

# Retrospective Analysis of Blood Culture Sample in the Context of Neonatal Sepsis in a Tertiary Care Hospital

Dr. R. Akshaya, Dr. S. Dhanapaul  
KADV Government Medical College  
Trichy

**Abstract:-** On the view of emerging antibiotic resistance and increased death occurring due to neonatal sepsis, this paper has been done to meet the needs of choosing drugs for empirical antibiotic therapy. The laboratory data of samples dating from 2012-2016 has been used here. The data is collected from KAPV GOVT MEDICAL COLLEGE MICROBIOLOGY DEPARTMENT and has been analyzed with the help of Whonet software. From the data we can find resistance of organism towards ampicillin, amoxicillin, ciprofloxacin, gentamycin, and sensitivity towards tazobactam and meropenem.

## I. INTRODUCTION

Neonatal sepsis is a clinical syndrome characterized by signs and symptoms of infection with or without accompanying bacteremia in the first month of life. The incidence of neonatal sepsis according to data from national neonatal perinatal database is 30 per 1000 live births<sup>[1]</sup>. Among intramural births, *Klebsiella pneumoniae* was the most frequently isolated organism (32.5%) followed by *Staphylococcus aureus* (13.6%). Among extramural neonates, *Klebsiella pneumoniae* was the most common

organism (27%) followed by *Staphylococcus aureus* (15%) and *Pseudomonas* (13%)<sup>[1]</sup>. Early onset sepsis (within 72 hours) occurs due to organisms prevalent in the maternal genital tract. Late onset sepsis (after 72 hours) occurs due to organisms thriving in home or hospital.

## II. METHOD OF STUDY

This is a retrospective cohort study done with the help of computational tool Whonet software. This is done with the help of microbiology laboratory data from January 2012-April 2016 from blood samples collected in Mahatma Gandhi government medical college hospital, Tiruchirappalli. Includes children in the age below 28 days and excludes children above the age of 28 days. SAMPLE SIZE: 7935 ISOLATES

## III. OBJECTIVE

The main aim of the study is to find out:

1. Common organisms isolated in our tertiary care hospital
2. Antimicrobial susceptibility pattern, resistance profile and the cross resistance among the antimicrobials using Scatter plot analysis.

## IV. RESULTS

➤ Sample Size: 7935 Isolates

Code	Organism	Number of isolates	(%)	Number of patients	2012	2013	2014	2015	2016
		2	0	2	2				
ci-	<i>Citrobacter</i> sp.	1	0	1				1	
en-	<i>Enterobacter</i> sp.	4	0	4	4				
ent	<i>Enterococcus</i> sp.	7	1	7	1	2	3	1	
eco	<i>Escherichia coli</i>	4	0	4		1	3		
kox	<i>Klebsiella oxytoca</i>	1	0	1	1				
kpn	<i>Klebsiella pneumoniae</i> ss. <i>pneumoniae</i>	112	10	112	21	14	43	33	1
kl-	<i>Klebsiella</i> sp.	1	0	1				1	
xxx	No growth	616	56	600	68	59	199	262	13
nor	Normal flora	347	32	343	40	32	145	124	2
ora	Oral flora	1	0	1		1			
sau	<i>Staphylococcus aureus</i> ss. <i>aureus</i>	4	0	4				2	2

