



STUDY ON PREVALENCE AND SENSITIVITY PATTERN OF MICROORGANISMS AT A PRIVATE CORPORATE HOSPITAL

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ABSTRACT

AMR (Antimicrobial Resistance) is a complex global public health challenge, and no single or simple strategy will be sufficient to fully contain the emergence and spread of infectious organisms that become resistant to the available antimicrobial drugs. The retrospective study was conducted for a period of 2 years at a 700-bedded multi-speciality

private tertiary care hospital at Coimbatore, Tamil Nadu. A total of 6591 cases were analyzed during retrospective study. Nineteen different micro-organisms were isolated of which major organisms identified were *S. pneumoniae* (27%), *Klebsiella species* (21.8%), *E. coli* (15.3%), *S. aureus* (10.6%), *Pseudomonas* (8.3%), *S. pyogenes* (7.3%). The retrospective data revealed that almost all organisms were highly sensitive to Imipenam. The evidence obtained indicated that AMR has a significant adverse impact on clinical outcomes and leads to higher costs due to consumption of health-care resources.

KEYWORDS: AMR (Antimicrobial Resistance), *S. pneumoniae*, *Klebsiella species*, *E. coli*, *S. aureus*, *Pseudomonas*, *S. pyogenes*.

INTRODUCTION

Use of antibacterial drugs has become widespread over several decades (although equitable access to antibacterial drugs is far from being available worldwide), and these drugs have been extensively misused in humans in ways that favour the selection and spread of resistant bacteria. Consequently, antibacterial drugs have become less effective or even ineffective, resulting in an accelerating global health security emergency that is rapidly outpacing available treatment options. It is essential to preserve the efficacy of existing drugs through measures to minimize the development and spread of resistance to them, while efforts to

develop new treatment options proceed. The burden of morbidity and mortality resulting from AMR in many infections and settings has serious consequences for individuals and society in terms of clinical outcomes and added costs.

The development of AMR is a natural phenomenon in microorganisms, and is accelerated by the selective pressure exerted by use and misuse of antimicrobial agents in humans and animals. The current lack of new antimicrobials on the horizon to replace those that become ineffective brings added urgency to the need to protect the efficacy of existing drugs.

The World Health Assembly, through several resolutions over the years, has called for intensified implementation of the global strategy, stressing the need for strengthened surveillance of AMR and enhanced laboratory capacity to carry it out, and reduction in the inappropriate use of antimicrobial drugs. Antibacterial resistance (ABR) involves bacteria that cause many common and life threatening infections acquired in hospitals and in the community, for which treatment is becoming difficult, or in some cases impossible.

In 2011, the health ministers of the region's Member States articulated their commitment to combat AMR through the Jaipur Declaration on AMR.

Despite the importance of these infections, there are major gaps in information concerning the extent, spread, evolution and impact of ABR. Urgency is added in particular by the lack of new therapeutic options in the development pipeline to replace those that lose their efficacy as bacteria become resistant to them. The collection of reliable information about the ABR situation through well-conducted surveillance is essential to inform strategies and prioritize interventions to tackle the problem. ABR surveillance should generate data to support action at all levels: local, national, regional and global.

STUDY BACKGROUND: Wide reports in literatures from different parts of the world revealed that antibiotics are used both widely and indiscriminately. RTIs comprise the most common indication for consulting a general practitioner, and obtaining an antibiotic prescription.

OBJECTIVES

- To conduct a retrospective study for a period of two years (January 2012 to February 2014) on the sensitivity pattern of micro organisms prevailing in the study hospital.

- To compare the retrospective antibiotic sensitivity pattern of micro organisms.
- To know the resistance pattern & prepare guidelines.

STUDY DESIGN: Retrospective study

STUDY DURATION: Two years (from 2012 to 2014).

STUDY SITE: 700- bedded multi- specialty private corporate hospital in South India.

PATIENT SELECTION

Inclusion criteria: All the inpatients and outpatients for whom culture and sensitivity was done.

Exclusion criteria: Those unwilling to participate in the study.

METHOD

The study was carried out in 700 bedded multi-specialty private corporate hospital in Tamil Nadu. The study was planned to understand the sensitivity pattern of micro-organisms to various antibiotics used in the hospital.

To conduct a retrospective analysis on the sensitivity pattern of micro organisms towards antibiotics in the study hospital for a period of two years (from 2012 to 2014).

