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TO STUDY AND COMPARE THE ANTIOBIOTIC SENSITIVITY PATTERN OF ORGANISMS INVOLVED IN INFECTIONS IN PATIENTS WITH SEVERE ACUTE MALNUTRITION (SAM).

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ABSTRACT

Severe acute malnutrition (SAM) defined by a very low weight for height (below -3z scores of the median WHO growth standards), is a devastating public health problem of epidemic proportions. Diminished immune functions render undernourished patients more susceptible to multiple infections and many severely malnourished children die from delay inappropriate treatment. This study was undertaken to study the antibiotic senstitivity pattern among organisms causing infections in patients with severe acute malnutrition so as to aid in developing a local antibiogram.

MATERIAL AND METHODS : In this study 72 children aged 6 months-60 months, classified as SAM children as per WHO criteria were included and their blood cultures and antibiotic sensitivity were studied and analysed.

RESULTS AND CONCLUSION : Our study shows that infections in patients with severe acute malnutrition is a common occurrence with gram negative organisms being more than gram positive organisms with E.coli being the most common culprit. As per our study, we recommended that the patients suffering with SAM with associated comorbidities, with high suspicion of sepsis should be started empirically with ceftriaxone or cefotaxime . In case of non improvement , or subtle response vancomycin (if gram positive suspected) or Amikacin (if Gram negative sepsis is suspected) may be added as an additional drug, finally until the blood culture and sensitivity results for the organisms are available.

KEYWORDS Severe acute malnutrition, sepsis, causative organism, antibiotic

INTRODUCTION :

Severe acute malnutrition (SAM) defined by a very low weight for height (below -3z scores of the median WHO growth standards), is a devastating public health problem of epidemic proportions. It is one of the leading causes of morbidity and mortality in childhood. Children with severe malnutrition are at risk of several life threatening problems like hypoglycemia, hypothermia, serious infections and severe electrolyte imbalance. [(1),(2),(3)].

Diminished immune functions render undernourished patients more susceptible to multiple infections and many severely malnourished children die from delay in appropriate treatment.[(4),(5),(6),(7)] Thus, knowing the commonly implicated organisms will be helpful in formulating an effective empirical regimen.

This study was undertaken to study the antibiotic senstitivity pattern among organisms causing infections in patients with severe acute malnutrition so as to aid in developing a local antibiogram.

OBJECTIVE :

To study and compare the antiobiotic sensitivity pattern of organisms involved in infections in patients with severe acute malnutrition (SAM).

MATERIAL AND METHODS :

In this study 72 children aged 6 months-60 months, classified as SAM children as per WHO criteria described before (in introduction), were admitted in pediatrics ward with obvious signs of infections such as hyperthermia, diarrhea, respiratory illness, urinary tract infections or with non obvious signs of infections such as hypothermia, poor oral acceptance, hypoglycemia are included in the study. Children aged below 6 months and above 60 months and whose parent/patient not giving consent were excluded.

Blood samples were collected on admission prior to administration of antibiotics as per the blood culture guidelines for phlebotomist collection of specimen for culture sensitivity. Quantity of blood-1 ml/year of child, in culture broth 10 times the quantity of blood. Site of collection is preferably peripheral vein, an area of 5 cm sterilized with 70% alcohol for 30 seconds in encircling pattern from centre to periphery then widening with 10% betadine for 60 seconds).

Results of culture sensitivity collected.

The information regarding of culture sensitivity reports arranged as systematic data.

OBSERVATIONS AND RESULTS :

TABLE 1
Age wise distribution

AGE	No of cases	Percent
< 1 yr	36	50.0
1-2 yr	31	43.1
>2 yr	5	6.9
Total	72	100.0

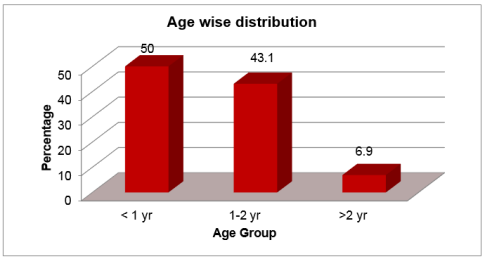

TABLE 2
Sex wise distribution

Sex	No Of Cases	Percent
Female	41	56.9
Male	31	43.1
Total	72	100.0

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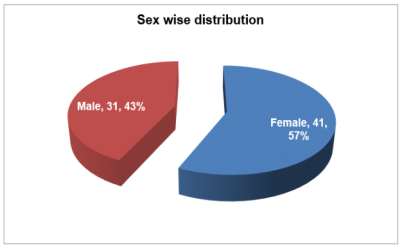


