Microbial spectrum and their antibiotic susceptibility pattern from patients with sepsis in medical emergency unit of a teaching hospital in Nigeria

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Abstract

Background: Sepsis is among the leading cause of morbidity and mortality worldwide. The study aimed to determine the microbial isolates and their antibiotics susceptibility pattern among patients with sepsis in Lagos University Teaching Hospital.
Methodology: It was a cross-sectional hospital-based study carried out in the adult medical emergency unit in patients with clinical diagnosis of suspected sepsis. Clinical samples were obtained and processed according to standard microbiological protocol.
Result: Three hundred patients were enrolled, of which 42.3% were male and 53.7% were female. There were (79, 26.3%) participants that showed blood culture positive. The predominant bacterial pathogens isolated from blood cultures were *Staphylococcus aureus* (23, 29.1%), followed by *Klebsiella pneumoniae* (15, 19.0%) and *Escherichia coli* (13, 16.5%). Blood cultures and other specimens such as urine, and wound biopsy showed a similar pattern. Over 50% of the bacterial isolates were resistant to commonly prescribed antibiotics, such as third-generation cephalosporins, penicillin, tetracycline, and erythromycin.
Conclusion: The study revealed that *Staphylococcus aureus*, *Klebsiella pneumoniae* and *Escherichia coli* were the most common pathogens isolated. The isolates showed high level of resistance to commonly prescribed antibiotics.

Spectre microbien et leur modèle de sensibilité aux antibiotiques chez des patients atteints de sepsis dans l'unité d'urgence médicale d'un hospital universitaire au Nigéria

Résumé
Contexte de l'étude: Le sepsis est l'une des principales causes de morbidité et de mortalité dans le monde. L'étude visait à déterminer les isolats microbiens et leur profil de sensibilité aux antibiotiques chez les patients atteints de sepsis à l'hôpital universitaire de Lagos.
Méthode de l'étude: Il s'agit d'une étude transversale réalisée en milieu hospitalier dans le service des urgences médicales pour adultes auprès de patients présentant un diagnostic clinique de suspicion de sepsis. Des échantillons cliniques ont été obtenus et traités selon un protocole microbiologique standard.
Résultats de étude: Trois cents patients ont été inclus, dont 42,3 % étaient des hommes et 53,7 % des femmes. Parmi les participants (79, 26,3 %), l'hémoculture était positive. Les pathogènes bactériens prédominants isolés des hémocultures étaient *Staphylococcus aureus* (23, 29,1 %), suivis de *Klebsiella pneumoniae* (15, 19,0 %) et *d'Escherichia coli* (13, 16,5 %). Les hémocultures et d'autres échantillons tels que l'urine et la biopsie de plaie ont montré une tendance similaire. Plus, de 50 % des isolats bactériens étaient résistants aux antibiotiques couramment prescrits, tels que les céphalosporines de troisième génération, la pénicilline, la tétracycline et l'érythromycine.
Conclusion: L'étude a révélé que Staphylococcus aureus, Klebsiella pneumoniae et Escherichia coli étaient les pathogènes les plus fréquemment isolés. Les isolats ont montré un niveau élevé de résistance aux antibiotiques couramment prescrits.
Mots-clés: Sepsis,staphylococcus aureus, klebsiella pneumoniae, escherichia coli

INTRODUCTION

Infectious diseases are among the leading cause of morbidity and mortality globally with the highest burden in developing countries (1). Bacterial infection can be localized or systemic and the major complication of severe bacterial infection is sepsis, a threatening systemic inflammatory response (2). Sepsis is a time-dependent medical condition that demands prompt management, with patients typically first encountering medical care in the emergency department (3). Physicians play a crucial role in the early recognition of sepsis, initiating resuscitation, and administering timely antibiotic therapy (4). Blood cultures are regarded as the most sensitive method for detecting bacteremia and are frequently observed in patients presenting with sepsis-related symptoms such as fever, chills, leukocytosis, and localized or systemic infection (5).

Each year, around 31.5 million cases of sepsis are reported globally, with mortality rates ranging between 20% and 50% (6). Sepsis represents a considerable portion of hospital-acquired infections and stands as one of the leading causes of death in the United States (7). Despite medical advancements, sepsis-related mortality remains high, reaching up to 30% in Europe and North America (8). In African countries, including Nigeria, sepsis is a major contributor to illness and death across all age groups, particularly among children and the elderly, with mortality rates nearing 53%, highlighting its significant health burden in developing nations (9).

Previous studies have reported wide range of bacterial pathogens isolated from patients with sepsis. The predominance of either the Gram positive or Gram-negative bacterial isolates is influenced by geographical location, patient's immune status and season. Some commonly isolated bacterial pathogens include Gram-negative bacteria such as *Escherichia coli*, *Klebsiella* species, *Pseudomonas aeroginosa*, *Neisseria meningitides*, *Haemophilus influenzae*. They also include Gram positive bacteria such as *Staphylococcus aureus*, *Coagulase negative staphylococci (CONs)*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus agalatiae* and *Enterococcus* species (10-12). The gold standard for diagnosis of sepsis is by isolation of the pathogen from blood culture, which takes some days to be ready and is also not routinely available in some hospitals in developing countries (13).

