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Rates of bacteremia among children presenting with highland malaria in Vihiga County, Kenya

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ABSTRACT

Malaria remains a major cause of pediatric morbidity and mortality in sub-Saharan Africa. In highland regions like Vihiga County, Kenya, where malaria transmission is unstable, children are especially vulnerable to severe disease and complications. Bacteremia is an increasingly recognized co-infection in children with malaria, yet its burden and clinical profile in highland settings remain poorly characterized. This study aimed to determine the prevalence and distribution of bacterial pathogens among children diagnosed with malaria in Vihiga County and to evaluate the association between sociodemographic and clinical characteristics and the occurrence of bacteremia in this population. A cross-sectional study was conducted among children aged ≤60 months presenting with malaria. Blood samples were collected for malaria microscopy, full blood counts, and aerobic blood cultures. Data on clinical and demographic variables were analyzed using descriptive statistics and logistic regression to determine associations with bacteremia. Out of 312 children with malaria, 34 (10.9%) were bacteremic. The most commonly isolated pathogens were non-typhoidal Salmonella spp. (44.1%), Escherichia coli (23.5%), and Staphylococcus aureus (14.7%). Significant predictors of bacteremia included age below 12 months (Odds Ratio [OR] = 2.3, 95% Confidence Interval [CI]: 1.3–4.1), high-grade fever (OR = 2.2, 95% CI: 1.1–4.0), pallor (OR = 2.8, 95% CI: 1.4–5.3), respiratory distress (OR = 3.4, 95% CI: 1.8–6.4), severe anemia (OR = 2.9, 95% CI: 1.5–5.6), underweight status (OR = 2.1, 95% CI: 1.2–3.5), and hospitalization (OR = 3.6, 95% CI: 2.0–6.2). Bacteremia was associated with significantly longer hospital stays and higher mortality (17.6% vs. 0.4%). The prevalence and pathogen profile of bacteremia in Vihiga County mirror those of other high-burden settings in Africa, with non-typhoidal Salmonella predominating. Clinical predictors identified in this study are consistent with previous literature and highlight the difficulty of clinically distinguishing malaria from co-infection in resource-limited settings. Bacteremia is a common and clinically significant co-infection among children with malaria in Vihiga County. It is associated with severe clinical manifestations and poor outcomes. Routine blood culture diagnostics should be integrated into pediatric malaria care in high-risk areas. Additionally, risk-based clinical screening tools should be implemented to guide early empirical antibiotic treatment for children presenting with malaria and features suggestive of bacteremia.

Keywords: Bacteremia, Highland Malaria, Malaria, Non-Typhoidal Salmonella, Pediatric Co-Infection

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I. INTRODUCTION

In sub-Saharan Africa, malaria continues to be a major cause of morbidity and mortality in children under five (Sarfo et al., 2023). Infections caused by malaria place a significant burden on communities and health systems (Andrade et al., 2022; Elnour et al., 2023). Malaria rates in this susceptible group have decreased in Kenya as a result of the national malaria control program's (NMCP) efforts (Nyawanda et al., 2024). However, because of unstable and epidemic-prone transmission, highland areas like Vihiga County continue to see sporadic outbreaks (Ahmed et al., 2020; Jumba et al., 2025). The varying incidence of malaria in these areas is associated with variations in climate, altitude, and ecosystem dynamics. Due to this, people in such areas are immunologically naive and often vulnerable during periods of high transmission (Jumba et al., 2025; Jumba et al., 2024). According to Opoka et al. (2024), children in these environments are especially susceptible to malarial sequelae such as severe anemia, cerebral malaria, hyperparasitemia, and co-infections (Opoka et al., 2024).