Table 1

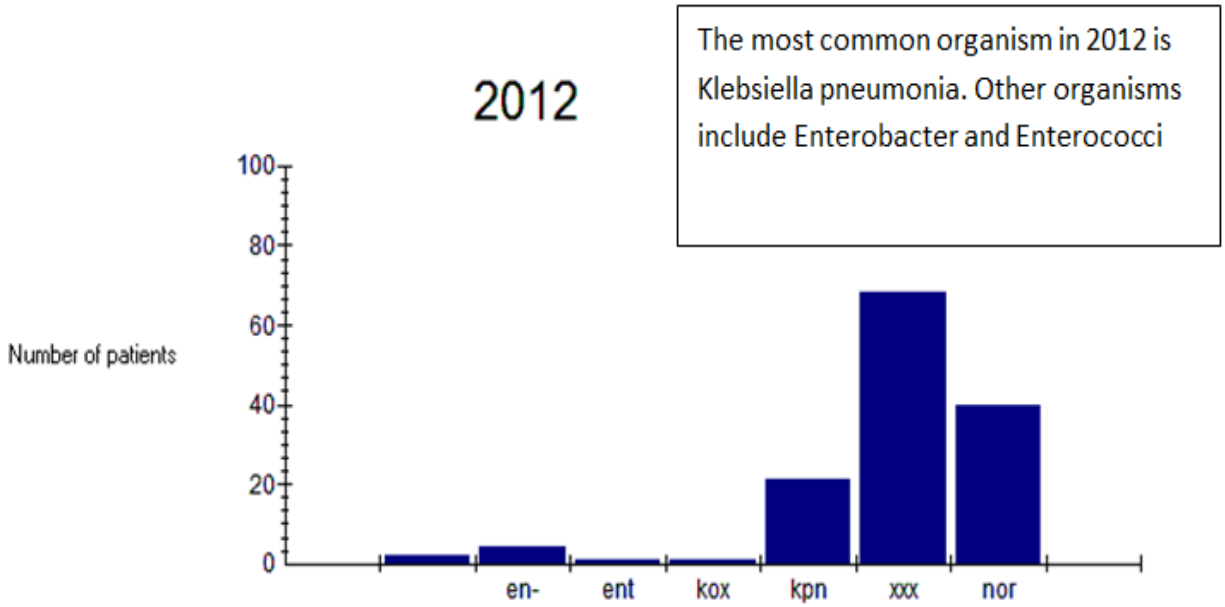


Fig 1

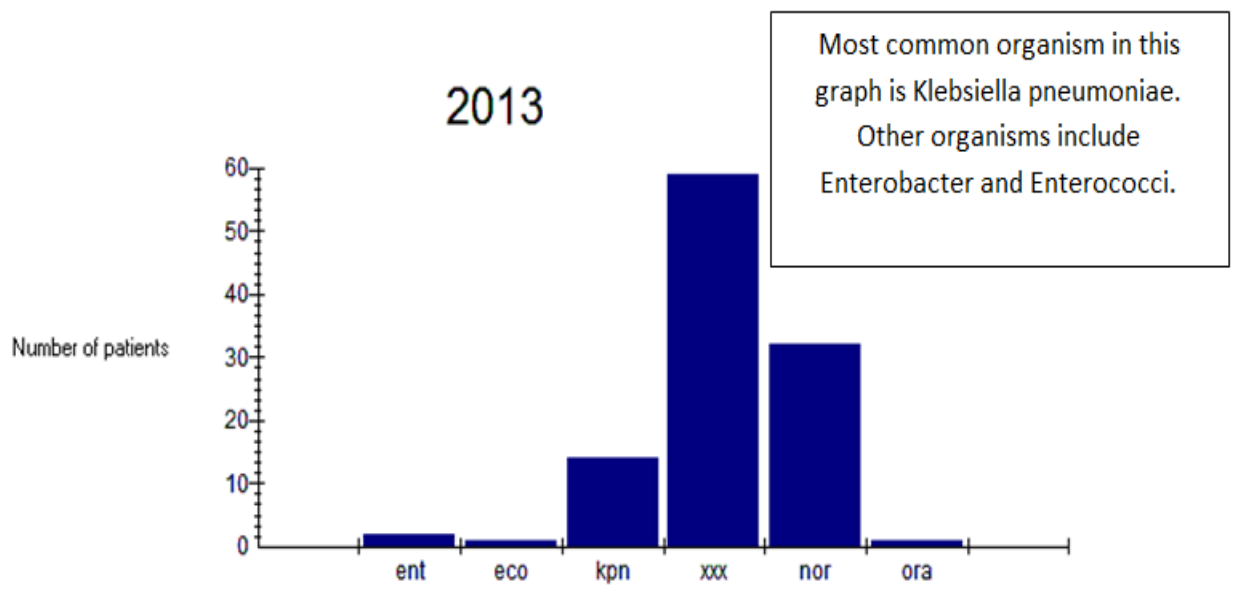
