxazole, where *S. Paratyphi A* shows 100% susceptibility. The susceptibility to ciprofloxacin was relatively low compared to other antibiotics, with *S. Typhi* showing a susceptibility rate of 2.1% and *S. Paratyphi A* showing a susceptibility rate of 6.9%. For the treatment of typhoid and paratyphoid fevers, the choice of antibiotics should be guided by local susceptibility patterns. These findings emphasize the limited effectiveness of ciprofloxacin in treating infections caused by this pathogen in 2023.

Table 5.1: Susceptibility pattern of *Salmonella* species from blood

AMA	Blood	
	<i>Salmonella Typhi</i> n=1098	<i>Salmonella Paratyphi A</i> n=240
Ampicillin	619 / 635 (97.5%)	93 / 93 (100%)
Azithromycin	640 / 657 (97.4%)	0 / 0 (-)
Cefixime	549 / 570 (96.3%)	70 / 73 (95.9%)
Cefotaxime	323 / 338 (95.6%)	7 / 7 (-)
Ceftriaxone	640 / 661 (96.8%)	96 / 96 (100%)
Chloramphenicol	597 / 608 (98.2%)	86 / 87 (98.9%)
Ciprofloxacin	14 / 674 (2.1%)	7 / 101 (6.9%)
Levofloxacin	10 / 55 (18.2%)	4 / 19 (-)
Ofloxacin	7 / 49 (14.3%)	2 / 19 (-)
Pefloxacin	24 / 379 (6.3%)	5 / 28 (-)
Trimethoprim-sulfamethoxazole	634 / 655 (96.8%)	95 / 95 (100%)

*Azithromycin sensitivity cutoff values are not given in CLSI for *Salmonella Paratyphi A*

Salmonella Typhi

The data provided reveals the sensitivity patterns of *Salmonella Typhi* to various antimicrobial agents in different regions of India (**Table 5.2**). In the South region, ampicillin exhibited a susceptibility rate of 99.5% (373/375), while in the North region; it was 95.7% (225/235). Across India the overall susceptibility rate was 97.5% (619/634). For trimethoprim-sulfamethoxazole, the West region showed 78.6% (22/28) susceptibility, the South region had a rate of 99.7% (374/375), the North region had a rate of 95.3% (223/234). Across India, Chloramphenicol demonstrated a susceptibility rate of 98.2% (597/608), while in the South region it was 99.7% (365/366), and 95.9% (215/224) in the North region.

The susceptibility patterns of cephalosporins varied across different regions of India. Ceftriaxone displayed a susceptibility rate of 96.8% (640/661) nationwide, with resistant strains identified in the North, South and West region. Ciprofloxacin susceptibility was found to be 1.6% (6/383) in the South region and 3.3% (8/245) in the North region. Across India, the overall ciprofloxacin susceptibility rate was 2% (14/674). Pefloxacin susceptibility rates were 20% (10/50) in the North region and 6.3% (24/379) across India. The observed findings underscore the significance of regional disparities in antimicrobial susceptibility, emphasizing the emergence of resistance, especially in cephalosporins and fluoroquinolones. Accurate understanding of these trends plays a crucial role in guiding effective treatment approaches and facilitating surveillance measures to address antimicrobial resistance in *Salmonella Typhi* infections.

Table 5.2: Susceptibility pattern of *S. Typhi* from blood across different regions of India

	National (n=1098)	North (n=498)	South (n=528)	West (n=47)	Central (n=23)	East (n=2)
Ceftriaxone	640 / 661 (96.8)	234 / 236 (99.2)	371 / 378 (98.1)	27 / 28 (96.4)	6 / 17 (-)	2 / 2 (-)
Azithromycin	640 / 657 (97.4)	233 / 236 (98.7)	364 / 375 (97.1)	27 / 28 (96.4)	14 / 16 (-)	2 / 2 (-)
Cefixime	549 / 570 (96.3)	222 / 233 (95.3)	318 / 324 (98.1)	1 / 2 (-)	8 / 9 (-)	0 / 2 (-)
Ampicillin	619 / 635 (97.5)	225 / 235 (95.7)	373 / 375 (99.5)	7 / 7 (-)	13 / 16 (-)	1 / 2 (-)
Chloramphenicol	597 / 608 (98.2)	215 / 224 (95.9)	365 / 366 (99.7)	9 / 9 (-)	6 / 7 (-)	2 / 2 (-)
Trimethoprim- sulfamethoxazole	634 / 655 (96.8)	223 / 234 (95.3)	374 / 375 (99.7)	22 / 28 (78.6)	13 / 16 (-)	2 / 2 (-)
Pefloxacin	24 / 379 (6.3)	10 / 50 (20)	12 / 323 (3.7)	2 / 4 (-)	0 / 0 (-)	0 / 2 (-)
Levofloxacin	10 / 55 (18.2)	10 / 47 (21.3)	0 / 1 (-)	0 / 0 (-)	0 / 7 (-)	0 / 0 (-)
Ciprofloxacin	14 / 674 (2.1)	8 / 245 (3.3)	6 / 383 (1.6)	0 / 28 (0)	0 / 16 (-)	0 / 2 (-)

Table 5.3 and Figure 5.1 represent yearly susceptibility trends of *Salmonella Typhi* isolated from blood. Ampicillin shows a general increase in susceptibility over the years, with a peak of 97.5% in 2020 and 2023 and slight dip in 2022 to 94.1%. Ceftriaxone showed high susceptibility rates overall, with a peak of 99.6% in 2021. Noticeable drop was observed to 93.8% in 2022 before slightly recovering to 96.8% in 2023. Cefixime displayed high susceptibility rates, with a highest of 99.4% in 2020 followed by slight decrease in recent years, down to 96.3% in 2023. Azithromycin susceptibility rates were consistently high, peaking at 99.5% in 2021. Despite a slight decrease to 96.8% in 2022, then a slight increase to 97.4% in 2023. Overall, ciprofloxacin showed very low susceptibility rates throughout the years, with a slight increase to 19.6% in 2021. A significant drop was noticed back to 2% in 2023. In case of levofloxacin variable susceptibility rates, with noticeable peaks and troughs was observed. The highest susceptibility was 30% in 2021 followed by lower rates in 2022 (6.4%) and 2023 (18%). Trimethoprim sulfamethoxazole and chloramphenicol generally displayed high and stable susceptibility rates, with a peak of 97% and 98 % respectively in 2023 and followed by a slight dip in 2022 to 93% and 95% was observed respectively.

Table 5.3: Yearly susceptibility trends of *S. Typhi* from blood

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

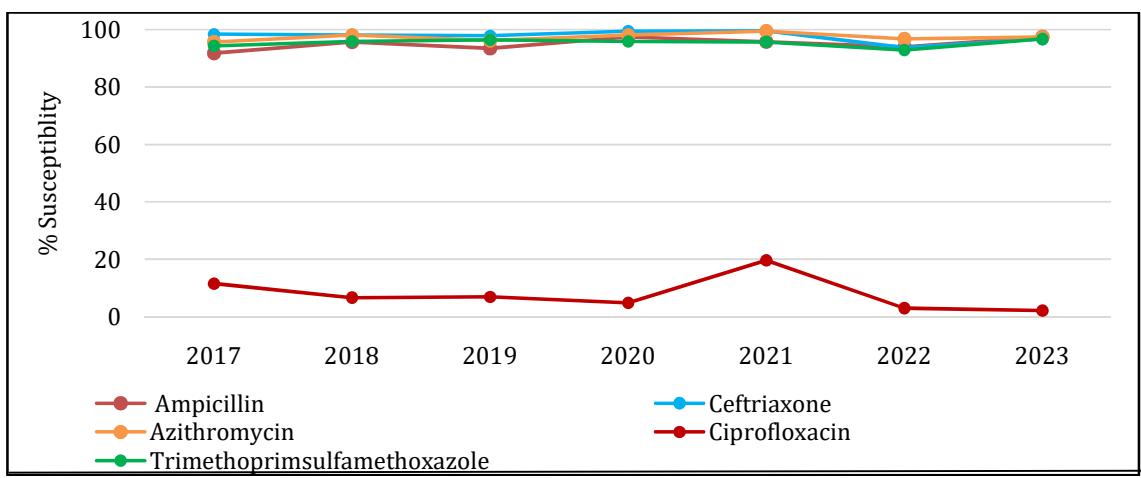


Figure 5.1: Yearly susceptibility trends of *S. Typhi* from blood

Ciprofloxacin MIC trend in *Salmonella Typhi*:

The data presented in **Figure 5.2a** and **Figure 5.2b** show a concerning trend in the creeping MIC of Ciprofloxacin for *Salmonella Typhi*. Although the majority of *S. Typhi* isolates exhibited intermediate sensitivity to ciprofloxacin during the years 2014-2016 (58%) and 2017-2019 (71%), these isolates were considered non susceptible overall.

Overall, the total ciprofloxacin sensitivity was 8% in 2014-2016 followed by 11.6% in 2017 and dropping to 4.9% by 2020, indicating high non susceptibility from the beginning. There was a brief improvement in 2021, with susceptibility rising to 19.6%. Susceptibility rates decreased again, reaching as low as 2% in 2023. This marked a significant increase in the MIC of Ciprofloxacin, indicating escalating resistance in *Salmonella Typhi*.

Mainly trend of increasing non susceptibility for ciprofloxacin was reflected in the MIC₉₀ values. While there were periods of slight improvement or stabilization, such as in 2017-2018 and 2022, the overall trajectory points towards higher resistance levels, with the peak MIC₉₀ of 128 µg/ml in 2023 being a significant concern. The fluctuating MIC₅₀ values also highlight variable susceptibility within the population, but the overall trend suggests increasing non susceptibility. This calls for continued surveillance, judicious use of antibiotics, and exploration of alternative treatment options to manage ciprofloxacin resistance in *Salmonella Typhi*.

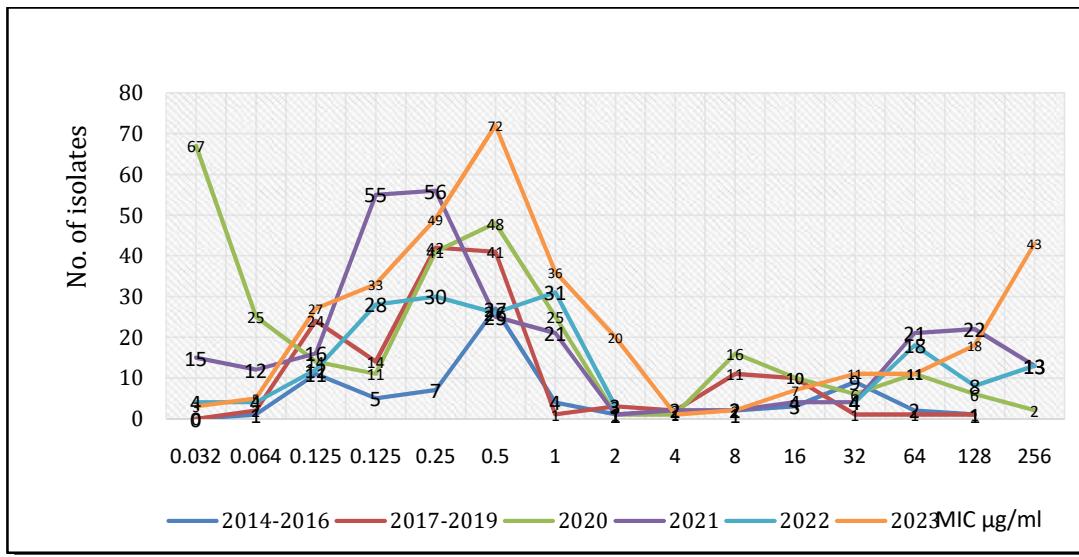


Figure 5.2 a: Ciprofloxacin MIC trends in *Salmonella Typhi* from pan India over a period of ten years

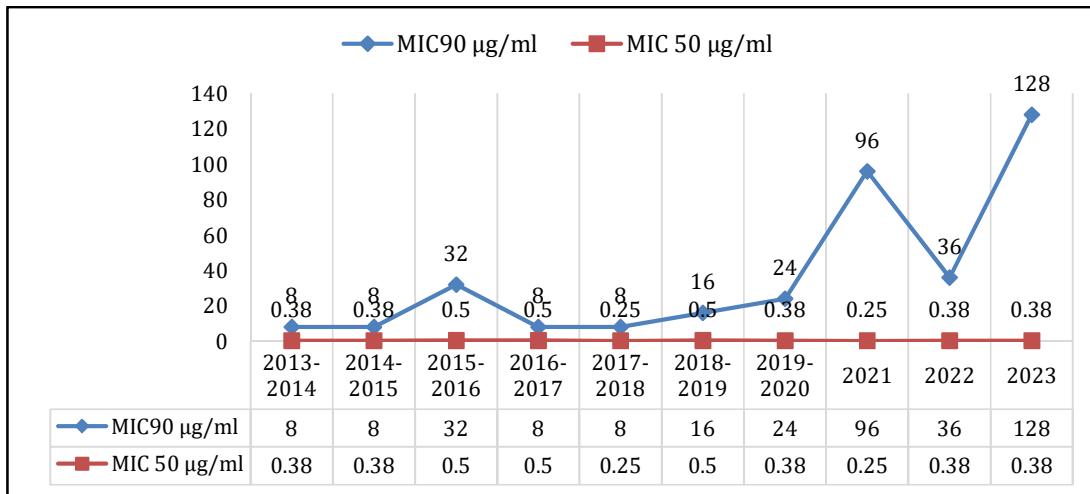


Figure 5.2 b: Comparison of MIC 50 and MIC90 of *S. Typhi* for Ceftriaxone in *S. Typhi* over a period of ten years

In order to examine the trend of ceftriaxone creeping minimum inhibitory concentration (MIC) over 10-year period, the data was divided into two groups for 6 years: 2014-2016 and 2017-2019 and the individual years of 2020, 2021, 2022 and 2023 were analysed separately for any recent change (**Figure 5.3a& b**). During the period of 2014-2016, maximum number of isolates showed a minimum inhibitory concentration (MIC) range of 0.032-0.064 µg/ml. Over the years, there's a noticeable fluctuation in the number of cases with lower MIC values (0.032 to 0.125 µg/mL). In 2020, there's a peak in cases with higher MIC values (0.125 µg/mL), which indicates a

period of reduced susceptibility but this trend seems to revert in 2021 and 2022 with more cases of lower MIC values.

In 2021 and 2022, the number of cases with very low MIC values (0.032 and 0.064 µg/mL) is quite high. However, the number of cases with high MIC values (>32 µg/mL) is minimal or absent in those years, indicating low resistance. In 2023, there's a slight resurgence in cases with high MIC values, indicating some level of increased resistance again, though it's not as high as in 2020. Total number of isolates with MIC range 0.125 to 0.19 has been increased during 2023 from previous years. During 2023, ceftriaxone resistance was observed in 5 isolates. The MIC₅₀ values suggest a generally high susceptibility among the bacterial isolates. The MIC₉₀ values, however, show varying patterns, with slight increases in MIC observed in 2023. These findings suggest a fluctuation in the MIC values of ceftriaxone over the years.

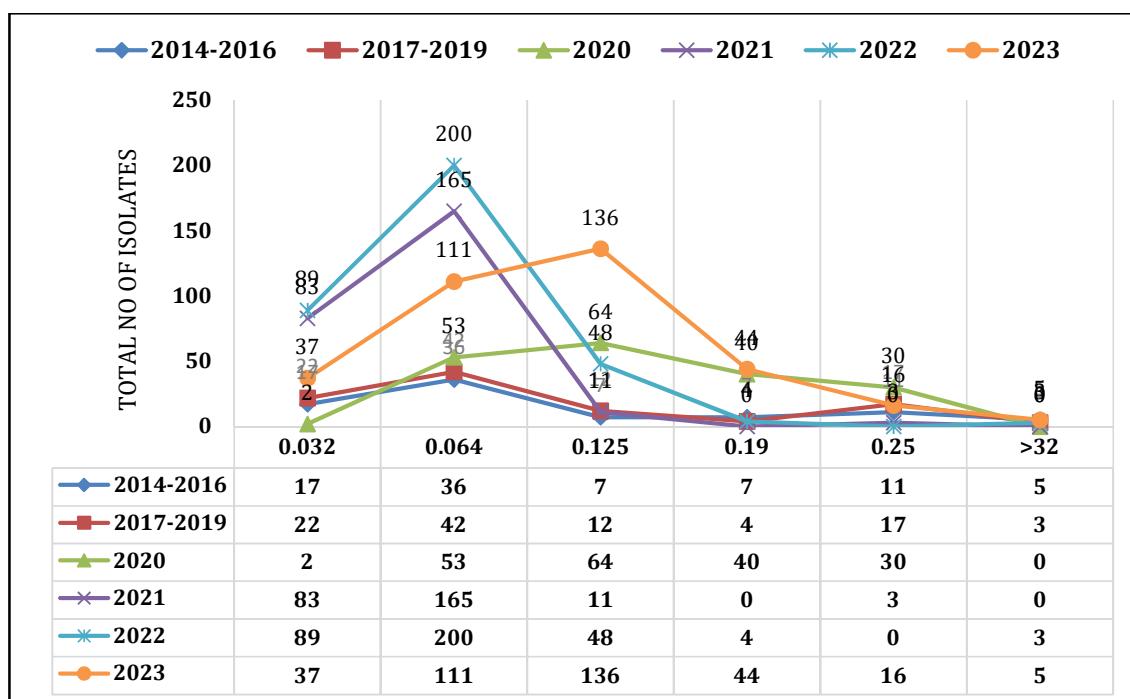


Figure 5.3 a: MIC trend for Ceftriaxone in *S. Typhi* from Pan India over a period of nine years

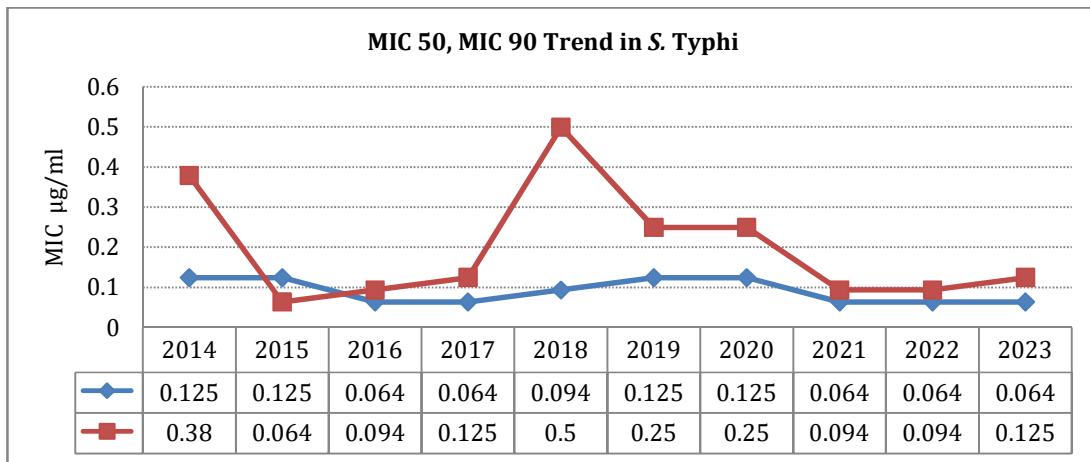


Figure 5.3 b: Comparison of MIC 50 and MIC90 of S. Typhi for Ceftriaxone in S. Typhi over a period of ten years

To understand the trend of azithromycin MIC over a 10-year period, the data was divided into two groups: 2014-2016 and 2017-2019. Additionally, the individual years of 2020, 2021, 2022 and 2023 were analysed separately (**Figure 5.4 a & b**) for any recent change. In the years 2014-2016 and 2017-2019, the majority of isolates showed a maximum concentration (MIC) range of 2-4 µg/ml. However, in the subsequent years 2020 to 2023, there was a shift in the distribution, with the maximum number of isolates falling in the 4-16 µg/ml MIC range. Though, none of the isolate in this study was resistant to azithromycin. However, it is evident that azithromycin MIC values have increased with time, suggesting a rise in MIC that could result in resistance. There has been a clear trend since 2017, with increasing MIC levels climbing substantially in 2021 and beginning to stabilise in 2023.

The MIC values for azithromycin against *Salmonella Typhi* from 2014 to 2023 revealed a fluctuating pattern in susceptibility. The MIC50 values generally varied between 4 to 12 µg/ml, indicating changes in the lower threshold of azithromycin effectiveness. The MIC90 values showed more variability, peaking significantly at 24 µg/ml in 2020, suggesting a temporary decrease that year and again decreased upto16µg/ml in 2023. Overall, while there are fluctuations, there is no consistent trend of increasing MIC, but the variations highlight the importance of continuous monitoring.

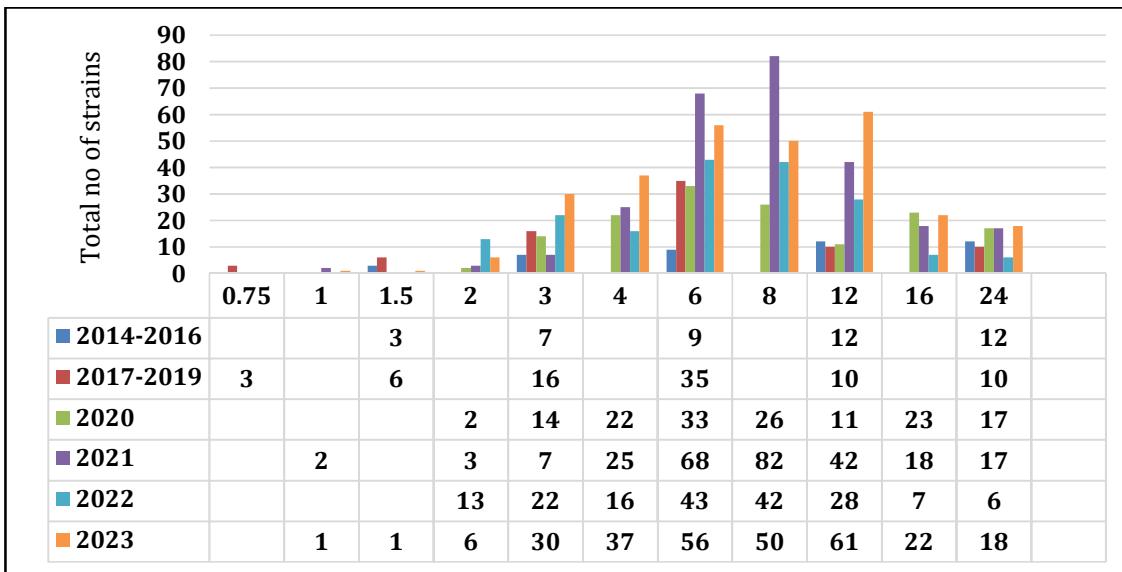


Figure 5.4 a: Azithromycin MIC trend in *S. Typhi* over a period of nine years from Pan India

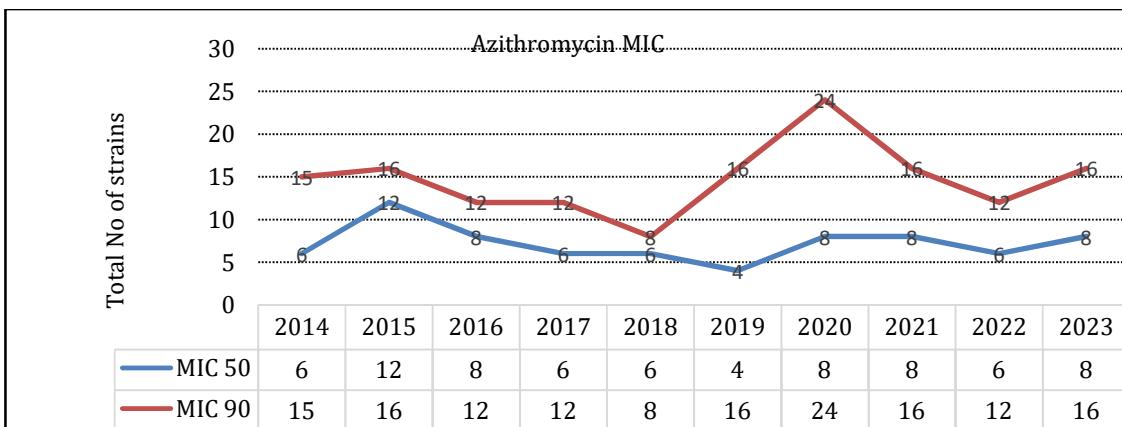


Figure 5.4 b: Comparison of MIC 50 and MIC90 of *S. Typhi* for Azithromycin in *S. Typhi* over a period of ten years

Salmonella Paratyphi A

The antibiotic susceptibility pattern of *S. Paratyphi A* from 2017 to 2023 shows that susceptibility to ampicillin in 2023 is 100% compared to 95% in 2017, as per the data presented in **Table 5.4 and Figure 5.5**. The susceptibility to chloramphenicol which was 100% in 2019 has dropped to 99% in 2023. Trimethoprim-sulmethoxazole showed 100% susceptibility in 2017 and 2018, but there was a significant variation in 2021 and 2022, with 98% and 99%, susceptibility respectively while another 100% susceptibility

report was seen in 2023. Ciprofloxacin resistance in *S. Paratyphi A* is high, and while there have been minor fluctuations, the overall sensitivity remains low.

Ciprofloxacin sensitivity dropped from 10% (4/40) in 2017 to 8.7% (4/46) in 2021. Only one isolate was found to be ciprofloxacin-sensitive in 2022. Ciprofloxacin sensitivity increases by up to 6.9% (7/101) in 2023. Ceftriaxone antimicrobial susceptibility has increased from 95% (38/40) in 2017 to 97.6% (122/125) in 2018 and 97.9% (139/142) in 2019. In 2020, 2021, and 2023, it was found to be 100% susceptible.

Cefixime exhibited susceptibility of 96.3% (26/27) in 2017, 100% (105/105) in 2018, 98.1% (105/107) in 2019, and 100% (31/31) in 2020 and 2021, in that order. It was 90% (72/80) susceptible in 2022 and 95.9% (70/73) susceptible in 2023. Azithromycin was not analysed as azithromycin susceptibility cutoff for *S. Paratyphi A* are not given in CLSI.

Table 5.4: Yearly susceptibility trends of *S. Paratyphi A* from blood

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

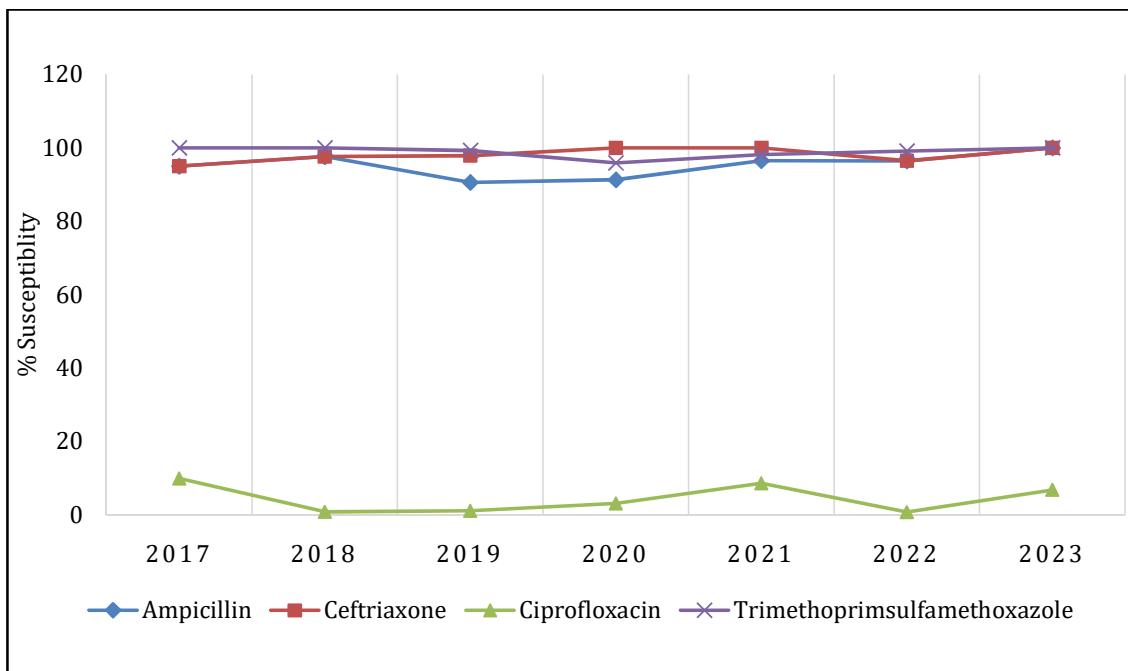


Figure 5.5: Yearly susceptibility trends of *S. Paratyphi A* from blood

Among *Salmonella* Paratyphi A, the majority of isolates exhibited an intermediate MIC range (0.125-0.5 µg/ml) for ciprofloxacin (**Figure 5.6**). However, a significant shift occurred in 2021, 2022 and 2023 with the emergence of isolates showing higher MIC ranges of 128 µg/ml to 256 µg/ml. In *S. Paratyphi A*, both MIC₅₀ and MIC₉₀ values for ciprofloxacin have increased over time. In 2014, the MIC₅₀ was observed to be 0.38 µg/ml, which gradually increased to 0.5 µg/ml by 2023. While the MIC₉₀ has continued to rise, reaching 1.5 µg/ml in 2023. It is noteworthy that fluoroquinolone resistance is higher in *S. Typhi* compared to *S. Paratyphi A* in 2023. For ceftriaxone resistance MIC range was 0.032 – 0.5 µg/mL (**Figure 5.7**). From 2017 to 2019, there was a shift towards higher MIC values, with the highest number of isolates falling between 0.125 and 0.25 µg/mL. In 2023, the highest number of isolates was recorded in the 0.064-0.125 µg/mL MIC range. Recognising the existence of isolates with creeping minimum inhibitory concentrations (MIC values) is crucial as it suggests a possibility of future resistance development. But none of the *Salmonella* Paratyphi A showed signs of ceftriaxone resistance.

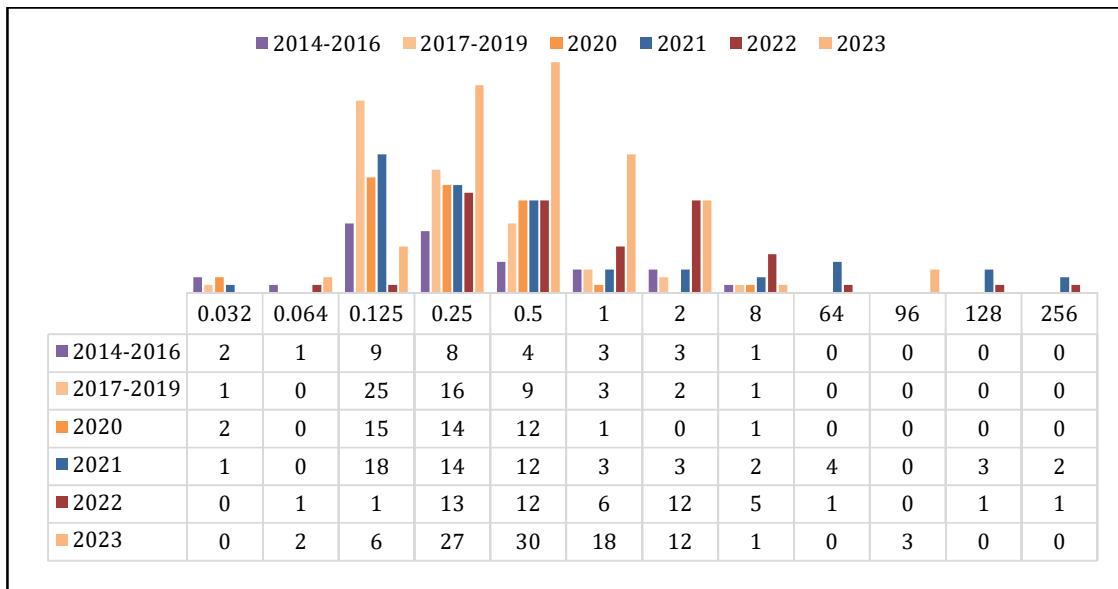


Figure 5.6: Ciprofloxacin MIC trends in *Salmonella Paratyphi A* from Pan India over a period of ten years

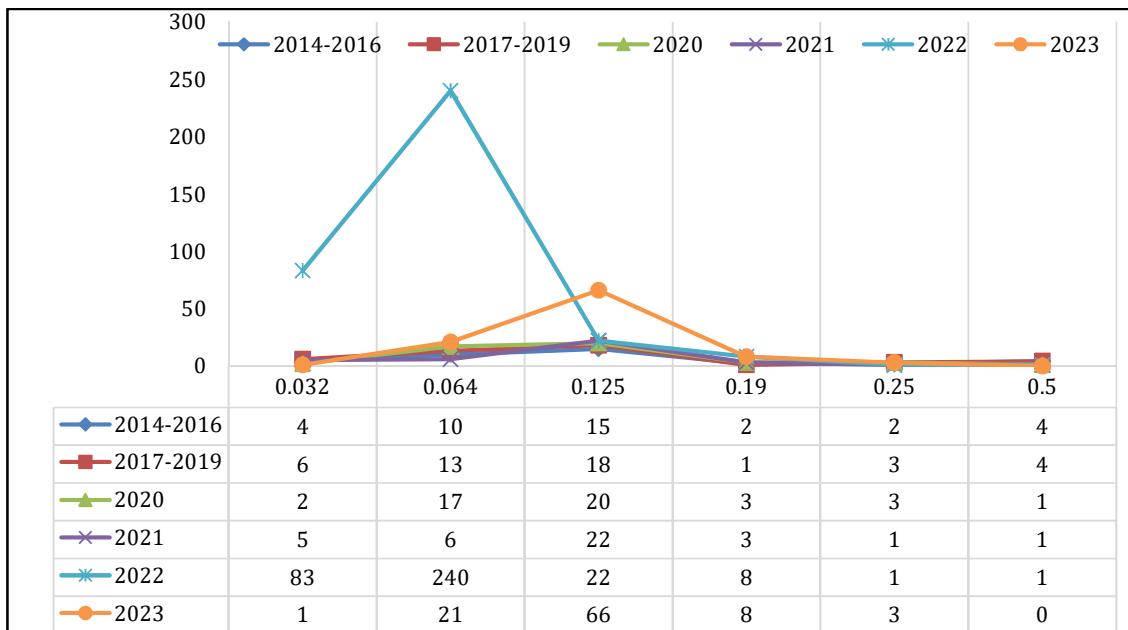


Figure 5.7: Ceftriaxone creeping MIC in *S. Paratyphi A* from pan India over a period of nine years

Molecular data and its relevance

We investigated resistance genes and their phenotypic correlation in typhoidal isolates to understand the resistance mechanisms at the molecular level. For this study, we

selected 25% of all representative samples from all centers. The relationships between resistance gene content identified from WGS was deciphered with the drug resistance profile for each corresponding clinical isolate (phenotype). The following observations were made on the basis of WGS analysis.

In *Salmonella* Typhi the ampicillin resistance is associated with the presence of beta-lactam genes which were observed in 2% strains (1/49) by WGS. In the entire strains blaTEM-1 D beta-lactam resistance gene was observed. The resistance genes encode for the predominant plasmid-mediated β -lactamases of Enterobacterales. Earlier reports for amoxicillin resistance in *Salmonella* from pan-India were also 2%.

In case of *Salmonella* Paratyphi A, all strains were sensitive. Other gene responsible for resistance rsmA, sdi A and marA were present. Chloramphenicol resistance determinants were observed in 2% strains (1/49) *Salmonella* Typhi by WGS. All non-susceptible strains harboured catA1 gene which encodes chloramphenicol acetyltransferase enzyme causing chloramphenicol resistance by chemical modification of the drug molecule, whereas ten isolates harboured the catI genes. Our findings are consistent with other studies reporting chloramphenicol susceptibility in *S. enterica*.

Trimethoprim-sulfamethoxazole were considered in combination for treatment as the first-line drug, co-trimoxazole. Out of 49 strains, trimethoprim resistance determining genes were found in 2% strains (1/49). Likewise, gene sul1 and sul2, encoding dihydropteroate synthases known to disseminate sulfamethoxazole resistance, were also detected in 2% strains (1/49).

Molecular determinants of resistance to fluoroquinolone including ciprofloxacin and pefloxacin antibiotics encoded by gyrA and parC, genes were detected in 72.3% strains by WGS. Mutations in gyrA and parC, was observed in 44.6% followed by only gyrA mutation in 48.9% isolates. The identified genes were associated with mutations in Quinolone Resistance Determining Region of DNA gyrase enzyme, the binding site for fluoroquinolone. Antimicrobial resistance to fluoroquinolones was 70% by both disc diffusion and E-test method. MIC distribution ranged between 2–256 mg/L and peaked at 12 mg/L. DNA Gyrase A mutations at position 83 (Ser-83→Phe, Ser-83→Tyr and Asp 87→ Phe) are the most prevalent resistance mechanisms for Fluoroquinolone in India, followed by Ser-80→Ile substitution in parC gene. Highly non-susceptible strains (with ciprofloxacin MIC > 8 mg/L) were found to be double or triple mutants with mutations in gyrA83, gyrA87 and parC80. Strains with moderate resistance to ciprofloxacin possessed single mutations in DNA gyrA gene at Ser83 position.

