HAI and AMR: The Indian Scenario- Results from India AMR Surveillance Network

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RESEARCH ARTICLE

Alarming rates of antimicrobial resistance and fungal sepsis in outborn neonates in North India

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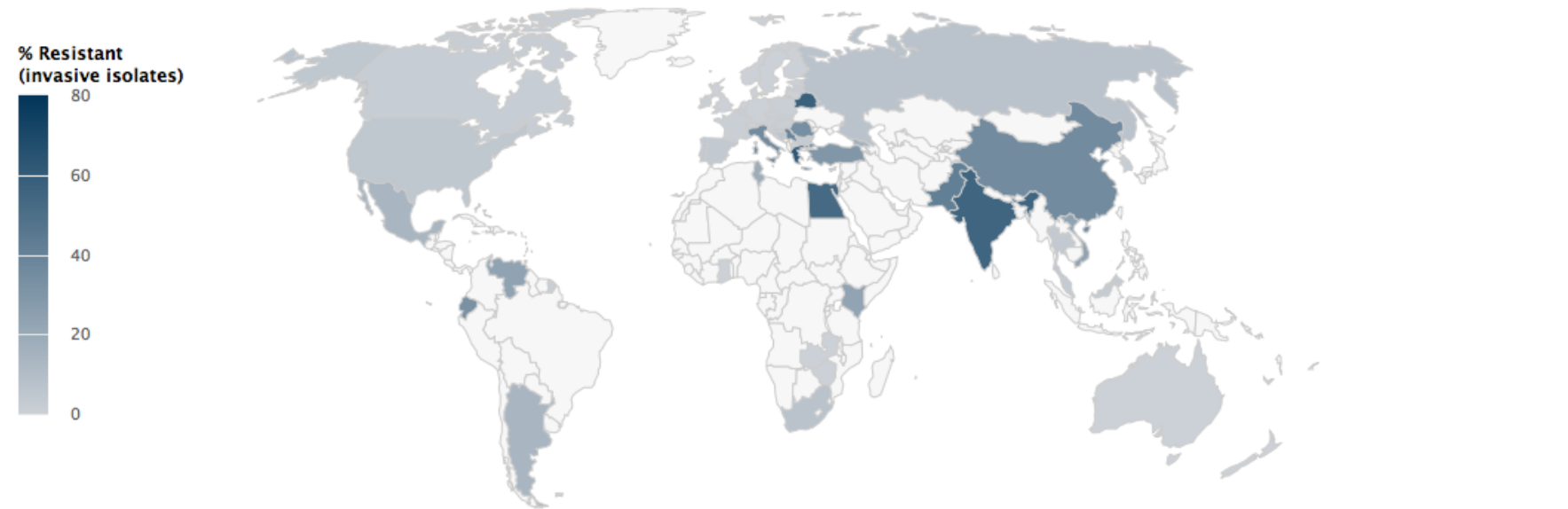
Antibiotic Resistance

Map | Trend | Chart

? Help

Resistance of *Klebsiella pneumoniae* to Carbapenems



Center for Disease Dynamics, Economics & Policy (cddep.org) © Natural Earth

Data includes aggregated resistance rates for isolates (includes intermediate resistance) from blood and cerebrospinal fluid (i.e., invasive) from inpatients of all ages. Because of differences in scope of collections and testing

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First Report on a Cluster of Colistin-Resistant *Klebsiella pneumoniae* Strains Isolated from a Tertiary Care Center in India: Whole-Genome Shotgun Sequencing

Purva Mathur,[a] Balaji Veeraraghavan,[b] Naveen Kumar Devanga Ragupathi,[b] Francis Yesurajan Inbanathan,[b] Surbhi Khurana,[a] Nidhi Bhardwaj,[a] Subodh Kumar,[a] Sushma Sagar,[a] Amit Gupta[a]

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Indian Journal of Medical Microbiology, (2016) 34(4): 495-499

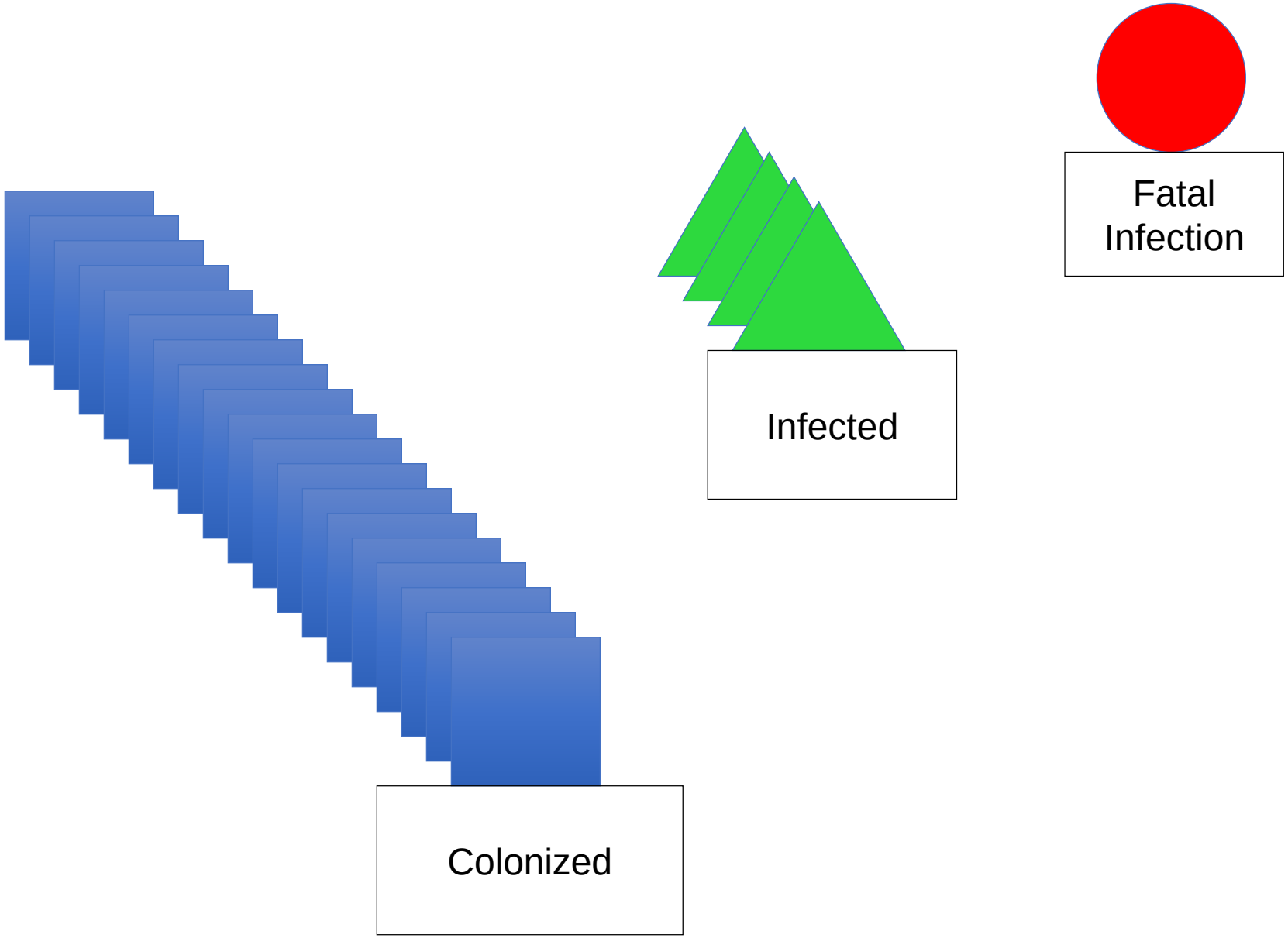
Original Article

Does the presence of *Klebsiella pneumoniae* carbapenemase and New Delhi metallo-β-lactamase-1 genes in pathogens lead to fatal outcome?