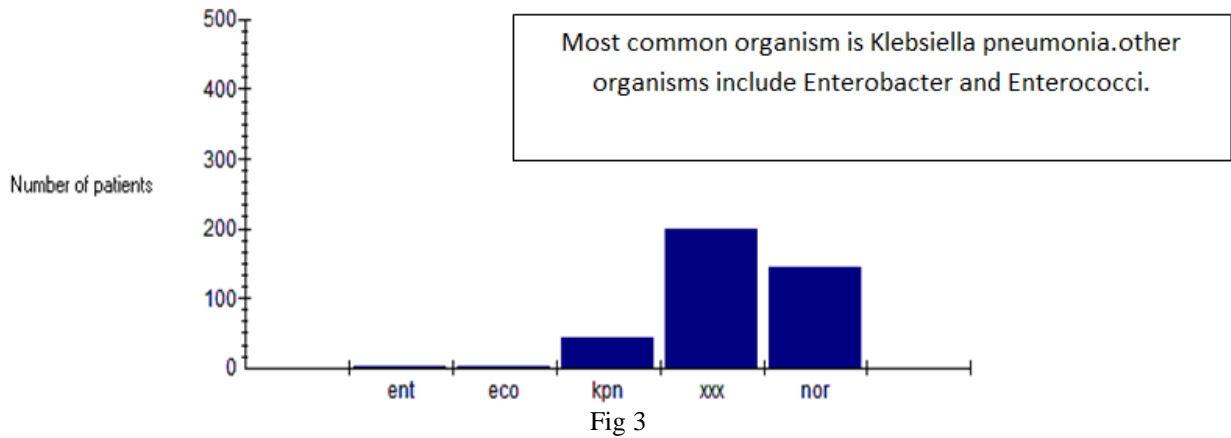
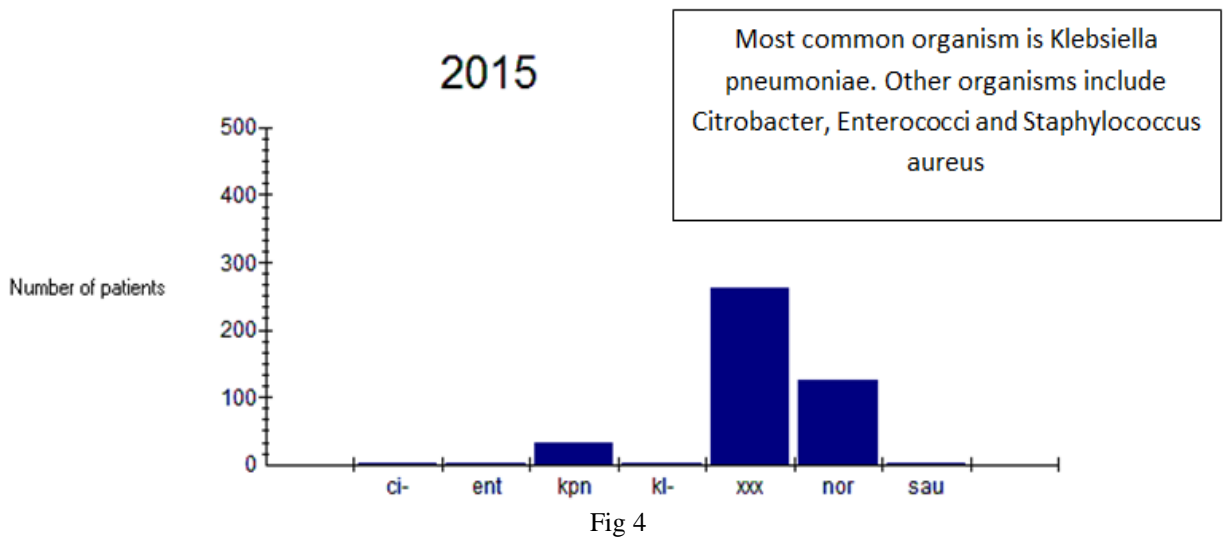