In case of *Salmonella* Paratyphi A, phenotypically 67% strains were intermediate and 34% were resistant to fluoroquinolone. Mutations in gyrA gene were detected in 100% of the strains. Double mutation in gyrAS83F and D87N was observed in one strain followed by triple mutation in only one strain. Other fluoroquinolone resistance mechanism CRP, acrR, marR, soxR, acrB, emrA, emrB, mdtk and rsmA were also present.

Although all the strains were cephalosporin sensitive Mutations in PBP3 gene at D350N, S357N, *Escherichia coli* ampC1 beta-lactamase, and *Escherichia coli* ampH beta-lactamase gene was present in all tested isolates. This clearly raises an alarm towards

the judicial use of these antibiotics. All isolates were azithromycin susceptible. Other genes responsible for macrolide resistance nalD, KpnE, CRP were also observed by WGS. *S. Typhi* can demonstrate resistance to multiple antibiotics by acquiring new resistance genes through horizontal genes transfer (HGT). The acquired antimicrobial resistance genes including aac(6')-Iaa, AAC(6')-Iy, aadA1, aph(3")-Ib, aph(6)-Id, strA, and strB that provided resistance to aminoglycosides were observed in 100% isolates (Table 6.6). In addition, *S. Typhi* isolates harboured the genes baeR, emrb, H-NS, marA, mdfA, mdtK, msbA, acrA, emrR, kpnE, kpnF, marR, sdiA, crp, soxR, and soxS that could confer multidrug resistance and were detected in all strains. The mds ABC complex, a multidrug transporter of *Salmonella*, comprising mdsA, mdsB, and mdsC units was also observed in all isolate. The mdsABC complex is recognized to contribute resistance against a diverse set of drugs and toxins. The identified multi-efflux pump mdtK gene, conferring resistance against the drugs, acriflavin, doxorubicin and norfloxacin, was observed in 100% of the isolates. The gene, sdiA, a multi-drug resistance pump regulator for AcraB, was also present in 100% of the isolates.

The pathogenicity and resistance profile of the various *Salmonella* isolates can be attributed to the presence of identified genes.

Multi-locus sequence typing (MLST) profile disclosed low genetic variation in housekeeping genes (aroC, dnaN, hemD, hisD, purE, sucA, and thrA) among *Salmonella* Typhi, *Salmonella* Paratyphi A and other *Salmonella* isolates. Two different sequence types (STs) including ST1 and ST2 were observed in *Salmonella* Typhi while *Salmonella* Paratyphi A was divided in ST 85 and ST129 respectively. ST1 was the predominant type, accounting for 70% of examined strains, whereas ST2 was observed in 29% of the strains (Table 6.5). In case of *S. Paratyphi A*, ST85 was observed in 1 and ST129 was observed in 3 isolates. *S. enteritidis* grouped as ST11.

In summary, our findings demonstrate a consistent correlation between the presence of resistance-associated genes or mutations and the observed antimicrobial susceptibility profile.

Clinical relevance of the study:

The analysis of antimicrobial susceptibility results highlights the importance of accurate diagnosis and appropriate antibiotic treatment for typhoid fever, considering the increasing resistance to antibiotics. The isolation trends revealed a dynamic pattern of *S. Typhi* prevalence and geographical distribution in India over a five-year period from 2017 to 2023. It is also important to highlight that the number of strains exhibiting higher MIC values has increased in 2021 and 2022, and 2023 indicating a potential shift towards reduced susceptibility to ciprofloxacin in recent years.

The fluctuations in the regional isolation rates of *S. Typhi* highlight the dynamic nature of the disease and its epidemiology across different regions of India. Factors such as population movement, healthcare facilities, sanitation, and climate variations could

have contributed to these variations in prevalence. Understanding these patterns is crucial for implementing targeted prevention and control strategies to reduce the burden of *S. Typhi* infections in India. Further research and surveillance efforts will be essential to monitor and respond to any future changes in the geographical distribution of the disease.

The historical development of antibiotic resistance demonstrates the gradual acquisition of resistance, leading to the designation of fluoroquinolones as the first-line drugs due to the emergence of multidrug-resistant strains.

Currently, third-generation cephalosporins and azithromycin are the available treatment options for multidrug-resistant and fluoroquinolone-resistant typhoid fever. However, the emergence of extensively drug-resistant (XDR) strains in Asian countries has severely limited the treatment choices. Continuous surveillance is necessary to prevent the spread of these XDR strains, considering the elimination of geographical boundaries due to travel and the dissemination of drug-resistant isolates.

In a small percentage of isolates, susceptibility was observed despite the presence of resistance genes, particularly for chloramphenicol and cotrimoxazole. Notably, no resistance to ceftriaxone or the presence of the CTXM-15 gene was detected in any typhoidal strain. Furthermore, none of the studied isolates exhibited resistance genes associated with azithromycin, indicating susceptibility to this antibiotic. Due to the small numbers of isolates from each regional center, no significant regional variations were observed in the distribution of resistance genes. However, when comparing different regions of India (East, West, North, and South), the presence of gyrase mutations other than S83F was observed primarily in strains from North and West India. On a national scale, the distribution of fluoroquinolone resistance mechanisms and genes exhibited variability.

Strains with intermediate ciprofloxacin susceptibility had single mutation at gyrA S83F or double mutation at gyrA S83F and parC S80I of the QRDR. While strains with higher ciprofloxacin MIC had triple mutation at gyrA at S83F, D87N and parC S80I or parE D420N. Mutation in parE gene at L416F, also was found in one isolate each with ciprofloxacin intermediate MIC.

Not all isolates showed a positive association of genetic mutations and phenotypic resistance, supporting the fact that mere presence of gene may not be sufficient to impart clinical resistance and many factors may come into play including expression of gene and antibiotic selection pressure. There was no significant difference in the distribution of mutation and antibiotic susceptibility across different regions. However, the presence of resistance mutation in susceptible strains is a cause of concern as it may lead to their expression on exposure to fluoroquinolones and subsequent emergence of ciprofloxacin resistance. Genotypic studies and continuous surveillance of antimicrobial resistance is therefore necessary to understand the evolving mechanism of resistance and their epidemiology.

While *S. Typhi* shows higher sensitivity rates to some antibiotics, such as ampicillin, chloramphenicol, and trimethoprim-sulfamethoxazole, its sensitivity to ciprofloxacin

has decreased over the years. The susceptibility patterns of *S. Paratyphi A* also exhibit variations across different antibiotics. These findings accentuate the importance of continued surveillance and the need for alternative treatment strategies to combat the rising levels of antibiotic resistance in typhoid fever.

Table 5.5.a: MLST grouping of all *Salmonella*

Organism	Sequence Type	Total Sequence Type/organism
<i>S. Typhi</i>	ST1, ST2	ST1- 30 ST2- 9
<i>S. Paratyphi A</i>	ST85, ST129	ST85- 1 ST129 -3
<i>S. Enteritidis</i>	ST11	ST11- 1

Table 5.5 b: Distribution of FQ resistance imparting mutations in DNA gyrases and topoisomerase IV of studied strains and coorelation with MIC

MIC ($\mu\text{g/ml}$)	Single Mutation	Double mutation	Triple mutation
0.064 (n=1)	<i>gyrAS83F</i> (n= 1)	-----	-----
0.125 (n=3)	<i>gyrAS83F</i> (n= 1) <i>parCS80 I</i> (n= 1) <i>gyrAS83Y</i> (n= 1)	-----	-----
0.75 (n=3)	<i>gyrAS83F</i> (n= 1) <i>gyrAS83Y</i> (n= 1)	<i>gyrAS83F, parCS80 I</i> (n= 1)	
0.25 (n=5)	<i>gyrAS83F</i> (n= 3) <i>gyrAS83Y</i> (n= 1)	- <i>gyrAS83F, parCS80 I</i> (n= 1)	-----
0.19 (n=4) Single-2 Double -2	<i>gyrAS83F</i> (n= 1) <i>gyrAS83Y</i> (n= 1) <i>gyrAD87N</i> (n=1)	<i>gyrAS83F, gyrAD87N</i> (n= 1)	-----
0.5 (n=5)	<i>gyrAS83F</i> (n= 3) <i>gyrAS83Y</i> (n= 1)	<i>gyrAS83F, parCS80 I</i> (n= 1)	-----
0.38 (n=5)	<i>gyrAS83F</i> (n= 4)	-----	<i>gyrA S83F, D87N parCS80I</i> (n=1)
1-256 (n=10)			<i>gyrA S83F, D87N parCS80I</i> (n=6) <i>gyrA S83F, S83Y, par C S80I</i> (n=4)

Table 5.6a: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from JIPMER

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	Er m C	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
2/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
3/ST	Np	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
4/ST	Np	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
5/ST	Np	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
6/ST	Np	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
7/S. Enteritidis	NP	NP	S	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
8/S. Enteritidis	NP	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR

P*- Present; NP*- Not present; I*- Intermediate; R*- Resistant; S**- Sensitive

CRP, acrA,acrR,marR, soxR,acrB,emrA,emrB,emrR,marA,mdtK,mdtM,rsmA,sdiA - Present in all isolates for FQ resistance

acrA, acrR, ampC1, ampH, marR, soxR,soxS,PBP3,KpnE,acrB,marA,sdiA- Present in all isolates for Cephalosporin resistance

CRP,KpnE,kpnF- Present in all isolates for Macrolide resistance

Table 5.6 b: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC 16

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine antibiotic	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	Erm C	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	NP	gyrA_S83Y	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	S
2/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	S

Table 5.6c: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC1

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	Erm C	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	NP	gyrA_S83F	S	Np	S	Np	S	NP	Np	Np	Np	Np	Np	Non-MDR
2/ST	Np	gyrB_S464F	I	Np	S	Np	S	P	Np	P	P	P	Np	MDR

Table 5.6d: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic from RC6

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	ErmC	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
2/ST	Np	gyrA_S83F	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
3/ST	Np	gyrA_S83F	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
4/ST	Np	gyrA_S83F	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
5/ST	Np	gyrA_S83F/D87N	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
6/ST	parE_L416F	gyrA_S83F,	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
	Np	Np	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR
7/SPA	NP	gyrA_S83F	I	Np	S	Np	Sensitive	Np	Np	Np	Np	Np	Np	non-MDR

Table 5.6e: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC 15

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	ErmC	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
2/ST	NP	NP	S	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
3/ST	NP	gyrA_S83Y	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR

Table 5.6f: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC 5

	Fluoroquinolone			Cephalospo rin	Macrolide		Ampicill in	diaminopyrimid ine	phenic ol	Sulfonami de	Phenoty pic Sensitivi ty			
	parC	gyrA	Phenoty pic Sensitivi ty	CTX-M-15	Phenoty pic Sensitivi ty	Erm C	Phenoty pic Sensitivi ty	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	
1/ST	NP	gyrA_S83Y	I	Np	S	Np	S	NP	Np	NP	NP	NP	NP	Non- MDR
2/ST	NP	gyrA_S83F	I	Np	S	Np	S	NP	Np	Np	Np	Np	Np	Non- MDR
3/ST	NP	gyrA_S83Y	I	Np	S	Np	S	NP	Np	Np	Np	Np	Np	Non- MDR
4/ST	NP	gyrA_S83Y	I	Np	S	Np	S	NP	Np	Np	Np	Np	Np	Non- MDR
5/ST	parC_S80I	gyrA_S83F/D 87N	R	Np	S	Np	S	NP	Np	Np	Np	Np	Np	Non- MDR
6/ST	NP	gyrA_S83Y	I	Np	S	Np	R	NP	Np	Np	Np	Np	Np	Non- MDR
7/ST	parE_D42 ON	gyrA_S83F,	I	Np	S	Np	S	NP	Np	Np	Np	Np	Np	Non- MDR

Table 5.6g: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC3

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	ErmC	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	NP	gyrA_S83Y	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
2/ST	parC_E84G	gyrA_S83F,	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
3/ST	parC_S80I	gyrA_S83Y	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
4/ST	parC_S80I	gyrA_S83Y	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
5/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR

Table 5.6h: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC8

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide			
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	ErmC	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenotypic Sensitivity
1/ST	NP	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
2/ST	NP	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
3/ST	parC_S80I	gyrA_S83F/D87N	R	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR
4/ST	NP	gyrA_S83F	I	Np	S	Np	S	Np	Np	Np	Np	Np	Np	Non-MDR

Table 5.6i: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC2

	Fluoroquinolone			Cephalosporin		Macrolide		Ampicillin	diaminopyrimidine	phenicol	Sulfonamide	Phenotypic Sensitivity		
	parC	gyrA	Phenotypic Sensitivity	CTX-M-15	Phenotypic Sensitivity	Erm C	Phenotypic Sensitivity	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	
1/ST	Np	gyrA_S83Y	I	NP	S	NP	R	Np	NP	NP	NP	Np	Np	Non-MDR
2/ST	Np	gyrA_S83F	I	NP	S	Np	S	Np	NP	NP	NP	Np	Np	Non-MDR
3/ST	Np	gyrA_S83F	I	NP	S	Np	S	Np	NP	NP	NP	Np	Np	Non-MDR
4/ST	parC_S80I	gyrA_S83F/D87N	R	NP	S	Np	S	Np	NP	NP	NP	Np	Np	Non-MDR
5/SPA	Np	gyrA_S83F	I	NP	S	Np	S	Np	NP	NP	NP	Np	Np	Non-MDR
6/SPA	Np	gyrA_S83F/D87N	R	NP	S	Np	S	Np	NP	NP	NP	Np	Np	Non-MDR

Table 5.6j: Genotyping analysis of antibiotic resistance by whole genome sequencing and comparison with phenotypic antibiotic sensitivity from RC 13

	Fluoroquinolone			Cephalosp orin			Macrolide		Ampicil lin	diaminopyrimi dine		phenic ol	Sulfonamide		
	parC	gyrA	Phenoty pic Sensitivi ty	CTX-M-15	Phenoty pic Sensitivi ty	ErmC	Phenoty pic Sensitivi ty	TEM-1	dfrA15	dfrA7	catI	Sul1	Sul2	Phenoty pic Sensitivi ty	
1/ST	parE_D42 0N	gyrA_S83Y, gyrA_S83F/D 87N;	I	NP	S	Prese nt	R	Present	Presen t	Presen t	Presen t	Prese nt	Prese nt	Prese nt	MDR
2/ST	parC_S80 I	gyrA_S83F/D 87N;	R	NP	S	NP	S	Np	NP	NP	NP	Np	Np	Np	Non- MDR
3/ST	NP	gyrA_S83F	I	NP	S	NP	R	NP	NP	NP	NP	NP	NP	NP	Non- MDR
4/ST	parC_S80 I	gyrA_S83F/D 87N	R	NP	S	Np	S	Np	NP	NP	NP	Np	Np	Np	Non- MDR
5/SPA	NP	gyrA_S83F	R	NP	S	NP	S	Np	NP	NP	NP	Np	Np	Np	Non- MDR

Chapter 6. Diarrheal pathogens

The antimicrobial susceptibility profile of *Aeromonas* spp. covering cefixime, imipenem, meropenem, tetracycline, and ciprofloxacin is detailed in **Table 6.1**. The data reveals a high susceptibility to meropenem (89%), while imipenem shows moderate susceptibility (63.9%). However, ciprofloxacin's susceptibility remains notably low at 20.9%. **Table 6.2** depicts annual trends in the susceptibility of *Aeromonas* spp. to selected antimicrobials. Susceptibility to carbapenems has shown improvement over time, with consistently high susceptibility to tetracycline. Despite a slight increase, ciprofloxacin susceptibility remains low at 20.9% in 2023 (**Figure 6.1**).

***Shigella* sp**

The taxonomic distribution of *Shigella* spp. in 2023 indicates a dominance of *Shigella flexneri* (n=25) over *Shigella sonnei* (n=15). *Shigella flexneri* exhibited the highest susceptibility to azithromycin (83.3%) and trimethoprim-sulfamethoxazole (79.2%). Conversely, *Shigella sonnei* showed the highest susceptibility to ampicillin (93.3%) and cefixime (92.9%). Both strains were completely resistant to ciprofloxacin (0% susceptibility), and Nalidixic acid showed no susceptibility, though the sample sizes for this antibiotic were small (**Table 6.3**). **Figure 6.2** and **Table 6.4** illustrate the antibiotic susceptibility trends for *Shigella flexneri* from 2017 to 2023. Among the tested antimicrobials, azithromycin consistently maintained high susceptibility, around 83.3%. Trimethoprim-sulfamethoxazole showed significant improvement, increasing from 7.7% in 2017 to 79.2% in 2023. However, cefixime and ampicillin exhibited moderate and decreasing susceptibility over the years. Yearly trends for *Shigella sonnei* highlight that beta-lactams (Ampicillin and Cefixime) generally showed high susceptibility, though with fluctuations. In recent years, there has been a slight decline in susceptibility to cefixime, but overall, the data remains consistent (**Table 6.5 and Figure 6.3**). Nalidixic acid has been ineffective across all years. Trimethoprim-sulfamethoxazole exhibited low to moderate susceptibility, with minor improvements observed over time.

Table 6.1: Susceptibility pattern of *Aeromonas* spp

AMA	Faeces n=181
Cefixime	0 / 0 (0%)
Ciprofloxacin	18 / 86 (20.9%)
Imipenem	53 / 83 (63.9%)
Meropenem	73 / 82 (89%)
Tetracycline	66 / 85 (77.6%)

Table 6.2: Yearly susceptibility trends of *Aeromonas* spp from faeces

AMA	Year 2017	Year 2018	Year 2019	Year 2020	Year 2021	Year 2022	Year 2023
	Total n=131	Total n=114	Total n=170	Total n=77	Total n=179	Total n=164	Total n=181
	(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%)
Imipenem	20/46 (43.5)	53/109 (48.6)	*1/2	*0/0	77/154 (50)	104 / 164 (63.4)	53 / 83 (63.9%)
Meropenem	26/48 (54.2)	71/109 (65.1)	*1/2	*0/0	118/153 (77.1)	138 / 164 (84.1)	73 / 82 (89%)
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%)
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%)

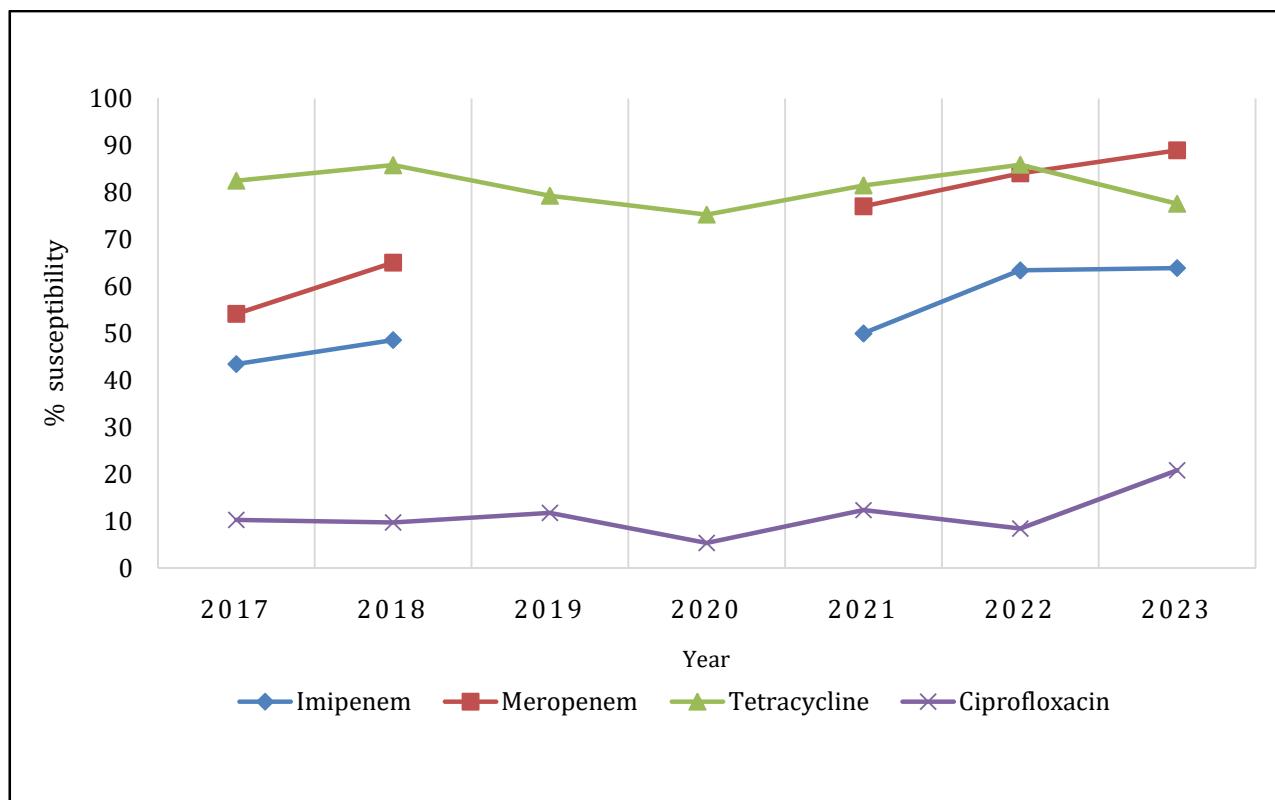


Figure 6.1: Yearly susceptibility trends of *Aeromonas* spp

Table 6.3: Susceptibility pattern of *Shigella* species

AMA	All Specimens	
	<i>Shigella flexneri</i> n=25	<i>Shigella sonnei</i> n=15
Ampicillin	4/25 (16)	*14/15 (-)
Azithromycin	20/24 (83.3)	*10/15 (-)
Cefixime	16/25 (64)	*13/14 (-)
Ciprofloxacin	0/25 (0)	*0/15 (-)
Nalidixic acid	*0/5 (-)	*0/1 (-)
Trimethoprim-sulfamethoxazole	19/24 (79.2)	*6/15 (-)

Table 6.4: Yearly susceptibility trends of *Shigella flexneri*

AMA	Year 2017	Year 2018	Year 2019	Year 2020	Year 2021	Year 2022	Year 2023
	Total n=89	Total n=47	Total n=95	Total n=55	Total n=37	Total n=37	Total n=25
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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)
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)
Nalidixic acid	0/24 (0)	*0/15	2/35 (5.7)	*2/13	*0/8	*0 / 8 (-)	*0/5 (-)
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)

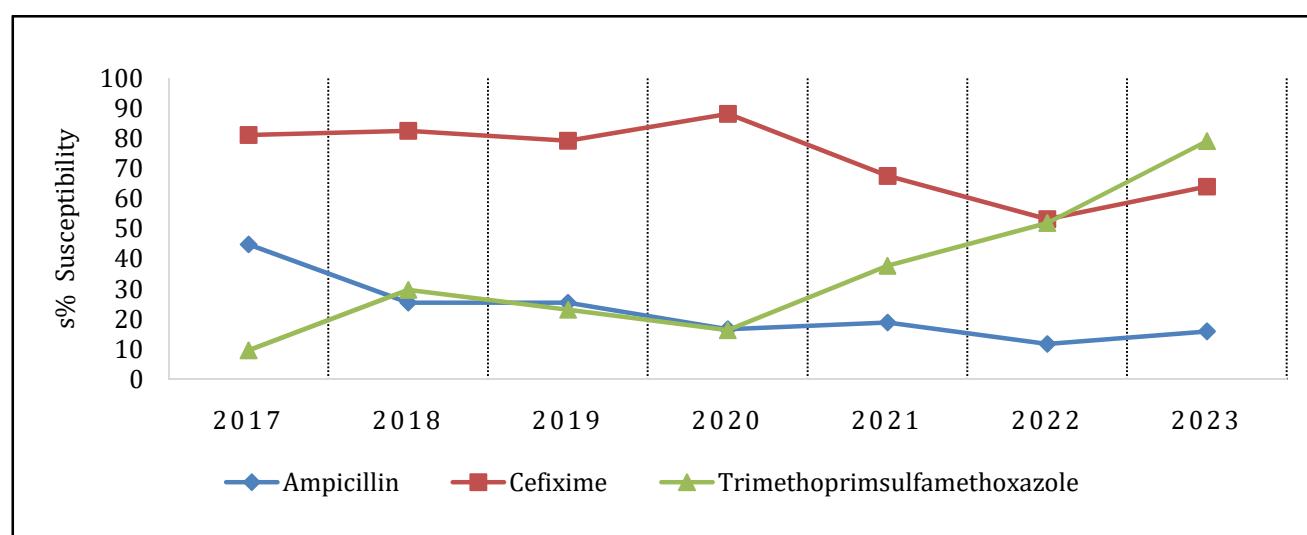


Figure 6.2: Yearly susceptibility trends of *Shigella flexneri*

Table 6.5: Yearly susceptibility trends of *Shigella sonnei*

AMA	Year 2017	Year 2018	Year 2019	Year 2020	Year 2021	Year 2022	Year 2023
	Total n=52	Total n=26	Total n=57	Total n=14	Total n= 41	Total n= 39	Total n=15
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Ampicillin	35/52 (67.3)	18/24 (75)	42/57 (73.7)	*10/14	22/40 (55)	30 / 39 (76.9)	*14/15 (-)
Cefixime	47/50 (94)	25/26 (96.2)	52/57 (91.2)	*12/13	31/39 (79.5)	31 / 39 (79.5)	*13/14 (-)
Nalidixic acid	*0/8	*0/1	*0/8	*0/0	*0/7 (-)	*0 / 4 (-)	*0/1 (-)
Trimethoprim- sulfamethoxazole	4/52 (7.7)	0/25 (0)	5/57 (8.8)	*1/13	9/41 (22)	9 / 39 (23.1)	*6/15 (-)

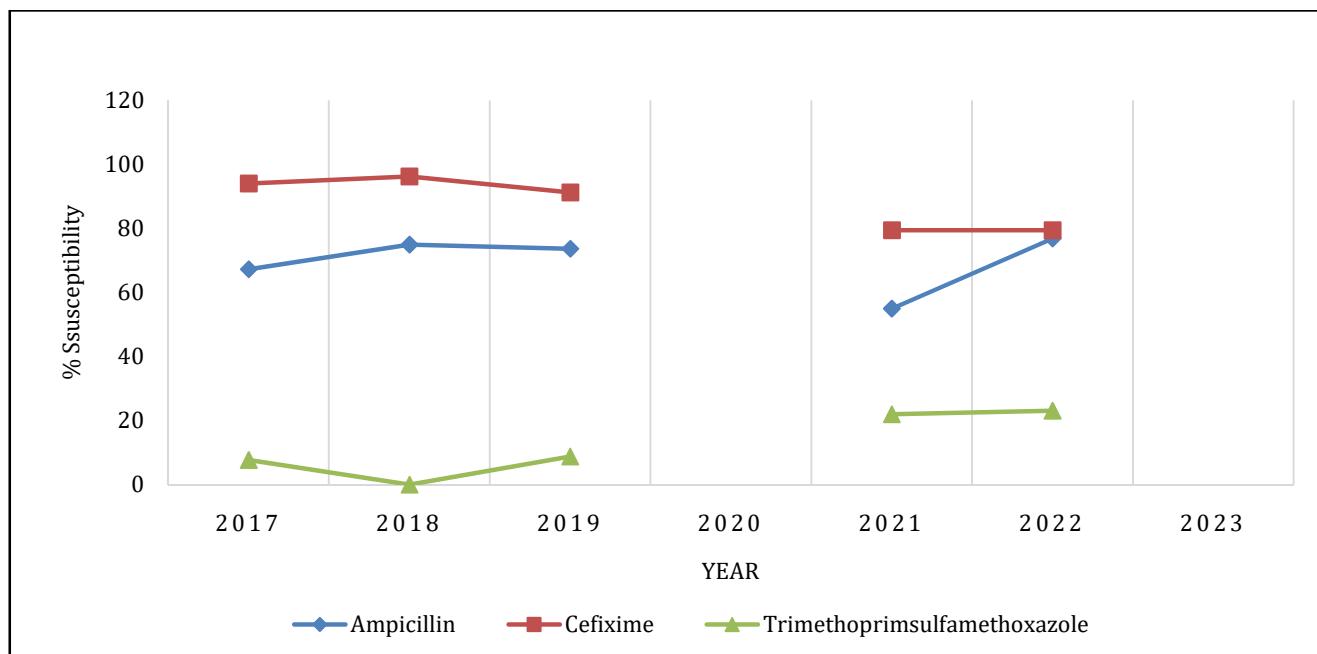


Figure 6.3: Yearly susceptibility trends of *Shigella sonnei*

***Vibrio cholerae* and *Vibrio* spp**

Table 6.6 presents the antibiotic susceptibility patterns of *Vibrio cholerae* based on 17 isolates. Among these isolates, 12 were susceptible to ampicillin, resulting in a susceptibility rate of approximately 70.6%. No data was available for nalidixic acid. Tetracycline showed a high susceptibility rate of around 88.2%, making it a consistently effective treatment option. Trimethoprim-sulfamethoxazole had a lower susceptibility rate, with only 7 out of 17 isolates being susceptible, corresponding to about 41.2%.

Yearly trends in susceptibility revealed varied patterns. Ampicillin showed notable improvements in susceptibility in 2021 and 2022, indicating an increasing effectiveness of this antibiotic. Tetracycline maintained consistently high susceptibility rates, underscoring its reliability as a treatment option for *Vibrio cholerae*. On the other hand, trimethoprim-sulfamethoxazole exhibited fluctuating susceptibility, with a significant decrease in 2021 followed by an improvement in 2022 (**Table 6.7 and Figure 6.4**).

Overall, the data suggests that while tetracycline remains a consistently effective treatment for *Vibrio cholerae*, ampicillin's effectiveness has been improving in recent years. Trimethoprim-sulfamethoxazole, however, shows more variable susceptibility rates, indicating the need for careful consideration when using it as a treatment option.

Table 6.6: Susceptibility pattern of *Vibrio cholerae* and *Vibrio* spp

	<i>Vibrio cholerae</i> n=17
Ampicillin	*12/17 (-)
Nalidixic acid	*0/0 (-)
Tetracycline	*15/17 (-)
Trimethoprim-sulfamethoxazole	*7/17 (-)

Table 6.7: Yearly susceptibility trends of *Vibrio cholerae*

AMA	Year 2017	Year 2018	Year 2019	Year 2020	Year 2021	Year 2022	Year 2023
	Total n=24	Total n=25	Total n=39	Total n=31	Total n=58	Total n=32	Total n=17
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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 (-)
Tetracycline	19/21 (90.5)	*7/10	36/38 (94.7)	31/31 (100)	55/58 (94.8)	29 / 32 (90.6)	*15/17 (-)
Nalidixic acid	*1/8	*0/4	*0/5	*1/1	*0/0	*0 / 1 (-)	*0/0 (-)
Trimethoprim- sulfamethoxazole	10/24 (41.7)	6/24 (25)	18/38 (47.4)	13/31 (41.9)	10/58 (17.2)	16 / 32 (50.0)	*7/17 (-)

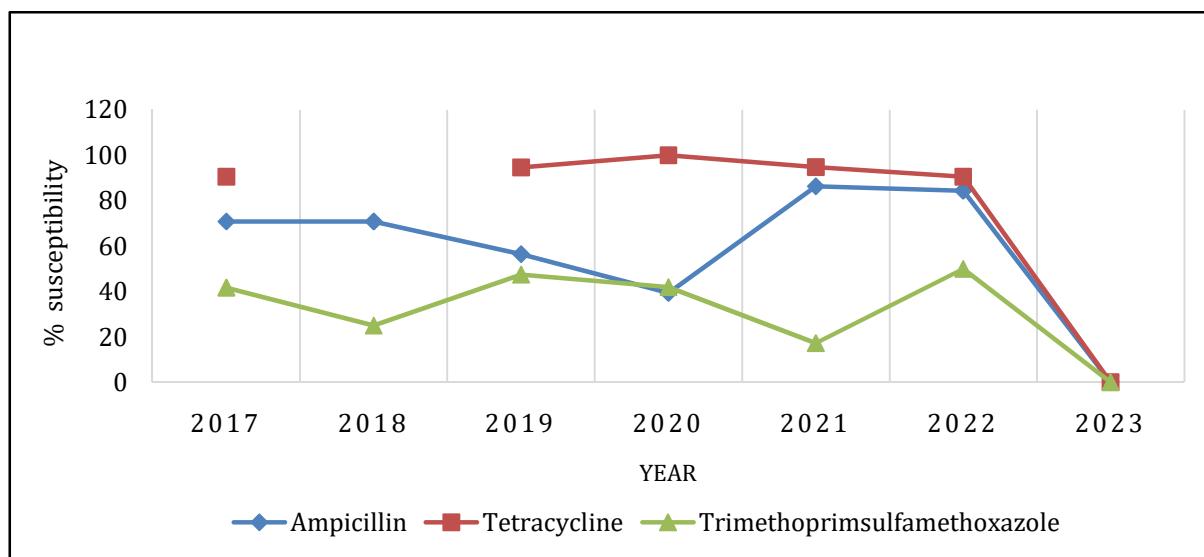


Figure 6.4: Yearly susceptibility trends of *Vibrio cholerae*

Diarrheagenic Escherichia coli (DEC)

Table 6.8 summarizes the antibiotic susceptibility profile of Diarrheagenic Escherichia coli (DEC). Among the 33 isolates tested, only 1 (3%) showed susceptibility to both ampicillin and cefixime. No data was available for azithromycin susceptibility in 2023. None of the 33 isolates (0%) were susceptible to ciprofloxacin or nalidixic acid. Regarding trimethoprim-sulfamethoxazole, 7 out of 33 isolates (21.2%) were susceptible. These findings indicate generally low susceptibility rates across the tested antibiotics for DEC, with Trimethoprim-sulfamethoxazole showing the highest susceptibility rate at 21.2%.

Table 6.9 provides a yearly overview of the susceptibility trends of Diarrheagenic Escherichia coli (DEC) to various antibiotics from 2019 to 2023. Susceptibility to ampicillin remained consistently low across all years, ranging from 0% to 4.5%. Cefixime exhibited varied susceptibility, with peaks observed in 2019 and 2021 and lower rates in other years. Similarly, susceptibility to nalidixic acid fluctuated, showing a notable increase in 2023. Trimethoprim-sulfamethoxazole displayed moderate susceptibility, with fluctuating rates over the years, reaching its lowest point in 2023 (**Figure 6.5**). These trends underscore the evolving antibiotic susceptibility patterns in DEC over time, highlighting the necessity for ongoing monitoring and adjustment of treatment strategies.

