

# Original Research Article

## **Bacterial isolates and drug susceptibility pattern of sterile body fluids at a tertiary care hospital in Northern India**

### **Abstract**

### **Background**

Body fluids obtained from sterile body sites are expected to be devoid of any pathogenic or commensal microorganisms. The cause of infected body fluids could be any pathological agents or skin contaminants harbored from intensive care units. This study identifies commonly isolated bacteria from these samples and their antibiotic sensitivity pattern.

### **Methods**

All body fluid samples (except blood, cerebrospinal fluid and contaminated samples) received in Bacteriology section of Department of Microbiology from November 2019 to May 2020 were included in our study. All positive cultures were subjected to identification by standard biochemical tests or MALDI-TOF-MS assay and antibiotic sensitivity testing by Kirby Bauer disc diffusion test.

### **Results**

Out of 363 samples of body fluids, 113 (31.12%) were found to be positive on bacterial culture and sensitivity. Male predominance among patients with liver disease was deemed statistically significant in comparison to those without liver disease. Comorbidities like hypertension and

encephalopathy among the patients with liver disease was statistically significant in comparison to those without liver disease. *Escherichia coli* was the most commonly isolated bacteria (20.35%) which was followed by *Pseudomonas spp* (15.92%) and *Klebsiella pneumoniae* (11.50%). Fifty one (45.13%) isolates in our study were Multidrug resistant. The isolation of MDR microorganisms from body fluid samples is statistically significant in cancer patients in our study. Among MDR microorganisms, *Klebsiella pneumoniae* was deemed most resistant with presence of Extended spectrum beta lactamase (ESBL) character and also showed complete resistance to Carbapenems but all isolates were susceptible to Colistin.

## **Conclusion**

This study shows spectrum of bacterial isolates observed from body fluid samples received in our laboratory and helps in empirical treatment of patients based on antibiotic susceptibility patterns. It also highlights importance of adhering to antibiotic sensitivity results and infection control practices to prevent spread of multidrug resistant infection in hospital environment.

**Keywords: Body Fluids, Multidrug resistance (MDR), Chronic liver disease (CLD), MALDI-TOF-MS, Antibiotic sensitivity pattern.**

## **Introduction**

Body sites are called sterile when they have no bacteria or other microorganisms as commensals in healthy condition. The infections caused in these sites could be either due to any pathological

agents or skin contaminants harbored from intensive care units [1]. The body fluids obtained from sterile body sites are similarly expected to be devoid of any pathogenic or commensal microorganisms. Sterile body fluids include cerebrospinal fluid (CSF), synovial fluid, pericardial fluid, pleural fluid and peritoneal dialysate fluid. Most common causative agents of pathogenic microorganisms infecting the sterile body fluids are lactose fermenting gram negative bacteria like *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter species* and *Citrobacter species*, non lactose fermenting gram negative bacteria like *Acinetobacter species*, *Burkholderia cepacia*, *Pseudomonas species* and gram positive organisms like *Methicillin resistant Staphylococcus aureus* and *Enterococcus species* which lead to morbid infections with poor outcome [2, 3].

The morbidity and ability to cause life threatening infections has rendered these cases a medical emergency that demands early diagnosis and suitable treatment. Due to low inoculum of pathogenic bacteria and early administration of empirical antibiotics there were fewer chances of retrieving positive cultures [4]. The difficulty in diagnosing the causative microorganism of body fluid infections and need for effectively managing the patients admitted to the intensive care unit has made it the need of the hour to frame an antibiotic policy and to know the common pathogenic microorganisms with appropriate antibiotic sensitivity pattern [5].

As far as we know, there is limited knowledge regarding the microbiological characteristics, bacterial spectrum and antimicrobial resistance in our geographical setting. The knowledge of the common pathogenic bacteria and their antibiotic susceptibility pattern is crucial for the clinicians to combat a range of infections and administer adequate antibiotics. So, this study conducted at a tertiary care centre in Northern India sheds light on the spectrum of bacterial isolates from the body fluid samples collected from outpatient department (OPD) and

inpatient department (IPD) patients at out centre along with their antibiotic susceptibility patterns.