Bacteremia, or the presence of live bacteria in the circulation, is one such co-infection that has emerged as a prevalent clinical problem (Smith & Nehring, 2025). It exacerbates systemic inflammation by impairing immunological responses and raising the possibility of adverse clinical outcomes (Donnelly et al., 2021). Bacteremia prevalence rates among children range from 6% to 12%, according to several studies conducted in western Kenya, particularly in areas with ecological similarities to Vihiga (Otambo et al., 2022; Salgado et al., 2021). Non-typhoidal Salmonella (NTS) species are commonly isolated and are typically associated with intestinal mucosal injury and hemolysis caused by malaria, which facilitates bacterial translocation (Nyirenda et al., 2018). *Escherichia coli* and *Staphylococcus aureus* are two other frequently isolated pathogens (Barua et al., 2024). Due to overlapping clinical signs and limited availability of microbiological testing in rural health institutions, the coexistence of bacteremia and malaria presents diagnostic and therapeutic challenges (Wilairata et al., 2022).

Despite the clinical significance of co-infections between malaria and bacteremia, there is a lack of information specific to highland areas like Vihiga County. Understanding the burden and bacterial causes of these co-infections in this population is crucial for improving antimicrobial stewardship, minimizing childhood mortality, and guiding empirical treatment protocols. The purpose of this study was to determine the prevalence of bacteremia in children in Vihiga County diagnosed with malaria and to examine the associated clinical characteristics and outcomes.

1.1 Statement of the Problem

Malaria is one of the leading causes of morbidity and mortality among children in sub-Saharan Africa, despite significant progress in its control. This is especially true in highland areas like Vihiga County, Kenya, where malaria transmission is unstable. Bacteremia is a prevalent and frequently neglected co-infection in children with malaria, according to an increasing number of studies. It increases the risk that the condition will be severe and possibly fatal. There is limited data on the load, variety, and clinical manifestations of bacteremia in children with malaria in highland environments like Vihiga. It is more probable that diagnoses will be missed or delayed, treatments will be incorrect, and results will be poor due to the lack of routine blood culture tests, restricted empirical antibiotic guidelines, and a lack of local data on how co-infections function together. This lack of knowledge and professional practice makes it more difficult to care for children and places more pressure on health systems. Determining the prevalence of bacteremia and the clinical manifestations in children with malaria residing in highland locations is crucial. Focused diagnostic, therapeutic, and policy measures that seek to reduce childhood mortality will benefit from this information.

1.2 Research Objectives

i. To determine the prevalence and distribution of bacterial pathogens among children diagnosed with malaria in Vihiga County, Kenya.
ii. To evaluate the association between sociodemographic and clinical characteristics and the occurrence of bacteremia in children with malaria.

II. LITERATURE REVIEW

2.1 Theoretical Review

2.1.1 Burden of Pediatric Malaria in Sub-Saharan Africa

In sub-Saharan Africa, malaria continues to be one of the leading causes of sickness and mortality among children. This region accounts for over 90% of all malaria cases and fatalities (WHO, 2021). Since their immune systems are still maturing, children under five are particularly vulnerable (Mambo et al., 2023). In highland regions such as Vihiga County, Kenya, malaria transmission is erratic and frequently prone to epidemics. Due to intermittent exposure to malaria, residents in these locations have lower levels of acquired immunity and are more likely to become critically ill during outbreaks (Ahmed et al., 2020). Despite ongoing efforts to control the disease, it remains a significant issue for communities and health systems in these transitory zones.

2.1.2 Bacteremia in Children with Malaria

Recent data indicates that bacteremia is a severe yet frequently unrecognized side effect of childhood disease. Between 6% and 12% of children with a malaria diagnosis also have bacterial bloodstream infections at the same time, according to research from Tanzania (Moyo et al., 2020), Burkina Faso (Maltha et al., 2014), and Kenya (Masika et al., 2017). In locations where blood cultures aren't performed frequently, it might be challenging to distinguish between severe malaria and bacteremia because they frequently have similar appearances. The risk of negative consequences, including prolonged hospital admissions and mortality, is significantly increased. Perhaps because malaria weakens the gut barrier, decreases the immune system, and promotes hemolysis, non-typhoidal Salmonella (NTS) is more likely to be prevalent (Nyirenda et al., 2018).

