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Original Research Article

Bacteriological Profile and Antimicrobial Resistance Patterns of Isolates from some Body Fluids at Al-Sader Teaching Hospital, Basrah/Iraq

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Abstract: The objective of this study was to identify the prevalence, distribution and the antimicrobial susceptibility profile of bacteria isolates obtained on different Body Fluids. Clinical samples analyzed were 308 clinical samples, comprising of blood, cerebrospinal fluid (CSF), and pleural fluid. Bacterial isolates have been determined and their distribution was evaluated as per sample type, age grouping and patient sex. More distribution isolates were tested in relation to antimicrobial susceptibility. Among 308 samples, 126 (39.6), were positive and highest positivity rate was reported in blood (64.6). *Staphylococcus aureus* (n=28), *S. hominis* (n=23), and *S. haemolyticus* (n=18) were the most common of all. The etiological picture depended on sample type: Coagulase-Negative Staphylococci (CoNS) dominated blood cultures whereas a co-dominant S. aureus (24.0%) and *Acinetobacter baumannii* (24.0) was also a worrying situation in CSF cultures. There were no statistically significant differences in the age distribution and sex of the patients of the isolates. Antimicrobial susceptibility testing showed that there was a high prevalence of Methicillin-Resistant *S. aureus* (MRSA, 64.3) and Methicillin-Resistant CoNS. In addition, *A. baumannii* showed alarming resistance (87.5%) to carbapenems. Importantly, all *Staphylococcus* species were completely susceptible to vancomycin and linezolid. The results demonstrate that there is a large presence of multidrug-resistant (MDR) pathogens, especially at such critical locations as CSF, with a high prevalence of MRSA/MRCoNS and extensively drug-resistant (XDR) *A. baumannii*. Such findings stress the necessity of active local monitoring to educate empirical treatment rules and enhance the processes of preventing infections.

Keywords: Body Fluids, Coagulase-Negative Staphylococci, *Staphylococcus Aureus*, *Acinetobacter Baumannii*, Antibiotic Susceptibility.

INTRODUCTION

Antimicrobial Resistance (AMR) is considered one of the most formidable health risks of the 21 st century which has weakened the capability of modern medicine to cure prevalent infections (Tang *et al*., 2023). It is estimated that around 1.27 million deaths were caused by AMR in 2019 alone all over the world, and it is expected to grow considerably unless an effective intervention is undertaken (WHO, 2020). Conflict areas and settings with poor healthcare infrastructure, like Iraq, are left to a further worsened crisis of AMR, where reports indicate that the pathogen has caused the deaths of thousands per year, and it has been estimated that the health sector is overloaded (IHME, 2025). The most crucial cases are bacterial infections of essential body fluids, including blood (bacteremia) (Thari *et al*., 2024), cerebral fluid (meningitis), and pleural fluid (pleurisy/empyema), which are highly severe and are considered to be accompanied by high morbidity and mortality rates (Teklehymanot *et al*., 2017). These are the conditions that necessitate empirical therapy with immediate therapeutic intervention before culture and sensitivity outcomes are obtained (Altaf *et al*., 2023). In order to make this early intervention work, local and current data on the most common patterns of bacteria and their resistance to antimicrobials in each healthcare facility is necessary (Salam *et al*., 2023). In this regard, there exists the urgent necessity of the Multidrug-

Resistant (MDR) pathogens surveillance which poses a threat to the effectiveness of the existing treatment options (Shetty *et al*., 2025). Among such pathogens, the major cause of hospital- and community-acquired infections, Methicillin-Resistant *Staphylococcus aureus* (MRSA), should be mentioned first, as well as *Acinetobacter baumannii*, which is extremely carbapenem-resistant (Carbapenem-Resistant A. baumannii - CRAB), and is rated as a critical priority by the World Health Organization (Pons *et al*., 2025). The growing prevalence of such pathogens in the local clinical area presents a high challenge to clinicians and requires an ongoing revision of treatment protocols (Kumar *et al*., 2024).

The resistance of bacteria to antibiotics is conditioned by various mechanisms that enable pathogens to avoid antimicrobial agents (Reygaert, 2018). These mechanisms encompass enzymatic inactivation, PBP2a in MRSA (Peacock and Paterson, 2015), target modification, and reduced permeability or active efflux of the drug, which is mainly carbapenemases in the CRAB (Kyriakidis *et al*., 2021). The fact that bacteria gain and transfer these resistance genes horizontally promotes the rapid dissemination of Multidrug-Resistant (MDR) strains, and local monitoring of these systems is essential to ensure the successful treatment of infections (Elshobary *et al*., 2025).

