ANTIBIOTIC RESISTANCE KLEBSIELLA SPECIES ISOLATED FROM CLINICAL SAMPLES IN A TERTIARY CARE HOSPITAL, SOUTH, GOA, INDIA

ABSTRACT

Klebsiella species is a common cause of hospital acquired infections (HAIs) and more antibiotic resistance patterns seen in this species. The purpose of this study was to identify the antibiotic resistance such as ESBL producer,carbapenem- resistant K.pneumoniae (CRKP) and study (Antibiogram) of Klebsiella species isolated from clinical samples in a tertiary care hospital in south Goa,India.The Klebsiella species was isolated from the hospital admitted patient process at Royal Hospital South Goa from April 2022 to Dec 2022. Identification of Klebsiella species isolate was done by analyzing microscopic examination, colony morphology ,performing biochemical testing and also process on Vitek 2 compact system for confirming species identification and their susceptibility. A total of 213 (21.82 %) Klebsiella species isolates were isolated from 976 total clinical bacterial isolates during the study. In this study two different species of Klebsiella were studied such as Klebsiella pneumoniae(20.59%) and Klebsiella oxytoca(1.22%) . Most of them were collected from patients aged more than 45 years old .Klebsiella pneumoniae were obtained from respiratory specimens (38.49%). Among all (90%) isolates showed sensitivity to Meropenem,Amikacin,Piperacillin/tazobactam (80%) isolates showed sensitivity to Cefoperazone/sulbactam (60%) isolates showed sensitivity to Levofloxacin, (100%) isolates showed sensitivity to Tigecycline .Most common Klebsiella species present in hospital acquired infection is Klebsiella pneumoniae. Klebsiella pneumoniae isolates demonstrated resistance to a wide range of antibiotics .

Keywords: Klebsiella pneumoniae, Klebsiella oxytoca Multidrug resistance,Antibiogram.

1. Introduction:

The widespread rod-shaped bacteria known as Klebsiella frequently live in the soil, water, and plants. Some Klebsiella strains are thought to be a normal component of the nasopharynx and gastrointestinal tract flora of people. In honour of the German bacteriologist Theodor Albrecht Edwin Klebs, V. Trevisan (1885) named the genus Klebsiella, family Enterobacteriaceae (1834-1913). According to microbiological classification, these microorganisms belong to the family Enterobacteriaceae and are facultative anaerobic gramme negative bacilli (GNB). The majority of these bacteria are non-motile and enclosed in a distinct polysaccharide-based capsule. They don't have any unique growth requirements and can thrive on standard laboratory culture media. The most significant species affecting humans is Klebsiella pneumoniae (K. pneumoniae), which causes a number of serious, life-threatening illnesses such pneumonia, septicemia, urinary tract, nosocomial, and opportunistic infections. German doctor and microbiologist Carl Friedlander documented K. pneumoniae isolated from respiratory samples of pneumonia patients for the first time in 1882.

Physiology and morphology of *Klebsiella pneumoniae*

K. pneumoniae is a bacterium with a wide range of physiological abilities. It lives in ecological environments and is frequently found in soil and water. In K. pneumoniae, atmospheric nitrogen gas is taken in and reduced via metabolic nitrogen fixation pathways to ammonia and amino acids. K. pneumoniae exclusively uses nitrogen fixation in anaerobic circumstances because oxygen can cause damage to some of the nitrogenase enzyme. The bacterium may defend itself from phagocytosis with the help of a prominent polysaccharide capsule, which makes it more virulent and harmful. This bacterium is isolated in the hospital environment from places like contaminated medical equipment, contaminated sink handles and drains, contaminated bar soaps, and contaminated cleaning supplies. With a huge genome covering more than 5 million base pairs and containing 5300 genes, it is a highly adaptable organism. It consists of a core genome that is rather stable and encodes metabolic and resistance factors. The genes that code for

virulence factors, antibiotic resistance, and certain catabolic pathways are found in this extremely changeable genome, allowing the organism to survive in a variety of conditions. This bacterium's typical biochemical traits include a negative oxidase test, a positive citrate utilization test, nitrate reduction, lysine decarboxylation, a positive urea hydrolysis test, and lactose fermentation. Multiple colony morphotypes of K. pneumoniae can be produced by isolates. Clinical samples frequently contain large, smooth, mucoid colonies. Typically, environmental sources yield small colonies with a rough, convex look. It is common to obtain the mucoid hypermucoviscous morphotype from respiratory and urinary system secretions.

