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# MALARIA PARASITEMIA IN RELATION TO SOCIODEMOGRAPHIC CHARACTERISTICS OF PATIENTS WITH DIFFERENT GENOTYPES ATTENDING HEALTH FACILITIES IN YOLA SOUTH AND YOLA NORTH LGA, ADAMAWA STATE

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**ABSTRACT**

Malaria, a life-threatening disease caused by *Plasmodium* parasites and transmitted through the bites of infected *Anopheles* mosquitoes, remains a significant public health challenge, particularly in sub-Saharan Africa. The aim of this study was to assess malaria parasitemia among patients with different hemoglobin genotypes attending health facilities in Yola North and South. A total of 300 blood samples were collected from patients with different hemoglobin genotype attending health facilities in Yola South and North. Blood samples for malaria diagnosis were processed using microscopy and rapid diagnostic tests [(RDTs)(One Step Malaria Antigen *P. falciparum* (HRP2)]. Data were analyzed using Statistical Package for Social Sciences (SPSS) version 22. There was an overall infection rate of 17.0%. The prevalence was slightly higher in Yola North (18.7%) compared to Yola South (15.3%). However, statistical analysis ($\chi^2 = 0.591$, $p = 0.442$) indicates that there was no statistical significance. Individuals with SS and SC genotypes had the highest prevalence (66.7% each), followed by those with the AA genotype (16.9%), while the lowest prevalence was recorded in AS individuals (5.9%). The chi-square test ($\chi^2 = 25.449$, $p = 0.000$) revealed a significant association between hemoglobin genotype and malaria parasitemia. Individuals aged 15–24 years had the highest prevalence (23.0%), while the lowest was observed among those aged 25–34 years (6.7%). The chi-square test ($\chi^2 = 6.536$, $p = 0.088$) suggests no statistically significant relationship between age and malaria prevalence. Individuals with secondary education had the highest prevalence (31.2%), while the lowest prevalence was recorded among those with tertiary education (12.5%). The chi-square test ($\chi^2 = 2.604$, $p = 0.457$) showed no significant association between educational attainment and malaria prevalence. Lastly, highest infection rate was recorded among tertiary workers (28.6%), while the lowest was observed among civil servants (13.8%). However, the chi-square test ($\chi^2 = 1.555$, $p = 0.670$) indicates no statistically significant association between occupation and malaria prevalence. This study highlights a moderate malaria prevalence (17.0%) in Yola North and Yola South, with a significant relationship between hemoglobin genotype and malaria susceptibility. Individuals with SS and SC genotypes were the most vulnerable, while those with AS had the lowest risk, supporting the protective effect of sickle cell trait against malaria. Other demographic factors such as age, gender, education, and occupation did not show statistically significant associations with malaria prevalence.

## 1. Introduction

Malaria remains one of the most devastating infectious diseases worldwide, causing significant morbidity and mortality, particularly in sub-Saharan Africa. Despite decades of concerted control efforts, the World Health Organization (2021) reports that Africa bears over 90% of global malaria cases and deaths, with children under five years old and pregnant women among the most vulnerable populations. In Nigeria, malaria continues to pose a serious public health threat, accounting for about 25% of the global malaria burden and contributing substantially to hospital admissions, outpatient visits, and mortality rates (WHO, 2021). *Plasmodium falciparum*, the most virulent malaria parasite, predominates in Nigeria and is transmitted by the female *Anopheles* mosquito. The parasite's ability to evade the host immune system and adapt to interventions complicates eradication efforts. In regions like Yola South and Yola North Local Government Areas (LGAs) of Adamawa State, malaria transmission is sustained by favorable