According to the above, the purpose of the study was to identify the bacterial profiles obtained on different body fluid samples (blood, cerebrospinal fluid, and pleural fluid) at Al-Sadr Teaching Hospital in Basrah/Iraq, and to observe the antimicrobial resistance pattern of those samples. It is hoped that the results will give the right local surveillance data that can be utilized to guide the empirical treatment choice, and can assist in development of effective local guidelines on infection control and resistance spread limitation.

MATERIALS AND METHODS

Sampling of Clinical Samples

Between February and November 2024, 308 clinical samples were isolated, and they were obtained among patients admitted to Al-Sadr Teaching Hospital, Basrah, Iraq, Samples which were collected were blood (n=130), pleural fluid (n=106) and cerebrospinal fluid (CSF) (n=72). Samples are transported to the Microbiology Laboratory in sterile, non-leakage samples.

Bacteria Isolation and Identification

Bacterial growth was continuously monitored by placing the blood samples in BacT/ALERT ortho blood culture bottles (bioMerieux, France) and incubating the samples in the BacT/ALERT microbial detection system as per the manufacturer protocol. The positive blood culture samples, pleural fluid and CSF were cultured on 5% sheep blood agar and the nutrient agar, and incubated at 5-10% CO 2 and aerobically at 37 C in 24 hours. A pure colony was obtained using streak plate method with a sterile loop and gram stained followed by cultivation on some selective and differential media including mannitol salt agar, XLD agar, MacConkey agar, Eosin methylene blue agar, and incubated at 37 C. The morphologies of the colonies, size, shape, color odor and pigments of the bacteria isolates were described. Gram-negative and Gram-positive bacteria were detected by some of the biochemical methods. Besides this, the result was certified using the VITEK 2 Compact system (bioMerieux, France).

Susceptibility of Microorganisms to Antimicrobials

The VITEK 2 Compact system was used to test the susceptibility of the bacteria to antibiotics. The experiment was used based on the instructions of the manufacturer. The antibiotics in the study under analysis consisted of 17 gram-negative and 14 gram-positive antibiotics. These gram-negative bacterial antibiotics were Piperacillin/ Tazobactam, Ampicillin, Ampicillin/ Sulbactam, Cefepime, Ceftazidime, Cefoxitin, Cefotaxime, Ceftriaxone, Trimethoprim/ Sulfamethoxazole, Amikacin, Gentamicin, Imipenem, Aztreonam, Meropenem, Levofloxacin, Ciprofloxacin, and Colistin. Whereas gram-positive bacterial antimicrobials, such as Oxacillin, Cefoxitin, Trimethoprim/Sulfamethoxazole, Vancomycin, Gentamicin, Erythromycin, Azithromycin, Tetracycline, Linezolid, Ciprofloxacin, Clindamycin, Doxycycline, Rifampicin and Levofloxacin. To interpret the results of antimicrobial susceptibility, used Clinical and Laboratory Standards Institute guidelines (CLSI, 2024).

Statistical Analysis

All statistical result calculations were conducted in the IBM SPSS Statistics (version 23). The percentages and frequencies of categorical variables were calculated with the help of descriptive statistics. Potential relationships among bacterial isolates and patient variables, including sex, type of sample and age group, were determined using the Chi-square (X^2) test. The p-value of below 0.05 was regarded as statistically significant.

RESULT AND DISCUSSION

Among 308 tested samples (blood, pleural fluid and CSF), 126 were positive cultures (39.6%). Positivity was different between samples with blood 64.6% (84/130), CSF 34.7% (25/72), and pleural fluid 16% (17/106). Results of blood samples were high with *Staphylococcus hominis* (26.2%) and *S. haemolyticus* (20.2) followed by *S. aureus* (16.7%),

Escherichia coli (15.5), and *Klebsiella pneumoniae* (9.5). Although it is less common in *Pseudomonas aeruginosa* (3.6%), Salmonella typhi (2.4%), and individual isolates (1.2%), respectively, each of, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Citrobacter freundii*, *Acinetobacter baumannii*, and Proteus mirabilis. The most frequent Pleural fluid Samples were S. aureus (47.1%), *K. pneumoniae* (23.5%), E. coli (17.6%), *A. baumannii* and *S. haemolyticus* (5.9% each). Further, the high bacteria detected in the CSF samples were *S. aureus* (24.0%), *A. baumannii* (24.0%), *S. epidermidis* (16.0%), *K. pneumoniae* (16.0%), *P. aeruginosa* (8.0%), and single isolates (4.0%); *S. hominis*, *S. pneumoniae* and *Neisseria meningitides* respectively.