## **Materials and Methods**

This retrospective, observational, single centre study was conducted from November 2019 to May 2020 in the Bacteriology section of the Department of Microbiology at a tertiary care centre. A total of 363 non repeat samples of clinically suspected infected body fluids were collected aseptically and the samples included in the study consist of pleural fluid, pericardial fluid, ascitic fluid and peritoneal dialysate fluid samples.

**Inclusion criteria:** All the samples received from patients with clinically suspected body fluid infections, from the OPD and IPD patients at our centre, irrespective of age and gender were included.

**Exclusion criteria:** 1) Blood samples, 2) Cerebrospinal fluid samples, 3) Contaminated samples, 4) Body fluids with delay in transportation for more than 2 hours.

**Sample processing:** The samples were collected at a combined receiving station, sent to the bacteriology section of the Department of Microbiology and processed in our laboratory according to the standard protocols. The samples were subjected to Grams' stain and culture. The culture media used were Blood agar, Mackonkey agar and Robertsons' cooked meat broth (RCM). Isolated colonies were observed on the Blood and Mackonkey agar plates and turbidity was observed in the RCM and the isolates were identified by Grams' stain and standard biochemical tests.

**Antimicrobial susceptibility testing:** The antibiotic sensitivity testing was performed for each of the bacterial isolates by Kirby Bauer Disc Diffusion method and Epsilometric test method according to the guidelines of CLSI [6]. Antibiotic discs containing Amikacin (30mcg), Ampicillin (10mcg), Ampicillin-Sulbactam (10/10mcg), Aztreonam (30mcg), Ceftazidime (30mcg), Ceftriaxzone (30mcg), Cefoperazone-Sulbactam (75/10mcg), Cefoxitin (30mcg), Ciprofloxacin(5mcg), Clindamycin (2mcg), Doxycycline(10mcg), Ertapenem (10mcg), Erythromycin (15mcg), Gentamicin (10mcg), Imipenem(10mcg), Levofloxacin (5mcg), Linezolid (30mcg), Meropenem (30mcg), Minocycline (30mcg), Tigecycline (15mcg), Trimethoprim-sulphamethoxazole (1.25/23.75mcg), Teicoplanin (30 mcg), Piperacillin-tazobactam (100/10mcg), Vancomycin (30mcg) and Colistin (0.016-256mcg) Epsilometric test strips were obtained from bioMérieux and used as per manufacturer's instructions. Briefly, inoculums were prepared for each bacterial isolate by adjusting the turbidity to 0.5 McFarland standard and spread on Muller-Hinton agar plates. Antibiotic discs and E-test strips were placed on the agar plates and incubated overnight at 37° C for 24 h. The zones of inhibition were measured and the isolates were classified as sensitive, intermediate, and resistant according to CLSI tables and guidelines [6].

Microbiological characteristics and drug resistance pattern were analyzed for all the samples included in the study. We further demonstrated the risk factors for isolation of MDR microorganisms, among which are *Pseudomonas* resistant to at least 3 antibiotic groups, carbapenemases-resistant and ESBL-producing Enterobacteriaceae, *Enterococcus* resistant to vancomycin, and *MRSA* [7, 8]. We also assessed the risk factors for isolating bacterial body fluid infections in patients with and without chronic liver disease.

The statistical analysis for our study was performed by observing frequencies. Quantitative variables were expressed as mean and SD. In the analysis of risk factors for MDR, the comparison between groups for categorical variables was estimated by using  $\chi^2$  tests. The results were presented as 95% CIs. Statistical analysis was performed using the software program IBM SPSS Statistics version 20.0 (SPSS Inc.), with  $p < 0.05$  considered as statistically significant.