2.1.3 Clinical Predictors and Implications for Case Management

Various clinical and demographic factors have been identified as predictors of bacteremia in pediatric malaria cases. Criteria include age under 12 months, presence of high-grade fever, difficulty in breathing, pallor, severe anemia, and malnutrition (Andersen et al., 2022; Anjorin et al., 2023). These characteristics are common in children with severe malaria, complicating the differentiation between uncomplicated malaria and co-infection. In the absence of microbiological tests, the selection of empirical antibiotic treatment is a critical and challenging decision (Ochayo et al., 2023; Wamalwa et al., 2024). The WHO guidelines currently lack specific recommendations for the simultaneous treatment of malaria and bacteremia, resulting in variability in treatment approaches across different endemic regions. Understanding local pathogen profiles and their clinical implications is essential for developing evidence-based management protocols, thus lowering preventable deaths in this vulnerable population.

III. METHODOLOGY

3.1 Study Design and Population

This cross-sectional study involved 312 children under five years of age diagnosed with malaria who attended healthcare facilities in the Vihiga Highlands of Western Kenya. The study population was categorized into two groups based on clinical diagnostic criteria: individuals with malaria (n = 278) and individuals with both malaria and bacteremia (n = 34).

3.2 Study Site

This research utilized samples obtained from Vihiga District Hospital in Western Kenya, a region characterized by intermittent transmission of *Plasmodium falciparum* malaria. The elevation above sea level varies between 1,300 m and 1,500 m (Ahmed et al., 2020). The malaria incidence rate from March to May is 27%.

3.3 Sample Size and Sampling Technique

This study utilized a systematic random sampling design, with the initial cases elected randomly from children with *P. falciparum* malaria seeking treatment at the hospital. The *k*th case subsequent to the initial point adhered to a systematic selection process. The *k*th case denotes the sampling interval, determined by dividing the estimated population (N) of children with *P. falciparum* malaria in Vihiga, reported as 7,125 (Ahmed et al., 2020), by the sample size (n) of 312. Consequently, every fifth case of malaria was selected until a sample size of 312 was achieved. The sample size was established according to Cochran (1977):

$$n = \frac{Z^2 p(1-p)}{e^2}$$

$n=1.96^2*0.27(1-0.27)/0.05^2$

Where:

n is the sample size, Z is normal deviation at desired confidence interval (1.96), *P* is the proportion of the cases (27%), I^2 is the degree of precision (5%)
= 312

3.4 Ethical Consideration

This protocol has been approved by the Masinde Muliro University of Science and Technology Institutional Ethical Review Committee, with the protocol number MMUST/IERC/021/2021. The study was authorized by the National Council on Science and Technology (NACOSTI) under license number NACOSTI/P/21/14703. All participants provided signed consent forms.

3.5 Data Collection

Children aged ≤60 months presenting with clinical features of malaria and confirmed *Plasmodium falciparum* infection via rapid diagnostic test (RDT) and microscopy were enrolled consecutively. Written informed consent was obtained from parents or guardians prior to inclusion in the study. A structured questionnaire was used to collect demographic information, presenting symptoms, nutritional status, and history of prior antibiotic use.

Comprehensive clinical assessments included measurement of temperature, weight, height/length, mid-upper arm circumference (MUAC), and respiratory rate. Blood samples were drawn aseptically for full blood count, malaria parasite quantification, and aerobic blood culture using standard pediatric blood culture bottles. The cultures were incubated and monitored for up to five days, and positive cultures were sub-cultured and identified using standard biochemical tests. Contaminants such as coagulase-negative staphylococci were excluded based on clinical correlation and repeat cultures. Data on treatment modalities, duration of hospital stay, need for blood transfusion, and in-hospital outcomes (discharge or death) were recorded.

3.6 Data Analysis

Data entry and analysis were conducted using SPSS version 25. Categorical variables were summarized using frequencies and percentages, while continuous variables were summarized using means or medians with interquartile ranges. Associations between bacteremia and clinical variables were tested using chi-square tests and logistic regression models. A P-value < 0.05 was considered statistically significant.