The prevalence of these species is in line with the worldwide trends, with *S. hominis* and *S. haemolyticus* commonly found in patients with bloodstream infections (Eltwisy *et al*., 2022; Asai *et al*., 2021). Although CoNS are common commensals of human skin and are typically regarded as the cause of contamination in blood cultures, their emerging impact as a significant cause of pleural infection, especially in healthcare-associated environments, is well-reported (Wu *et al.,* 2022). *S. aureus* a high rate which is consistent with its growing role as a primary cause of pleural infection especially in healthcare-associated settings (Alelign *et al*., 2022; Roy *et al*., 2021). *K. pneumoniae* and *E. coli* are also in line with the etiology of community-acquired and healthcare-associated pleural infections (Hassan *et al*., 2021). A. baumannii isolating at this CSF culture gives high frequency which is a critical finding. *A. baumannii* is a well-known nosocomial pathogen, and the mortality rate related to meningitis caused by this organism is high and, sometimes, up to 37.8% despite the fact that neurosurgical procedures may be the cause of this infection (Fursova *et al*., 2023; Wang *et al*., 2024). S. aureus is also considered to be co-dominant and S. epidermidis is also present, which also indicates a considerable burden of healthcare-associated central nervous system infections (Suthar and Sankhyan, 2019). Lastly, *Neisseria meningitides* isolation is a typical outcome of the community-acquired bacterial meningitis, a health issue that necessitates an immediate response by the health authorities (Van de Beek *et al*., 2021).

Table 1: Distribution of pathogenic bacterial isolates from blood, pleural fluid, and cerebrospinal fluid (CSF) samples

Sample Type	Total Samples	Positive Cultures	Negative Cultures	Bacteria Isolated	No. of Isolates	Percentage (%)
Blood	130	84	46	*Staphylococcus hominis*	22	26.2
				Staphylococcus haemolyticus	17	20.2
				Staphylococcus aureus	14	16.7
				Staphylococcus epidermidis	1	1.2
				Streptococcus pneumoniae	1	1.2
				Escherichia coli	13	15.5
				Klebsiella pneumoniae	8	9.5
				Pseudomonas aeruginosa	3	3.6
				Salmonella typhi	2	2.4
				Acinetobacter baumannii	1	1.2
				Proteus mirabilis	1	1.2
				Citrobacter freundii	1	1.2
					1	1.2
Pleural fluid	106	17	89	*Staphylococcus aureus*	8	47.1
				Staphylococcus haemolyticus	1	5.9
				Klebsiella pneumoniae	4	23.5
				Escherichia coli	3	17.6
				Acinetobacter baumannii	1	5.9
Cerebrospinal Fluid (CSF)	72	25	47	*Staphylococcus aureus*	6	24
				Staphylococcus epidermidis	4	16
					1	4
					1	4

Sample Type	Total Samples	Positive Cultures	Negative Cultures	Bacteria Isolated	No. of Isolates	Percentage (%)
				Staphylococcus hominis *Neisseria meningitidis* *Streptococcus pneumoniae* *Acinetobacter baumannii* *Klebsiella pneumoniae* *Pseudomonas aeruginosa*	1 6 4 2	4 24 16 8
Total	**308**	**126**	**182**			

Pearson Chi-Square= 63.929, df= 24, p-value= 0.001

The result of the distribution of 126 bacteria among five age groups (Figure 1), *S. aureus* was the most frequently identified pathogen (n = 28), followed by *S. hominis* (n = 23) and *S. haemolyticus* (n = 18). On the other hand, gram-negative bacteria such as *E. coli* (n = 16) and *K. pneumoniae* (n = 16) were also prominent among the isolates. Although numerical differences were present, particularly the higher counts of *S. aureus* and *S. hominis* in adults aged (40–59 years), the distribution of isolates across age categories did not show statistically significant variation.

