ORIGINAL RESEARCH

Microbiological Profile and its Antibiotic Susceptibility Pattern Pleural fluid sample in a tertiary care centre

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ABSTRACT
Background: Pleural infection is a clinical problem that affects all ages but is most common in children and elderly patients.sterile body areas Patients may experience severe morbidity and mortality if they become contaminated with germs. The current study is intended to identify the bacterial profile and trend of antibiotic resistance associated with pleural fluid infection in a tertiary care centre. **Material method:** Using aseptic measures, a thoracocentesis was used to obtain pleural fluid samples. The study comprised all specimens of pleural fluid from July 2023 to December 2023 from the departments of medicine, paediatrics, and TB Chest for Culture and Sensitivity to Microbiology. **Result:** Total sample of Pleural fluid received from July 2023 to December 2023 were 495 out of which 70 (14.2%) showed growth while 425 (85.8%) samples were sterile. Majority of isolates were Gram negative bacilli 77 %. **Conclusion:** Antimicrobial resistance has increased in both gram positive and gram negative bacteria as a result of the careless use of antibiotics. Patients' knowledge of the harmful effects of antibiotic overuse and misuse must be raised, and empirical treatment should be promoted.
Key words: Pleural fluid, *Klebsiella*, Antibiotic Resistance

INTRODUCTION

Pleural infection is a clinical problem that affects all ages but is most common in children and elderly patients.sterile body areas Patients may experience severe morbidity and mortality if they become contaminated with germs [1]. Since these infections frequently pose a serious risk to life, they have a higher clinical urgency [2]. Numerous microorganisms, including viruses, fungi, bacteria, and parasites, are suspected of being the infectious cause of pleural effusion. Even one colony may have considerable effects on a potentially dangerous organism [3]. Poor outcomes are linked to pleural effusion and empyema, which are the major manifestations of intrathoracic illness [4].

Bacterial-related pleural infections now account for 14.9% of cases worldwide, with a 20% fatality rate [5, 6]

Bacterial invasion of the sterile pleural space or trans-diaphragmatic spreads of abdominal infection are the most common causes of infection. These infections are closely linked to immune-compromised states, thoracic injuries, chest trauma, chest tube drainage, complications from hospital and community-acquired pneumonia, and other behavioural factors (alcohol misuse and cigarette smoking) [7, 8, 9,10,11] patterns of antibiotic sensitivity and the bacteriological profile of sterile bodily fluids. To ensure appropriate diagnosis and prudent administration of antibiotics, thereby minimising morbidity and mortality, microbiologists, doctors, infectious disease experts, and antibiotic policymakers must have a thorough understanding of the bacteriological profile and drug susceptibility patterns [12].

The current study is intended to identify the bacterial profile and trend of antibiotic resistance associated with pleural fluid infection in a tertiary care centre.

MATERIAL METHOD

Using aseptic measures, a thoracocentesis was used to obtain pleural fluid samples. The study comprised all specimens of pleural fluid from July 2023 to December 2023 from the departments of medicine, paediatrics, and TB Chest for Culture and Sensitivity

to Microbiology. All of the fluids were received for gram staining, after which they were inoculated on culture mediums such as Mac Conkey medium and blood agar, and they were left to incubate for a whole night at 37ºC. The isolate was identified by routine, conventional biochemical testing, and any growth was reported. Using the Kirby Bauer disc diffusion method and CLSI recommendations, antibiotic susceptibility testing wasconducted.

RESULT

Total sample of Pleural fluid received from July 2023 to December 2023 were 495 out of which 70 (14.2%) showed growth while 425 (85.8%) samples were sterile. Majority of isolates were Gram negative bacilli 77 % of which most common was *Pseudomonas aeroginosa*30% followed by*Klebsiella*14%, *Acinetobacter* 11%,*E.coli* 10%. Among gram positive spectrum, *Staphylococcus aureus* was isolated from (10%) samples. Males 51 (73%) were more commonly affected then females 19 (27%) as shown table 2.

