

Pseudomonas aeruginosa

Table 5.3: Resistance percentages of *Pseudomonas aeruginosa* isolated from different specimen (except faeces).

AMA	Blood	LRT	Pus	CSF	Urine
	n=545	n=2526	n=1980	n=61	n=430
Amikacin	172/542 (31.7)	648/2525 (25.7)	584/1969 (29.7)	29/57 (50.9)	231/430 (53.7)
Cefepime	162/442 (36.7)	732/2184 (33.5)	621/1790 (34.7)	32/57 (56.1)	222/418 (53.1)
Ceftazidime	175/527 (33.2)	735/2446 (30)	605/1895 (31.9)	29/61 (47.5)	207/427 (48.5)
Ciprofloxacin	143/416 (34.4)	703/1931 (36.4)	792/1956 (40.5)	38/58 (65.5)	251/424 (59.2)
Colistin	8/193 (4.1)	7/852 (0.8)	3/750 (0.4)	0/30 (0)	2/229 (0.9)
Gentamicin	143/347 (41.2)	586/1460 (40.1)	674/1743 (38.7)	32/52 (61.5)	245/425 (57.6)
Imipenem	159/536 (29.7)	610/2435 (25.1)	323/1959 (16.5)	22/56 (39.3)	122/425 (28.7)
Levofloxacin	167/497 (33.6)	824/2383 (34.6)	729/1818 (40.1)	40/58 (69)	253/418 (60.5)
Meropenem	150/496 (30.2)	652/2229 (29.3)	391/1742 (22.4)	27/59 (45.8)	195/426 (45.8)
Piperacillin-tazobactam	112/508 (22)	514/2435 (21.1)	386/1890 (20.4)	18/56 (32.1)	133/426 (31.2)
Tobramycin	128/393 (32.6)	595/2145 (27.7)	539/1622 (33.2)	28/49 (57.1)	197/334 (59)

Salmonella Paratyphi A

Table 3.2 Susceptibility pattern of *Salmonella Paratyphi A* from Blood across different regions of India

Antibiotic	National (n=101)		North (n=80)		Central (n=0)		East (n=0)		West (n=11)		South (n=10)	
	n= (%)	% Range	n= (%)	% Range	n= (%)	% Range	n= (%)	% Range	n= (%)	% Range	n= (%)	% Range
Ampicillin	98/101 (97)	98	77/80 (96)	100	0/0 (-)	-	0/0 (-)	-	11/11 (100)	100	10/10 (100)	100
Cefixime	88/88 (100)	100	80/80 (100)	100	0/0 (-)	-	0/0 (-)	-	1/1 (100)	100	8/8 (100)	100
Ceftriaxone	101/101 (100)	100	80/80 (100)	100	0/0 (-)	-	0/0 (-)	-	11/11 (100)	100	10/10 (100)	100
Chloramphenicol	98/98 (100)	100	77/77 (100)	100	0/0 (-)	-	0/0 (-)	-	11/11 (100)	100	10/10 (100)	100
Ciprofloxacin	1/97 (1)	-	1/80 (1)	-	0/0 (-)	-	0/0 (-)	-	0/11 (-)	-	0/6 (-)	-
Pefloxacin	1/14 (7)	-	1/11 (9)	-	0/0 (-)	-	0/0 (-)	-	0/0 (-)	-	0/3 (-)	-
Trimethoprim-sulfamethoxazole	99/99 (100)	100	79/79 (100)	100	0/0 (-)	-	0/0 (-)	-	11/11 (100)	100	9/9 (100)	100

Table 3.2 shows antibiotic susceptibility pattern of *Salmonella Paratyphi A* from blood and it shows that *Salmonella Paratyphi A* become completely resistant to ciprofloxacin as the susceptibility to the drug was 1% only.

No MDR was found in *Paratyphi A*. Ampicillin susceptibility was 97% while chloramphenicol and cotrimoxazole was 100% susceptible from North India. Third generation cephalosporins (Ceftriaxone and cefixime) were 100% susceptible.