## Results

### Demographics

Out of the 363 samples of clinically suspected infected body fluids, 113 (31.12%) were found to be positive on bacterial culture and sensitivity. Among these culture positive patients a majority of 39 (34.50 %) were in the age group of 41 to 60 years followed by 21 to 40 years and 61- 80 years which was 33 and 23 cases respectively. In our study, samples from male patients were more predominant than samples from women, 74 (65.5%) patients were men and 39 (34.5%) patients were women respectively. Among the patients belonging to the age group of 41-60 years, male patients were predominant. The mean age of the patients suffering from liver disease in this study is  $41.82 \pm 20.80$ , while the mean age among those without liver disease is  $42.16 \pm 21.33$  and the male predominance among the patients with liver disease was deemed statistically significant in comparison to those without liver disease, as seen in Table 1. Out of the 113 culture positive samples, 63 (55.8%) were ascitic fluid samples, 38 (33.6%) were pleural fluid samples, 6 (5.3%) were peritoneal dialysate fluid samples, 4 (3.5%) were pericardial fluid samples and 2 (1.8%) were synovial fluid samples (Fig. 1). *Escherichia coli* was the most

common isolated bacteria (20.35%) which was followed by *Pseudomonas spp* (15.92%) and *Klebsiella pneumoniae* (11.50%) as observed in Fig. 2.

Among the clinical characteristics of the patients included in our study, the patients were divided into two groups of those with liver disease and those without liver disease, as demonstrated in Table 1. Among the comorbidities taken into account among the patients included in our study group hypertension and encephalopathy among the patients with liver disease was statistically significant in comparison to those without liver disease.

Multidrug resistance (MDR) was commonly encountered when reporting antibiotic sensitivity testing of the isolates included in our study. Fifty one (45.13%) isolates in our study were Multidrug resistant. The mean age of patients suffering from body fluid infections with MDR microorganisms is  $44.41 \pm 18.33$ . Male predominance is observed in this study in cases of MDR infections of body fluids. The most common comorbidities encountered among the multidrug resistant isolates were anemia (78.43%), chronic liver disease (45.09%), chronic kidney disease (41.17%), post-operative patients (39.21%), hypertension (31.37%), pleural effusion (29.41%) and malignancy (23.53%). Table 2 demonstrates that the isolation of MDR microorganisms from body fluid samples is a statistically significant in the patients suffering from malignancies in our study. The mean length of hospitalization in the patients from our study is  $25.24 \pm 19.62$  days, the mean total leukocyte count and the mean SAAG ratio of the samples from which the MDR microorganisms were isolated is  $16221.57 \pm 10400.81$  per cubic mm and  $1.59 \pm 1.117$  respectively.

### **Microbiological Characteristics**

The microorganisms most frequently isolated from the body fluid samples *Escherichia coli* was the most common isolated bacteria (20.35%) which was followed by *Pseudomonas spp* (15.92%) and *Klebsiella pneumoniae* (11.50%) as observed in Fig. 2. The microorganism mostly commonly isolated from ascitic fluid samples was *Escherichia coli* (14/23, 60.86%) followed by *Klebsiella pneumoniae* (9/13, 69.23%) and *Pseudomonas spp* (44.44%). The patients were grouped into two groups of patients with (55 patients) and without (58 patients) chronic liver disease, as demonstrated in the Table 1. Twenty three (41.81%) MDR microorganisms were isolated from the patients with chronic liver disease, while 28 (48.27%) MDR microorganisms were isolated from patients without liver disease. The most common microorganisms isolated among the patients with chronic liver disease were *Escherichia coli* (15, 27.27%) followed by *Pseudomonas spp* (10, 18.18%) and *Klebsiella pneumoniae* (6, 10.91%), of the above mentioned microorganisms 40%, 50% and 100% of the respective microorganisms were MDR. Among the gram positive microorganism, *Methicillin Resistant Staphylococcus aureus* was isolated in 2 (1.8%) and *Enterococcus spp* was isolated in 12 (10.6%) body fluid samples.

### **Multidrug Resistance**

Fifty one (45.13%) isolates from body fluid samples in our study were Multidrug resistant. Out of the most commonly isolated gram negative bacteria, *Klebsiella pneumoniae* seems to be the most resistant to most of the first line drugs for lactose fermenting gram negative bacteria; it is completely resistant to Ciprofloxacin, Ceftazidime and Ceftriaxzone, and Cefoperazone-Sulbactam, thus showing the presence of Extended spectrum beta lactamase (ESBL) character and showed Carbapenem resistance by complete resistance to Imipenem, Meropenem and Ertapenem and all isolates were susceptible to Colistin (Table 3).