Infections caused by *Klebsiella species*

The most prevalent bacterium in a variety of nosocomial and community-acquired diseases is K. pneumoniae. Numerous nosocomial infections, including pneumonia, urinary tract infections, bacteremia, wound infections, intra abdominal infections, and neonatal septicemia, are brought on by this bacterium. Klebsiella species has been linked to community-acquired illnesses, including invasive and systemic diseases including liver abscess, meningitis, endophthalmitis, and septic arthritis in diabetics and immunocompromised people, in addition to being a nosocomial pathogen. 17-20 Its high rate of intrinsic resistance to antimicrobials, including antibiotics and disinfectants, is one of the factors contributing to its success as a nosocomial disease. In people with cystic fibrosis, chronic lung infections are also linked to pathogenic K. pneumoniae stains. 21 K. pneumoniae can sporadically invade parts of the human body include the intestine, throat, skin, and nasal mucosa. Hospitalization, broad-spectrum antibiotic therapy, physical barrier disruption (skin or mucous membrane), the presence of indwelling invasive devices, and/or immune defence system malfunction are all associated with higher rates of colonisation. K. pneumoniae is therefore primarily a nosocomial pathogen linked to respiratory tract infections, such as ventilator-associated pneumonia (VAP), urinary tract infections (UTIs), burn wound infections, soft tissue infections, bacteraemia, bone and joint infections, and a variety of systemic infections, especially in immunosuppressed patients. Urinary tract infections, acute lower respiratory tract infections, bacteremia, liver abscess, meningitis, and endophthalmitis are the community-acquired illnesses brought on by pathogenic K. pneumoniae. The purulent infections that result in liver abscesses are strongly related with the mucoid hypervirulent or hypermucoviscous phenotype of K. pneumoniae.

Virulence factors of Klebsiella species

Klebsiella species has a variety of cell-associated and secreted virulence agents at its disposal. Capsular polysaccharide, fimbrial adhesins, biofilm, and lipopolysaccharide are some of the critical cell-associated virulence factors that let a cell survive in a variety of environmental circumstances and aid in the establishment of infections. Hemolysins, proteases, cytotoxins, siderophores, exotoxins, etc. are the most common extracellular or secreted virulence agents. A cell density-regulating mechanism known as quorum sensing coordinates the production of many virulence agents (QS). K. pneumoniae has a polysaccharide capsule that offers resistance to the host's phagocytic defense system. Fimbrial adhesins enable the bacterial colonization and biofilm formation by allowing the bacteria to adhere to the surfaces of the host cells. The mannose sensitive type 1 and the mannose resistant type 3 fimbrial adhesins, two important bacterial fimbriae, confer adhesion of K. pneumoniae to the host cells. Type 1 adhesins usually attach to epithelial cells in the urogenital, respiratory, and intestinal tracts that have mannose-containing trisaccharides of the host glycoproteins. Only Type 3 adhesins can agglutinate erythrocytes that have been treated with tannin. Quorum sensing, a system of cell-to-cell communication including signalling molecules known as autoinducers, regulates the growth of biofilms. Siderophores, which chelate iron and are secreted by K. pneumoniae, are essential for bacterial growth, multiplication, and increased pathogenicity. The two most significant iron chelating siderophores released by K. pneumoniae are the enterobactins of the phenolate and aerobactins of the hydroxamate types.