Early and appropriate antibiotic therapy improves clinical outcome of patients with sepsis. In fact, Consensus guidelines recommended antibiotic administration within one hour of diagnosis of sepsis (2). Antimicrobial therapy in most cases of sepsis is commenced empirically before the results of blood culture (14). Nonetheless, many bacterial pathogens have developed resistance to antibiotic regimens and currently a serious public health concern worldwide. The reason for the antimicrobial resistance includes but limited to increase antibiotic use, antibiotic misuse in patients and livestock, and poor infection control (15). Therefore, a good knowledge of local bacterial profile and antimicrobial susceptibility patterns from accurate bacteriological data of clinically relevant specimens is needed to provide guidance towards an empirical therapy before definitive sensitivity patterns are available.

However, there are only a few recent studies from tertiary health facilities in Nigeria, which have studied the organisms causing sepsis in adult medical emergency unit and their susceptibility pattern (10,11). This study was therefore carried out to determine the baseline information on the local bacterial pathogens causing sepsis and their antibiotics susceptibility pattern to enable physicians initiating empirical therapy on the choice of antibiotics in adult medical emergency unit of Lagos University Teaching Hospital (LUTH).

MATERIALS AND METHODS

Study area

This study was conducted in Lagos University Teaching Hospital (LUTH), Lagos State which is in Southwest region of Nigeria. Lagos University Teaching Hospital is a tertiary hospital located in Idi-Araba in Surulere local government area of Lagos state. It is a 760-beded hospital with 22 wards, adult accident and emergency unit, children emergency room and one intensive care unit. Adult medical emergency unit is where the adult patients with medical emergencies are admitted and attended to before transferring to medical ward for continuous management.

Study design

This was a hospital based cross-sectional study of patients with clinical diagnosis of sepsis at the adult medical emergency unit of Lagos University Teaching Hospital. Clinical diagnosis of sepsis was made by managing physicians. The selection of participants was done using systematic consecutive sampling technique.

Inclusion criteria

Criteria used for clinical diagnosis of sepsis include tachycardia, tachypnoea, fever or hypothermia and presence of leukocytosis, leukopenia or 10% band forms. A case of sepsis is defined as life threatening organ dysfunction caused by a dysregulated host response to infection (16)

Exclusion criteria

Patients presenting with fever, tachypnoea, and tachycardia, along with signs of acute trauma but without any indications of localized or systemic infection, were exempted from the study.

Study population

The participants were between the ages of 18 years and above. The study was carried out from 1st May 2019 to 30th April 2020.

Sample collection and analysis

Blood was collected from all the participants with clinical diagnosis of sepsis for culture. In patients with known primary focus of infection, clinically relevant specimens such as sputum, pus, wound specimen, and urine were also collected for culture.

Appropriate venous site was located and carefully disinfected with 70% isopropyl alcohol and tincture of iodine. The blood volume collected was 20ml in each set (10ml per bottle of aerobic and anaerobic culture bottles based on the 1:10 blood to broth ratio guideline) (17). The bottles were transported to the Clinical Microbiology Laboratory for incubation.

The blood culture bottles were incubated in BACTEC 9050 automated blood culture system (Becton Dickinson Diagnostic Instrument Systems, Sparks, Md) at 37^{0}C for 3 to 5 days in both aerobic and anaerobic blood culture bottles. The bottles were removed from the BACTEC machine when they flagged positive or after 5 days of incubation. Samples were taken from positive bottles and sub-cultured on MacConkey and 5% sheep blood agar media. Blood agar media were incubated in CO_2 enriched condition and MacConkey agar media were incubated in ambient air for 18 to 24 hours. There was no strict anaerobe that was isolated from the anaerobic blood culture. Other specimens were also cultured and processed following macroscopy, microscopy, culture in appropriate media and biochemical identification. Bacterial isolated were identified using standard laboratory procedure including Microbact commercial identification kit (Oxoid, United Kingdom) and Vitek 2 compact system (bioMerieux, France) (17,18). Organisms that grew in both culture sets with consistent clinical features were regarded as pathogens. Some bacterial species that are often regarded as normal skin flora such as coagulase negative staphylococci were classified as pathogens only in patients with background severe immunosuppression or had prosthetic heart valve (17).

Antibiotics susceptibility test and choice of antibiotics:

Antibiotics susceptibility test was done using Kirby-Bauer disc diffusion methods and antibiotics used for different organisms were chosen based on Clinical Laboratory Standard Institute (CLSI) (19). Two Mueller Hinton agar plates were used for each isolate and five antibiotic discs were placed in 90mm agar plate (19).