Fig 2

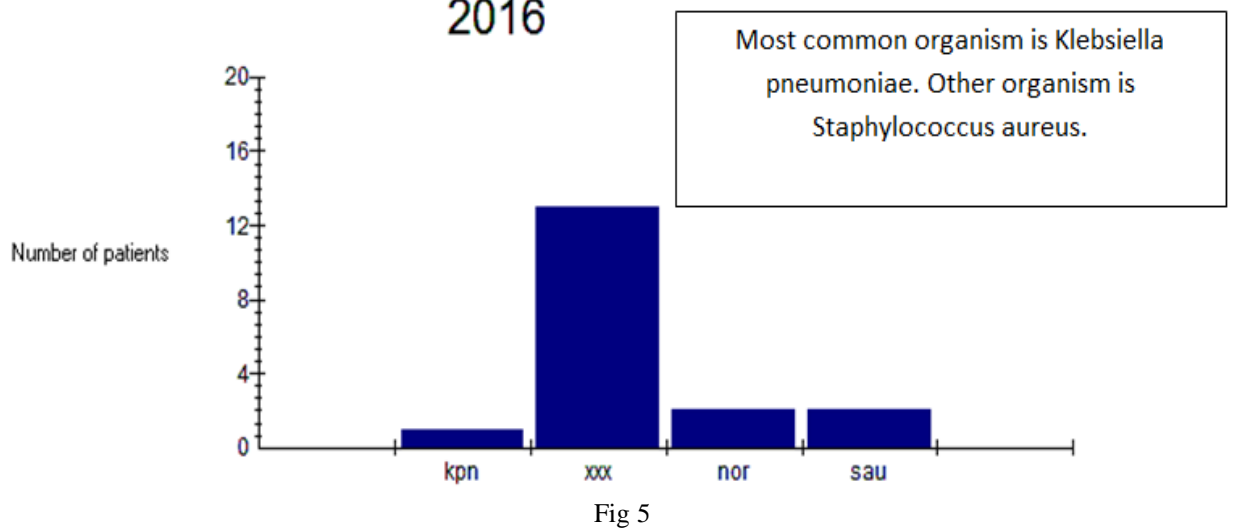
### 2014



### 2015



### 2016



**V. RESISTANCE SCATTERPLOT DISPLAYING CROSS RESISTANCE**

	AMP	AMP	CEF	CEF	CIP	CIP	SXT	SXT	AMC	AMC	AMK	AMK	GEN	GEN	MEM	MEM	OFX	OFX	TZB	TZB
AMP																				
AMP			4.3	95.6	12.9	87.1	50	50			46.2	53.8	50	50	100		100		27.3	72.8
CEF					4.2	2.2					3.2	3.2	4.3	2.9	3.1				1.5	3.1
CEF					14.7	79.1			2.2	95.6	43.7	50	47.4	45.7	97		66.7	33.3	32.3	63.1
CIP							14.6	4.8	2.2	22.2			11	8.5	17.6		---		6.8	11
CIP							25	56.1		75.5			46.6	32.9	82.4				24.6	49.3
SXT									8.3	8.3	22.8	14.6	27.3	6	28.9	3.3			17	24
SXT									16.7	66.7	38.6	23.9	35.5	31.2	64.5	3.3	100		21	38
AMC											2.7	1.3			3.1	1.2	8.3		3.8	0.6
AMC											52.2	43.8		72.7	92.6	3.1	61.7	25	26.1	69.3
AMK													51.7		55.1				28.7	
AMK													3.9	40	40.5	3.3	42.9	42.9	9.7	26.4
GEN															45.2	2.6			21.1	40.1
GEN															51.1	1.1	83.3	16.7	12.4	26.4
MEM																	81.8	9.1	36.3	59.3
MEM																	9.1			4.3
OFX																			20	60
OFX																				20
TZB																				
TZB																				

Table 2:- KLEBSIELLA PNEUMONIAE [graph 6]