The *Acinetobacter spp* isolates obtained in our study were most susceptible to second line drugs like Minocycline, Tigecycline and drug of last resort Colistin, with 83.33% susceptibility to each drug, followed by Amikacin, to which only 50% of microorganisms were susceptible. The microorganism was most resistant to Ceftazidime, Ceftriaxone and Cefoperazone Sulbactam, with 16.67% susceptibility to each isolate.

The *Pseudomonas spp* isolates obtained from our study were most susceptible to second line drugs like Minocycline and Colistin, with 75% and 93.75% susceptibility respectively to each of these drugs, followed by Amikacin and Piperacillin - Tazobactam, to each of which the microorganism was 37.50% sensitive. The microorganism was most resistant to Aztreonam followed by Ceftazidime, with a susceptibility of 18.75% and 25% respectively (Table 3).

The Gram positive cocci isolated from the samples in our study were grouped into *Coagulase negative Staphylococcus*, *Coagulase positive Staphylococcus* and *Enterococcus spp*. Of all the gram positive microorganisms isolated from these samples *Coagulase positive* and *coagulase negative Staphylococcus* and *Enterococcus* isolates were most sensitive to Doxycycline, with 81.48%, 90.90% and 68.18%, respectively, followed by Amikacin among the *Coagulase positive Staphylococcus* and *Coagulase negative Staphylococcus*, with a susceptibility of 100% and 82.60% respectively, All the *Coagulase positive Staphylococcus* and *Coagulase negative Staphylococcus* were susceptible to Vancomycin and in case of Teicoplanin all *Coagulase positive Staphylococcus* were susceptible but 91.30% were susceptible among *Coagulase negative Staphylococcus*. Among the isolates of *Enterococcus spp* susceptibility to Linezolid and Minocycline was 91.67% and 83.33% respectively, thus proving that 15.7% of the *Enterococci* isolates were multidrug resistant (Table 4). The risk factors associated with the acquisition of multidrug resistance are increased length of stay in the hospital, patient comorbidities like

immunosuppression, chronic liver disease, heart disease, diabetes mellitus and malignancy. Malignancy was a statistically significant risk factor for acquiring multidrug resistance in our study.

## Discussion

The spectrum of pathogenic microorganism causing body fluid infections along with their antibiotic susceptibility patterns changes from one geographical region to another from one time to another. The increase in incidence of comorbidities, immunocompromised conditions and increase in length of hospital stay have combined to render ideally sterile ascitic and pleural fluids samples infected [9].

In our study, 31.13% of samples were bacterial culture positive, which was in agreement with the other studies were 30%, 31% positive cultures were noted [10, 11].

The predominant microorganisms isolated in our study were *Escherichia coli* (23), *CONS* (23), followed by *Pseudomonas species* (18), *Klebsiella pneumoniae* (13), *Enterococcus species* (12), *Acinetobacter baumannii* (6), *Streptococcus species* (4), *Enterobacter species* (3), *Staphylococcus aureus* (3), *Burkholderia cepacia* (2), *Proteus mirabilis* (2), *Yeast like cells* (2), *Citrobacter freundii* (1) and *Chryseobacterium indologenes* (1).

The most common organism isolated from pleural fluid was *Escherichia coli* (7) and these findings correlates with the findings of studies by Sharma *et al*, Sujatha *et al* and Evans *et al* where the most common causative agent of pleural fluid infections was *Escherichia coli* [10-12]. While the second most common microorganism to cause pleural infections in our study was *Pseudomonas spp* (6) in contrast to *Acinetobacter spp* in the study by Sharma *et al* and *Klebsiella pneumoniae* in studies by Sujatha *et al* and Evans *et al*.

Our study represents the ability of the aerobic gram negative bacteria to predominantly cause purulent pleural fluid infections. In studies by Jain *et al*, Gupta *et al* and Mohanty *et al* a similar finding was observed that the gram negative bacteria were more commonly isolated from the purulent infections of pleural fluid [13 - 15]. In our study, the gram positive microorganisms isolated from pleural fluid infections consist mainly of *Enterococcus species* followed by *Staphylococcus aureus*. The isolation of aerobic gram negative bacteria or isolation of multiple pathogenic bacteria holds poor prognosis and thus arises need of rigorous antimicrobial therapy [5].