Foxman, B. (2010). The epidemiology of urinary tract infection. Nature Reviews Urology, 7(12), 653–660.

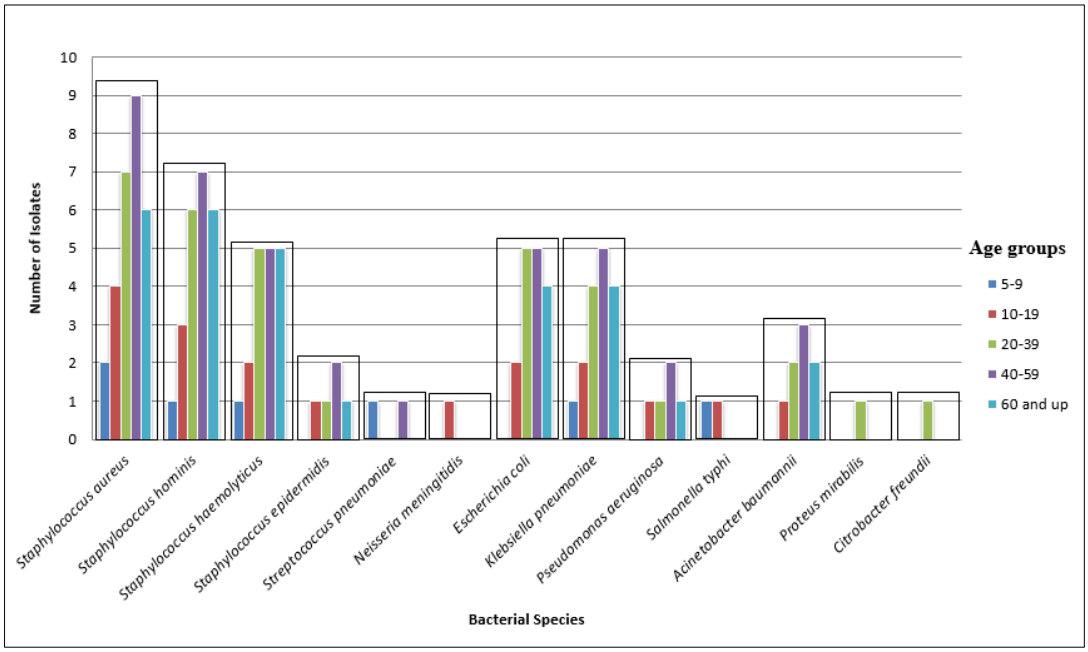

Figure 1: Distribution of bacteria which were isolated in cerebrospinal fluid, blood and pleural fluid based on age groups. Pearson Chi-Square= 41.216, df= 48, p-value= 0.745

According to patient sex, the 126 bacterial species (69 males and 57 female isolates) distribution did not differ significantly. Although there were no statistically significant differences between the males and females, *S. aureus* was the most common bacteria observed in the study with 17 and 11 isolates of males and females respectively (n=28). *S. hominis* was followed by 12 isolates in males and 11 in females (total = 23) and *S. haemolyticus* was present in 10 and 8 males and females respectively (total = 18). *E. coli* was just as prominent as *K. pneumoniae* among gram-negative bacteria, with 16 isolates each, *E. coli* with a higher frequency in females and *K. pneumoniae* with an equal occurrence in both sexes.

Nonetheless, the numerical trends were observed, such as the increased number of *S. aureus* and *S. hominis* in the middle-aged and old groups (Patil *et al*., 2024; Keogh *et al*., 2025). Nonetheless, the distribution of the isolates among all the age groups was not statistically significant. This notwithstanding, *S. aureus* and *S. hominis* were more commonly found in males, and this aligns with some of the studies stating a higher occurrence of *S. aureus* bloodstream infection in men

(Serra *et al*., 2023). Whereas *E. coli* was more common in females, just as it has been repeatedly reported elsewhere, especially in literature on urinary tract infections (Baba *et al*., 2015).