RESULTS

A total of 6591 cases were analyzed during retrospective study. Nineteen different micro-organisms were isolated of which major organisms identified were *S.pneumoniae*(27%), *Klebsiella species* (21.8%), *E. coli* (15.3%), *S.aureus*(10.6%), *Pseudomonas*(8.3%), *S.pyogenes*(7.3%). **Sriram *et al* (2013)** conducted similar study which also reported that *E.coli*(38.3%), *Klebsiella species* (19.25%), *S. pneumonia* (16%),*S.aureus*(11.6%), *Pseudomonas*(7.9%) were commonly isolated micro-organisms.

S.pneumoniae was highly prevalent in sputum specimen (68.6%), *E.coli* was common in urine specimen (76.4%), *S.pyogenes* was present more in throat swab specimen (56.3%), *Klebsiella* were more commonly isolated from urine sample (41.7%) and from tracheal sample (11.7%), *S.aureus* from pus culture (42.9%). **Khavane K *et al* (2010)**, in a similar study reported that *E.coli* was highly prevalent in urine sample (n=17) and *Klebsiella species* were more common in sputum specimen (n=7).

The retrospective data revealed that almost all organisms were highly sensitive to Imipenem. It was found that Imipenem showed high sensitivity in *Salmonella sps.*(100%), *S.pneumoniae* (97.9%), *S.aureus*(97.6%), *Pseudomonas aeruginosa* (97.4%); *S.pyogenes* showed better activity to Linezolid(92.5%); *Proteus vulgaris* showed high sensitivity towards Cefepime/tazobactam (100%). Similarly Cefaperazone/Sulbactam is highly efficient against *S.epidermidis*(100%). Similar study was conducted by Shamataj K et al (2012) which revealed that organisms like *Klebsiella* were highly sensitive to Imipenem(38.8%).

In the class of various cephalosporins prescribed to the patients, cefepime tazobactam was found highly effective against *S.pyogenes*, *S.pneumonia* *S.aureus*, *Klebsiella sps* and *Pseudomonas sps*. In the class of carbapenams, imipenam was highly active against the major organisms viz, *S.pyogenes*(91.9%), *S.pneumonia* (97.9%), *S.aureus* (97.6%), *Klebsiella sps*(79.3) and *Pseudomonas sps*(97.4%) followed by meropenam. Whereas in case of fluoroquinolones, ofloxacin was found to be more active against *S.pyogenes*(51.1%)and *S.aureus*(49.3%, while levofloxacin showed more activity against *S.pneumoniae*, *Klebsiella sps* and *Pseudomonas sps*.

In penicillins, piperacillin tazobactam was found to have excellent activity against *S.pyogenes*, *S.pneumonia* *S.aureus* *Klebsiella sps* and *Pseudomonas sp* [CHART1,2,3].

According to **WHO Report on global status of ABR and Surveillance (2014)** –

- ✓ *E. coli*: resistance to third generation Cephalosporins, including resistance conferred by ESBLs and to FQ.
- ✓ *K. pneumonia*: resistance to third generation Cephalosporins, including resistance conferred by ESBLs and to Carbapenems.
- ✓ *S.aureus*: resistance to beta-lactam antibiotics (Methicillin, Methicillin resistant *S. aureus*).
- ✓ *S. pneumonia*: resistance or non-susceptibility to penicillin (or both).^[51]

Table:1. Sensitivity Pattern– Retrospective Study (January 2012 To February 2014) (N= 6591)