Table 1: Positivity rate of total samples (n= 495)

	Number	Percentage %
Positive samples	70	14.2%
Negative samples	425	85.8%
Total samples	495	

Table 2: Gender wise distribution based on culture positivity

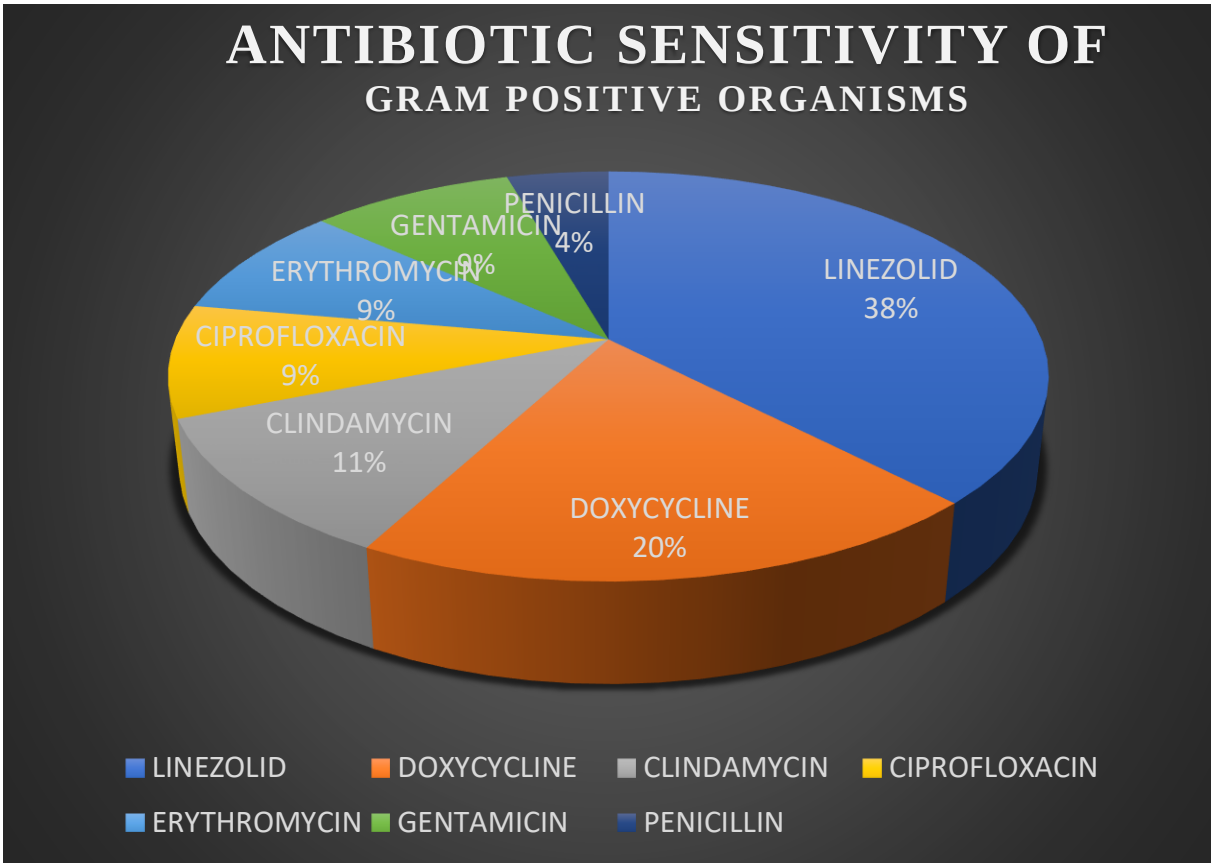
Male patients	Female patients	Total no. of isolates
51 (73%)	19 (27%)	70