Table 2.4.1: Yearly susceptibility trend of *E. coli* isolated from all samples (except faeces and urine)

AMA	Year-2016	Year-2017	Year-2018	Year-2019
	(S%)	(S%)	(S%)	(S%)
Amikacin	796/961 (82.8)	4788/6048 (79.2)	7070/8911 (79.3)	9862/12453 (79.2)
Cefazolin	0/0	0/8	2/6	0/1
Cefotaxime	165/928 (17.8)	879/5747 (15.3)	1274/7817 (16.3)	1531/10569 (14.5)
Ceftazidime	244/977 (25)	1295/5513 (23.5)	1398/5956 (23.5)	1496/7492 (20)
Ciprofloxacin	151/745 (20.3)	1028/5368 (19.2)	1889/8450 (22.4)	2414/11613 (20.8)
Colistin	0/0	494/498 (99.2)	824/833 (98.9)	1589/1595 (99.6)
Ertapenem	514/705 (72.9)	3104/4605 (67.4)	4528/6877 (65.8)	6612/9309 (71)
Fosfomycin	0/0	5/7	2/3	0/0
Imipenem	699/814 (85.9)	4699/5773 (81.4)	6453/8873 (72.7)	6433/10158 (63.3)
Levofloxacin	2/4	140/889 (15.7)	600/3493 (17.2)	1138/5987 (19)
Meropenem	792/981 (80.7)	4158/5678 (73.2)	5873/8403 (69.9)	9039/12072 (74.9)
Nitrofurantoin	1/3	12/14	18/23 (78.3)	2/2
Piperacillin-tazobactam	607/1009 (60.2)	3424/6030 (56.8)	4857/8960 (54.2)	6580/12030 (54.7)
Trimethoprim-sulfamethoxazole	1/3	10/25 (40)	12/24 (50)	2/2

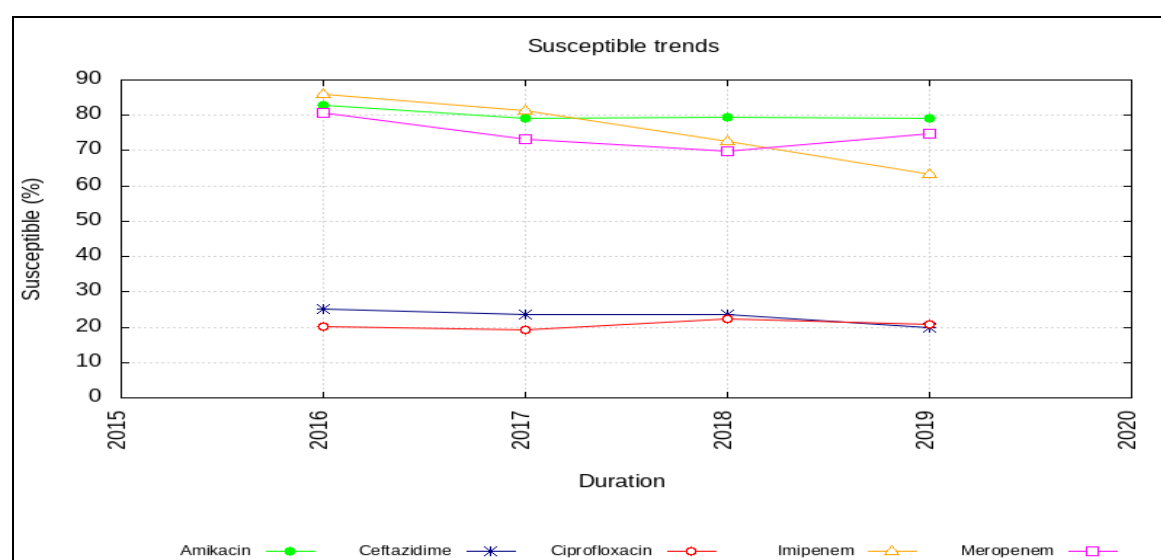


Figure 2.4.1: Yearly susceptibility trend of *E. coli* isolated from all samples (except faeces and urine)

