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ANTIBIOTICS RESISTANCE PATTERN IN MALNOURISHED CHILDREN SUFFERING FROM ACUTE SEVERE BACTERIAL INFECTIONS AT CMC CHILDREN'S HOSPITAL, LARKANA

Original Research

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ABSTRACT

Background: Severe acute malnutrition (SAM) significantly compromises immunity in children, increasing their vulnerability to life-threatening bacterial infections. These infections often present with nonspecific symptoms and are further complicated by rising antimicrobial resistance. Early detection and understanding of pathogen distribution and antibiotic susceptibility patterns are critical for timely intervention, particularly in resource-limited regions such as Larkana, Pakistan.

Objective: To assess the frequency of acute bacterial infections and determine the antibiotic resistance patterns in children with SAM admitted to healthcare facilities in Larkana.

Methods: A cross-sectional study was conducted from October 2023 to September 2024 at the nutrition ward of Chandka Medical College and a private pediatric facility in Larkana. A total of 105 children aged 5 to 60 months, clinically diagnosed with SAM, were included. Blood samples were collected aseptically before initiating antibiotic therapy. Bacterial identification and antibiotic susceptibility testing were performed using standard microbiological protocols. Demographic, clinical, and laboratory data were recorded and analyzed using SPSS version 25.

Results: Of the 105 children, 67% presented with fever, 63% with diarrhea, 54% with dehydration, 42% with vomiting, 41% with edema, and 30% with cough. Blood cultures were positive in 33 cases (31%). Escherichia coli was the most frequently isolated pathogen (39%), followed by Klebsiella pneumoniae (27%), Staphylococcus aureus (12%), Pseudomonas aeruginosa (9%), and both Streptococcus pneumoniae and Haemophilus influenzae type b (6% each). E. coli showed 85% sensitivity to imipenem, and K. pneumoniae showed 78% sensitivity to amikacin. High resistance was noted against ampicillin and multiple cephalosporins.

Conclusion: Children with SAM, particularly those under one year, are highly susceptible to bacterial infections. The emergence of antibiotic-resistant pathogens underscores the need for localized antibiotic stewardship and evidence-based treatment protocols to improve pediatric outcomes in malnutrition-endemic areas.

Keywords: Anti-Bacterial Agents; Blood Culture; Child, Preschool; Malnutrition; Microbial Sensitivity Tests; Pakistan; Pediatric Infections.

INTRODUCTION

Malnutrition, as defined by the World Health Organization (WHO), is a cellular-level imbalance between nutrient intake and the body's energy demands, often resulting from deficiencies in both macronutrients and micronutrients (1). Although the terms malnutrition and protein-energy malnutrition are sometimes used interchangeably, the latter specifically refers to the most critical form of nutritional deficiency, particularly in young children. Globally, children affected by malnutrition are at significantly greater risk of infections and death, with protein-energy malnutrition implicated in approximately 35% of all deaths among children under the age of five (2,3). Alarmingly, 20–30% of infants experience some degree of malnutrition within the first six months of life, often as a consequence of low birth weight and inadequate postnatal nutrition (4). Growth faltering and nutritional deficiencies typically become clinically apparent between the ages of four to six months, a period during which the immune system is still developing and highly vulnerable. Studies have also noted the presence of septicemia in up to 25% of malnourished children, a condition that underscores the fragile immune function in this population (5). A major challenge in addressing this issue is the lack of a robust, nationwide surveillance system capable of tracking antibiotic resistance patterns in pediatric bloodstream infections, thereby impeding timely and effective therapeutic interventions (6). Severe acute malnutrition compromises immune system development, increasing susceptibility to infections from opportunistic and pathogenic microorganisms (7). It leads to physiological changes in the intestinal lining, including damaged and blunted microvilli, reduced immune cells in Peyer's patches, and lower levels of secretory immunoglobulin A (IgA), collectively known as nutritionally acquired immunodeficiency syndrome (8). This impaired immune defense not only makes children more prone to infections but also perpetuates a vicious cycle where infection exacerbates nutrient loss and further weakens immune response.

