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Bacteriological Analysis of Sputum Sample Associated with Lower Respiratoy Tract Infection" Of East Godavari District, Coastal Andhra Pradesh

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Abstract

To identify and characterize bacterial pathogens in sputum samples from patients with suspected LRTIs. Determining which bacteria are responsible for the infection helps guide effective treatment. Through culture and sensitivity testing, clinicians can identify which antibiotics the pathogen is sensitive or resistant to, reducing the risk of antimicrobial resistance. Some bacteria may be present without causing disease. Proper analysis helps differentiate harmless colonization from active infection. Monitor disease progression or treatment response: Serial sputum samples can track how well a patient is responding to therapy.

Keywords: Bacteriological Analysis, Sputum Sample, Lower Respiratory Tract Infection, East Godavari District, Coastal Andhra Pradesh".

1. Introduction

Infection of the respiratory system is a common disease in the community. Respiratory infections (Reid PT, Innes JA) based on the region of the infection are divided into upper respiratory infections and lower respiratory tract infections (LRTIs). In general, the cause of respiratory tract infections is various microorganisms, but the most are due to bacterial and viral infection. The mortality rate is very high in baby, children, elderly, and especially in countries with low- and medium-income per capita. LRTIs are among the most common infectious diseases affecting humans worldwide. They are important causes of morbidity and mortality for all age groups, and each year approximately 7 million people die as a direct consequence of acute and chronic respiratory infections.

The World Health Organization report in 2012 said that LRTIs, especially pneumonia rank fourth as the leading cause of death in the world and at the same time, the leading cause of death from infectious diseases. Lower respiratory tract infections (LRTIs) represent a significant global health

burden, accounting for substantial morbidity and mortality, particularly among vulnerable populations such as children, the elderly, and immune compromised individuals. LRTIs encompass a spectrum of diseases, including bronchitis, bronchiolitis, and pneumonia, which are primarily caused by a diverse array of bacterial, viral, and, less commonly, fungal pathogens. Among these etiological agents, bacteria play a pivotal role, especially in severe and community- or hospital-acquired cases. Accurate and timely identification of the causative bacterial pathogens is essential for the effective clinical management of LRTIs. This is particularly important in the context of rising antimicrobial resistance, which necessitates precise and targeted antibiotic therapy to improve patient outcomes and limit the spread of resistant strains. The bacteriological analysis of sputum samples remains one of the cornerstone diagnostic modalities for the detection and characterization of bacterial pathogens in LRTIs.

Sputum, a mixture of saliva and secretions from the lower airways, serves as a non-invasive and readily obtainable specimen for microbiological investigation. However, the diagnostic utility of sputum analysis is heavily dependent on the quality of the sample, Ziyade N,Aksu B,Yagri as contamination with or pharyngeal flora can compromise the accuracy of results. Therefore, stringent criteria for sample collection, macroscopic and microscopic examination, and laboratory processing are imperative to ensure the reliability of bacteriological findings. Each type of LRTI vary in the epidemiology, pathogenesis, clinical presentation, and outcome. The factors that contribute to the rising incidence of LRTIs in hospitals include underlying lung diseases, diabetes mellitus, malignancy, immunosuppressant drugs, in appropriate antibiotic therapeutic. Microscopic examination and culture of respiratory specimens remain the main stay of laboratory diagnosis of LRTIs. But procurement of good quality specimens is essential for the accurate reporting of results. Many studies have observed that the majority of the respiratory bacterial pathogens are Gram negative. The etiological agents of LRTIs and their antibiotic susceptibility profile vary from area to area. Streptococcus pneumoniae, Klebsiella pneumoniae, Escherichia coli, Pseudomonas species, Acinetobacter species and other Non-Fermentative Gram-Negative Bacilli (NFGNB) have often been recovered from LRTIs.

