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Research Article

Frequency of Isolation and Antimicrobial Susceptibility of Bacteria Isolated from Bloodstream of Septicemic Patients at Pediatric Hospital-Benghazi

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Abstract

Septicemia, a typical reason for morbidity and mortality among neonates and children is caused by a large spectrum of common bacteria. Rapid development of the septicemic neonates and children is caused by a wide spectrum of constantly changing bacteria. Prompt recognition of the infectious agent and the use of effective antimicrobial agents is the key determinant of positive outcome during this serious medical emergency. The study design was prospective, observational and included 4,278 consecutive blood samples of suspected septicemic patients in Pediatric Hospital - Benghazi from January 2011 to January 2020. 1098 (27%) samples showed no growth of bacteria, while 3180 (74.3%) samples showed the growth. Place distribution of samples for septicemic patients were: 68% from patients admitted in medical department in Pediatrics Hospital-Benghazi, 17% from patients admitted in pediatrics ICU and 15% from patients admitted in neonatal ICU. Gender distribution showed male predominance, 2290 (53.53%) male vs. 1635 (38.22%) female. After microscopic examination, samples were cultured for bacterial identification and antibiotic susceptibility. The common isolated pathogens were *Staphylococcus albus* 1471 (46.3%), followed by *Staphylococcus epidermidis* 1099 (34.6%), *Streptococcus* spp 135 (4.2%), *Staphylococcus aureus* 125 (4%), *Escherichia coli* 103 (3.2%), *Klebsiella* spp. 83 (2.6%), *Gram* negative *bacilli* 74 (2.3%), *Pseudomonas aeruginosa* 23 (0.7%), Fungi 16 (0.5%), *Enterococcus faecalis* 14 (0.4%), *Proteus* spp. and *Staphylococcus cereus* 11 (0.3%) each, *Staphylococcus* coagulase negative 8 (0.3%), *Salmonella* spp. 4 (0.1%), while the lowest was *Staphylococcus* spp. 3 (0.1%). The majority of cases were isolated in autumn 1909 (60%) followed by winter and spring 572 (18%), while the lowest incidence was observed in summer 127 (4%). Most of the gram positive organisms were sensitive to Amikacin, Ciprofloxacin and Vancomycin. Gram negative isolates were mainly sensitive to Colistin followed by Amikacin and Imipenem. In wake of high incidence, morbidity and mortality related to infection in neonates and children, there was a need for monitoring, at regular intervals, to understand the dynamic infectious agents' profiles and their condition patterns, thus to formulate policies for the most optimal use of antibiotics and infection control.

Keywords: *Bacteriological; Profile; Susceptibility; Pattern; Septicemic Children*

Introduction

Septicemia could be a common reason for morbidity and mortality in neonates and children despite advanced measures for early diagnosing and treatment, introduction of latest antimicrobial agents, significant progress in hygiene and aggressive enteral feeding [1]. Pediatric infections are outlined as a clinical syndrome of sepsis presenting with general signs and symptoms of infection within the initial four weeks of life [2]. A pair of on the premise of your time or postnatal age of onset, neonatal sepsis may be classified into early

onset neonatal sepsis (within seventy-two hours to seven days of birth) and late onset sepsis (7th day to 1 month of birth) [3]. Early onset infections are thought to be normally transmitted vertically from mother to child. Late onset neonatal infections are primarily caused by bacteria thriving in external surroundings i.e. they›re either Community or Hospital non-inheritable, largely acquired from the hands of the care takers, however is also acquired throughout delivery by vertical transmission from the mother [3,4]. Sepsis in youngsters in Pediatrics ICU (PICU) could be a common reason for morbidity and mortality. Most of the infections in PICU are nosocomial. The longer the stay, larger is the contact of patient with the health care personnel, higher are the probabilities of infection through exposure to environmental organisms and invasive procedures, which may result in sepsis. Risk factors for infection in PICU are prolonged central blood vessel tubing use, receipt of extracorporeal membrane oxygenation, mechanical ventilation, dialysis and total parenteral nutrition. A wide variety of bacteria can cause septicemia in neonates and children and this bacteriological profile is constantly changing. The common gram-positive organisms are *Staphylococcus aureus*, both Methicillin Sensitive *Staphylococcus aureus* (MSSA) and Methicillin Resistant *Staphylococcus aureus* (MRSA), Group B *Streptococcus* and Coagulase Negative *Staphylococci* (CoNS). Gram negative organisms are *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter* spp, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Listeria* sp. *E. coli* and Group B *Streptococci* (GBS) most frequently cause EOS, being members of the maternal genitourinary tract which may ascend through birth canal to amniotic fluid either through intact amniotic membranes or after their rupture [2,5]. *Klebsiella* sp, *Enterobacter* sp, *Citrobacter* sp, *Pseudomonas* sp, CoNS and *Staphylococcus aureus*, both Methicillin sensitive and resistant are more common causes of late onset septicemia. Both neonates and children are vulnerable to infections resulting in septicemia which makes the information of bacteriological profile, access to effective antibiotics within the region or hospital and observation of the same essential [2]. The shortcomings of low sensitivity of blood culture and reporting delay of 24 - 72h have been overcome within the last decade with the arrival of machine-controlled continuous blood culture watching systems [6]. Most typical presenting clinical symptoms in children are fever, tachycardia, hyperventilation, cool extremities, color changes, hypotension, mental status changes and anuria.

Objective of the Study

The present study was designed for isolation and identification of the causative microorganisms of septicaemia in neonates and paediatric patients and selecting their antibiotic regimens, therefore creating a policy recommendation for rational prophylactic and therapeutic use of antibiotics in the hospital.

Materials and Methods

Study populations

The study design was prospective, observational and included 4,278 consecutive blood samples of suspected septicemic patients in Pediatric Hospital - Benghazi from January 2011 to January 2020. After microscopic examination, samples were cultured for bacterial identification and antibiotic susceptibility.

Laboratory analysis

Cultures of blood were performed at the Pediatric Hospital Laboratories in Benghazi. When samples were collected, they were transported in trans-isolate medium at ambient temperature to the Pediatric Hospital Laboratories. Sediment from a centrifuged specimen of blood was cultured on blood agar (BA), MacConkey agar (MA) and Vitox-enriched Chocolate agar (CA) plates. Plates were incubated for 24 - 48h at 35°C in an aerobic atmosphere (BA and MA), an anaerobic atmosphere (BA) or in an incubator at a gas concentration of 5% CO_2 (CA). Isolates from cultures were identified by standard methods. All bacterial isolates were tested for *in vitro* antibiotic disc sensitivity.

Statistical analysis: The data were analyzed by SPSS 22.

Treatment

Antibiotic treatment varied from patient to patient. The antibiotics were used during the study period for all specimens so AMC- Augmentin, AMP- Ampicillin, G- Gentamicin, VA- Vancomycin, FD- Fusidic acid, AK- Amikacin, CAR- Carbapenem, E- Erythromycin, PRL- Clarithromycin, IMP- Imipenem, AML- Amoxicillin, P- Penicillin G, OX-Oxacillin, CFX- Ceftriaxone, CN- Cloxacillin, F- Fosfomycin, NA- Nalidixic acid, PIP- Piperacillin, SMZ- Sulfamethoxazole, FOX- Flucloxacillin, C- Colistin and CIP-Ciprofloxacin were the antibiotics that demonstrated *in-vitro* activity regularly against all culture organisms.