Children with malnutrition are particularly vulnerable to infections of the gastrointestinal, respiratory, and urinary tracts due to weakened mucosal integrity, diminished cellular immunity, lower opsonin levels, and reduced phagocytic capacity. Deficiency in essential micronutrients like vitamin A further compromises immune defenses (9,10). In light of this, the WHO recommends the empirical use of antibiotics during the initial management of children with severe acute malnutrition. However, the effectiveness of such interventions is highly contingent upon knowledge of local bacterial prevalence and resistance profiles to guide appropriate antibiotic selection. Given the high morbidity and mortality associated with malnutrition-related infections, particularly in resource-limited settings, this study aims to evaluate the spectrum of bacterial pathogens and their antimicrobial resistance patterns in children suffering from severe acute malnutrition. The objective is to inform more targeted and effective antibiotic strategies that align with local resistance data, ultimately improving clinical outcomes in this vulnerable population.

METHODS

This cross-sectional study was conducted over a 12-month period from October 2023 to September 2024 and involved children diagnosed with Severe Acute Malnutrition (SAM) who were admitted to the nutrition ward of Chandka Medical College and a nearby private healthcare facility in Larkana, Sindh, Pakistan. Ethical approval for the study was obtained from the institutional review board prior to commencement, and written informed consent was obtained from the parents or legal guardians of all participating children. The study enrolled a total of 108 children aged between 5 and 60 months who were clinically diagnosed with SAM and presented with signs of acute bacterial infection upon hospital admission. The inclusion criteria comprised children within the defined age group with confirmed SAM, exhibiting clinical signs of infection, and who had not received antibiotics for more than 48 hours before sample collection. Children with moderate or mild malnutrition, chronic comorbidities, incomplete clinical data, or those who expired before the collection of biological specimens were excluded to ensure data validity and minimize confounding factors. While the inclusion of children who had received antibiotics within 48 hours may slightly affect culture sensitivity, it was deemed necessary for real-world relevance where early empirical antibiotic therapy is standard in acute care (11).

Data collection involved both structured questionnaires and microbiological investigations. The questionnaire captured demographic details, clinical symptoms, nutritional status, medical history, and hospitalization records. Blood samples were collected aseptically prior to the administration of antibiotics to ensure accuracy in identifying causative pathogens. These samples were processed in the hospital's microbiology laboratory using standard culture techniques to isolate bacterial organisms and assess their antibiotic susceptibility profiles

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using disc diffusion and minimum inhibitory concentration (MIC) methods as per Clinical and Laboratory Standards Institute (CLSI) guidelines. All data were initially recorded in Microsoft Excel to maintain organization and accuracy. Following data cleaning and validation, statistical analysis was conducted using SPSS (Statistical Package for the Social Sciences) to determine the frequency of bacterial isolates and evaluate antibiotic sensitivity patterns among the isolates recovered from SAM patients. Descriptive statistics were used to summarize the demographic and clinical characteristics, while frequencies and percentages were calculated to describe pathogen distribution and resistance trends. This methodological approach ensured systematic evaluation of regional bacterial profiles and antibiotic resistance in a vulnerable pediatric population.

RESULTS

A total of 105 children with severe acute malnutrition were included in the study. The age distribution showed that 52% of the children were between 5–13 months, 37% were 14–25 months, and 11% were aged 26–69 months. Male children comprised 59% of the sample, while 41% were female. The majority of participants (57%) belonged to rural areas, and 72% had a history of breastfeeding. Regarding hospitalization, 59% of children stayed for less than 7 days, while 41% had prolonged admissions exceeding one week. Among the clinical presentations observed in children with severe acute malnutrition, fever was the most common symptom, reported in 67% of cases. Diarrhea followed at 63%, dehydration was recorded in 54%, vomiting in 42%, and edema in 41% of cases. Cough was the least commonly reported, present in 30% of the children. Blood cultures collected from these patients indicated that 31% were positive for bacterial growth, confirming bloodstream infection, while 69% were culture-negative. Escherichia coli emerged as the most prevalent bacterial isolate, accounting for 39% of the positive cultures. Klebsiella pneumoniae was found in 27% of cases, Staphylococcus aureus in 12%, and Pseudomonas aeruginosa in 9%. Streptococcus pneumoniae and Haemophilus influenzae type b were each detected in 6% of the cases.