	AMP	AMP	CEF	CEF	CIP	CIP	SXT	SXT	AMC	AMC	AMK	AMK	GEN	GEN	MEM	MEM	OFX	OFX	TZB	TZB
AMP																				
AMP				100		100		100						100						
CEF					33.3						50		33.3		20.8					
CEF					33.3	33.3				100	50		66.7	75	4.2				100	
CIP							50	25		100			50	25					100	
CIP								25						25	100					
SXT										100	25	12.5	25	8.3		38.5			44.4	11.1
SXT											37.5	25	33.3	33.3	53.8	7.7			22.2	22.2
AMC													3.4	2.6						
AMC											63.6	36.4	43.1	49.5	100				66.6	33.3
AMK													42.1	26.3	66.7				50	16.7
AMK														31.6	29.2	4.2			16.7	16.7
GEN															38.5				37.5	
GEN															54	7.7			25	37.5
MEM																			60	40
MEM																				
OFX																				
OFX																				
TZB																				
TZB																				

Table 3:- ESCHERICHIA COLI [graph 7]

On accordance with the analysis with laboratory data (2012-2016) we can find that **klebsiella 791scherich[112 isolates]** is the most common 791scheric.other organisms include **enterobacter [4] enterococci[7] and 791scherichia coli[4]**.

On 791scherich data we can further to find out resistance pattern exhibited by microbes drugs such as ampicillin amoxicillin cefotaxime,sulphamethoxazole,amikacin gentamycin,ofloxacin,meropenem and tazobactam.

With drug 791scherichia testing klebsiella 791scherich has exhibited resistance towards ampicillin cefotaxime ciprofloxacin and amikacin with sensitivity towards meropenem and ofloxacin.<sup>[a]</sup>

On similar testing 791scherichia coli has exhibited resistance towards ampicillin amoxicillin gentamycin sulphamethoxazole cefotaxime and ciprofloxacin with sensitivity towards tazobactam and meropenem.<sup>[b]</sup>

On analyzing resistance scatterplot pattern we can find that klebsiella 791scherich has cross resistance against ampicillin-cefotaxime(95.6%) cefotaxime-ciprofloxacin(79%) cefotaxime-amoxicillin(95.6%) ciprofloxacin-amoxicillin(76%) and has the greatest cross sensitivity against meropenem ofloxacin(82%)<sup>(graph 6)</sup>

On analyzing resistance scatterplot pattern we can find that 791scherichia coli has cross resistance against ampicillin cefotaxime, ampicillin ciprofloxacin, ampicillin sulphamethoxazole, ampicillin gentamycin and cefotaxime amoxicillin<sup>(graph 7)</sup>

**VI. DISCUSSION**

In this study gram negative organisms forms the major causative organism the reason probably being vaginal and fecal flora of mother and the environment where the delivery occurs.

From the above results one can obviously notice an increasing trend of resistance towards ampicillin amoxicillin ciprofloxacin cefotaxime gentamycin and sensitive towards tazobactam and meropenem.

On reference with an article (neonatal sepsis:high antibiotic resistance of the bacterial pathogens in a neonatal intensive care unit in a tertiary care hospital by arpita jigar shah and summaiya A.mulla) we can see gram negative organisms(52%) and gram positive organisms(45%) are the main cause of sepsis.prematurity and lowbirthweight were found in 70% of cases.escherichia coli is the most common organism followed by klebsiella pneumoniae while in gram positive coagulase negative staphylococci followed by staphylococcus aureus. According to antibiogram in their hospital resistance is seen towards ampicillin amikacin and gentamycin and sensitivity towards higher generation cephalosporins and carbapenems<sup>[2]</sup>,here resistance exhibited towards ampicillin amikacin and gentamycin is in accordance with our results.

On reference with the article "tackling antimicrobial resistance in neonatal sepsis" by laura folgori and sally j eljis ,they have noticed a resistance pattern towards the commonly used empirical regimen amoxicillin and gentamycin and they have replaced it with a combination of fosfomycin and amikacin.<sup>[3]</sup>Again the resistance pattern exhibited by the organisms is similar to our results.

On reference with the Lamia mohsen and Nermin Ramy "emerging antimicrobial resistance in early and late onset neonatal sepsis" , klebsiella pneumoniae and coagulase negative staphylococcus are found to be the common organisms.these bacilli shows high resistance towards ampicillin amoxicillin cephalosporin piperacillin and tazobactam with lesser resistance towards amikacin and gentamycin.<sup>[4]</sup>this paper also confirms our findings however we have sensitivity towards tazobactam.