Quality control measures

Two sets of blood culture bottles were collected aseptically to minimize contamination and strict adherence to the manufacturer's guideline to guarantee quality result. Reference organisms were used as quality control in both biochemical identification and antibiotic susceptibility testing of the organisms. The reference organisms used were *Escherichia coli ATCC 25922 and Pseudomonas aeruginosa ATCC 27853* for Gram negative bacilli. The organisms used for Gram positive cocci quality controls were *Staphylococcus aureus ATCC 25923* and *Enterococcus faecalis ATCC 29212 (19)*

Data collection and analysis

The data collected was entered and analysed using the International Business Machine Statistical Package for Social Sciences (IBM SPSS) statistics for windows, version 25 (IBM Corp., Armonk, New York, USA). The data was presented in frequency tables and summary statistics. Bivariate analysis including chi-square was used to determine the relation between variables. The confidence interval of 95% was used and p-value < 0.05 was considered significant.

RESULT

Demographic and baseline characteristics of the participants

A total of 300 patients with clinical diagnosis of sepsis were enrolled into the study. None of the

patients were recruited more than once. The recruited participants were 127 males (42.3%) and 173 females (53.7%). Their ages ranged from 20 to 82 years, and the mean age was 44.9 ± 14.5 years (Table 1). The primary sites of the bacterial infection included respiratory tract, urogenital system (UGS), skin and soft tissue, central nervous system (CNS), gastrointestinal tract (GIT) and others. Respiratory tract infection (40%) was the most frequent primary source of infection (Figure 1).

Prevalence of bacteremia among patients

All the patients recruited for the study were classified as bacteremic (positive culture growth) and non-bacteremic (negative culture growth) groups based on the presence or absence of pathogenic bacterial isolate from their blood culture. Of the total participants, (79, 26.3%) were found to be bacteremic while (221, 73.7%) were non-bacteremic. However, no statistically significant association was found between the bacteremic and non-bacteremic groups with regard to the demographic characteristics of the patients (P=0.680) (Table 2).

Bacterial pathogens isolated from the blood culture

There were more Gram-negative bacilli (48, 60.8%) than Gram positive cocci (31, 39.2%) isolated from the blood culture. However, *Staphylococcus aureus* (23, 29.1%) was the most common pathogen isolated followed by *Klebsiella pneumoniae* (15, 19.0%), *Escherichia coli* (13, 16.5%) and *Coagulase Negative Staphylococci (mostly from patients with severe immunosuppression such as HIV/AIDS and prosthetic heart valve)*. Other pathogens isolated were *Klebsiella oxytoca*, *Enterobacter aerogenes*, *Proteus mirabilis, Serratia marcescens*, *Providencia rettgeri*, *Citrobacter freundii*, *Acinetobacter* species, *Pseudomonas aeruginosa* and *Enterococcus* species (Table 3)

Bacterial pathogens isolated from other specimens from primary sites of infection

Other specimens cultured based on the identified primary focus of infection included urine, sputum, wound specimen, pus aspirate, and ascitic fluid. The most predominant bacterial pathogens from urine and sputum were *Escherichia coli* (31.8%), and *Klebsiella pneumoniae* (33.3%) respectively. However, *Staphylococcus aureus* was the most common pathogen isolated from wound specimen (11/34, 32.4%), pus aspirate (2/5, 40.0%), and ascitic fluid (1/1, 100%) (Table 4).

Antibiotics Susceptibility Tests

The antibiotic susceptibility profiles of the isolated bacterial pathogens were categorized into four groups: Gram-negative bacilli from blood cultures, Gram-negative bacilli from other specimens, Gram-positive cocci from blood cultures, and Gram-positive cocci from other specimens. Among the Gram-negative bacilli isolated from blood, 85% were susceptible to meropenem, 77% to piperacillin-tazobactam, 65% to amikacin, 62% to gentamicin, 60% to cefepime, and 56% to levofloxacin. However, their susceptibility to cefuroxime, cefotaxime, ceftriaxone, ciprofloxacin, and amoxicillin-clavulanate was below 50% (Table 5).

The antibiotic susceptibility patterns of Gram-negative bacilli isolated from other primary focus sites were also assessed. They showed 87% susceptibility to meropenem, 78% to piperacillin-tazobactam, 67% to levofloxacin, and 60% to cefepime. However, their susceptibility to cefotaxime, ceftriaxone, and amoxicillin-clavulanate was less than 50% (Table 6).

Three species of Gram-positive cocci were isolated from blood cultures: *Staphylococcus aureus*, coagulase-negative staphylococci, and *Enterococcus* species. These Gram-positive cocci showed 100% susceptibility to vancomycin, 90% to linezolid, 71% to levofloxacin, 61% to amikacin, and 58% to clindamycin. However, their susceptibility was less than 50% for penicillin, trimethoprim-sulfamethoxazole, erythromycin, and tetracycline (Table 7).

