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Aerobic Bacterial Profile and Antibiogram of Pus Isolates: A Six-Month Retrospective Study in a Tertiary Care Teaching Hospital, Krishnagiri, Tamil Nadu

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ABSTRACT

Background: Wound infections contribute significantly to morbidity and involve diverse bacterial pathogens. Identification of causative organisms and their antimicrobial susceptibility patterns is essential for effective treatment and control of antimicrobial resistance.
Objective: To determine the aerobic bacterial profile and antibiogram of pus isolates in a tertiary care teaching hospital.
Materials and Methods: This retrospective study was conducted in the Department of Microbiology from January to June 2025. All pus and wound specimens received for aerobic culture were included. Bacterial identification was performed using standard microbiological methods, and antimicrobial susceptibility testing was carried out using the VITEK 2 Compact system. Results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) 2025 guidelines.
Results: Out of 333 pus and wound specimens processed, 223 (67.0%) were culture positive. Among these, 198 (88.8%) were pathogenic isolates and 25 (11.2%) were commensals. Gram-negative bacilli predominated (162; 81.8%) over Gram-positive cocci (36; 18.2%). Among Gram-positive cocci, Staphylococcus aureus was the most common isolate (30; 15.2%), followed by Enterococcus spp. (6; 3.0%). Among Gram-negative bacilli, the predominant isolates were Escherichia coli (52; 26.3%), Klebsiella pneumoniae (30; 15.2%), Proteus spp. (17; 8.6%), Pseudomonas spp. (16; 8.1%), and Acinetobacter baumannii complex (15; 7.6%). Other Gram-negative isolates included Enterobacter cloacae complex (12; 6.1%), Morganella spp., Providencia spp., and Serratia spp. (8; 4.0%), Citrobacter spp. (5; 2.5%), and Burkholderia spp. (2; 1.0%). Resistance included methicillin-resistant Staphylococcus aureus (18/30; 60%), carbapenem-resistant E. coli (9/52; 17.3%), and multidrug-resistant K. pneumoniae (18/30; 60%). Gram-positive isolates showed high susceptibility to vancomycin, teicoplanin, linezolid, and tigecycline, while Gram-negative isolates were more susceptible to carbapenems, amikacin, and fosfomycin.
Conclusion: Gram-negative bacilli predominated, with a considerable burden of multidrug-resistant organisms. Continuous surveillance of local bacterial profiles and antibiogram patterns is essential to guide empirical therapy and strengthen antimicrobial stewardship.

Keywords*: Pus culture; Aerobic bacteria; CLSI; Antibiogram; Antimicrobial resistance.*

INTRODUCTION

Wound infections are a significant cause of morbidity and are associated with delayed healing and prolonged hospitalization, particularly in developing countries [1]. They commonly occur following surgical procedures, trauma, and burns, and are frequently influenced by underlying comorbid conditions. These infections are caused by a wide range of aerobic bacterial pathogens, including Gram-positive cocci and Gram-negative bacilli [2].

The increasing burden of antimicrobial resistance (AMR) among wound pathogens poses a major challenge to effective treatment and infection control [3]. Inappropriate and empirical antibiotic use has contributed to the emergence of multidrug-resistant (MDR) organisms, resulting in therapeutic failure, increased healthcare costs, and poor clinical outcomes [4]. Therefore, continuous surveillance of the local bacterial spectrum and antimicrobial susceptibility patterns is essential for guiding empirical therapy and improving patient care [5].

Studies from Tamil Nadu and other regions of South India have reported a predominance of Gram-negative bacilli in wound infections, with *Escherichia coli* and *Klebsiella pneumoniae* being frequently isolated [6,7]. In addition, the increasing prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) and carbapenem-resistant Enterobacteriaceae has further complicated the management of wound infections [8,11].

Hence, the present study was undertaken to determine the aerobic bacterial profile and antimicrobial susceptibility pattern of pus isolates in a tertiary care teaching hospital in Krishnagiri, Tamil Nadu.

MATERIALS AND METHODS

Study Design and Setting

This retrospective study was conducted in the Department of Microbiology of a tertiary care teaching hospital in Krishnagiri, Tamil Nadu, over a period of six- months (January to June 2025).

Study Population

All pus and wound specimens received for aerobic bacterial culture during the study period were included. Duplicate samples from the same patient and improperly collected specimens were excluded.