***P Mathur, S Sagar, S Kumar, V Sharma, D Gupta, S Lalwani, R Rani, A Muruganantham**

Abstract

Introduction: Infections due to multidrug-resistant (MDR) pathogens are a medical challenge. There is considerable apprehension among clinicians regarding pathogens reported as carrying New Delhi metallo-β-lactamase-1 (NDM) and *Klebsiella pneumoniae* carbapenemase (KPC) genes from their patients. In the face of extremely high rates of antimicrobial resistance, it is essential to gauge the clinical significance of isolation of pathogens carrying these genes from clinical samples. This study compares the outcome of patients infected with pathogens carrying NDM/KPC genes versus those without these genes. **Methods:** The study was conducted over a 1-year period at a Level-1 trauma centre. Hospital-acquired infections were diagnosed on the basis of CDC's criteria. The correlation of isolation of a multi-resistant pathogen carrying KPC or NDM genes with the clinical outcome was ascertained. **Results:** A total of 276 consecutive patients admitted to the Intensive Care Units/wards of the JPNA Trauma Centre were included in this study. Of the 371 isolates recovered from these patients, 116 were from patients who had a fatal outcome. The difference in prevalence of bla_{NDM} and bla_{KPC} was not significant in any genera of Gram-negative pathogens isolated from patients who survived versus those who had a fatal outcome. **Conclusion:** Isolation of MDR pathogens carrying NDM/KPC genes from clinical samples is not always a harbinger of a fatal outcome. Efforts should be made to prevent cross-transmission of these pathogens.


Fatal
Infection
Infected
Colonized

Magnitude of HAIs

- > 1.5 million people suffer from HAIs at any time
- Prevalence in developing countries:> 40 %
- HAIs kill more people every year than AIDS, Breast Cancer and Accidents put together

- Annual Direct cost of managing HAIs:
  - 6.4 billion $ US
  - 13-24 billion £ in Europe

- 30-70% of HAIs are preventable

- **If a preventive program can reduce prevalence by just 7%, the entire cost of the program is recovered.**

- **Extremely cost effective**

Surveillance

- 1/3rd of HAIs can be prevented by systematic surveillance & implementation of standard preventive guidelines.

  - SENIC Study

- HCAI surveillance systems are in place at national/sub-national level in many developed countries.

- Only 23 developing countries (23/147 [15.6%]) reported a functioning national surveillance system in a survey conducted by the WHO's First Global Patient Safety Challenge.

http://www.who.int/gpsc/country_work/summary_20100430_en.pdf

- Very scanty data available from the vast majority of low- and middle-income countries.
- Only nine published studies reported HCAI data at national level.
- HCAI rates markedly higher than those in developed countries.
- Rates vary from 5% to 19% (most studies report values higher than 10%)

ICMR
AMR Network

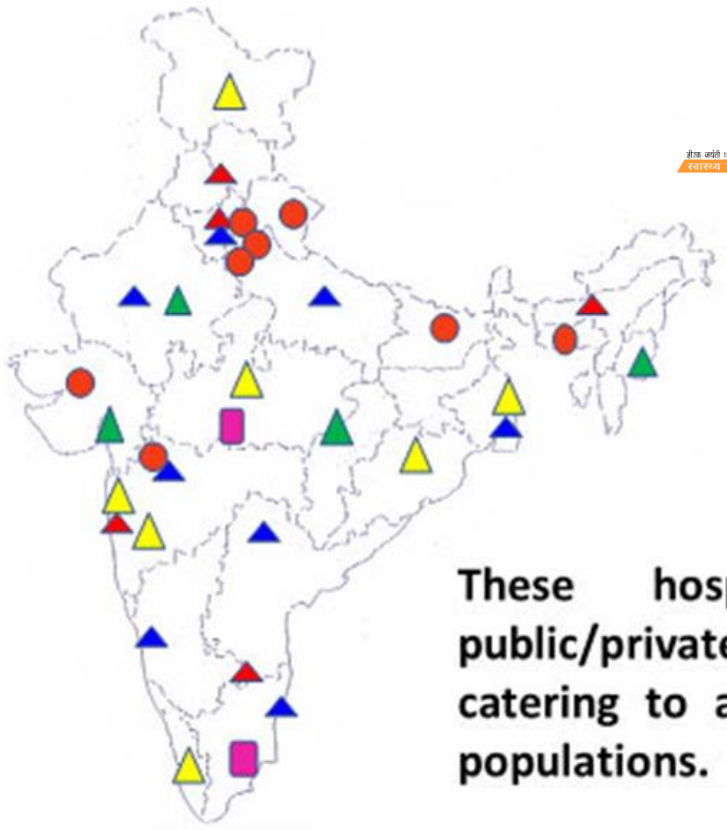
AIIMS
Systematic Surveillance of Hospital acquired Infection

CDC-GHSA:
Pan India Network

- **Surveillance**
- **Infection Control**
- **Laboratory Strengthening**
- **EQAS**
- **AMSP**

Layered on AMR

Capacity Building and Strengthening of Hospital Infection Control to detect and prevent antimicrobial resistance in India



These hospitals are a mix of public/private/missionary/army hospitals, catering to a diverse category of patient populations.

Participating Facilities
50

- ICMR- AIIMS Centers- 25
- NCDC Centers- 5
- Facilities under Swachhtta Action Plan - 6
- Voluntary Participation -14

- More Centers being planned to be trained/ included

Total ICUs included in the surveillance

ICU Type	Number
Medical ICU	24
Neonatal ICU	15
Pediatric Medical ICU	14
Medical/Surgical ICU	12
Surgical ICU	11
Cardiothoracic Surgical ICU	5
Gastrointestinal ICU	3
Repiratory ICU	3
Trauma ICU	3
Pediatric Medical/Surgical ICU	3
High Dependency Unit	2
Neurosurgical ICU	2
Burn ICU	1
Cardiac ICU	1
Neurologic ICU	1
Oncologic Medical ICU	1
Oncologic Surgical ICU	1
Total ICU	**102**

Data from May, 2017 to May, 2019

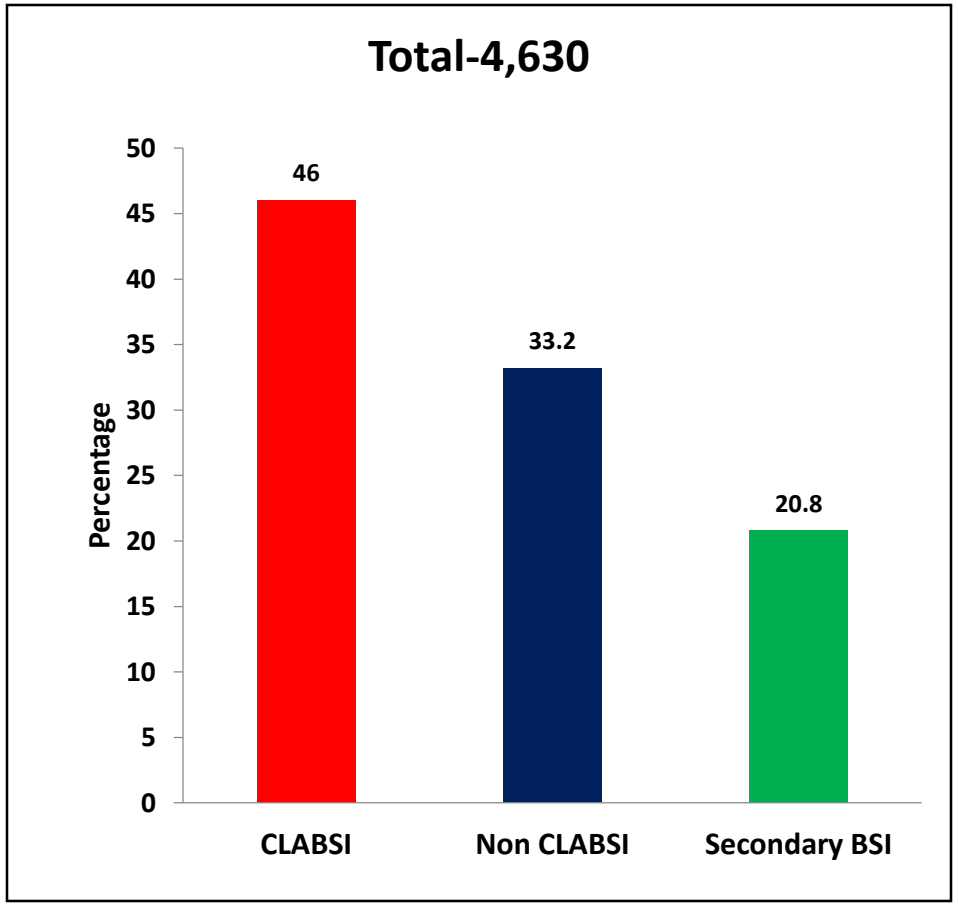
Patient Days	**7,51,672**
Central Line Days	**2,34,544**
Urinary Catheter Days	**4,26,840**