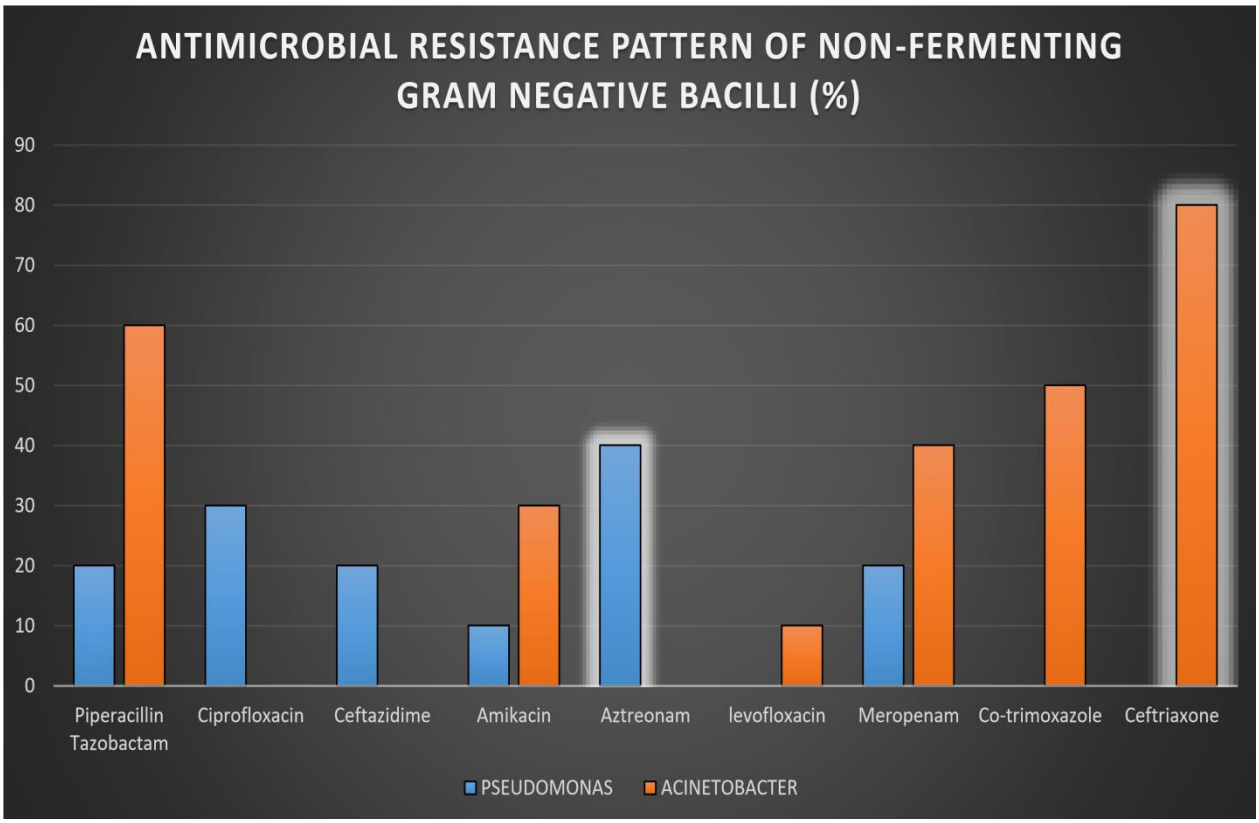
Table 3: Distribution of organisms isolated

BACTERIAL ISOLATE	NO.	%
Pseudomonas aeruginosa	21	30%
Klebsiella pneumoniae	10	14%
Acinetobacter baumanii	8	11%
Staphylococcus aureus	7	10%
Coagulase negative staphylococcus	7	10%
Escherichia coli	7	10%
Acinetobacter spp.	3	4.2%
Enterobacter	2	2.8%
Enterococcus	1	1.4%
Proteus mirabilis	1	1.4%
Citrobacter species	1	1.4%
Streptococcus pneumoniae	1	1.4%
Acinetobacter lauffi	1	1.4%
TOTAL	70	

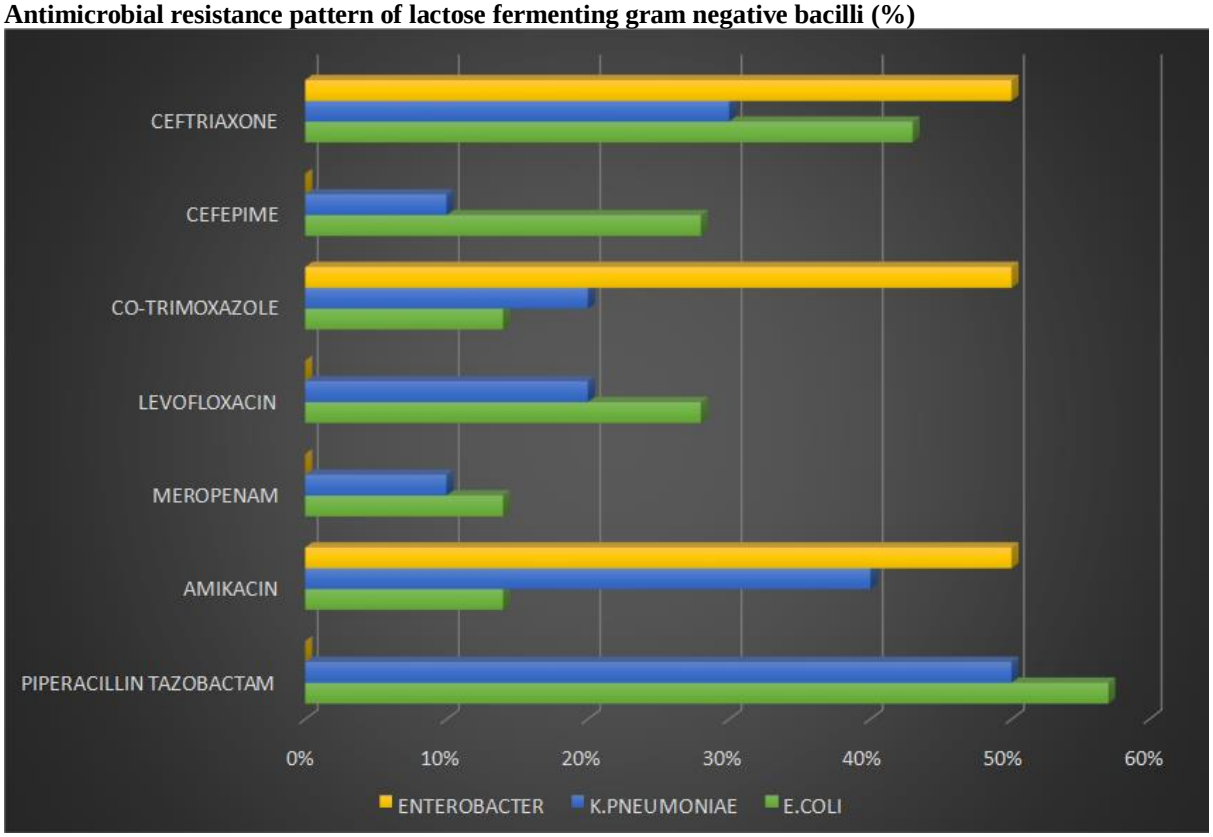
Table 4: Percentage of growth of gram positive and gram negative bacteria