Analysis of antibiotic susceptibility patterns in the 33 culture-positive cases revealed that Escherichia coli (n=13) showed 85% sensitivity to imipenem and nitrofurantoin, while demonstrating resistance to ampicillin and ceftriaxone. Klebsiella pneumoniae (n=9) was 78% sensitive to amikacin and meropenem but exhibited high resistance to cefotaxime and ampicillin. Pseudomonas aeruginosa (n=3) isolates were 67% sensitive to piperacillin-tazobactam and tobramycin, with notable resistance to ceftazidime and cefepime. Staphylococcus aureus (n=4) showed 75% susceptibility to vancomycin and linezolid and was commonly resistant to penicillin and erythromycin. All isolates of Streptococcus pneumoniae (n=2) and Haemophilus influenzae type b (n=2) were 100% sensitive to ceftriaxone and levofloxacin, and azithromycin and cefuroxime respectively, with consistent resistance to tetracycline, trimethoprim, ampicillin, and chloramphenicol depending on the organism. Subgroup analysis of culture positivity across demographic variables revealed notable differences in infection rates. Among children aged 5–13 months, 33% (18 out of 54) had positive blood cultures, compared to 28% (11 out of 39) in the 14–25 months group and 33% (4 out of 12) in the 26–69 months group. Gender-based comparison showed a slightly higher culture positivity in males (31%, 19 out of 62) than females (33%, 14 out of 43). Hospital stay duration also influenced infection prevalence, with 29% (18 out of 62) of those staying longer than 7 days showing culture positivity, compared to 24% (15 out of 62) in those discharged earlier.

Table 1: Demographic Overview of Pediatric Patients with Severe Acute Malnutrition

Variable	Category	Frequency (n=105)	%
Age (Years)	05-13	54	52
	14-25	39	37
	26-69	12	11
Gender	Male	62	59
	Female	43	41
Residency	Rural	60	57
	Urban	45	43
Feeding	Breastfeeding	76	72
	Not Breastfeeding	28	28
Hospital Stay Duration	<7 Days	62	59
	>7 Days	43	41

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Table 2: Antibiotic Susceptibility and Resistance Patterns of Bacterial Isolates Identified in Clinical Samples

Organism	No of Isolates	Most Effective Antibiotics	Sensitivity rate (%)	Sensitive cases	Frequently Resistant To
Escherichia coli (E. coli)	13	Imipenem, Nitrofurantoin	85%	11	Ampicillin, Ceftriaxone
Klebsiella pneumoniae	9	Amikacin, Meropenem	78%	7	Cefotaxime, Ampicillin
Pseudomonas aeruginosa	3	Piperacillin-Tazobactam, Tobramycin	67%	2	Ceftazidime, Cefepime
Staphylococcus aureus	4	Vancomycin, Linezolid	75%	3	Penicillin, Erythromycin
Streptococcus pneumoniae	2	Ceftriaxone, Levofloxacin	100%	2	Tetracycline, Trimethoprim
Haemophilus influenzae (type b)	2	Azithromycin, Cefuroxime	100%	2	Ampicillin, Chloramphenicol

Table 3: Subgroup Analysis of Culture Positivity

Variable	Category	Total Cases	Culture Positive (n)	Culture Positive (%)
Age Group (months)	05–13	54	18	33.3%
	14–25	39	11	28.2%
	26–69	12	4	33.3%
Gender	Male	62	19	30.6%
	Female	43	14	32.6%
Hospital Stay Duration	<7 Days	62	15	24.2%
	>7 Days	43	18	41.9%