The Gram positive cocci isolates from other specimens demonstrated 100% susceptibility to vancomycin, 87% to linezolid, 67% to clindamycin, 65% to levofloxacin, and 52% to amikacin. However, their susceptibility rates were below 50% for penicillin, tetracycline, and erythromycin (Table 7).

DISCUSSION

Blood culture remains the established standard for diagnosing the causative agents of sepsis, a condition that significantly contributes to the overall healthcare burden worldwide. It has been demonstrated that there exists a correlation between treatment delay and the mortality rate in cases of septic shock. Therefore, having a thorough understanding of the microbial profile is crucial for prompt management (20). The rate of bacterial isolation in this study was found to be

26.3%, a figure consistent with findings in other developing countries where similar investigations have been conducted. For instance, studies in Uganda (26%) (21), Zambia (24.2%) (22), and even Nigeria, which reported a bacterial isolation rate of 23.4% as indicated by Kingsley's research team (11). Previous studies have also noted lower rates, such as 15.8% in Ethiopia and 18.2% in Nigeria, respectively (11, 23).

The potential reasons behind these variations may stem from factors such as the duration of the study, the characteristics of the study population, age groups, and geographical locations. Additionally, the methods employed for culturing can have a significant impact on the results. For instance, it has been established that semi-automated systems such the BactAlert blood culture system and BACTEC systems tend to yield higher rates of bacterial isolation (24). Another contributing factor to the variability in isolation rates could be prior antibiotic use, as some patients may have already received antibiotics before their presentation at the emergency unit, particularly in tertiary hospitals. Furthermore, it was noted that the gender and age of the patients did not exhibit statistically significant differences in culture positivity ($P > 0.05$), which aligns with the findings reported by Kingsley's research team (11).

In this study, the most prevalent primary source of infection was lower respiratory tract infections, closely followed by urogenital infections, a pattern consistent with previous findings reported by Isa and colleagues (9). A majority of these infections (60.8%) were attributed to Gram-negative bacteria, while the remaining 39.2% were caused by Gram-positive bacteria. These figures agree with the results of earlier studies conducted in North-central Nigeria, where the distribution was 69.3% Gram-negative and 30.7% Gram-positive, and in Tanzania, where it was 69.7% Gram-negative and 30.3% Gram-positive, as reported by Nwadioha et al and Meremo A et al, respectively (10, 25). A similar pattern emerged in Zimbabwe, mirroring our findings, where Swamy and his colleagues documented 52.6% Gram-negative bacteria, 44.8% Gram-positive cocci, and 2.6% yeast (26).

However, it's worth noting that in other developing countries, such as Northwest Ethiopia, Gram-positive bacteria have been documented as the predominant culprits behind sepsis, with a breakdown of 69% Gram-positive and 31% Gram-negative bacteria (12). The variation in the causative agents may arise from differences in culture methods, the characteristics of the study population, the presence of co-morbidities, and geographical locations.

Staphylococcus aureus accounted for 29.1% of the isolates, making it the most prevalent, followed by *Klebsiella pneumoniae* at 19.0%, *Escherichia coli* at 16.5%, and Coagulase Negative *Staphylococci* at 8.8% out of a total of 79 cases. These findings are in line with previous studies conducted in other countries (27, 28). Notably, Swamy and colleagues also observed a similar pattern in their study, where Coagulase Negative Staphylococci was the primary pathogen, followed by *Klebsiella pneumoniae* (26).

It's important to note that the isolation rate of *Staphylococcus aureus* in this study is lower than the rates of 55.3% and 40% reported in Uyo (11) and Ethiopia (23), respectively. *Staphylococcus* species are often encountered as contaminants on the skin during blood collection, particularly Coagulase Negative *Staphylococci* (26) Therefore, it's crucial to distinguish between true pathogens and contaminants by correlating the results with the clinical status of the patients (26). Moreso, in this study true pathogen was defined by isolation of same organism in both sets of culture bottles with clinical features suggestive of sepsis (17). *Klebsiella pneumoniae* and *Escherichia coli* accounted for 19.0% and 16.5% of bacteremia cases, which is consistent with findings from other Nigerian studies (10, 11). The profile and frequency of bacterial pathogens varied depending on the usage of medical devices, the age of the patients, their immune status, the presence of co-morbidities, and hospital infection prevention and control practices. The bacterial composition identified in sepsis patients can serve as a valuable guide for physicians in selecting the most suitable antibiotics for empirical therapy in the emergency unit. This suggests that a combination of antibiotics that effectively targets both Gram-negative bacteria (such as *Klebsiella pneumoniae* and *Escherichia coli*) and Gram-positive cocci (specifically *Staphylococcus aureus*) would be a sound choice for empirical therapy at LUTH, aligning with the prevalent local microbiological profile.