Table 6.8: Susceptibility pattern of DEC

	<i>Escherichia coli</i> Diarrheagenic n=33
Ampicillin	1/33 (3)
Azithromycin	*0/0 (-)
Cefixime	1/33 (3)
Ciprofloxacin	0/33 (0)
Nalidixic acid	5/32 (15.6)
Trimethoprim-sulfamethoxazole	7/33 (21.2)

Table 6.9: Yearly susceptibility trend of DEC

AMA	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	Total n=134	Total n=102	Total n=88	Total n=189	Total n=33
	(S%)	(S%)	(S%)	(S%)	(S%)
Ampicillin	6/132 (4.5)	1/102 (1)	0/87 (0)	6 / 189 (3.2)	1/33 (3)
Cefixime	17/129 (13.2)	11/100 (11)	12/87 (13.8)	6 / 189 (3.2)	1/33 (3)
Nalidixic acid	14/122 (11.5)	11/98 (11.2)	7/87 (8)	15 / 164 (9.1)	5/32 (15.6)
Trimethoprim-sulfamethoxazole	45/133 (33.8)	32/102 (31.4)	32/88 (36.4)	56 / 186 (30.1)	7/33 (21.2)

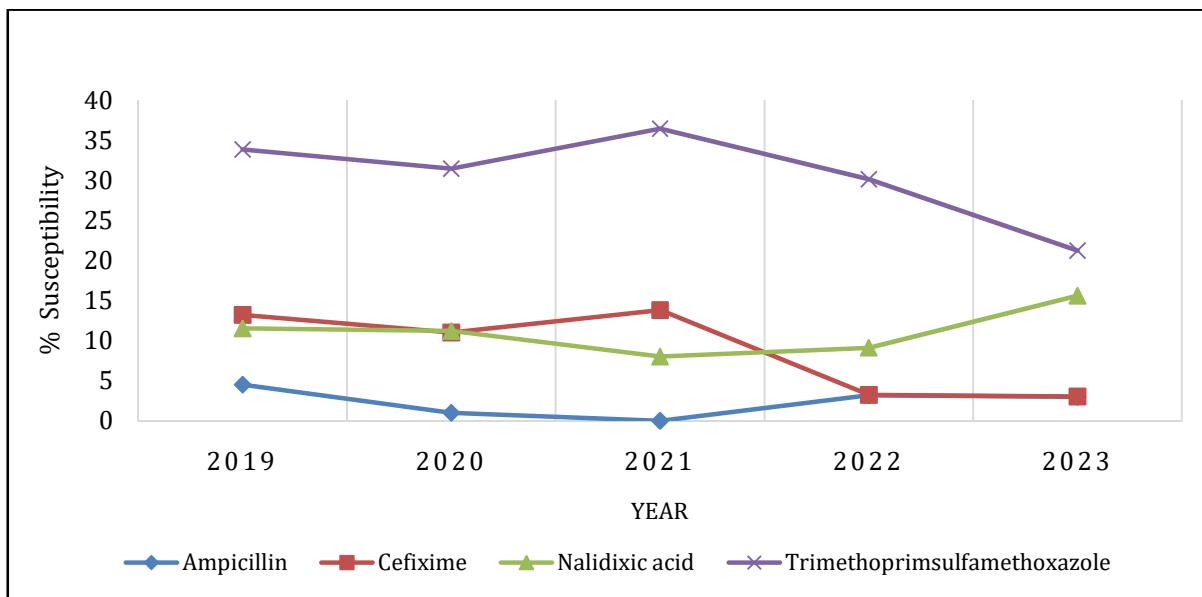


Figure 6.5: Yearly susceptibility trend of DEC

Summary

The antimicrobial resistance patterns observed in diarrheal pathogens during 2023 are as follows: *Aeromonas* spp. demonstrated high susceptibility to meropenem (89%) and tetracycline (77.6%), moderate susceptibility to imipenem (63.9%), and low susceptibility to ciprofloxacin (20.9%). Trends indicate an increase in the efficacy of imipenem and meropenem over time. *Shigella flexneri* exhibited high susceptibility to azithromycin (83.3%) and trimethoprim-sulfamethoxazole (79.2%), moderate susceptibility to cefixime (64%), and no efficacy to

fluoroquinolones. Yearly trends showed a decreased susceptibility to ampicillin and cefixime over the years, while trimethoprim-sulfamethoxazole exhibited a marked increase in susceptibility from 7.7% in 2017 to 79.2% in 2023. *Vibrio cholerae* maintained high susceptibility to tetracycline (88.2%) and ampicillin (70.6%), with fluctuating but notable efficacy of trimethoprim-sulfamethoxazole (41.2%). Conversely, diarrheagenic *Escherichia coli* (DEC) exhibited very low susceptibility to ampicillin (3%) and cefixime (3%), with moderate susceptibility to trimethoprim-sulfamethoxazole (21.2%). Yearly data also indicated reduced susceptibility to all tested antimicrobials from 2017 to 2023.

Molecular biology

The antimicrobial resistance (AMR) gene profiles of diarrheal bacterial pathogens collected from multiple centers, focusing on EPEC, *Shigella flexneri*, *Shigella sonnei*, *Salmonella* spp., and *Campylobacter* spp. The analysis identified several key resistance genes, including TEM, OXA, dfrA, sul1/2, CTX-M, qnrS/B, tetA/B, mphA, and mphA/ermC. In EPEC isolates (n=25), TEM and OXA were the most prevalent, found in 40% and 24% of isolates, respectively. *Shigella flexneri* (n=12) showed high prevalence of OXA-1 (58.33%) and dfrA (100%). *Shigella sonnei* (n=20) predominantly carried dfrA (100%) and tetA/B (45%). For *Salmonella* spp. (n=329), the most common genes were CTX-M (17.93%) and dfrA (11.24%). *Campylobacter* isolates (n=4) exhibited a varied profile with each gene (OXA, dfrA, sul1/2, tetO/tetR) present in 25% of isolates.

These findings underscore the significant presence of AMR genes across different pathogens, indicating an ongoing need for robust surveillance and targeted interventions to manage and mitigate the spread of antimicrobial resistance.

Clinical relevance and treatment guidelines

Clinically, the changing AMR susceptibility profile of diarrheagenic pathogens, highlight the need for continuous surveillance and adaptive treatment strategies. Rising AMR trends in *Aeromonas* spp. and *Shigella* spp. necessitate vigilant monitoring, while the high efficacy of tetracycline against *Vibrio cholerae* suggests its reliability as a first-line treatment. Low susceptibility of DEC to common antimicrobials underscores the need for alternative treatments. Treatment guidelines recommend using meropenem and tetracycline for *Aeromonas* spp., azithromycin and trimethoprim-sulfamethoxazole for *Shigella flexneri*, azithromycin and cefixime for *Shigella sonnei*, tetracycline for *Vibrio cholerae*, and close monitoring of trimethoprim-sulfamethoxazole efficacy for DEC.

Chapter 7. *Staphylococci and Enterococci*

A total of 8900 *S. aureus*, 6895 CoNS and 2746 enterococci isolates collected across India were analysed in the year 2023. The total number of isolates in 2023 was slightly higher than in 2022 particularly for CoNS.

S. aureus

A total of 8900 isolates of *S. aureus* were reported from different centres across India. Identification of MRSA was done by testing susceptibility to cefoxitin (7017) and/or oxacillin (4071). The overall proportion of MRSA was 44.5% and 64.1% based on the 2 methods respectively. The proportion of MRSA in 2023 was similar to 2022 (44.5%) (**Table 7.1**). There was a discrepancy in the MRSA rates detected by oxacillin MIC and cefoxitin DD/MIC (64.1% vs 44.5%). This discrepancy could be because of the smaller number of isolates tested against oxacillin than cefoxitin. Moreover the same isolates may not have been tested by both the methods. As per CLSI guidelines, an isolate of *S.aureus* may be identified as MRSA using cefoxitin and /or oxacillin. On some occasions, only one of the two methods may be positive for eg: *mecC* isolates may sometimes be cefoxitin sensitive but oxacillin resistant. This could explain the few isolates of MRSA in table 4.1 which demonstrated susceptibility to cefoxitin or oxacillin. Susceptibility to tetracycline, clindamycin co-trimoxazole, erythromycin and ciprofloxacin, was higher among MSSA when compared to MRSA. The anti MRSA antibiotics such as vancomycin and tigecycline showed excellent in vitro activity (100% against MRSA isolates). Linezolid resistance was encountered in MRSA, MSSA as well as CoNS isolates (1%, 0.2% and 0.7% respectively). These rates were slightly reduced than those encountered in 2022. Teicoplanin susceptibility was 100% among MRSA and CoNS isolates.

Table 7.2 shows the susceptibility pattern of *S. aureus* and CoNS across different hospital locations. As expected, the overall MRSA rates among *S.aureus* were lowest in the OPD isolates (39.6%) while it was moderate among ward isolates (46.7%) and higher among in the ICU isolates (48.2%).The susceptibility to most antibiotics was least among ICU isolates and highest among OPD isolates of *S.aureus* including MRSA and CoNS. However, among *S.aureus*, susceptibility to ciprofloxacin was slightly higher among ICU and OPD isolates than ward although the difference was not significant like previous year. When compared to the previous year linezolid resistance rates were slightly reduced among MRSA, CoNS and MSSA isolates 2.1 to 1.1 %, 0.9 to 0.7%, and 0.6 to 0.2% respectively. No teicoplanin resistance was encountered among MRSA, MSSA and CoNS.

Table 7.1: Percentage susceptibility of *S. aureus*, MSSA, MRSA and CoNS isolated from all samples

AMA	All Specimens			
	<i>S. aureus</i> n=8900	MSSA n=4539	MRSA n=4311	CoNS n=6895
Cefoxitin	3901 / 7017 (55.5)	3901 / 3901 (100.0)	0 / 3116 (-)	705 / 3500 (20.1)
Oxacillin	1689 / 4072 (35.9)	1689 / 1689 (100.0)	0 / 2383 (-)	487 / 3621 (13.4)
Vancomycin	8850 / 8850 (100)	4539 / 4539 (100)	4311 / 4311 (100)	4788 / 4788 (100)
Teicoplanin	4444 / 4444 (100)	1875 / 1875 (100)	2402 / 2402 (100)	2137 / 2137 (100)
Erythromycin	3226 / 8133 (39.7)	2299 / 4299 (53.5)	927 / 3834 (24.2)	684 / 4720 (14.5)
Tetracycline	5667 / 6530 (86.8)	3278 / 3552 (92.3)	2389 / 2978 (80.2)	1788 / 3747 (47.7)
Tigecycline	2470 / 2470 (100)	1106 / 1106 (100)	1364 / 1364 (100)	-
Ciprofloxacin	1972 / 8864 (22.3)	1568 / 4553 (34.4)	404 / 4311 (9.4)	1958 / 6895 (28.4)
Clindamycin	6464 / 8786 (73.6)	3811 / 4506 (84.6)	2653 / 4280 (62.0)	2326 / 6895 (33.7)
Trimethoprim-sulfamethoxazole	6645 / 8850 (75.1)	3853 / 4539 (84.9)	2792 / 4311 (64.8)	3789 / 6895 (55)
Linezolid	8794 / 8850 (99.4)	4528 / 4539 (99.8)	4266 / 4311 (99.0)	6849 / 6895 (99.3)

Table 7.2: Location-wise susceptibility of *S. aureus*, MSSA, MRSA and CoNS from all samples

AMA	<i>Staphylococcus aureus</i>				MSSA				MRSA				CoNS			
	Total n=8900	OPD n=3504	Ward n=4597	ICU n=799	Total n=4539	OPD n=2003	Ward n=2148	ICU n=388	Total n=431 1	OPD n=147 8	Ward n=242 7	ICU n=40 6	Total n=689 5	OPD n=15 55	Ward n=378 6	ICU n=15 54
	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)
Cefoxitin	3954 / 7017 (56.3)	1886 / 3121 (60.4)	1713 / 3211 (53.3)	355 / 685 (51.8)	3901 / 3901 (100.0)	1871 / 1871 (100.0)	1686 / 1686 (100.0)	344 / 344 (100.0)	0 / 3117 (-))	0 / 1251 (-)	0 / 1525 (-)	0 / 341 (-)	705 / 3500 (20.1)	257 / 1074 (23.9)	287 / 1459 (19.7)	161 / 967 (16.6)
Oxacillin	1737 / 4071 (42.7)	605 / 1282 (47.2)	1003 / 2478 (40.5)	129 / 311 (41.5)	1689 / 1689 (100.0)	589 / 589 (100.0)	975 / 975 (100.0)	125 / 125 (100.0)	0 / 2382 (-))	0 / 693 (-)	0 / 1503 (-)	0 / 186 (-)	487 / 3621 (13.4)	91 / 515 (17.7)	349 / 2458 (14.2)	47 / 648 (7.3)
Vancomycin	8850 / 8850 (100)	3481 / 3481 (100)	4575 / 4575 (100)	794 / 794 (100)	4539 / 4539 (100)	2003 / 2003 (100)	2148 / 2148 (100)	388 / 388 (100)	4311/ 4311 (100)	1478/ 1478 (100)	2427 / 2427 (100)	406 / 406 (100)	6895 / 6895 (100)	1555 / 1555 (100)	3786 / 3786 (100)	1554 / 1554 (100)
Teicoplanin	4277 / 4277 (100))	1643 / 1643 (100)	2228 / 2228 (100)	406 / 406 (100)	1875 / 1875 (100)	806 / 806 (100)	897 / 897 (100.0)	172 / 172 (100)	2402 / 2402 (100)	837 / 837 (100)	1331 / 1331 (100)	234 / 234 (100)	2914 / 2914 (100)	481 / 481 (100)	1882 / 1882 (100)	551 / 551 (100)
Erythromycin	3226 / 8126 (39.7)	1390 / 3404 (40.8)	1554 / 3975 (39.1)	282 / 747 (37.8)	2299 / 4308 (53.4)	1037 / 1964 (52.8)	1055 / 1966 (53.7)	207 / 378 (54.8)	927 / 3867 (24.0)	353 / 1455 (24.3)	499 / 2041 (24.4)	75 / 371 (20.2)	684 / 4720 (14.5)	222 / 1177 (18.9)	323 / 2339 (13.8)	139 / 1204 (11.5)
Tetracycline	5667 / 6530 (86.8)	2508 / 2872 (87.3)	2687 / 3062 (87.8)	472 / 596 (79.2)	3278 / 3552 (92.3)	1531 / 1678 (91.2)	1489 / 1590 (93.6)	258 / 284 (90.8)	2389 / 2994 (79.8)	977 / 1200 (81.4)	1198 / 1481 (80.9)	214 / 313 (68.4)	1788 / 3747 (47.7)	455 / 1082 (42.1)	939 / 1645 (57.1)	394 / 1020 (38.6)
Tigecycline	2470 / 2470 (100)	1060 / 1060 (100)	1225 / 1225 (100)	185 / 185 (100)	1106 / 1106 (100)	501 / 501 (100)	536 / 536 (100)	69 / 69 (100)	1364 / 1364 (100)	559 / 559 (100)	689 / 689 (100)	116 / 116 (100)	-	-	-	-

Ciprofloxacin	1972 / 8850 (22.3)	812 / 3481 (23.3)	971 / 4575 (21.2)	189 / 794 (23.8)	1568 / 4553 (34.4)	684 / 2007 (34.1)	734 / 2158 (34.0)	150 / 388 (38.7)	404 / 4340 (9.3)	128 / 1494 (8.6)	237 / 2438 (9.7)	39 / 408 (9.6)	1958 / 6895 (28.4)	521 / 1555 (33.5)	1093 / 3786 (28.9)	344 / 1554 (22.1)
Clindamycin	6464 / 8786 (73.6)	2667 / 3443 (77.5)	3262 / 4555 (71.6)	535 / 788 (67.9)	3811 / 4516 (84.4)	1672 / 1978 (84.5)	1815 / 2149 (84.5)	324 / 389 (83.3)	2653 / 4332 (61.2)	995 / 1486 (67.0)	1447 / 2438 (59.4)	211 / 408 (51.7)	2326 / 6895 (33.7)	638 / 1555 (41)	1278 / 3786 (33.8)	410 / 1554 (26.4)
Trimethoprim-sulfamethoxazole	6645 / 8850 (75.1)	2750 / 3481 (79)	3328 / 4575 (72.7)	567 / 794 (71.4)	3853 / 4542 (84.8)	1730 / 2003 (86.4)	1805 / 2150 (84.0)	318 / 389 (81.7)	2792 / 4343 (64.3)	1020 / 1494 (68.3)	1523 / 2442 (62.4)	249 / 407 (61.2)	3789 / 6895 (55)	902 / 1555 (58)	2083 / 3786 (55)	804 / 1554 (51.7)
Linezolid	8794 / 8850 (99.4)	3461 / 3481 (99.4)	4551 / 4575 (99.5)	782 / 794 (98.5)	4528 / 4539 (99.8)	1998 / 2003 (99.8)	2144 / 2148 (99.8)	386 / 388 (99.5)	4266 / 4312 (98.9)	1463 / 1479 (98.9)	2407 / 2427 (99.2)	396 / 406 (97.5)	6849 / 6895 (99.3)	1544 / 1555 (99.3)	3773 / 3786 (99.7)	1532 / 1554 (98.6)

*Although all isolates were found susceptible to vancomycin by MIC, a few of the isolates were found to be hVISA by PAP-AUC analysis.

Center wise analysis

As per **Table 7.3**, there were significant differences in MRSA rates observed between the various regional centres, the highest rate in the isolates from RC16 and RC01 (74.7% and 63.8%). The lowest MRSA rates were observed from the RC07 (28.9%) and RC04 (27%) based on cefoxitin test results. However it should be noted that in RC02 and RC21 oxacillin resistance was used to identify MRSA rather than cefoxitin (1692 vs 23 and 67 vs 21, respectively). This variation in MRSA rates across centres may be indicative of the differences in the antibiotic prescription practices and usage in the different regions. It could also reflect different methodologies adopted across centres to identify MRSA. Ciprofloxacin susceptibility was extremely low across all the centres. The susceptibility rate of other antibiotics varied widely between the centres for many of the antibiotics like erythromycin (11.7% in RC 16 to 65.7% in RC 07), tetracycline (23.9 % in RC19 to 96.5% in RC08), clindamycin (51.8% in RC19 to 97.7 % in RC08), co-trimoxazole (45.9% in RC06 to 94.7 % in RC03). Linezolid resistance ranged from 0.1% in RC 02 to 9.4% in RC 12.

Most of the *S. aureus* isolates were obtained from superficial infections followed by blood stream and deep infections. MRSA rates differed based on the source of isolation, with isolates from deep infection demonstrating highest rates (45.6%) while those from superficial infections showed the lowest rates (44.1%) although the difference was not significant. 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, co-trimoxazole was more evident in MSSA when compared to MRSA.

Table 7.3: Antimicrobial Susceptibility (AMS) Percentage RC wise of *Staphylococcus aureus* from all samples except faeces and urine

RC/ Antibiotics	Cefoxitin (n=6805)	Oxacillin (n=4020)	Vancomycin (n=8629)	Teicoplanin (n=4171)	Erythromycin (n=7945)	Tetracycline (n=6353)	Tigecycline (n=2397)	Ciprofloxacin (n=8629)	Clindamycin (n=8601)	Trimethoprim-sulfamethoxazole (n=8629)	Linezolid (n=8629)
	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	124 / 343 (36.2)	0 / 0 (-)	343 / 343 (100)	1 / 1 (-)	132 / 343 (38.5)	274 / 343 (79.9)	0 / 1 (0)	44 / 343 (12.8)	223 / 339 (65.8)	287 / 343 (83.7)	343 / 343 (100)
RC2	13 / 23 (-)	577 / 1692 (34.1)	1691 / 1693 (99.9)	844 / 844 (100)	343 / 1035 (33.1)	6 / 7 (-)	2 / 3 (0)	101 / 1693 (6)	897 / 1692 (53)	850 / 1693 (50.2)	1692 / 1693 (99.9)
RC3	189 / 338 (55.9)	0 / 0 (0)	338 / 338 (100)	1 / 1 (0)	161 / 338 (47.6)	200 / 216 (92.6)	0 / 0 (-)	308 / 338 (91.1)	199 / 338 (58.9)	320 / 338 (94.7)	334 / 338 (98.8)
RC4	1531 / 2098 (73)	62 / 371 (16.7)	2099 / 2099 (100)	720 / 720 (100)	1201 / 2099 (57.2)	1962 / 2099 (93.5)	666 / 666 (100)	809 / 2099 (38.5)	1801 / 2099 (85.8)	1952 / 2099 (93)	2099 / 2099 (100)
RC5	139 / 231 (60.2)	144 / 236 (61)	236 / 236 (100)	162 / 162 (100)	61 / 235 (26)	195 / 226 (86.3)	14 / 14 (-)	39 / 236 (16.5)	229 / 236 (97)	163 / 236 (69.1)	236 / 236 (100)
RC6	139 / 329 (42.2)	13 / 38 (34.2)	338 / 338 (100)	335 / 335 (100)	102 / 338 (30.2)	272 / 320 (85)	16 / 18 (-)	13 / 338 (3.8)	228 / 338 (67.5)	155 / 338 (45.9)	336 / 338 (99.4)
RC7	27 / 38 (71.1)	27 / 61 (44.3)	77 / 77 (100)	65 / 65 (100)	26 / 75 (34.7)	61 / 73 (83.6)	58 / 58 (100)	10 / 77 (13)	61 / 73 (83.6)	46 / 77 (59.7)	77 / 77 (100)
RC8	170 / 257 (66.1)	170 / 260 (65.4)	260 / 260 (100)	260 / 260 (100)	94 / 257 (36.6)	251 / 260 (96.5)	260 / 260 (100)	50 / 260 (19.2)	254 / 260 (97.7)	199 / 260 (76.5)	259 / 260 (99.6)
RC9	149 / 309 (48.2)	0 / 0 (0)	309 / 309 (100)	0 / 0 (0)	87 / 290 (30)	276 / 309 (89.3)	0 / 0 (0)	46 / 309 (14.9)	244 / 291 (83.8)	270 / 309 (87.4)	307 / 309 (99.4)
RC10	275 / 408 (67.4)	0 / 0 (0)	408 / 408 (100)	408 / 408 (100)	164 / 408 (40.2)	0 / 0 (0)	0 / 0 (0)	66 / 408 (16.2)	310 / 408 (76)	362 / 408 (88.7)	408 / 408 (100)

RC11	63 / 231 (27.3)	68 / 230 (29.6)	232 / 232 (100)	231 / 231 (100)	73 / 232 (31.5)	183 / 232 (78.9)	46 / 46 (100)	15 / 232 (6.5)	180 / 232 (77.6)	126 / 232 (54.3)	232 / 232 (100)
RC12	91 / 187 (48.7)	87 / 183 (47.5)	191 / 191 (100)	190 / 190 (100)	72 / 191 (37.7)	166 / 190 (87.4)	189 / 189 (100)	4 / 191 (2.1)	153 / 191 (80.1)	92 / 191 (48.2)	173 / 191 (90.6)
RC13	38 / 74 (51.4)	7 / 20 (-)	76 / 76 (100)	21 / 21 (-)	13 / 75 (17.3)	39 / 49 (79.6)	18 / 18 (-)	10 / 76 (13.2)	41 / 76 (53.9)	63 / 76 (82.9)	76 / 76 (100)
RC14	436 / 699 (62.4)	437 / 700 (62.4)	700 / 700 (100)	700 / 700 (100)	304 / 700 (43.4)	697 / 700 (99.6)	700 / 700 (100)	161 / 700 (23)	683 / 700 (97.6)	600 / 700 (85.7)	700 / 700 (100)
RC15	110 / 251 (43.8)	0 / 0 (0)	251 / 251 (100)	0 / 0 (0)	84 / 251 (33.5)	224 / 251 (89.2)	0 / 0 (0)	24 / 251 (9.6)	151 / 250 (60.4)	239 / 251 (95.2)	251 / 251 (100)
RC16	143 / 565 (25.3)	0 / 0 (0)	565 / 565 (100)	0 / 0 (0)	66 / 565 (11.7)	439 / 565 (77.7)	203 / 203 (100)	112 / 565 (19.8)	349 / 565 (61.8)	398 / 565 (70.4)	545 / 565 (96.5)
RC17	60 / 106 (56.6)	62 / 106 (58.5)	108 / 108 (100)	108 / 108 (100)	71 / 108 (65.7)	83 / 108 (76.9)	108 / 108 (100)	64 / 108 (59.3)	70 / 108 (64.8)	64 / 108 (59.3)	108 / 108 (100)
RC19	118 / 276 (42.8)	0 / 0 (0)	276 / 276 (100)	0 / 0 (0)	79 / 276 (28.6)	66 / 276 (23.9)	0 / 2 (0)	30 / 276 (10.9)	143 / 276 (51.8)	181 / 276 (65.6)	275 / 276 (99.6)
RC20	6 / 21 (-)	18 / 56 (32.1)	60 / 60 (100)	58 / 58 (100)	19 / 60 (31.7)	59 / 60 (98.3)	47 / 47 (100)	3 / 60 (5)	56 / 60 (93.3)	49 / 60 (81.7)	60 / 60 (100)
RC21	8 / 21 (-)	40 / 67 (59.7)	69 / 69 (100)	67 / 67 (100)	10 / 69 (14.5)	63 / 69 (91.3)	64 / 64 (100)	8 / 69 (11.6)	53 / 69 (76.8)	49 / 69 (71)	65 / 69 (94.2)
Total	3829 / 6805 (56.3)	1712 / 4020 (42.6)	8593 / 8629 (100)	4171 / 4171 (100)	3162 / 7945 (39.8)	5516 / 6353 (86.8)	2397 / 2397 (100)	1917 / 8629 (22.2)	6325 / 8601 (73.5)	6465 / 8629 (74.9)	8576 / 8629 (99.4)

Table 7.4 and Figure 7.1 depicts the comparison of the susceptibility rates of *S.aureus* in 2023 with the rates seen between 2017-22. Overall MRSA rates have increased each year from 2017 to 2023 (32.9% to 43.7%). Susceptibility to most antibiotics showed almost similar rates as in the previous years. Resistance to tigecycline was not seen in 2016 but it appeared in a small number of isolates in 2017 and 2018 (0.5%), 2019 (0.4%), 2021 (0.8%). No tigecycline resistance was observed among 2022 and 2023 isolates. Cefoxitin resistance, the surrogate marker for MRSA, was observed nearly twice as frequently among CoNS compared to *S. aureus* (79.9% vs 43.7%). **Table 7.5** depicts the susceptibility rates of staphylococci from blood. MRSA rate was slightly higher among blood isolates when compared to the overall rate (47.7% vs 43.7%). CoNS were more commonly isolated from blood than *S.aureus* from the different centres across India. Cefoxitin resistance was observed more commonly among CoNS than the *S.aureus* (84% vs 47.7%). When compared to MRSA, MSSA was more susceptible to tetracycline, co-trimoxazole, clindamycin, erythromycin and ciprofloxacin. The anti MRSA antibiotics such as linezolid, tigecycline and vancomycin showed excellent in vitro activity. As seen from **Table 7.6**, around 44.4% of the total *S.aureus* and 7.4% of CoNS isolates were from superficial infections. MRSA rate was 44.1%. When compared to MRSA, MSSA was more susceptible to tetracycline, co-trimoxazole, clindamycin, erythromycin and ciprofloxacin. The anti MRSA antibiotics such as teicoplanin, linezolid, tigecycline and vancomycin showed excellent in vitro activity linezolid resistance was reduced in CoNS isolates (2.3% and 1%), when compared to 2022.

As seen from **Table 7.7**, the proportion of MRSA from deep seated infections is higher than the overall rate (45.6% vs 44.5%) The anti MRSA antibiotics such as tigecycline and vancomycin showed excellent in vitro activity. Linezolid resistance was slightly reduced in CoNS isolates, when compared to 2022 (1.1% and 0.8%) respectively.

Table 7.4: Year wise susceptibility trends of *Staphylococcus aureus* from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	Total n=5708	Total n=8644	Total n=12320	Total n=6281	Total n=8827	Total n=9415	Total n=8850
	(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)
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)
Vancomycin	2602/2602 (100)	4640/4640 (100)	6996/6996 (100)	3846/3846 (100)	6203/6204 (100)	7731/7731 (100)	8850 / 8850 (100)
Teicoplanin	5233/5257 (99.5)	6544/6697 (97.7)	6194/6269 (98.8)	2043/2050 (99.7)	3351/3356 (99.9)	3450/3466 (99.5)	4277 / 4277 (100)
Erythromycin	2755/5570 (49.5)	3593/8102 (44.3)	4803/11975 (40.1)	2594/6096 (42.6)	3617/8355 (43.3)	3586/9282 (38.6)	3226 / 8126 (39.7)
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)
Tigecycline	433/435 (99.5)	1529/1536 (99.5)	2902/2914 (99.6)	1559/1559 (100)	2113/2131 (99.2)	2314/2452 (94.4)	2470 / 2470 (100)
Ciprofloxacin	1224/5260 (23.3)	1497/8094 (18.5)	1990/11200 (17.8)	1101/5845 (18.8)	1455/8341 (17.4)	1948/9050 (21.5)	1972 / 8850 (22.3)
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)
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)
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)

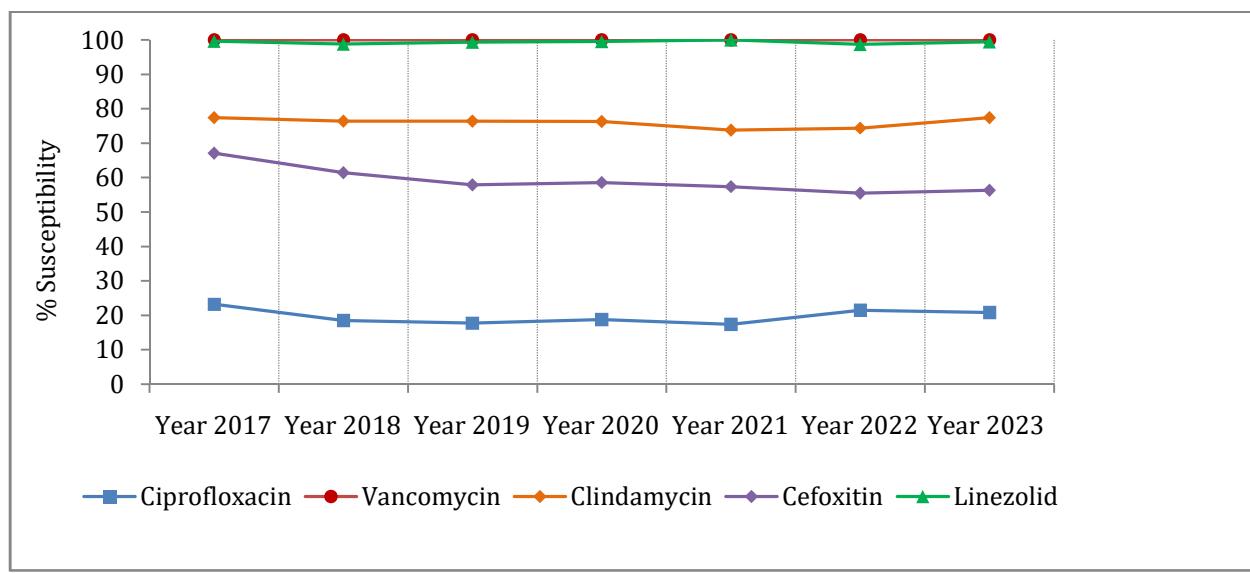


Figure 7.1: Year wise susceptibility trends of *S. aureus* from all samples

Table 7.5: Susceptible percentages of staphylococci isolated from blood

	<i>S. aureus</i> n=1472	MSSA n=699	MRSA n=773	CoNS n=5672
Cefoxitin	599 / 1146 (52.3)	589 / 589 (100.0)	0 / 557 (-)	412 / 2581 (16)
Oxacillin	289 / 682 (42.4)	277 / 277 (100.0)	0 / 405 (-)	390 / 3250 (12)
Vancomycin	1472 / 1472 (100)	699 / 699 (100)	773 / 773 (100)	5672 / 5672 (100)
Teicoplanin	898 / 898 (100)	444 / 444 (100.0)	454 / 454 (100)	2605 / 2605 (100)
Erythromycin	510 / 1337 (38.1)	358 / 673 (53.2)	152 / 690 (22.0)	442 / 3696 (12)
Tetracycline	940 / 1103 (85.2)	502 / 542 (92.6)	438 / 565 (77.5)	1208 / 2833 (42.6)
Tigecycline	478 / 478 (100)	230 / 230 (100)	248 / 248 (100)	-
Ciprofloxacin	444 / 1472 (30.2)	308 / 699 (44.06)	136 / 778 (17.5)	1519 / 5672 (26.8)
Clindamycin	1040 / 1467 (70.9)	584 / 699 (83.5)	456 / 783 (58.2)	1758 / 5672 (31)
Trimethoprim-sulfamethoxazole	1046 / 1472 (71.1)	591 / 699 (84.5)	455 / 778 (58.5)	3078 / 5672 (54.3)
Linezolid	1468 / 1472 (99.7)	699 / 699 (100.0)	769 / 773 (99.5)	5643 / 5672 (99.5)

Table 7.6: Susceptible percentages of staphylococci isolated from Superficial Infections

	<i>S. aureus</i> n=3956	MSSA n=2117	MRSA n=1833	CoNS n=515
Cefoxitin	1978 / 3538 (55.9)	1956 / 1956 (100.0)	0 / 1582 (-)	147 / 487 (30.2)
Oxacillin	694 / 1515 (45.8)	674 / 674 (100.0)	0 / 841 (-)	20 / 55 (36.4)
Vancomycin	3950 / 3950 (100)	2117 / 2117 (100)	1833 / 1833 (100)	515 / 515 (100)
Teicoplanin	1799 / 1799 (100)	766 / 766 (100)	1033 / 1033 (100)	75 / 75 (100)
Erythromycin	1523 / 3754 (40.6)	1132 / 2055 (55.1)	391 / 1714 (22.8)	118 / 512 (23)
Tetracycline	2952 / 3399 (86.8)	1719 / 1861 (92.4)	1233 / 1548 (79.7)	321 / 500 (64.2)
Tigecycline	1320 / 1320 (100)	551 / 551 (100)	769 / 769 (100)	0 / 4 (-)
Ciprofloxacin	842 / 3950 (21.3)	735 / 2117 (34.7)	107 / 1833 (5.83)	197 / 515 (38.3)
Clindamycin	3059 / 3933 (77.8)	1834 / 2112 (86.8)	1225 / 1833 (66.2)	266 / 515 (51.7)
Trimethoprim-sulfamethoxazole	3135 / 3950 (79.4)	1856 / 2117 (87.6)	1279 / 1833 (69.7)	291 / 515 (56.5)
Linezolid	3916 / 3950 (99.1)	2110 / 2117 (99.7)	1806 / 1833 (98.5)	510 / 515 (99)

Table 7.7: Susceptible percentages of staphylococci isolated from Deep Infections

AMA	Deep Infection			
	<i>S. aureus</i> n=1330	MSSA n=565	MRSA n=743	CoNS n=128
Cefoxitin	365 / 671 (54.4)	356 / 356 (100.0)	0 / 315 (-)	26 / 58 (44.8)
Oxacillin	389 / 1008 (38.6)	380 / 380 (100.0)	0 / 628 (-)	17 / 82 (20.7)
Vancomycin	1308 / 1308 (100)	565 / 565 (100)	743 / 743 (100)	128 / 128 (100)
Teicoplanin	770 / 770 (100)	317 / 317 (100.0)	453 / 453 (100.0)	56 / 56 (100)
Erythromycin	464 / 1218 (38.1)	271 / 541 (50.1)	193 / 680 (28.4)	20 / 83 (24.1)
Tetracycline	522 / 584 (89.4)	277 / 298 (93.0)	245 / 286 (85.7)	35 / 51 (68.6)
Tigecycline	267 / 267 (100)	135 / 135 (100)	132 / 132 (100)	0 / 0 (-)
Ciprofloxacin	145 / 1308 (11.1)	120 / 565 (21.2)	25 / 743 (3.36)	35 / 128 (27.3)
Clindamycin	915 / 1307 (70)	468 / 564 (83.0)	447 / 743 (60.1)	48 / 128 (37.5)
Trimethoprim-sulfamethoxazole	852 / 1308 (65.1)	420 / 565 (74.3)	432 / 743 (58.1)	73 / 128 (57)
Linezolid	1304 / 1308 (99.7)	564 / 565 (99.8)	740 / 743 (99.6)	127 / 128 (99.2)

Table 7.8 and figure 7.2 depict trends in antimicrobial susceptibility among MSSA isolates across the 7 years of study (2017-23). Although *S.aureus*, overall, 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 increase in the susceptibility rates to clindamycin and co-trimoxazole. The unusual occurrence of linezolid resistance rates was slightly reduced in MSSA isolates (0.6 to 0.2%).

Table 7.9 and figure 7.3 depict trends in antimicrobial resistance in MRSA isolates across the 7 years (2017-23). Susceptibility rates across the years were similar to most antibiotics except co-trimoxazole which showed a slightly decreased in the susceptibility rates in 2023 than the 2022 (69 to 64 %). The Vancomycin and teicoplanin susceptibility rates are 100 %. Linezolid resistance was slightly reduced 2.1% to 1% respectively.