Results

Four thousand and two hundred seventy-eight (4278) suspected septicemia cases were examined using culture in microbiology laboratory in Pediatric Hospital - Benghazi from January 2011 to January 2020.

Comparison between the cases according to the gender age

Table 1 shows that 2290 (53.53%) were male [where 1815 (42.43%) positive and 475 (11.10%) no growth], while 1635 (38.22%) were female [where 1236 (28.89%) positive and 399 (9.33%) no growth].

	Culture				Total
	No growth		Positive		
Gender / Age	Female	Male	Female	Male	
> 5 years	106 2.48%	118 2.76%	60 1.40%	69 1.61%	353 8.25%
< 5 years	399 9.33%	475 11.10%	1236 28.89%	1815 42.43%	3925 91.75%
Total	1098 25.67%		3180 74.33%		4278 100%

Table 1: *Culture depending upon gender and age.*

Distribution of cases positive and negative for septicemic patients at Pediatric Hospital from January 2011 to January 2020

Table 2 shows that the number of samples that showed no growth of bacteria is 1,098 samples (27%), while the number of samples that showed growth of bacteria was 3,180 samples (74.3%).

Culture	Frequency	Percent
No growth	1098	25.7
Positive	3180	74.3
Total	4278	100

Table 2: *Distribution of samples.*

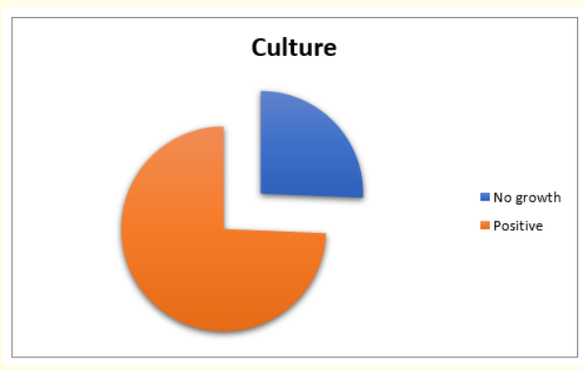

Figure 1: *Distribution of samples.*

Place distribution of samples for septicemic patients at Pediatric Hospital from January 2011 to January 2020

Figure 2 shows place distribution of samples for septicemic patients at Pediatric Hospital from January 2011 to January 2020. 68% from patients admitted in medical department in Pediatrics Hospital -Benghazi, 17% from patients admitted in pediatrics ICU and 15% from patients admitted in neonatal ICU.

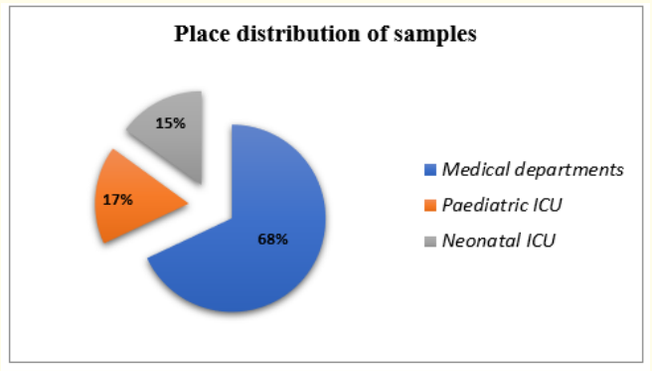

Figure 2: *Place distribution of samples for septicemic patients at Pediatric Hospital from January 2011 to January 2020.*

Organisms isolated from blood cultures of septicemic patients at Pediatric Hospital from January 2011 to January 2020

Table 3 and figure 3 show that the common isolated pathogens were *Staphylococcus albus* 1471 (46.3%), followed by *Staphylococcus epidermidis* 1099 (34.6%), *Streptococcus* spp. 135 (4.2%), *Staphylococcus aureus 125 (4%), Escherichia coli* 103 (3.2%), *Klebsiella* spp. 83 (2.6%), *Gram negative bacilli* 74 (2.3%), *Pseudomonas aeruginosa*23 (0.7%), Fungal growth 16 (0.5%), *Enterococcus faecalis 14 (0.4%), Proteus* spp. and *Staphylococcus cereus* 11 (0.3%) equally, *Staphylococcus* coagulase negative 8 (0.3%), *Salmonella* spp. 4 (0.1%), while the lowest was *Staphylococcus* spp. 3 (0.1%).

Microorganism	Frequency	Percent
Enterococcus faecalis	14	0.4%
Escherichia coli	103	3.2%
Fungal growth	16	0.5%
Gram negative bacilli	74	2.3%
Klebsiella spp	83	2.6%
Proteus spp	11	0.3
Pseudomonas aeruginosa	23	0.7%
Salmonella spp	4	0.1%
Staphylococcus albus	1471	46.3%
Staphylococcus aureus	125	4%
Staphylococcus cereus	11	0.3%
Staphylococcus coagulase negative	8	0.3%
Staphylococcus epidermidis	1099	34.6%
Staphylococcus spp	3	0.1%
Streptococcus spp	135	4.2%
Total	3180	100%

Table 3*: Distribution of microorganisms from 2011 to 2020.*

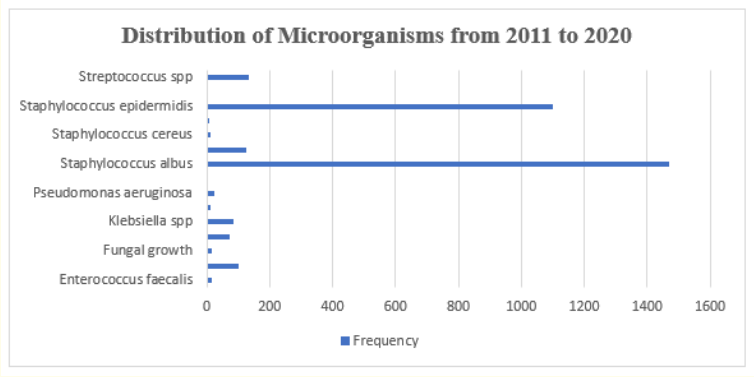

Figure 3: *Distribution of microorganisms from 2011 to 2020.*

Table 4 and figure 4 show the distribution of common isolated pathogens in 2011. *Staphylococcus epidermidis* 64 (43%), followed by *Staphylococcus albus* 45 (30.2%), *Escherichia coli* and *Streptococcus* spp. 10 (6.7%) equally, *Klebsiella* spp. 7 (4.7%), *Staphylococcus aureus* 5 (3.4%), while the lowest were *Enterococcus faecalis* and *Proteus* spp. 1 (0.7%) equally.

