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Sputum Culture Patterns in Children with Severe Acute Malnutrition (SAM) Admitted in A Paediatric Ward of A Tertiary Care Hospital

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Abstract

Background: Severe Acute Malnutrition (SAM) remains a major public health challenge in developing countries and is associated with increased susceptibility to infections, particularly respiratory tract infections. Pneumonia is a leading cause of morbidity and mortality among malnourished children. Microbiological evaluation of respiratory specimens such as sputum culture helps in identifying causative pathogens and guiding appropriate antimicrobial therapy.

Objectives: To analyze sputum culture positivity, bacteriological profile, and antimicrobial susceptibility patterns among children diagnosed with Severe Acute Malnutrition admitted to a paediatrics inpatient department.

Materials and Methods: This retrospective, record-based observational study was conducted in the

Paediatrics ward of a tertiary care teaching hospital. Inpatient records of 25 children aged 6–59 months diagnosed with SAM and subjected to sputum culture for clinically suspected lower respiratory tract infection were reviewed. Sputum samples were processed using standard microbiological techniques. Organism identification and antimicrobial susceptibility testing were performed according to CLSI guidelines.

Results: Out of 25 SAM children, sputum culture was positive in 14 cases (56%). Gram-negative bacilli predominated. Klebsiella pneumoniae was the most common isolate followed by Staphylococcus aureus and Pseudomonas aeruginosa. High resistance was observed to ampicillin and first-generation cephalosporins, while better sensitivity was noted with aminoglycosides and third-generation cephalosporins.

Conclusion: Children with SAM are highly susceptible to severe respiratory infections caused predominantly by Gram-negative organisms. Periodic surveillance of sputum culture patterns in SAM is essential for rational antibiotic use and reduction of mortality.

Keywords: Severe acute malnutrition, SAM, sputum culture, pneumonia, paediatrics, retrospective study

Introduction

Severe Acute Malnutrition (SAM) is a life-threatening condition affecting millions of children worldwide, particularly in low- and middle-income countries. According to the World Health Organization, SAM is defined by a weight-for-height Z-score less than −3, visible severe wasting, or presence of nutritional edema [1]. Malnutrition compromises both innate and adaptive immunity, predisposing children to frequent and severe infections.

Respiratory tract infections, especially pneumonia, are the most common causes of hospitalization and death among children with SAM[2]. Altered immune responses, micronutrient deficiencies, and impaired mucosal barriers contribute to increased vulnerability to bacterial pathogens [3].

Microbiological diagnosis in SAM-associated pneumonia is challenging due to atypical clinical presentation and overlapping symptoms. Sputum culture, though technically difficult in young children, provides valuable information regarding the etiological agents and their antimicrobial susceptibility patterns [4].

Understanding the local bacteriological profile of respiratory infections in SAM children is crucial for guiding empirical therapy, reducing antimicrobial resistance, and improving clinical outcomes. The present study was undertaken to analyze sputum culture patterns among SAM children admitted to a Paediatrics ward.

Materials and Methods

Study Design- Retrospective, record-based observational study.

Study Setting- Department of Paediatrics in collaboration with the Department of Microbiology at a tertiary care teaching hospital.

Study Duration- Records over a period of 18 months were reviewed.

Study Population- A total of 25 children diagnosed with Severe Acute Malnutrition and admitted to the paediatrics inpatient department with clinical suspicion of lower respiratory tract infection were included.

Inclusion Criteria

- Children aged 6–59 months
- Diagnosed with Severe Acute Malnutrition as per WHO criteria
- Admitted in paediatrics IPD
- Sputum sample sent for culture and sensitivity

Exclusion Criteria

- Incomplete medical or microbiology records

- Children already on antibiotics for more than 72 hours prior to sample collection
- Known congenital lung disease or immunodeficiency

Ethical Considerations-Approval was obtained from the Institutional Ethics Committee.

Sample Collection and Microbiological Processing

Sputum Collection

- Expectorated or induced sputum samples
- Collected in sterile, leak-proof containers
- Samples transported immediately to the microbiology laboratory

Culture and Identification

- Gram staining for sample adequacy
- Culture on Blood agar and MacConkey agar
- Incubation at 37°C for 18–24 hours
- Identification based on colony morphology, Gram stain, and standard biochemical tests

Antimicrobial Susceptibility Testing

- Kirby–Bauer disc diffusion method
- Interpretation as per CLSI guidelines [5]

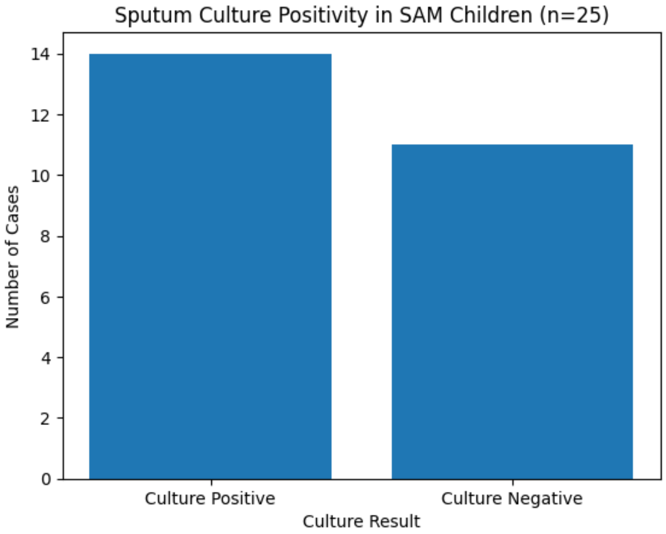
Results

Demographic Profile

Parameter	Number (%)
Total cases	25
Male	14 (56%)
Female	11 (44%)
Mean age	22.4 ± 10.6 months