Table 7.8: Year wise susceptibility trends of MSSA from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	Total n=3819	Total n=5135	Total n=7029	Total n=3655	Total n=5273	Total n=5050	Total n=4539
	(S%)						
Cefoxitin	3801/3801 (100)	4857/4857 (100)	6255/6255 (100)	3388/3388 (100)	3845/3845 (100)	4525/4525 (100)	3901 / 3901 (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)
Vancomycin	1935/1935 (100)	3041/3041 (100)	3986/3986 (100)	2153/2153 (100)	4010/4010 (100)	4323/4335 (99.7)	4539 / 4539 (100)
Teicoplanin	3509/3517 (99.8)	3642/3682 (98.9)	3391/3419 (99.2)	1074/1075 (99.9)	1945/1949 (99.8)	1720/1724 (99.8)	1875 / 1875 (100.0)
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)
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)
Tigecycline	300/302 (99.3)	902/902 (100)	1608/1613 (99.7)	861/861 (100)	1102/1112 (99.1)	1091/1136 (96)	1106 / 1106 (100)
Ciprofloxacin	1051/3524 (29.8)	1167/4816 (24.2)	1587/6452 (24.6)	888/3386 (26.2)	1112/4971 (22.4)	1412/4879 (28.9)	1568 / 4553 (34.4)
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)
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)
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)

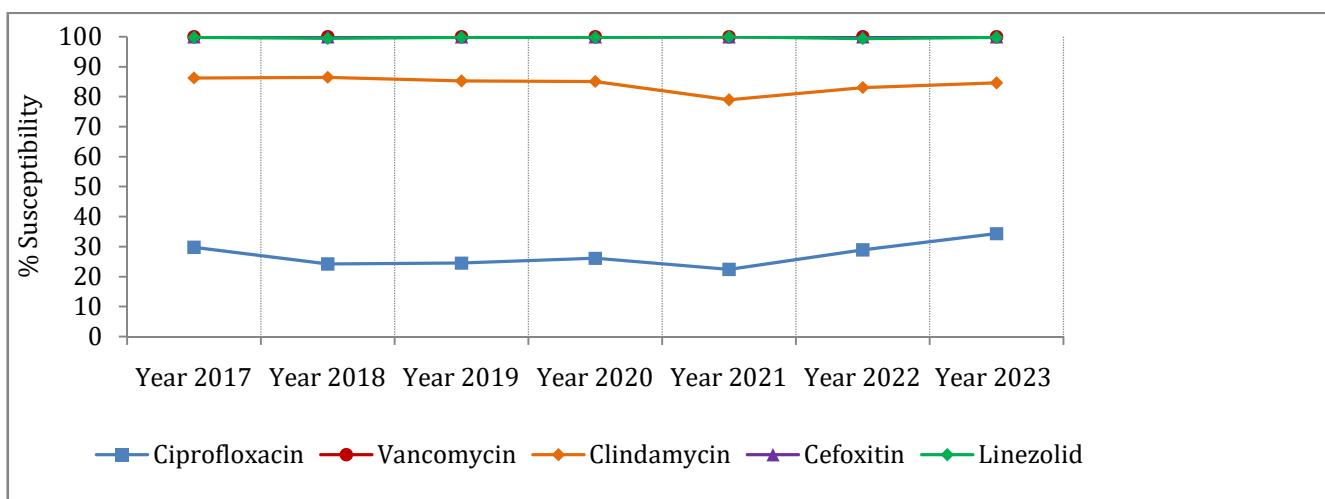


Figure 7.2: Year wise susceptibility trends of MSSA from all samples

Table 7.9: Year wise susceptibility trends of MRSA from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	Total n=1870	Total n=3445	Total n=5185	Total n=2582	Total n=3423	Total n=4266	Total n=4311
	(S%)						
Cefoxitin	0/1867 (0)	0/3062 (0)	0/4578 (0)	0/2399 (0)	24/2895 (0.8)	132/3862 (3.4)	0 / 3116 (-)
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)	0 / 2383 (-)
Vancomycin	667/667 (100)	1581/1581 (100)	2960/2960 (100)	1676/1676 (100)	2153/2154 (100)	3315/3348 (99)	4311 / 4311 (100)
Teicoplanin	1719/1735 (99.1)	2848/2956 (96.3)	2729/2775 (98.3)	948/953 (99.5)	1369/1370 (99.9)	1690/1700 (99.4)	2402 / 2402 (100)
Erythromycin	494/1813 (27.2)	822/3228 (25.5)	1251/4988 (25.1)	621/2490 (24.9)	917/3274 (28)	1009/4230 (23.9)	927 / 3834 (24.2)
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)
Tigecycline	133/133 (100)	627/634 (98.9)	1280/1286 (99.5)	694/694 (100)	990/998 (99.2)	1195/1281 (93.3)	1364 / 1364 (100)
Ciprofloxacin	165/1718 (9.6)	323/3222 (10)	397/4654 (8.5)	204/2417 (8.4)	328/3257 (10.1)	524/4096 (12.8)	404 / 4311 (9.4)
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)
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)
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)

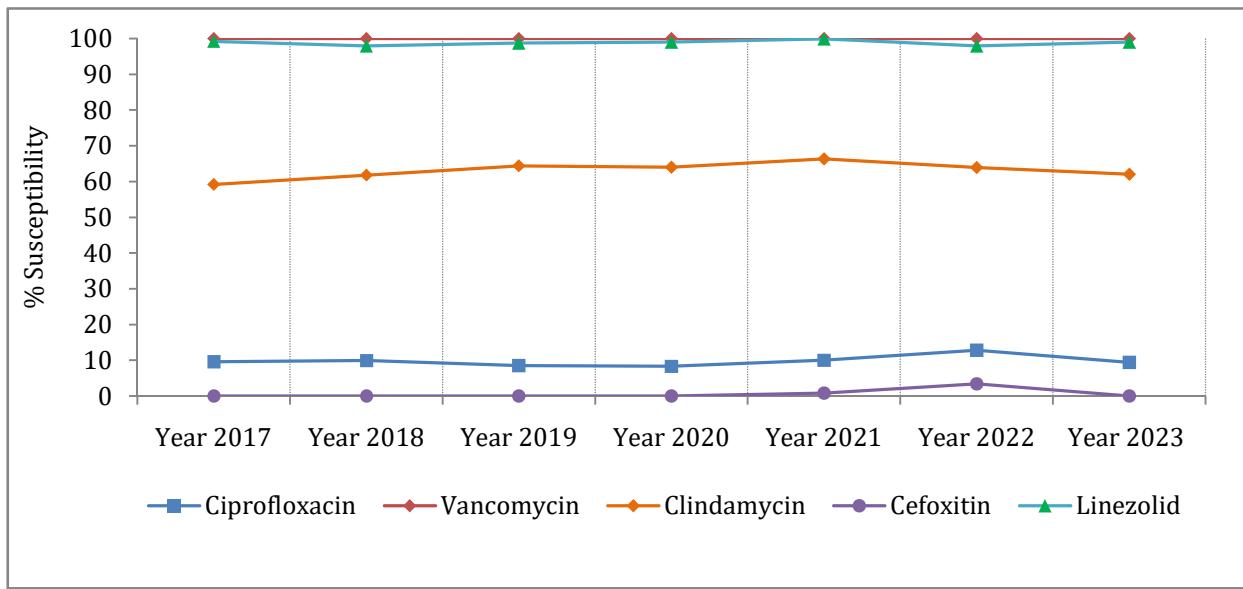


Figure 7.3: Year wise susceptibility trends of MRSA from all samples

Coagulase negative staphylococci

The common species were *S.haemolyticus*, *S.epidermidis*, *S.hominis*, *S.lugdunensis* and *S.saprophyticus*. Cefoxitin resistance was highest in *S.haemolyticus* (88.7 %) followed by *S.hominis* (80%) and *S.epidermidis* (76.3%). With the exception of teicoplanin, and vancomycin, *S.haemolyticus* exhibited much lower rates of susceptibility to all antibiotics when compared to the other species. Linezolid resistance rates remained unchanged in *S.epidermidis* and *S.hominis* while it was slightly higher among *S.haemolyticus* (0.7 to 1.3%), *S.lugdunensis* (3.1 to 6.2%) and *S.saprophyticus* (2 to 3.4%) encountered in 2023 CoNS isolates (**Table 7.10**). It can be clearly observed that there is a decrease in the susceptibility rates for most of the antibiotics except trimethoprim-sulfamethoxazole in 2022 and 2023.

Table 7.11 and figure 7.4 depict trends in antimicrobial susceptibility among CoNS isolates across the 7 years of study (2017-23). CoNS, overall, showed increasing trends of resistance to cefoxitin, erythromycin, tetracycline, ciprofloxacin and clindamycin over the years however, there was only a marginal increase in the susceptibility rates to co-trimoxazole. Linezolid resistance rates were slightly reduced in CoNS isolates (0.9 to 0.7 %) compared to 2022 but was lower than in 2018 and 2019.

Table 7.10: Susceptibility percentages of CoNS isolated from all specimens

AMA	All Specimens					
	<i>S. haemolyticus</i> n=2262	<i>S. epidermidis</i> n=2056	<i>S. hominis</i> n=1408	<i>S. spp.</i> n=1010	<i>S. lugdunensis</i> n=130	<i>S. saprophyticus</i> n=29
Cefoxitin	160 / 1418 (11.3)	232 / 977 (23.7)	146 / 731 (20)	62 / 224 (27.7)	86 / 127 (67.7)	19 / 23 (82.6)
Vancomycin	2262 / 2262 (100)	2056 / 2056 (100)	1408 / 1408 (100)	1010 / 1010 (100)	130 / 130 (100)	29 / 29 (100)
Teicoplanin	735 / 735 (100)	995 / 995 (100)	567 / 567 (100)	578 / 578 (100)	23 / 23 (100)	16 / 16 (100)
Erythromycin	162 / 1799 (9)	232 / 1347 (17.2)	133 / 1047 (12.7)	94 / 372 (25.3)	54 / 129 (41.9)	9 / 26 (34.6)
Tetracycline	643 / 1504 (42.8)	524 / 1057 (49.6)	344 / 827 (41.6)	156 / 214 (72.9)	96 / 120 (80)	25 / 25 (100)
Ciprofloxacin	388 / 2262 (17.2)	653 / 2056 (31.8)	439 / 1408 (31.2)	359 / 1010 (35.5)	91 / 130 (70)	28 / 29 (96.6)
Clindamycin	525 / 2262 (23.2)	752 / 2056 (36.6)	578 / 1408 (41.1)	358 / 1010 (35.4)	93 / 130 (71.5)	20 / 29 (69)
Linezolid	2247 / 2262 (99.3)	2048 / 2056 (99.6)	1405 / 1408 (99.8)	999 / 1010 (98.9)	122 / 130 (93.8)	28 / 29 (96.6)
Trimethoprim sulfamethoxazole	1072 / 2262 (47.4)	1161 / 2056 (56.5)	789 / 1408 (56)	636 / 1010 (63)	106 / 130 (81.5)	25 / 29 (86.2)

Table 7.11: Year wise susceptibility trends of CoNS from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	Total n=2830	Total n=4016	Total n=3571	Total n=2018	Total n=2655	Total n=6333	Total n=6895
	(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)
Vancomycin	718/718 (100)	1619/1679 (96.4)	1681/1691 (99.4)	890/890 (100)	1374/1377 (99.8)	5633/5680 (99.2)	6895 / 6895 (100)
Teicoplanin	2212/2236 (98.9)	2912/3083 (94.5)	1324/1379 (96)	229/238 (96.2)	497/518 (95.9)	1701/1771 (96)	2914 / 2914 (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)
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)
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)
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)
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)
Trimethoprim-sulfamethoxazole	923/1940 (47.6)	1579/3452 (45.7)	1687/3428 (49.2)	861/1935 (44.5)	1224/2610 (46.9)	2347/4356 (53.8)	3789 / 6895 (55)

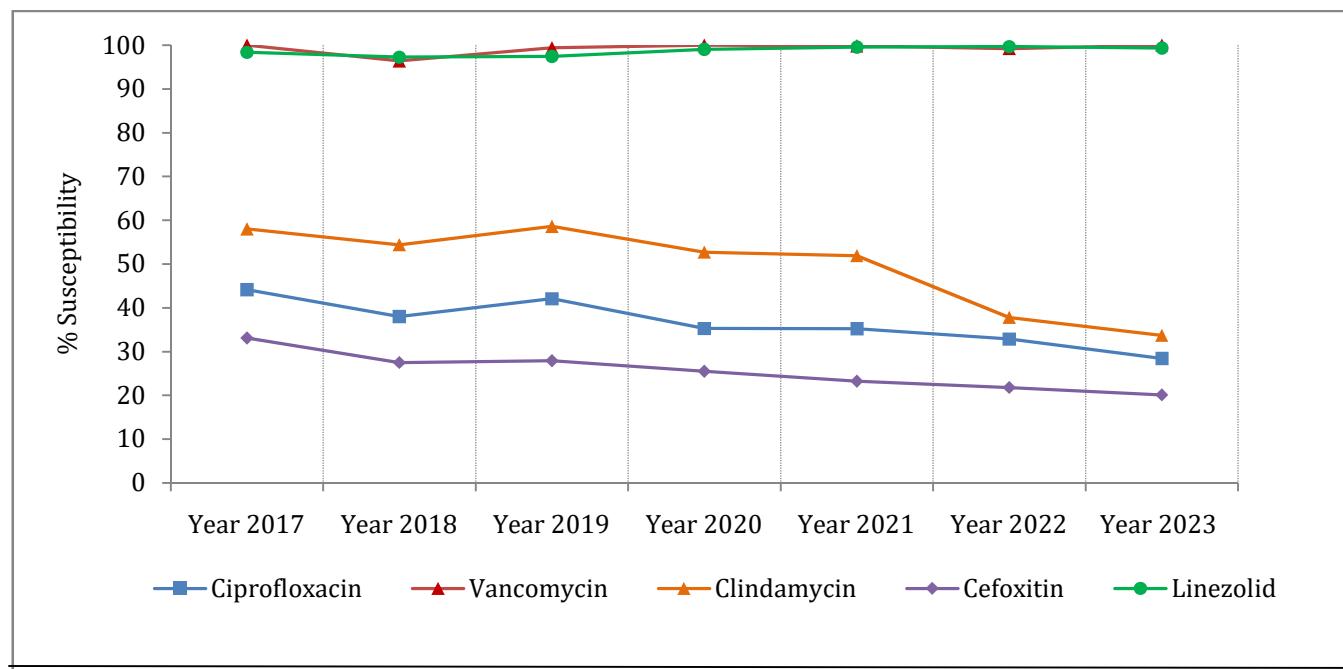


Figure 7.4: Year wise susceptibility trends of CoNS from all samples

Enterococci

E. faecalis is usually the commonest species followed by *E. faecium*. However in 2021 and 2022, *E. faecium* was found to be the predominant species. This trend was reversed in 2023 where *E. faecalis* was found to be more 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 17.5 % (2023) slightly increased than the rate in 2022 (16.7%). However, the rate was 5 times higher in *E. faecium* compared to *E. faecalis* (29.6% vs 5.8%). Isolates from blood (both the species) appear to be more resistant when compared to isolates from superficial and deep infections in *E. faecium* isolates. Although the numbers are too small for significance, vancomycin resistance among CSF isolates was much higher than the overall rate (**Table 7.12**). The susceptibility to all the antibiotics was higher among *E. faecalis* isolates when compared to *E. faecium*. The difference was particularly marked for ampicillin and nitrofurantoin (**Table 7.13**).

Table 7.12: Susceptibility pattern of enterococci from all samples except urine

AMA	All Specimens (except urine)		Blood		Superficial Infection		Deep Infection		CSF	
	<i>Enterococcus faecalis</i> n=1866	<i>Enterococcus faecium</i> n=1804	<i>Enterococcus faecalis</i> n=545	<i>Enterococcus faecium</i> n=731	<i>Enterococcus faecalis</i> n=650	<i>Enterococcus faecium</i> n=377	<i>Enterococcus faecalis</i> n=153	<i>Enterococcus faecium</i> n=159	<i>E. faecalis</i> n=29	<i>E. faecium</i> n=33
Ampicillin	1394 / 1804 (77.3)	334 / 1699 (19.7)	340 / 524 (64.9)	119 / 684 (17.4)	534 / 644 (82.9)	95 / 374 (25.4)	134 / 150 (89.3)	27 / 149 (18.1)	16 / 29 (-)	10 / 32 (31.3)
Vancomycin	1756 / 1866 (94.1)	1269 / 1804 (70.3)	488 / 545 (89.5)	452 / 731 (61.8)	630 / 650 (96.9)	293 / 377 (77.7)	151 / 153 (98.7)	114 / 159 (71.7)	24 / 29 (-)	20 / 33 (60.6)
Teicoplanin	1655 / 1779 (93)	1130 / 1567 (72.1)	440 / 502 (87.6)	399 / 615 (64.9)	613 / 642 (95.5)	283 / 364 (77.7)	145 / 147 (98.6)	107 / 153 (69.9)	21 / 24 (-)	18 / 27 (-)
Gentamicin HL	975 / 1763 (55.3)	594 / 1691 (35.1)	271 / 527 (51.4)	212 / 681 (31.1)	342 / 619 (55.3)	121 / 339 (35.7)	86 / 142 (60.6)	57 / 153 (37.3)	14 / 28 (-)	15 / 32 (46.9)
Linezolid	1823 / 1866 (97.7)	1676 / 1804 (92.9)	532 / 545 (97.6)	662 / 731 (90.6)	639 / 650 (98.3)	353 / 377 (93.6)	150 / 153 (98)	147 / 159 (92.5)	28 / 29 (-)	33 / 33 (100)

Table 7.13: Susceptibility pattern of enterococci from urine

AMA	Urine	
	<i>Enterococcus faecalis</i> n=1595	<i>Enterococcus faecium</i> n=942
Ampicillin	1019 / 1543 (66)	145 / 900 (16.1)
Vancomycin	1511 / 1595 (94.7)	688 / 942 (73)
Teicoplanin	1425 / 1549 (92)	667 / 908 (73.5)
Gentamicin HL	603 / 1363 (44.2)	320 / 801 (40)
Ciprofloxacin	174 / 1532 (11.4)	39 / 861 (4.5)
Nitrofurantoin	1220 / 1531 (79.7)	310 / 824 (37.6)
Linezolid	1537 / 1595 (96.4)	868 / 942 (92.1)

As expected, most antibiotics showed lower susceptibility rates among ICU isolates when compared to ward isolates. This difference was noted in *E.faecalis* species (except for fosfomycin) in that susceptibility rate were slightly higher in ICU isolates than the ward isolates (**Table 7.14**). **Table 7.15** and **figure 7.5** depict the year wise susceptibility rates of *E. faecium*. The susceptibility rates showed a slight increase for ampicillin in 2023 when compared to 2022 while there was a slight reduction in susceptibility to high-level gentamicin, nitrofurantoin vancomycin, linezolid and teicoplanin. Compared to the index year of 2017, there was a significant reduction in susceptibility to nitrofurantoin from 2017 to 2023.

Table 7.14: Susceptibility pattern of enterococci from all samples across OPD, Ward and ICU

AMA	<i>Enterococcus faecalis</i>				<i>Enterococcus faecium</i>			
	Total n=3461	OPD n=1272	Ward n=1633	ICU n=556	Total n=2746	OPD n=460	Ward n=1631	ICU n=655
	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)	(S %)
Ampicillin	2413 / 3347 (72.1)	1004 / 1245 (80.6)	1084 / 1556 (69.7)	325 / 546 (59.5)	479 / 2599 (18.4)	140 / 449 (31.2)	263 / 1517 (17.3)	76 / 633 (-)
Vancomycin	3267 / 3461 (94.4)	1226 / 1272 (96.4)	1534 / 1633 (93.9)	507 / 556 (91.2)	1957 / 2746 (71.3)	378 / 460 (82.2)	1180 / 1631 (72.3)	399 / 655 (60.9)
Teicoplanin	3080 / 3328 (92.5)	1159 / 1234 (93.9)	1442 / 1552 (92.9)	479 / 542 (88.4)	1797 / 2475 (72.6)	356 / 436 (81.7)	1060 / 1437 (73.8)	381 / 602 (63.3)
Gentamicin HL	1578 / 3126 (50.5)	581 / 1080 (53.8)	782 / 1531 (51.1)	215 / 515 (41.7)	914 / 2492 (36.7)	191 / 414 (46.1)	550 / 1516 (36.3)	173 / 562 (30.8)
Ciprofloxacin	205 / 1805 (11.4)	102 / 866 (11.8)	83 / 731 (11.4)	20 / 208 (9.6)	50 / 1112 (4.5)	23 / 235 (9.7)	21 / 612 (3.4)	6 / 265 (2.2)
Nitrofurantoin	1321 / 1651 (80)	714 / 819 (87.2)	492 / 650 (75.7)	115 / 182 (63.2)	318 / 878 (36.2)	99 / 211 (46.9)	171 / 490 (34.9)	48 / 177 (27.1)
Fosfomycin	945 / 1247 (75.8)	400 / 537 (74.5)	427 / 559 (76.4)	118 / 151 (78.1)	NT	NT	NT	NT
Linezolid	3360 / 3461 (97.1)	1240 / 1272 (97.5)	1583 / 1633 (96.9)	537 / 556 (96.6)	2544 / 2746 (92.6)	426 / 460 (92.6)	1519 / 1631 (93.1)	599 / 655 (91.5)

Table 7.15: Year wise susceptibility trends of *Enterococcus faecium* from all samples

AMA	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021	Year-2022	Year-2023
	Total n=937	Total n=1476	Total n=2700	Total n=1994	Total n=2422	Total n=2998	Total n=2746
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)	(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)
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)
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)
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)
Ciprofloxacin	10/230 (4.3)	26/446 (5.8)	79/984 (8.0)	38/544 (7.0)	47/640 (7.3)	140 / 1141 (12.3)	50 / 1112 (4.5)
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)
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)

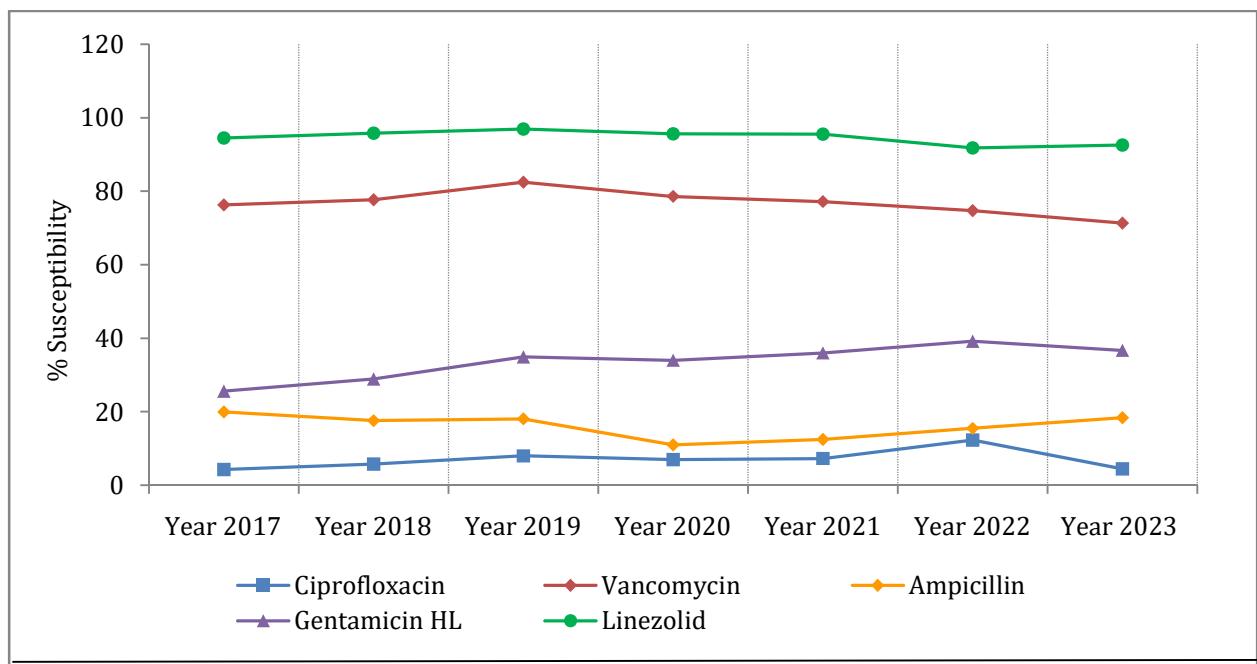


Figure 7.5: Year wise susceptibility trends of *Enterococcus faecium* from all samples

Table 7.16. In *Enterococcus faecium* the susceptibility rates to vancomycin ranged from 48.4% to 97 % across regional centres. Though the overall VRE rate is 29.7% slightly increased compared to 2022 (27%), there were significant differences observed between the various regional centres, the highest VRE rate in the isolates from RC03 and RC06 (43.4% and 51.6%). The lowest VRE rates were observed from the RC06 (3.3%) and RC19 (9.6%). Susceptibility to linezolid was high (>90%) in most centres. However, RC06 and RC21 reported a very low susceptibility rate of 66.2% and 67.7% respectively. Susceptibility to ampicillin was found to be lowest in the range of (3.3% to 47%), while susceptibility to high level gentamicin ranged between 15.9% to 64.3%.

Table 7.16: Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Enterococcus faecium* from total (Except faeces & urine)

RC/ Antibiotics	Ampicillin (n=1699)	Vancomycin (n=1804)	Teicoplanin (n=1567)	Gentamicin_HL (n=1691)	Linezolid (n=1804)
	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	12 / 94 (12.8)	58 / 94 (61.7)	60 / 94 (63.8)	30 / 89 (33.7)	93 / 94 (98.9)
RC2	73 / 423 (17.3)	267 / 423 (63.1)	137 / 202 (67.8)	94 / 418 (22.5)	419 / 423 (99.1)
RC3	6 / 53 (11.3)	30 / 53 (56.6)	31 / 52 (59.6)	15 / 53 (28.3)	49 / 53 (92.5)
RC4	89 / 402 (22.1)	314 / 402 (78.1)	316 / 402 (78.6)	168 / 401 (41.9)	387 / 402 (96.3)
RC5	12 / 43 (27.9)	42 / 51 (82.4)	42 / 51 (82.4)	23 / 51 (45.1)	50 / 51 (98)
RC6	7 / 150 (4.7)	76 / 157 (48.4)	78 / 157 (49.7)	24 / 151 (15.9)	104 / 157 (66.2)
RC7	7 / 16 ()	17 / 22 (77.3)	13 / 20 (-)	15 / 17 (-)	19 / 22 (-)
RC8	-	44 / 67 (65.7)	46 / 67 (68.7)	29 / 67 (43.3)	61 / 67 (91)
RC9	16 / 34 (47.1)	33 / 34 (97.1)	33 / 34 (97.1)	18 / 34 (52.9)	32 / 34 (94.1)
RC10	6 / 113 (5.3)	77 / 113 (68.1)	78 / 113 (69)	37 / 90 (41.1)	110 / 113 (97.3)
RC11	1 / 30 (3.3)	21 / 32 (65.6)	21 / 32 (65.6)	8 / 31 (25.8)	31 / 32 (96.9)
RC12	10 / 61 (16.4)	44 / 61 (72.1)	44 / 60 (73.3)	6 / 8 (-)	54 / 61 (88.5)
RC13	12 / 28 (-)	22 / 28 (78.6)	21 / 27 (-)	15 / 24 (-)	28 / 28 (100)
RC14	0 / 3 (-)	2 / 3 (-)	2 / 3 (-)	0 / 3 (-)	3 / 3 (-)
RC15	7 / 25 (28)	26 / 27 (-)	24 / 26 (-)	14 / 24 (-)	24 / 27 (-)
RC16	8 / 30 (26.7)	29 / 30 (96.7)	28 / 30 (93.3)	20 / 29 (-)	28 / 30 (93.3)
RC17	14 / 14 (-)	13 / 14 (-)	14 / 14 (-)	12 / 14 (-)	14 / 14 (-)
RC18	1 / 4 (-)	4 / 4 (-)	3 / 3 (-)	3 / 4 (-)	4 / 4 (-)
RC19	26 / 83 (31.3)	75 / 83 (90.4)	70 / 83 (84.3)	22 / 83 (26.5)	82 / 83 (98.8)
RC20	15 / 44 (34.1)	37 / 44 (84.1)	28 / 35 (80)	27 / 42 (64.3)	42 / 44 (95.5)
RC21	12 / 49 (24.5)	38 / 62 (61.3)	41 / 62 (66.1)	14 / 58 (24.1)	42 / 62 (67.7)
Total	334 / 1699 (19.7)	1269 / 1804 (70.3)	1130 / 1567 (72.1)	594 / 1691 (35.1)	1676 / 1804 (92.9)

Enterococcus faecalis

Table 7.17 and figure 7.6 depict the trends in antibiotic susceptibility rates in *E. faecalis* from 2017-2023. Lower susceptibility trends were observed for all antibiotics in 2023 isolates when compared to 2022 except for ampicillin (71% to 72.1 %).

Table 7.17: 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
	Total n=1034	Total n=2014	Total n=2895	Total n=2101	Total n=2373	Total n=3240	Total n=3461
	(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)
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)
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)
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)
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)
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)
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)
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)

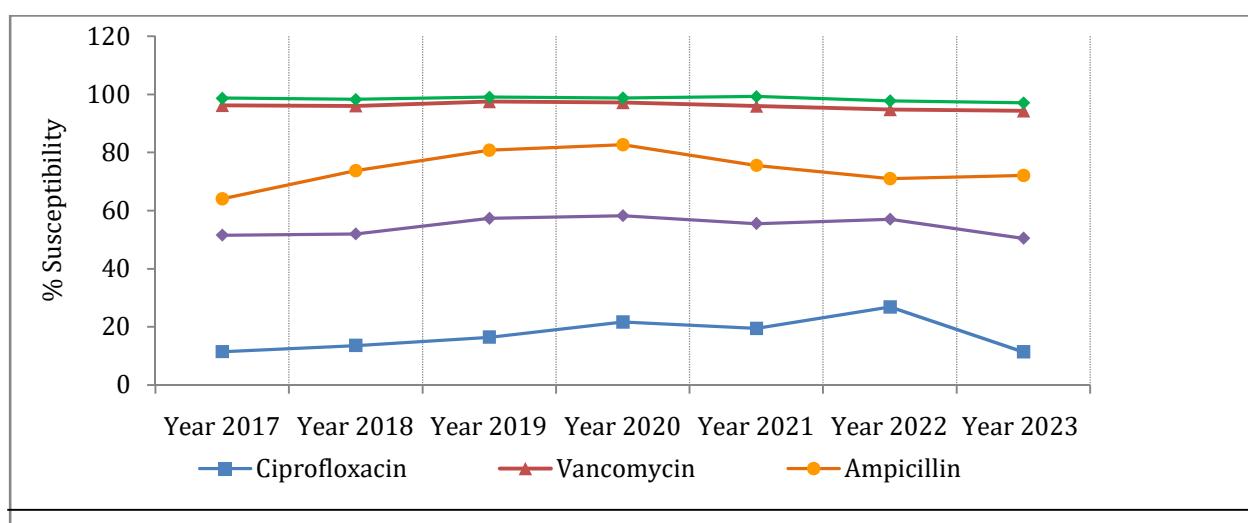


Figure 7.6: Year wise susceptibility trends of *Enterococcus faecalis* from all samples

In *E. faecalis* the susceptibility rates of vancomycin (75.6% to 100%) and teicoplanin ranged from (76.5% to 100 %) from most of the regional centres (**Table 7.18**). Though the overall VRE rate slightly increased 5.7% to 5.9%, there were significant differences observed between the various regional centres, the highest rate in the isolates from RC19 and RC01 (16.7% and 24.4%). The lowest VRE rates were observed from the RC03 (1.3%) and RC04 (1.9%). Susceptibility to linezolid was high in most of the centres in the range between 83.1% to 100%. Linezolid resistance was found to be the higher in the RC09 (16.9%) centre. The overall high level gentamicin susceptibility rate was at 55.3% which is the least recorded rate when compared to the other antibiotics. Susceptibility to ampicillin was found to be lowest in the range of (33.3% to 35.3%), while in the high level gentamicin moderate susceptibility was recorded in the range of (33.8% to 87.9%) across the centres.

Table 7.18 Antimicrobial Susceptibilities (AMS) Percentage RC wise of *Enterococcus faecalis* from Total (Except Faeces & Urine)

RC/ Antibiotics	Ampicillin (n=1804)	Vancomycin (n=1866)	Teicoplanin (n=1779)	Gentamicin HL (n=1763)	Linezolid (n=1866)
	n(%)	n(%)	n(%)	n(%)	n(%)
RC1	15 / 45 (33.3)	34 / 45 (75.6)	37 / 45 (82.2)	26 / 44 (59.1)	44 / 45 (97.8)
RC2	94 / 117 (80.3)	110 / 117 (94)	39 / 43 (90.7)	53 / 117 (45.3)	115 / 117 (98.3)
RC3	49 / 54 (90.7)	52 / 54 (96.3)	53 / 54 (98.1)	35 / 54 (64.8)	51 / 54 (94.4)
RC4	562 / 619 (90.8)	612 / 619 (98.9)	611 / 619 (98.7)	346 / 619 (55.9)	619 / 619 (100)
RC5	38 / 38 (100)	42 / 42 (100)	42 / 42 (100)	25 / 42 (59.5)	42 / 42 (100)
RC6	58 / 63 (92.1)	59 / 63 (93.7)	57 / 63 (90.5)	13 / 62 (21)	63 / 63 (100)
RC7	6 / 12 (-)	24 / 27 (-)	20 / 24 (83.3)	13 / 16 (-)	25 / 27 (92.6)
RC8	0 / 0 (-)	36 / 36 (100)	36 / 36 (100)	25 / 36 (69.4)	35 / 36 (97.2)
RC9	55 / 83 (66.3)	75 / 83 (90.4)	76 / 81 (93.8)	49 / 82 (59.8)	69 / 83 (83.1)
RC10	246 / 246 (100)	246 / 246 (100)	246 / 246 (100)	142 / 189 (75.1)	246 / 246 (100)
RC11	17 / 19 (-)	17 / 19 (-)	18 / 19 (-)	9 / 18 (-)	19 / 19 (-)
RC12	20 / 24 (-)	21 / 24 (-)	24 / 24 (-)	1 / 1 (-)	23 / 24 (-)
RC13	10 / 15 (-)	14 / 15 (-)	11 / 12 (-)	6 / 10 (-)	15 / 15 (-)
RC14	2 / 2 (-)	2 / 2 (-)	2 / 2 (-)	2 / 2 (-)	2 / 2 (-)
RC15	17 / 21 (-)	20 / 22 (-)	21 / 21 (-)	15 / 21 (-)	20 / 22 (-)
RC16	31 / 68 (45.6)	66 / 68 (97.1)	52 / 68 (76.5)	50 / 68 (73.5)	60 / 68 (88.2)
RC17	55 / 58 (94.8)	54 / 58 (93.1)	54 / 58 (93.1)	51 / 58 (87.9)	58 / 58 (100)
RC18	2 / 3 (-)	3 / 3 (-)	2 / 2 (-)	1 / 3 (-)	3 / 3 (-)
RC19	97 / 275 (35.3)	229 / 275 (83.3)	221 / 275 (80.4)	93 / 275 (33.8)	274 / 275 (99.6)
RC20	15 / 28 (53.6)	26 / 29 (-)	23 / 26 (-)	16 / 27 (-)	26 / 29 (-)
RC21	5 / 14 (-)	14 / 19 (-)	10 / 19 (-)	4 / 19 (-)	14 / 19 (-)
Total	1394 / 1804 (77.3)	1756 / 1866 (94.1)	1655 / 1779 (93)	975 / 1763 (55.3)	1823 / 1866 (97.7)

PCR for resistance genes

The MRSA phenotype was conferred by *mecA* gene as determined by PCR of all randomly selected isolates from all centres. Since all were *mecA* positive, *mecC* gene PCR was not performed. Recently plasmid mediated *mecB* and *mecD* genes have been reported in *S.aureus* which may complicate detection methods even further. Unlike previous years, none of the randomly tested MSSA isolates (269) harboured *mecA* gene. Among the non-beta lactam antibiotics, macrolide resistance was conferred either through *ermA/ermC/msrA/B* genes. In the present study, the overall prevalence of *ermC* genes was high (34%) followed by *msrA/B* (24%) and *ermC* and *msrA/B* together was (6.1%). None of the isolates harboured *ermB* genes. These genes are usually found among streptococci. Resistance to the high-level mupirocin (200 μ g) was conferred by *mup A* gene in all mupirocin resistant isolates (**Table: 7.19A**).

Full blown vancomycin resistance was not encountered in 2023. Although there were no VRSA or VISA identified among the 2023 isolates of MRSA, some of the isolates were found to be hVISA when tested by PAP/AUC analysis. Of the 100 MRSA isolates from JIPMER subjected to PAP-AUC, 7 were identified as hVISA (7%), while 12/312 were identified as hVISA (3.8%) from other centres. The overall rate of hVISA was 4.6% (19/412). Mupirocin resistance among MRSA isolates slightly decreased from 7% to 4.7%. These rates have remained almost the same for last 3 years possibly suggesting that mupirocin resistance genes exert a large fitness cost on MRSA. Resistance to tigecycline was not seen in 2016 but it appeared in a small number of isolates in 2017 and 2018 (0.5%), 2019 (0.4%), 2021 (0.8%). In 2022 and 2023, none of the isolates exhibited tigecycline resistance.

MIC₅₀ of different antibiotics against MRSA isolates

There was a slight decrease in MIC 50 level of vancomycin in a few centres like RC04, RC03, RC01, RC06 and RC12 isolates, (1 to 0.75 μ g/ml), and in the RC09 (0.75 to 0.5 μ g/ml), while in the isolates from RC20 and RC02, the value remained the same at 0.75 μ g/ml. The median MIC for linezolid among RC09 isolates increased slightly (0.5 to 0.75 μ g/ml), but in RC04, RC03, RC20, RC12, it slightly decreased compared to 2022. The value in isolates from RC06, RC01, RC02 remained unchanged. In the case of daptomycin, MIC level was slightly lower among all the centres except RC12 where it has remained same (0.25 μ g/ml) as last year. Tigecycline median MIC increased slightly in all the centres ranges between (0.032 to 0.25 μ g/ml), but remained the same in RC06 (0.064 μ g/ml). Teicoplanin MICs lightly increased in RC09 (0.38 to 0.75 μ g/ml) and RC03 (0.25 to 0.5 μ g/ml), while it decreased in RC20 (1 to 0.5 μ g/ml) and RC12 (0.75 to 0.5 μ g/ml). The value remained same as the previous year in RC04 (0.75 μ g/ml) and in

RC01 (0.5 μ g/ml). Although vancomycin may continue to be used for serious MRSA infections, it is better to use alternate drugs if the MIC value is close to the breakpoint as such isolates are likely to be hVISA leading to poor response to therapy. As susceptibility to daptomycin continues to be close to 100% among MRSA isolates, this antimicrobial may be considered as alternative agents besides vancomycin and linezolid except for respiratory infections. This may also remove some of these selection pressures on antimicrobial resistant genes as exerted by these agents. Vancomycin MIC in the majority of the hVISA isolates were in the ranges of 1 μ g/ (9), 0.75 μ g/ml (6), 0.5 μ g/ml (3) and 1.5 μ g/ml (1).