The gram negative bacteria most commonly isolated from ascitic fluid samples included in our study was *Escherichia coli* (14), followed by *Klebsiella pneumoniae* (9) and *Pseudomonas spp* (8) which is correlates with the studies conducted by Arroyo *et al* and Chawla *et al* which showed *Escherichia coli* as the most common microorganism causing peritonitis [16, 17]. In a study by Harshika *et al*, non lactose fermenting bacteria were the most commonly isolated microorganisms from the ascitic fluid samples disagrees with the findings of our study but dissimilarity in the spectrum of pathogenic bacteria causing peritonitis also depends upon the geographical area of isolation [5].

In our study setting, very few samples of pericardial fluid samples were obtained, which is only 4% of body fluid samples received in our laboratory were culture positive. Out of the 4 culture positive pericardial fluid samples, one sample showed culture of *Staphylococcus aureus* as seen in a study by Reuter *et al* [18]. Very rare cases of pericardial fluid infections are noted in literature and these infections can lead to life threatening complications like cardiac tamponade and constrictive pericarditis [5]. The most common underlying causes of pericardial infections

include people undergoing haemodialysis, those suffering from AIDS, those undergoing chemotherapy and thoracic surgery [19, 20].

In our study, the gram negative bacteria were almost completely susceptible to drug of last resort, Colistin, followed by good sensitivity for drugs like Minocycline and Tigecycline. A decreasing sensitivity of the gram negative bacterial isolates to carbapenems was noted in our study, in contrast to good susceptibility to carbapenems seen in a studies conducted by Harshika *et al* [5] and Sharma *et al* [10]. The isolates in our study were relatively resistant to Ceftazidime, Ceftriaxzone, Ciprofloxacin and Cefoperazone Sulbactam, which corroborates with studies conducted by Tullu *et al* [21].

Gram positive bacteria isolated in our study were highly sensitive to Vancomycin, Teicoplanin and Linezolid which is in agreement with the study by Sujatha *et al* [11] but disagrees with the complete resistance to Gentamicin shown in our study. The *Pseudomonas species* isolated in our study were highly sensitive for Colistin and Minocycline. Only 37.5% isolates of *Pseudomonas species* were susceptible to Piperacillin- Tazobactam which is in contrast to a study conduct by Harshika *et al* [5].

Thus, evaluation of the results of antimicrobial resistance to the isolates is suggestive of rapid emergence of multidrug resistance. Ability to attain the resistant genes from other resistant microorganisms has lead to rise of multidrug resistance through the years. Before seeking treatment at a tertiary care centre, most patients are subjected to unnecessary antimicrobial therapy that renders them resistant to most first line antibiotics given to treat a specific microorganism. Lack of proper antimicrobial stewardship program and no adherence to the antibiotic susceptibility testing has lead to increased antimicrobial resistance.

## **Conclusion**

This study shows spectrum of bacterial isolates observed from the body fluid samples received in our laboratory and helps in guiding the empirical treatment of patients based on antibiotic susceptibility patterns. The increase in the incidence of multidrug resistance also points out the need to implement strict adherence to the antibiotic sensitivity. The spread of multidrug resistant and extensively drug resistant microorganisms can also be curtailed by strict adherence to infection control practices, educating the health care workers and patients about hand hygiene and make them aware about the morbidity of suffering from a multidrug resistant infection.

## COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

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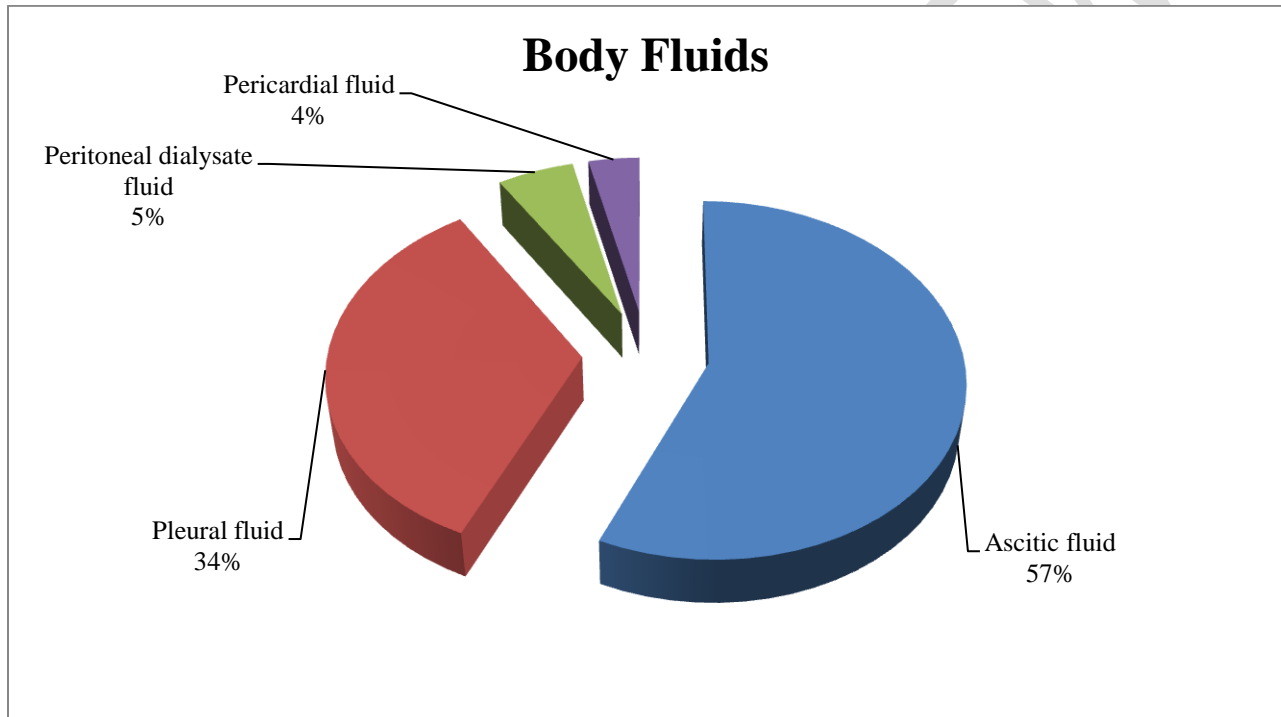
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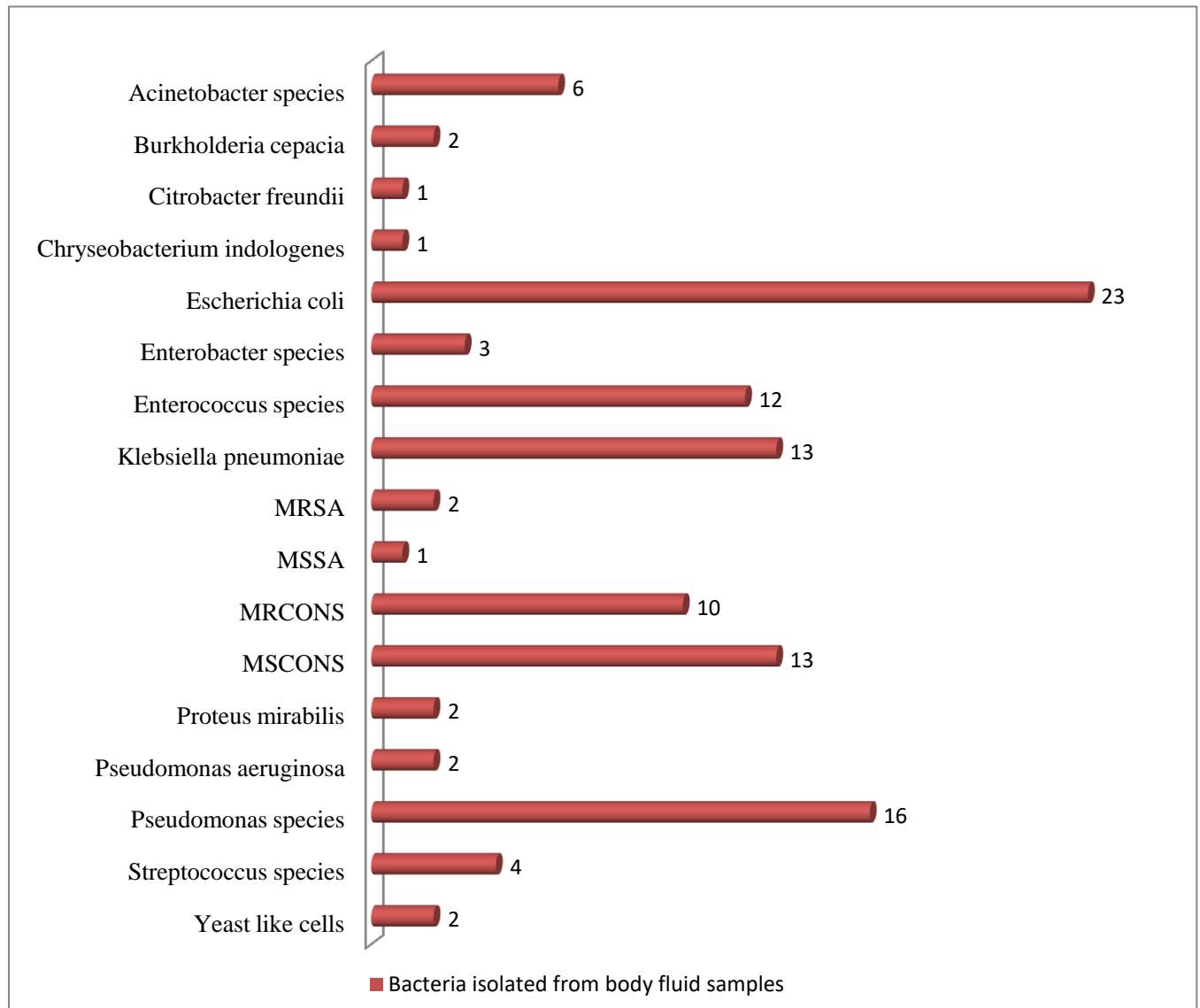
**Fig 1. Distribution of types of infected body fluid samples received in our laboratory**