Blood Stream Infections
BSIs

May, 2017 to May, 2019

Total	**4,630**

BSI Type	Number
CLABSI	2,129 (46%)
Non CLABSI	1,536 (33.2)
Secondary BSI	965 (20.8%)
Total	4,630



BSI Rates

Patient Days	7,51,672	Total BSI Rate	6.16
Central Line Days	2,34,544	CLABSI Rate	9.07
CLABSI	2,129 (46%)	Sec. BSI Rate	1.28
NON- CLABSI	1536 (33.2%)	Non-CLABSI Rate	2.04
Secondary BSI	965 (20.8%)		

ICU- wise distribution of BSI

ICU Type	Number of BSI cases
Medical/Surgical ICU	986 (21.3)
Medical ICU	888 (19.2)
Neonatal ICU	854 (18.4)
Surgical ICU	425 (9.2)
Trauma ICU	543 (11.7)
Pediatric Medical ICU	327 (7.1)
Gastrointestinal ICU	149 (3.1)
Neurosurgical ICU	95 (2.1)
Cardiothoracic Surgical ICU	86 (1.9)
High Dependency Unit	84 (1.8)
Respiratory ICU	79 (1.7)
Pediatric Medical/Surgical ICU	38 (0.8)
Oncologic Medical ICU	27 (0.6)
Burn ICU	24 (0.5)
Neurologic ICU	13 (0.3)
Oncologic Surgical ICU	7 (0.2)
Cardiac ICU	5 (0.1)
Total BSI	4630

Basic demographics, Fatality and Length of stay

Gender	Number	Age range	Age median
Male	3,011 (65%)	- 4 to 95	34
Female	1619	- 3 to 95	48

Average length of stay	24 days
Range of Stay	3 to 1,703 days
Median	21 days

14 day fatal outcome	1,736 (37.5%)
Final fatal outcome	471 + 1,736= 2,207 (47.7%)

Distribution of BSI cases by duration of events

	Median	Range
Duration between date of admission and date of event	9	2 – 1,467

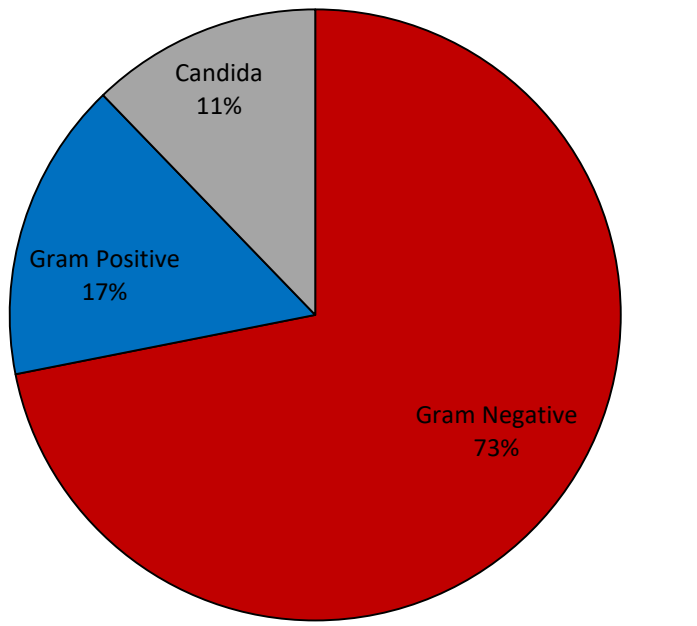
Duration of stay btw date of admission in unit and DOE (Days)	Number of patients	Duration of stay btw date of admission in unit and DOE (Days)	Number of patients
		35	5
3	405	36	2
4	187	37	2
5	155	38	3
6	145	39	8
7	129	42	3
8	89	43	1
9	89	44	1
10	63	45	2
11	54	46	2
12	42	47	1
13	36	48	3
14	39	49	3
15	17	50	1
16	21	51	4
17	22	53	1
18	18	55	2
19	15	56	1
20	11	57	2
21	18	59	1
22	14	60	2
23	6	61	1
24	12	62	1
25	11	68	1
26	10	74	1
27	12	77	1
28	6	83	1
29	8	85	1
30	9	90	3
31	7	96	1
32	5	102	1
33	3	146	1
34	4		

Distribution of CLABSI cases by location of central lines

Location of central line	No. of CLABSI cases (%)
Jugular	1354 (63.1)
Subclavian	451 (21)
Umbilical	210 (9.8)
Femoral	71 (3.3)
Branchial	29 (1.4)
Multiple	30 (1.4)
Total	2,145

Organisms causing BSI

Organism Type	Number
Gram Negative	3,651
Gram Positive	835
Candida	530
Total	5,016



Distribution of organisms

Distribution of organisms causing BSI

S. No.	Name of organism	Number (%)
1	***Acinetobacter sp.***	**1195 (24.6)**
2	***Klebsiella sp.***	**1165 (24)**
3	***Candida sp.***	**515 (10.6)**
4	***Staphylococcus sp.***	**422 (8.7)**
5	***Enterococcus sp.***	**404 (8.3)**
6	***Pseudomonas sp.***	**324 (6.8)**
7	***Escherichia sp.***	**259 (5.3)**
8	***Burkholderia sp.***	**212 (4.4)**
9	***Enterobacter sp.***	**186 (3.8)**
10	***Stenotrophomonas spp.***	**60 (1.2)**
11	***Citrobacter sp.***	**56 (1.2)**
12	***Serratia spp.***	**56 (1.2)**
13	**Others**	**162 (3.3)**
Total		5,016

Percentage distribution of Gram Negative Organisms causing BSI

Organisms	Number (%)
Acinetobacter spp.	1195 (33.7)
Klebsiella spp.	1165 (32.0)
Pseudomonas spp.	324 (8.9)
Escherichia coli	259 (7.1)
Burkholderia spp.	212 (5.8)
Enterobacter spp.	186 (5.1)
Stenotrophomonas spp.	60 (1.6)
Citrobacter spp.	56 (1.5)
Serratia spp.	56 (1.5)
Proteus spp.	23 (0.6)
Chryseobacterium spp.	15 (0.4)
Others	*101 (2.8)*
Total	3652

Organisms	Number (%)
Klebsiella pneumoniae	1118/1165 (96)
Burkholderia cepaciae	195/212 (92.0)
Pseudomonas aeruginosa	271/324 (83.6)
Acinetobacter baumannii	990/1195 (83.0)
Enterobacter cloacae	91/185 (49.1)
Citrobacter freundii	26/56 (46.4)
Citrobacter koseri	11/34 (32.4)
Enterobacter aerogenes	53/185 (28.6)

Percentage distribution of Gram Positive Organisms

Organisms	Number (%)
Staphylococcus spp.	422 (50.5)
Enterococcus spp.	404 (48.4)
Streptococcus spp.	6 (0.7)
Leuconostoc pseudomesenteroides	2 (0.2)
Weissella confusa	1 (0.1)
Total	835

Organism Name	Number (%)
Staphylococcus aureus	343/422 (81.3)
Enterococcus faecium	249/404 (61.6)
Enterococcus spp.	83/404 (20.5)
Staphylococcus spp.	79/422 (18.7)
Enterococcus faecalis	72/404 (17.8)

Percentage distribution of Candida

Organisms	Number (%)
Candida spp.	515 (97.2)
Trichosporon ashaii	4 (0.8)
Cryptococcus neoformans	4 (0.8)
Geotrichum capitatum	1 (0.2)
Kodamaea ohmeri	3 (0.6)
Yeast spp.	3 (0.6)
Total	530