TABLE - 3
Culture positive Organisms Gram staining

	Gram Stain	
	Gram Positive	Gram Negative
Result	26.67%	73.34%

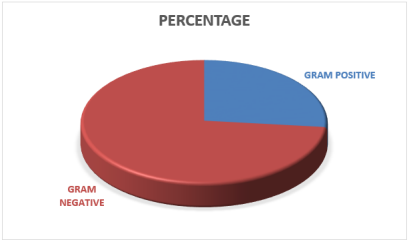


TABLE - 4
Blood culture results

Blood Culture	No of cases	Percent
Positive	30	41.7
Sterile	42	58.3
Total	72	100.0

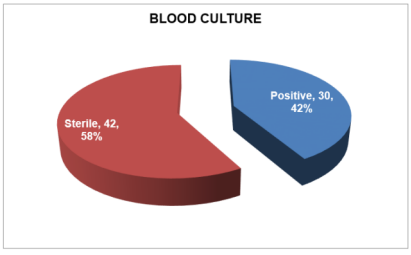


TABLE - 5
Blood culture organisms

Blood Culture Organizms	No of cases	Percent
E.Coli	10	33.34
H Influenzae	1	3.34
Kleibseilla	3	10.0
Non Lactose Fermenter Gram Negative Bacilli R	1	3.34
Proteus	2	6.67
Psuedomonas Aurogenosa	2	6.67
Salmonella	4	13.34
Staph. Aureus	6	20.0
Streptococci Pnuemoniae	1	3.34
Total	30	100.0

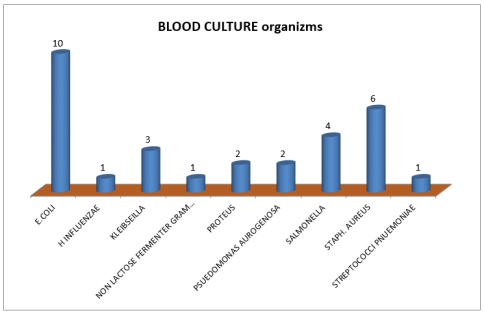
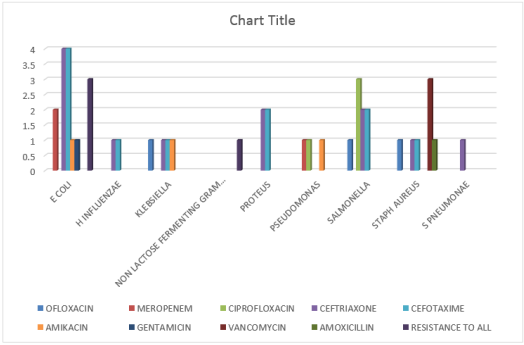


TABLE - 6
Sensitivity to antibiotics

Blood Culture Organizms	Ofloxacin	Meropenem	Cipro	Ceftriaxone	Cefotaxim	Amikacin	Genta	Vanco	Amox	Resistance To All
E.Coli		2		4	4	1	1			3
H Influenzae				1	1					
Kleibseilla	1			1	1	1				
Non Lactose Fermenter Gram Negetive Bacilli R										1
Proteus				2	2					
Psuedomonas Aurogenosa		1	1			1				
Salmonella	1		3	2	2					
Staph. Aureus	1			1	1			3	1	
Streptococci Pnuemoniae				1						



Our study included a total number of 72 cases of severe acute malnutrition with suspected sepsis were admitted and their blood cultures and sensitivity pattern were studied with following results :

1) Children <1 yr constituted 50% (36/72) of cases, whereas children aged between 1-2 yr constituted 43.1% (31/72) and >2 yr 6.9% (5/72) respectively.

2) The cases as per gender are females 56.9% (41/72) and males 43.1% (31/72) respectively.

3) Of the blood culture results in our study, 41.7% (30/72) were culture positive and 58.3% (42/72) were found sterile respectively.

4) Gram negative organisms (73.34%) were more common cause of bactereamia than gram positive ones (26.67%).

5) In positive blood culture results the organisms in decreasing order of frequency are E.Coli 33.34% (10/30), Staph. aureus 20% (6/30),Salmonella 13.24% (4/30), Kleibseilla 10.0% (3/30), Proteus and Psuedomonas aerogenosa 6.67% each. (2/30) and Streptococcous pnuemoniae, H.influenzae, and non-lactose fermenting gram negative bacteriae 3.34% (1/30) each respectively.