(N= 113)



**Fig 2. Rate of bacteria isolated from the body fluid cultures performed in the laboratory**

**(N=113)**



*MSCONS- Methicillin sensitive coagulase negative Staphylococcus*

*MRCONS- Methicillin resistant coagulase negative Staphylococcus*

*MSSA- Methicillin sensitive Staphylococcus aureus*

**Table 1. Demographic characteristics of patients and risk factors for bacterial body fluid infections with and without chronic liver disease (CLD) (N=113)**

	With CLD (n=55)	Without CLD (n=58)	P-value
<b>Demographics</b>			
Age, years, mean (SD)	41.82 ± 20.80	42.16 ± 21.33	0.9318
Gender, male/female	43:12	31:27	<b>0.006*</b>
<b>Comorbidities</b>			
Diabetes mellitus, %	14	11	0.406
Chronic kidney disease, %	17	24	0.247
Heart disease, %	7	13	0.178
Hypertension, %	23	13	<b>0.027*</b>
Pleural effusion, %	16	26	0.084
COPD, %	4	7	0.390
Malignancy, %	6	11	0.231
Encephalopathy, %	21	5	<b>&lt;0.001*</b>
Organ transplant, %	4	1	0.152
Post operative patients, %	17	20	0.686
Anemia, %	42	44	0.950
<b>Other parameters</b>			

Length of hospital stay, mean (SD)	22.38 ± 15.61	25.12 ± 19.08	0.407
Total leukocyte count, mean (SD)	15378.18 ± 10473.77	14076 ± 9262.49	0.485
SAAG ratio, mean (SD)	1.82 ± 0.905	1.52 ± 0.978	0.093
Death, %	16	18	0.822

\* p-value <0.05 is significant

**Table 2. Demographic characteristics of patients and risk factors for isolation Multidrug resistant microorganisms in patients with purulent infections (N=51)**