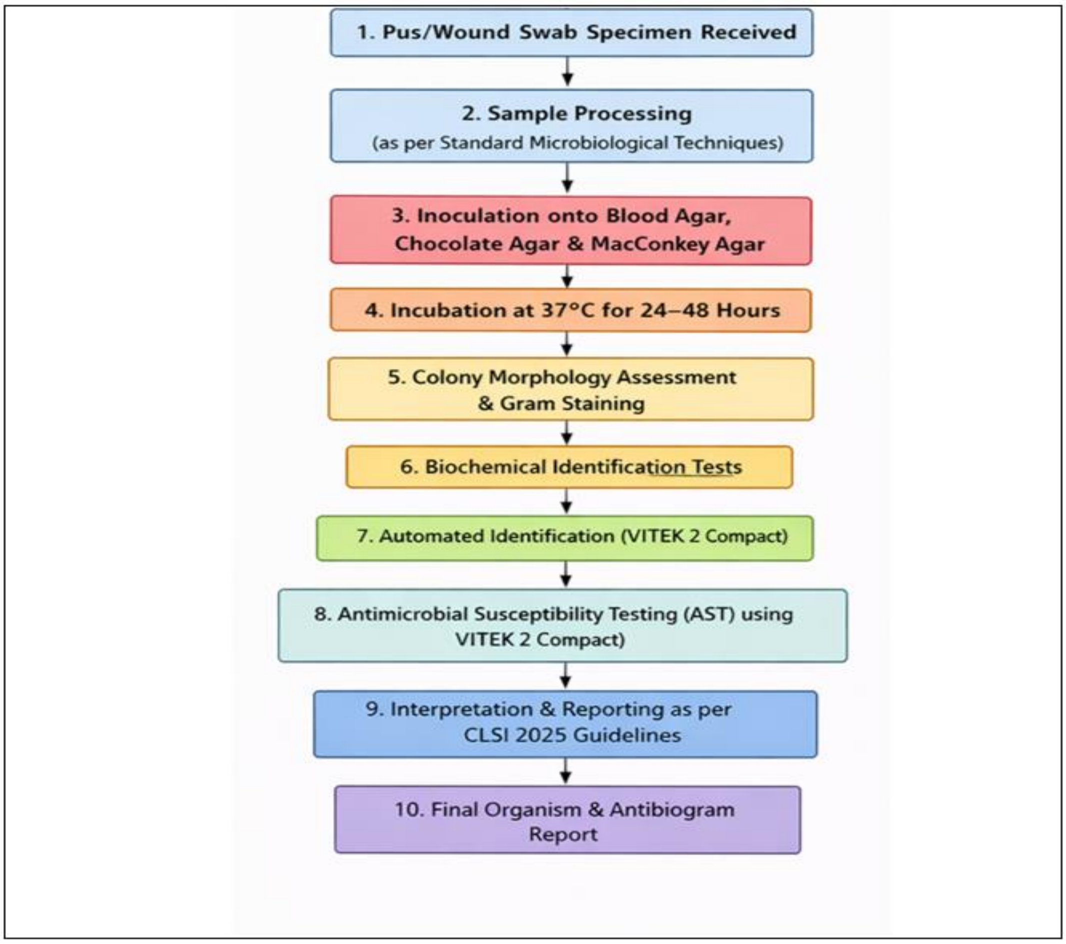

Figure 1: Workflow of Bacteriological Processing and Antimicrobial Susceptibility Testing of Pus/Wound Specimens

Data Analysis
Data were entered into Microsoft Excel and analyzed using descriptive statistics. Results were expressed as frequencies and percentages.

RESULTS

During the study period (January–June 2025), a total of 333 pus and wound swab specimens were received for aerobic culture and sensitivity testing. Out of these, 223 (67.0%) specimens yielded bacterial growth, while 110 (33.0%) showed no growth.