Organisms	Number (%)
Candida tropicalis	138 (26.8)
Candida parapsilosis	77 (15)
Candida glabrata	76 (14.8)
Candida albicans	64 (12.4)
Candida auris	51 (9.9)
Candida utilis	47 (9.1)
Candida spp.	33 (6.4)
Candida pelliculosa	16 (3.1)
Non albican candida	7 (1.4)
Candida haemulonii	3 (0.6)
Candida lusitaniae	3 (0.6)
Total	515

CLABSI

S. No.	Organism	No. (%)
1	*Acinetobacter sp.*	504 (21)
2	*Klebsiella sp.*	480 (20)
3	*Candida sp.*	258 (10.8)
4	*Enterococcus sp.*	224 (9.3)
5	*Pseudomonas sp.*	180 (7.5)
6	*Burkholderia sp.*	182 (7.6)
7	*Staphylococcus sp.*	162 (6.7)
8	*Enterobacter sp.*	110 (4.6)
9	*Escherichia sp.*	108 (4.5)
10	*Stenotrophomonas sp.*	46 (1.9)
11	*Serratia sp.*	33 (1.4)
12	Others	117 (4.9)
Total		2404

Non-CLABSI

S. No.	Organism	No. (%)
1	*Klebsiella sp.*	344 (21.2)
2	*Acinetobacter sp.*	333 (20.6)
3	*Staphylococcus sp.*	225 (13.9)
4	*Candida sp.*	210 (13)
5	*Enterococcus sp.*	156 (9.6)
6	*Escherichia sp.*	98 (6)
7	*Enterobacter sp.*	68 (4.2)
8	*Pseudomonas sp.*	57 (3.5)
9	*Citrobacter sp.*	28 (1.7)
10	*Burkholderia sp.*	27 (1.7)
11	Others	74 (4.5)
Total		1620

Secondary

S. No.	Organism	No. (%)
1	Acinetobacter sp.	357 (36)
2	*Klebsiella sp.*	341(34.4)
3	*Pseudomonas sp.*	87(8.8)
4	*Escherichia sp.*	53(5.3)
5	*Candida sp.*	50(5)
6	*Staphylococcus sp.*	36(3.6)
7	*Enterococcus sp.*	24(2.4)
8	*Enterobacter sp.*	9(0.9)
9	*Serratia sp.*	9(0.9)
10	Others	26(2.6)
Total		992

AMR

Antimicrobials	*Klebsiella pneumoniae* 1,118	*E. coli* 259	*Enterobacter sp.* 187
Aminoglycoside	66.7	42.9	36.2
Quinolone	78.3	83.9	41.6
Third Gen Cephalosporin	91.2	90.5	71.4
Carbapenem	62.4	47.4	Mero 31.4 (58/170) Imipenem: 88.4 (63/164)
Tigecycline	26.9	3.1	7.3
Colistin			

Antimicrobials	*Acinetobacter baumannii* 990	*Pseudomonas aeruginosa* 271
Aminoglycoside	82.3	59.4
Quinolone	88.2	59.6
Third Gen Cephalosporin	92	64.4
Carbapenem	86	62.9
Tigecycline	11.4	
Colistin		
Piperacillin Tazobactam		44.4
Aztreonam		53.2

Colistin Resistance in BSI cases

Organism name	Number	%R
Acinetobacter baumanni	**20/614**	**3.26**
E. coli	**2/166**	**1.2**
Klebsiella pneumoniae	**57/701**	**8.13**
Pseudomonas aeruginosa	**4/167**	**2.39**
Enterobacter spp	**5/88**	**5.68**

Staphylococcus aureus; n= 344

Antibiotic name	Number	%R
Ciprofloxacin	129/192	67.2
Clindamycin	163/285	57.2
Daptomycin	2/61	3.3
Erythromycin	235/323	72.8
Cefoxitin	128/191	67.0
Gentamicin	86/235	36.6
Linezolid	9/273	3.3
Oxacillin	51/98	52.0
Rifampicin	12/51	23.5
Trimethoprim/Sulfamethoxazole	104/218	47.7
Teicoplanin	0	0
Tigecycline	4/67	6.0
Vancomycin	0	0

Antimicrobials	*Enterococcus faecium* *n= 249*	*Enterococcus faecalis* *n= 72*
Gentamicin-High	84.2	66.7
Linezolid	9.4	3.8
Vancomycin	32.3	11.4

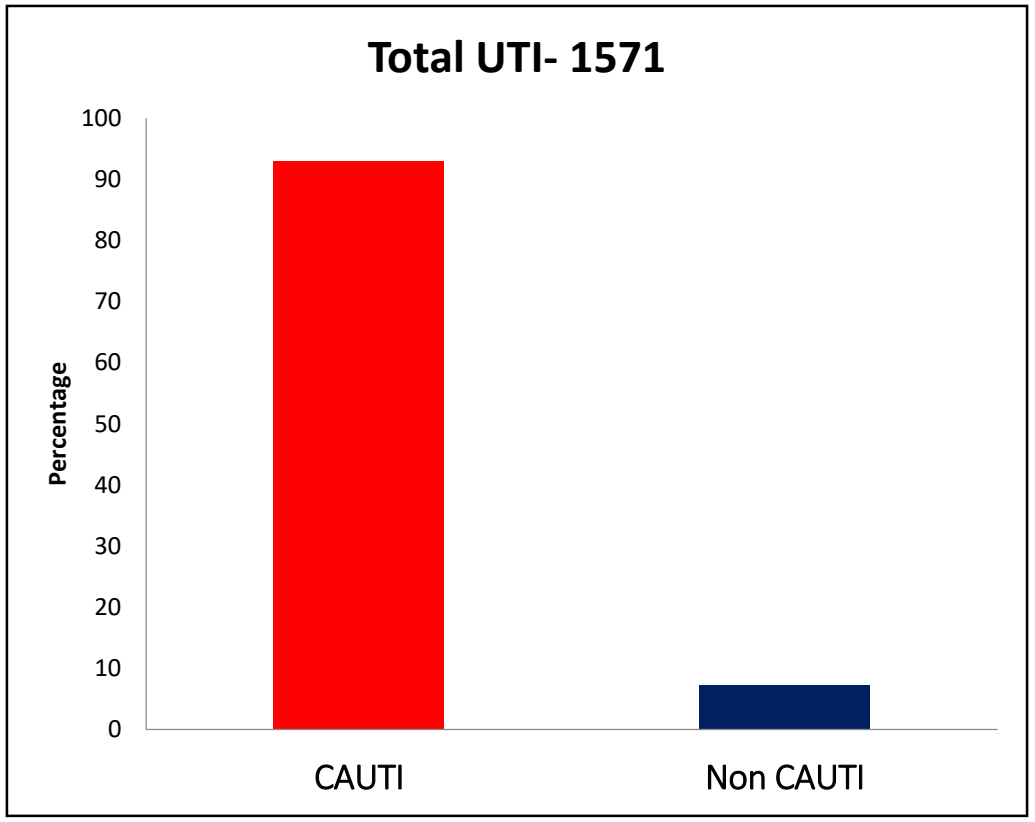
Candida spp.; n= 62

Antibiotic name	Number	%R
Caspofungin	5/35	14.3
Fluconazole	14/45	31.1
FLUCY	7/29	24.1
Voriconazole	4/46	8.7

UTI

Data from May, 2017 to May, 2019

UTI Type	Number
CAUTI	1456 (92.6%)
Non CAUTI	115
Total	1,571



UTI Rates

Patient Days	7,51,672
Urinary Catheter Days	4,26,840
CAUTI	1,456 (92.3%)
NON- CAUTI	115 (7.3%)

Total UTI Rate	2.09
CAUTI Rate	3.41
NON-CAUTI Rate	0.15

Number of UTI cases- ICU wise

ICU Type	Number of UTI cases
Medical/Surgical ICU	362
Medical ICU	483
Surgical ICU	150
Pediatric Medical ICU	111
Neurosurgical ICU	23
Trauma ICU	207
Oncologic Medical ICU	23
Gastrointestinal ICU	20
High Dependency Unit	36
Neonatal ICU	21
Pediatric Medical/Surgical ICU	9
Neurologic ICU	13
Respiratory ICU	20
Oncologic Surgical ICU	7
Anaesthesia / Medicals	77
Cardiothoracic Surgical ICUs	9
Total	1,571