6) Of culture positive organisms to different drugs, maximum 40% (12/30) were sensitive to ceftriaxone of which 33.34% (4/12) were E.Coli, 16.67% (2/12) were Proteus and Salmonella each and 8.34% (1/12) each of Kleibseilla, H.influenzae, Staph. aureus and Streptoccus pnuemoniae. 36,67% (11/30) of cases were sensitive to cefotaxime, of which 36.36% (4/11) were E.coli, 18.18% (2/11) were Salmonella and Proteus each, and 9.09% (1/11) were Klebseilla, H.influenzae, and Staph aureus each. 13.34% (4/30) were sensitive to ciprofloxacin of which 75% (3/4) were Salmonella and 25% (1/4) were Psuedomonas aerugenosa. 10% (3/30) of each organisms were sensitive to ofloxacin, meropenem, amikacin, and vancomycin. ofloxacin sensitivity was in 33.34% (1/3) each of Salmonella, H.influenzae, and Staph. aureus.

Among meropenem sensitivity isolates, 66.67% (2/3) were E.Coli and 33.34% (1/3) were Psuedomonas. Among amikacin sensitivity isolated 33.34% (1/3) were E.Coli, Kleibseilla, and Psuedomonas each. Among vancomycin sensitive isolates all (3/3) organisms were Staph aureus.

Among organisms sensitive for gentamicin E.Coli and amoxycillin [Staph. aureus {1/1}] were 3.34% (1/30). 13.34% (4/30) culture positive organisms were resistant to all, of which 75% (3/4) were E.Coli and 25% (1/4) were non lactose fermenting gram negative bacteria.

DISCUSSION :

In our study, the maximum number of patients admitted were 50%(36/72) of <1yr, 43.1% (31/72) between 1-2 year and 6.9% (5/72) >2 year. So the maximum number of patients who were admitted in our set up belonged to < 2 year of age which is nearly 93%. This is in accordance with study done by Mahama Sakaa et al[8] in which the number of patients under two years of age was 63.2% of which 26.4% (92/348) were between 6 -11 months and 36.8% (128/348) patients were between 12-23 months of age.

Regarding sex distribution our study had female prelidiction for admission as 56.9% (41/72) were females and 43.1% (31/72) were males. It is in accordance to national trends of our country having the under five mortality rate higher for females than males. As per SRS 2010, U5MR stood at 64 for females whereas it is 55 for males [3],[9].

In our study blood culture was positive in 42% (30/72) of patients, while culture of 58% (42/72) of patients remained sterile, as compared to studies conducted by Babirekre-Iriso et al[10] who observed the prevalence of bacteremia to be 22% in their study and Noorani et al[11] found 28.9% of their patients to be bacteraemic.

Among the organisms causing bactereamia, gram negative organisms (73.34%) were found to be a more common cause of bactereamia than gram positive ones (26.67%). This is in conjunction with studies conducted by Noorani et al[11], Babirekere-Isors et al[10] found predominance of gram negative organisms (77%) in causing septicemia. Bachou et al[12] too found predominance of gram negative organisms (58%) in causing bactereamia. Others with predominance of gram negative organisms in their studies were Shimles et al[13] with 36%, Berkowitz et al[14] with 19%, and Noorani et al[11]. Whereas gram positive dominance as a cause of sepsis were found in studies of Issac et al[15]. Phillip C. Hill et al[16] estimated 73% organisms as gram positive in causing sepsis.

Our study had E.coli as the predominant organism among bactereamic patients accounting for 33.34% of culture positive patients, followed by Staph aureus in 20% of culture positive patients, Salmonella in 13.34%, Klebseilla in 10%, Proteus and Psuedomonas in 6.67% each and lastly H.influenzae, Streptococcus pnuemoniae and non lactose fermenting gram negative bacilli 3.34% each. Comparing our results to other studies as Babirekerelroso et al[10] had 67% of organisms as E.Coli and Salmonella, Bachou et al[12] found 39.4% Salmonella, 26.3% Staph aureus and 13.2% Streptococcus pneumonia, whereas Issac[15] found Staph aureus, as most common organism in his study.