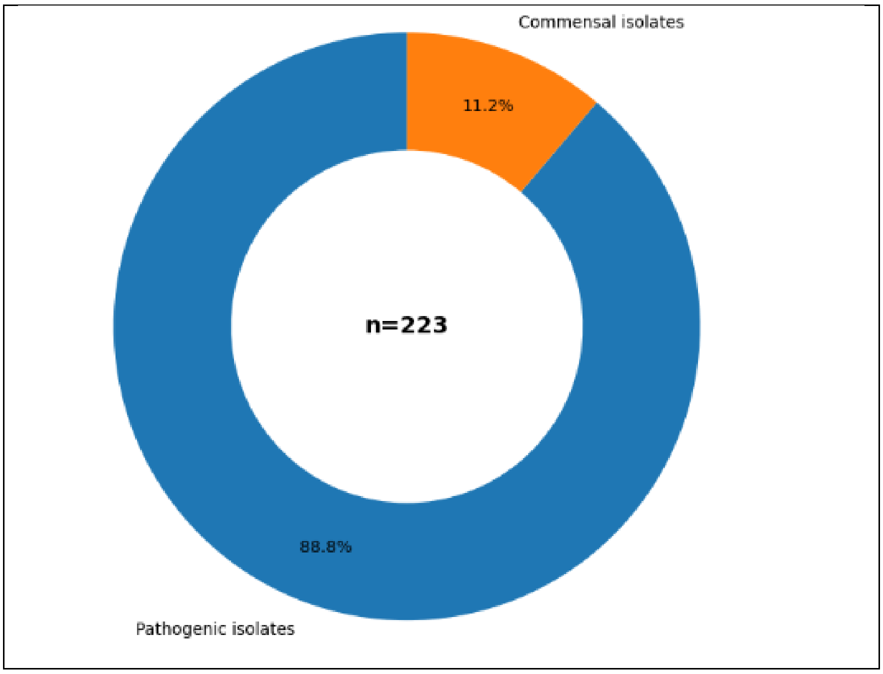

Figure 2: Distribution of Pathogenic and Commensal Isolates among Culture-Positive Samples (n=223)

Among the culture-positive specimens, 198 (88.8%) isolates were identified as pathogenic organisms, whereas 25 (11.2%) were reported as commensal isolates.

Table 1: Distribution of Aerobic Bacterial Pathogens Isolated from Pus/Wound Specimens (n = 198)

Gram Reaction	**Organism**	**Number (n)**	**Percentage (%)**
Gram-positive cocci (n = 36)	*Staphylococcus aureus*	30	15.2
	Enterococcus spp.	6	3.0
	Total GPC	**36**	**18.2**
Gram-negative bacilli (n = 162)	*Escherichia coli*	52	26.3
	Klebsiella pneumoniae	30	15.2
	Proteus spp.	17	8.6
	Pseudomonas spp.	16	8.1
	Acinetobacter baumannii complex	15	7.6
	Enterobacter cloacae complex	12	6.1
	Morganella spp./*Providencia* spp./*Serratia* spp.	8	4.0
	Citrobacter spp.	5	2.5
	Burkholderia spp.	2	1.0
	Total GNB	**162**	**81.8**
Total pathogenic isolates		**198**	**100**

Note: Percentages are calculated out of total pathogenic isolates (n = 198).

A total of 198 pathogenic isolates were analyzed for bacterial distribution and antibiogram. Gram-negative bacilli (162; 81.8%) predominated over Gram-positive cocci (36; 18.2%).

Among Gram-positive cocci, *Staphylococcus aureus* was the most common isolate (30; 15.2%), followed by *Enterococcus spp.* (6; 3.0%).

Among Gram-negative bacilli, the most frequently isolated organism was *Escherichia coli* (52; 26.3%), followed by *Klebsiella pneumoniae* (30; 15.2%), *Proteus spp.* (17; 8.6%), *Pseudomonas spp.* (16; 8.1%), and *Acinetobacter baumannii complex* (15; 7.6%). Other isolates included *Enterobacter cloacae complex* (12; 6.1%), *Morganella spp./Providencia spp./Serratia spp.* (8; 4.0%), *Citrobacter spp.* (5; 2.5%), and *Burkholderia spp.* (2; 1.0%).

Table 2: Antibiotic susceptibility pattern of Gram-positive cocci isolates

Antibiotic	Staphylococcus spp. (n=30) Sensitive n (%)	Enterococcus spp. (n=6) Sensitive n (%)
Cefoxitin (MRSA marker)	11 (36.7)	—
Clindamycin	19 (63.3)	—
Erythromycin	13 (43.3)	1 (16.7)
Gentamicin / High-level Gentamicin	19 (63.3)	3 (50.0)
Ciprofloxacin	3 (10.0)	1 (16.7)
Levofloxacin	4 (13.3)	1 (16.7)
Linezolid	25 (83.3)	6 (100)
Vancomycin	30 (100)	6 (100)
Teicoplanin	30 (100)	6 (100)

Note: Data expressed as number sensitive (%). MRSA prevalence among *Staphylococcus* isolates = 18/30 (60%). (—) not tested / not applicable.