Gender	Number	Age Range	Age Median
Male	938 (59.7%)	-1 to 95	40
Female	633	-1 to 90	39

Average length of stay in Unit	33
Range of Stay	3-213
Median of Stay	23

14 day fatal outcome	369 (23.5%)
Final fatal outcome	549 (34.9%)

Duration of events

	Median	Range
Duration between date of admission and date of event	11	3 – 1217

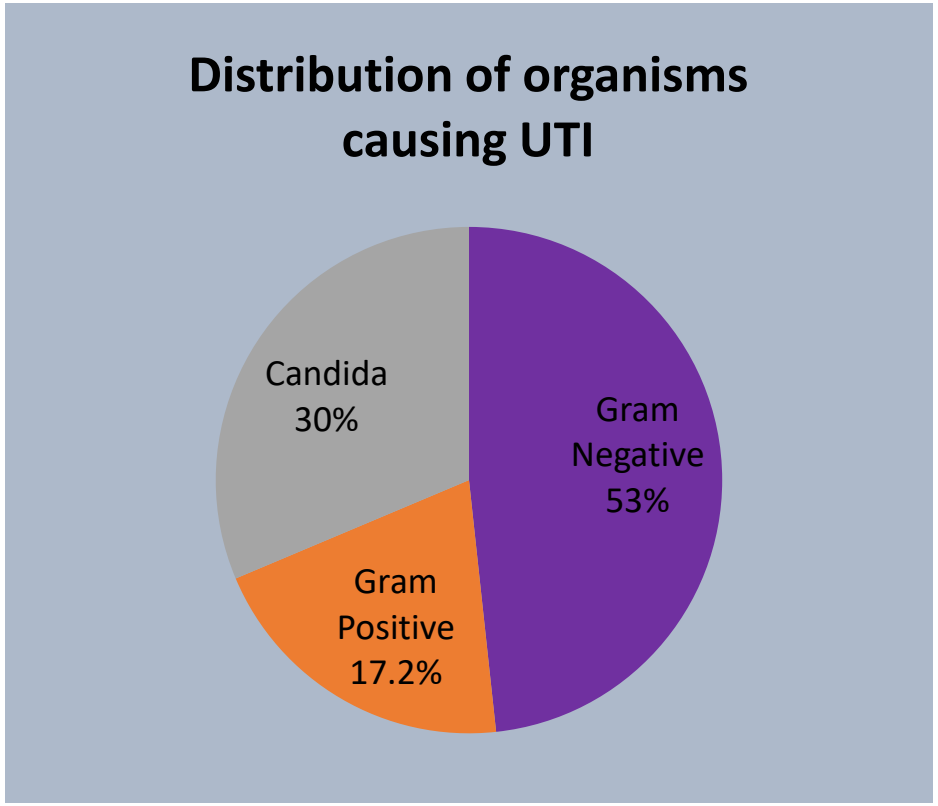
Duration between DOA in unit and DEO (Days)	Patients	Duration between DOA in unit and DEO (Days)	Patients
		31	3
3	126	32	3
4	59	33	1
5	34	35	2
6	36	36	1
7	30	37	2
8	34	39	2
9	19	40	2
10	23	42	2
11	22	45	2
12	10	48	1
13	13	50	2
14	15	51	1
15	9	53	2
16	19	54	3
17	8	60	1
18	7	61	1
19	7	63	1
20	8	66	1
21	2	68	1
22	4	77	1
23	2	78	1
24	3	80	1
25	5	81	1
26	3	90	1
27	3	144	1
28	4	173	1
29	2	333	1
30	6		

Distribution of organisms causing UTI

S. No.	Organism	Number (%)
1	*Candida sp.*	478(29.2)
2	*Escherichia sp.*	286 (17.4)
3	*Enterococcus sp.*	269 (16.4)
4	*Klebsiella sp.*	233 (14.2)
5	*Pseudomonas sp.*	140 (8.5)
6	*Acinetobacter sp.*	84 (5.1)
7	*Enterobacter sp.*	20 (1.2)
8	*Proteus sp.*	33 (2)
9	*Providencia sp.*	33 (2)
10	*Citrobacter sp.*	14 (0.9)
11	*Staphylococcus sp.*	13 (0.8)
12	Others	35 (2.1)
Total		1,638

Organisms causing UTI

Organism Type	Number
Gram Negative	867
Candida	489
Gram Positive	282
Total	1,638



Gram Negative Organisms causing UTI

Organism Name (total - 1638)	Number (%)
Escherichia coli	286 (17.5)
Klebsiella spp.	233 (14.2)
Pseudomonas spp.	140 (8.5)
Acinetobacter spp.	84 (5.1)
Proteus spp.	33 (2.0)
Providencia spp.	33 (2.0)
Enterobacter spp.	20 (1.2)

Organism Name (Species level)	Number (%)
Klebsiella pneumoniae	203/233 (87.1)
Pseudomonas aeruginosa	120/140 (85.7)
Acinetobacter baumannii	70/84 (83.3)
Proteus mirabilis	29/33 (87.9)
Enterobacter aerogenes	4/20 (20.0)
Enterobacter cloacae	6/20 (30.0)

Gram Positive Organisms causing UTI

Organism Name	Number (%)
Enterococcus faecium	133 (47.2)
Enterococcus spp.	83 (29.4)
Enterococcus faecalis	53 (18.8)
Staphylococcus aureus	10 (3.5)
Staphylococcus spp.	3 (1.1)
Total	282

Distribution of Candida sp causing UTI

Organism Name	Number (%)
Candida spp.	139 (28.4)
Candida tropicalis	114 (23.3)
Candida albicans	120 (24.5)
Candida auris	15 (3.1)
Candida glabrata	26 (5.3)
Candida parapsilosis	15 (3.1)
Trichosporon ashaii	11 (2.2)
Candida utilis	5 (1.0)
Candida non-albicans	44 (9.0)
Total	489

AMR

Antimicrobials	*Klebsiella pneumoniae 203*	*E. coli 286*
Aminoglycoside	70	44.6
Quinolone	83.7	74.8
Third Gen Cephalosporin	95.1	88.5
Carbapenem	71.3	52.1
Tigecycline	23.2	1.3
Colistin		

Antimicrobials	*Acinetobacter baumannii* 70	*Pseudomonas aeruginosa* 120
Aminoglycoside	82	73.7
Quinolone	94.6	77.8
Third Gen Cephalosporin	97.1	80.9
Carbapenem	87	66
Tigecycline		
Colistin		
Piperacillin Tazobactam		55
Aztreonam		57.1

Antimicrobials	*Enterococcus faecium* *n= 249*	*Enterococcus faecalis* *n= 72*
Gentamicin-High	71.4	89.4
Linezolid	2.9	10.9
Vancomycin	17.3	46.6
Nitrofurantoin	35.1	61.4

Candida spp.; N= 139

Antibiotic name	Number	%R
Voriconazole	27/28	96
Caspofungin	3/24	13
Flucy	2/22	9
Fluconazole	2/28	7
Mica	1/21	5