Organism	No. of Patients Infected	Amikacin	Amoxicillin/Clavulanic acid	Cotrimoxazole	Ceftriaxone	Ciprofloxacin	Ofloxacin	Netillin	Sparfloxacin	Cloxacillin	Piperacillin/Tazobactam	Cefepime / tazobactam	Cefoperazone/Sulbactam	Meropenem	Imipenem	Vancomycin	Teicoplanin	Levofloxacin	Polymixin B	Nalidixic acid	Azithromycin	Linezolid	cefuroxime	Nitrofurantoin	Norfloxacin
<i>E.coli</i>	1011	810	166	226	320	204	454	708	252	0	829	926	708	728	818	4	4	346	405	23	336	9	34	481	90
<i>K.pneumoniae</i>	1439	1151	229	319	435	364	717	880	455	3	1050	1323	1246	1206	1141	26	13	747	745	52	647	26	39	418	96
<i>S.pneumoniae</i>	1783	1074	1170	210	1241	390	908	1195	554	63	1593	1648	1583	1616	1746	1606	636	957	16	2	1005	1647	211	15	11
<i>P.aerogenosa</i>	547	431	54	50	129	260	260	297	190	5	395	480	441	425	533	3	1	270	304	2	187	3	4	73	29
<i>S.aureus</i>	699	540	231	128	405	162	345	482	226	33	564	595	591	612	682	641	209	323	3	9	328	653	69	111	12
<i>S.pyogenes</i>	481	281	305	64	357	136	246	307	179	11	434	437	392	423	471	425	138	219	3	3	247	445	74	9	3
<i>S.epidermidis</i>	86	68	42	12	39	17	45	62	25	1	68	74	86	70	36	78	34	62	3	0	55	80	7	1	0
<i>S.saprophyticus</i>	179	146	81	31	67	25	94	184	57	5	138	141	157	159	177	160	81	108	7	1	97	157	7	101	7
<i>Proteus vulgaris</i>	23	20	11	5	13	10	15	11	7	0	17	23	15	20	22	0	0	6	3	1	1	0	0	8	2
<i>Proteus mirabilis</i>	28	21	11	6	19	11	16	11	9	0	22	23	25	28	28	0	0	19	8	1	6	0	1	5	5
<i>Enterobacter</i>	25	23	12	23	10	9	12	15	10	0	22	22	13	19	21	0	0	5	8	2	3	0	1	16	4
<i>Actinobacter</i>	148	74	29	12	14	15	49	15	76	0	67	122	121	71	143	0	0	50	79	0	31	0	2	4	2
<i>Staphylococcus</i>	34	28	13	5	15	11	11	21	15	4	23	33	22	24	34	33	7	12	0	0	4	32	0	4	0
<i>Streptococci</i>	66	31	46	10	38	16	32	37	18	0	58	49	57	59	65	51	20	32	0	0	42	61	13	1	0
<i>Salmonella</i>	21	17	5	5	11	8	13	14	7	0	14	19	18	19	21	0	0	14	5	0	9	0	0	11	3
<i>Pneumococci</i>	13	5	8	0	7	3	4	6	4	0	12	12	10	10	10	12	4	8	0	0	7	12	4	0	0
<i>Gram negative bacilli</i>	6	2	0	1	2	3	3	4	4	0	5	5	6	5	6	0	0	4	2	0	3	0	1	3	1
<i>Nesseria</i>	2	1	2	0	0	0	1	1	0	0	1	2	2	2	2	0	0	1	1	0	2	0	1	0	0
<i>Non Lactose Fermenters</i>	1	1	0	0	0	0	0	1	0	0	1	1	1	1	1	0	0	1	0	0	0	0	0	1	0