The antibiotic susceptibility testing of the isolates revealed concerning trends, as the bacterial samples demonstrated limited sensitivity to commonly used antibiotics. For bloodstream infections, only 40-47% of *Klebsiella pneumoniae* strains were susceptible to second and third-generation cephalosporins, while just 38-54% of *Escherichia coli* isolates showed susceptibility to the same class of

antibiotics. However, on a more encouraging note, over 60% of Gram-negative bacilli were susceptible to piperacillin-tazobactam, cefepime, gentamicin, and levofloxacin, with a significant 80% responding to carbapenems, particularly meropenem. The susceptibility patterns of organisms isolated from other infection sites mirrored those of bloodstream pathogens, though they exhibited greater resistance to third-generation cephalosporins. *Staphylococcus aureus* and other Gram-positive cocci displayed limited susceptibility to penicillin, trimethoprim-sulfamethoxazole, and tetracycline in bloodstream infections, with isolates from other sites showing even higher resistance to most tested antibiotics. They demonstrated moderate sensitivity to gentamicin, cefepime, levofloxacin, and clindamycin. Notably, all Gram-positive bacteria were fully susceptible to vancomycin.

This susceptibility pattern aligns with previous studies conducted in Nigeria, where bacterial isolates showed resistance to second-generation cephalosporins but remained highly sensitive to vancomycin and carbapenems (11, 29, 30). The increased resistance to third-generation cephalosporins, trimethoprim-sulfamethoxazole, and tetracycline can be attributed to the common practice in the region, where these medications are readily available over the counter at pharmacies and roadside chemist shops, allowing patients to purchase them without a prescription (29). Even in tertiary hospitals, third-generation cephalosporins, like ceftriaxone, are frequently administered for medical or surgical prophylaxis, sometimes when antibiotics are not ultimately needed (31).

Therefore, healthcare providers and other key stakeholders must collaborate to promote the responsible use of antibiotics to reduce the growing incidence of multidrug-resistant bacterial pathogens. Carbapenems and vancomycin should be reserved for situations where first-line antibiotics have proven ineffective.

CONCLUSION

The current study reveals a bacterial isolation rate of 26.3% from blood cultures during the survey period. The most frequently encountered bacterial isolates were *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Escherichia coli*. Notably, the prevalence of multidrug-resistant bacterial pathogens, particularly against commonly prescribed antibiotics, was significant.

Furthermore, there is evidence of emerging resistance to carbapenems, with sensitivity rates falling below 100% for both enterobacteriaceae and non-enterobacteriaceae. Consequently, it is of importance to establish continuous antibiotic susceptibility surveillance for blood culture isolates. This measure is essential for promoting the rational use of antibiotics and implementing antimicrobial stewardship programs within medical emergency units.

Limitation of this study: This is a small-scale study with significant findings that could have had a much broader impact if we had sufficient funding to conduct it as a multicenter, large-scale research project. This would have allowed us to generate an antibiogram. Nevertheless, these findings pave the way for more comprehensive future studies.

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Data Availability: The dataset presented in this study can be found online according to the journal's standard protocol.

Ethical approval and consent to participate: Ethical clearance was gotten from LUTH Health Research Ethics Committee and a written consent was also obtained from all the patients that participated in the study. Ethical Number: ADM/DCST/HREC/APP/2771

Conflicting interests: The authors have no conflicts of interest.

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Table 1: Demographic and baseline characteristics of the participants

Characteristics	Frequency (%) (n = 300)
Sex	
Male	127 (42.3)
Female	173 (57.7)
Age group (Years)	
20-29	48(16.0)
30-39	75(25.0)
40-49	60(20.0)
50-59	68(22.7)
60-69	32(10.7)
=70	17(5.7)
Mean±SD	44.93±14.5