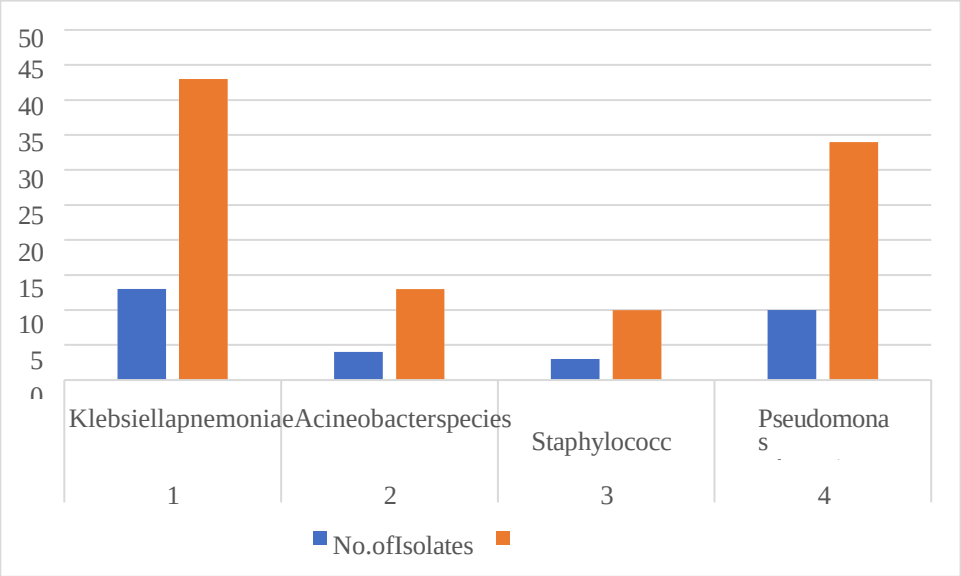
The most common bacterial pathogens isolated from LRTIs in some studies were Klebsiella pneumoniae (K. pneumoniae) and Pseudomonas aeruginosa (P.aeruginosa). But non-fermentative gram-negative bacilli were the most common Gram-negative bacteria followed by Klebsiella species. Hospitalised patients become colonized rapidly with Gram-negative bacilli and it is often impossible to determine their clinical significance. The standard bacteriological workflow involves the initial assessment of sputum quality using followed by direct microscopic examination (e.g., Gram staining) to provide preliminary information on the presence and type of bacteria as well as the inflammatory response. Subsequent culture and sensitivity testing enable the isolation, identification, and antibiotic susceptibility profiling of the causative organism.

MATERIAL & METHODS: A total number of 50 sputum samples were collected (García-Vázquez E) from clinically suspected severe cough, difficulty breathing, skin turning blue due to lack of oxygen these symptoms are observed from the patients in Kakinada corporate hospital, Eat Godavari district, Andhra Pradesh, were studied during the period of two month, .urine samples were collected and processing was done in the laboratory.

RESULTS: "A total number of 50 sputum samples were collected from the patients in the department of Microbiology, Corporate Hospital, Kakinada during the period from May 2023 to June 2023."

Organism wise distribution of cases

S.no	Organisms	No.ofIsolates	Percentage(%)
1	Klebsiellapnemoniae	13	43
2	Acineobacterspecies	4	13
3	StaphylococcusAureus	3	10
4	PseudomonasAeruginosa	10	34
	Total	30	100



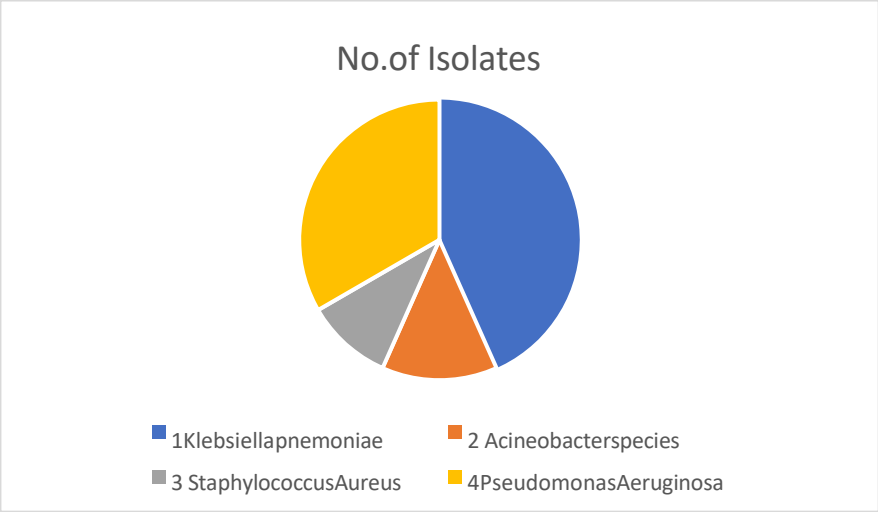
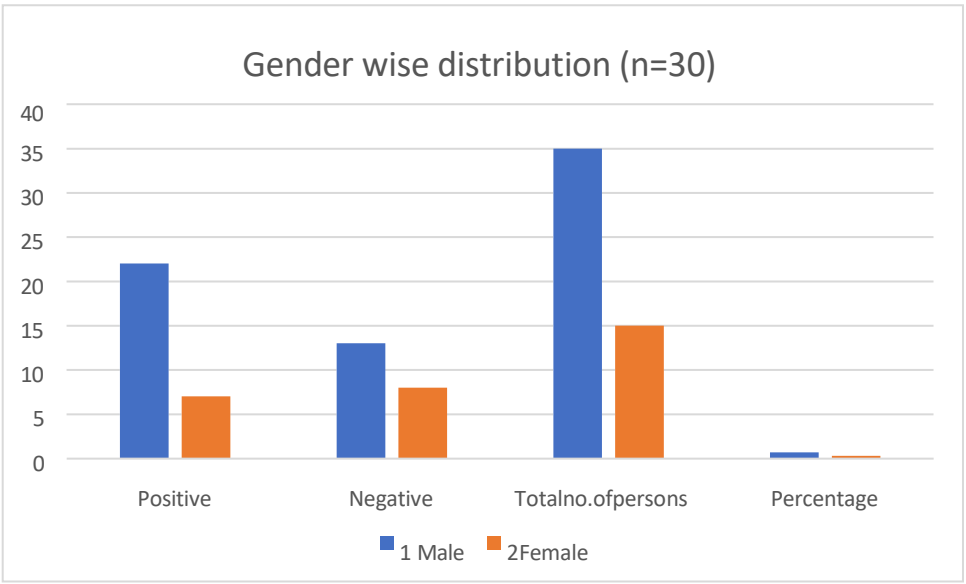