ICMR initiative on AMR Surveillance and Antimicrobial Stewardship

Dr Kamini Walia, Program officer Antimicrobial Resistance Initiative

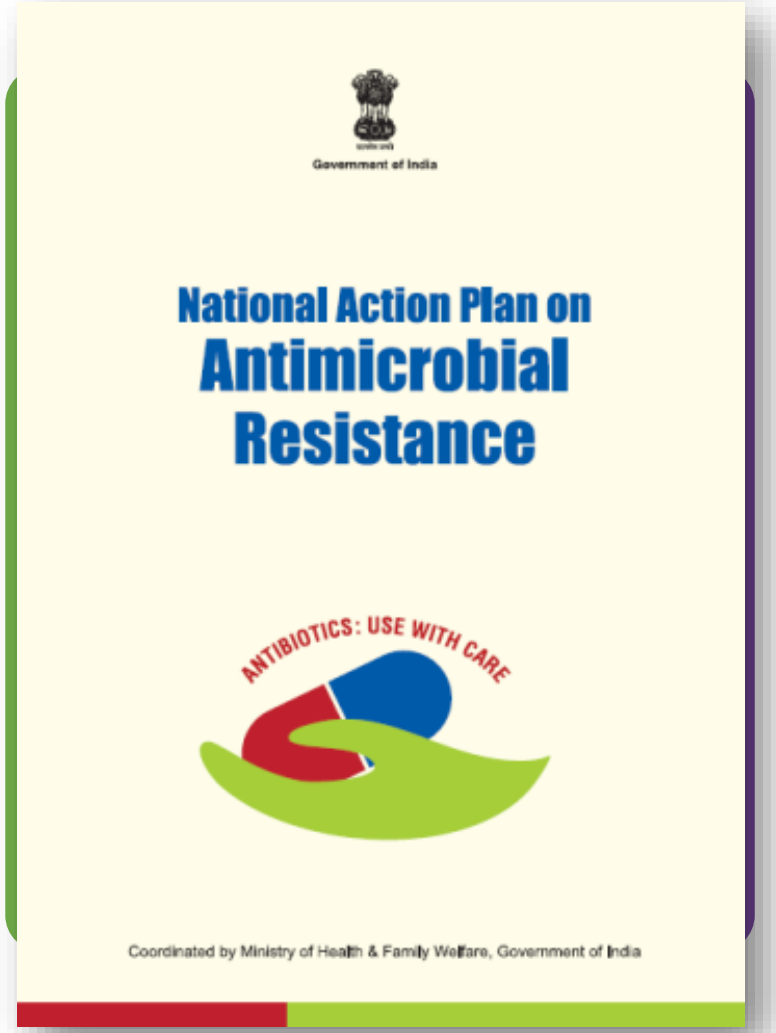
NAP-AMR

1. Awareness & understanding

- Communication & IEC
- Education, Training

2. Knowledge & evidence

- Surveillance of AMR
  AM residues
- Laboratories



5. Innovations R&D Finance

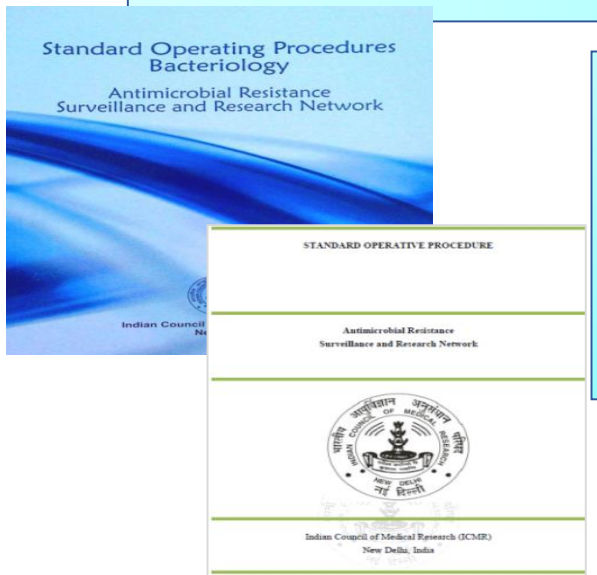
- New medicines, diagnostics, vaccines
- Innovations
- Investments