IV. FINDINGS & DISCUSSIONS

4.1 Demographic and Clinical Characteristics between Malaria-Only and Malaria–Bacteremia Groups

A total of 312 children were enrolled in the study. Out of the total, 34 children (10.9%) were found to have bacteremia. Table 1 presents a comparative analysis of demographic and clinical characteristics between children with malaria only and those co-infected with malaria and bacteremia. The findings reveal that children with both malaria and bacteremia were significantly younger, with a median age of 7.4 months compared to 9.3 months among those with malaria alone. Although the proportion of males was slightly higher in the co-infected group (55.9% vs. 53.0%), this difference was not statistically significant. Clinically, children with bacteremia exhibited more severe presentations. They had significantly higher fevers, with a median temperature of 39.2°C compared to 38.5°C in the malaria-only group. Pallor was also more prevalent in co-infected children (73.0% vs. 51.0%), suggesting a greater burden of anemia. Similarly, respiratory distress was observed in nearly half (47.0%) of the children with bacteremia, compared to only 20.0% of those with malaria alone. These findings point to a heightened severity of illness in the presence of bacteremia.

The study also found that severe anemia was more pronounced in co-infected children, with lower median hemoglobin levels (5.9 g/dL) than in those with malaria alone (6.5 g/dL). Nutritional status, assessed using WHO Z-scores, revealed that children with bacteremia were more underweight (median Z-score: -2.3) than their counterparts (-1.9), indicating a potential link between malnutrition and susceptibility to bacterial infections. In terms of health service utilization, children with both infections were more likely to be hospitalized (85.0% vs. 59.0%) and had longer hospital stays (6.5 days vs. 4.0 days), reflecting the complexity and severity of their clinical condition. The mortality rate among children with bacteremia was substantially higher at 17.6%, compared to just 0.4% in those with malaria alone.

Table 1
Showing Demographic and Clinical of the Study Participants

Characteristic	Malaria, n =278	Malaria + Bacteremia, n =34	*P*
Age, mos	9.3 (4.2)	7.4 (5.1)	<0.001[a]
Male gender, no. (%)	147 (53.0)	19 (55.9)	0.770[b]
High grade fever, (>39.0 ˚C)	38.5 (0.8)	39.2 (0.9)	0.030[a]
Pallor, no. (%)	142 (51.0)	25 (73.0)	0.020[b]
Respiratory distress, no. (%)	56 (20.0)	16 (47.0)	0.010[b]
Severe anemia, (Hb <6 g/dl)	6.5 (0.7)	5.9 (0.6)	0.020[a]
Underweight (WHO Z-score)	-1.9 (0.3)	-2.3 (0.4)	0.030[a]
Hospitalization, no. (%)	164 (59.0)	29 (85.0)	<0.001[b]
Hospital stay, (days)	4.0 (1.0)	6.5 (1.2)	<0.001[a]
Mortality, no. (%)	1.0 (0.4)	6.0 (17.6)	0.040[b]

Demographic and clinical characteristics of study participants, comparing malaria and malaria with bacteremia. Data analysis was conducted using [a]Mann-Whitney-U test for continuous and [b]Chi-square for categorical data. Values in bold are significant *P*-values.

4.2 Distribution of Isolated Bacteria in Co-Infected Children

Data on the distribution of bacterial pathogens isolated from children with bacteremia is presented in Figure 1 below. The figure shows that non-typhoidal Salmonella was the most frequently isolated organism, accounting for 15 of the total isolates, which represents nearly half of all identified pathogens. This finding reinforces the well-documented association between malaria and invasive non-typhoidal Salmonella infections, particularly in endemic regions. *Escherichia coli* was the second most common isolate with 8 occurrences, indicating its significance as a bloodstream pathogen in co-infected children, potentially linked to gastrointestinal translocation under conditions of immune compromise or mucosal barrier dysfunction. *Staphylococcus aureus* was identified in 5 cases, while *Klebsiella pneumoniae* and other miscellaneous bacteria each accounted for 3 isolates.