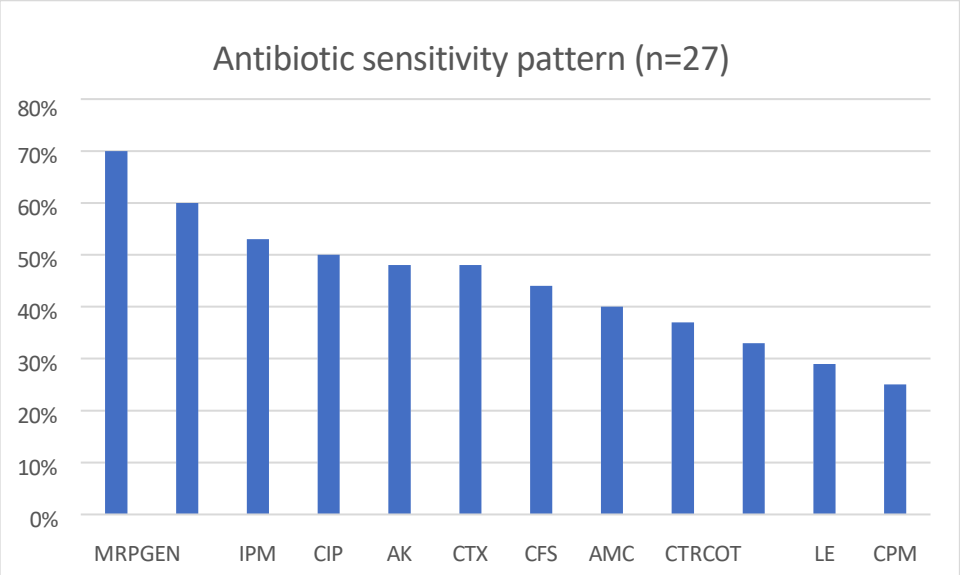
Table.2: Gender wise distribution of cases (n=30)

S.no	Gender	Positive	Negative	Total no.of persons	Percentage
1	**Male**	22	13	35	70%
2	**Female**	7	8	15	30%



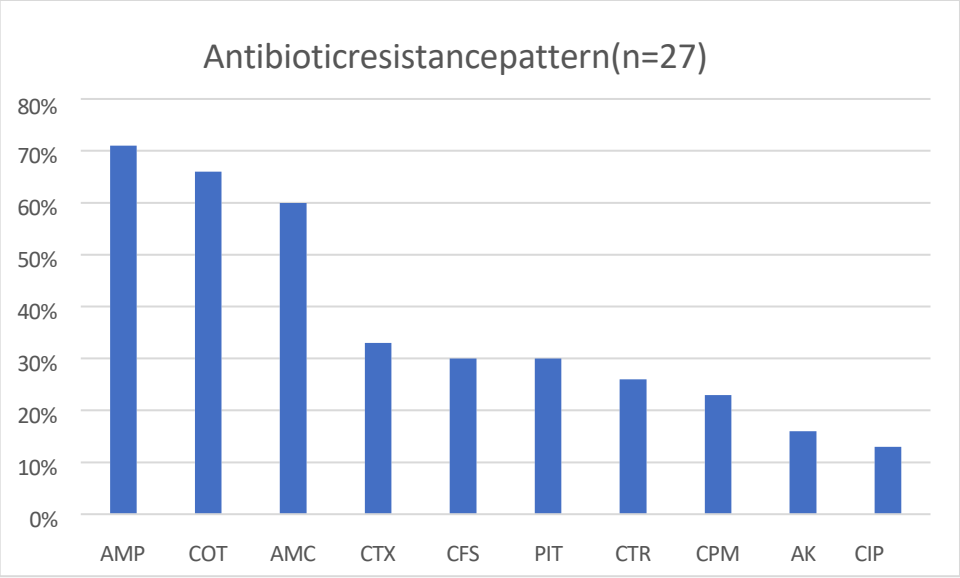
Antibiotic sensitivity pattern of gram-negative organisms.