Vancomycin variable Enterococcus

There were 355 isolates of vancomycin susceptible enterococci (158 *E. faecium* and 197 *E. faecalis*) which were screened for VVE (by van A PCR). None of the isolates was identified as VVE. Antibiotic resistance genes among phenotypically resistant and sensitive isolates of *S. aureus*, CoNS and enterococci from nodal and regional centres are depicted in **Table 7.19A and 7.19B respectively**. All vancomycin resistant enterococci carried the vanA gene only. Among susceptible *S. aureus* isolates, the msrA/B and ermC genes were found 4% (8/215) and 5% (10/215) while it was found 4 isolates in 2022. VVE was identified in 5 isolates in 2020 and 3 isolates in 2021. However, there was no VVE detected in 2022 and 2023.

All MRSA isolates were mediated by mecA gene. No other mec gene was detected. Among the macrolide resistance genes, ermC was found more commonly among the isolates from regional centres when compared to JIPMER isolates (51% vs 34%). The percentage of macrolide resistant *S. aureus* carrying msr genes were decreased among JIPMER isolates and in other regional centres slightly increased when compared to 2023 (44 to 33% vs 24 to 28.6%). The genes coding for mupirocin resistance (mupA gene) and linezolid resistance (cfr gene) remained the same in the current year compared to the previous years.

Biocide resistance genes (*qacA/B* and *smr*) among MRSA and VRE isolates

412 isolates of MRSA and 128 VRE isolates were tested for the presence of *qacA/B* and *Smr* genes. The overall prevalence of *qacA/B* and *smr* genes in MRSA isolates was 1.2% (5/412) and 0.7% (3/412) respectively. In *Enterococcus*, *qacA/B* was detected in 2.3 % (3/128) isolates while none had *smr* genes. Among MRSA isolates, *qacA/B* and *smr* genes slightly decreased from 1.9 % in 2022 to 1.2% in 2023 while in enterococci 4.3 to 2.3%. Most disinfectant-resistance genes are plasmid borne and can spread between staphylococcal species.

Table- 7.19 A: Antibiotic resistance genes among phenotypically resistant isolates of *S. aureus* and enterococci from nodal and regional centres

S.No	Phenotypic resistance	Genes detected	Nodal center (No.positive /no tested)	Regional centers (No.positive /no tested)
1	Methicillin resistant <i>S.aureus</i> (MRSA)	<i>mecA</i>	<i>mecA</i> : 100/100 (100%)	<i>mecA</i> :312/312 (100%)
2	Erythromycin resistant <i>S.aureus</i>	<i>erm A</i> , <i>erm B</i> and <i>erm C</i>	<i>erm A</i> :3/76 (3.9%) <i>erm B</i> :0/76 <i>erm C</i> :28/76 (36.8%) <i>msrA/B</i> : 40/76 (52.6%) <i>ermA</i> and <i>ermC</i> :1/76 (1.3%) <i>ermC</i> and <i>msrA/B</i> : 4/76 (5.2%) Negative for <i>ermA,B,C</i> and <i>msr A/B</i> genes: 0/76	<i>erm A</i> :1/379 (0.2%) <i>erm B</i> :0/379 <i>erm C</i> :194/379 (51 %) <i>msrA/B</i> : 124/379 (33 %) <i>ermC</i> and <i>msrA/B</i> : 33/379 (9%) <i>ermA</i> and <i>msrA/B</i> : 2/379 (0.5 %) Negative for <i>ermA,B,C</i> and <i>msr A/B</i> genes: 22 / 379 (6 %)
3	Mupirocin resistant <i>S.aureus</i>	<i>mupA</i> and <i>mupB</i>	<i>mup A</i> :27/27 (100 %) <i>mup B</i> :0/27	<i>mup A</i> :7/7 (100 %) <i>mup B</i> :0/7
4	Linezolid resistant MRSA	<i>cfr</i>	<i>Nil</i>	<i>cfr</i> : 4/4 (100%)
5	Vancomycin resistant Enterococci (VRE)	<i>vanA</i> , <i>vanB</i> , <i>vanC₁/C₂</i>	<i>vanA</i> :61/61 (100%) <i>vanB</i> :0/61 <i>vanC₁/C₂</i> :0/61	<i>vanA</i> :67/67 (100%) <i>vanB</i> :0/67 <i>vanC₁/C₂</i> :0/67

Table- 7.19 B: Antibiotic resistance genes among phenotypically sensitive isolates of *S.aureus* and enterococci from nodal and regional centres

S.No	Phenotypic resistance	Genes detected	Nodal center (No.positive /no tested)	Regional centers (No.positive /no tested)
1	Methicillin sensitive <i>S.aureus</i> (MSSA)	<i>mecA</i>	<i>mecA</i> : 0/57	<i>mecA</i> :0/257
2	Erythromycin sensitive <i>S.aureus</i>	<i>erm A</i> , <i>erm B</i> and <i>erm C</i>	<i>erm A</i> :0/57 <i>erm B</i> :0/57 <i>erm C</i> :0/57 <i>msrA/B</i> : 0/57 <i>ermA</i> and <i>ermC</i> :0/57 <i>ermC</i> and <i>msrA/B</i> : 0/57 <i>ermA</i> and <i>msrA/B</i> : 0/57 Negative for <i>ermA,B,C</i> and <i>msr A/B</i> genes: 57/57	<i>erm A</i> :0/15 <i>erm B</i> :0/215 <i>erm C</i> :10/215 (5%) <i>msrA/B</i> : 8/215 (4%) <i>ermA</i> and <i>ermC</i> : 0/263 <i>ermC</i> and <i>msrA/B</i> : 1/215(0.4%) <i>ermA</i> and <i>msrA/B</i> : 0/263 <i>ermC</i> and <i>msrB</i> : 0/263 Negative for <i>ermA,B,C</i> and <i>msr A/B</i> genes : 196/215 (91%)
3	Vancomycin sensitive enterococci	<i>vanA</i> , <i>vanB</i> , <i>vanC₁/C₂</i>	<i>vanA</i> :0/41 <i>vanB</i> :0/41 <i>vanC₁/C₂</i> :0/41	<i>vanA</i> :0/321 <i>vanB</i> :0/321 <i>vanC₁/C₂</i> :0/321

Mutations identified in hVISA isolates

Candidate genes in hVISA genomes were analysed for amino acid substitutions. These candidate genes included *vraSR*, *vraT*, *graSR*, and *walKR*, (regulates the electrical potential of cell membrane); *saeS* (virulence regulator), *mprF* (multiple peptide resistance factor) gene which is involved in the production of wall-teichoic acid (WTA). In addition, all the genomes were screened for the mutations of *rpoB* gene encoding for β subunit of bacterial RNA polymerase. Mutations were analysed for the hVISA study isolates using VSSA reference genome (MSSA476 NC002953). In the present study, whole-genome analysis of hVISA ($n = 54$) revealed distinct amino acid substitutions in eight candidate genes (Table 7.20). However, none of the tested isolates showed mutations in *walR* genes. Several mutations which were identified in an earlier study were also detected in our study. For eg. *vraR* (T24K), *rpoB* (L466S), *graS* (T224I,Y737F) were found only in 7 isolates, in *saeS*, S227N was more common and in *mprF* A26V , K47N were predominant. When compared to the other genes, mutations in the *graS* and *mprF* were more frequently observed.

Among hVISA, T224I 23/54 (42.5%) was identified as the predominant mutation in *graS* followed by A26V20/54 (37%) substitution in *mprF* and D148E 14/54 (26%) in *graR*. A strong link was seen between hVISA phenotype and the mutations identified in *graS* (T224I) and *graR* (D148E). Of these mutations, T224I and D148E were identified in various STs. M81I substitution was most commonly seen in *vraR* genes among the hVISA strains which belonged to ST772, ST672, ST239 and D148E substitution in *graR* genes were associated with ST672 and ST772.

Table 7.20: Amino acid substitutions observed in the candidate genes of hVISA isolates

S.No	Lab ID	walK	walR	graS	graR	vraR	vraS	rpoB	saeS	mprF
RC01	211964	-	-	L26F,T224I	-	R121I, K38N	-	-	-	-
RC13	270815	-	-	K146E,D218N,	-	-	-	D148E	-	I9V,A26V,K47N
RC21	293579	-	-	-		E59D, M81I	-	-	-	A26V
RC15	268928	-	-	I59L,L26F	D148Q,	M81I	-	-	N227S, E268K	-
RC15	292118	E239K	-	I59L,L26F,T224I	-	-	-	-	E268K	A26V,E692Q
RC17	257340	-	-	I59L	D148Q,	M81I	-	-	-	E692Q,P267S
RC17	257342	-	-	L26F,T224I	-	R121I, K38N	-	-	-	A26V,K47N,, F413L,
RC06	287446	R22K, A468T	-	L26F,T224I	D148Q,	-	-	-	N227S,	P267S
RC15	292919	-	-	I59L,T224I	-	E59D	-	-	N227S, E268K	A26V,P267S
RC17	245326	-	-	Y156F,D218N	D148Q,	-	-	M309V	-	19V,A26V,
RC06	243766	-	-	T224I	D148Q,	M81I	-	-	N227S, E268K	A26V,E692Q
RC06	292780	-	-	L26F,T224I	D148Q	K38N	-	-	N227S,	A26V,E692Q
RC04	322189	-	-	T224I D218N,	S207R	T24K	V15G	H481N Y737F	S227N S351T	F194YK522 N,L575I
RC04	333471	R222K	-	I59L	D148E	E59D, M81I	-	-	-	A26V
RC04	331100	-	-	I59L F245Y,I247V,Y261I	D148E D148ES 207R	E59D	-	V309M Y737F	S351T	E692Q,K 47N,
RC03	327750	-	-	T224I	D148Q	E59D, M81I	-	-	-	A26V
RC03	358665	-	-	T224I	-	K38N	-	-	D269N	L53F,P267S

RC02	364401		-	D218N,F245Y,	D148ES207 R	-	-	Y737F	S351T	A26V,K47N,D160N,F174L,
RC02	375399	-	-	L26F,T224I	D148E, D148Q	K38N	-	-	N227S,	A26V,E692Q
RC02	375465	-	-	-		E59D, M81I	-	-	-	-
RC14	322810	-	-	M15K,M55L,Y62F,	D148E	E59D -	-	Y737F	E268K S351T	A26V, K47N,K522N,L575I
RC14	376982	-	-	-		E59D, M81I	-	-	-	A26V
RC15	335113	-	-	T224I	-	K38N	-	-	D269N	L53F,
RC15	373890	-	-	-		E59D, M81I	-	-	-	A26V
RC15	374125	A468T	-	D218N,Y219H, F245Y,	D148E S207R	-	-	Y737F	S351T	F174L,
RC09	315999	-	-	S104L,E108D, D218N,	-	-	-	D148E	-	I9V,K47N
RC09	319660	A468T	-	D218N,Y219H,F245Y,	D148ES207 R	-	-	Y737F	S351T	K47N,D160N,F174L,
RC09	324755	-	-	T224I	-	K38N	-	-	D269N	L53F,P267S
RC05	331702	-	-		-	K38N	-	-	D269N	L53F,
RC05	350383	-	-	T224I	-	K38N	-	-	D269N	L53F,P267S
RC17	361218	A468T	-	L59I D218N,F245Y,	D148H D148ES207 R	E59D -	-	Y737F	N227S S351T	A26V,K47N,D160N,F174L,
RC06	366998	-	-	S104L,	-	-	-	D148E	-	I9V

RC08	368268	A468T	-	L26F D218N,Y219H,F245Y,	-	K38N -	-	Y737F	S351T	K47N,F174L,
RC04	330443	-	-	L26F,T224I	D148E, D148Q	K38N	-	-	N227S,	E692Q
RC05	350416	-	-	-	-	K38N	-	-		
RC15	372765	-	-	D218N,Y219H,F245Y,	D148ES207 R	-	-	Y737F	S351T	K47N,D160N,F174L,
RC09	338779	-	-	T224I	-	K38N	-	-	-	A26V,L53F,P267S
RC04	423817	-	-	-	-	K38N	-	-	D269N	P267S
RC04	425430	-	-	Y224I,L26F	-	K38N	-	L466S	K268E	A26V,L53F,P267S
RC04	437295	-	-	L26F,T224I	D148E, D148Q	K38N	-	-	N227S,	A26V,E692Q
RC04	457718	-	-	-	-	-	-	-	D269N	L53F,P267S
RC04	457719	-	-	-	-	K38N	-	-	-	-
RC13	402661	-	-	E112D	-	-	-	-	-	-
RC13	467187	-	-	T224I,Y182F	S207R	-	-	-	D269N	A26V,L53F,P267S
RC06	433210	-	-	L26F,L59I	D148E, D148Q	K38N	-	-	N227S,D269N	-E692Q
RC08	456767	-	-	T224I	-	K38N	-	-	D269N	,P267S
RC10	425546	-	-	T224I	-	K38N	-	-	D269N	L53F,P267S

RC06	459647	A469T	-	Y219H,S259A	V136I	K38N	-	-	D269N	L53F,P267S
RC12	447246	-	-	I59L,L26F,T224I	D148E	M81I	-	-	N227S, E268K	-P267S
RC12	459954	-	-	S104L,T167A	S207R	-	-	Y737F	S351T	L406I,T409I
RC10	434704	-	-	-	D148E	E59D	-	-	N227S	-E692Q
RC05	456133	-	-	T224I	D148Q	T24K	-	-	N227S,	E692Q
RC1	466128	-		L59I	-	E59D	-	-	N227S,D269N	A26V,E692Q
RC15	457213	-		I59L,L26F,	D148E	M81I	-	-	E268K	-

Transcriptome sequencing

Transcriptome sequencing and analysis was carried out for 2 isolates of *S. aureus* strains [resistant (hVISA) and sensitive (VSSA)]. RNA sequencing libraries were prepared using NEBNext UltraII Directional RNA library preparation reagents and workflow. The libraries were paired-end sequenced on Illumina NovaSeq 6000 sequencer for 150 cycles. The raw data were pre-processed by trimming adapters, and removing low-quality reads and ribosomal RNA contamination removal steps. Around 26.6 million reads were retained after removing non-coding reads and pre-processing steps. The pre-processed data was aligned to respective *Staphylococcus aureus* [*S. aureus* NCTC8325] genome. From the respective genome alignment, around 2400 genes were identified as being expressed. The read statistics, alignment details and the obtained absolute read count as well TPM matrix have been provided as a primary analysis results for all the samples. For differential regulation study, combinations of control and treatment samples were analysed for both sensitive strains. Differentially regulated genes, their corresponding pathway details, functional GO annotation and the plots generated were reported separately.

From the analysis results, we observed that some of the gene of interests such as **WalK**, **graR**, **saeS**, **vraS**, **graS** [which were involved in signaling, sensing mechanisms and regulatory systems in *S. aureus*] were identified as being expressed with maximum number of reads.

Clinical relevance and treatment guidance

The proportion of MRSA and VRE was found to be higher among blood isolates than from other specimens which are a cause for concern. Although vancomycin susceptibility remains very high among MRSA isolates, the occurrence of hVISA which is not usually detected in most clinical laboratories is worrisome as it may lead to therapeutic failure. Although vancomycin may continue to be used for serious MRSA infections, it is better to use alternate drugs if the MIC value is close to the breakpoint as such isolates are likely to be hVISA. As susceptibility to daptomycin continues to be close to 100% among MRSA isolates, this antimicrobial may be considered as alternative agents besides vancomycin and linezolid for infections other than those of the respiratory tract. This may also remove some of the selection pressure on antimicrobial resistance genes exerted by these agents. The decision to start vancomycin empirically for serious *S. aureus* infections depends on the MRSA rates in that centre. In centres where MRSA rates are high, vancomycin or linezolid may be used as empirical therapy with de-escalation if required. On the other hand, in centres where MRSA rates are low, Beta lactams may be used as empirical therapy with escalation to glycopeptides/linezolid/ daptomycin as required. For skin and soft tissue infections, the possibility of using tetracyclines and or clindamycin may be considered as susceptibility

rates to these two antibiotics continue to be high. Levonadifloxacin was tested on 886 isolates of MRSA, and all of them were shown to be susceptible. As per available literature, it appears to be highly efficient against acute bacterial skin and skin structure infections, as well as bacteraemia and diabetic foot infections. Ceftaroline also showed excellent in vitro efficacy with 90.1% of MRSA isolates being susceptible. While it is relatively easy to assign clinical significance to *S. aureus* and *Enterococcus* species, the same is not true for CoNS. They are often dismissed as colonizers though they are being increasingly recognized as opportunistic pathogens, particularly *S. haemolyticus*. Another feature of importance is that these isolates are often multi drug resistant; the genes are carried on mobile elements which make transfer of resistance a distinct possibility. In cases where there is a strong possibility of CoNS being pathogens, it may be prudent to use either vancomycin or linezolid as the rates of resistance to beta lactams are extremely high. The numbers of *E. faecium* was almost equal to *E. faecalis* across most centres of India. This could signify a worrisome trend as this species is far more drug resistant when compared to *E. faecalis*. In serious infections, such as meningitis or bacteraemia, linezolid may be tried as empirical therapy, with de-escalation if indicated. In centres which reported linezolid resistance in enterococci, daptomycin may be considered an alternative. The detection of *Enterococcus* species other than faecalis and faecium in high numbers is also significant as some of these species are intrinsically resistant to glycopeptides. Hence, speciation of enterococci is of clinical significance and is not just an academic exercise.

Chapter 8. Fungal pathogens

Total number of fungal isolates studied during the year 2023 was 2981. The antifungal susceptibility testing (AFST) profiling of *Candida* species (*C. tropicalis*, *C. albicans*, *C. glabrata*, *C. parapsilosis*, *C. auris*, *C. krusei*) isolated from all specimens revealed 90.8% fluconazole susceptibility in *C. albicans*, 92.5% in *C. tropicalis*, and 88.6% in *C. parapsilosis* but only 2.7% in *C. auris*; 97.5% voriconazole susceptibility in *C. krusei*, 87.9% in *C. albicans*, 88.2% in *C. parapsilosis* and 14.5% in *C. auris* (Table 1). *C. auris* showed variable resistance to echinocandins (caspofungin- 24.8%, anidulafungin-14% and micafungin -7.6%) (**Table 8.1**). *C. parapsilosis* which is generally reported as less susceptible to echinocandins, exhibited significant susceptibility to echinocandins (caspofungin-99.2%, anidulafungin- 98.3% and micafungin - 94.7%) in the present study (**Table 8.1**). Notably, 5.5-8.2% of *C. tropicalis* isolates were resistant to echinocandins which is of serious concern. Additionally, *C. glabrata* showed quite low susceptibility to caspofungin (72.2%) and micafungin (82.9%). Although two most common human fungal pathogens (*C. albicans* and *C. tropicalis*) showed the azole susceptibility in > 90%, increasing resistance rate over the recent years among these species is a major health concern. Moreover, *C. auris* showed very low susceptibility to fluconazole (2.7%) and voriconazole (14.5%). *C. tropicalis* isolated from urine was more susceptible to anidulafungin (100 %) compared to isolates obtained from blood (90.1%) (**Tables 8.2 and 8.3**). Further, decrease in antifungal susceptibility to majority of the antifungals among *C. albicans*, *C. tropicalis*, *C. parapsilosis* and *C. glabrata* needs to be cautiously monitored.

Table 8.1: Susceptibility pattern of *Candida* species isolated from all samples

AMA	<i>Candida</i> <i>tropicalis</i> n=706	<i>Candida</i> <i>albicans</i> n=746	<i>Candida</i> <i>glabrata</i> n=316	<i>Candida</i> <i>parapsilosis</i> n=202	<i>Candida</i> <i>auris</i> n=240	<i>Candida</i> <i>krusei</i> n=63
Anidulafungin	167 / 180 (92.8%)	116 / 122 (95.1%)	75 / 81 (92.6%)	58 / 59 (98.3%)	49 / 57 (86%)	26 / 26 (100%)
Caspofungin	378 / 400 (94.5%)	352 / 388 (90.7%)	135 / 187 (72.2%)	126 / 127 (99.2%)	82 / 109 (75.2%)	24 / 39 (61.5%)
Micafungin	281 / 301 (93.4%)	198 / 214 (92.5%)	116 / 140 (82.9%)	90 / 95 (94.7%)	85 / 92 (92.4%)	30 / 32 (93.8%)
Fluconazole	368 / 398 (92.5%)	347 / 382 (90.8%)	146 / 160 (91.3%)	109 / 123 (88.6%)	3 / 110 (2.7%)	15 / 40 (37.5%)
Voriconazole	356 / 400 (89%)	334 / 380 (87.9%)	115 / 183 (62.8%)	112 / 127 (88.2%)	16 / 110 (14.5%)	39 / 40 (97.5%)

Table 8.2: Susceptibility pattern of *Candida* species isolated from blood

AMA	<i>Candida tropicalis</i> n=313	<i>Candida albicans</i> n=171	<i>Candida auris</i> n=154	<i>Candida glabrata</i> n=115	<i>Candida krusei</i> n=27	<i>Candida parapsilosis</i> n=166
Anidulafungin	109 / 121 (90.1%)	48 / 51 (94.1%)	30 / 36 (83.3%)	43 / 47 (91.5%)	16 / 16 (100%)	48 / 49 (98%)
Caspofungin	190 / 206 (92.2%)	93 / 101 (92.1%)	50 / 70 (71.4%)	50 / 83 (60.2%)	9 / 19 (47.4%)	109 / 110 (99.1%)
Micafungin	163 / 174 (93.7%)	72 / 78 (92.3%)	53 / 59 (89.8%)	54 / 69 (78.3%)	16 / 17 (94.1%)	76 / 80 (95%)
Fluconazole	190 / 206 (92.2%)	91 / 97 (93.8%)	3 / 70 (4.3%)	54 / 63 (85.7%)	6 / 19 (31.6%)	96 / 106 (90.6%)
Voriconazole	183 / 208 (88%)	89 / 101 (88.1%)	14 / 70 (20%)	57 / 83 (68.7%)	18 / 19 (94.7%)	97 / 110 (88.2%)

Table 8.3: Susceptibility pattern of *Candida* species isolated from urine

AMA	<i>Candida tropicalis</i> n=156	<i>Candida albicans</i> n=136	<i>Candida glabrata</i> n=74	<i>Candida auris</i> n=56	<i>Candida parapsilosis</i> n=9
Anidulafungin	22 / 22 (100%)	27 / 27 (100%)	12 / 13 (-)	15 / 17 (-)	5 / 5 (-)
Caspofungin	82 / 82 (100%)	78 / 84 (92.9%)	29 / 35 (82.9%)	21 / 24 (87.5%)	8 / 8 (-)
Micafungin	69 / 70 (98.6%)	65 / 72 (90.3%)	28 / 29 (96.6%)	23 / 24 (95.8%)	7 / 8 (-)
Fluconazole	75 / 81 (92.6%)	75 / 84 (89.3%)	30 / 33 (90.9%)	0 / 24 (0%)	4 / 8 (-)
Voriconazole	75 / 82 (91.5%)	74 / 81 (91.4%)	19 / 34 (55.9%)	0 / 24 (0%)	7 / 8 (-)

* Less than 20 samples

The antifungal susceptibility testing (AFST) profiling of *Aspergillus* species isolated from all specimens is mentioned in **Table 8.4**. *A. flavus* and *A. fumigatus* were among the leading moulds isolated from clinical samples. A considerable rate of amphotericin B resistance was observed in *Aspergillus flavus* (30.8%) and *A. fumigatus* (51.13%). Moreover, 4.5% *A. fumigatus* isolates depicted resistance to voriconazole.

Table 8.4: Susceptibility pattern of *Aspergillus* species isolated from all samples

AMA	<i>Aspergillus flavus</i> (n=250)	<i>Aspergillus fumigatus</i> (n=178)
Amphotericin B	173/250 (69.20%)	87/178 (48.87%)
Caspofungin	250/250 (100%)	178/178 (100%)
Itraconazole	243/250 (97.5%)	171/178 (96.06%)
Posaconazole	250/250 (100%)	161/178 (90.44%)
Voriconazole	248/250 (99.2%)	170/178 (95.50%)

Invasive infections due to multidrug-resistant *C. auris* continue to be reported across many centres (**Figure 8.1**). *C. auris* was isolated from seven centres, highest number of *C. auris* isolates were from Chandigarh (RC2=40), followed by New Delhi (RC6=19) and Kolkata (RC8=14). Echinocandin resistant *C. auris* was isolated from two centres (RC21, RC8). Susceptibility trends of six *Candida* species have been shown in **figure 8.2**.

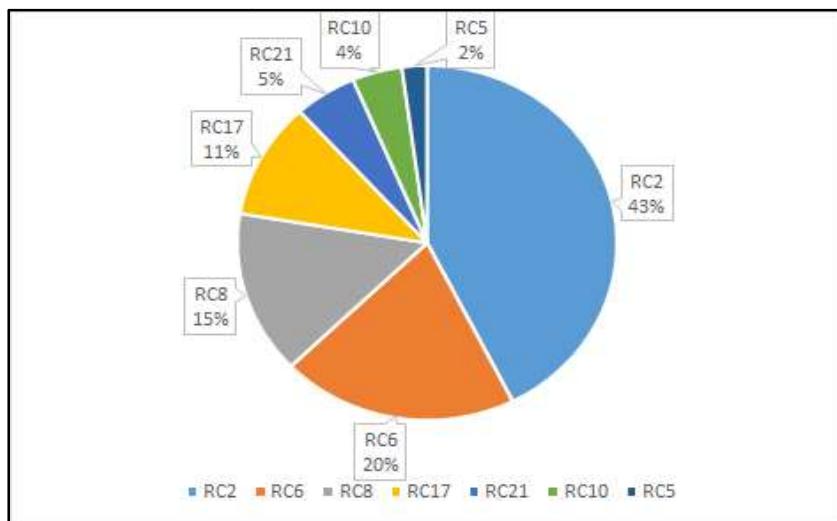
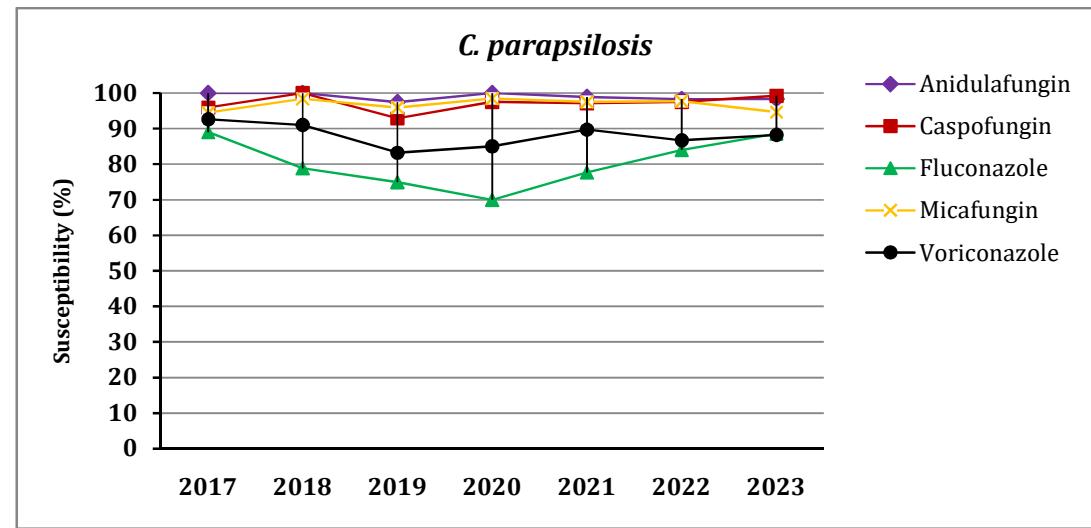
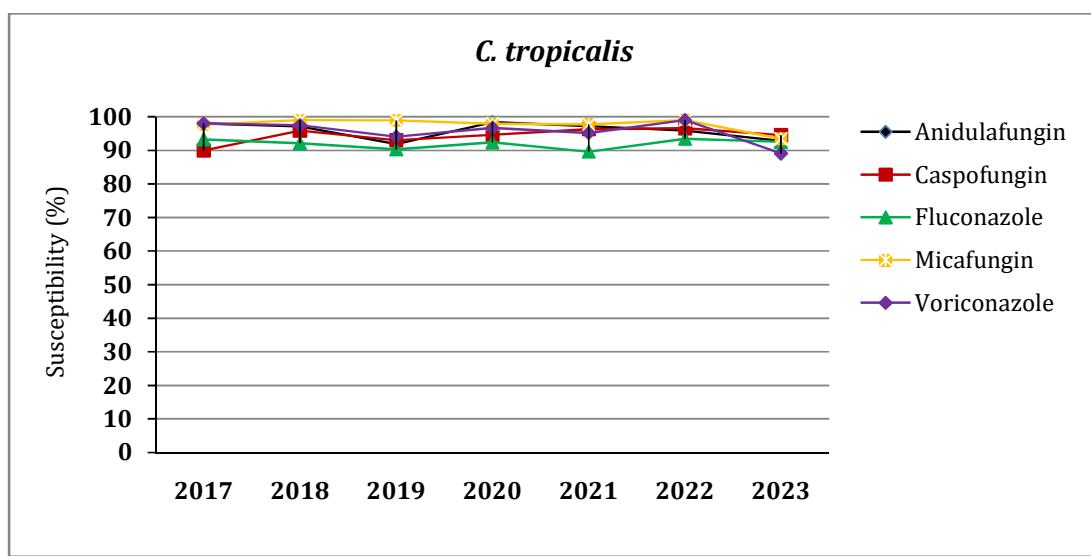
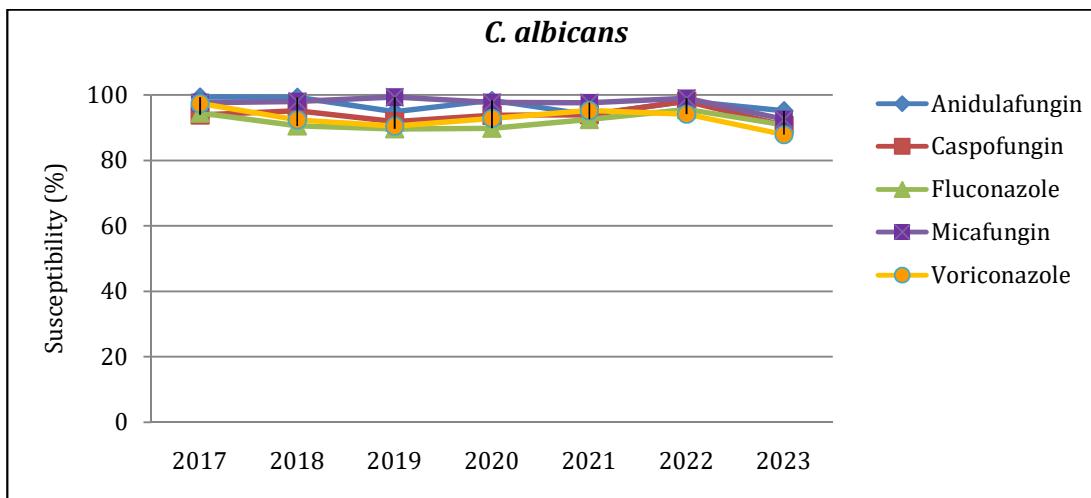


Figure 8.1: Distribution of *C. auris* from different regional centers



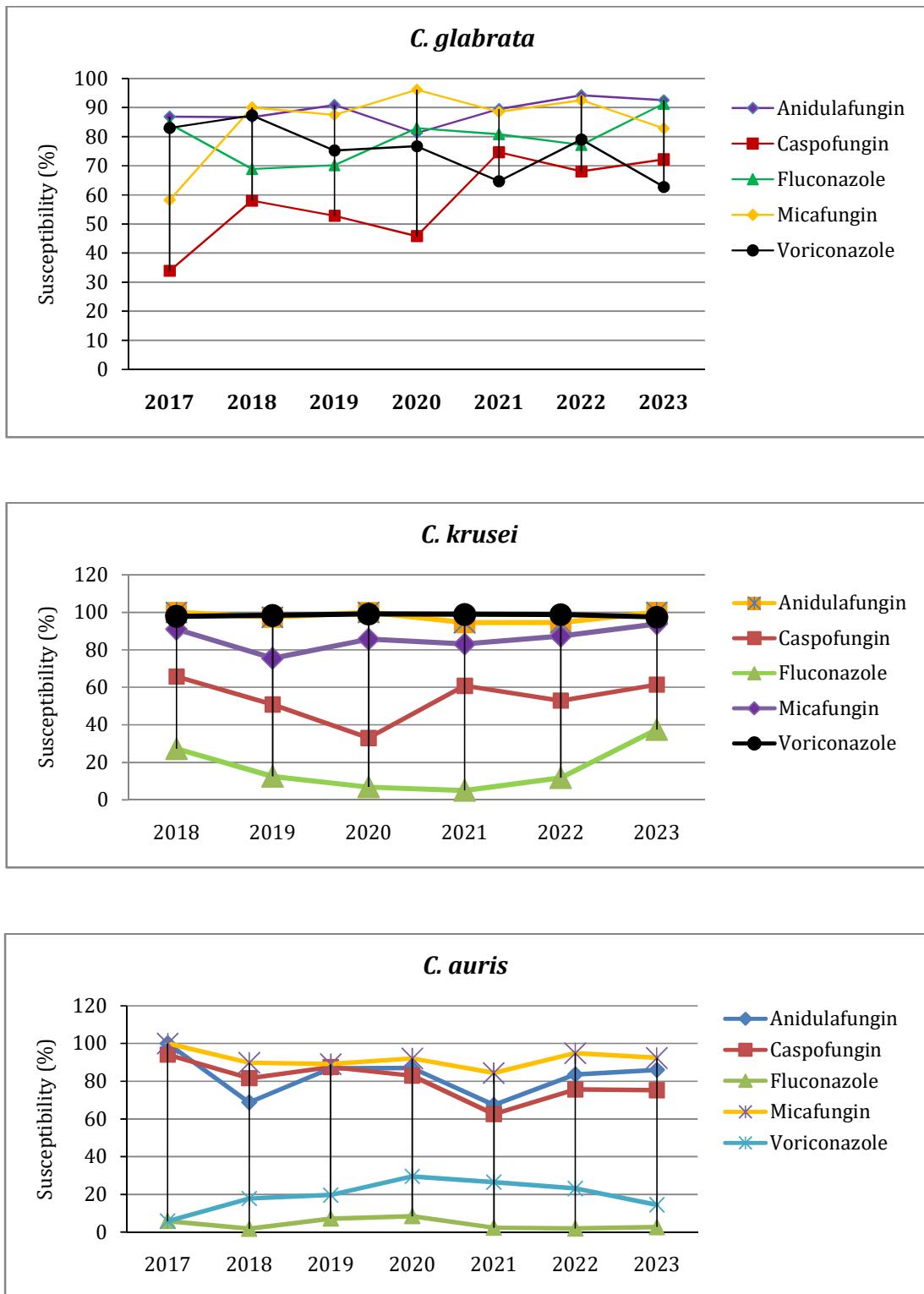


Figure 8.2: Susceptibility trends over the years in six major yeast species

Characterization of resistance mechanism

1. Phenotypic characterisation and molecular attributes of heteroresistance and tolerance to azole antifungals in *C. tropicalis*

A total of 1029 *C. tropicalis* isolates were screened for resistance by CLSI-BMD technique. 91 (8.84%) were resistant to at least one of the azoles, 922 (89.6%) were susceptible to all azoles and 16 (1.55%) were susceptible dose dependent to at least one of the azoles. Amongst the susceptible *C. tropicalis*, 38 (3.69%) were observed to exhibit trailing growth phenomenon. Among these 38 isolates, 100% showed trailing to fluconazole but only 39.47% (15/38) to voriconazole, 26.32% (10/38) to isavuconazole and 23.68% (9/38) to both itraconazole and posaconazole. 8 isolates showed trailing phenomena to all azoles. The zone diameters in millimeters were recorded for the isolates tested against sterile disks of fluconazole (25 µg, 50 µg, 100 µg) and voriconazole (1 µg, 2 µg, 4 µg). For the isolates that had micro colonies growing within the zone of inhibition, the disk diffusion for fluconazole (25 µg) was repeated for colonies both from within (marked as 'i') and outside (marked as 'o') the zone of inhibition. The susceptibility pattern was identical to that of the parental isolates for all of them, i.e., a similar zone diameter with reproduction of the micro colonies was observed in all the isolates.