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climatic conditions for mosquito breeding, including high temperatures, abundant rainfall, and poor environmental sanitation. Consequently, malaria remains a major cause of hospital visits and an ongoing threat to socio-economic development in the region (Afolabi *et al*., 2020). Interestingly, malaria has played a significant role in shaping human genetics through natural selection. One of the most prominent examples is the distribution of hemoglobinopathies, particularly the sickle cell gene (HbS). The sickle cell gene mutation, which causes red blood cells to assume a rigid, sickle shape under low oxygen conditions, offers a survival advantage in malaria-endemic regions when inherited heterozygous sickle cell trait (HbAS) (Allison, 1954). Individuals with the sickle cell trait are partially protected against severe *P. falciparum* infection, which explains why the gene has persisted at high frequencies in malaria-endemic regions despite its detrimental effects when inherited in homozygous form (HbSS), leading to sickle cell anemia (Williams *et al*., 2005).

The coexistence of malaria and sickle cell disease (SCD) poses unique health challenges in sub-Saharan Africa (Serjeant, 2013). While HbAS confers partial immunity, individuals with sickle cell anemia face compounded risks when infected with malaria. The parasite-induced destruction of red blood cells exacerbates the chronic hemolytic anemia inherent in SCD, often triggering severe complications, crises, and increased mortality risk (Aidoo *et al*., 2002). In areas like Yola South and Yola North LGAs, where both malaria and SCD are prevalent, understanding this interaction is crucial for designing effective public health strategies.

Despite extensive global and national research, limited studies have focused specifically on how malaria parasitemia varies among patients with different hemoglobin genotypes at the local level in northeastern Nigeria. As genetic traits like the sickle cell gene directly affect malaria outcomes, local empirical data are essential for developing targeted prevention and management strategies. This gap underscores the need for focused research in Adamawa State, where health facilities frequently attend to patients suffering from both malaria and sickle cell disorders.

Malaria and sickle cell disease (SCD) represent significant public health challenges in sub-Saharan Africa, particularly in regions like northeastern Nigeria. Despite ongoing efforts to control malaria and manage SCD, the dual burden of these conditions continues to exert a heavy toll on affected populations. In Yola North and South, the endemic nature of malaria and the prevalent rates of hemoglobinopathies, including sickle cell trait (SCT), present unique health challenges and opportunities for research.

Middle-aged adults (35-44 years) in this region face a high risk of malaria infection, which can lead to severe health complications and even death (Emeka, 2011). Simultaneously, SCT, while typically asymptomatic, has been associated with a protective effect against severe malaria caused by Plasmodium falciparum. Understanding the prevalence and interaction between malaria parasitemia and SCT in this demographic is critical for developing effective public health strategies.

However, there is a paucity of comprehensive data on the prevalence of malaria parasitemia and SCT among middle-aged adults in Yola North and South. This gap in knowledge hinders the ability to design targeted interventions that can address the dual burden of malaria and SCT. Furthermore, the potential correlation between SCT and malaria parasitemia in this population remains underexplored, limiting our understanding of how genetic factors may influence malaria susceptibility and outcomes.

## 2. Material and Methods

### 2.1 Description of the Study Area

This study was carried out in Yola North and South are located in Adamawa State, northeastern Nigeria. These areas experience a tropical climate with distinct wet and dry seasons. The region is characterized by a mix of urban and rural settlements, with Yola North being more urbanized compared to Yola South. The primary economic activities in these areas include agriculture, trading, and services. The healthcare infrastructure includes several public and private health facilities that cater to the medical needs of the population. Malaria transmission is perennial, with peaks during the rainy season from April to October. Sickle cell disease and Sickle cell Traits are also prevalent, reflecting the genetic background of the population.

### 2.2 Research Design

This study utilized a cross-sectional research design to determine the prevalence of malaria parasitemia among patients with different hemoglobin genotypes attending health facilities in Yola South and North. This design is appropriate for estimating the prevalence of conditions within a specific population at a particular point in time. It allows for the collection of data on various variables simultaneously, providing a snapshot of the health status of the study population.

### 2.3 Ethical Approval

Ethical approval for the study was obtained from the Adamawa State Ministry of Health with the approval no ADHREC 08/11/2024/065, and all procedures were conducted in accordance with ethical guidelines for human research.