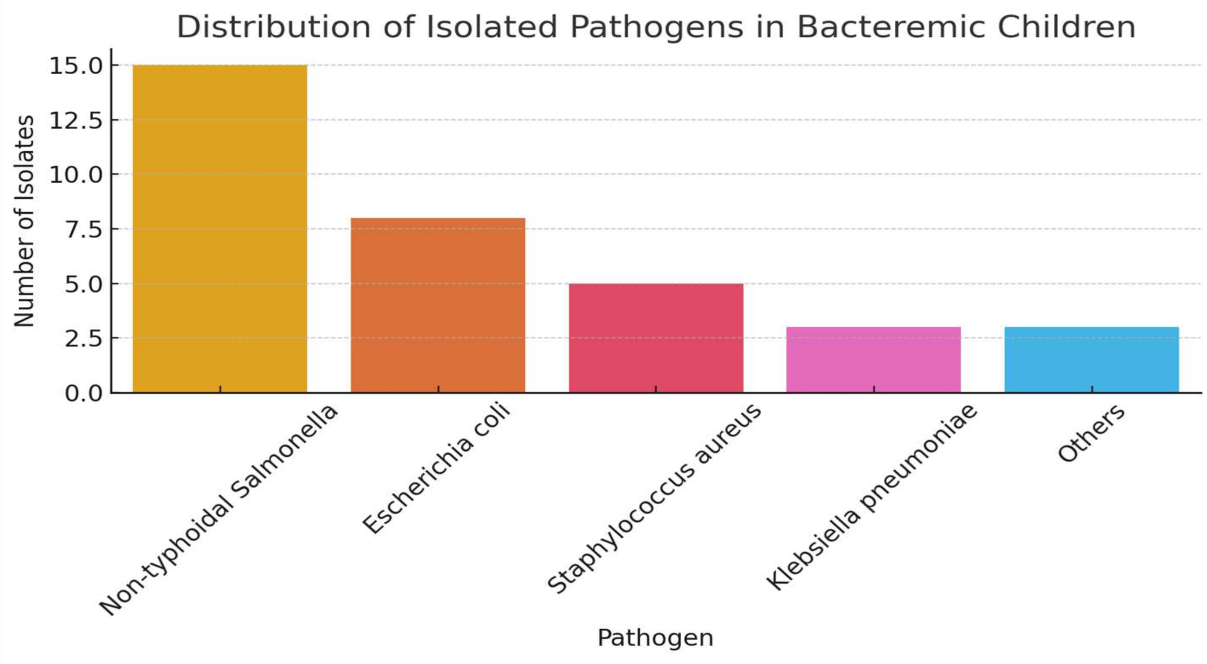

Figure 1
Distribution of Bacterial Pathogens Isolated from Blood Cultures of Children with Malaria-Associated Bacteremia

4.3 Association between Clinical Predictors and Bacteremia in Children with Malaria

Data on the strength and significance of associations between selected sociodemographic and clinical variables and bacteremia in children with malaria are presented in Figure 2 below. Hospitalization had the strongest association, with an Odds Ratio [OR] of 3.6 (95% Confidence Interval [CI]: 2.0–6.2, P = 0.001), indicating that hospitalized children were over three times more likely to have bacteremia compared to those not admitted. Respiratory distress was also strongly associated (OR = 3.4, 95% CI: 1.8–6.4, P = 0.01), reflecting the severity of illness in co-infected children. Similarly, severe anemia was a significant predictor (OR = 2.9, 95% CI: 1.5–5.6, P = 0.02), as was pallor (OR = 2.8, 95% CI: 1.4–5.3, P = 0.02), both pointing to hematologic compromise as a key feature of bacteremia in malaria cases. High-grade fever (OR = 2.2, 95% CI: 1.1–4.0, P = 0.03) and underweight nutritional status (OR = 2.1, 95% CI: 1.2–3.5, P = 0.03) also showed significant associations. Notably, age below 12 months was associated with more than twice the odds of bacteremia (OR = 2.3, 95% CI: 1.3–4.1, P = 0.01), suggesting that infants represent a particularly vulnerable group.