Microorganism	Frequency	Percent
Enterococcus faecalis	1	0.7%
Escherichia coli	10	6.7%
Fungal growth	4	2.7%
Klebsiella spp	7	4.7%
Proteus spp	1	0.7%
Pseudomonas aeruginosa	2	1.3%
Staphylococcus albus	45	30.2%
Staphylococcus aureus	5	3.4%
Staphylococcus epidermidis	64	43%
Streptococcus spp	10	6.7%
Total	149	100%

Table 4: *Distribution of microorganisms in 2011.*

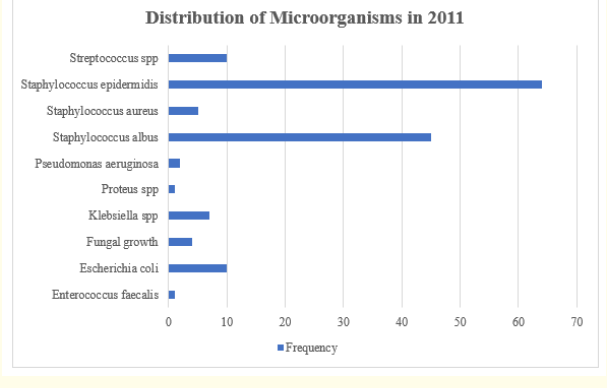

Figure 4: *Distribution of microorganisms in 2011.*

Table 5 and figure 5 show the distribution of common isolated pathogens in 2012. *Staphylococcus albus* 389 (63.6%), followed by *Staphylococcus epidermidis* 118 (19.3%), *Escherichia coli* 28 (4.6%), *Staphylococcus aureus* 26 (4.2%), *Streptococcus* spp 21 (3.4%), *Enterococcus faecalis* and *Klebsiella* spp. 15 (2.5%) equally, *Pseudomonas aeruginosa* 4 (0.7%), while the lowest were Fungal growth, Gram negative *bacilli*, *Salmonella* spp. and *Staphylococcus cereus* 1 (0.2%) equally.

Microorganism	Frequency	Percent
Enterococcus faecalis	15	0.8%
Escherichia coli	28	4.6%
Fungal growth	1	0.2%
Gram negative *bacilli*	1	0.2%
Klebsiella spp	15	2.5%
Proteus spp	2	0.3%
Pseudomonas aeruginosa	4	0.7%
Salmonella spp	1	0.2%
Staphylococcus albus	389	63.6%
Staphylococcus aureus	26	4.2%
Staphylococcus cereus	1	0.2%
Staphylococcus epidermidis	118	19.3%
Streptococcus spp	21	3.4%
Total	612	100%

Table 5: *Distribution of microorganisms in 2012.*

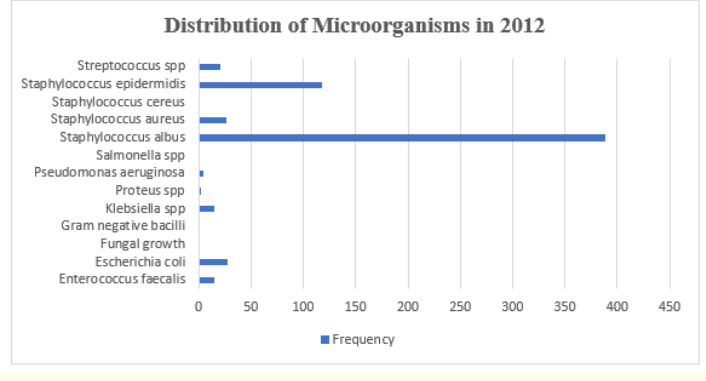

Figure 5: *Distribution of microorganisms in 2012.*

Table 6 and figure 6 show the distribution of common isolated pathogens in 2013. *Staphylococcus albus* 255 (47%), followed by *Staphylococcus epidermidis* 234 (43.2%), *Streptococcus* spp. 19 (3.5%), *Staphylococcus aureus* 13 (2.4%), *Klebsiella* spp. and *Escherichia coli* 5 (0.9%) equally, *Pseudomonas aeruginosa* 4 (0.7%), Fungal growth 3 (0.6%), while the lowest were *Enterococcus faecalis*, *Salmonella* spp., *Staphylococcus cereus* and *Proteus* spp. 1 (0.2%) equally.

Microorganism	Frequency	Percent
Enterococcus faecalis	1	0.2%
Escherichia coli	5	0.9%
Fungal growth	3	0.6%
Klebsiella spp	5	0.9%
Proteus spp	1	0.2%
Pseudomonas aeruginosa	4	0.7%
Salmonella spp.	1	0.2%
Staphylococcus albus	255	47%
Staphylococcus aureus	13	2.4%
Staphylococcus cereus	1	0.2%
Staphylococcus epidermidis	234	43.2%
Streptococcus spp	19	3.5%
Total	542	100%

Table 6: *Distribution of microorganisms in 2013.*

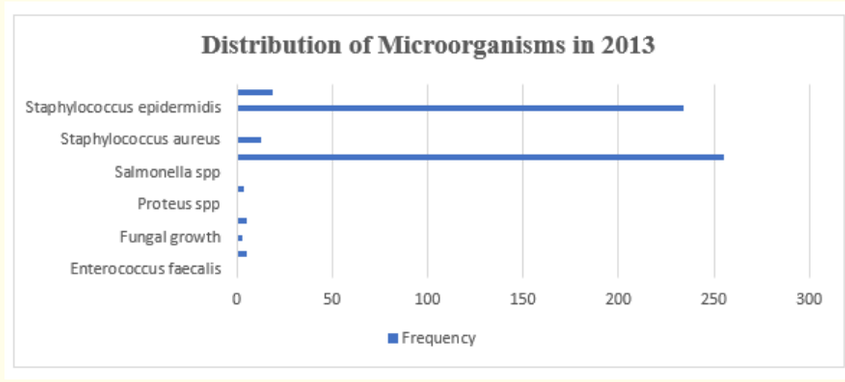

Figure 6: *Distribution of microorganisms in 2013.*

Table 7 and figure 7 show the distribution of common isolated pathogens in 2014. *Staphylococcus epidermidis* 64 (43%), followed by *Staphylococcus albus* 45 (30.2%), *Streptococcus* spp. and *Escherichia coli* 10 (6.7%) equally, *Klebsiella* spp. 7 (4.7%), *Staphylococcus aureus* 5 (3.4%), Fungal growth (2.7%), *Pseudomonas aeruginosa* 2 (1.3%), while the lowest were *Enterococcus faecalis* and *Proteus* spp. 1 (0.7%) equally.

Microorganism	Frequency	Percent
Enterococcus faecalis	1	0.7%
Escherichia coli	10	6.7%
Fungal growth	4	2.7%
Klebsiella spp	7	4.7%
Proteus spp	1	0.7%
Pseudomonas aeruginosa	2	1.3%
Staphylococcus albus	45	30.2%
Staphylococcus aureus	5	3.4%
Staphylococcus epidermidis	64	43%
Streptococcus spp	10	6.7%
Total	149	100%

Table 7: *Distribution of microorganisms in 2014.*

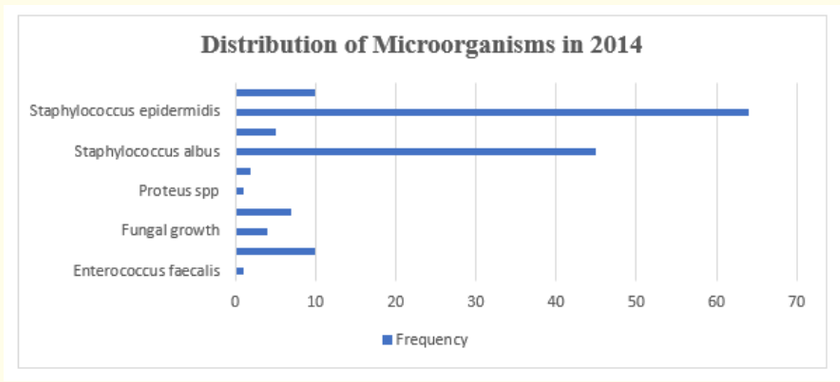

Figure 7: *Distribution of microorganisms in 2014.*

Table 8 and figure 8 show the distribution of common isolated pathogens in 2015. *Staphylococcus albus* 389 (63.6%), followed by *Staphylococcus epidermidis* 118 (19.3%), *Escherichia coli* 28 (4.6%), *Staphylococcus aureus* 26 (4.2%), *Streptococcus* spp 21 (3.4%), *Enterococcus faecalis* and *Klebsiella* spp. 15 (2.5%) equally, *Pseudomonas aeruginosa* 4 (0.7%), while the lowest were Fungal growth, Gram negative *bacilli*, *Salmonella* spp. and *Staphylococcus cereus* 1 (0.2%) equally.