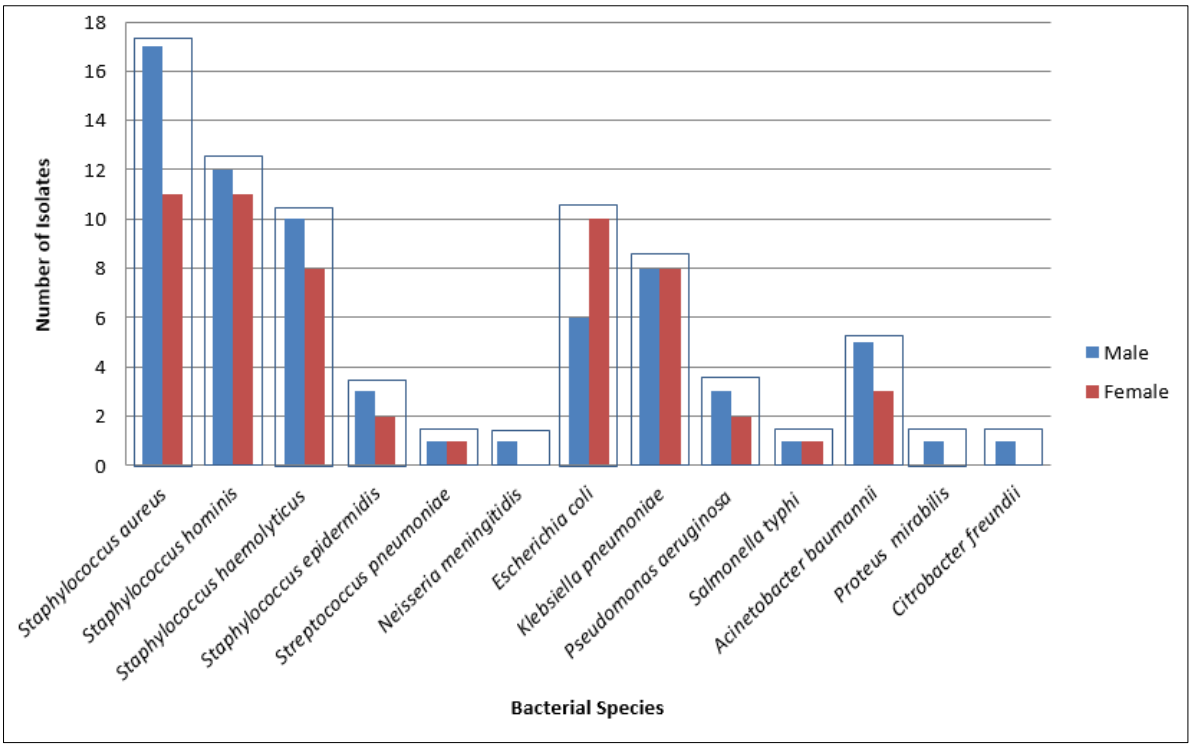

Figure 2: The distribution of pathogenic bacteria isolated from body fluids (blood, cerebrospinal fluid, and pleural fluid) according to sex. Pearson Chi-Square= 5.357, df= 12, p-value= 0. 945

The antimicrobial susceptibility and profile of the four gram-negative bacteria studied revealed a very high sensitivity to resistance to several classes of antibiotics. *E. coli* (N=16) was highly resistant to a variety of antibiotics, the top being ampicillin (93.8%), trimethoprim-sulfamethoxazole (75%), ceftriaxone, ampicillin/ sulbactam, and ciprofloxacin (62.5% each). There were also moderate rates of resistance to ceftazidime (50%), cefotaxime, aztreonam, and levofloxacin (56.2% each). Conversely, the meropenem (18.8%), imipenem, gentamicin (12.5% each) and amikacin (6.2) had low resistance. *P. aeruginosa* (N=5) exhibited various resistance rates with the highest levels being observed in the piperacillin-tazobactam, ceftazidime, and aztreonam (60% in all cases). The other antibiotics had moderate resistance (40%), and reduced resistance with trimethoprim/sulfamethoxazole (20%). *A. baumannii* (N=8) proved to have the most threatening resistance profile. Resistance to cefotaxime, ceftazidime, ceftriaxone, meropenem and imipenem (87.5%) then to piperacillin/tazobactam, ampicillin and ampicillin/ sulbactam, cefepime, aztreonam, ciprofloxacin and levofloxacin were high (75%). The amikacin (25 %) and colistin (12.5 %) achieved less resistance. High resistance to ampicillin (87.5%), ceftriaxone (81.2%), and trimethoprim sulfas (75%) was also demonstrated in *K. pneumoniae* (N=16). Subsequently, extended-spectrum cephalosporins (4.625% to 68.8%). low resistance observed to gentamicin (12.5%), amikacin (6.2%).