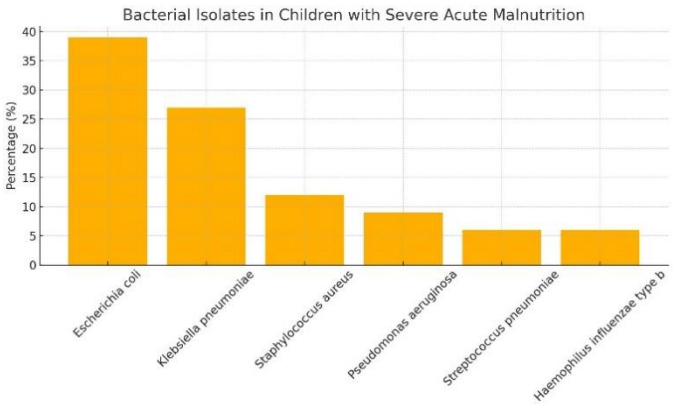


Figure 1 Bacterial Isolates in Children with Severe Acute Malnutrition

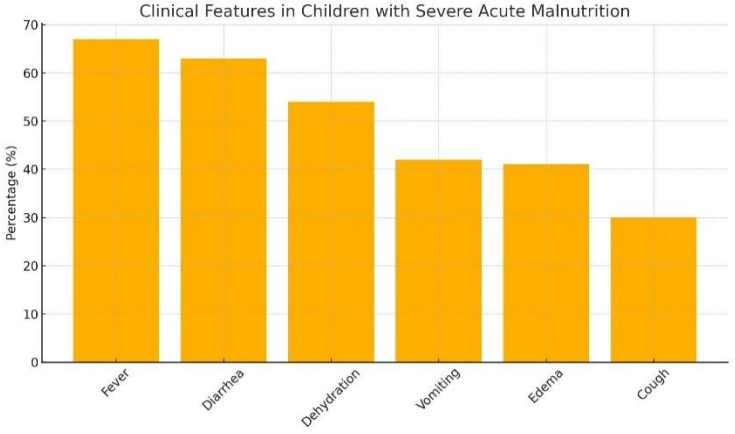
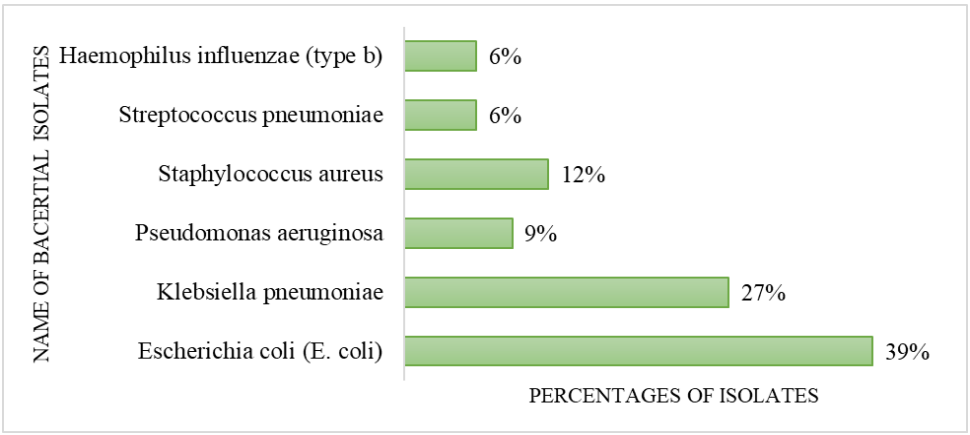
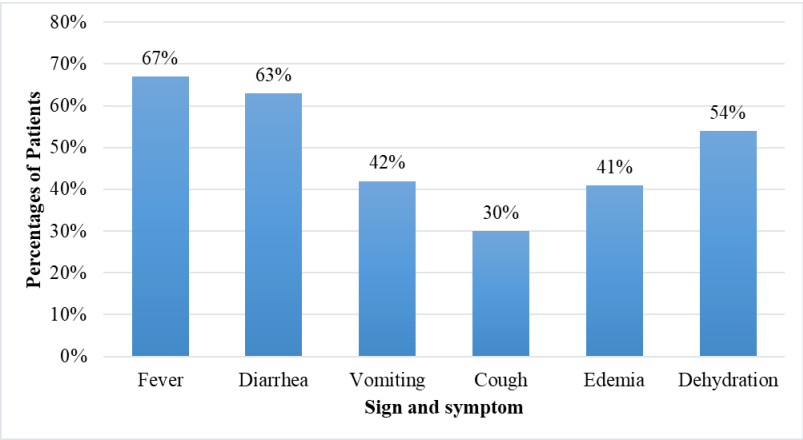
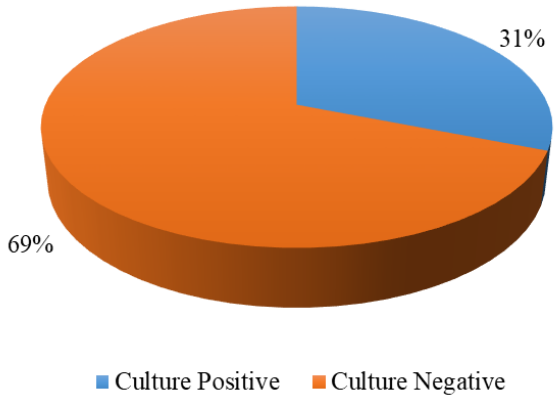