On reference with the article "neonatal sepsis and antibiotic resistance in developing countries" by bates matthew ,escherichia coli klebsiella pneumoniae and staphylococcus aureus were found to be the common organisms.it is noticed that klebsiella exhibited resistance towards ampicillin and cefotaxime and escherichia coli towards ampicillin alone.staphylococcus aureus exhibited resistance towards cotrimoxazole with sensitivity towards methicillin.<sup>[5]</sup>This provides a support to our findings.

<b>KLEBSIELLA PNEUMONIAE<sup>[a]</sup></b>	<b><u>RESISTANCE:</u></b> AMPICILLIN CEFOTAXIME CIPROFLOXACIN AMIKACIN  <b><u>SENSITIVE:</u></b> MEROPENEM OFLOXACIN
<b>ESCHERICHIA COLI<sup>[b]</sup></b>	<b><u>RESITANCE:</u></b> AMPICILLIN CEFOTAXIME CIPROFLOXACIN SULPHAMETHOXZOLE GENTAMYCIN AMOXCILLIN <b><u>SENSITIVE:</u></b> TAZOBACTAM MEROPENEM

Table 4

On reference with the article "bacteriological profile and antimicrobial sensitivity pattern in neonatal sepsis:a study from north india" by geeta gathwala and mohit gupta ,a total of three hundred and fifty six microbes were isolated of which pseudomonas aeruginosa is found to be the commonest .in their study resistance to third generation cephalosporins was rampant.gram negative bacilli exhibited sensitivity towards piperacillin tazobactam and carbapenems. gram positive organisms exhibited sensitivity towards linezolid and vancomycin.<sup>[6]</sup>

On reference with the article "aetiology ,antibiotic resistance and risk factors for neonatal sepsis in a large referral center in zambia" by mwila kambwe john tembo and others, klebsiella was the most common organism followed by coagulase negative staphylococcus,staphylococcus aureus and escherichia coli .a resistance is noted towards third generation cephalosporins<sup>[7]</sup>.

## VII. CONCLUSION

We can see a pattern of emerging antibiotic resistance and hence wise use of antibiotics seems to be the need of hour. Surveillance should be conducted at regular intervals and empirical treatment regimen should be employed based on the susceptibility pattern. We can observe a large amount of normal flora which can be avoided by taking aseptic precautions before blood collection.

## REFERENCES

- [1]. Report of national neonatal perinatal database(national neonatology forum)
- [2]. Arpita jigar shah and Sumaiya A Mulla "high antibiotic resistance of the bacterial pathogens in a neonatal intensive care unit in a tertiary care hospital "JOURNAL OF CLINICAL NEONATOLOGY (www.ncbi.nlm.nih.gov)
- [3]. Laura Folgron and Sally J Ellis "tackling antimicrobial resistance in neonatal sepsis" THE LANCET GLOBAL HEALTH (www.thelancet.com)
- [4]. Lamia mohsen and Nermin Ramy "emerging antimicrobial resistance in early and late onset neonatal sepsis" BIOMEDICALCENTRAL(www.aricjournal.biomedcentral.com)
- [5]. Battes Matthew "neonatal sepsis and antibiotic resistance in developing countries" THE PEDIATRIC INFECTIOUS DISEASE JOURNAL(<http://journal.lww.com>)
- [6]. Geeta Gathwala and Mohit Gupta "bacteriological profile and antimicrobial sensitivity pattern in neonatal sepsis:a study from north India" INTERNATIONAL JOURNAL OF RESEARCH IN MEDICAL SCIENCES([www.msjonline.org](http://www.msjonline.org))/april 2017/volume 5/issue
- [7]. John Tembo and Mwillla Kambwe "etiology ,antibiotic resistance and risk factors for neonatal sepsis in a large referral center in Zambia" PEDIATRIC INFECTIOUS DISEASE JOURNAL 2016(<http://ncbi.nlm.nih.gov>)