The profile of antibiotic resistance of the four *Staphylococcus* species (Table 3) showed that in *S. aureus* (N=28), the greatest resistance was to oxacillin and cefoxitin (64.3%), which indicates the existence of a high prevalence of methicillin-resistant *S. aureus*. The erythromycin and azithromycin resistance (53.6% and 42.9% respectively) was also highly expressed. Conversely, the lesser levels of resistance were determined by doxycycline (17.9%), and rifampicin (7.1%). No resistance to vancomycin and linezolid detected. *S. hominis* (N=23) was very resistant to cefoxitin (60.9%), oxacillin (56.5%), erythromycin (52.2%), and azithromycin (43.5%). Rifampicin (8.7%), indicated the lower resistance, and no resistance was detected to linezolid and vancomycin. The high antibiotic resistance of *S. haemolyticus* (N=18) were also noted on cefoxitin and oxacillin (66.7% each against them), followed by erythromycin (55.6%). Conversely, rifampicin (5.6%). Conversely, there was no resistance to vancomycin and linezolid susceptibility. *S. epidermidis* (N=5) had lower rates of resistance in general, with cefoxitin, oxacillin, erythromycin, azithromycin, levofloxacin, ciprofloxacin, and clindamycin resistance all being 40 %. Gentamicin, trimethoprim/sulfamethoxazole, doxycycline and tetracycline (20%) recorded the low resistance. all isolates were susceptible to vancomycin and linezsolid.

Table 2: Antibiotic resistance profiles of gram-negative clinical isolates (*E. coli*, *P. aeruginosa*, *A. baumannii*, and *K. pneumoniae*)

NO.	Antibiotics	*E. coli* (N=16)		*P. aeruginosa* (N=5)		*Acinetobacter baumannii* (N=8)		*K. pneumoniae* (N=16)	
		Number of Resistant isolates	Resistant isolates %	Number of Resistant isolates	Resistant isolates %	Number of Resistant isolates	Resistant isolates %	Number of Resistant isolates	Resistant isolates %
1	Piperacillin/Tazobactam	6	37.5	3	60	6	75	10	62.5
2	Ampicillin	15	93.8	-	-	6	75	14	87.5
3	Ampicillin/ sulbactam	10	62.5	-	-	6	75	12	75
4	Cefoxitin	-	-	0	0	-	-	-	-
5	Cefotaxime	9	56.2	2	40	7	87.5	11	68.8
6	Ceftazidime	8	50	3	60	7	87.5	10	62.5
7	Ceftriaxone	10	62.5	2	40	7	87.5	13	81.2
8	Cefepime	7	43.8	2	40	6	75	10	62.5
9	Trimethoprim/Sulfamethoxazole	12	75	1	20	5	62.5	12	75
10	Aztreonam	9	56.2	3	60	6	75	9	56.2
11	Meropenem	3	18.8	2	40	7	87.5	6	37.5
12	Imipenem	2	12.5	2	40	7	87.5	5	31.2
13	Amikacin	1	6.2	0	0	2	25	1	6.2
14	Gentamicin	2	12.5	2	40	4	50	2	12.5
15	Ciprofloxacin	10	62.5	2	40	6	75	10	62.5
16	Levofloxacin	9	56.2	2	40	6	75	9	56.2
17	Colistin	0	0	0	0	1	12.5	0	0
Total									

Pearson Chi-Square= 30.448, df= 45, p-value= 0.952

Table 3: Antimicrobial resistance patterns of gram-positive *Staphylococcus* Species Isolated from some body fluids

NO.	Antibiotics	*Staphylococcus aureus* (N=28)		*Staphylococcus hominis* (N=23)		*Staphylococcus haemolyticus* (N=18)		*Staphylococcus epidermidis* (N=5)	
		Number of Resistant isolates	Resistant isolates %	Number of Resistant isolates	Resistant isolates %	Number of Resistant isolates	Resistant isolates %	Number of Resistant isolates	Resistant isolates %
1	Cefoxitin Sceen	18	64.3	14	60.9	12	66.7	2	40
2	Oxacillin	18	64.3	13	56.5	12	66.7	2	40
3	Gentamicin	6	21.4	5	21.7	4	22.2	1	20
4	Trimethoprim/Sulfamethoxazole	10	35.7	8	34.8	7	38.9	1	20
5	Vancomycin	0	0	0	0	0	0	0	0
6	Erythromycin	15	53.6	12	52.2	10	55.6	2	40
7	Azithromycin	12	42.9	10	43.5	9	50	2	40
8	Linezolid	0	0	0	0	0	0	0	0
9	Doxycycline	5	17.9	4	17.4	3	16.7	1	20
10	Tetracycline	6	21.4	4	17.4	3	16.7	1	20
11	Clindamycin	7	25	6	26.1	5	27.8	2	40
12	Rifampicin	2	7.1	2	8.7	1	5.6	0	0
13	Levofloxacin	8	28.6	6	26.1	5	27.8	2	40
14	Ciprofloxacin	9	32.1	7	30.4	6	33.3	2	40
Total									