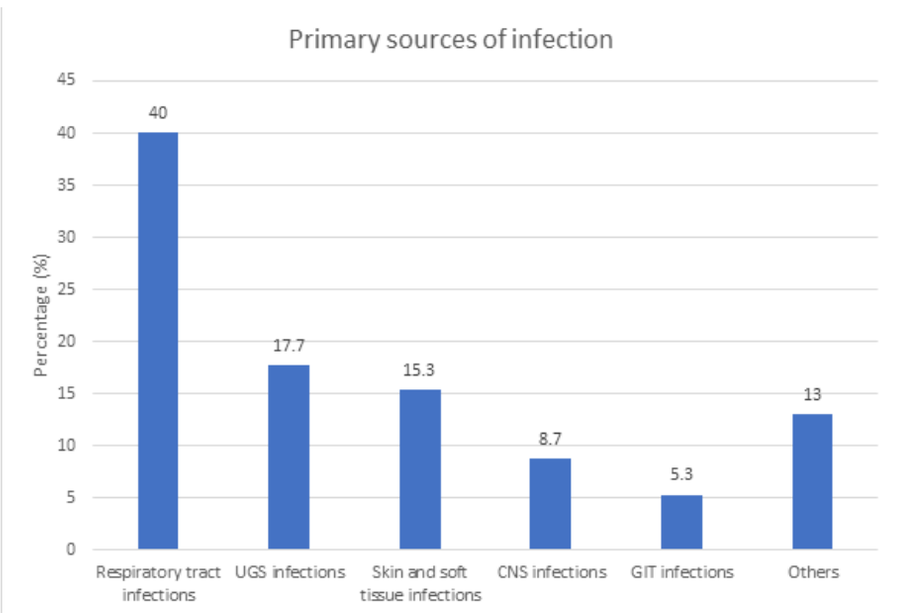

Figure 1: Primary focus of infection among the participants
Key: UGS: Urogenital system, CNS: Central nervous system, GIT: Gastrointestinal tract.

Table 2: Association between culture growth and demographic characteristics

	Culture Positive group n=79 (%)	Culture Negative group n=221(%)	Chi-square	p-value
Gender (n)				
Male (127)	35 (27.6)	92 (72.4)	0.171	0.680
Female (173)	44 (25.4)	129 (74.6)		
Age group in years (n)				
20-29 (48)	11 (22.9)	37 (77.1)	3.579	0.612
30-39 (75)	18 (24)	57 (76.0)		
40-49 (56)	13 (23.2)	43 (76.8)		
50-59 (68)	22 (32.4)	46 (67.6)		
60-69 (32)	11 (34.4)	21(65.6)		
=70 (17)	4 (23.5)	13 (76.5)		

Table 3: Bacterial pathogens isolated from blood culture

Isolate	Frequency	Percentage
Gram Positive Cocci		
Staphylococcus aureus	23	29.1
Coagulate Negative Staphylococcus (CONs)	7	8.8
Enterococcus faecalis	1	1.3
Total	**31**	**39.2**
Gram Negative Bacilli		
Escherichia coli	13	16.5
Klebsiella pneumoniae	15	19.0
Pseudomonas aeruginosa	2	2.5
Klebsiella oxytoca	3	3.8
Acinetobacter baumannii	3	3.8
Enterobacter aerogenes	2	2.5
Proteus mirabilis	2	2.5
Serratia marcescens	2	2.5
Acinetobacter lwoffii	2	2.5
Providencia rettgeri	2	2.5
Citrobacter freundii	1	1.3
Enterobacter agglomerans	1	1.3
Total	48	60.8
Grand total	**79**	**100.0**

Table 4: Bacterial pathogens isolated from other clinical specimens

Isolate	Urine (%)	Sputum (%)	Wound Specimen (%)	Pus Aspirate (%)	Ascitic Fluid (%)	Other (%)	Total
Gram Positive Cocci							
Staphylococcus aureus	1 (4.5)	4 (16.0)	10 (31.3)	2 (40.0)	1 (100.0)	1 (25.0)	19 (21.3)
Coagulate Negative Staphylococcus (CONs)	6 (27.3)	0 (0.0)	2 (6.3)	1 (20.0)	0 (0.0)	1 (25.0)	10 (11.2)
Enterococcus faecalis	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Streptococcus pneumoniae	0 (0.0)	1 (4.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
Enterococcus faecium	1 (4.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
Total	**8 (36.4)**	**5 (20.0)**	**12 (37.5)**	**3 (60.0)**	**1 (100.0)**	**2 (50,0)**	**31 (34.8)**
Gram Negative Bacilli							
Escherichia coli	7 (31.8)	5 (20.0)	3 (9.4)	1 (20.0)	0 (0.0)	1 (25.0)	17 (19.1)
Klebsiella pneumoniae	1 (4.5)	8 (32.0)	3 (9.4)	0 (0.0)	0 (0.0)	1 (25.0)	13 (14.6)
Pseudomonas aeruginosa	1 (4.5)	0 (0.0)	6 (18.8)	0 (0.0)	0 (0.0)	0 (0.0)	7 (7.9)
Klebsiella oxytoca	0 (0.0)	3 (12.0)	2 (6.3)	0 (0.0)	0 (0.0)	0 (0.0)	5 (5.6)
Acinetobacter baumannii	2 (9.0)	0 (0.0)	2 (6.3)	0 (0.0)	0 (0.0)	0 (0.0)	4 (4.5)
Enterobacter aerogenes	1 (4.5)	2 (8.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (3.4)
Proteus mirabilis	0 (0.0)	0 (0.0)	1 (3.1)	1 (20.0)	0 (0.0)	0 (0.0)	2 (2.2)
Citrobacter koseri	0 (0.0)	2 (8.0)	1 (3.1)	0 (0.0)	0 (0.0)	0 (0.0)	3 (3.4)
Serratia marcescens	1 (4.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
Acinetobacter lwoffii	1 (4.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
Providencia rettgeri	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Citrobacter freundii	0 (0.0)	0 (0.0)	1 (3.1)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
Enterobacter agglomerans	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
Pseudomonas fluorescens	0 (0.0)	0 (0.0)	1 (3.1)	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
Total	14 (63.6)	20 (80.0)	20 (62.5)	2 (40.0)	0 (0.0)	2 (50.0)	58 (65.2)
Grand total	**22 (100.0)**	**25 (100.0)**	**32 (100.0)**	**5 (100.0)**	**1 (100.0)**	**4 (100.0)**	**89 (100.0)**