Antibiotic resistance in *Klebsiella species*

K. pneumoniae infections picked up in hospitals frequently exhibit a stronger correlation with drug resistance. This bacteria exhibits inherent, acquired, and adaptive mechanisms of antibiotic resistance, with some overlap between these categories. The failure of the antibiotic to accumulate in the cell causes intrinsic resistance, whereas changes in the antibiotic's target sites or enzymatic inactivation of the medication cause acquired and adaptive resistance. Due to its poor outer membrane permeability and active antibiotic efflux, K. pneumoniae is innately resistant to a number of antibiotics. This makes it a challenging infection to treat, along with the constrained absorption through its outer membrane and secondary resistance mediated by the -

lactamases. Changes in the control of resistance genes may result from chromosomal mutations in the organism's DNA. Plasmids, transposons, and bacteriophages can also be used to obtain resistance genes from other bacteria. When compared to chromosomal mutation, acquired resistance genes mostly confer resistance to -lactams and aminoglycosides, while the latter frequently results in fluoroquinolone resistance. Extended-spectrum -lactamase (ESBL) generating and multidrug resistant K. pneumoniae (MDR-KP) are quickly becoming problems in clinical practise. When an isolate of K. pneumoniae displays in vitro resistance to at least three classes of antibiotics, including cephalosporins, carbapenems, aminoglycosides, and fluoroquinolones, it is referred to as MDR-KP. Due to incorrect empiric medication, MDR is a widespread clinical issue that is frequently linked to considerable morbidity, death, and increased economic burden. Carbapenems have been the go-to medication for treating MDR infections for a time. But recently, carbapenem resistance has spread rapidly and is frequently caused by enzymes called metallo—lactamases (MBLs), which break down carbapenems. Imipenemase (blaIMP), Verona imipenemase (blaVIM), and New Delhi metallo-beta-lactamase-1 (blaNDM-1) are a few examples of the genes that encode these enzymes and are found either on the bacterial chromosome or in a plasmid. 24 Therefore, it is necessary to reevaluate therapeutic approaches for the quick and successful empiric treatment of infections brought on by MDR isolates. A significant factor in treatment failure, which results in high mortality rates, is inappropriate initial empiric therapy.

LIMITATIONS OF THE RESEARCH

The study's limitation is that it could only detect the presence of the NDM-1 gene, one of numerous MBL genes, in imipenem-resistant isolates of K. pneumoniae, leaving open the possibility that other genes encoding carbapenamases may have gone undetected. Since siderophores are one of the main iron chelating molecules that confer higher virulence to K. pneumoniae strains, their detection would have added more significance along with other virulence factors.

1. SCOPE FOR FUTURE WORK

This work emphasises the stronger correlation between K. pneumoniae clinical isolate virulence parameters and ESBL development. It would be ideal to develop agents that can combat the most important virulence factor, such as quorum sensing among MDR and virulent bacteria, for successful treatment of these infections because many of these virulence factors and even antibiotic resistance are closely related to bacterial cross talk that occurs as a part of quorum sensing.

2. OBJECTIVES OF THE STUDY

To isolate and identify K. pneumoniae from various clinical samples.

To study the antibiogram pattern of these isolates.

To phenotypically detect ESBL production in cephalosporin resistant K. pneumoniae isolates.

- To determine the overall susceptibility of *K. pneumoniae* against clinically important antimicrobial agents
- To evaluate different combinations of newer beta lactam/beta lactamase inhibitors against

K. pneumoniae and screen its activity against isolates from bacteremia and

- pneumonia

Aim: Hypothesis: Convergence of antimicrobial resistance and virulence factor contributes to severity and increased mortality in invasive infections caused by *K. pneumoniae.*

REVIEW OF LITERATURE

A gram-negative, non-motile, encapsulated rod-shaped bacterium called Klebsiella pneumoniae grows well on common culture media. They are widely dispersed throughout the natural world. They exist as saprophytes in sewage and soil and as commensals in both human and animal intestine (Podschun and Ullmann, 1998).