6. Leadership

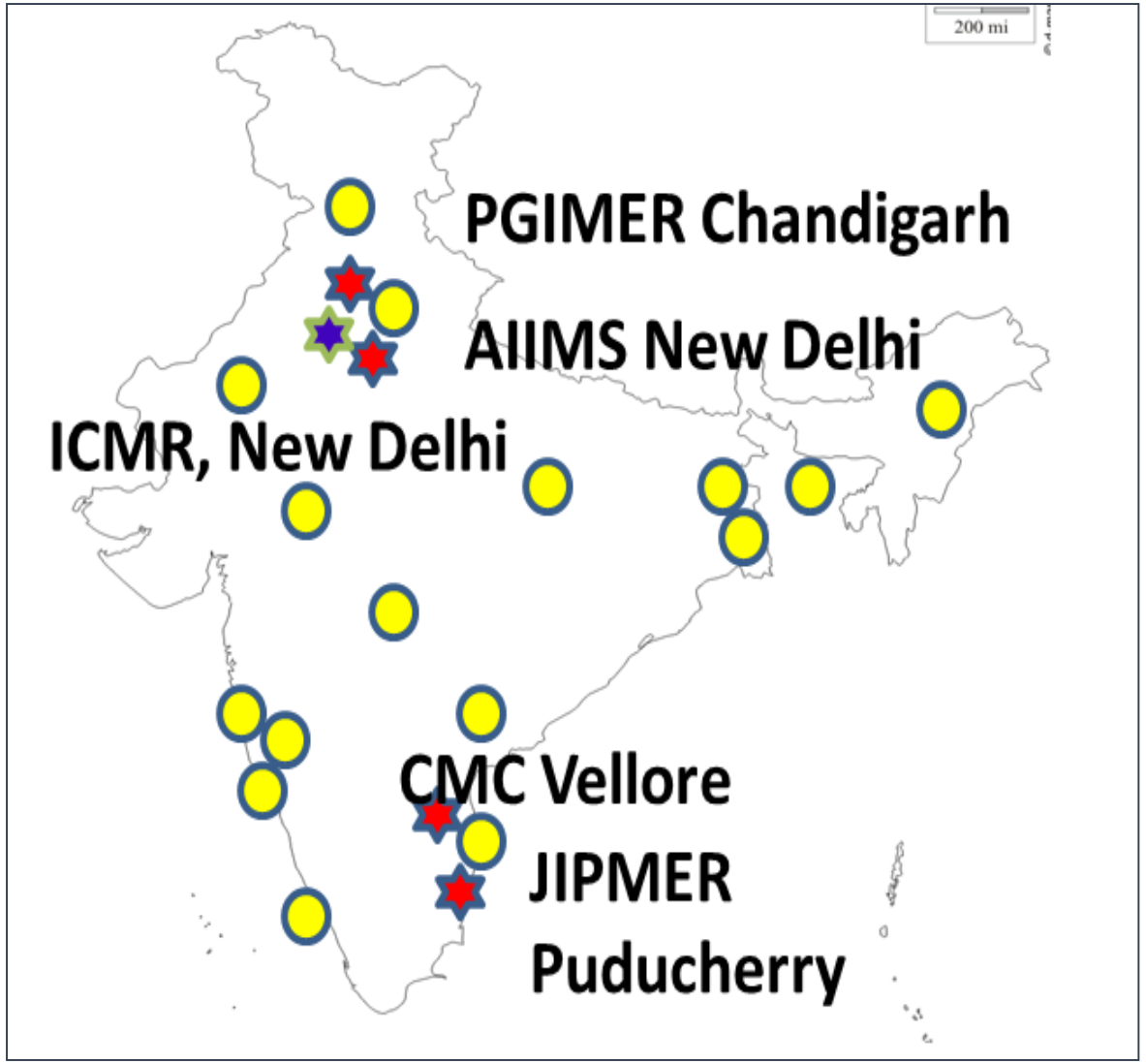
- International
- National
- States/UTs

Antimicrobial Research & Surveillance Network at ICMR

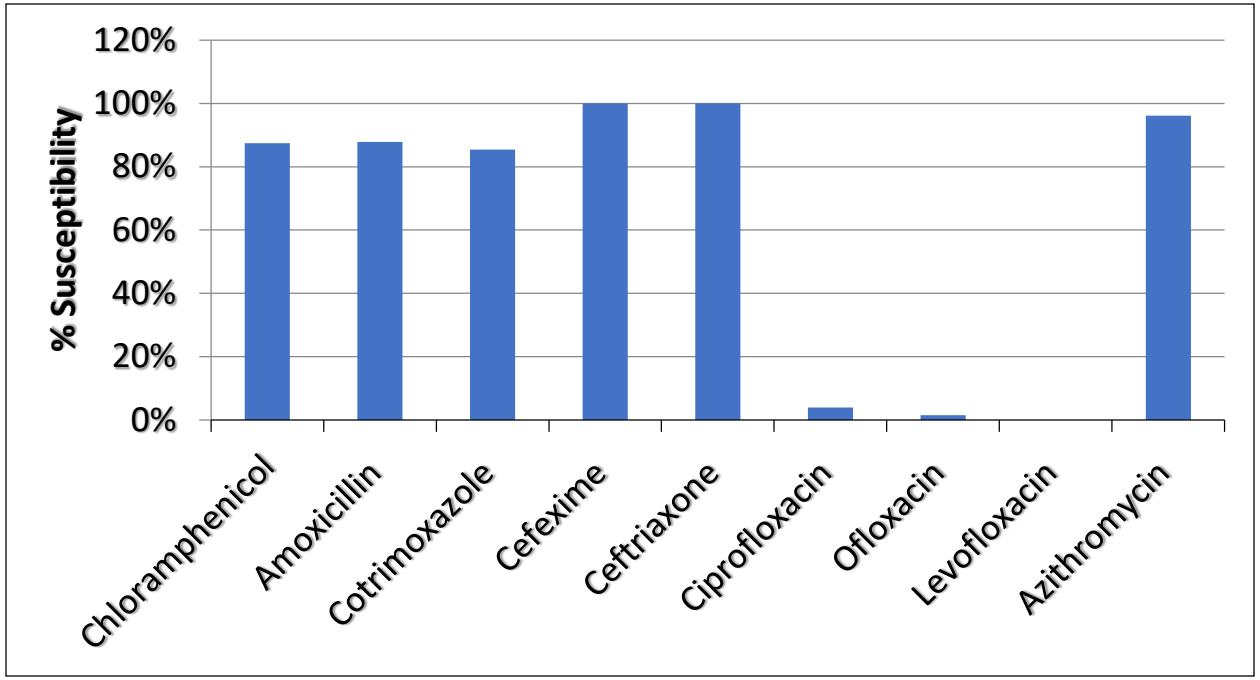
- *Enterobacteriaceae* / sepsis
- Gram negative non-fermenters
- Enteric fever organisms
- Diarrhoeagenic organisms
- MRSA, Enterococcus
- Fungal pathogens

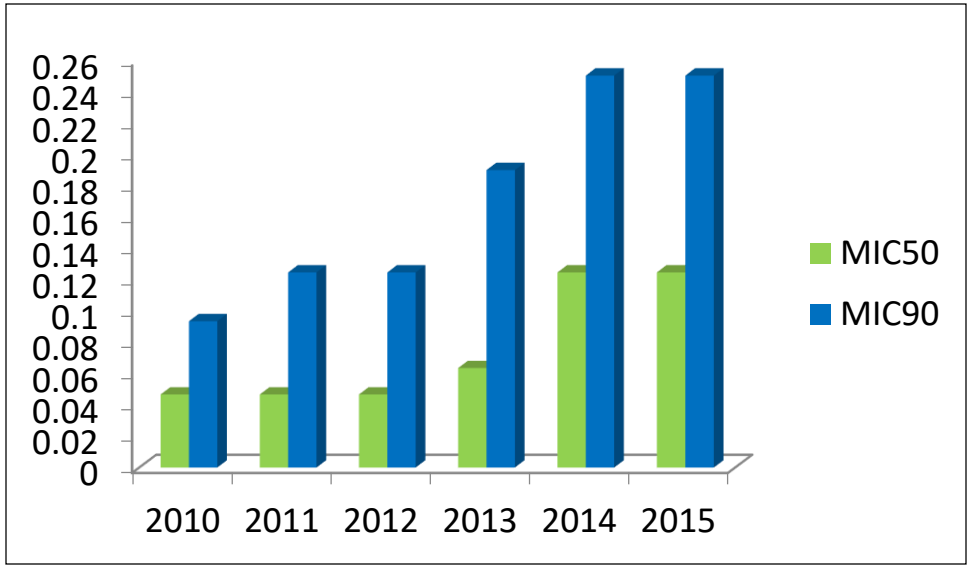


- *Standardisation*
- *Harmonisation*
- *SOPs*
- *EQAS*



Present Cumulative Antibiogram of Typhoidal Salmonellae



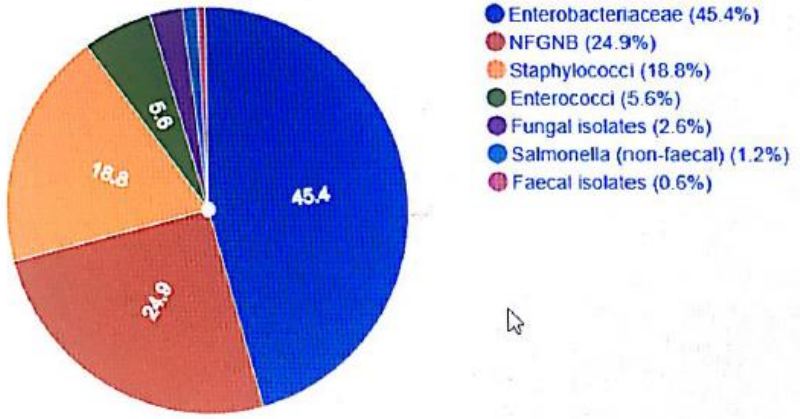


Increasing MIC to ceftriaxone in *Salmonella typhi*

- ***S.typhi*** multidrug resistance (MDR) : 100% sensitive to ampicillin, chloramphenicol and cotrimoxazole, cefixime
- High resistance to FQ, Ciprofloxacn **in** *S. typhi* is increasingly reported

Gram negatives are of serious concern

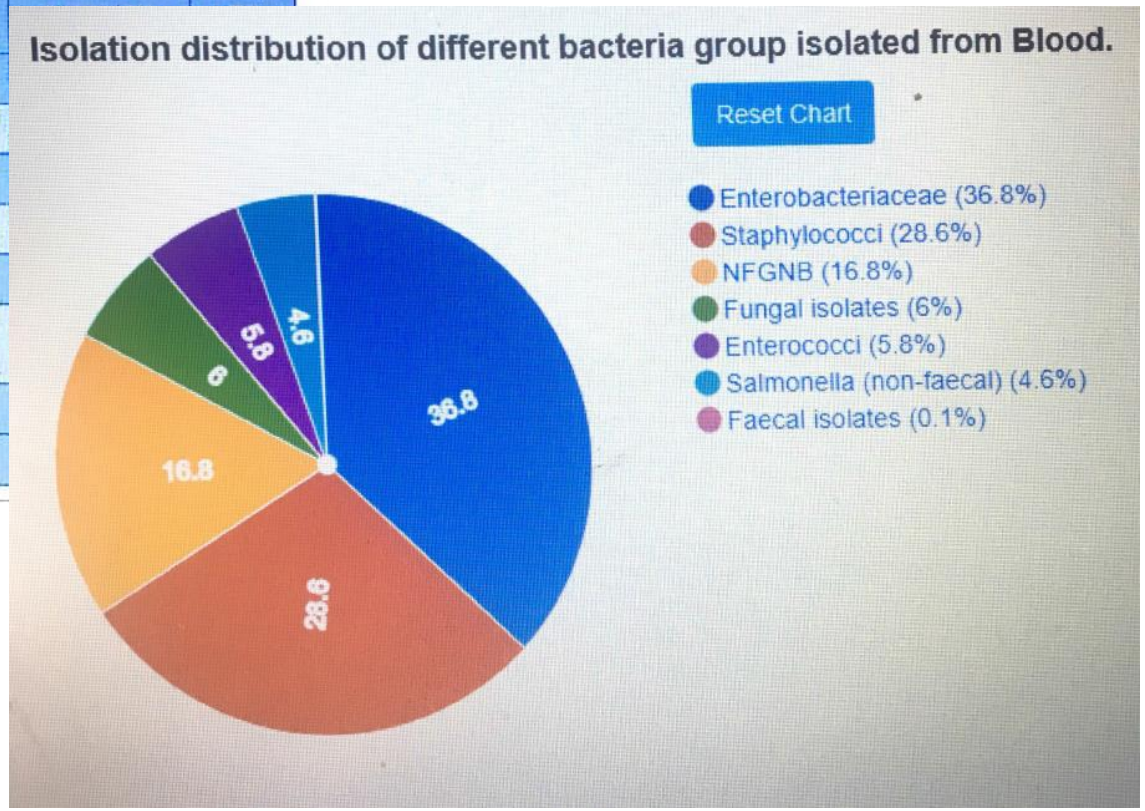
Isolation distribution of different bacteria group isolated from all specimens.