Table 5: Antibiotics susceptibility profile of Gram negative bacilli from blood culture

	NAME OF ISOLATE	TOTAL NO	CEPTA (%)	AMIKA (%)	CIPRO (%)	LEVOF (%)	CEFTRI (%)	CEFUR (%)	CEFTA (%)	CEFTRIME (%)	PIPERA (%)	AUGM (%)	AMPIC	TRIME-SUL (%)	MERO (%)	IMIPEN (%)
1	*Klebsiella pneumoniae*	15	8(53)	10(67)	8(53)	9(60)	**6(40)**	7(47)	6(40)	NT	8(53)	10(67)	7(47)	**NT**	5(33)	13(86)	NT
2	*E coli*	13	10(77)	9(69)	6(46)	7(54)	5(38)	7(54)	7(54)	NT	8(62)	10(77)	8(62)	**NT**	5(38)	**11(85)**	NT
3	*Klebsiella oxytoca*	3	2(67)	2(67)	1(33)	2(67)	1(33)	2(67)	2(67)	NT	2(67)	3(100)	2(67)	**NT**	1(33)	3(100)	NT
4	*Proteus mirabilis*	2	1(50)	1(50)	0(0)	0(0)	**0(0)**	1(50)	1(50)	NT	1(50)	1(50)	0(0)	**NT**	0(0)	2(100)	NT
5	*Enterobacter aerogenes*	2	1(50)	1(50)	0(0)	1(50)	0	1(50)	1(50)	NT	2(100)	1(50)	1(50)	**NT**	0(0)	1(50)	NT
6	*Enterobacter agglomerans*	1	1(100)	1(100)	0	1(100)	0	1(100)	1(100)	NT	1(100)	1(100)	1(100)	**NT**	NT	1(100)	NT
7	*Citrobacter freundii*	1	0(0)	1(100)	0	0	0	1(100)	0(0)	NT	1(100)	1(100)	0(0)	**NT**	0(0)	1(100)	NT
8	*Serratia marcescens*	2	2(100)	2(100)	1(50)	1(50)	0(0)	1(50)	1(50)	NT	2(100)	2(100)	1(50)	**NT**	0(0)	2(100)	NT
9	*Providencia rettgeri*	2	1(50)	1(50)	1(50)	2(100)	1(50)	1(50)	1(50)	NT	1(50)	2(100)	1(50)	**NT**	NT	2(100)	NT
10	*Acinetobacter lwoffii*	2	1(50)	1(50)	1(50)	2(100)	NT	NT	NT	1(50)	1(50)	2(100)	NT	**2(100)**	2(100)	2(100)	NT
11	*Acinetobacter baumannii*	3	1(33)	1(33)	1(33)	1(33)	NT	NT	NT	1(33)	1(33)	2(67)	NT	**2(67)**	1(33)	2(67)	NT
12	*Psedomonas aeruginosa*	2	1(50)	1(50)	0(0)	1(50)	NT	NT	NT	1(50)	1(50)	2(100)	NT	**NT**	1(50)	1(50)	1(50)
13	Total	48	30(62)	31(65)	19(40)	27(56)	13(27)	22(46)	20(42)	3(6)	29(60)	37(77)	21(44)	4(8)	10(21)	41(85)	1(2)

Note: NT = Not tested

Over 60% of the Gram-negative bacilli isolated from blood culture are susceptible to gentamicin, amikacin, cefepime, piperacillin tazobactam and meropenem.

Table 6: Antibiotics susceptibility profile of Gram negative baccilli isolated from other specimens