Microorganism	Frequency	Percent
Enterococcus faecalis	15	0.8%
Escherichia coli	28	4.6%
Fungal growth	1	0.2%
Gram negative *bacilli*	1	0.2%
Klebsiella spp	15	2.5%
Proteus spp	2	0.3%
Pseudomonas aeruginosa	4	0.7%
Salmonella spp	1	0.2%
Staphylococcus albus	389	63.6%
Staphylococcus aureus	26	4.2%
Staphylococcus cereus	1	0.2%
Staphylococcus epidermidis	118	19.3%
Streptococcus spp	21	3.4%
Total	612	100%

Table 8*: Distribution of microorganisms in 2015.*

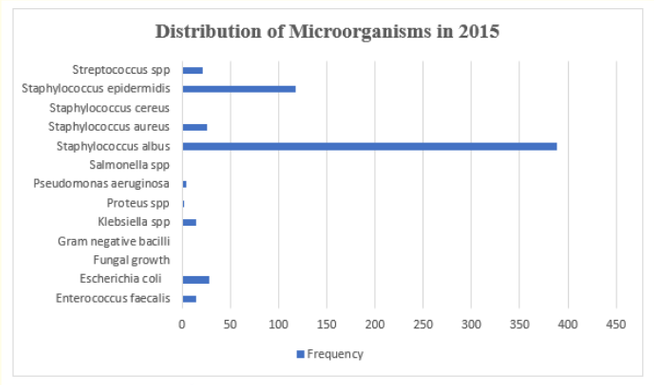

Figure 8: *Distribution of microorganisms in 2015.*

Table 9 and figure 9 show the distribution of commonly isolated pathogens in 2016. *Staphylococcus albus* 255 (47%), followed by *Staphylococcus epidermidis* 234 (43.2%), *Streptococcus* spp. 19 (3.5%), *Staphylococcus aureus* 13 (2.4%), *Klebsiella* spp. and *Escherichia coli* 5 (0.9%) equally, *Pseudomonas aeruginosa* 4 (0.7%), Fungal growth 3 (0.6%), while the lowest were *Enterococcus faecalis*, *Salmonella* spp., *Staphylococcus cereus* and *Proteus* spp. 1 (0.2%) equally.

Microorganism	Frequency	Percent
Enterococcus faecalis	1	0.2%
Escherichia coli	5	0.9%
Fungal growth	3	0.6%
Klebsiella spp	5	0.9%
Proteus spp	1	0.2%
Pseudomonas aeruginosa	4	0.7%
Salmonella spp.	1	0.2%
Staphylococcus albus	255	47%
Staphylococcus aureus	13	2.4%
Staphylococcus cereus	1	0.2%
Staphylococcus epidermidis	234	43.2%
Streptococcus spp.	19	3.5%
Total	542	100%

Table 9: *Distribution of microorganisms in 2016.*

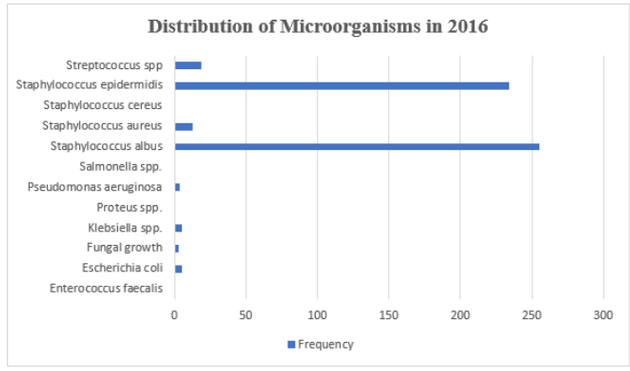

Figure 9: *Distribution of microorganisms in 2016.*

Table 10 and figure 10 show the distribution of common isolated pathogens in 2017. *Staphylococcus epidermidis* 22 (45.8%), followed by *Klebsiella* spp. 8 (16.7%), *Staphylococcus albus* 7 (14.6%), *Escherichia coli* 4 (8.3%), *Streptococcus spp.* 3 (6.3%), *Staphylococcus* spp 2 (4.2%), while the lowest were Gram negative *bacilli* and *Staphylococcus aureus* 1 (0.2%) equally.

Microorganism	Frequency	Percent
Escherichia coli	4	8.3%
Gram negative *bacilli*	1	2.1%
Klebsiella spp	8	16.7%
Staphylococcus albus	7	14.6%
Staphylococcus aureus	1	2.1%
Staphylococcus epidermidis	22	45.8%
Staphylococcus spp	2	4.2%
Streptococcus spp	3	6.3%
Total	48	100%

Table 10: *Distribution of microorganisms in 2017.*

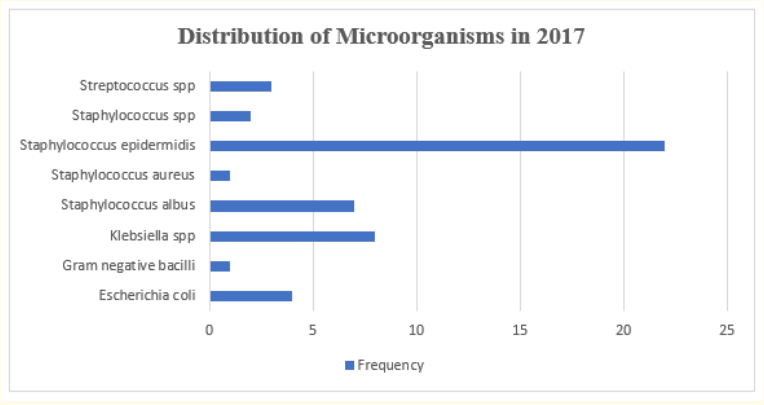

Figure 10: *Distribution of microorganisms in 2017.*

Table 11 and figure 11 show the distribution of common isolated pathogens in 2018. *Staphylococcus epidermidis* 27 (41.5%), followed by Gram negative *bacilli* 16 (24.6%), *Staphylococcus albus* 7 (10.8%), *Escherichia coli* 5 (7.7%), *Klebsiella* spp. and *Staphylococcus aureus* 3 (4.6%) equally, *Streptococcus* spp. 2 (3.1%), while the lowest were *Staphylococcus cereus* and *Proteus* spp. 1 (1.5%) equally.