Of culture positive organisms to different drugs, maximum 40% (12/30) were sensitive to ceftriaxone of which 33.34% (4/12) were E.Coli, 16.67% (2/12) were Proteus and Salmonella each and 8.34% (1/12) each of Kleibseilla, H.influenzae, Staph. aureus and Streptoccus pnuemoniae. 36,67% (11/30) of cases were sensitive to cefotaxime, of which 36.36% (4/11) were E.coli, 18.18% (2/11) were Salmonella and Proteus each, and 9.09% (1/11) were Klebseilla, H.influenzae, and Staph aureus each. 13.34% (4/30) were sensitive to ciprofloxacin of which 75% (3/4) were Salmonella and 25% (1/4) were Psuedomonas aerugenosa. 10% (3/30) of each organisms were sensitive to ofloxacin, meropenem, amikacin, and vancomycin. ofloxacin sensitivity was in 33.34% (1/3) each of Salmonella, H.influenzae, and Staph. aureus.

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CONCLUSION :

Our study shows that infections in patients with severe acute malnutrition is a common occurrence with gram negative organisms being more than gram positive organisms with E.coli being the most common culprit. As per our study, we recommended that the patients suffering with SAM with associated comorbidities, with high suspicion of sepsis should be started empirically with ceftriaxone or cefotaxime . In case of non improvement, or subtle response vancomycin (if gram positive suspected) or Amikacin (if Gram negative sepsis is suspected) may be added as an additional drug, finally until the blood culture and sensitivity results for the organisms are available.

References

1. World Health Organisation Department of child and adolescent Health development Management of the child with serious infection or severe malnutrition Guidelines for care at the first referral level in developing countries. WHO/FCH/CAH/00.
2. National family health survey India 2005-2006.Pg 19.
3. Sample Registration System-2010.
4. Scrimshaw NS, San Giovanni JP, Synergism of nutrition, infection, and immunity; an overview. Am. J. Clin. Nutr. 1997; 66:464S-77S.
5. Ambrus JL, Sr, Ambrus JL Jr (2004). Nutrition and infectious diseases in developing countries and problems of acquired immunodeficiency. Exp. Biol. Med (Maywood) 229: 464-472.
6. Woodward B (1998). Proteins, calories and immune defences: Nutr. Rev. 56: S84-S92.
7. Field CJ, Johnson IR, Schley PD (2002).I Nutrients and their role in host resistance to infections J. Leukoc Biol. 71:16-32.
8. Mahama Saaka, Shaibu Mohammed Osman, Anthony Amponsem, Juventus B. Ziem, Alhassan Abdul-Mumin, Prosper Akanbong, Ernestina Yirkyio, Eliasu Yakubu, and Sean Ervin. Treatment Outcome of Severe Acute Malnutrition cases at the Tamale Teaching Hospital. Journal of Nutr. And Metabolism Volume 2015.
9. Children in India 2012- A Statistical Appraisal Social Statistics Division Central Statistics Office Ministry of statistics and Programme Implementation Government of India. Page 9-40.
10. Babirekere-Iriso, Musoke P, Kekitinwa A. Bacteraemia in severly malnourished in an HIV-endemic setting. Department of Paediatrics, Mulago Hospital, Kampala, Uganda. Ann. Trop. Paediatr. 2006, Dec; 26(4): 319-28.
11. Noorani N, Macharia WM, Oyatsi D, Revathi G. Bacterial isolates in severely malnourished children at Kenyatta. National Hospital, Nairobi, East Afr. Med J. 1994 Apr; 71(4): 264-7.
12. Bachou H, Tylleskar, T, Kaddu Mulindwa DH. Bacteraemia among severely malnourished children infected and uninfected with the human immunodeficiency virus-1 in Kampala, Uganda. BMC Infect Dis. 2006; 6; 160.
13. Shimeles D, Lulseged S; Clinical profile and pattern of infection in Ethiopian children with severe protein-energy malnutrition. Department of Paediatrics and Child Health, Faculty of Medicine, Addis Ababa University, Ethiopia. East Afr. Medical J. 1994 April 71(4): 264-7.
14. Berkowitz FE. Bacteremia in hospitalized black South African children: A one-year study emphasizing nosocomial bacteremia and bacteremia in severely malnourished children. Am. J. Dis. Child. 1984; 138(6): 551-556.
15. Issac H. Pattern of bacterial infections among the severely malnourished in Pediatric wards of Muhimbili Medical Centre. Dissertation for Med. UDSM 1990.
16. Philip C. Hill, Charles O Onyeama, Usman NA, Ikumapayi, Ousman Seeka, Samuel Ameyaw, Naomi Simmonds, Simon A Donkor, Stephen R. Howie, Mary Tapgun,1 Tumani Corrah, 1 and Richard A. Adegbolal Bacteraemia in patients admitted to an urban hospital in West Africa. East Afr. Med J. 2005 Jul; 82(7): 343-8.