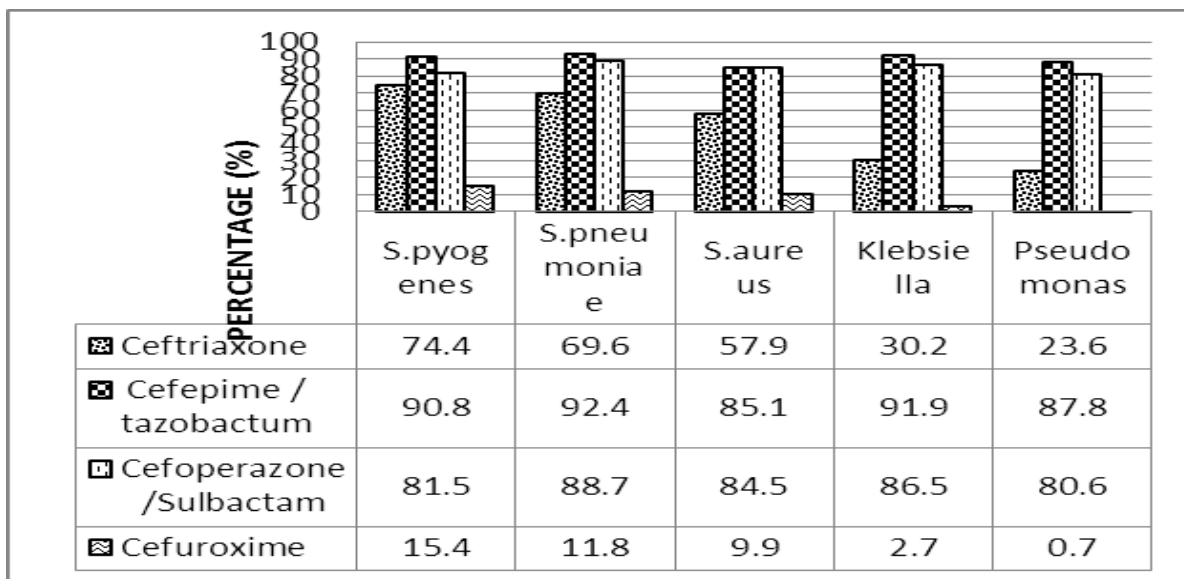


Chart: 1. Microbial sensitivity towards cephalosporins-retrospective (n=6591)

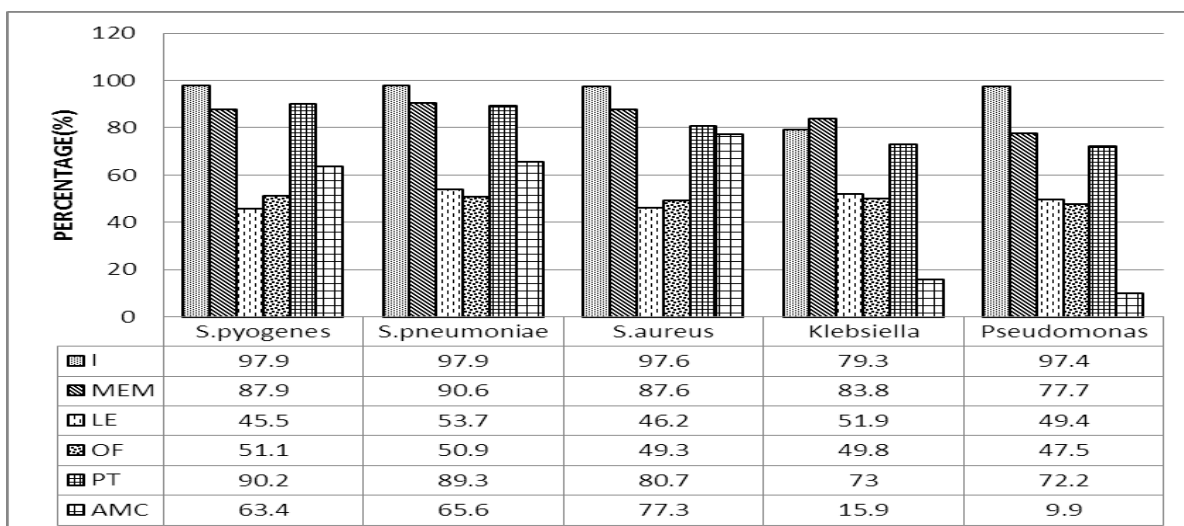


Chart: 2. Microbial sensitivity towards other antibiotics-retrospective (n=6591)

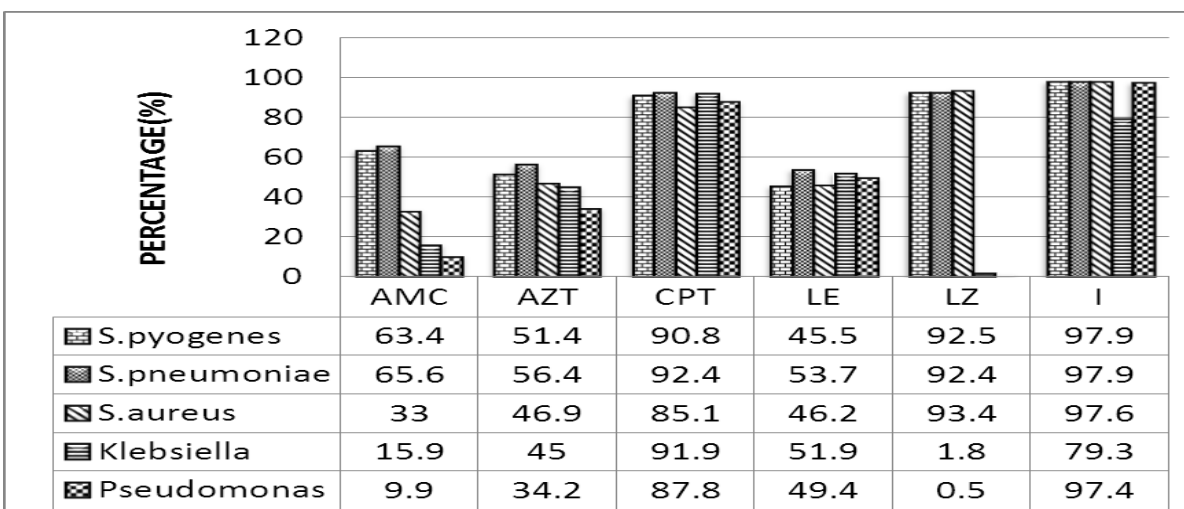


Chart: 3. Microbial susceptibility towards most effective antibiotics- retrospective (n=6591)