Gram Positive Cocci	23%	Gram Negative Bacilli	77 %
Staphlococcus aureus	10%	Pseudomonas aeruginosa	30%
Coagulase negative staphylococcus	10%	Escherichia coli	10%
Streptococcus pneumoniae	1.4%	Klebsiella pneumoniae	14%
Enterococcus	1.4%	Acinetobacter baumanii	11%
		Enterobacter spp.	2.8%
		Proteus mirabilis	1.4%
		Citrobacter spp.	1.4%
		Acinetobacter lauffi	1.4%
		Acinetobacter spp.	4.2%





Antimicrobial resistance pattern of lactose fermenting gram negative bacilli (%)



DISCUSSION

Patients with pleural effusion frequently have pleural infection, which necessitates the early and intensive antimicrobial therapy initiation. Therefore, it is essential to identify the causal organisms in order to choose the best antibiotic course and enhance patient outcomes [13]Previous studies shown the wide regional heterogeneity and diversity of the bacteriology profile in pleural effusion. Previous research has demonstrated that the majority of infections in individuals with pleural infections were caused by aerobic gram-positiveorganisms. But in low- and middle-income nations, things seem to be turning around, as gram negative bacteria are now recognised as important culprits in a variety of thoracic illnesses [14, 15]In this study, 495 samples of pleural fluid were received in the department of microbiology, out of which 70 (14.2%) were found to be growth-positive. Mohanty et al. showed similar growth, which is comparable to our study [15].Males (51,73%) were more commonly affected than females (19,27%) as shown in Table 2. A study done by Soniya Saxena *et al*. [9] shows males are more commonly affected than females, which concords with the present study [16].Among the 70 culture-positive isolates, 77% were gram negative bacilli. The predominant pathogens were Pseudomonas (30%), followed by Klebsiella (11%), *E. coli (10%), S. aureus (10%),* and CONS (10%). This finding was similar to a study conducted by Bajare B et al [17]. Antibiotic-resistant pattern in gram negative bacteria among pseudomonas: maximum resistance was shown by aztreonam, followed by ciprofloxacin, piperacillin-tazobactam, ceftazidime, meropenem, and amikacin.Among Acinetobacter, maximum resistance was shown by ceftriaxone, followed by piperacillin-tazobactam, cotrimoxazole, meropenem, amikacin, and levofloxacin.In lactose-fermenting bacteria, among Klebsiella, high resistance is shown by piperacillin-tazobactam, amikacin, levofloxacin=cotrimoxazole, meropenem, and cefepime.Among Escherichia coli, maximum resistance was shown by piperacillin-tazobactam, ceftriaxone, cefepime=levofloxacin, and cotrimoxazole=meropenem. Numerous researchers from the current study have observed variations in the patterns of antibiotic susceptibility. These variations can be attributed to a number of factors, including the population being studied, geographic variations, institution-based variation, patient socioeconomic status, local patterns of antibiotic resistance in the area, local hospital-based antibiotic policies, and hospital infection control practices of healthcare personnel.

CONCLUSION

Antimicrobial resistance has increased in both gram positive and gram negative bacteria as a result of the careless use of antibiotics. Patients' knowledge of the harmful effects of antibiotic overuse and misuse must be raised, and empirical treatment should be promoted. An effective hospital-based antibiotic policy must also be developed.

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