Table 6.19: Antibiotic resistance genes phenotypically resistant isolates of *S. aureus*, CoNS and enterococci from nodal and regional centers

S.No	Phenotypic resistance	Genes detected	Nodal center (No. positive /no tested)	Regional centers (No. positive /no tested)	National (No. positive /no tested)
1	Methicillin resistant <i>S. aureus</i> (MRSA)	<i>mecA</i>	<i>mecA</i> : 102/105 (97.1%)	<i>mecA</i> : 286/287 (99.7%)	<i>mecA</i> : 388/392 (99.0%)
2	Erythromycin resistance (<i>S. aureus</i>)	<i>erm A</i> , <i>erm B</i> and <i>erm C</i>	<i>erm A</i> :35/145 (24.1%) <i>erm B</i> :0/145 (0%) <i>erm C</i> :72/145 (49.6%) Negative for <i>ermA</i> , <i>B</i> , <i>C</i> :38/145 (26.2%)	<i>erm A</i> : 10 /482 (2.1%) <i>erm B</i> : 0/482 (0%) <i>erm C</i> : 121/482 (25.1%) <i>ermA</i> and <i>C</i> : 9/482 (1.9%) Negative for <i>ermA</i> , <i>B</i> , <i>C</i> : 342 /482 (70.9%)	<i>erm A</i> : 45/627 (7.2%) <i>erm B</i> : 0/627 (0%) <i>erm C</i> : 193/627 (30.8%) <i>ermA</i> and <i>C</i> : 9/482 (1.9%) Negative for <i>ermA</i> , <i>B</i> , <i>C</i> : 380/627 (60.6%)
3	Mupirocin resistance (<i>S. aureus</i>)	<i>mupA</i> and <i>mupB</i>	<i>mup A</i> : 30/35 (85.7%) <i>mup B</i> : 0/35 (0%)	<i>mup A</i> :5/5 <i>mup B</i> :0/5	<i>mup A</i> :35/40 (87.5%) <i>mup B</i> :0/40 (0%)
4	Linezolid resistant MRSA and MR CoNS	<i>cfr</i>	<i>cfr</i> : 1/1 (MRSA) 3/3 (CoNS)	<i>cfr</i> :1/1(MRSA)	<i>cfr</i> : 2/2 (MRSA) 3/3 (CoNS)
5	Vancomycin resistant Enterococci (VRE)	<i>vanA</i> , <i>vanB</i> , <i>vanC</i> ₁ / <i>C</i> ₂	<i>vanA</i> :97/97 (100%) <i>vanB</i> :0/97 (0%) <i>vanC</i> ₁ / <i>C</i> ₂ :0/97 (0%)	<i>vanA</i> :85/85 (100%) <i>vanB</i> : 0/85 (0%) <i>vanC</i> ₁ / <i>C</i> ₂ : 0/85 (0%)	<i>vanA</i> :182/182 (100%) <i>vanB</i> : 0/182 (0%) <i>vanC</i> ₁ / <i>C</i> ₂ : 0/182 (0%)