Bacteria (Group/Sub-group/Species)	Number of	Percent
Enterobacteriaceae		
NFGNB		
Staphylococci		
Enterococci		
Fungal isolates		
Salmonella (non-faecal)		
Faecal isolates		
Total		

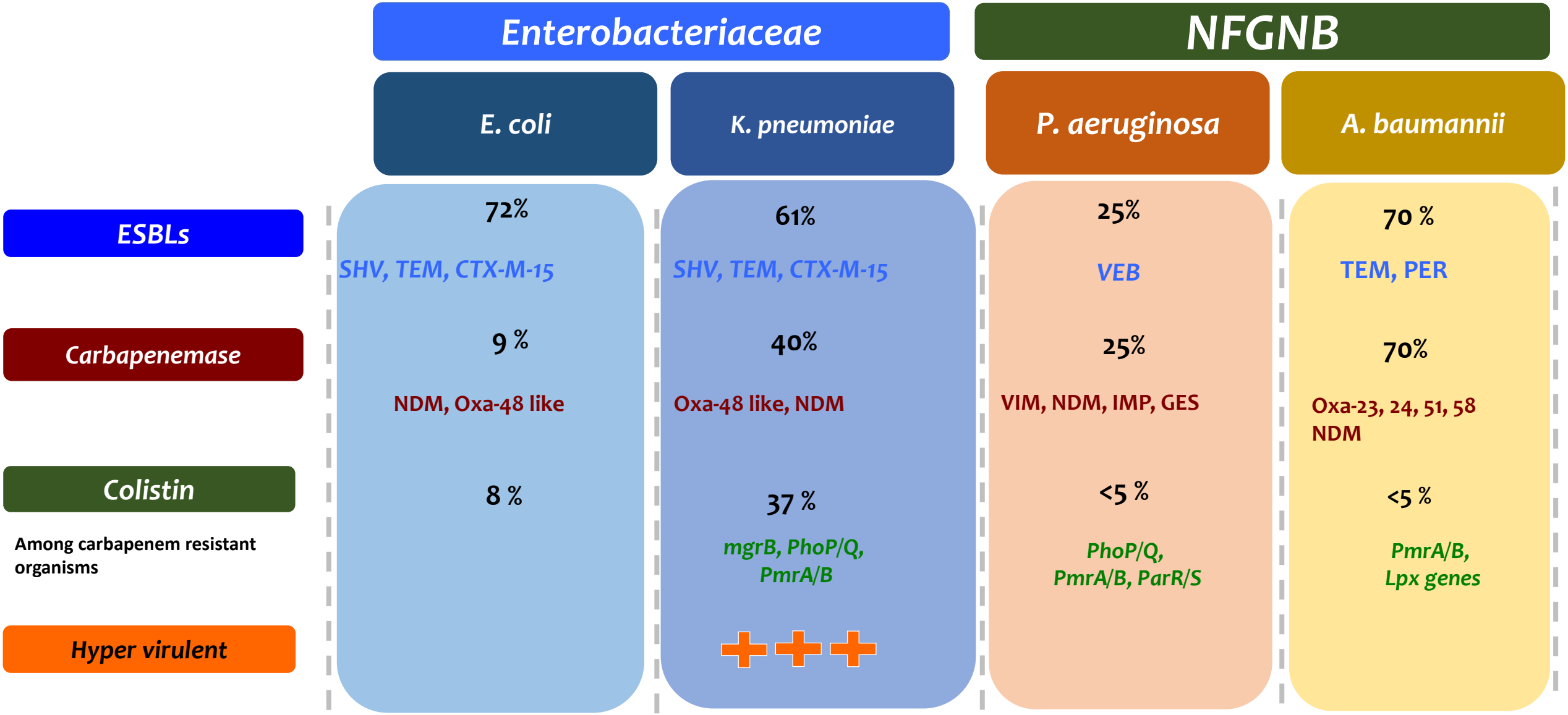
Notes:

1. Blood includes: Blood-central catheter, Blood-peripheral and Peripheral catheter-blood



Current antimicrobial susceptibility profile, molecular resistance mechanisms, common mobile genetic elements and lineages observed in India

	Cephalosporin		Carbapenems		Colistin* (among carbapenem resistance)		MGEs	Lineages
	Percentage resistance	Molecular mechanism of resistance	Percentage resistance	Molecular mechanism of resistance	Percentage resistance	Molecular mechanism of resistance (chromosomal mutations)	Associated with resistance	International/ Indian high risk clones
E. coli	Up to 70%	bla_{SHV}, bla_{TEM}, bla_{OXA-1}, $bla_{CTX-M-15}$	Up to 10%	bla_{NDM}, $bla_{OXA-48\ like}$	8%	Scanty information on chromosomal mutations	IncFII - 93% IncFIA - 87% IncFIB (AP001918) - 63% IncL1-40 Col (BS512) - 43 Integron - Class 1	ST131/ST167
K. pneumoniae	Up to 60%	bla_{SHV}, bla_{TEM}, $bla_{CTX-M-15}$	Up to 40%	$bla_{OXA-48like}$, bla_{NDM}	37%	Mutations in *mgrB, PhoP/Q, PmrA/B*	ColKP3-44 IncFIB - 24 IncR - 24 IncFIA - 22 IncFIB (pQil) - 22 Integron - Class 1	ST258/ST14, ST231
P. aeruginosa	Up to 25%	bla_{VEB}	Up to 25%	bla_{VIM}, bla_{NDM}, bla_{IMP}	<5%	Mutations in *PhoP/Q, PmrA/B, ParR/S*	IncP Integron - Class 1	ST111, ST233, ST235, ST244, ST357/ST664, ST1047, ST823, ST773
A. baumannii	Up to 70%	bla_{TEM}, bla_{PER}	Up to 70%	$bla_{OXA-23/24like}$, bla_{NDM}	<5%	Mutations in *PmrA/B, Lpx*	Integron - Class 1 Insertion sequences - ISAba1	ST457, ST195/ ST862


Enterobacteriaceae
NFGNB
E. coli
K. pneumoniae
P. aeruginosa
A. baumannii
ESBLs
Carbapenemase
Colistin
Among carbapenem resistant organisms
Hyper virulent
72%
SHV, TEM, CTX-M-15
9 %
NDM, Oxa-48 like
8 %
61%
SHV, TEM, CTX-M-15
40%
Oxa-48 like, NDM
37 %
mgrB, PhoP/Q, PmrA/B
+++
25%
VEB
25%
VIM, NDM, IMP, GES
<5 %
PhoP/Q, PmrA/B, ParR/S
70 %
TEM, PER
70%
Oxa-23, 24, 51, 58
NDM
<5 %
PmrA/B, Lpx genes

Antimicrobial Stewardship

- Using evidence for treatment guidelines
- Infection control guidelines
- Antimicrobial Stewardship guidelines
- AMSP workshops led by ID physicians
- 60 medical colleges/hospitals both Govt and Private
- More than 300 staff trained
- One year AMSP projects initiated in ICMR-AMR network hospitals

- Creating Antibiogram for the hospital
- Creating Antibiotic Policy (HAI & Choice) based on the hospital antibiogram, including surgical prophylaxis
- Carry out Culture of cultures: point prevalence study 1 day in 3 months
- Carry out Antibiotic consumption in ICUs using ICMR tool (DOTS/DDD)
- Initiate audit : Carbapenem, Polymyxin prescriptions in ICU
- Initiate Formulary restriction for Polymyxins (Colistin)
- Carry out workshops for Education: One event for own hospital and one for hospitals and practitioners in the region


Faleminderit
danke
謝謝
teşekkür ederim
thank you
gracias
спасибо
dank je
tapadh leat
mochchakkeram
bedankt
hvala
dziękuję
go raibh maith agat
obrigado
sukriya
kop khun krap
arigato
takk
dakujem
grazie
terima kasih
merci
감사합니다
ευχαριστώ
мерси