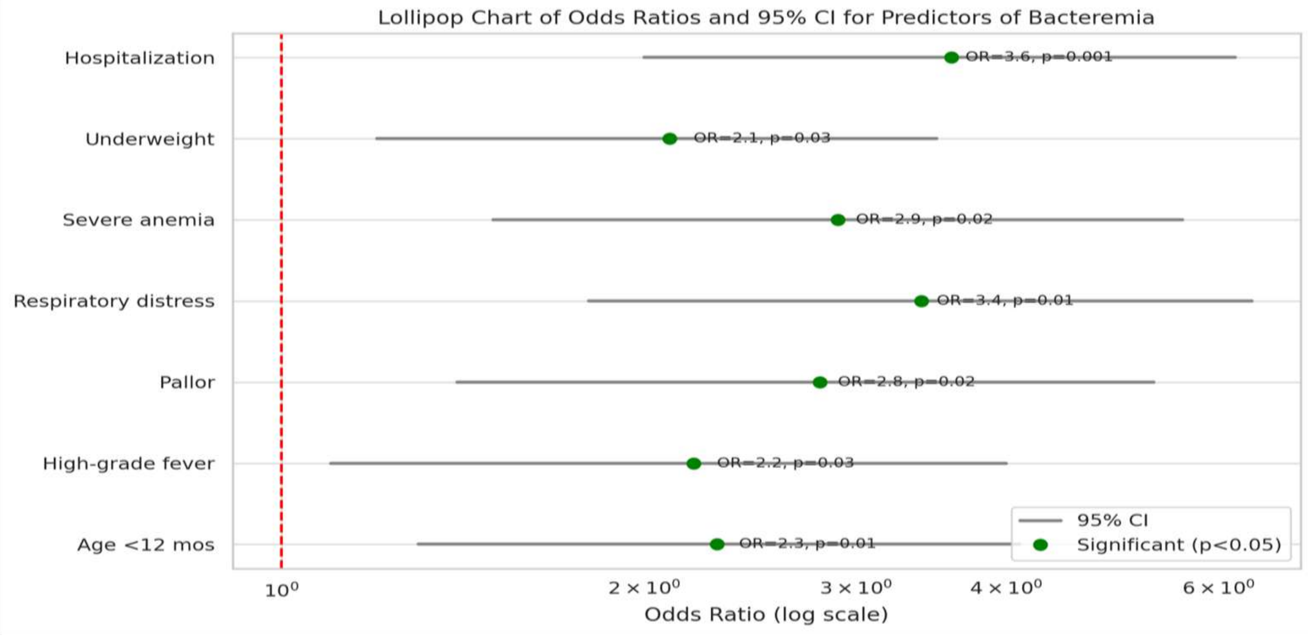

Figure 2

Odds Ratios and 95% Confidence Intervals for Selected Sociodemographic and Clinical Predictors of Bacteremia in Children with Malaria.

4.4 Discussion

This study provides critical insights into the burden and clinical profile of bacteremia among children presenting with malaria in Vihiga County, a highland region of Kenya characterized by unstable malaria transmission. The findings reveal that approximately 10.9% of children with malaria had concurrent bacteremia, a figure that aligns closely with estimates from other studies in western Kenya and other malaria-endemic areas in sub-Saharan Africa. For instance, Oshagbemi et al. (2023) reported a bacteremia prevalence of 15.4% among children with malaria across several sub-Saharan countries, with non-typhoidal Salmonella being the predominant pathogen. This similarity underscores a consistent pattern of bacterial co-infection in regions where malaria is endemic, especially among vulnerable pediatric populations.

Non-typhoidal Salmonella was the most frequently isolated organism, accounting for 44.1% of all bacteremia cases. This aligns with previous studies documenting a strong epidemiological link between NTS and malaria, possibly due to malaria-induced hemolysis and gut barrier dysfunction facilitating bacterial translocation (Akullian et al., 2018; Shahunjā et al., 2015). The high proportions of *Escherichia coli* and *Staphylococcus aureus* further reflect global patterns of pediatric bacteremia; however, their prominence in highland regions like Vihiga warrants further investigation into environmental and host-specific risk factors.