Microorganism	Frequency	Percent
Escherichia coli	5	7.7%
Gram negative *bacilli*	16	24.6%
Klebsiella spp	3	4.6%
Proteus spp	1	1.5%
Staphylococcus albus	7	10.8%
Staphylococcus aureus	3	4.6%
Staphylococcus cereus	1	1.5%
Staphylococcus epidermidis	27	41.5%
Streptococcus spp	2	3.1%
Total	65	100%

Table 11: *Distribution of microorganisms in 2018.*

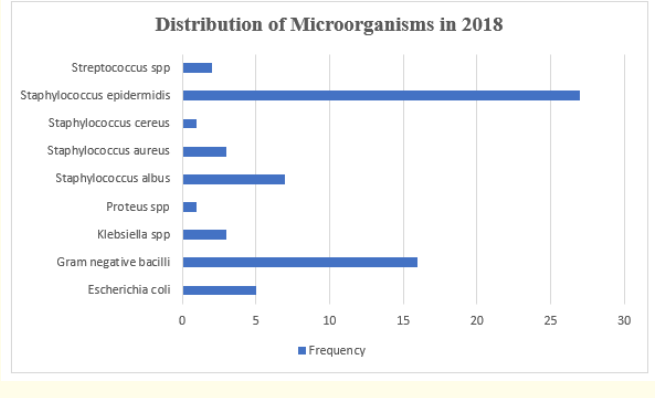

Figure 11: *Distribution of microorganisms in 2018.*

Table 12 and figure 12 show the distribution of common isolated pathogens in 2019. *Staphylococcus epidermidis* 122 (47.3%), followed by Gram negative *bacilli* 40 (15.5%), *Staphylococcus albus* 34 (13.2%), *Staphylococcus aureus* 20 (7.8%), *Streptococcus* spp 16 (6.2%), *Klebsiella* spp. 10 (3.9%), *Escherichia coli* 7 (2.7%), *Pseudomonas aeruginosa* and *Staphylococcus cereus* 3 (1.2%) equally, *Proteus* spp. 2 (0.8%), while the lowest was *Staphylococcus* spp. 1 (0.4%).

Microorganism	Frequency	Percent
Escherichia coli	7	2.7%
Gram negative *bacilli*	40	15.5%
Klebsiella spp	10	3.9%
Proteus spp	2	0.8%
Pseudomonas aeruginosa	3	1.2%
Staphylococcus albus	34	13.2%
Staphylococcus aureus	20	7.8%
Staphylococcus cereus	3	1.2%
Staphylococcus epidermidis	122	47.3%
Staphylococcus spp	1	0.4%
Streptococcus spp	16	6.2%
Total	258	100%

Table 12: *Distribution of microorganisms in 2019.*

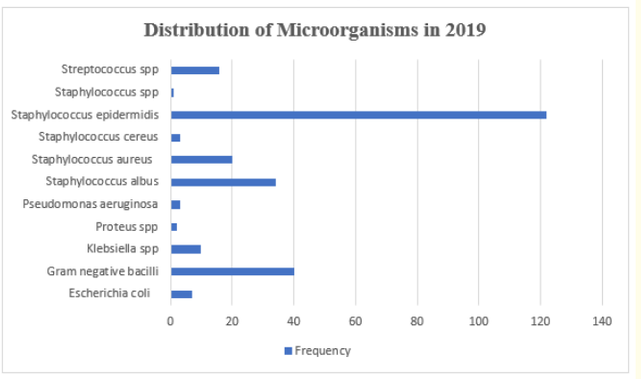

Figure 12: *Distribution of microorganisms in 2019.*

Table 13 and figure 13 show the distribution of common isolated pathogens in 2020. *Staphylococcus epidermidis* 96 (47.3%), followed by *Staphylococcus albus* 45 (22.2%), Gram negative *bacilli* 15 (7.4%), *Streptococcus* spp. 14 (6.9%), *Staphylococcus aureus* 13 (6.4%), *Klebsiella* spp. and *Staphylococcus* coagulase negative 8 (3.9%) equally, *Staphylococcus cereus* 3 (1.5%), while the lowest were *Escherichia coli* 1 (0.5%).

Microorganism	Frequency	Percent
Escherichia coli	1	0.5%
Gram negative *bacilli*	15	7.4%
Klebsiella spp	8	3.9%
Staphylococcus albus	45	22.2%
Staphylococcus aureus	13	6.4%
Staphylococcus cereus	3	1.5%
Staphylococcus coagulase negative	8	3.9%
Staphylococcus epidermidis	96	47.3%
Streptococcus spp	14	6.9%
Total	203	100%

Table 13: *Distribution of microorganisms in 2020.*

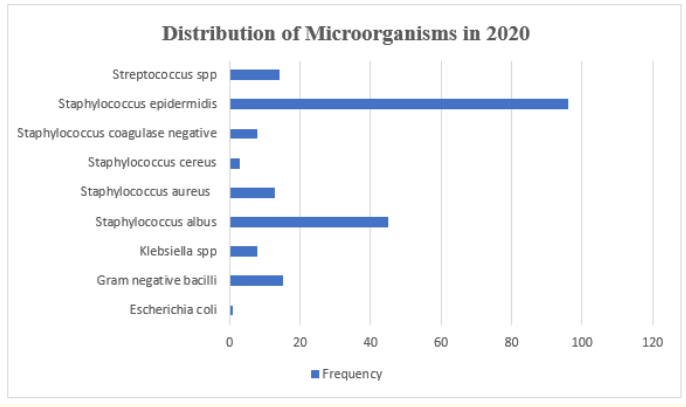

Figure 13: *Distribution of microorganisms in 2020.*

Seasonal variations in the bacterial pathogens isolated from septicemia blood at Benghazi Pediatric hospital from January 2011 to January 2020

The majority of cases were isolated in autumn 1909 (60%) followed by winter and spring 572 (18%), while the lowest incidence was observed in summer 127 (4%).

Seasons	Autumn	Winter	Spring	Summer	Total
Growth	1909 (60%)	572 (18%)	572 (18%)	127 (4%)	3180 (100%)

Table 14: *Seasonal variations in the bacterial pathogens isolated from septicemia blood at Benghazi Pediatric hospital from January 2011 to January 2020.*

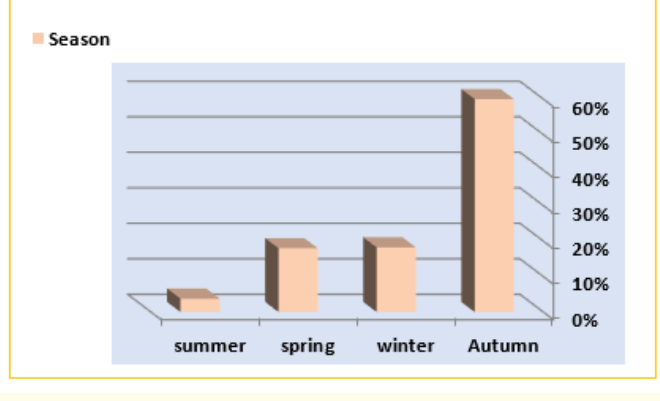

Figure 14: *Seasonal variations of the isolated bacterial septicemia from blood at Benghazi Pediatric hospital from January 2011 to January 2020.*

Susceptibility patterns of various bacteria isolated from blood at Benghazi Pediatric Hospital from January 2011 to January 2020

Uniform antibiogram was used during the study period for all specimens. AMC-Augmentin, AMP- Ampicillin, G- Gentamicin, VA-Vancomycin, FD- Fusidic acid, AK-Amikacin, CAR- Carbapenem, E- Erythromycin, CRL- Clarithromycin, G- Gentamycin, IMP- Imipenem, AML- Amoxicillin, P- Penicillin G, OX- Oxacillin, CFX- Ceftriaxone, AM- Ampicillin, CN- Cloxacillin, F- Fosfomycin, NA- Nalidixic acid, PIP-Piperacillin, SMZ- Sulfamethoxazole, FOX- Flucloxacillin, C- Colistin and CIP- Ciprofloxacin were the antibiotics that demonstrated *in-vitro* activity universally against all culture organisms.