Pearson Chi-Square= 3.669, df= 33, p-value= 1.000

The investigation of the four studied Gram-negative bacteria, *E. coli*, *P. aeruginosa*, *A. baumannii*, and *K. pneumoniae*, reported previously shows a worrying pattern of multi-drug resistance (MDR) in various classes of antibiotics (Sahoo *et al*., 2025). Higher-level resistance to cephalosporins is a common characteristic of the four Gram-negative isolates, which can indicate the presence of Extended-Spectrum Beta-Lactamase (ESBL) production, a significant issue of public health concern (Gauba and Rahman, 2023). There was also high resistance to fluoroquinolones (ciprofloxacin and levofloxacin). More importantly, *E. coli* and *K. pneumoniae* had low resistance to carbapenems (meropenem and

imipenem) and aminoglycosides (gentamicin and amikacin), indicating that they can still be considered effective agents in treating severe infections caused by them (Muteeb, 2023). *A. baumannii* showed the most concerning pattern of antibiotic resistance as it was highly resistant to carbapenems (meropenem and imipenem) a characteristic of extensively drug-resistant (XDR) strains (Yehya *et al*., 2025). The development of many resistance mechanisms through antibiotic resistance efforts and strategies resulted in the development of resistance. Such mechanisms are antibiotic inactivating/modifying enzymes, remodelling of outer membrane porins, increased efflux pump activity, and targets of antibiotics change (Gauba and Rahman 2023). The current patterns of antibiotic resistance to 4 *Staphylococcus* species are in line with past studies that recorded high levels of resistance to oxacillin and cefoxitin in both *S. aureus* and coagulase-negative staphylococci (Humphries *et al*., 2020). This agreement is indicative of a large-scale dissemination of methicillin-resistant isolates, which can be explained by the fact that the *mecA* gene encoding a modified penicillin-binding protein (PBP2a) with a lower affinity to β-lactam antibiotics is carried (Idrees *et al*., 2023). On the same note, the significant resistance to erythromycin and azithromycin recorded in all the examined species is consistent with the reports made by (Haliman *et al*., 2022). The most common ways of bacterial resistance to macrolides is a mutation of one or more of the binding site nucleotides. Even though azithromycin is reported to exhibit various and two-step mechanism of the inhibition of the ribosome activity of certain species, the specific mode of action should be elaborated more (Jelić and Antolović, 2016). Rifampicin (Garbacz *et al*., 2021) and doxycycline demonstrate lower resistance rates that can be compared to the findings of other studies (Bora *et al*., 2018). Notably, the full susceptibility of all isolates to vancomycin and linezolid is consistent with the reports that emphasize the retained efficacy of the particular antibiotics in relation to *Staphylococcus* species (Husain *et al*., 2018).

CONCLUSION

The test of 308 clinical samples, the distinct pathogen distribution of the samples of varying types, the prevalence of CoNS in blood and highly virulent and nosocomial pathogens such as *A. baumannii* in CSF, proves the need of site-specific empirical treatment regimes. The prevalence of gram-positive isolates with high rates of Methicillin-Resistant *S. aureus* (MRSA) and Methicillin-Resistant Coagulase-Negative Staphylococci (MRCoNS) presents a serious risk of antimicrobial resistance and the alarming, extensively drug-resistant (XDR) phenotype of *A. baumannii* (87.5% carbapenems resistance). It is important to mention that the full vulnerability of all *Staphylococcus* isolates to vancomycin and linezolid confirms its further application as the important therapeutic agent. In general, these results indicate that the ongoing local surveillance and evidence-based optimization of empirical antimicrobial treatment should be considered to enhance clinical outcomes and reduce the evolution of antimicrobial resistance.

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