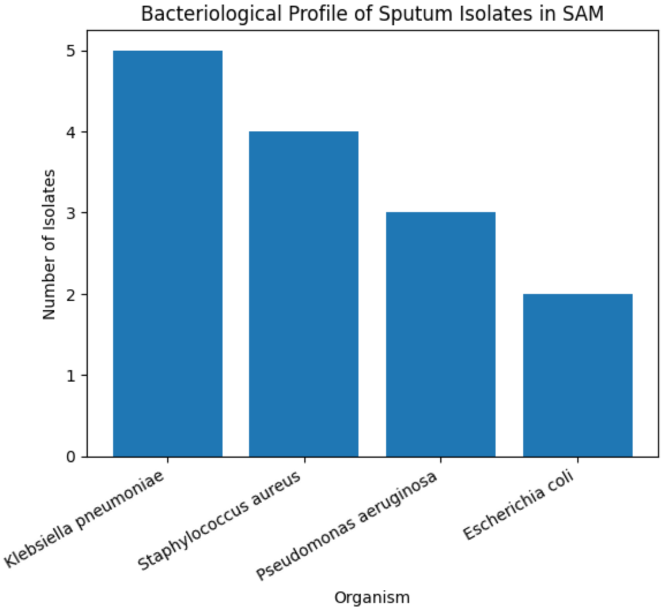
Sputum Culture Positivity-

- Culture positive: 14 cases (56%)
- Culture negative: 11 cases (44%)

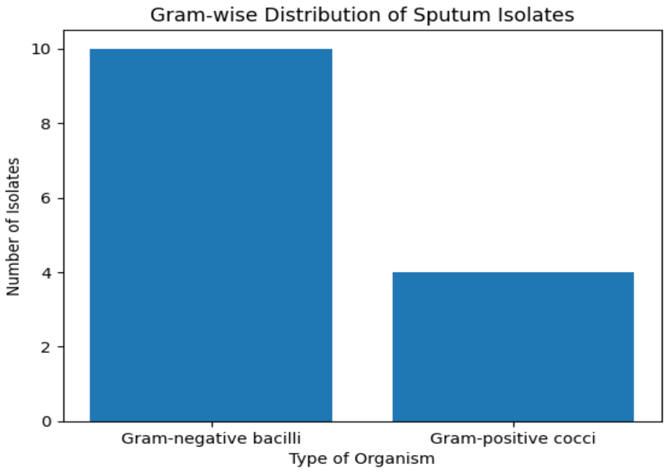


Bacteriological Profile of Isolates-

Organism	Number (%)
Klebsiella pneumoniae	5 (35.7%)
Staphylococcus aureus	4 (28.6%)
Pseudomonas aeruginosa	3 (21.4%)
Escherichia coli	2 (14.3%)



- Gram-negative bacilli: 10 (71.4%)
- Gram-positive cocci: 4 (28.6%)



Antimicrobial Susceptibility Pattern-

Gram-negative isolates

- High resistance: Ampicillin, Cotrimoxazole
- Moderate sensitivity: Cefotaxime, Ciprofloxacin
- High sensitivity: Amikacin, Piperacillin–tazobactam

Gram-positive isolates

- Staphylococcus aureus showed good sensitivity to clindamycin and vancomycin
- Methicillin resistance noted in one isolate

Discussion

The present retrospective study highlights a high sputum culture positivity rate (56%) among SAM children with respiratory symptoms, emphasizing their vulnerability to bacterial infections. Similar findings have been reported in previous studies where malnutrition was strongly associated with severe pneumonia and bacterial isolation [6,7].

Klebsiella pneumoniae emerged as the predominant pathogen, consistent with hospital-based studies reporting Gram-negative predominance in malnourished children [8]. The isolation of Pseudomonas aeruginosa suggests possible nosocomial acquisition or prolonged hospitalization.

High resistance to commonly used first-line antibiotics such as ampicillin raises concern and underscores the need for culture-guided therapy. Aminoglycosides and extended-spectrum beta-lactams demonstrated better efficacy, supporting their role in severe infections among SAM children [9].

Limitations

- Small sample size
- Retrospective design
- Single-center study
- Viral and atypical pathogens were not assessed

Conclusion

Children with Severe Acute Malnutrition admitted to paediatrics wards show a high burden of bacterial respiratory infections. Gram-negative organisms predominate, with significant antimicrobial resistance. Routine sputum culture and periodic surveillance of pathogen patterns are essential for optimizing antimicrobial therapy and improving survival in SAM children.

Recommendations

- Early microbiological evaluation in SAM children with respiratory symptoms
- Judicious use of antibiotics based on local antibiogram
- Strengthening infection control practices in paediatrics wards

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