Table 4.8: Year wise susceptibility trends of MSSA from All samples

AMA	Year-2016	Year-2017	Year-2018	Year-2019	Year-2020	Year-2021
	Total n=686	Total n=3819	Total n=5135	Total n=7029	Total n=3655	Total n=5273
	(S%)	(S%)	(S%)	(S%)	(S%)	(S%)
Cefoxitin	686/686 (100)	3801/3801 (100)	4857/4857 (100)	6255/6255 (100)	3388/3388 (100)	3845/3845 (100)
Oxacillin	*0/0	306/306 (100)	1187/1187 (100)	2195/2195 (100)	1100/1100 (100)	2399/2399 (100)
Penicillin	59/557 (10.6)	248/2393 (10.4)	218/2068 (10.5)	410/3729 (11)	231/1931 (12)	203/2131 (9.5)
Vancomycin	428/428 (100)	1935/1935 (100)	3041/3041 (100)	3986/3986 (100)	2153/2153 (100)	4010/4010 (100)
Teicoplanin	636/636 (100)	3509/3517 (99.8)	3642/3682 (98.9)	3391/3419 (99.2)	1074/1075 (99.9)	1945/1949 (99.8)
Erythromycin	419/684 (61.3)	2251/3739 (60.2)	2757/4841 (57)	3527/6895 (51.2)	1962/3570 (55)	2665/4975 (53.6)
Tetracycline	528/557 (94.8)	2508/2665 (94.1)	3809/4137 (92.1)	5383/5791 (93)	2838/3047 (93.1)	3297/3579 (92.1)
Tigecycline	*0/0	300/302 (99.3)	902/902 (100)	1608/1613 (99.7)	861/861 (100)	1102/1112 (99.1)
Ciprofloxacin	168/609 (27.6)	1051/3524 (29.8)	1167/4816 (24.2)	1587/6452 (24.6)	888/3386 (26.2)	1112/4971 (22.4)
Clindamycin	561/661 (84.9)	3162/3666 (86.3)	4341/5021 (86.5)	5837/6839 (85.3)	3021/3548 (85.1)	4057/5137 (79)
Trimethoprim- sulfamethoxazole	414/629 (65.8)	2202/2959 (74.4)	3030/4499 (67.3)	4750/6475 (73.4)	2425/3344 (72.5)	2884/3927 (73.4)
Linezolid	634/634 (100)	3630/3636 (99.8)	4775/4800 (99.5)	6433/6448 (99.8)	3343/3349 (99.8)	4838/4839 (100)
Mupirocin High Level	434/440 (98.6)	2119/2139 (99.1)	2414/2441 (98.9)	2775/2820 (98.4)	1564/1600 (97.8)	1436/1460 (98.4)

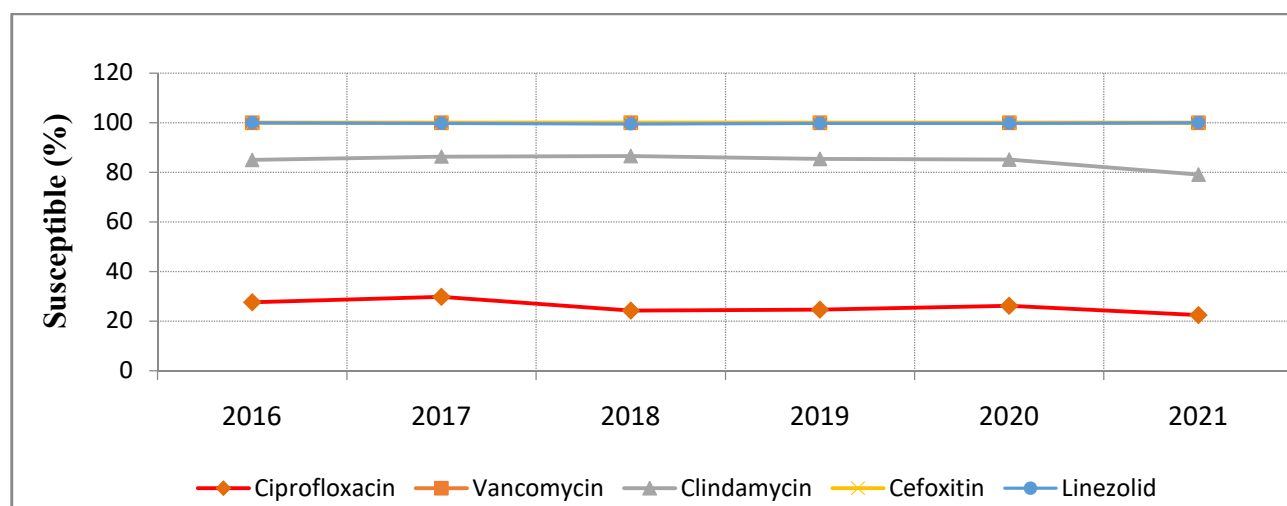


Figure 4.2: Year wise susceptibility trends of MSSA from All Samples

Gram negative organisms predominated as the cause of BSIs in our network, as shown in Table 9.10.