	NAME OF ISOLATE	TOTAL ISO	CENT	AMIC	CIPRO (%)	LEVO	CEFE	CEFAZ	CEFTI	CEFT	CEFEP	PIPERA TAZ	AMOXY CLA	AMPICILLIN-CLI	TRIMET CLI	MEROP	IMIPE
1	*E.coli*	17	14(82)	11(65)	12(76)	14(82)	7(41)	9(53)	10(59)	NT	11(65)	15(88)	11(65)	**NT**	NT	16(94)	NT
2	*Klebsiella pneumoniae*	13	6(46)	7(54)	5(38)	6(46)	4(31)	6(46)	6(46)	NT	8(62)	10(77)	8(62)	**NT**	NT	11(85)	NT
3	*Klebsiella oxytoca*	5	2(40)	2(40)	2(40)	3(60)	1(20)	2(40)	2(40)	NT	3(60)	3(60)	2(40)	**NT**	NT	4(80)	NT
4	*Proteus mirabilis*	2	1(50)	1(50)	1(50)	2(100)	0	1(50)	1(50)	NT	2(100)	2(100)	1(50)	**NT**	NT	2(100)	NT
5	*Enterobacter aerogenes*	3	1(33)	1(33)	1(33)	2(67)	1(33)	2(67)	2(67)	NT	2(67)	2(67)	1(33)	**NT**	NT	2(67)	NT
6	*Citrobacter koseri*	3	2(67)	2(67)	1(33)	2(67)	1(33)	1(33)	1(33)	NT	2(67)	2(67)	2(67)	**NT**	NT	3(100)	NT
7	*Citrobacter freundii*	1	0	1(100)	0	0	0	0	0	NT	1(100)	1(100)	0	**NT**	NT	1(100)	NT
8	*Serratia marcescens*	1	1(100)	1(100)	0	1(100)	0	0	0	NT	1(100)	1(100)	0	**NT**	NT	1(100)	NT
9	*Pseudomonas flourescens*	1	1(100)	0	1(100)	1(100)	NT	NT	NT	0	1(100)	1(100)	NT	**NT**	NT	1(100)	1(100)
10	*Acinetobacter lwoffii*	1	1(100)	1(100)	0	1(100)	NT	NT	NT	1(100)	NT	1(100)	NT	**1**(100)	0	1(100)	NT
11	*Acinetobacter baumannii*	4	1(25)	1(25)	2(50)	2(50)	NT	NT	NT	1(25)	NT	2(50)	NT	**2(50)**	1(25)	3(75)	NT
12	*Psedomonas aeruginosa*	7	4(57)	3(43)	4(57)	5(71)	3(43)	NT	NT	3(43)	4(57)	5(71)	3(43)	**NT**	NT	6(86)	6(86)
14	Total	58	34(59)	31(53)	29(50)	39(67)	17(29)	21(36)	22(38)	4(7)	35(60)	45(78)	28(48)	**3(5)**	1(2)	51(87)	6(10)

Key: NT - Not tested

Over 60% of the Gram-negative bacilli isolated from other specimens were susceptible to levofloxacin, cefepime, piperacillin tazobactam and meropenem.

Table 7: Antibiotics susceptibility profile of Gram positive cocci

S/N	ISOLATE	TOTAL NO. IS	PENIC LIN	GENTAM ICIN (%)	AMIK IN	ERYT OM	CIPRO OX	LEVO OX	CLINI MY	TRIM HO	TETR YC	NITR ID	CL	LINEZ LID	VANC YCI
Gram positive cocci from blood culture															
1	*Staphylococcus aureus*	23	11(48)	12 (54)	14 (61)	12 (52)	13 (57)	16 (67)	14(61)	11 (48)	9 (39)	NT	NT	22(96)	23 (100)
2	*Coagulase negative staphylococci*	7	3(43)	4(57)	5(71)	3(43)	4 (57)	5 (71)	4 (57)	3 (43)	2 (29)	NT	NT	5 (71)	7 (100)
3	*Enterococcus spp*	1	0	NT	NT	0	1 (100)	1(100)	NT	NT	0	1 (100)	0	1 (100)	1 (100)
	TOTAL	31	14(45)	16(52)	19 (61)	15(48)	18(58)	22(71)	18(58)	14(45)	11(35)	1(3)	0	28(90)	31(100)
Gram positive cocci from other specimens															
1	*Staphylococcus aureus*	19	9(43)	10(53)	12(63)	10(53)	12(63)	13(68)	13(68)	8(42)	4(21)	NT	NT	17 (89.5)	19(100)
2	*Coagulase negative staphylococci*	10	3(30)	4(40)	4(40)	3(30)	5(50)	6(60)	7(70)	7(70)	2(20)	NT	NT	9(90)	10(100)
3	*Enterococcus spp*	1	0	NT	NT	0	0	0	NT	NT	0	1 (100)	0	1 (100)	1 (100)
4	*Streptococcus pneumoniae*	1	1 (100)	NT	NT	1 (100)	1 (100)	1 (100)	1 (100)	NT	1 (100)	NT	0	1 (100)	1 (100)
	Total	31	13 (41)	14(45)	16 (52)	14(45)	18(58)	20(65)	21(67)	15(48)	7(23)	1(3)	0	27 (87)	31(100)

Key: NT - Not tested

Over 70% of the Gram-positive cocci isolated from blood culture were susceptible to levofloxacin, linezolid and vancomycin.

Over 60% of Gram positive cocci isolated from other specimens were susceptible to levofloxacin, clindamycin, linezolid and vancomycin.