Figure 2 Clinical Features in Children with Severe Acute Malnutrition







DISCUSSION

This study evaluated 105 children aged 5 to 60 months diagnosed with severe acute malnutrition (SAM), revealing key insights into the age-related vulnerability, clinical manifestations, and microbiological profiles associated with SAM-related infections. The highest frequency of SAM was observed in children aged 6 to 12 months, accounting for 38% of cases. This finding may be linked to early cessation of breastfeeding, delayed initiation of complementary feeding, and inadequate intake of essential nutrients during a critical developmental window (12,13). The mean age of participants was 20.47 ± 13.13 months, and although gender distribution showed a slight male predominance (59%), infection rates remained similar across both sexes, reflecting the non-gendered nature of malnutrition-associated immune compromise. Fever emerged as the most frequently reported symptom, contrasting with findings from other studies where respiratory symptoms were more dominant (14). This difference may be attributed to the immunosuppressive nature of malnutrition, which blunts the classical signs of infection, leading to less pronounced respiratory manifestations despite the presence of underlying disease. The study emphasized the high burden of bacterial infections in malnourished children, particularly gastroenteritis, respiratory tract infections, bloodstream infections, and urinary tract infections. Gastroenteritis was particularly prevalent, often resulting from bacterial overgrowth in the small intestine and presenting as watery diarrhea with varying degrees of dehydration (15,16). Dehydration not only worsens anthropometric indicators such as body weight and mid-upper arm circumference but also increases the risk of mortality if not promptly addressed. Respiratory infections also posed a diagnostic challenge in this cohort due to atypical or muted clinical presentations. Infections such as measles and tuberculosis were commonly associated with SAM, with measles being closely linked to vitamin A deficiency (17).

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Blood cultures revealed a 31% positivity rate, which was considerably higher than that reported in comparable studies, such as one from Niger that reported a 9.1% rate (18). This higher yield may be explained by timely blood collection before antibiotic initiation, ensuring more accurate detection of bloodstream infections. Among the isolates, Escherichia coli was the most frequently identified pathogen, consistent with trends observed in similar pediatric settings (19). E. coli demonstrated high susceptibility to imipenem and nitrofurantoin but exhibited resistance to commonly used agents such as ampicillin and ceftriaxone. These resistance patterns align with regional data on extended-spectrum beta-lactamase (ESBL) producing strains, which complicate treatment regimens and call for routine susceptibility testing to guide empirical therapy (20). Klebsiella pneumoniae, the second most common isolate, also displayed resistance to older beta-lactam antibiotics but retained susceptibility to amikacin and meropenem, reflecting antimicrobial sensitivity patterns previously noted in low- and middle-income countries (19,20). Pseudomonas aeruginosa, though less frequently isolated, showed favorable responses to piperacillin-tazobactam and tobramycin, supporting their continued utility in high-risk patients. However, resistance to third-generation cephalosporins remains a growing concern, particularly in pediatric intensive care settings (21). Staphylococcus aureus was responsive to vancomycin and linezolid, which remain reliable options for treating methicillin-resistant strains. These results support existing recommendations advocating the use of glycopeptides and oxazolidinones in resistant staphylococcal infections (19,21).

The study provides valuable regional data on pathogen profiles and antibiotic sensitivity in children with SAM, offering actionable evidence to guide empirical treatment strategies. One of its strengths lies in the pre-antibiotic timing of blood sample collection, enhancing culture accuracy. Additionally, the study's focus on a vulnerable population with limited prior exposure to antibiotics strengthens the reliability of resistance data. However, the study had limitations, including its single-region setting, which may reduce generalizability. Furthermore, data on clinical outcomes such as recovery time, mortality, or antibiotic response were not collected, limiting the assessment of therapeutic effectiveness. The absence of advanced diagnostic tools, such as molecular assays, may have resulted in underdiagnosis of fastidious organisms. Future research should include multicentric data with larger sample sizes, outcome tracking, and molecular resistance profiling. There is also a need to integrate routine antibiotic stewardship programs in pediatric nutrition wards to curb the development of resistance. Overall, this study underscores the urgent need for targeted antibiotic protocols based on local resistance patterns to improve the management and outcomes of infections in children with severe acute malnutrition.

CONCLUSION

This study concludes that children suffering from severe acute malnutrition are particularly vulnerable to bacterial infections, with common clinical signs including fever, diarrhea, and dehydration. The findings highlight the predominance of gram-negative organisms such as Escherichia coli and Klebsiella pneumoniae, which demonstrated notable antibiotic sensitivity patterns. These outcomes underscore the critical need for routine blood culture testing, locally tailored antibiograms, and evidence-based treatment protocols to ensure timely and appropriate management. Strengthening diagnostic practices and antimicrobial stewardship in pediatric nutrition wards can significantly enhance clinical outcomes for this high-risk population.

AUTHOR CONTRIBUTION

Author	Contribution
Ishfaque Ahmed Mugher*	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Delijan Mugheri	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Beenish Ghafar	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Ammar Ali	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Vinay Kumar Jesrani	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Abdul Jabbar Mugheri	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published

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