Table 3: Antibiotic susceptibility pattern of Gram-negative bacilli isolates

Antibiotic	*E. coli* (n=52)	*K. pneumoniae* (n=30)	*Citrobacter spp.* (n=5)	*Enterobacter spp.* (n=12)	*Proteus spp.* (n=17)	*Morganella/Serratia/Providencia* (n=8)	*P. aeruginosa* (n=16)	*A. baumannii* (n=15)
Amikacin	45 (87%)	10 (33%)	5 (100%)	10 (83%)	15 (88%)	8 (100%)	13 (81%)	1 (7%)
Gentamicin	29 (56%)	10 (33%)	4 (80%)	6 (50%)	13 (76%)	5 (63%)	11 (69%)	1 (7%)
Ciprofloxacin	0 (0%)	5 (17%)	3 (60%)	4 (33%)	2 (12%)	0 (0%)	2 (13%)	1 (7%)
Levofloxacin	42 (80%)	9 (30%)	3 (60%)	3 (25%)	4 (25%)	3 (60%)	13 (81%)	2 (13%)
Piperacillin/ Tazobactam	24 (46%)	7 (23%)	0 (0%)	0 (0%)	15 (88%)	5 (63%)	8 (50%)	1 (7%)
Cefepime	9 (17%)	6 (20%)	5 (100%)	6 (50%)	10 (59%)	4 (50%)	12 (75%)	1 (7%)
Imipenem	43 (83%)	7 (23%)	5 (100%)	9 (75%)	3 (25%)	1 (13%)	8 (50%)	1 (7%)
Meropenem	29 (56%)	10 (33%)	5 (100%)	11 (92%)	4 (25%)	0 (0%)	12 (75%)	1 (7%)
Colistin	0 (0%)	0 (0%)	5 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Tigecycline	51 (98%)	28 (93%)	0 (0%)	0 (0%)	0 (0%)	1 (13%)	0 (0%)	8 (100%)

Table 4: Major Resistance Patterns Observed among Common Pathogens

Organism	Resistance Pattern	Resistant isolates / Total isolates	Percentage (%)
Staphylococcus aureus	MRSA	18 / 30	60.0
Escherichia coli	Carbapenem-resistant (CRE)	9 / 52	17.3
Klebsiella pneumoniae	Multidrug-resistant (MDR)	18 / 30	60.0

Note: MRSA – Methicillin-resistant *Staphylococcus aureus*; CRE – Carbapenem-resistant Enterobacterales; MDR – Multidrug-resistant.

Regarding resistance patterns, methicillin-resistant *Staphylococcus aureus* (MRSA) accounted for 60% (18/30) of *S. aureus* isolates. Carbapenem resistance in *E. coli* was noted in 17.3% (9/52) isolates. Additionally, multidrug resistance in *Klebsiella pneumoniae* was observed in 60% (18/30) isolates. Gram-positive isolates showed high susceptibility to vancomycin, teicoplanin, linezolid, and tigecycline, whereas Gram-negative isolates demonstrated better susceptibility to carbapenems, amikacin, and fosfomycin.

DISCUSSION

In the present study, pus and wound infections were predominantly caused by Gram-negative bacilli, particularly the Enterobacterales, which is consistent with observations from Tamil Nadu and other Indian settings reporting a shift towards Gram-negative pathogens in wound infections [6,7]. The predominance of *Escherichia coli* and *Klebsiella pneumoniae* highlights their major contribution to wound and postoperative infections. This shift towards Gram-negative pathogens may be linked to increasing healthcare-associated infections and selective antibiotic pressure.

A notable finding was the high proportion of methicillin-resistant *Staphylococcus aureus* (MRSA) (60%). MRSA remains a major cause of skin and soft tissue infections globally and is associated with limited treatment options and increased morbidity [8]. In this study, vancomycin, teicoplanin, and linezolid retained excellent activity against Gram-positive cocci, supporting their continued usefulness in managing serious MRSA-associated infections [9].

The detection of carbapenem-resistant *E. coli* and multidrug-resistant *K. pneumoniae* is of significant concern, as these organisms severely restrict therapeutic choices and may contribute to treatment failure. Similar resistance trends have been reported in Indian surveillance data, reflecting the growing burden of resistant Enterobacterales [5]. The global rise of antimicrobial resistance, as highlighted by WHO, is strongly influenced by inappropriate antibiotic use and inadequate infection prevention measures [3,4].

Overall, the findings of this study emphasize the need for routine culture and susceptibility testing, continuous monitoring of local antibiogram patterns, and strict implementation of antimicrobial stewardship programs. Such measures are essential to guide appropriate empirical therapy, reduce the spread of multidrug-resistant organisms, and improve patient outcomes [3,5].

CONCLUSION

Gram-negative organisms, particularly Enterobacterales, were the most common isolates from pus and wound specimens, with a considerable proportion showing multidrug resistance. This reflects the increasing challenge in selecting effective empirical therapy for wound infections. Regular evaluation of local bacteriological trends and antibiogram data is essential to guide rational empirical treatment and to strengthen infection control and antimicrobial stewardship practices.

Limitations

This was a retrospective single-center study conducted over a limited duration, which may restrict generalizability. Only aerobic bacterial isolates were evaluated; anaerobic and fungal pathogens were not included, which may have led to underestimation of the true etiological agents. Clinical correlation with patient risk factors, prior antibiotic exposure, and outcomes could not be assessed. Molecular characterization of resistance mechanisms was not performed.

Conflict of Interest: None declared.

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