Klebsiella bacterial isolates were highly susceptibility to Colistin (46.3%) and highly resistant towards Cloxacillin (36.6%) as shown in figure 15.

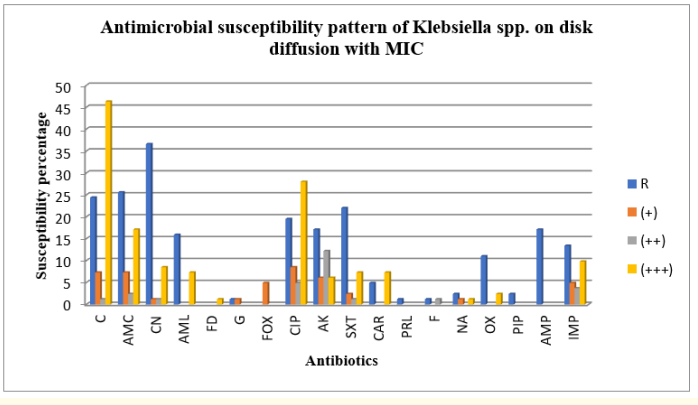

Figure 15: *Antimicrobial susceptibility pattern of Klebsiella spp. on disc diffusion with MIC.*

Proteus bacteria isolates were highly susceptible to Colistin and Augmentin (63.6%) and highly resistant towards Cloxacillin (27.3%) as is shown figure 16.

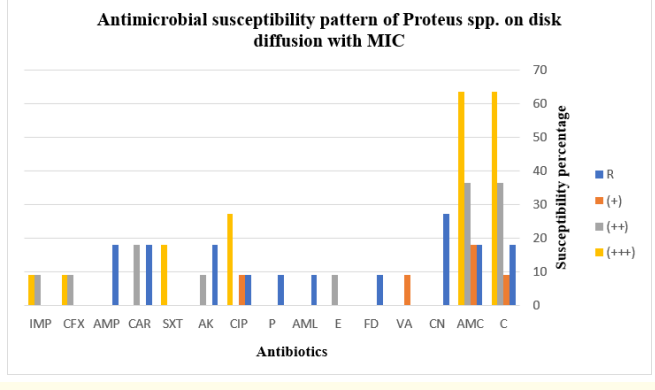

Figure 16: *Antimicrobial susceptibility pattern of Proteus spp. on disc diffusion with MIC.*

Escherichia coli bacterial isolates were highly susceptible to Colistin (38.8%) and highly resistant towards Amoxicillin (18.4%) as shown in figure 17.

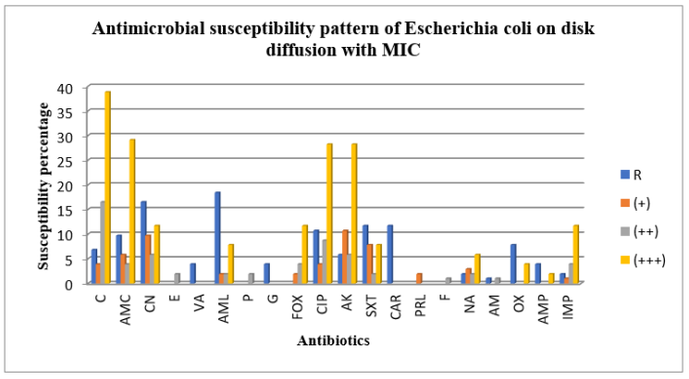

Figure 17: *Antimicrobial susceptibility pattern of Escherichia coli on disc diffusion with MIC.*

Enterococcus faecalis bacterial isolates were highly susceptible to Amikacin (75%) and highly resistant towards Fusidic acid (75%) as shown in figure 18.

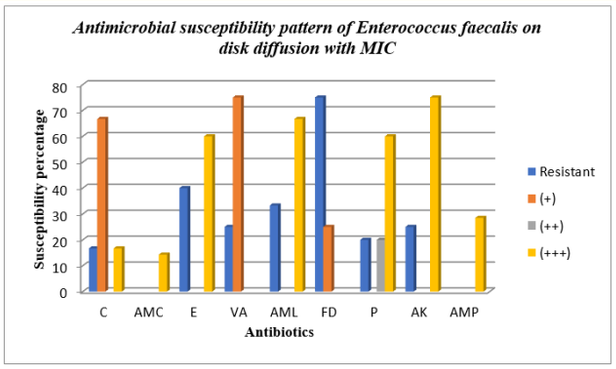

Figure 18: *Antimicrobial susceptibility pattern of Enterococcus faecalis on disc diffusion with MIC.*

Gram negative *bacilli* isolates were highly susceptible to Amikacin and Ciprofloxacin (45.9%) and highly resistant towards Colistin (35.1%) as shown in figure 19.

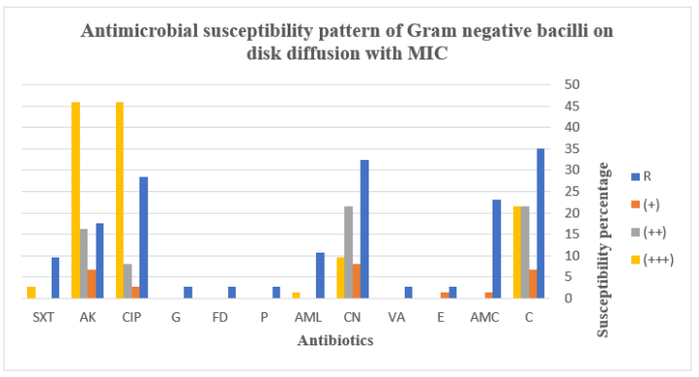

Figure 19: *Antimicrobial susceptibility pattern of Gram-negative bacilli on disc diffusion with MIC.*

Staphylococcus albus bacterial isolates were highly susceptible to Ciprofloxacin, Augmentin, Oxacillin and Colistin (100%) and highly resistant towards Fosfomycin and Ampicillin (100%) as shown in figure 20.

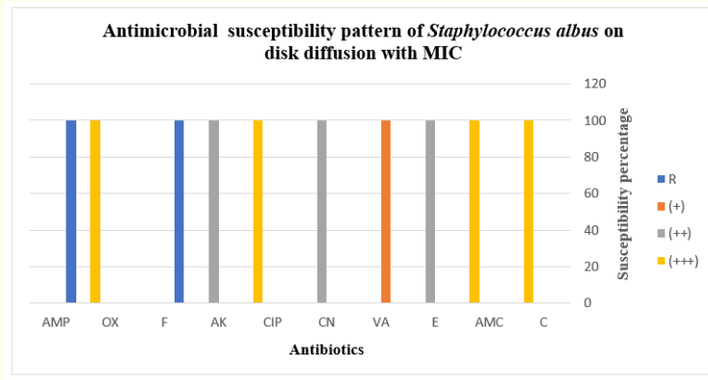

Figure 20: *Antimicrobial susceptibility pattern of Staphylococcus albus on disc diffusion with MIC.*

Pseudomonas aeruginosa bacterial isolates were highly susceptible to Ciprofloxacin (60.9%) and highly resistant towards Augmentin (39.1%) as shown in figure 21.