Sanger sequencing for ERG11 gene was done to analyze for the presence of mutations in ERG11 gene. The sequences were aligned against the ERG11 gene sequence of *C. tropicalis* retrieved from NCBI with known mutations, Y132F and S154F. These mutations or any other non-synonymous mutations in ERG11 were absent in the isolates exhibiting trailing phenomenon. The results of population analysis profiling (PAP) were plotted as CFU/ml on y-axis against increasing drug concentrations on x-axis. To quantitate fluconazole heteroresistance, the area under curve (AUC) was normalized by taking an AUC-ratio (AUCR) calculated against the AUC of a well characterized *C. glabrata* 1646 heteroresistance reference strain (**Figure 8.3**). The trailing isolate (Tr3) yielded an AUCR of 0.857221 and the fluconazole susceptible strain CtS had an AUCR of 0.143392. Current CLSI guidelines do not focus on identifying the phenomena of drug tolerance and heteroresistance (both are subpopulation in a single colony of isogenic susceptible cells) strains. In our routine practice, these isolates (strains with MIC₅₀ below the cut-off but can grow up to a very high concentration of drug *in-vitro*) report as susceptible as per the current CLSI Antifungal Susceptibility Testing (AFST) guidelines. But these isolates pose a threat of developing a resistant phenotype gradually on antifungal exposure in a patient body leading to the treatment failure or persistence. This study records the incidence of heteroresistance/tolerance in *C. tropicalis* from a tertiary care center in India. After categorizing and identifying these heteroresistant and tolerant *C. tropicalis* isolates from true-resistant and susceptible strains, clinicians will be informed about their phenotypes to prevent the induction of resistance among those isolates.

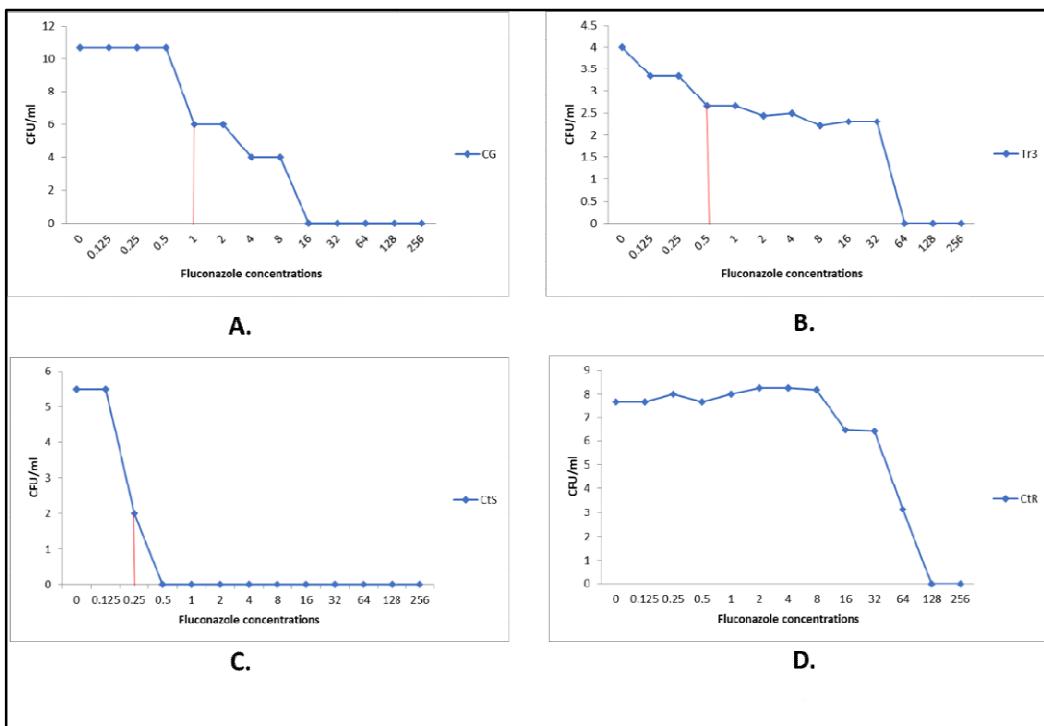


Figure 8.3. PAP assay of *C. glabrata* 1646 heteroresistance reference strain CG (3A), *C. tropicalis* trailing isolate Tr3 (3B), *C. tropicalis* susceptible isolate CtS (3C) and *C. tropicalis* resistant isolate CtR (3D) in RPMI-1640.

2. Antifungal resistance profile and dynamics of azole resistance of *Candida auris* in a large collection of clinical isolates over thirteen years period

596 *C. auris* isolates were screened where fluconazole had the highest resistance (~80%) and 43% isolates being above the fluconazole ECOFF (128 µg/ml). Amphotericin B had the second highest rate of resistance (~53%) with 7.4% of isolates being above the ECOFF (2 µg/ml). Voriconazole showed 28% of resistance with 11.5% isolates above the ECOFF (1 µg/ml). 12% of the total isolates were resistant to caspofungin and 36% of isolates had MIC beyond the ECOFF (0.5 µg/ml). Though as per CDC tentative cut off, none of the isolates were resistant to Posaconazole but 35.6% isolates had higher MIC beyond the ECOFF (0.125 µg/ml). Anidulafungin and micafungin had the least %resistance (1.1% and 1.5% respectively) whereas 14% and 4.7% of isolates had MICs beyond their ECOFFs (0.5 µg/ml for both).

The patterns of increase in antifungal resistance over the period of 13 years were analyzed. **Figure 8.4** represents the trendline of developing resistance for three classes of antifungals. Amphotericin B showed the R square value 0.9 which is almost near 1 and hence, denotes a steady rate of increase in amphotericin B resistance over time. Caspofungin had R square value 0.679 which is moderately considerable though a slow but increasing pattern is observed since 2017. Fluconazole had a constant resistance

rate over the time (R square value 0.00088). For mutation analysis, the respective gene sequences of 30 flu resistant and 15 flu susceptible isolates were aligned with the reference sequence of the CDC clade I type strain AR0387 by ClustalX2 and multiple sequence alignment was performed by using BioEdit software. In the *ERG11* gene two nonsynonymous mutations were noticed at 395 and 428 positions. No nonsynonymous SNP was noticed in three flu-susceptible isolates (wildtype). Out of the rest 12 flu-susceptible isolates, 11 isolates had A395T mutation, and one isolate showed A428G mutations. Out of 30 flu-resistant isolates, 17 isolates had A428G, and 13 isolates had A395T mutations. A total of 235 randomly selected *C. auris* isolates were submitted for STR genotyping. All isolates were allocated to clade I (South Asian clade) and 32 different genotypes were found, varying in three markers at most (**Figure 8.5**). When compared to 610 previously genotyped *C. auris* isolates from 20 countries, seven genotypes were previously found in other countries, mostly from India. Isolates were further analyzed based on the state of origin, year of isolation and antifungal susceptibility. Based on all these three variables, isolates did not cluster, with most genotypes consisting of isolates from multiple states, years and varying susceptibility.

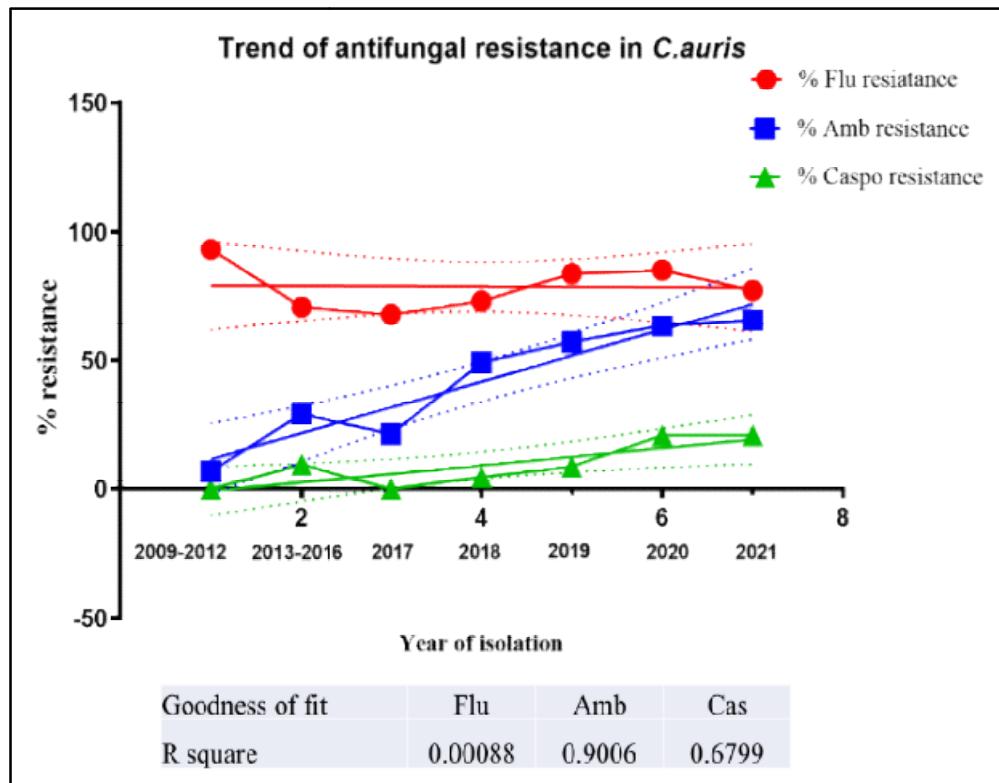


Figure 8.4: Trend analysis of drug resistance against three major antifungals in *C. auris*

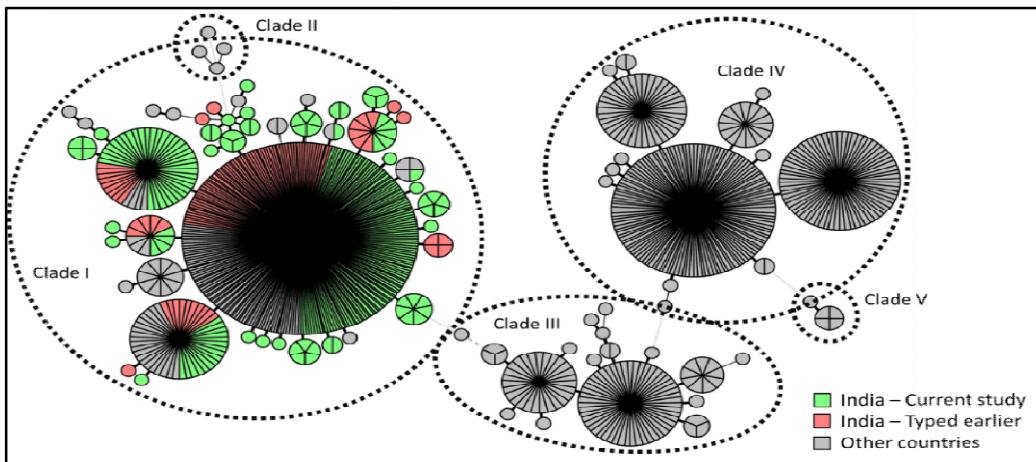


Figure 8.5: Minimum spanning tree of 845 *Candida auris* isolates, of which 235 were genotyped in the present study and compared to 610 previously published isolates.

Branch lengths indicate similarity between isolates, with thick solid lines (variation in one marker), thin solid lines (variation in two markers), thin dashed lines (variation in three markers), and thin dotted lines (variation in more four or more markers).

3. The genotypic diversity and molecular basis of fluconazole resistance in *Candida parapsilosis*

A total of 76 (13.3%) isolates exhibited reduced susceptibility to fluconazole, of which 48 (8.4%) were resistant ($\text{MIC} \geq 8 \mu\text{g/mL}$) while 28 (4.9%) isolates exhibited susceptible dose-dependent phenotype ($\text{MIC}, 4 \mu\text{g/mL}$). Among 48 fluconazole-resistant isolates, 6 (12.5%) were cross-resistant to voriconazole ($\text{MIC} \geq 1 \mu\text{G/mL}$), while 6 (12.5%) had MIC higher than the epidemiological cut off value for Amphotericin B ($\text{MIC } 1\mu\text{g/mL}$). Sequencing analysis of *ERG11* gene revealed three homozygous mutations K143R, Y132F mutation and R398I in fluconazole-resistant isolates. About 71.4% (20/28) of the fluconazole-resistant isolates exhibited K143R mutations. Among these isolates 35.7% (10/20) of the isolates showed amino acid substitution at K143R in combination with R398I. 17.85% (5/28) were wild type for *ERG11*. Only 10.7% (3/28) of the fluconazole resistant isolates carried amino acid substitution at Y132F in *ERG11* gene. Phylogenetic relatedness of 69 *C. parapsilosis* isolates was investigated using STR genotyping, resulting in the identification of 66 different genotypes (Figure 8.6). Three genotypes were shared by two isolates each, of which one genotype consisted of two fluconazole resistant isolates, while the others were susceptible. Furthermore, isolates 11 and 43, both harboring the K143R mutation in *ERG11*, were closely related showing a zygoty difference in one allele only. In the current study, only small clusters that shared the same fluconazole susceptibility and *ERG11* mutations clustered together.

Several isolates displayed closely related STR profiles while displaying a different *ERG11* phenotype and fluconazole MIC.

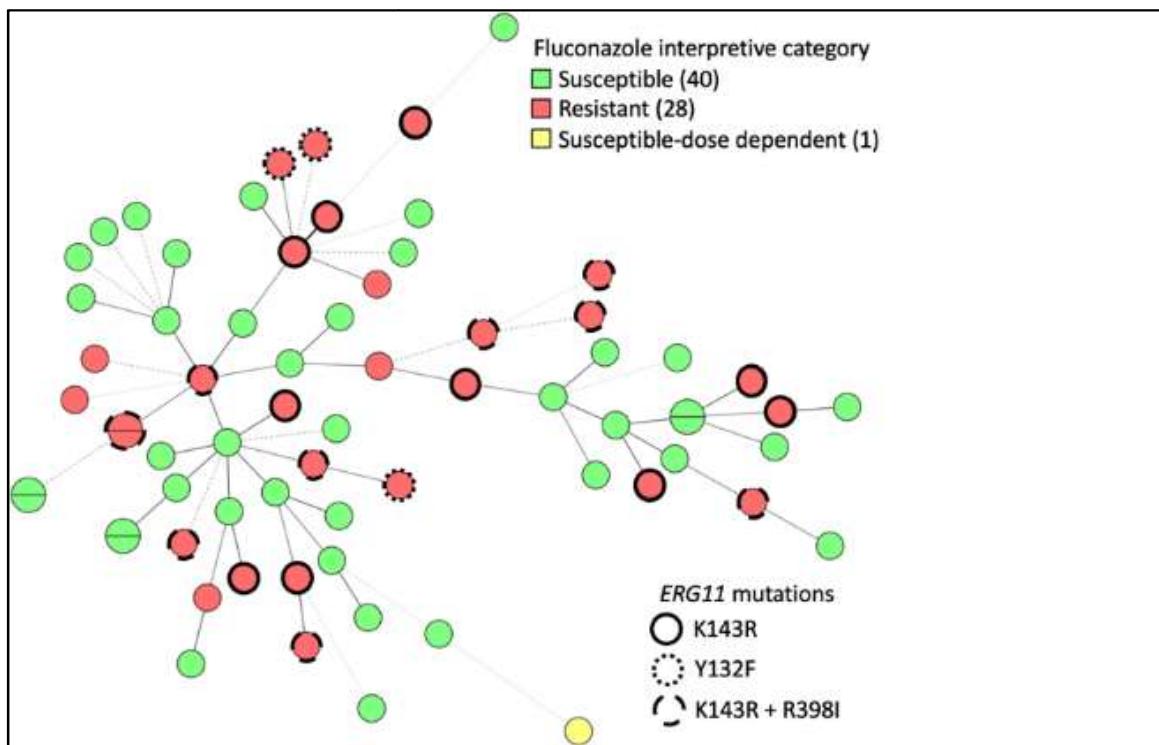


Figure 8.6: Minimum-spanning tree of 69 *Candida parapsilosis* isolates. Branch lengths indicate the similarity between isolates with thick solid lines (variation in one allele), thin solid lines (variation in two alleles), thin dashed lines (variation in three alleles), and thin dotted lines (variation in four or more alleles). Numbers per fluconazole interpretive category are shown in the color key and isolates ID are displayed next to each sample. Isolates without demarcation are *ERG11* wild type.

Clinical relevance and treatment guidance:

C. tropicalis and *C. albicans* were reported as leading candidemia agents as seen earlier, followed by *C. glabrata*. The isolation of *C. auris* was reasonably high. Resistance rate against echinocandins was low (<5%) for most of the species, making them the most suitable drugs for treatment. Among echinocandins, caspofungin susceptibility increased in *C. glabrata* (72% vs 68.1%) and *C. krusei* (61.5% vs 52.9%) compared to previous years. Micafungin showed slightly reduced susceptibility in *C. albicans* (92.5% vs 99%), *C. tropicalis* (93.5% vs 99%), and *C. auris* (92.4% vs 94.9%) this year. The slight decrease in susceptibility of voriconazole in *C. tropicalis*, *C. albicans*, *C. parapsilosis* and considerable decrease in *C. glabrata* is concerning. *C. auris* showed further decrease

in voriconazole susceptibility as compared to previous years (14.2% vs 23.1%). However, compared to previous years, higher voriconazole susceptibility was noticed in *C. tropicalis* (89% vs 56%) and *C. parapsilosis* (88.2% vs 86.7%). A constant decrease in fluconazole resistance in *C. parapsilosis* was noticed from previous years (12% vs. 17% and 22%). Among the moulds, higher amphotericin B resistance was observed compared to previous year in *Aspergillus flavus* (30.8% vs 12.17%) and *A. fumigatus* (51.13% vs 30.77%). The drug of choice, voriconazole, also depicted higher resistance in *A. fumigatus* compared to previous year (4.5% vs 1.1%).

As per the susceptibility patterns, echinocandins and fluconazole seem to be the best treatment option for *C. albicans* and *C. tropicalis* infections. Increased fluconazole was reported in *C. parapsilosis* spp. this year, hence, echinocandins can be recommended in the infections caused by these species. Declining susceptibility of *C. glabrata* to caspofungin, micafungin, fluconazole and voriconazole justifies anidulafungin as better treatment options against *C. glabrata* infections. Echinocandins (more specifically anidulafungin) and voriconazole are the suitable treatment choices for invasive infections due to *C. krusei*. *C. auris* infections with near complete resistance to azoles can be better treated with echinocandins as suggested by the antibiogram of the current report. The rise in amphotericin B and voriconazole resistance in *Aspergillus* species is quite concerning and needs to be investigated.

Chapter 9. *Streptococcus pneumoniae*

Serotype distribution and antimicrobial susceptibility profile of invasive and non-invasive *S. pneumoniae* in India for the year 2023

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

Serotype Distribution

A total of 149 invasive [Children below the age of 5 years (n= 37), adult and children above 5 years of age (n=112)] and 216 non-invasive [Children below the age of 5 years (n= 14), adult and children above 5 years of age (n= 202)]. *S. pneumoniae* isolated in the year 2023 were included in the analysis. The majority of the invasive isolates were from blood (n=131), followed by CSF (n=14) and sterile fluids (n=4). The serotype distribution among the invasive and non-invasive isolates of *S. pneumoniae* is depicted in **Figure 9.1 and Table 9.1**. PCV13 serotypes were the predominant ones, with serotype 14, 19F, 19A, and 6B being the major ones among the invasive isolates. Among the non-invasive, serotype 19F, 15B, 19A, 9V and 11A were the major serotypes. The other non-invasive serotypes were highly diverse.

Pneumosil (PCV10 Sii) percentage serotype coverage is 52 % and 44 % for invasive and the non-invasive serotypes, respectively. Among the serotypes not included in the Pneumosil (PCV10Sii), the serotype 4 constitutes 0.5 % and 2.0 % of the invasive and non-invasive serotypes. The serotype 18C constitutes 2.7 and 3.2 percentage of the invasive and non-invasive serotypes. Serotype 3 alone constitutes 10%, together of the invasive and non-invasive serotypes.

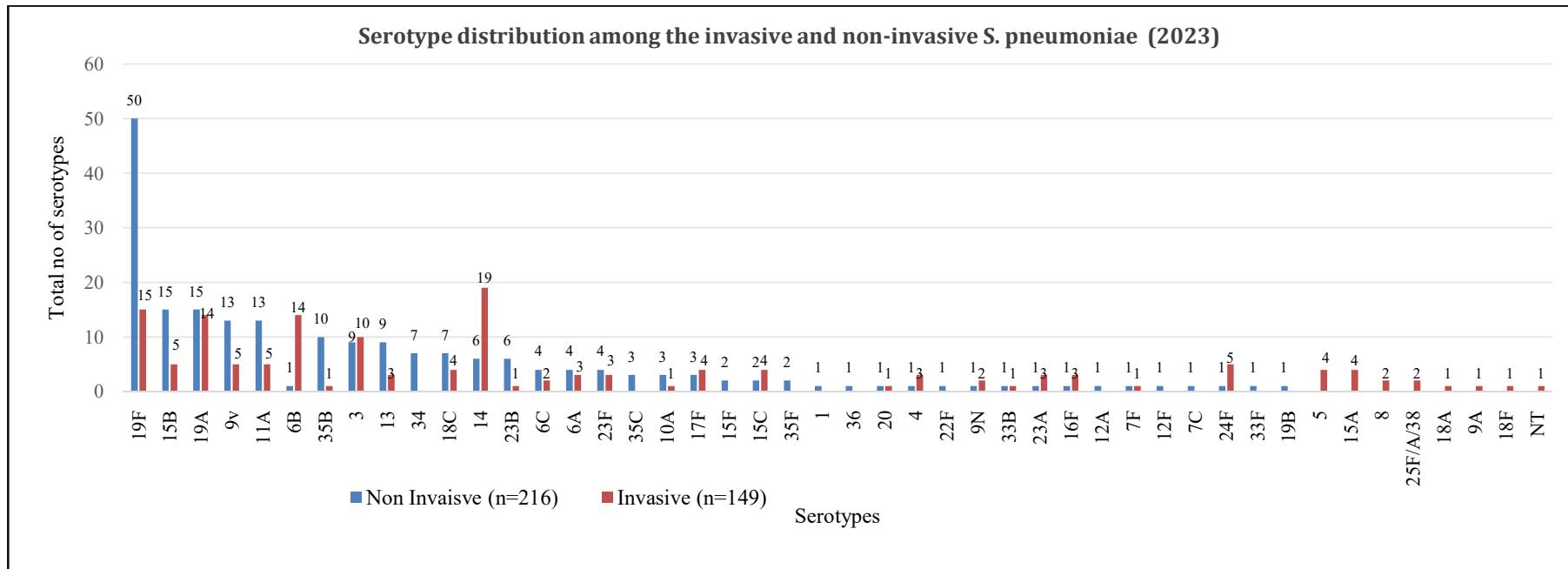


Figure 9.1: The serotype distribution of invasive (n=149) and non-invasive (n=216) isolates of *S. pneumoniae*. (NT indicates non typeable)

Table 9.1: The number of serotypes among the invasive and non-invasive isolates of *Streptococcus pneumoniae*

Serotype	Non Invasive (n=216)	Invasive (n=149)
19F	50	15
15B	15	5
19A	15	14
9v	13	5
11A	13	5
6B	1	14
35B	10	1
3	9	10
13	9	3
34	7	0
18C	7	4
14	6	19
23B	6	1
6C	4	2
6A	4	3
23F	4	3
35C	3	0
10A	3	1
17F	3	4
15F	2	0
15C	2	4
35F	2	0
20	1	1
4	1	3
5	0	4
9N	1	2
33B	1	1
23A	1	3
16F	1	3
7F	1	1
24F	1	5
15A	0	4
8	0	2
25F/A/38	0	2

One serotype each of 12A, NT, 12F, 7C, 33F, 22F, 1, 36 and 19B was seen among the non-invasive and serotypes 18A, 9A, 18F among the invasive specimens

Antimicrobial Susceptibility Profile

The penicillin and cefotaxime antimicrobial susceptibility percentage of invasive *S. pneumoniae* isolates were calculated based on meningeal or non-meningeal criteria (**Table 9.2 and Figure 9.2**). The penicillin and cefotaxime non susceptibility was high in meningeal isolates compared to the non-meningeal isolates. The antimicrobial susceptibility profile for atibiotics other than penicillin and cefotaxime is given (**Table 9.3 and Figure 9.3**). The antimicrobial susceptibility profile of non invasive isolates is depicted in **table 9.4** and **figure 9.4**.

Table 9.2: Number of *S. pneumoniae* invasive isolates susceptible to penicillin and cefotaxime

	Penicillin		Cefotaxime	
	Meningeal (n=11)	Non Meningeal (n=63)	Meningeal (n=11)	Non Meningeal (n=63)
<i>S.pneumoniae</i>	27.27%	98.41%	81.80%	100%
	(3/11)	(62/63)	(9/11)	(63/63)

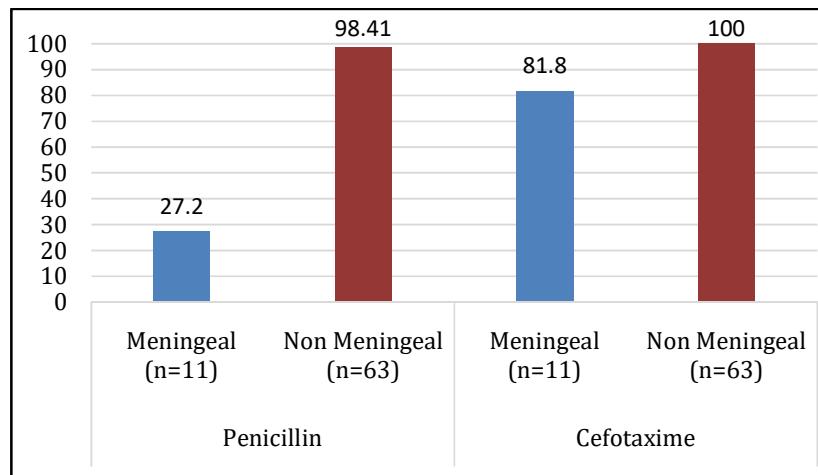


Figure 9.2: Penicillin and cefotaxime antimicrobial susceptibility of invasive isolates of *S. pneumoniae*

Table 9.3: Number of invasive *S. pneumoniae* isolates susceptible to Erythromycin, Levofloxacin, Linezolid, Vancomycin, Chloramphenicol, Cotrimoxazole

Antibiotics	Number of isolates susceptible, n=74(%)
Erythromycin	18(24.3)
Levofloxacin	71(95.9)
Linezolid	74(100)
Vancomycin	74(100)
Chloramphenicol	69 (93.2)
Cotrimoxazole	20(27)

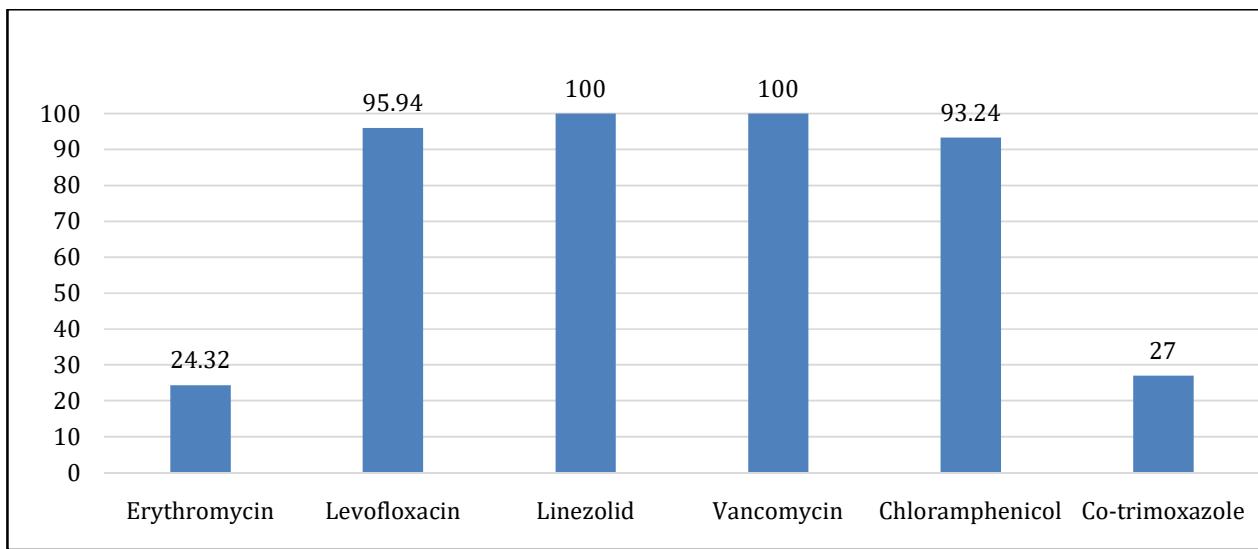


Figure 9.3: Antimicrobial susceptibility profile of invasive isolates of *S. pneumoniae* for antibiotics other than Penicillin and cefotaxime

Table 9.4: Number of non-invasive *S. pneumoniae* isolates susceptible to levofloxacin, Erythromycin and Penicillin

Antibiotics	No of susceptible isolates (%)
Penicillin(n=43)	41(95)
Erythromycin(n=86)	32(37)
Levofloxacin(n=90)	87 (96)

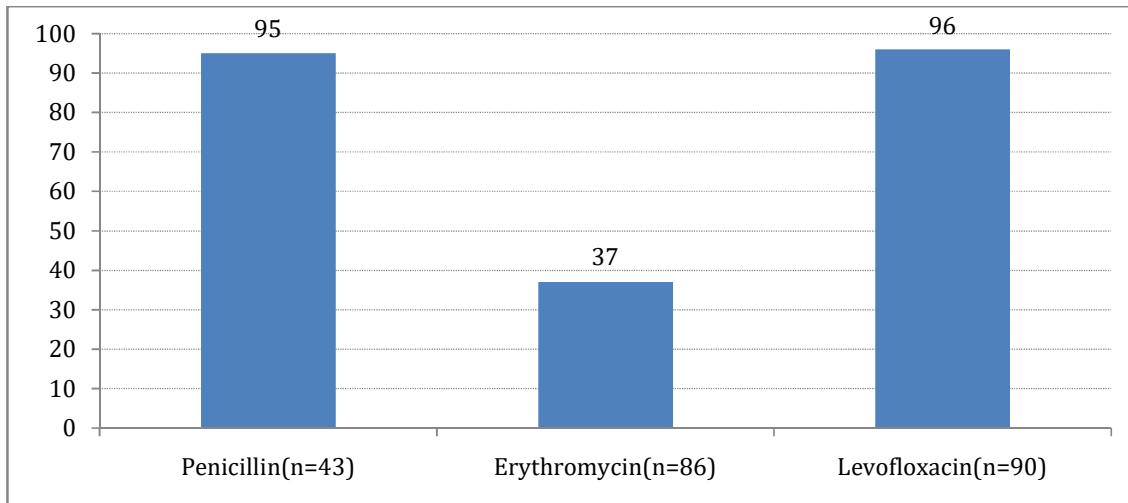


Figure 9.4: Antimicrobial Susceptibility profile of non-invasive *S.pneumoniae* isolates

Summary

Pneumosil (PCV10 Sii) percentage serotype coverage is 52% and 44% for invasive and the non-invasive serotypes, respectively. Compared to 2022, two serotypes (15B and 11A) has become predominant and has come under top five serotypes among the noninvasive isolates. The impact of replacement of PCV13 vaccine by Peumosil (Sii) has to be monitored since, serotype 4 and 18C is predominant in the non invasive group, and whereas serotype 3 is predominant among both the invasive and non-invasive serotypes. Together the serotypes 3, 4 and 18C constitute an additional 11% and 8 % in the invasive and non-invasive isolates. The antimicrobial non-susceptibility to penicillin and cefotaxime in meningeal isolates is decreasing gradually. Hence, monotherapy with either of these antibiotics is not recommended for meningeal infections.

Chapter 10. Health Care-Associated Infections

This chapter provides comprehensive details of bloodstream infections (BSIs), urinary tract infections (UTIs) and Ventilator associated pneumonia (VAP) reported from January 2023 to December 2023 from a network of 39 hospitals across India. The network hospitals in this report are part of the ICMR's AMR network and hospitals that have voluntarily joined the network. The methodology, standard operating procedures (SOPs) and training modules for healthcare-associated infection (HAI) surveillance are provided on our website www.haisindia.com. During the period from January 2023 to December 2023, a total of 103 intensive care units (ICUs) from the 39 centers reported HAI rates to our centralized database. Medical and Trauma ICUs accounted for 23.3% and 15.5% of the total ICUs in our network.

The cumulative patient days for the network for this period was 5,97,777. A total of 1,91,083 central line days and 3,33,850 urinary catheter days were reported during this period. A total of 3,815 episodes of BSIs and 1,110 episodes of UTIs were reported, accounting for the total BSI rate to be 6.38 per 1,000 patient days and the total UTI rate to be 1.86 per 1,000 patient days. A fatal outcome (14-day outcome) was reported in 35% of BSIs and 20.7% 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 patient's 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 73.6% of all BSI cases while 8.8% were due to fungal pathogens. For UTI, GNB accounted for 59.3% of cases. *Klebsiella* spp. (36.1%) was the most common GNB and *Enterococcus* spp. (51.3%) was the most common Gram-positive cocci (GPC) causing BSIs. 80% of *Klebsiella pneumoniae* and 91% of *Acinetobacter baumannii* causing BSIs were imipenem resistant. Nearly 63% of *Staphylococcus aureus* and around 42.7% 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 generation of quality assured HAI data and to assess 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 till 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 10.1**.

Table 10.1: Distribution of ICUs in the network

Name of ICU	Number (%)
Medical ICU	24 (23.3)
Trauma ICU	16 (15.5)
Pediatric Medical ICU	11 (10.7)
Surgical ICU	11 (10.7)
Neurosurgical ICU	7 (6.8)
Medical/Surgical ICU	6 (5.8)
Neonatal ICU	5 (4.9)
High Dependency Unit	4 (3.9)
Pediatric Medical/Surgical ICU	4 (3.9)
Gastrointestinal ICU	3 (2.9)
Anesthesia ICU	3 (2.9)
Cardiothoracic Surgical ICU	2 (1.9)
Respiratory ICU	2 (1.9)
Neurologic ICU	2 (1.9)
Cardiac ICU	1 (1.0)
Oncologic Medical ICU	1 (1.0)
Oncologic Surgical ICU	1 (1.0)
Total	103

This surveillance focused on BSIs (Primary and Secondary BSIs) and UTIs (Catheter associated and non-catheter associated). Blood and urine cultures were taken into consideration for fulfilling the surveillance definitions (www.haisindia.com). The distribution of organisms from blood and urine cultures is shown in **table 10.2**. *Enterobacteriales* were the most common, followed by NF-GNBs. The denominators for calculation of HAI rates during this period are shown in **table 10.3**.

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

Isolate	Culture positive					
	Total (N=5492)		Blood (N= 4287)		Urine (N=1205)	
	N	%	N	%	N	%
<i>Enterobacteriales</i>	2,056	37.4	1,561	36.4	495	41.1
<i>NF-GNB</i>	1,667	30.3	1,468	34.2	199	16.5
<i>Enterococci</i>	613	11.1	387	9.0	226	18.8
<i>Candida spp.</i>	628	11.4	378	8.8	250	20.7
<i>Staphylococci</i>	355	6.5	349	8.1	6	0.5
Others	174	3.2	145	3.4	29	2.4

Table 10.3: Denominator Data

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

Network level BSI data

A total of 3,815 cases of BSIs were reported by the network. The distribution (types) of BSI cases is shown in **table 10.4**.

Table 10.4: Types of BSI cases

Type of BSI cases	No. of BSI cases (%)
CLABSI	1,586 (41.6)
Non-CLABSI	1,666 (43.7)
Secondary BSI	563 (14.7)
Total	3,815

The total BSI rate in our network was 6.4/1,000 patient days, with the CLABSI rate being 8.3/ 1,000 central line days. The rates of BSIs, Primary BSIs, CLABSI and Secondary BSIs are shown in **table 10.5**. The trend of BSI rates in the surveillance network for three years (2021-2023) is depicted in **Figure 10.1**. 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 10.6** compares the rates of BSIs across the

different ICU types in our network. Of the 3,815 cases of BSIs, males accounted for 64.7%, as shown in **table 10.7**. However, no interpretation can be made from this data. It may reflect a higher admission rate in the ICUs.