Table: 2. Specimen vs. Organism – retrospective study(January 2012-February 2014) (n=6591)

Organism	Number of patients infected	Urine	Tracheal	Semen	Throat swab	Pus cells	Sputum	Wound	Catheter tip	Blood	Bronchial fluid	Endotracheal	Ear swab	Pleural	CSF	Rectal	Vaginal	Umbilical	Motion	Suction tube	Aspiration fluid	Urethral
<i>E.coli</i>	1011	773	26	17	2	141	13	10	6	1	3	2	4	2	1	0	3	0	0	0	4	0
<i>Klebsiella pneumonia</i>	1439	600	169	13	63	216	245	23	7	0	6	22	2	2	3	0	4	1	0	0	1	0
<i>S.pneumoniae</i>	1783	3	16	0	510	8	1223	2	1	0	1	7	1	2	1	0	0	0	1	0	1	0
<i>Pseudomonas aeruginosa</i>	547	172	52	9	22	169	72	18	2	1	6	3	11	1	0	0	2	0	0	0	1	0
<i>S.aureus</i>	699	153	20	19	63	300	73	18	3	10	1	1	8	1	0	0	5	0	14	0	1	0
<i>S.pyogenes</i>	481	5	4	6	271	21	167	3	0	1	0	1	1	0	0	0	1	0	0	0	0	0
<i>S.epidermidis</i>	86	2	7	4	5	41	12	3	0	0	0	4	0	0	0	0	0	0	0	0	0	0
<i>S.saprophyticus</i>	179	167	0	10	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Proteus vulgaris</i>	23	12	0	0	0	9	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Proteus mirabilis</i>	28	15	0	0	0	12	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Enterobacter</i>	25	19	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
<i>Acinetobacter</i>	148	8	61	0	4	13	26	4	1	1	2	23	0	0	1	0	0	0	0	0	0	0
<i>Staphylococcus</i>	34	6	4	1	3	5	6	0	0	0	0	1	1	0	0	0	1	0	1	0	0	0
<i>Streptococci</i>	66	23	3	2	9	0	26	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Salmonella typhi</i>	21	17	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	0
<i>Pneumococci</i>	13	0	0	0	4	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Gram negative bacilli</i>	6	4	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Nesseria</i>	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Non Lactose fermentor</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table: 3. Frequency of multiple organisms isolated – retrospective (n= 6591)

ORGANISMS	NO. ISOLATED (n= 6591)
<i>Pseudomonas</i> + <i>E.coli</i>	4
<i>Pseudomonas</i> + <i>Klebsiella</i>	9
<i>Pseudomonas</i> + <i>S. aureus</i>	4
<i>S.pneumoniae</i> + <i>Klebsiella</i>	16
<i>Klebsiella</i> + <i>E.coli</i>	1
<i>Klebsiella</i> + <i>S. aureus</i>	3
<i>S. aureus</i> + <i>E.coli</i>	3
<i>S.pneumoniae</i> + <i>S.epidermidis</i>	1
<i>K.pneumoniae</i> + <i>S.pyogenes</i>	7
<i>Pseudomonas</i> + <i>S.pneumoniae</i>	1
<i>E.coli</i> + <i>S.pneumoniae</i>	1

CONCLUSION

Antimicrobial resistance (AMR) threatens the effective prevention and treatment of an ever-increasing range of infections caused by bacteria, parasites, viruses and fungi. Very high rates of resistance have been observed in bacteria that cause common health-care associated and community-acquired infections (e.g. urinary tract infection, pneumonia) in all WHO regions. AMR has a significant adverse impact on clinical outcomes and leads to higher cost due to consumption of health-care resources. The scarcity of new class of antibacterial drugs for Gram negative bacteria adds additional urgency.

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