Several clinical features significantly associated with bacteremia included high-grade fever, pallor, respiratory distress, severe anemia, underweight status, and hospitalization. Notably, respiratory distress had an odds ratio (OR) of 3.4 (95% CI: 1.8–6.4), consistent with studies by Ogunkunle et al. (2022) and Rineer et al. (2023), which found respiratory symptoms to be common in children with bacteremia and malaria, often mimicking severe malaria syndromes. Severe anemia (OR = 2.9, 95% CI: 1.5–5.6) was another strong predictor, aligning with observations by Opoka et al. (2024), who reported that bacteremic children with malaria frequently presented with hemoglobin levels below 6 g/dL, likely due to compounded effects of malaria-induced hemolysis and inflammatory anemia from bacterial infections. Underweight status (OR = 2.1, 95% CI: 1.2–3.5) underscores the role of nutritional compromise as a risk factor for invasive bacterial infections, consistent with findings from Tanzania and Malawi, where malnutrition impairs mucosal immunity and increases gut permeability, predisposing children to systemic infections (Ndovie et al., 2025; Sunguya et al., 2011).

One of the most striking findings was the markedly higher mortality among children with bacteremia (17.6%) compared to those with malaria alone (0.4%). This echoes multiple reports indicating that mortality is nearly eight times higher in children with bacteremia, emphasizing the life-threatening nature of co-infection (Hollowell et al., 2023; Kamau et al., 2020). Additionally, children with bacteremia experienced longer hospital stays and higher hospitalization rates, reflecting the clinical complexity and resource burden associated with these cases.

From a clinical perspective, these findings reinforce the necessity for heightened vigilance and proactive screening for bacteremia in children presenting with malaria, especially among those under one year of age, severely anemic, undernourished, or exhibiting respiratory symptoms. Routine blood cultures and empirical antibiotics targeting NTS and other Gram-negative pathogens should be integrated into management protocols for high-risk malaria cases.

Furthermore, the strong association between bacteremia, nutritional deficits, and hematological compromise highlights the importance of a comprehensive child health approach—combining infection control, nutritional rehabilitation, and early detection of systemic illness—particularly in resource-limited settings like Vihiga. Such strategies are especially critical in rural and highland areas, where access to diagnostics and second-line antibiotics remains limited. Although bacteremia in highland regions like Vihiga is less studied compared to lowland or coastal zones, our findings suggest that the pathogen profile and clinical severity may be equally, if not more, pronounced, given the potentially lower immunity resulting from sporadic malaria exposure. This underscores the urgent need for further localized research and health system strengthening in highland endemic areas.

V. CONCLUSION & RECOMMENDATIONS

5.1 Conclusion

Bacteremia is a common and clinically significant co-infection among children presenting with malaria in Vihiga County. The study highlights the urgent need for integrated diagnostic and treatment strategies that address both malaria and potential bacterial infections. Given the associated risks of severe anemia, respiratory distress, prolonged hospitalization, and mortality, routine blood culture diagnostics and the timely initiation of empirical antibiotic therapy should be considered essential components of pediatric malaria care in highland regions. Strengthening local laboratory capacity, ensuring access to appropriate antimicrobial agents, and developing evidence-based treatment guidelines will be crucial in mitigating the burden of malaria-bacteremia co-infections. Additionally, policymakers and healthcare providers must prioritize investments in child health services that are responsive to the dual burden of infectious diseases in endemic areas. Future research, policy action, and targeted clinical interventions are warranted to improve outcomes and reduce mortality in this vulnerable pediatric population.

5.2 Recommendations

The identified burden and spectrum of bacterial co-infections suggest that health facilities in Vihiga County and similar highland settings should be equipped with routine blood culture diagnostics. This will enable accurate detection of bacterial pathogens among children with malaria, guide targeted antimicrobial therapy, and reduce inappropriate antibiotic use. Based on the established associations between sociodemographic and clinical characteristics (such as age <12 months, severe anemia, pallor, and respiratory distress) and bacteremia, the Ministry of Health should develop and adopt clinical screening tools or checklists. These should guide frontline healthcare workers in identifying high-risk children with malaria for prompt empirical antibiotic therapy and referral.

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