Classical K.pneumoniae

The strains of Klebsiella pneumoniae that are most frequently identified are known as classical Klebsiella pneumoniae (cKP). They are able to spread nosocomial infections and quickly develop resistance to many antimicrobial drug classes (W. Li et al., 2014). Pneumonia, bacteremia, urinary tract infections, intra-abdominal infections, infections due to intravascular devices, surgical site infections, and soft tissue infections are the most frequent illnesses brought on by cKP (Pomakova et al., 2012). Antimicrobial resistance has made it more difficult to treat common diseases such as urinary tract infections and the life-threatening pneumonia and bacteremia these bacteria produce (Paczosa and Mecsas, 2016).

Hypervirulent Klebsiella species

The novel form of Klebsiella pneumoniae known as hypervirulent Klebsiella pneumoniae (hvKP) was first identified in Taiwan in 1986. On an agar plate, they appear as hyperviscous colonies. The hvKP strains can result in life-threatening infections in young, healthy people with a functioning immune system (W. Li et al., 2014). They are frequently reported from extra hepatic diseases including septic endophthalmitis, community acquired liver abscess (CA-PLA), and others (T. Qu et al., 2015). A string test can be used to identify hyperviscous stresses. When a bacteriology loop can stretch the bacterial colonies produced on an agar plate to produce >5mm length string, the string test is deemed successful (Shon et al., 2013). On big plasmids, the genetic elements that code for their hypervirulence are found. The majority of hvKP infections have been linked to Asia. Recently, there have been more reports of them everywhere. hvKP has an outer membrane made up of lipoproteins, a lipid bilayer with related proteins, and lipopolysaccharides, just as other Enterobacteriaceae. The outside portion of the membrane contains the capsular polysaccharide. The distinctive structural characteristic of this strain is the excessive synthesis of capsular polysaccharides, which is mediated by RmpA and/or RmpA2. In hvKP, the most prevalent capsule types are K1, K2, K5, K20, K54, and K57. Aerobactin is the other component connected to hvKP.

In the past, antimicrobials that were frequently used to treat bacteria could still affect hvKP. Recently, reports of extensively drug resistant (XDR) and multidrug resistant (MDR) hvKP from various parts of the world have been made (Russo and Marr, 2019).

Epidemiology

The earliest reports of hypervirulent K. pneumoniae came from Taiwan. Since then, numerous nations, including those in Asia, Europe, and America, have noted their intermittent spread. In Taiwan, China, South Korea, and Iran, the hvKP epidemic expanded. In other parts of the world, the prevalence of hvKP was lower. Later, reports of this bacterium's hypermucoviscosity phenotype came from Spain, Canada, Brazil, and Algeria. In China, invasive infections accounted for 22.8% of hvKP isolates. According to another investigation, hvKP accounted for 90.9% of the microorganisms causing pyogenic liver abscess. hvKP strains were found in patients with bacteremia in South Korea. These strains (88.8%) were found in extrahepatic abscesses according to a Taiwanese study. K. pneumoniae liver abscess is now regarded as an endemic illness in Taiwan (C.-R. Lee et al.,2017). In Canada, Brazil, and Algeria, the prevalence rates of hvKP were 8.2%, 6.7%, and 9.2%, respectively (C.-R. Lee et al.,2017). Two studies in India have so far documented hvKP (Kotekani and Kotigadde, 2018; Shankar et al., 2018).

Guo et al. reported that in China, among those with hvKP, 42.9% had the K2 serotype and 23.8% had the K1 serotype (Guo et al., 2017). Zhao et al. discovered that 68.75% of K. pneumoniae positive for hypermucoviscosity belonged to the K2 serotype (Zhao et al., 2016). K1 and K2 capsular serotypes were prevalent among hvKP strains, according to a South Korean investigation (Kim et al., 2017). There have also been reports of K1 and K2 serotypes in hvKP from Europe and America (C.-R. Lee et al.,2017).