Demographics and risk factors	MDR microorganisms (n= 51/113, 45.10%)	P-value	95% CI
<b>Demographics</b>			
Age, years, mean (SD)	44.41 ± 18.33	0.268	39.25 – 49.56
Gender, male/female %	62.74/37.26	0.578	1.24 – 1.51
<b>Comorbidities</b>			
Diabetes mellitus, %	14 (27.45%)	0.216	1.60 – 1.85
Chronic liver disease, %	23 (45.09%)	0.491	1.41 – 1.69
Chronic kidney disease, %	21 (41.17%)	0.327	1.45 – 1.73
Heart disease, %	11 (21.56%)	0.328	1.67 – 1.90
Hypertension, %	16 (31.37%)	0.920	1.55 – 1.82
Pleural effusion, %	15 (29.41%)	0.122	1.58 – 1.84
COPD, %	6 (11.76%)	0.509	1.79 – 1.97
Malignancy, %	12 (23.53%)	<b>0.022*</b>	1.64 – 1.89
Encephalopathy, %	11 (21.56%)	0.741	1.67 – 1.90
Organ transplant, %	1 (1.96%)	0.248	1.94 – 2.0
Post operative patients, %	20 (39.21%)	0.184	1.47 – 1.75
Anemia, %	40 (78.43%)	0.599	1.10 – 1.33
<b>Other parameters</b>			
Length of hospital stay, mean (SD)	25.24 ± 19.62	0.426	19.72 – 30.75
Total leukocyte count, mean (SD)	16221.57 ± 10400.81	0.140	13296.29 – 19146.84
SAAG ratio, mean (SD)	1.59 ± 1.117	0.446	1.27 – 1.90
Death, %	19 (37.25%)	0.132	1.24 – 1.51

\* p-value <0.05 is significant

**Table 3: Percentage Sensitivity pattern for first and second line drugs in most commonly isolated Gram negative bacilli**

<b>Antibiotics</b>	<b>E. coli % sensitivity</b>	<b>Acinetobacter species % sensitivity</b>	<b>K. pneumoniae % sensitivity</b>	<b>Pseudomonas species % sensitivity</b>
<b>Amikacin</b>	73.91%	50.00%	15.38%	37.50%
<b>Ceftazidime</b>	8.69%	16.67%	0.00%	25.00%
<b>Ceftriaxzone</b>	0.00%	16.67%	0.00%	-
<b>Ciprofloxacin</b>	8.69%	33.33%	0.00%	-
<b>Levofloxacin</b>	-	-	-	37.5%
<b>Cefoperazone- Sulbactam</b>	34.78%	16.67%	0.00%	31.25%
<b>Imipenem</b>	60.87%	33.33%	0.00%	31.25%
<b>Meropenem</b>	60.87%	33.33%	0.00%	31.25%
<b>Ertapenem</b>	52.17%	-	0.00%	-
<b>Colistin</b>	100.00%	83.33%	100.00%	93.75%
<b>Tigecycline</b>	100.00%	83.33%	69.23%	-
<b>Minocycline</b>	95.65%	83.33%	69.23%	75.00%
<b>Aztreonam</b>	-	-	-	18.75%

<b>Piperacillin- Tazobactam</b>	-	-	-	37.5%
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**Table 4. Percentage Sensitivity pattern for first and second line drugs in most commonly isolated Gram positive cocci**

<b>Antibiotics</b>	<b>Coagulase positive Staphylococcus % sensitivity</b>	<b>Coagulase negative Staphylococcus % sensitivity</b>	<b>Enterococcus % sensitivity</b>
<b>Ampicillin</b>	-	-	25%
<b>Ampicillin- Sulbactam</b>	66.67%	47.83%	41.67%
<b>Amikacin</b>	100%	82.60%	-
<b>Clindamycin</b>	33.33%	60.87%	-
<b>Cefoxitin</b>	33.33%	56.52%	-
<b>Doxycycline</b>	100%	73.91%	83.33%
<b>Erythromycin</b>	0%	13.04%	-
<b>Gentamicin</b>	0%	0%	33.33%
<b>Levofloxacin</b>	0%	26.08%	16.67%
<b>Vancomycin</b>	100%	100%	41.67%
<b>Teicoplanin</b>	100%	91.30%	41.67%
<b>Linezolid</b>	-	-	91.67%
<b>Minocycline</b>	-	-	83.33%

UNDER PEER REVIEW