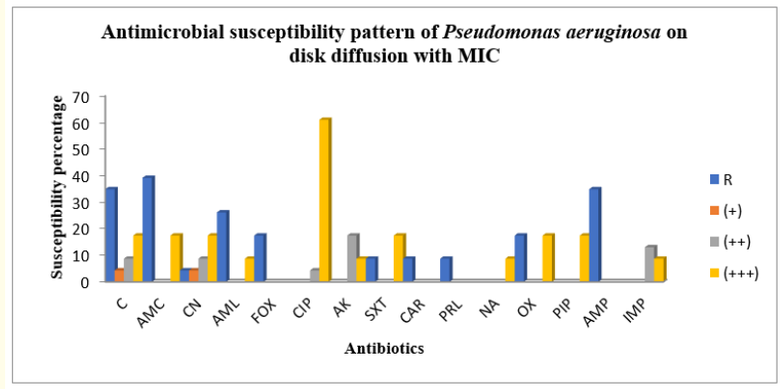

Figure 21: *Antimicrobial susceptibility pattern of Pseudomonas aeruginosa on disc diffusion with MIC.*

Staphylococcus coagulase negative bacterial isolates were highly susceptible to Imipenem and Colistin (25%), followed by Vancomycin (37.5%) and Cloxacillin (25%), and resistant towards most antibiotics by (12.5%) as shown in figure 22.

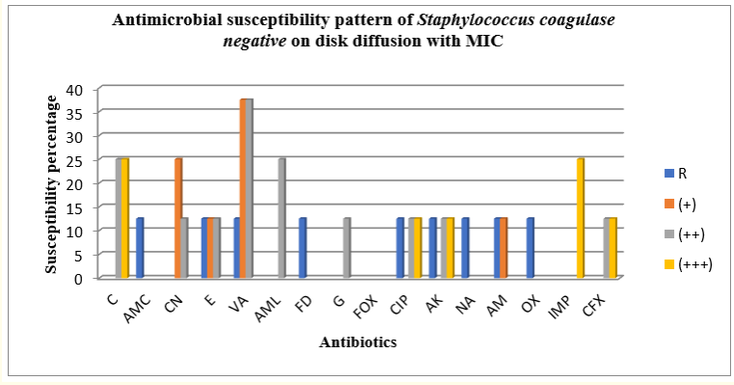

Figure 22: *Antimicrobial susceptibility pattern of Staphylococcus coagulase negative on disc diffusion with MIC.*

Staphylococcus epidermidis bacterial isolates were highly susceptible to Augmentin, Fusidic acid, Penicillin G, Gentamicin (97%) and Colistin (96.8%) followed by Cloxacillin (96.8%) as shown in figure 23.

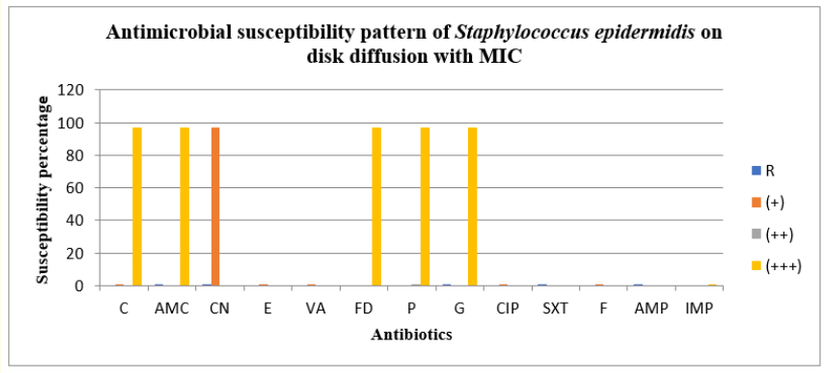

Figure 23: *Antimicrobial susceptibility pattern of Staphylococcus epidermidis on disc diffusion with MIC.*

Staphylococcus cereus bacterial isolates demonstrated high susceptibility to Imipenem (15%), followed by Oxacillin (10%), and resistance towards Vancomycin (20%) as shown in figure 24.

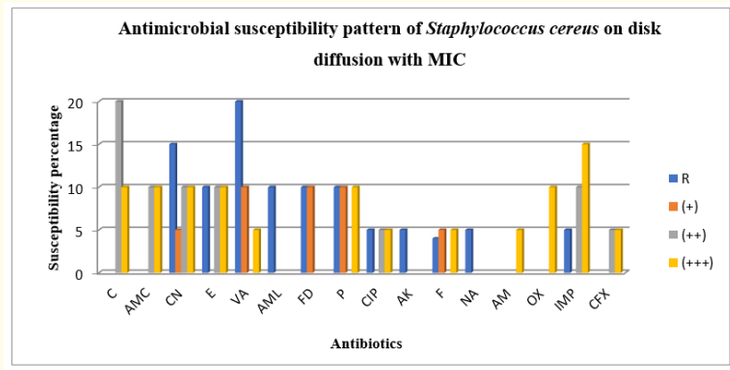

Figure 24: *Antimicrobial susceptibility pattern of Staphylococcus cereus on disc diffusion with MIC.*

Staphylococcus aureus bacterial isolates were highly susceptible to Ciprofloxacin (40%), followed by Colistin (37.6%), and resistant towards Erythromycin (18.4%) as shown in figure 25.

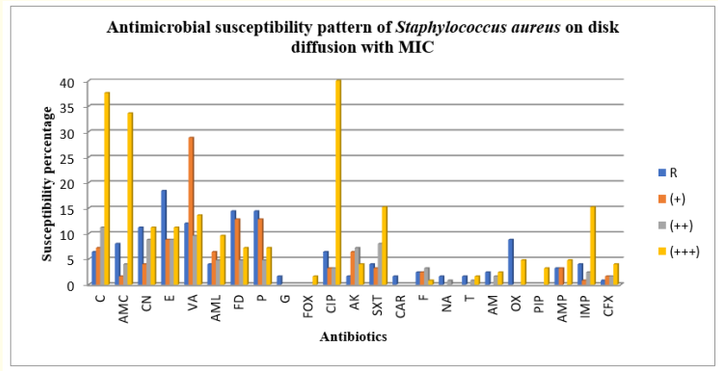

Figure 25: *Antimicrobial susceptibility pattern of Staphylococcus aureus on disc diffusion with MIC.*

Salmonella bacterial isolates were highly susceptible to Imipenem, Sulfamethoxazole, Ciprofloxacin, Gentamicin and Colistin (50%) as shown in figure 26.