Table 10.5: BSI rates

Indicator	Rates
Total BSI rate (per 1,000 patient days)	6.4
Primary BSI rate (per 1,000 patient days)	5.4
CLABSI rate (per 1,000 central line days)	8.3
Secondary BSI rate (per 1,000 patient days)	0.9

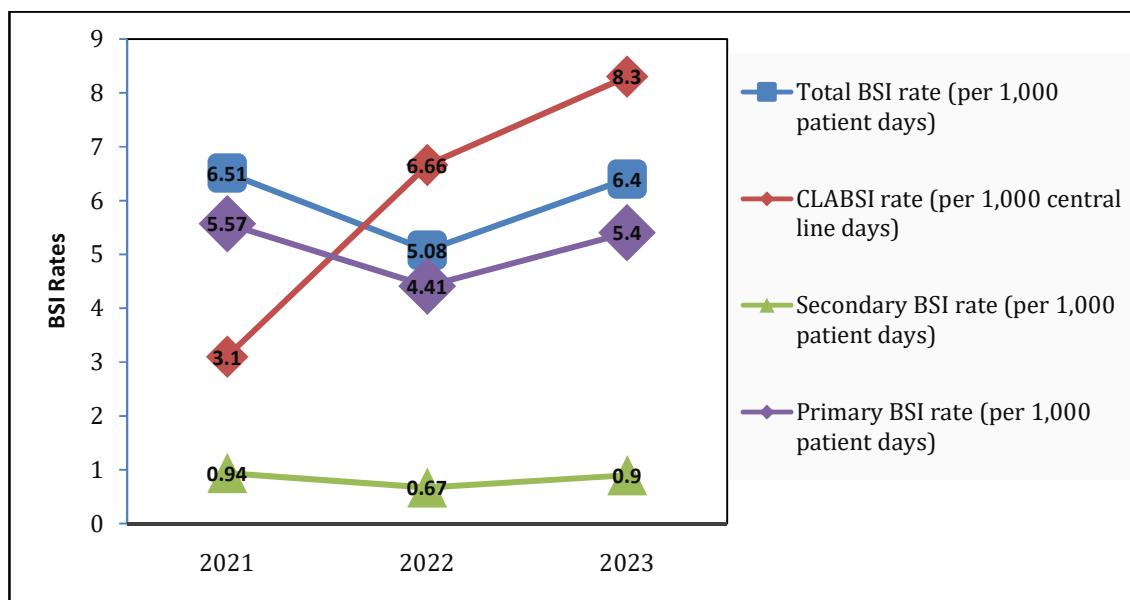


Figure 10.1: Trend of BSI rates in the surveillance network of Indian hospitals over three years (2021-2023).

Table 10.6: Distribution of BSI cases by ICUs

Types of ICUs	No. of BSI cases (Percentage)	Total BSI rate (per 1,000 patient days)
Neonatal ICU	1,030 (27)	9.4
Medical ICU	949 (24.9)	7.9
Medical/Surgical ICU	462 (12.1)	6.7
Trauma ICU	418 (11)	11.2
Surgical ICU	214 (5.6)	8.2
Pediatric ICU	178 (4.7)	3.8
Gastrointestinal ICU	126 (3.3)	13.7
Anaesthesia ICU	123 (3.2)	8.2
High Dependency Unit	71 (1.9)	3.9
Pediatric Medical/Surgical ICU	66 (1.7)	2.5
Neuro Surgery ICU	44 (1.2)	5.1
Respiratory ICU	39 (1)	6.6
Neurologic ICU	37 (1)	9.4
Oncologic Medical ICU	21 (0.6)	6.8
Oncologic Surgical ICU	18 (0.5)	6.3
Cardiothoracic ICU	12 (0.3)	2.3
Cardiac ICU	7 (0.2)	0.9
Total	3,815	6.4

Table 10.7: Distribution of BSI cases by gender and age

Gender	No. of BSI cases (%)
Males	2,468 (64.7)
Females	1,347 (35.3)
Total	3,815

	Median (Years)	Range (Years)
Age of males	31	0–95
Age of females	26	0–93

Table 10.8 shows the duration of stay in the ICUs and the duration between ICU admission and the development of BSI. 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 35%. 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 12% of BSI cases were discharged in 14 days. Table 10.9 shows the short-term outcomes of BSI cases. A total of 4,287 pathogens were isolated from the BSI cases. Gram-negative organisms predominated as the cause of BSIs in our network, as shown in **table 10.10** and **figure 10.2**. The genus level distribution in Gram-negative and Gram-positive organisms and species distribution of *Candida* causing overall BSIs is shown in **tables 10.11-10.13**. *Enterococcus* spp. was the most common Gram-positive organism; *Klebsiella* spp. was the most common Gram-negative organism and *Candida tropicalis* was the most common fungal pathogen.

Table 10.8: Median and range of ICU stay for BSI cases

	Median (Days)	Range (Days)
Duration of stay in the unit	19	3-424
Duration between date of admission and date of event	7	3- 219

Table 10.9: Outcomes of BSIs

14-day outcome	No. of BSI cases (%)
Died	1,335 (35.0)
Still in surveillance unit	1,121 (29.4)
Transferred to other ward/unit within same hospital	597 (15.60)
Discharged	456 (11.9)
LAMA	253 (6.6)
Transferred to other hospitals	49 (1.3)
Unknown	4 (0.1)
Total	3,815

Table 10.10: Distribution of organisms causing BSIs

S.No.	Type of organisms	Number (%)
1	Gram-negative organisms	3,154 (73.6)
2	Gram-positive organisms	754 (17.6)
3	Fungal pathogens	379 (8.8)
Total		4,287

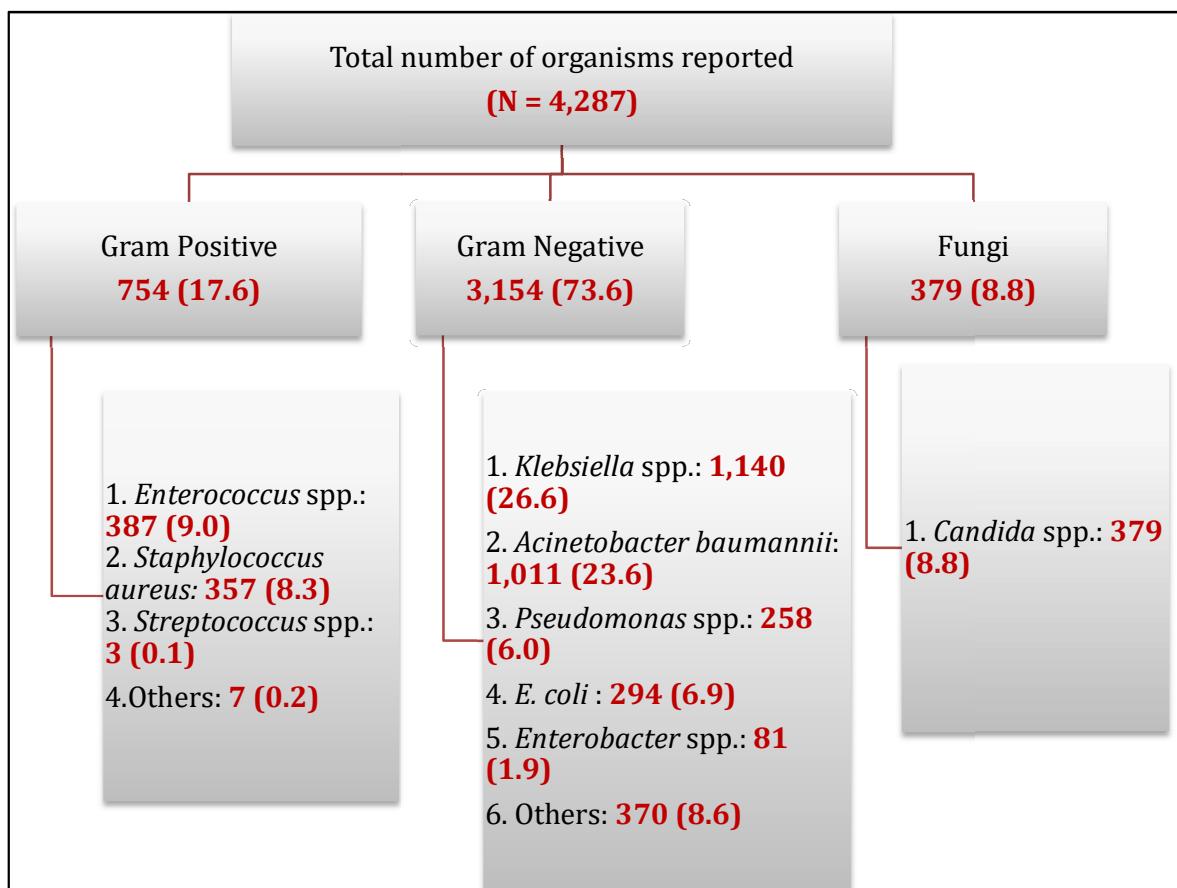


Figure 10.2: Distribution of organisms causing BSIs

Table 10.11: Distribution of Gram-positive organisms causing BSIs (Total BSIs)

S.No.	Name of organism	Number (%)
1	<i>Enterococcus</i> spp.	387 (9.0)
2	<i>Staphylococcus aureus</i>	357 (8.3)
3	<i>Streptococcus</i> spp.	3 (0.1)
4	Others	7 (0.2)
Total Gram-positive organisms		754 (17.6)

Table 10.12: Distribution of Gram-negative organisms causing BSI (Genus level)

S. No.	Name of organism	Number (%)
1	<i>Klebsiella</i> spp.	1,140 (26.6)
2	<i>Acinetobacter</i> spp.	1,011 (23.6)
3	<i>Escherichia coli</i>	294 (6.9)
4	<i>Pseudomonas</i> spp.	258 (6.0)
5	<i>Burkholderia</i> spp.	119 (2.8)
6	<i>Enterobacter</i> spp.	81 (1.9)
7	<i>Stenotrophomonas</i> spp.	57 (1.3)
8	<i>Serratia</i> spp.	49 (1.1)
9	<i>Elizabethkingia</i> spp.	25 (0.6)
10	<i>Proteus</i> spp.	19 (0.4)
11	<i>Citrobacter</i> spp.	18 (0.4)
12	<i>Ralstonia</i> spp.	18 (0.4)
13	<i>Chryseobacterium</i> spp.	16 (0.4)
14	<i>Achromobacter</i> spp.	15 (0.3)
15	Others	34 (0.8)
Total Gram-negative organisms		3,154 (73.6)

Table 10.13: Distribution of *Candida* species causing BSIs

S. No.	Name of organism	Number (%)
1	<i>Candida tropicalis</i>	134 (3.1)
2	<i>Candida parapsilosis</i>	67 (1.6)
3	<i>Candida albicans</i>	66 (1.5)
4	<i>Candida auris</i>	38 (0.9)
5	<i>Candida</i> spp.	23 (0.5)
6	<i>Candida glabrata</i>	21 (0.5)
7	<i>Candida krusei</i>	7 (0.2)
8	<i>Candida utilis</i>	7 (0.2)
9	<i>Candida guilliermondii</i>	6 (0.1)
10	<i>Candida pelliculosa</i>	4 (0.1)
11	<i>Candida rugosa</i>	4 (0.1)
12	<i>Candida metapsilosis</i>	1 (0.02)
13	<i>Candida non-albicans</i>	1 (0.02)
Total		379 (8.8)

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 10.14** shows the locations of central lines in our surveillance data. Even in CLABSIs, Gram-negative pathogens predominated over Gram-positive (**Table 10.15**). A high proportion of CLABSIs were caused due to *Candida* species in our network. The distribution of Gram-positive, Gram-negative and *Candida* species causing CLABSIs is shown in **tables 10.16-10.18**.

Table 10.14: Location of central lines

Location of central line	No. of CLABSI cases (%)
Jugular	1,366 (35.8)
Subclavian	425 (11.1)
Umbilical	299 (7.8)
Brachial	17 (0.4)
Femoral	192 (5.0)
Other	53 (1.4)
Total	2,352

*Multiple central lines possible in a single patient

Table 10.15: Distribution of organisms causing CLABSIs

S. No.	Name of organism	Number (%)
1	Gram-positive organisms	320 (16.8)
2	Gram-negative organisms	1,357 (71.2)
3	Fungal pathogens	229 (12.0)
Total organisms		1,906

Table 10.16: Distribution of Gram-positive organisms causing CLABSIs

S. No.	Name of organism	Number (%)
1	<i>Enterococcus</i> spp.	197 (10.3)
2	<i>Staphylococcus aureus</i>	116 (6.1)
3	Others	7 (0.4)
Total Gram-positive organisms		320 (16.8)

Table 10.17: Distribution of Gram-negative organisms causing CLABSIs (Genus level)

S. No.	Name of organism	Number (%)
1	<i>Klebsiella</i> spp.	472 (24.8)
2	<i>Acinetobacter</i> spp.	394 (20.7)
3	<i>Pseudomonas</i> spp.	109 (5.7)
4	<i>Escherichia coli</i>	105 (5.5)
5	<i>Burkholderia</i> spp.	83 (4.4)
6	<i>Enterobacter</i> spp.	43 (2.3)
7	<i>Stenotrophomonas</i> spp.	32 (1.7)
8	<i>Serratia</i> spp.	30 (1.6)
9	<i>Elizabethkingia</i> spp.	22 (1.2)
10	<i>Ralstonia</i> spp.	16 (0.8)
11	<i>Achromobacter</i> spp.	11 (0.6)
12	<i>Chryseobacterium</i> spp.	11 (0.6)
13	Others	29 (1.5)
Total Gram-negative organisms		1,357 (71.2)

Table 10.18: Distribution of *Candida* species causing CLABSIs

S. No.	Name of organism	Number (%)
1	<i>Candida tropicalis</i>	76 (4.0)
2	<i>Candida parapsilosis</i>	45 (2.4)
3	<i>Candida albicans</i>	39 (2.0)
4	<i>Candida auris</i>	31 (1.6)
5	<i>Candida</i> spp.	14 (0.7)
6	<i>Candida glabrata</i>	9 (0.5)
7	<i>Candida krusei</i>	5 (0.3)
8	<i>Candida guilliermondii</i>	3 (0.2)
9	<i>Candida pelliculosa</i>	3 (0.2)
10	<i>Candida rugosa</i>	3 (0.2)
11	<i>Candida metapsilosis</i>	1 (0.1)
Total		229 (12.0)

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 \geq two calendar days. The organism distribution of Non- CLABSI Primary BSIs is shown in **tables 10.19-10.22**.

Table 10.19: Distribution of organisms causing Non-CLABSI Primary BSIs

S.No.	Name of organism	Number (%)
1	Gram-positive organisms	409 (22.6)
2	Gram-negative organisms	1,268 (70.1)
3	Fungi	132 (7.3)
	Total	1,809

Table 10.20: Distribution of gram-positive organisms causing Non-CLABSI Primary BSIs

S. No.	Name of organism	Number (%)
1	<i>Staphylococcus aureus</i>	229 (12.7)
2	<i>Enterococcus</i> spp.	177 (9.8)
3	Others	3 (0.2)
	Total Gram-positive organisms	409 (22.6)

Table 10.21: Distribution of Gram-negative organisms causing Non-CLABSI Primary BSIs (Genus level)

S. No.	Name of organism	Number (%)
1	<i>Klebsiella</i> spp.	470 (26.0)
2	<i>Acinetobacter</i> spp.	382 (21.1)
3	<i>Escherichia coli</i>	153 (8.5)
4	<i>Pseudomonas</i> spp.	111 (6.1)
5	<i>Enterobacter</i> spp.	37 (2.0)
6	<i>Burkholderia</i> spp.	32 (1.8)
7	<i>Stenotrophomonas</i> spp.	23 (1.3)
8	<i>Citrobacter</i> spp.	13 (0.7)
9	<i>Serratia</i> spp.	11 (0.6)
10	Others	36 (2.0)
	Total Gram-negative organisms	1,268 (70.1)

Table 10.22: Distribution of *Candida* species causing Non-CLABSI Primary BSIs

S. No.	Name of organism	Number (%)
1	<i>Candida tropicalis</i>	51 (2.8)
2	<i>Candida albicans</i>	25 (1.4)
3	<i>Candida parapsilosis</i>	22 (1.2)
4	<i>Candida glabrata</i>	9 (0.5)
5	<i>Candida</i> spp.	7 (0.4)
6	<i>Candida utilis</i>	7 (0.4)
7	<i>Candida auris</i>	3 (0.2)
8	<i>Candida guilliermondii</i>	3 (0.2)
9	<i>Candida krusei</i>	2 (0.1)
10	<i>Candida non albicans</i>	1 (0.1)
11	<i>Candida pelliculosa</i>	1 (0.1)
12	<i>Candida rugosa</i>	1 (0.1)
Total <i>Candida</i> sp.		132 (7.3)

Data of Secondary BSIs

Secondary BSIs are those cases of BSIs in which a source of infection is found at some other body site and bacteremia is secondary to a primary source. The organism distribution in cases of secondary BSIs is shown in **tables 10.23-10.26**.

Table 10.23: Distribution of organisms causing Secondary BSI

S. No.	Name of organism	Number (%)
1	Gram-positive organisms	25 (4.4)
2	Gram-negative organisms	529 (92.5)
3	<i>Candida</i> spp.	18 (3.1)
Total		572

Table 10.24: Distribution of Gram-positive organisms causing Secondary BSI

S.No.	Name of organism	Number (%)
1	<i>Staphylococcus</i> spp.	12 (2.1)
2	<i>Enterococcus</i> spp.	13 (2.3)
Total Gram-positive organisms		25 (4.4)

Table 10.25: Distribution of Gram-negative organisms causing Secondary BSIs (Genus level)

S. No.	Name of organism	Number (%)
1	<i>Acinetobacter</i> spp.	235 (41.1)
2	<i>Klebsiella</i> spp.	198 (34.6)
3	<i>Pseudomonas</i> spp.	38 (6.6)
4	<i>Escherichia coli</i>	36 (6.3)
5	<i>Serratia</i> spp.	8 (1.4)
6	<i>Burkholderia</i> spp.	4 (0.7)
7	<i>Proteus</i> spp.	4 (0.7)
8	Others	6 (1.0)
Total Gram-negative organisms		529 (92.5)

Table 10.26: Distribution of *Candida* species causing Secondary BSIs

S. No.	Name of organism	Number (%)
1	<i>Candida tropicalis</i>	7 (1.2)
2	<i>Candida auris</i>	4 (0.7)
3	<i>Candida glabrata</i>	3 (0.5)
4	<i>Candida albicans</i>	2 (0.3)
5	<i>Candida</i> spp.	2 (0.3)
Total		18 (3.1)

AMS profile in isolates causing BSIs

A high rate of resistance was seen against third-generation cephalosporins, carbapenems, fluoroquinolones and aminoglycosides in *Klebsiella pneumoniae*, *Escherichia coli* and *Acinetobacter baumannii* causing BSIs. The rate of resistance in *Pseudomonas aeruginosa* was less as compared to these. Minocycline and Tigecycline appear to be a promising alternative in *Klebsiella* and *Acinetobacter* spp. (**Table 10.27**). Almost 40% strains of *Enterococcus faecium* causing BSIs were vancomycin-resistant (**Table 10.28**) and nearly 64% strains of *Staphylococcus aureus* were resistant to oxacillin (**Table 10.29**). AMS profile of organisms causing BSI over three years (2021-2023) is shown (**Figure 10.3 and 10.4**).

Table 10.27: Antimicrobial susceptibility (AMS) pattern for Gram-negative organisms causing BSIs in HAI surveillance network, 2023

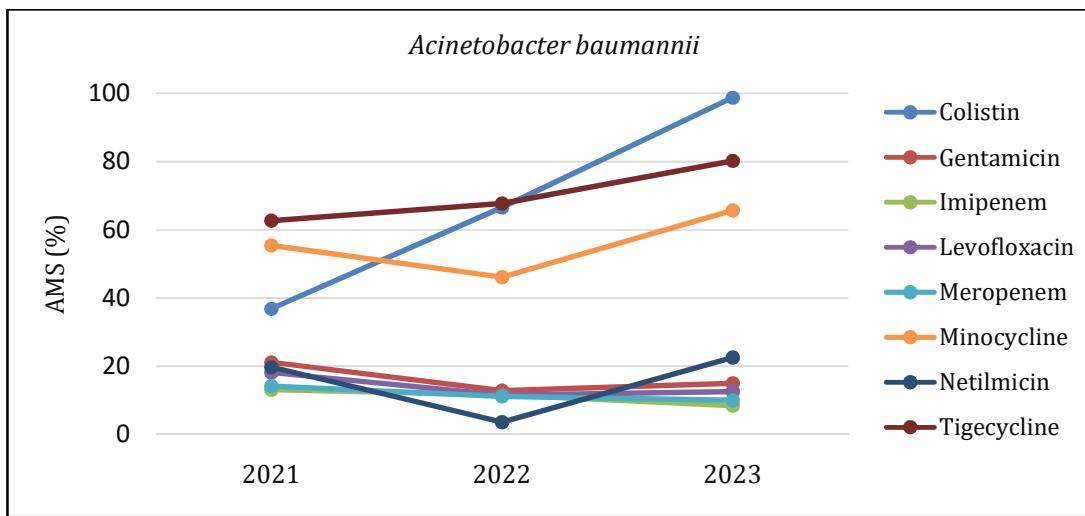
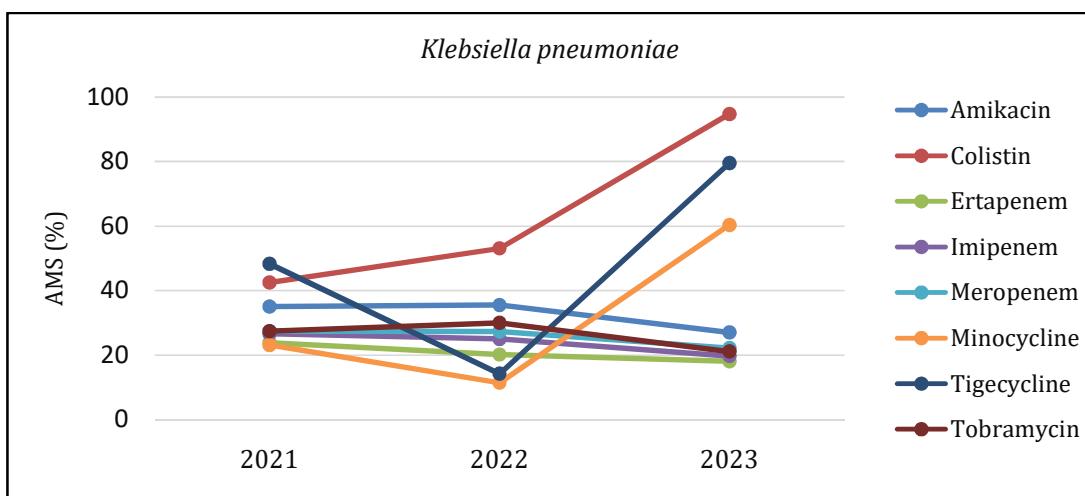
Antibiotics	<i>Klebsiella pneumoniae</i> (N = 1,054)	<i>Escherichia coli</i> (N = 294)	<i>Acinetobacter baumannii</i> (N = 895)	<i>Pseudomonas aeruginosa</i> (N = 194)
	% S	% S	% S	% S
Amoxicillin-Clavulanate	36/465 (7.7)	9/121 (7.4)	3/26 (11.5)	1/7
Amikacin	265/982 (27.0)	150/279 (53.8)	106/820 (12.9)	76/148 (51.3)
Ampicillin	3/136 (1.5)	11/133 (8.3)	2/32 (6.3)	-
Cefazolin	15/447 (3.4)	8/126 (6.4)	-	1/8
Cefepime	111/969 (11.4)	54/260 (20.8)	65/720 (9.0)	73/178 (41.0)
Cefotaxime	42/491 (8.5)	16/141 (11.4)	20/283 (7.1)	2/2
Ceftazidime	50/415 (12.1)	10/109 (9.2)	59/784 (7.5)	75/174 (43.1)
Ceftriaxone	66/814 (8.1)	25/203 (12.3)	20/252 (7.9)	6/13
Ciprofloxacin	142/952 (14.9)	42/269 (15.6)	94/802 (11.7)	87/179 (48.6)
Colistin	547/577 (94.8)	131/131 (100)	569/576 (98.8)	89/94 (94.7)
Ertapenem	123/679 (18.1)	68/179 (38.0)	2/26 (7.7)	-
Gentamicin	284/942 (30.1)	127/256 (49.6)	111/738 (15.0)	51/108 (47.2)
Imipenem	191/968 (19.7)	103/272 (37.9)	71/832 (8.5)	73/181 (40.3)
Levofloxacin	104/502 (20.7)	35/133 (26.3)	72/573 (12.6)	53/143 (37.1)
Meropenem	222/1,001 (22.2)	120/277 (43.3)	85/845 (10.1)	79/179 (44.1)
Minocycline	183/303 (60.4)	42/75 (56.0)	412/627 (65.7)	4/9
Netilmicin	7/81 (8.6)	9/9	12/53 (22.6)	12/32 (37.5)
Piperacillin	-	-	11/146 (7.5)	16/38 (42.1)
Tetracycline	124/223 (55.6)	13/42 (30.1)	37/169 (21.9)	-
Tigecycline	109/137 (79.6)	33/38 (86.8)	61/76 (80.3)	-
Tobramycin	56/266 (21.1)	24/53 (45.3)	65/364 (17.9)	44/94 (46.8)

Table 10.28: AMS pattern for *Enterococcus* species causing BSI, 2023

Antibiotics	<i>Enterococcus faecalis</i> (N = 96)	<i>Enterococcus faecium</i> (N = 246)	<i>Enterococcus</i> spp. (N = 41)
	% S	% S	% S
Ampicillin	41/74 (55.4)	13/151 (8.6)	14/34 (41.2)
Ciprofloxacin	18/70 (25.7)	8/159 (5.0)	14/30 (46.7)
Gentamicin	2/5	2/4	-
Linezolid	59/65 (90.8)	175/208 (84.1)	33/34 (97.1)
Teicoplanin	64/73 (87.7)	111/204 (54.4)	14/21 (66.7)
Vancomycin	78/92 (84.8)	137/239 (57.3)	29/38 (76.3)
Tetracycline	16/42 (38.1)	13/104 (12.5)	4/10

Table 10.29: AMS pattern for *Staphylococcus aureus* causing BSIs, 2023

Antibiotics	<i>Staphylococcus aureus</i> (N = 219)	
	% S	
Erythromycin	38/189 (20.1)	
Ciprofloxacin	77/174 (44.2)	
Oxacillin	24/64 (37.5)	
Clindamycin	84/181 (46.4)	
Trimethoprim/Sulfamethoxazole	99/133 (74.4)	
Tetracycline	51/65 (78.5)	
Teicoplanin	57/60 (95.0)	
Linezolid	161/162 (99.4)	
Vancomycin	92/92 (100)	



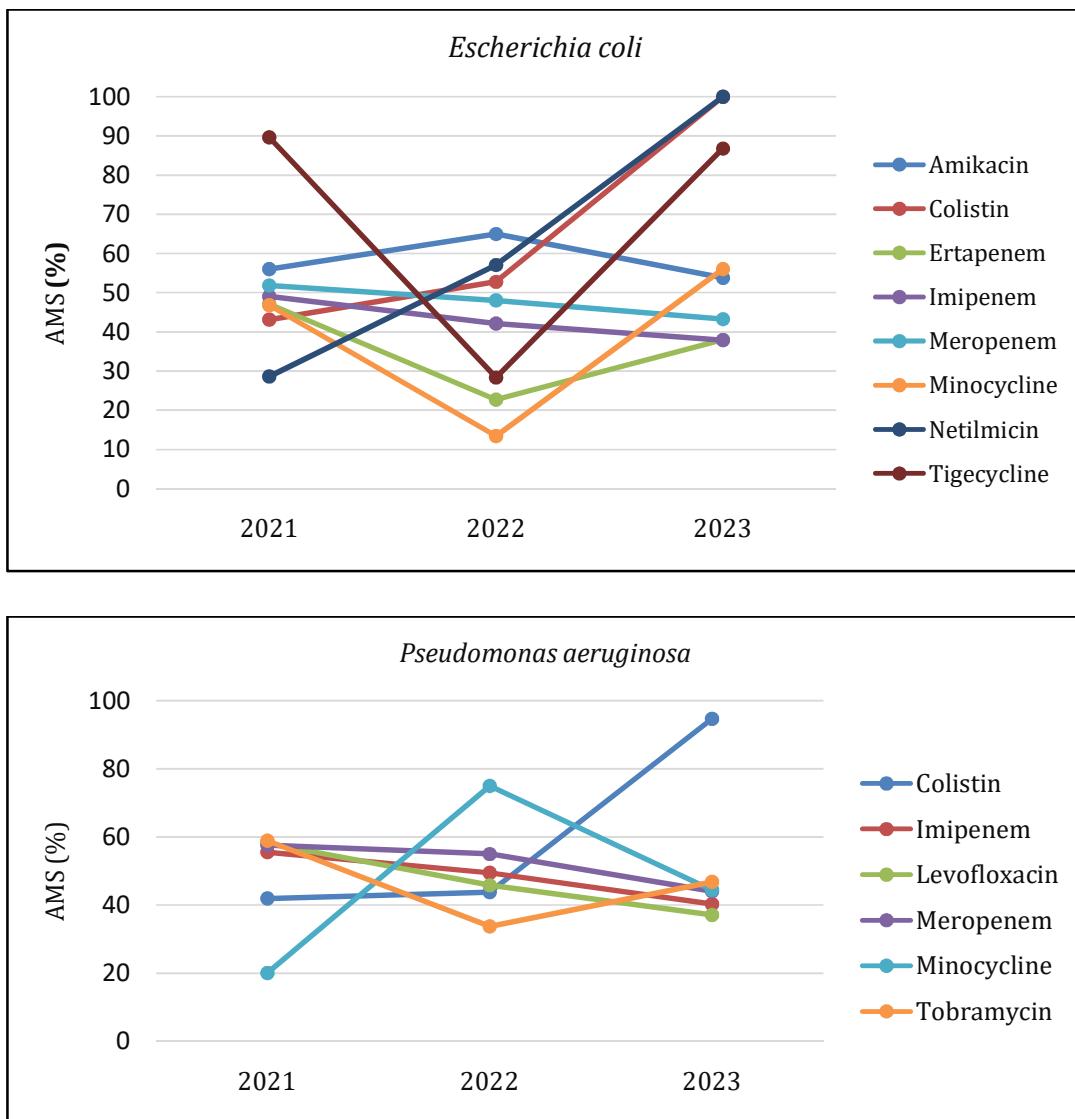
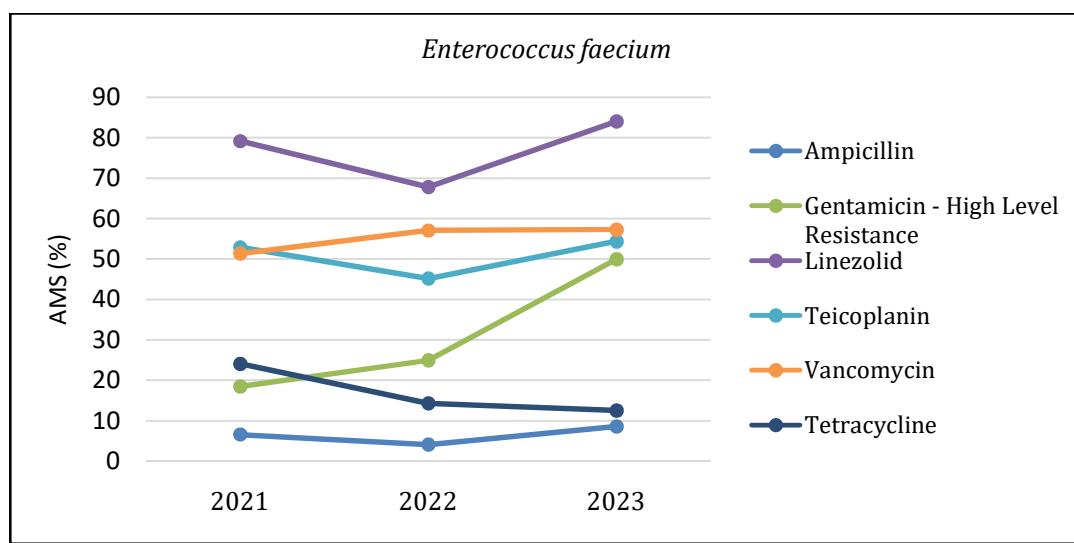
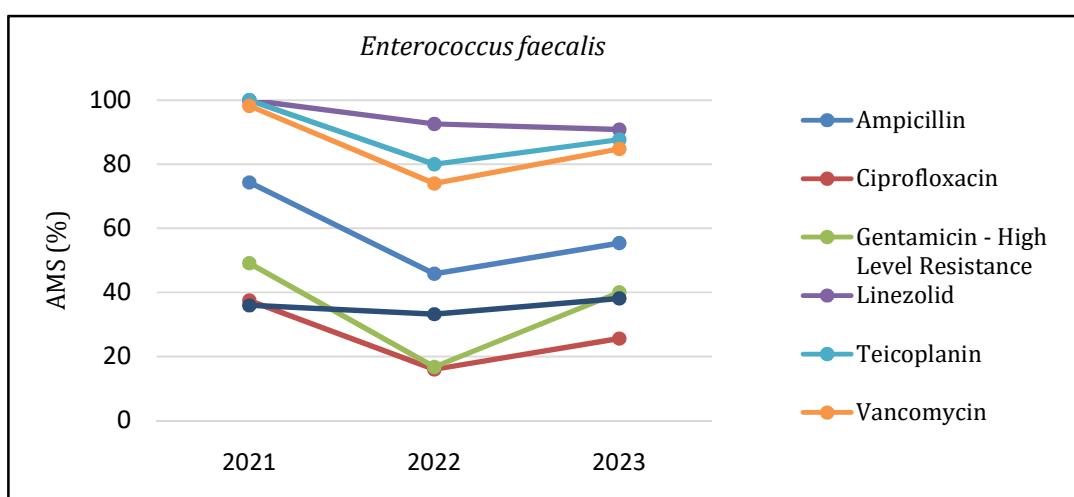
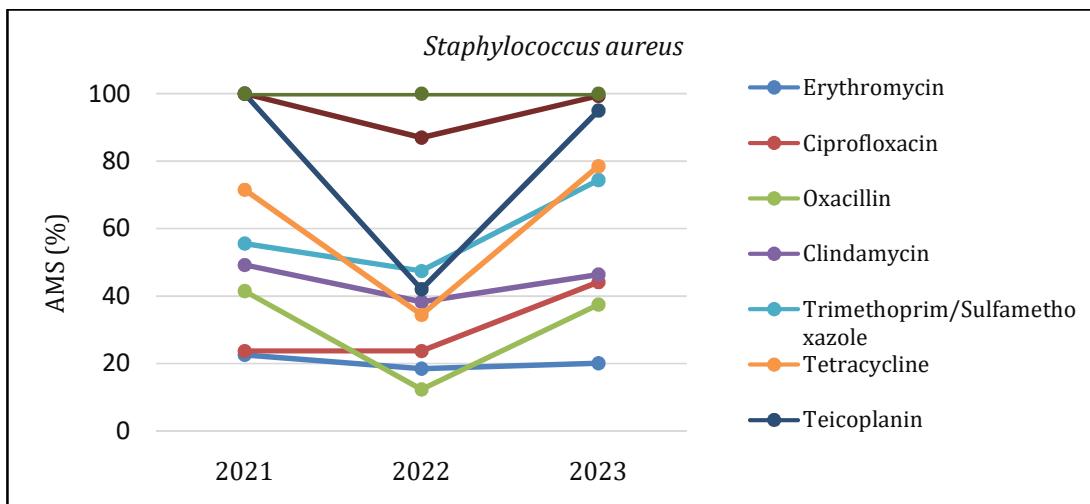


Figure 10.3: AMS profile of Gram-negative organisms (*Klebsiella pneumonia*, *Acinetobacter baumannii*, *Escherichia coli*, *Pseudomonas aeruginosa*) in the surveillance network over three years (2021-2023)



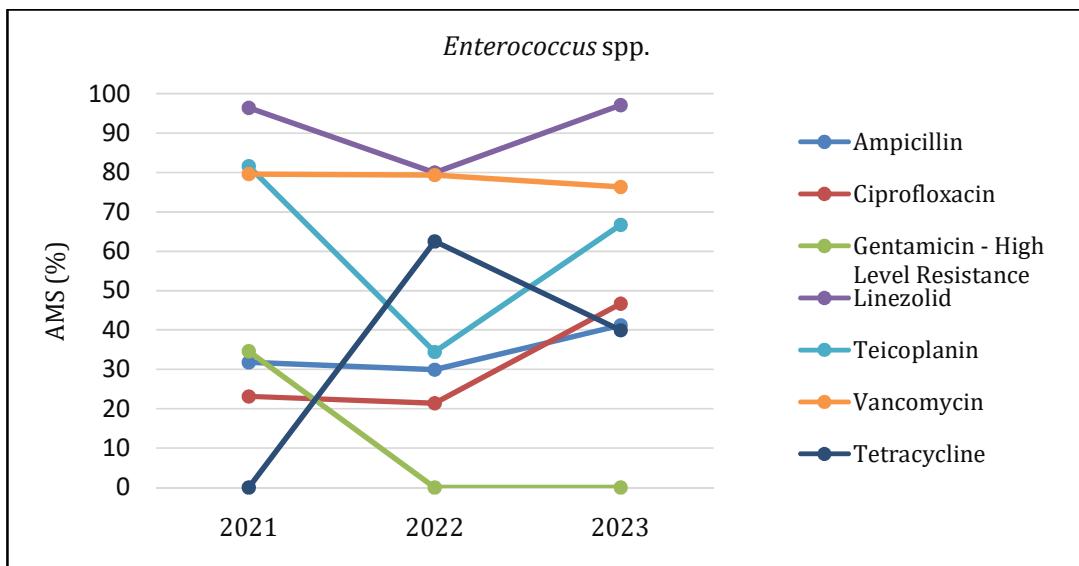


Figure 10.4: AMS profile of Gram-positive organisms (*Staphylococcus aureus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus spp.*) in the surveillance network over three years (2021-2023)

Urinary Tract Infections (UTI) data

A total of 1,110 cases of UTIs were reported. The distribution and profile of UTIs are shown in **Table 10.30**. The catheter-associated UTI (CAUTI) rate was 3.0/1,000 urinary catheter days, as shown in **Table 10.31**. The rates of total UTIs were compared against different types of ICUs since the morbidity of patients varies with the different types of ICUs. **Table 10.32** compares the rates of UTIs across the different ICU types in our network. The trend of UTI rates in the surveillance network for three years (2021-2023) is shown in **Figure 10.5**. **Table 10.33** shows that UTI cases were more common in males than females.