Numerous investigations have shown a link between rmpA and hypermucoviscosity (Liu et al., 2014;Struve et al., 2015; Wu et al., 2017). Despite the high correlation between hvKP and rmpA, certain isolates carrying the rmpA gene did not have hyperviscosity, according to Yu et al (Yu et al., 2006). According to a recent study, some rmpA positive isolates lack hyperviscosity and exhibit poor virulence because the rmpA and rmpA2 genes are simultaneously mutating in the absence of chromosomal rmpA. (Yu et al., 2015).

According to one study, aerobactin is a vital component of hvKP's growth and survival in both human and animal models, indicating that it is a key component of virulence (Russo et al., 2014). Between 69 and 96% of Chinese people with hvKP carry this gene (Guo et al., 2016, 2017; Sun et

al., 2016; Yan et al., 2016; Ye et al., 2016; Zhang et al., 2016; Zhao et al., 2016; Wu et al., 2017; Zhan et al., 2017). In Taiwan, the prevalence of aerobactin in K1 and K2 serotypes was 100%. (Yu et al., 2008).

Both healthy people and people with underlying medical issues can contract illnesses from hypervirulent K. pneumoniae strains. The fact that they induce primary liver abscesses in persons without underlying liver disease is what stands out most about them (Kim et al., 2009; Wang et al., 1998). Due to haematogenous spread from the liver, these liver infections have the potential to cause a variety of additional metastatic infections. For instance, in Taiwan, community-acquired K.pneumoniae meningitis is seen as an infection following a liver abscess (Fang et al., 2007; Keller et al., 2013; Bei Li et al., 2014). Cellulitis, necrotizing fasciitis, and myositis are examples of severe skin and soft tissue infections that can be brought on by it. Endophthalmitis and abscesses in other tissues, such as the neck, lungs, and kidneys, are also brought on by hypervirulent strains (N.-C. Cheng et al., 2015; Fang et al., 2007; Huang et al., 2005; Keller et al., 2013; Bei Li et al., 2014). These hypervirulent K. pneumoniae strains are more likely to cause infections at several places as a result of metastatic dissemination (Russo and Marr, 2019). The defining hallmark of hvKP is the development of infection in the community. But reports of hvKP-related hospital acquired ventilator associated pneumonia come from China (Liu and Guo, 2018; Yan et al., 2016). They also induce various pulmonary infections such empyema, lung abscess, and septic pulmonary emboli in addition to lobar pneumonia (Y.-T. Lin et al., 2010). The majority of genitourinary tract infections caused by hvKP are the result of hematogenous dissemination from an earlier bacteremia. Additionally, local abscess formation brought on by bacteremic dissemination has been seen in the prostate, perinephric area, and kidneys (Russo and Marr, 2019). A common and severe consequence of hvKP site-specific infections is bacteremia (Lee et al., 2006). People with hvKP bacteria are more likely than those with cKP infection to have positive blood cultures before the original site of infection is found or cultured (Wu et al., 2017). They can potentially result in endocarditis, a very uncommon manifestation of hvKP illness. There has been one instance of hypervirulent K. pneumoniae linked native valve endocarditis recorded, however purulent pericarditis has been documented more frequently (Rivero et al., 2010; Balestrino et al., 2008), either as a direct result of pyogenic liver abscess or by hematogenous dissemination (Balestrino et al., 2008; Hentzien et al., 2017). A few hvKP infections that are less frequent include epididymitis, ocular cellulitis, and Bartholin's abscess (Russo and Marr, 2019). Bacteremia in India has been linked to hvKP, according to research (Shankar et al., 2018).

History

The German bacteriologist Edwin Klebs is honoured with the naming of the genus Klebsiella. In honour of Carl Friedlander, who discovered this bacteria as one of the etiological factors for pneumonia, it is also known as Friedlander's bacterium (Friedlander, 1882.