The genus level distribution in Gram negative & Gram positive organisms and species distribution of *Candida* causing overall BSIs is shown in table 9.11 to 9.13. *Enterococcus* sp. 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 9.4: Types of BSI cases

Type of BSI cases	No. of BSI cases (%)
CLABSI	1,468 (47.7)
Non-CLABSI	1,166 (37.9)
Secondary BSI	446 (14.5)
Total	3,080

Table 9.5: BSI rates

Indicator	Rates
Total BSI rate(per 1,000 patient days)	6.51
Primary BSI rate (per 1,000 patient days)	5.57
CLABSI rate(per 1,000 central line days)	3.10
Secondary BSI rate (per1,000 patient days)	0.94

Table 9.6: Distribution of BSI cases by ICUs

Type of ICUs	No. of BSI cases (Percentage)	Total BSI rate (per 1,000 patient days)
Medical ICU	1,049(34)	8.50
Neonatal ICU	540(17.5)	5.09
Medical/Surgical ICU	412(13.4)	7.33
Surgical ICU	247(8.0)	8.53
Trauma ICU	236(7.7)	14.23
COVID ICU	208(6.8)	4.80
Pediatric Medical ICU (PICU)	175(5.7)	3.89
Gastrointestinal ICU	44(1.4)	7.32
Neurologic ICU	44(1.4)	13.71
Respiratory ICU	25(0.8)	7.55
High Dependency Unit (HDU)	24(0.8)	1.86
Oncologic Surgical ICU	20(0.7)	6.39
Oncologic Medical ICU	18(0.6)	6.92
Burn ICU	16(0.5)	15.37
Cardiothoracic ICU	11(0.4)	2.21
Pediatric Medical/Surgical ICU	9(0.3)	2.64
Cardiac ICU	2(0.1)	0.61
Total	3,080	5.70

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

S.No.	Name of organism	Number (Percentage)
1	<i>Klebsiella spp.</i>	159 (20.5)
2	<i>Acinetobacter sp.</i>	163 (21.0)
3	<i>Burkholderia spp.</i>	48 (6.2)
4	<i>Pseudomonas spp.</i>	38 (4.9)
5	<i>Escherichia sp.</i>	41 (5.3)
6	<i>Enterobacter spp.</i>	24 (3.1)
7	<i>Stenotrophomonas spp.</i>	12 (1.5)
8	<i>Serratia spp.</i>	13 (1.7)
9	<i>Elizabethkingia spp.</i>	6 (0.8)
10	<i>Providencia spp.</i>	3 (0.4)
11	<i>Others</i>	43 (5.5)
Total Gram-negative organisms		550 (70.9)

Table 10.18: Distribution of *Candida* sp causing CLABSIs

S. No.	Name of organism	Number (%)
1	<i>Candida tropicalis</i>	29 (3.7)
2	<i>Candida sp.</i>	11 (1.4)
3	<i>Candida auris</i>	14 (1.8)
4	<i>Candida albicans</i>	16 (2.1)
5	<i>Candida parapsilosis</i>	12 (1.5)
6	<i>Candida glabrata</i>	9 (1.2)
7	<i>Candida pelliculosa</i>	1 (0.1)
8	Other <i>Candida</i>	3 (0.4)
Total		95 (12.2)

Data of Primary Non-CLABSIs

Non-CLABSI Primary BSIs are the BSI cases for which no secondary sources are traced and that do not have a central line in place for $\geq$ 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	148 (20.2)
2	Gram-negative organisms	539 (73.6)
3	Fungi	45 (6.2)
Total		732