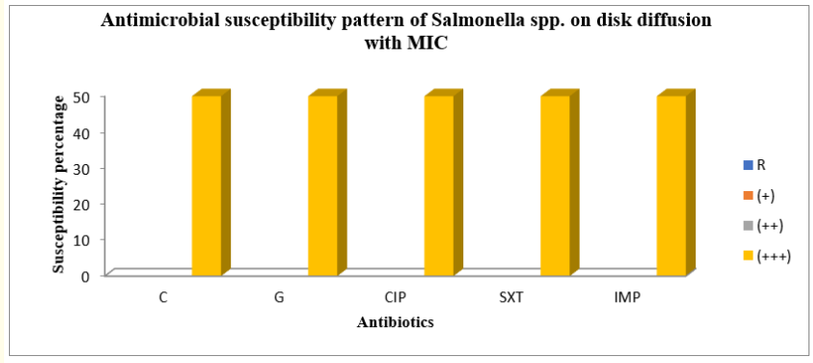

Figure 26: *Antimicrobial susceptibility pattern of Salmonella spp. on disc diffusion with MIC.*

Isolated Fungal growths were highly susceptibility to Ampicillin (12.5%), followed by Vancomycin and Ciprofloxacin (12.5%) as shown in figure 27.

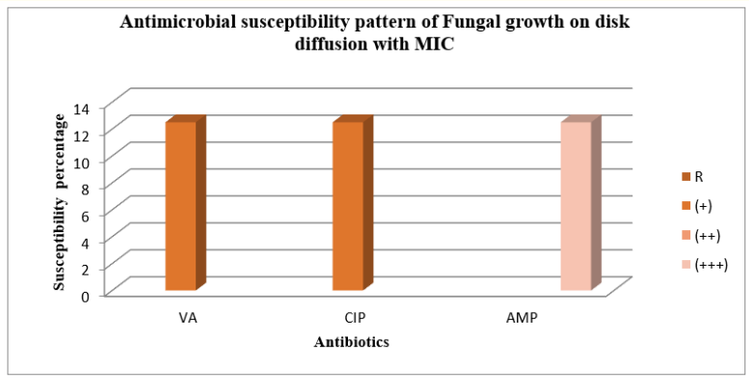

Figure 27: *Antimicrobial susceptibility pattern of Fungal growth on disc diffusion with MIC.*

Staphylococcus species isolates were highly susceptibility to Amikacin and Erythromycin (33.3%), and resistant to Ampicillin, Fusidic acid and Sulfamethoxazole (33.3%), as shown in figure 28.

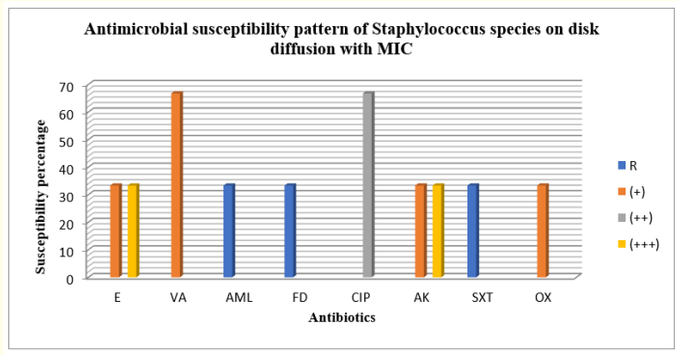

Figure 28: *Antimicrobial susceptibility pattern of Staphylococcus species on disc diffusion with MIC.*

Streptococcus species isolates demonstrated high susceptibility to Augmentin (19.9%), followed by Colistin (18.1%), and resistance to Vancomycin (6.6%) as shown in figure 29.

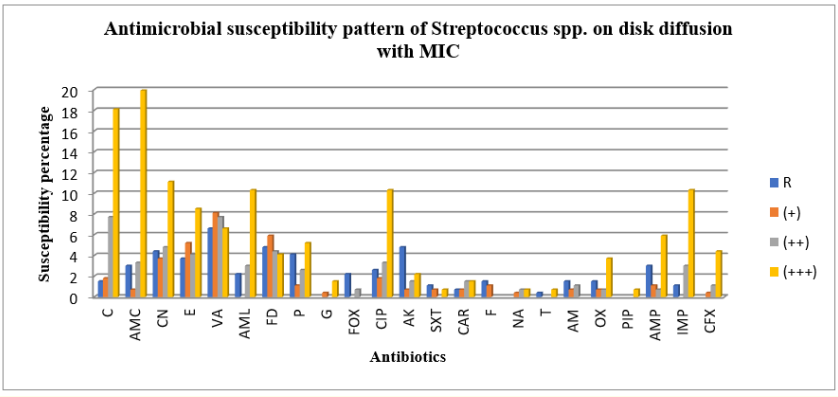

Figure 29: *Antimicrobial susceptibility pattern of Streptococcus spp. on disc diffusion with MIC.*

Discussion

Septicemia, a life-threatening emergency, is a common cause of morbidity and mortality in youngsters, particularly neonates. It poses a serious challenge to pediatricians worldwide, and especially in developing countries such as Libya. In our study, the incidence of microbiologically detected septicemia in clinically suspected patients in NICU was lower (15%) as compared to 44.2% in NICU in Hyderabad, 41.3% in Nepal, 39% in Tanzania and 43.2% in Korea [7-10]. The incidence of septicemia in PICU in our study was 17%, which is lower than the results obtained by Tsering., *et al.* in Sikkim, 36% and Becerra., *et al.* in Lima, Peru 20% [11,12]. The 15% blood culture positivity in neonates with Late Onset Sepsis could be due to relatively high mortality and delay in arrival to a tertiary care center like ours because of low socioeconomic status and rural backgrounds of most patient families [7,13].

Sundaram V and Shrestha., *et al*. reported an increase in the incidence of neonatal sepsis caused by *S. aureus* (43.3% and 56.8% resp.) and a decrease in the incidence of sepsis in neonates caused by gram-negative *bacilli*, our study confirms the same findings [14,15]. A higher number of *Staphylococcus* species were resistant to Erythromycin and Fosfomycin. In our study as well, *Staphylococcus* species were the most common cause of septicemia in NICU (15%), and in PICU (17%). *Staphylococcus aureus* isolates in our study were mostly susceptible to Ciprofloxacin followed by Colistin (Polymyxin E) and Augmentin in contrast to study by Sharma and Srinivasa., *et al*. [16,17] that demonstrated maximum susceptibility of Gram-negative isolates to Colistin followed by Amikacin and Imipenem. These results suggest that the WHO recommended antibiotics Ampicillin and Gentamicin may no longer be effective for the treatment of neonatal sepsis as the sensitivity of *Klebsiella* and *E coli* to these drugs was low.

E. coli and *Klebsiella* spp, like most gram-negative bacteria showed a high resistance to third generation Cephalosporins, and Fluoroquinolones. This was highly in agreement with Movahedian and Aurangzebetal [13,18]. The high resistance of those organisms to third generation Cephalosporins may be attributed to the frequent production of extended spectrum beta lactamase (ESBL) by these organisms. Differences in ESBL production are reportable by varied authors [19,20].

Conclusion

Pediatric sepsis is often preventable by strict adherence of health care workers to the sanitary pointers, particularly hand washing. Screening of health care providers ought to be done and those found infected should be treated. Establishing the national antibiotic policy, with involvement of microbiologists and its subsequent enforcement within the hospitals to stop the indiscriminative use of antibiotics, could improve the clinical outcomes and decrease an economic burden on the patient's family and the hospital system.

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