MATERIAL AND METHOD:-

Sample collection:-

The Klebsiella species was isolated from the hospital admitted patients process at Royal Hospital South Goa from April 2022 to Dec 2022. Identification of Klebsiella species isolate was done by analyzing microscopic examination, colony morphology and also process on Vitek 2 compact system for confirming species identification and their susceptibility. A total of 213 (21.82 %) Klebsiella species isolates were isolated from 976 total clinical bacterial isolates during the study. In this study two different species of Klebsiella were studied such as Klebsiella pneumoniae(20.59%) and Klebsiella oxytoca(1.22%) . Most of them were collected from patients aged more than 45 years old .Commonly used antibiotics were identified for each species. Further comparisons were done to study change in Klebsiella species collected from different sites and their sensitivity patterns.K. pneumoniae isolates from cultures of clinical samples from suspected cases of respiratory tract infections (sputum, bronchoalveolar lavage, and endo-tracheal aspirates), urinary tract infections (midstream and catheterized urine), blood stream infections (blood, central line tips, umbilical catheter tips), skin and soft tissue infections (wound swabs, pus), were included in the study during the study period. The microbiology department received these clinical samples for the typical bacteriological diagnostic.

Selection criteria

Inclusion criteria

- The study used one strain of K. pneumoniae per subject.
- The investigation comprised K. pneumoniae isolates that were isolated as pure culture from clinical samples.

Exclusion standards

- K. pneumoniae strains found in mid-stream clean-catch urine samples that don't meet the Kass criteria for severe bacteriuria (a colony count of 105 CFU/mL).
- K. pneumoniae was isolated from exudate samples, and the direct smear stained with Gram's stain revealed no pus cells (absence of pus cells could suggest bacterial surface

colonization).

- When there are no clinical symptoms or evidence of a bloodstream infection, K. pneumoniae is isolated from a single blood culture (BSI).

K. pneumoniae's role as a surface colonizer or pathogen was determined when it was isolated from non-sterile sites like respiratory tract and wound swabs based on the presence of pure growth in culture, the presence of the bacteria along with inflammatory cells on direct Gram's stain microscopy performed on the sample, and the presence of clinical signs and symptoms in the patient.

Storage and preservation of K. pneumoniae isolates

20% glycerol broth was used to store K. pneumoniae isolates for a lengthy period of time. It was made by mixing 800 liters of nutritional broth with 200 liters of sterile, autoclaved glycerol in a cryogenic vial. An isolated K. pneumoniae sample was injected into nutritional broth and cultured there for 18 to 24 hours at 37°C. A sterile container containing 150 mL of glycerol received 850 mL of nutrient broth culture before being vortexed. The glycerol broth was kept at -80°C right away. By freezing the suspension at 35°C and then streaking it over Luria Bertani agar, the bacteria were collected. Additionally, duplicate isolates were kept by inoculating them into semisolid nutritional agar that was covered in sterile paraffin oil at 4°C.

Isolation and identification:-

For Urine ,Tissue a loop full of samples streak on 5% sheep blood agar(BA) and Macconkey agar(Mac) with selective supplements (HiMedia Laboratories, Mumbai, India) and incubated at 37^{o}c for 24hrs. For Blood culture (8-10ml) withdrawn from suspected patients were inoculated directly into BD BACTEC PLUS-Aerobic/F Medium vials (30 mL) and processed using BACTEC 9050/Fx40 automated blood culture system . Bacterial growth in the culture bottle was streaked on previously discussed Blood and Macconkey agar medium and incubated at 37^{o}c for 24hrs. Then proceed for Gram stain and After Gram stain make a suspension 0.5 Mcfarland standard as per CLSI Guidelines. The bacterial isolates were identified to the species level by the VITEK2 system (BioMérieux, Lyon, France)/BD M50 Phoenix . The antimicrobial susceptibility (MIC) values derived from the VITEK 2 compact system according to clinical and laboratory standards(CLSI and EUCAST)guidelines.