Organisms	MRP	GEN	IPM	CIP	AK	CTX	CFS	AMC	CTR	COT	LE	CPM
Klebsiella pneumonia (13)	12 92%	10 76%	11 84%	8 61%	6 46%	9 69%	8 61%	8 61%	9 69%	6 46%	7 53%	1 7%
pseudomonas aeruginosa(10)	7 70%	4 40%	4 40%	6 60%	5 50%	3 30%	3 30%	2 20%	-	2 20%	-	6 60%
Acinetobacter species(4)	2 50%	4 100%	1 25%	1 25%	2 50%	1 50%	1 25%	1 25%	2 50%	1 25%	1 25%	-
TOTAL	21 70%	18 60%	16 53%	15 50%	13 48%	13 48%	12 44%	11 40%	10 37 %	9 33%	8 29 %	7 25%



Antibiotic resistance pattern of gram negative organisms

Organisms	AMP	COT	AMC	CTX	CFS	PIT	CTR	CPM	AK	CIP
Klebsiella pneumoniae(13)	12 92%	8 61%	8 61%	4 30%	5 38%	3 23%	4 30%	2 15%	2 15%	1 7%
pseudomonas aeruginosa(10)	5 50%	9 90%	7 70%	2 20%	2 20%	4 40%	2 20%	3 30%	1 10%	1 10%
Acinetobacter species(4)	4 100%	3 75%	3 75%	4 100%	2 50%	2 50%	2 50%	2 50%	2 50%	2 %
TOTAL	21 71%	20 66%	18 60%	10 33%	9 30%	9 30%	8 26%	7 23%	5 16%	4 13%



Discussion

These biochemical tests, along with colony morphology, pigment production, lactose fermentation. (and non-lactose fermentation), Gram staining, oxidase test, and catalase test, were all used to identify the bacteria, 50 (100%) sputum samples were analyzed for our study; 30 (60%) of the samples had positive results, and remaining 20 samples were negative results. Mostly Gram-negative bacteria were obtained in our study. Many other studies have obtained similar results. The Gram-negative predominance in our study might partly be due to the unequal distribution of patients with community-acquired and hospital-acquired infections and also due to the spread of antibiotic resistance in the hospital setting. The most common bacteria isolated in our study were Pseudomonas aeruginosa (34%), Klebsiella pneumonia (43%) and Acinetobacter spp. (13%). Multiple drug resistance is a growing concern among respiratory pathogens, particularly those causing hospital-acquired infections. The common MDR isolates K. pneumonia and Acinetobacter spp and. P. aeruginosa was comparatively more susceptible to antibiotics. on MDR Gram-negative bacilli causing lower respiratory infections. They had K. pneumonia and Acinetobacter spp. as the commonest MDR isolates. Another salient issue is the growing .Acinetobacter species have emerged as a major cause of healthcare-associated infections, particularly hospital-acquired and ventilator-associated pneumonia. Ewig S,Schloch termeier.

Conclusion

LRTIs are among the most common infectious diseases in humans worldwide. Among the acute manifestation s of LRTI, which remains an important public health problems. Demographic factors like age and some predisposing factors like hospitalization can lead to change in the causative agent of LRTI. In the present study the bacteriology laboratory received 50 sputum samples from patients who were thought to bacterial illnesses and processed them for culture. 30 sputum samples tested positive for bacterial growth. From sputum samples of individuals with lower respiratory infections, Klebsiella pneumonia was the most frequently isolated organism (43%), followed by Pseudomonas. Sputum samples were isolated frequently from patients who were male (70%) and from those who were between the ages of 60 and 79. The most sensitive drugs were imipenem, meropenem, gentamycin, and ciprofloxacin for gram negative organisms. The Gram positive bacteria Staphylococcus aureus most sensitive drugs were vancomycin, linezoid, teicoplanin, amikacin. Acinetobacter most sensitive drug was gentamycin. To reduce the inappropriate use of antibiotics, proper diagnosis, identification of the causing agents, and knowledge of their anti microbial sensitivity pattern were crucial. In the current study, LRTIs were more common in males than in females, with a higher incidence in the age group of 56-65 years among males.

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