Table 10.30: Type of UTI cases

Type of UTI cases	No. of UTI cases (%)
CAUTI (catheter-associated UTIs)	1,001 (90.2)
Non-CAUTI	109 (9.8)
Total	1,110

Table 10.31: UTI rates

S.No.	Indicator	Rates
1	UTI incidence rate (per 1,000 patient days)	1.9
2	CAUTI rate (per 1,000 urinary catheter days)	3.0

Table 10.32: Distribution of UTI cases by ICUs

Type of ICUs	No. of UTI cases (%)	UTI Rate (per 1,000 patient days)
Medical ICU	376 (33.9)	5.7
Medical/Surgical ICU	137 (12.3)	3.6
Trauma ICU	121 (10.9)	5.7
Surgical ICU	88 (7.9)	6.1
Anaesthesia	84 (7.6)	10.8
High Dependency Unit	61 (5.5)	5.5
Neuro Surgery ICU	49 (4.4)	8.9
Gastrointestinal ICU	37 (3.3)	7.6
Pediatric ICU	34 (3.1)	1.2
Neurologic ICU	26 (2.3)	7.0
Neonatal ICU	25 (2.2)	0.4
Oncologic Surgical ICU	25 (2.2)	15.7
Pediatric Medical/Surgical ICU	20 (1.8)	1.3
Oncologic Medical ICU	19 (1.7)	11.0
Respiratory ICU	5 (0.5)	1.4
Cardiothoracic ICU	2 (0.2)	0.7
Cardiac ICU	1 (0.1)	0.2
Total	1,110	1.9

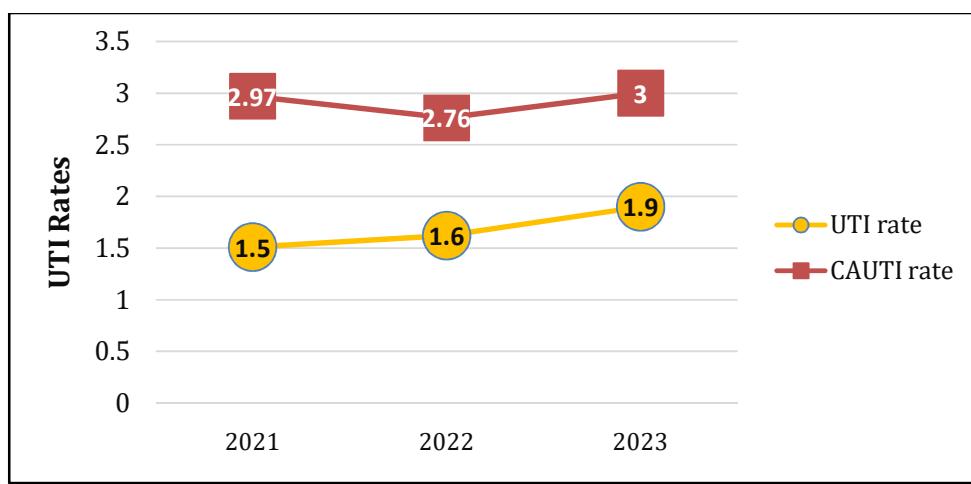


Figure 10.5: Trend of UTI rates in the surveillance network of Indian hospitals over three years (2021-2023)

Table 10.33: Distribution of UTI cases by gender and age

Gender	No. of UTI cases (%)
Males	663 (59.7)
Females	447 (40.3)
Total	1,110

	Median	Range (Days)
Age of males	42	0 – 95
Age of females	42	0 – 88

Table 10.34 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 20.7%. This may not be the actual attributable mortality, since severe primary illness or other underlying co-morbidities may be contributing to the fatal outcome. 19.6% of UTI cases were discharged at 14-day. **Table 10.35** shows the short-term outcomes of UTI cases. A total of 1,205 pathogens were isolated from the UTI cases. Gram-negative organisms predominated as the cause of UTIs in our network, as shown in **Table 10.36-10.38**.

Table 10.34: Duration between ICU admission and development of UTI

	Median	Range
Duration of stay in the unit	20	3–233
Duration between date of admission and date of event	12	3–339

Table 10.35: Outcome of UTI cases

14-day outcome	No. of UTI cases (%)
Died	230 (20.7)
Discharged	218 (19.6)
LAMA	58 (5.2)
Still in surveillance unit	341 (30.7)
Transferred to other hospital	6 (0.5)
Transferred to other ward/unit within the hospital	256 (23.1)
Unknown	1 (0.1)
Total	1,110

Table 10.36: Distribution of organisms causing UTI

S.No.	Name of organism	Number (%)
1	Gram-negative organisms	715 (59.3)
2	Gram-positive organisms	232 (19.3)
3	Fungal pathogens ^{oo}	258 (21.4)
	Total	1,205

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

Table 10.37: Distribution of organisms causing UTI (Genus level)

S. No.	Name of organism	Number (%)
1	<i>Candida</i> spp.	252 (20.9)
2	<i>Escherichia coli</i>	236 (19.6)
3	<i>Enterococcus</i> spp.	226 (18.8)
4	<i>Klebsiella</i> spp.	197 (16.3)
5	<i>Pseudomonas</i> spp.	134 (11.1)
6	<i>Acinetobacter</i> spp.	58 (4.8)
7	<i>Providencia</i> spp.	29 (2.4)
8	<i>Proteus</i> spp.	21 (1.7)
9	<i>Chryseobacterium</i> spp.	8 (0.7)
10	<i>Enterobacter</i> spp.	8 (0.7)
11	<i>Stenotrophomonas</i> spp.	6 (0.5)
12	<i>Staphylococcus aureus</i>	6 (0.5)
13	<i>Morganella morganii</i>	6 (0.5)
14	<i>Myroides</i> spp.	5 (0.4)
15	<i>Citrobacter</i> spp.	4 (0.3)
16	<i>Trichosporon</i> spp.	4 (0.3)
17	<i>Serratia</i> spp.	2 (0.2)
18	Others	2 (0.2)
19	<i>Burkholderia</i> spp.	1 (0.1)
	Total	1,205

Table 10.38: Distribution of organisms (Species level) causing UTI

S. No.	Name of organism	Number (%)
1	<i>Escherichia coli</i>	236 (19.6)
2	<i>Klebsiella pneumoniae</i>	176 (14.6)
3	<i>Enterococcus faecium</i>	133 (11.0)
4	<i>Pseudomonas aeruginosa</i>	123 (10.2)
5	<i>Candida albicans</i>	69 (5.7)
6	<i>Candida tropicalis</i>	67 (5.6)
7	<i>Candida</i> spp.	62 (5.0)
8	<i>Enterococcus</i> spp.	51 (4.2)
9	<i>Acinetobacter baumannii</i>	52 (4.3)
10	<i>Enterococcus faecalis</i>	42 (3.5)
11	<i>Providencia rettgeri</i>	23 (1.9)
12	<i>Proteus mirabilis</i>	18 (1.5)
13	<i>Candida parapsilosis</i>	15 (1.2)
14	<i>Candida glabrata</i>	12 (1.0)
15	<i>Candida auris</i>	11 (0.9)
16	<i>Klebsiella</i> spp.	11 (0.9)
17	Others	104 (8.6)
	Total	1,205

AMS profile of organisms causing UTI

A high rate of resistance was seen against third-generation cephalosporins, carbapenems, fluoroquinolones, colistin, and aminoglycosides in *Klebsiella pneumoniae*, *Escherichia coli* and *Acinetobacter baumannii* and *Pseudomonas aeruginosa* causing UTIs; nearly 60% isolates of *Enterococcus faecium* were vancomycin-resistant (**Table 10.39-10.41**). AMS profile of organisms causing UTI over three years is shown in **Figure 10.6 and 10.7**.

Table 10.39: AMS pattern for Gram-negative organisms causing UTIs in HAI surveillance network, 2023

Antimicrobials	Organisms			
	<i>Klebsiella pneumoniae</i> (N=177)	<i>Escherichia coli</i> (N=236)	<i>Acinetobacter baumannii</i> (N=52)	<i>Pseudomonas aeruginosa</i> (N=123)
Amikacin	39/169 (23.1)	132/232 (56.9)	9/50 (18.0)	31/119 (26.1)
Ampicillin	1/26 (3.9)	2/109 (1.8)	-	-
Cefazolin	3/50 (6.0)	8/89 (9.0)	-	-
Cefepime	12/140 (8.6)	25/165 (15.2)	4/44 (9.1)	25/121 (20.7)
Cefotaxime	7/104 (6.7)	10/142 (7.0)	-	-
Ceftazidime	4/72 (5.6)	7/98 (7.1)	4/40 (10.0)	22/116 (19.0)
Ceftriaxone	7/122 (5.7)	10/153 (6.5)	-	2/2
Ciprofloxacin	8/149 (5.4)	13/203 (6.4)	6/45 (13.3)	23/117 (19.7)
Colistin	84/91 (92.3)	86/95 (93.5)	12/12	50/53 (94.3)
Ertapenem	15/92 (16.3)	75/144 (52.1)	1/3	-
Gentamicin	35/153 (22.9)	107/206 (51.9)	8/42 (19.1)	24/73 (32.9)
Imipenem	32/155 (20.7)	82/183 (44.8)	4/46 (8.7)	18/112 (16.1)
Levofloxacin	7/85 (8.2)	5/90 (5.6)	4/31 (12.9)	14/94 (14.9)
Meropenem	29/147 (19.7)	81/182 (44.5)	4/44 (9.1)	23/117 (19.7)
Minocycline	25/53 (47.2)	37/52 (71.2)	27/36 (75.0)	1/4
Netilmicin	-	8/11	-	8/61 (13.1)
Piperacillin	-	-	-	5/38 (13.2)
Piperacillin/Tazobactam	24/158 (15.2)	71/208 (34.1)	8/48 (16.7)	33/117 (28.2)
Tetracycline	28/55 (50.9)	18/57 (31.6)	6/24 (25.0)	-
Tigecycline	14/19	23/25 (92.0)	2/4	-
Tobramycin	4/24 (16.7)	10/31 (32.3)	1/21 (4.8)	15/84 (17.9)
Amoxicillin/Clavulanate	5/83 (6.0)	11/96 (11.5)	-	-

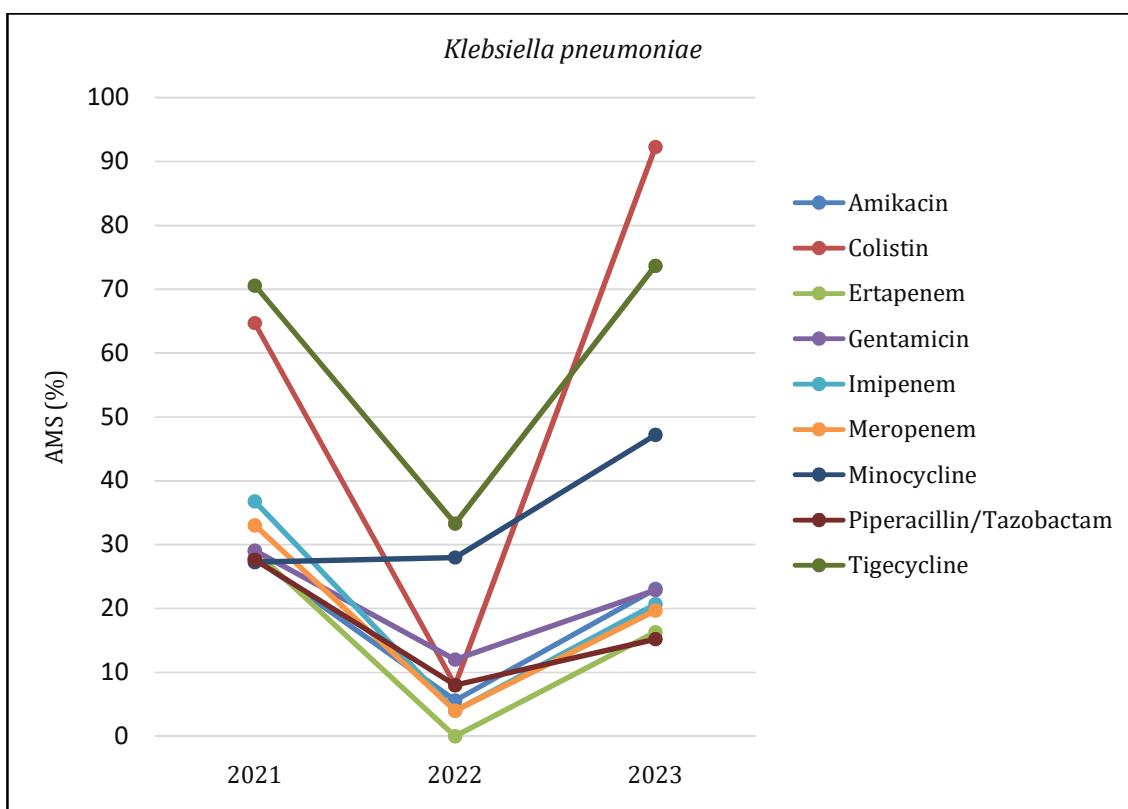
Table 10.40: AMS pattern for *Enterococcus* species causing UTI, 2023

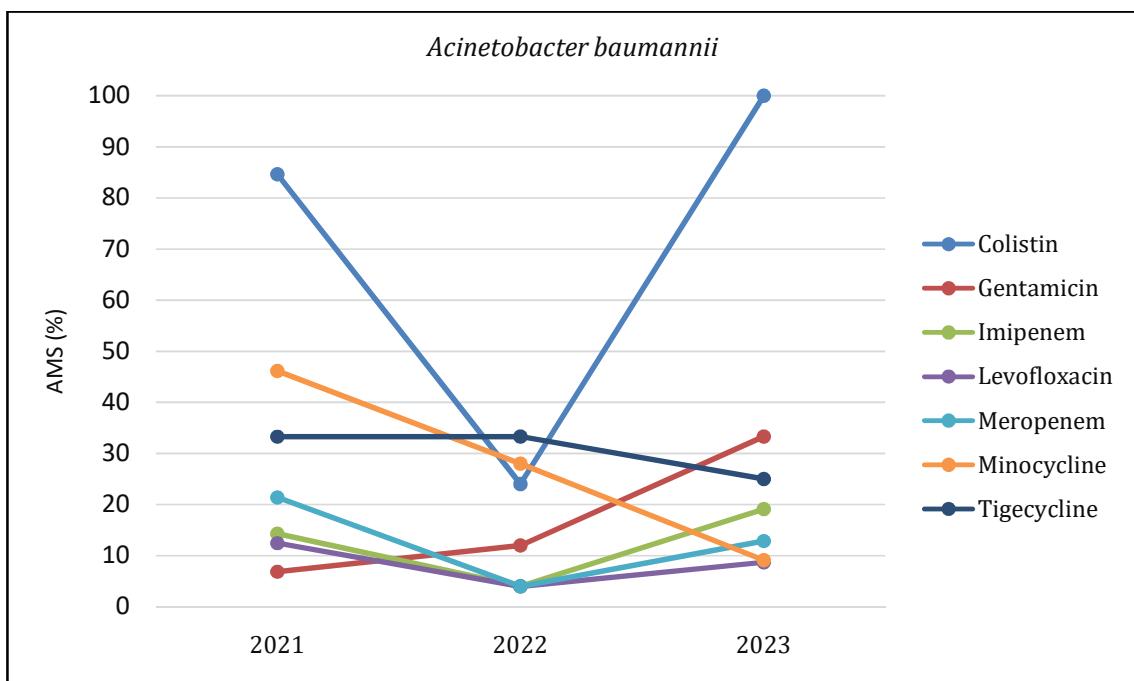
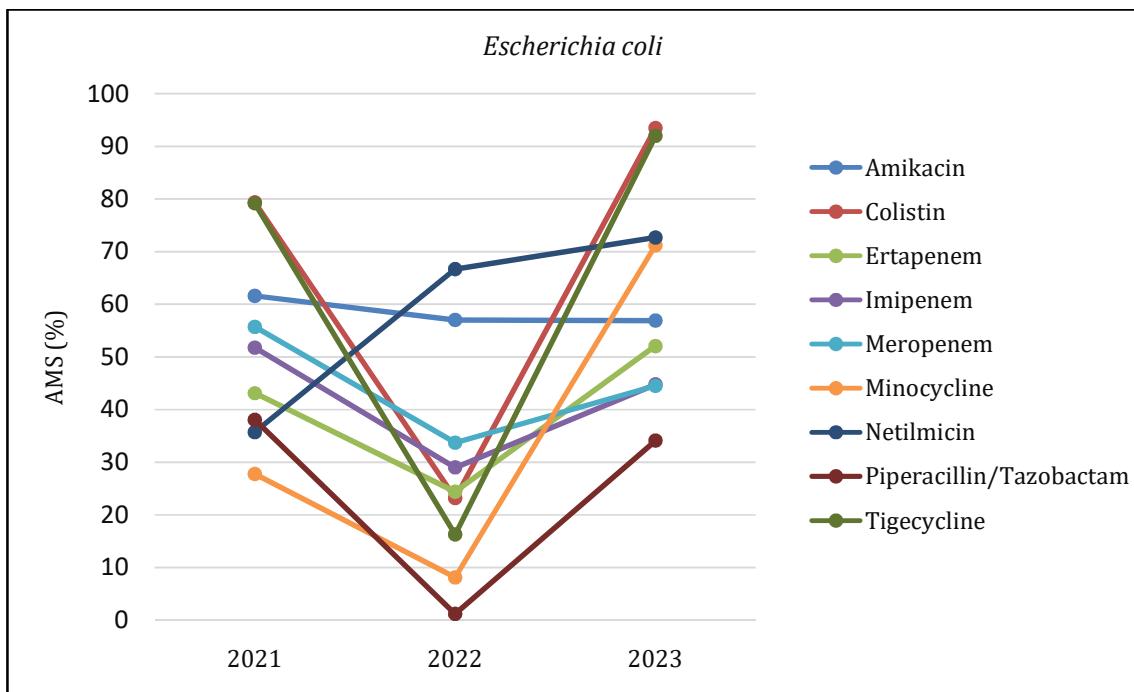
Antimicrobials	Organisms		
	<i>Enterococcus faecalis</i> (N=42)	<i>Enterococcus faecium</i> (N=133)	<i>Enterococcus</i> spp. (N=51)
	(%)S	(%)S	(%)S
Ampicillin	9/32 (28.1)	6/95 (6.3)	9/37 (24.3)
Ciprofloxacin	6/35 (17.1)	5/113 (4.4)	8/40 (20.0)
Linezolid	32/35 (91.4)	86/103 (83.5)	39/44 (88.6)
Nitrofurantoin	22/32 (68.7)	25/86 (29.1)	19/44 (43.2)
Teicoplanin	16/18	50/90 (55.6)	8/14
Tetracycline	2/15	6/66 (9.1)	3/16
Vancomycin	33/40 (82.5)	77/129 (59.7)	38/44 (86.4)
Fosfomycin	15/28 (53.6)	14/25 (56.0)	7/8

Table 10.41: AMS pattern for *Staphylococcus aureus* causing UTI, 2023

Antimicrobials	Organisms	
	<i>Staphylococcus aureus</i> (N=6) [∞]	Sensitive/Tested(%)
Clindamycin		2/2
Erythromycin		1/3
Linezolid		4/4
Rifampicin		-
Teicoplanin		2/2
Tetracycline		1/1
Tigecycline		-
Trimethoprim/Sulfamethoxazole		2/3
Vancomycin		2/2

[∞]numbers too low





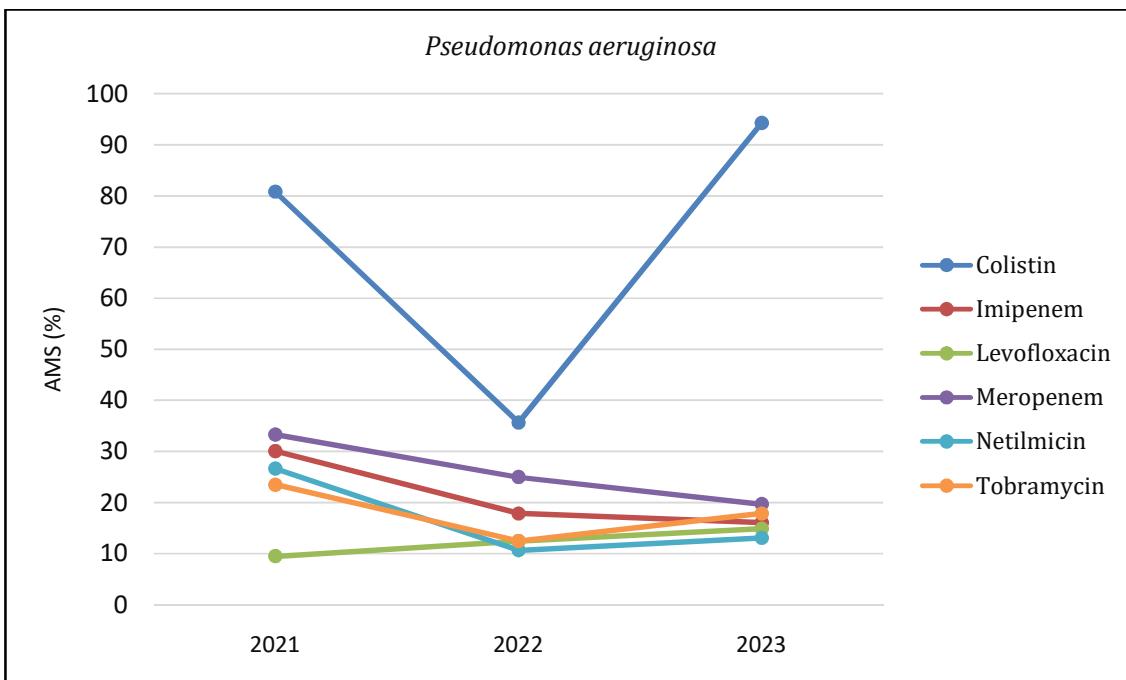
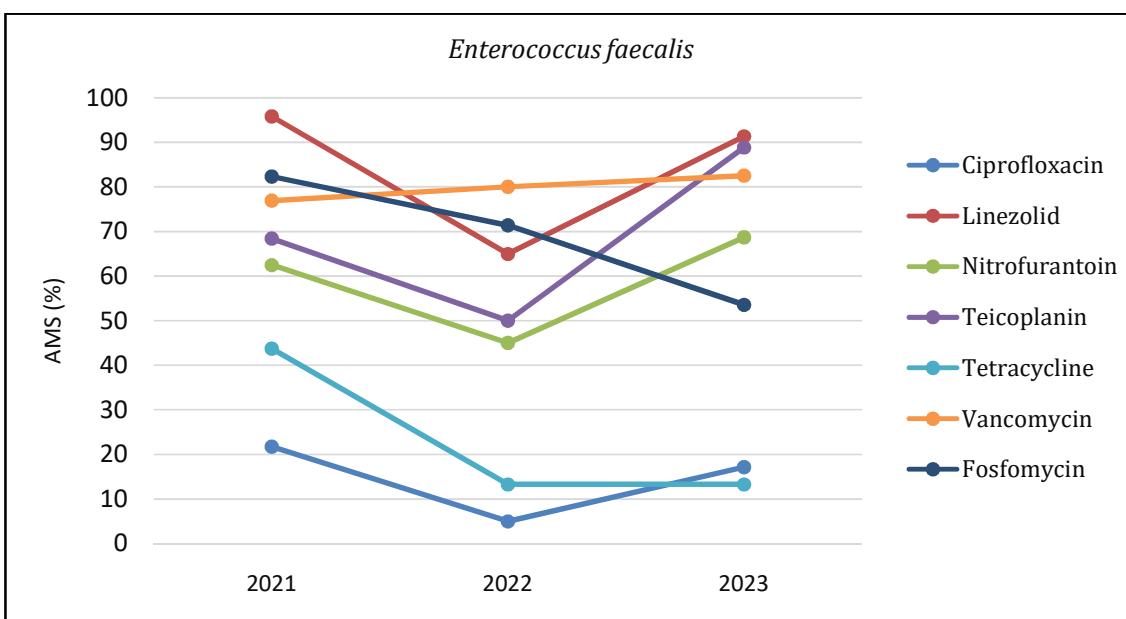


Figure 10.6: AMS profile of Gram-negative organisms (*Klebsiella pneumonia*, *Escherichia coli*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*) in the surveillance network over three years (2021-2023)



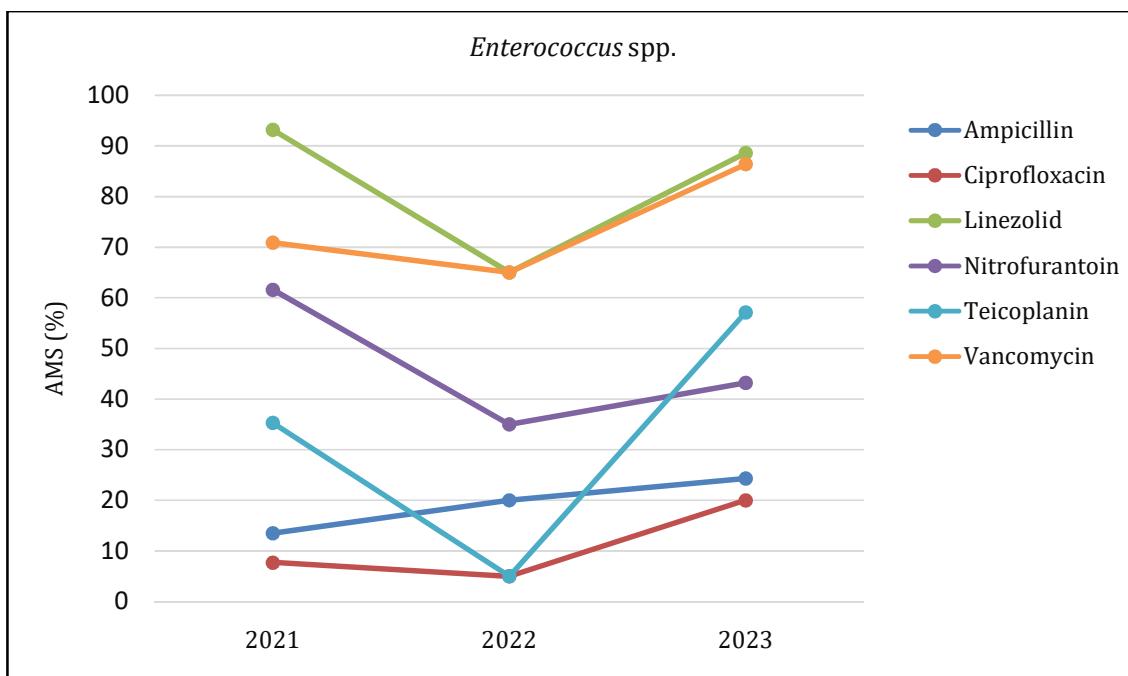
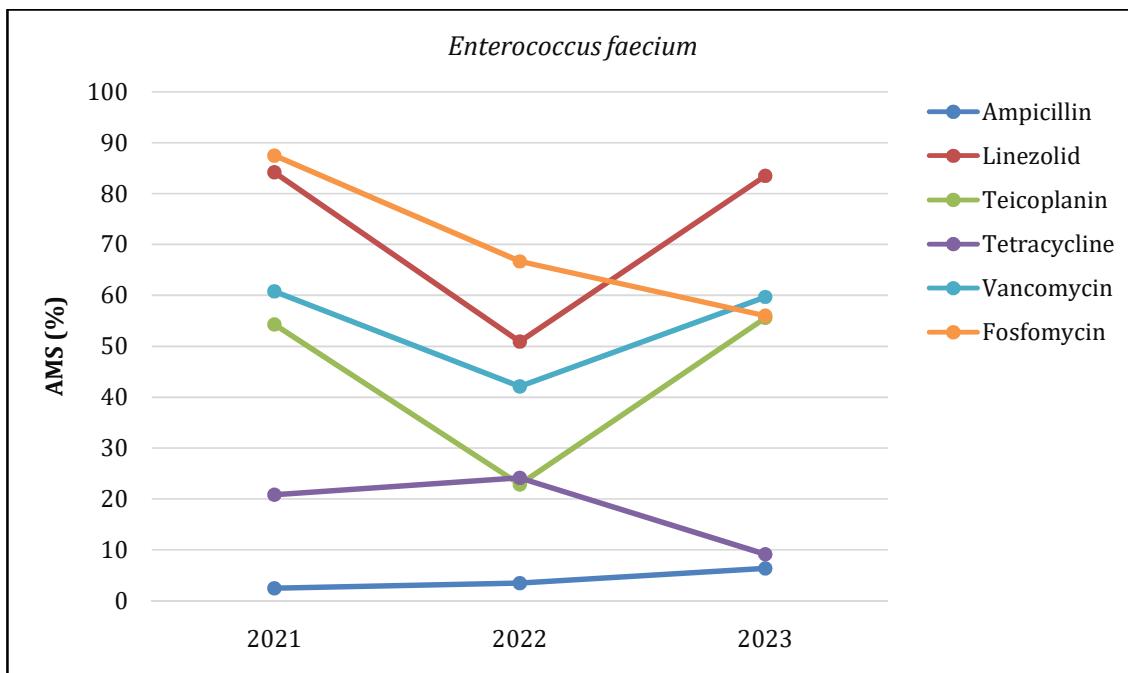


Figure 10.7: AMS profile of Gram-positive organisms (*Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus spp.*) in the surveillance network over three years (2021-2023)

Ventilator-Associated Pneumonia data

Surveillance for VAP was started towards the end of 2023 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 preliminary findings from a few hospitals in the network (**Table 10.42**). A total of 310 VAP events were reported, giving a VAP rate of 7.6/1,000 ventilator days (**Table 10.43**). A total of 429 organisms were recovered, of which *Acinetobacter* spp. was the most common (**Table 10.44**). AMS pattern for Gram-negative organisms isolated from VAP patients is shown (**Table 10.45**).

Table 10.42: ICU-wise distribution of total patient days and ventilator days (2023)

Type of ICUs	Patient Days	Ventilator Days
Medical ICU	45,357	19,525
Neurosurgical ICU	15,157	6,436
Pediatric ICU	13,056	4,349
Medical/Surgical ICU	10,499	4,235
Neuro Surgery ward	8,928	2,020
Surgical ICU	4,669	1,415
Cardiac ICU	3,812	615
HDU	2,691	0
Respiratory ICU	2,510	1,160
Gastrointestinal ICU	3,565	563
Total	1,10,244	40,318

Table 10.43: Demographic details of VAP patients under HAI surveillance network, 2023

S. No.	Features	Patient No. (%) (N=310)
1.	Gender <ul style="list-style-type: none"> ▪ Male ▪ Female 	226 (72.9) 84(27.0)
2.	Age: median (range) <ul style="list-style-type: none"> ▪ <=18 ▪ >18 	40 (0 – 88) years 54 (17.4) 256 (82.6)
3.	Time to infection <ul style="list-style-type: none"> ▪ Within 7 days ▪ 7 – 14 days ▪ 14 - 21 days ▪ 21+ days 	172(55.5) 78(25.2) 33(10.6) 27(8.7)
4	Outcome 14-day Outcome <ul style="list-style-type: none"> ▪ Still in a surveillance unit ▪ Died ▪ Transferred to another ward/t within the hospital ▪ Discharged ▪ LAMA ▪ Transferred to other hospitals Final Outcome <ul style="list-style-type: none"> ▪ Died ▪ Discharged ▪ LAMA ▪ Transferred to other Hospital ▪ Unknown 	98 (31.6) 112 (36.1) 72 (23.2) 16 (5.2) 6 (1.9) 6 (1.9) 144 (46.5) 102 (32.9) 8(2.6) 6 (1.9) 50 (16.1)

Table 10.44: Distribution of organisms isolated from VAP patients (2023)

Organism	Count	Percent
<i>Acinetobacter</i> spp.	187	43.6
<i>Klebsiella</i> spp.	76	17.7
<i>Pseudomonas</i> spp.	75	17.5
<i>Escherichia coli</i>	21	4.9
<i>Staphylococcus aureus</i>	17	4.0
<i>Stenotrophomonas maltophilia</i>	14	3.3
<i>Proteus</i> spp.	11	2.6
<i>Serratia marcescens</i>	9	2.1
<i>Providencia stuartii</i>	5	1.2
<i>Elizabethkingia</i> spp.	4	0.9
<i>Citrobacter</i> spp.	4	0.9
Others	4	0.9
<i>Burkholderia cepaciae</i>	2	0.5
Total	429	

Table 10.45: AMS pattern for Gram-negative organisms isolated from VAP patients (2023)

	<i>Enterobacteriales</i> (N = 118)	<i>Acinetobacter baumannii</i> (N = 187)	<i>Pseudomonas aeruginosa</i> (N = 75)
Antibiotics	% S	% S	% S
Amoxicillin-Clavulanate	13/67 (19.4)	11/71 (15.5)	10/20 (50.0)
Amikacin	39/113 (34.5)	5/183 (2.7)	31/60 (51.7)
Ampicillin	13/67 (19.4)	11/71 (15.5)	10/20 (50.0)
Cefazolin	10/45 (22.2)	11/71 (15.5)	10/20 (50.0)
Cefepime	18/112 (16.1)	5/171 (2.9)	20/70 (28.6)
Cefotaxime	12/68 (17.6)	1/65 (1.5)	10/20 (50.0)
Ceftazidime	11/52 (21.2)	3/169 (1.8)	27/71 (38.0)
Ceftriaxone	12/45 (26.7)	11/71 (15.5)	10/20 (50.0)
Ciprofloxacin	17/115 (14.8)	3/181 (1.7)	25/68 (36.8)
Colistin	53/66 (80.3)	123/126 (97.6)	26/27 (96.3)
Gentamicin	34/110 (30.9)	9/175 (5.1)	15/36 (41.7)
Imipenem	30/113 (26.5)	6/179 (3.4)	22/69 (31.9)
Levofloxacin	13/68 (19.1)	6/143 (4.2)	18/68 (26.5)
Meropenem	30/112 (26.8)	7/185 (3.8)	26/72 (36.1)
Minocycline	25/56 (44.6)	84/156 (53.8)	10/20 (50.0)
Netilmicin	13/67 (19.4)	3/12	8/13
Piperacillin	13/67 (19.4)	1/32 (3.1)	10/20 (50.0)
Tetracycline	10/28 (35.7)	10/39 (25.6)	10/20 (50.0)
Tigecycline	34/58 (58.6)	11/71 (15.5)	-
Tobramycin	13/67 (19.4)	5/53 (9.4)	20/41 (48.8)

Annexure I**List of participating centers**

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AIIMS, New Delhi CMC, Vellore JIPMER, Puducherry PGIMER, Chandigarh	AFMC, Pune AIIMS Bhopal AIIMS Jodhpur Apollo Hospital, Chennai Assam Medical College and Hospital, Assam IPGMR, Kolkata JPN Apex Trauma Center, New Delhi KGMU, Lucknow KMC, Manipal LTMMC&GH Mumbai MGIMS, Wardha NIMS, Hyderabad PD Hinduja Hospital, Mumbai RIMS, Imphal Sir Ganga Ram Hospital, New Delhi Tata Medical Center, Kolkata SKIMS, Srinagar

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