Statistical Method:-

The resistance of Pseudomonas spp. to individual antimicrobials was presented in absolute numbers and percentages .In Ms Excel using percentage formula check the resistance antimicrobial pattern of Klebsiella species.

RESULT AND DISCUSSION:-.

In this study two different species of Klebsiella were studied such as Klebsiella pneumoniae(20.59%) and Klebsiella oxytoca(1.22%) .

Most of them were collected from patients aged more than 45 years old .

Klebsiella pneumoniae were obtained from respiratory specimens (38.49%). Among all (90%) isolates showed sensitivity to Meropenem,Amikacin,Piperacillin/tazobactam (80%) isolates showed sensitivity to Cefoperazone/sulbactam (60%) isolates showed sensitivity to Levofloxacin, (100%) isolates showed sensitivity to Tigecycline .

Most common Klebsiella species present in hospital acquired infection is Klebsiella pneumoniae.

Klebsiella pneumoniae isolates demonstrated resistance to a wide range of antibiotics .

For Klebsiella pneumoniae and Klebsiella oxytoca in Tissue specimen the drug of choice will be meropenem,amikacin, cefoperazone/sulbactam,and piperacillin statistically proven.

4 patient identified on vitek 2 compact system as Klebsiella pneumoniae (ESBL) and 2 patients are Carbapanamase producer

Klebsiella pneumoniae(ESBL,MDR,carbapanamase producer) in Urine and Respiratory specimens the drug of choice will be Tigycycline and meropenem statistically proven.

In Table (2) Antimicrobial Resistance pattern for Klebsiella species is shown in %.

Table no.1: - Klebsiella species identified in clinical isolates(IN PATIENT).

sr. no	Total no.Klebsiella pneumoniae	Total no. Klebsiella oxytoca	Summation	specimen

1	27	0	**27**	Blood
2	58	6	**64**	Urine
3	82	2	**84**	Respiratory infection
4	34	4	**38**	wound/ Tissue
TOTAL	201	12	**213**	

Table no.2:- Resistance pattern for Klebsiella species in %.

Organisms	**Specimen**	**Meropenem (%)**	**Amikacin (%)**	**Tigecycline (%)**	**Levofloxacin (%)**	**Cefoperazone/sulbactam (%)**	**Piperacillin/tazobactam (%)**
K.pneumoniae	BLOOD	92.59±1	74.04±1	100±1	51.85±1	77.77±1	81.48±1
	URINE	93.10±1	86.20±1	100±1	72.41±1	87.93±1	87.93±1
	RESPIRATORY	93.90±1	91.46±1	100±1	74.39±1	91.46±1	91.46±1
	TISSUE	100±1	94.11±1	100±1	79.41±1	100±1	100±1

K.oxytoca	URINE	**100**±1	**100**±1	**100**±1	50.00±1	**100**±1	**100**±1
		100±1	**100**±1	**100**±1		**100**±1	**100**±1
	RESPIRATORY				50.00±1		
		100±1	**100**±1	**100**±1		**100**±1	**100**±1
	TISSUE				50.00±1		

CONCLUSION:-

- For Klebsiella pneumoniae and Klebsiella oxytoca in Tissue specimen the drug of choice will be meropenem,amikacin, cefoperazone/sulbactam,and piperacillin statistically proven.
- 4 patient identified on vitek 2 compact system as Klebsiella pneumoniae (ESBL) and 2 patients are Carbapanamase producer
- Klebsiella pneumoniae(ESBL,MDR,carbapanamase producer) in Urine and Respiratory specimens the drug of choice will be Tigycycline and meropenem statistically proven.
- Early clinical suspicion, along with appropriate culture processes (MIC) and awareness among health care providers is needed for effective control of infection.
- Antibiogram study helps Medical professionals in a locality to choose appropriate evidence based antibiotics . And also helps in initiating treatment for emergency cases while waiting for a culture and sensitivity report.

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