Table 10.28: % Susceptibility of *Enterococcus* species causing BSI, 2022

Antibiotics	<i>Enterococcus faecalis</i>	<i>Enterococcus faecium</i>	<i>Enterococcus spp.</i>
	(N = 28)	(N = 89)	(N = 35)
Ampicillin	45.8	4.1	30.0
Ciprofloxacin	16.0	7.4	21.4
Gentamicin	16.7	25.0	1/1 (100)
Linezolid	92.6	67.8	80.0
Teicoplanin	80.0	45.2	34.5
Vancomycin	74.0	57.1	79.4
Tetracycline	33.3	14.3	62.5

Table 10.29: % Susceptibility of *Staphylococcus aureus* causing BSIs, 2022

Antibiotics	<i>Staphylococcus aureus</i> (N = 137)
Erythromycin	18.5
Ciprofloxacin	23.8
Oxacillin	12.3
Clindamycin	38.3
Trimethoprim/Sulfamethoxazole	47.5
Tetracycline	34.5
Teicoplanin	42.0
Linezolid	87
Vancomycin	100

Urinary Tract Infections (UTI) data

A total of 505 cases of UTIs were reported. The distribution and profile of UTIs is shown in table 10.30. The catheter associated UTI (CAUTI) rate was 2.76/1,000 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.

Table 10.30: Type of UTI cases

Type of UTI cases	No. of UTI cases (%)
CAUTI (catheter associated UTIs)	462 (91.5)
Non-CAUTI	43 (8.5)
Total	505

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**

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 <i>Enterococcus</i>	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%)

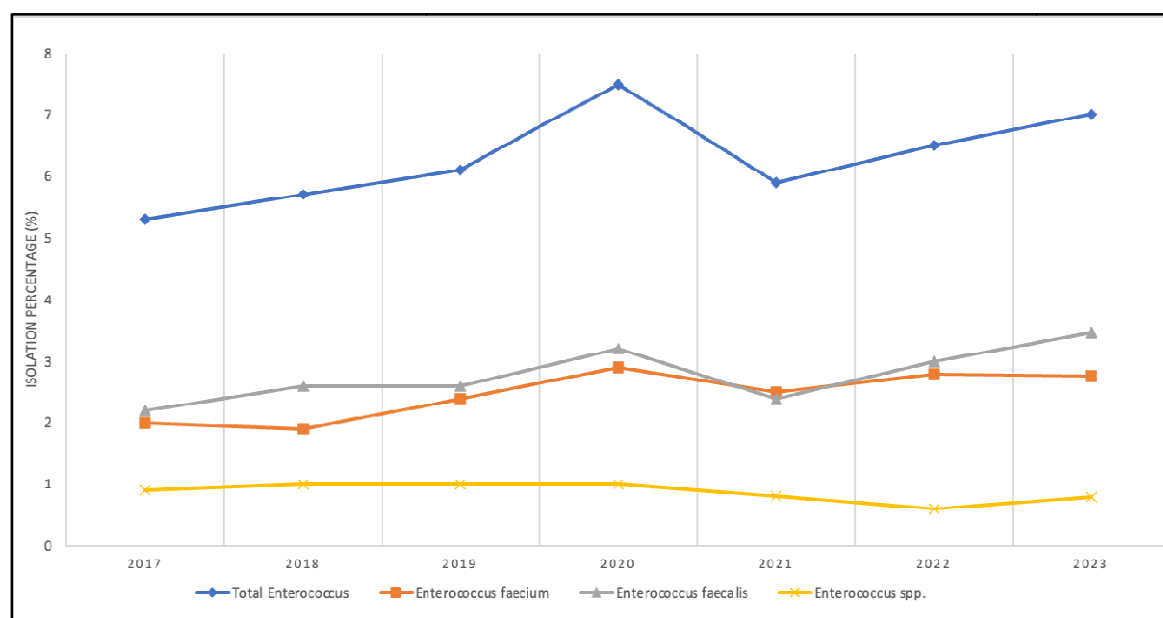


Figure 1.14: Yearly isolation trends of *Enterococcus* species

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 (S %)	OPD n=407 (S %)	Ward n=837 (S %)	ICU n=245 (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 (S %)	OPD n= 135 (S %)	Ward n=170 (S %)	ICU n=100 (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%)