### 2.4 Sample Collection

A total sample size of 300 was obtained using the Cochran's formula for sample size determination. The blood samples were collected from patients with different hemoglobin genotype attending health facilities in Yola South and North. Informed consent was obtained from all participants before data and sample collection. Participants for this study included patients attending health facilities in Yola North and South. The inclusion criteria were as follows;

1. Participant must be a patient attending a health facility in this location.
2. Must agree to sign the consent form. Exclusion criteria include any one that falls outside the above categories.

Blood samples were collected by trained phlebotomists using standard venipuncture techniques. Approximately 5 mL of blood were drawn from each participant and divided into two aliquots: one for malaria diagnosis and the other for hemoglobin electrophoresis.

The samples were immediately analyzed within the health facilities by trained technicians for malaria and SCT.

### 2.5 Sample Processing

Blood samples for malaria diagnosis were processed using microscopy and rapid diagnostic tests (RDTs) (One Step Malaria Antigen *P. falciparum* (HRP2). Thick and thin blood smears were prepared, stained with Giemsa, and examined under a microscope by experienced laboratory technicians to identify *Plasmodium* parasites. RDTs were used as a supplementary diagnostic tool to confirm malaria infection.

For SCT detection, hemoglobin electrophoresis was performed on the second aliquot of blood. Samples were processed at a central laboratory equipped with High Performance Liquid Chromatography system. This method allows for the accurate differentiation between hemoglobin variants, including HbA, HbS, and HbC.

### 2.6 Data Analysis

Data were analyzed using Statistical Package for Social Sciences (SPSS) version 22. Descriptive statistics were used to summarize demographic characteristics of the study population, including age, gender, and residency. Prevalence rates of malaria parasitemia and SCT were calculated with 95% confidence intervals. Chi-square test was used to assess associations between demographic variables and the presence of malaria parasitemia/parasite density and SCT with p-value set at $p \leq 0.05$.

## 3. Results

Table 1: Prevalence of malaria parasitemia among patients attending health facilities in Yola South and Yola North.

| Location | Malaria Parasitemia | |
|---|---|---|
| | No. Examined | No. Infected (%) |
| Yola North | 150 | 28(18.7) |
| Yola South | 150 | 23(15.3) |
| Total | 300 | 51(17.0) |

$\chi^2$=0.591; p=0.442; NS (Not significant)

Table 2: Malaria parasitemia among patients with different hemoglobin genotypes (AA, AS, SS, SC) attending health facilities in Yola South and Yola North.

| Haemoglobin Genotype | Malaria Parasitemia | |
|---|---|---|
| | No. Examined | No. Infected (%) |
| AA | 237 | 40(16.9) |
| AS | 51 | 3(5.9) |
| SS | 9 | 6(66.7) |
| SC | 3 | 2(66.7) |
| Total | 300 | 51(17.0) |

$\chi^2$=25.449; p=0.000; Excellent clear significance marking.

Key: AA = Normal Haemoglobin Genotype, AS= Sickle cell carrier, SS =Sickler, SC = Compound Heterozygous Hemoglobin SC Disease, $\chi^2$ =Chi-Square

Table 3: Distribution of malaria in relation to age among patients attending health facilities in Yola south and Yola North

| Age (Years) | Malaria Parasitemia | |
|---|---|---|
| | No. Examined | No. Infected (%) |
| 15-24 | 135 | 31(23.0) |
| 25-34 | 15 | 1(6.7) |
| 35-44 | 86 | 11(12.8) |
| 45 and above | 64 | 8(12.5) |
| Total | 300 | 51(17.0) |

$\chi^2$=6.536; p=0.088

Table 4: Distribution of malaria in relation to gender among patients attending health facilities in Yola south and Yola North

| Gender | Malaria Parasitemia | |
|---|---|---|
| | No. Examined | No. Infected (%) |
| Male | 159 | 26(16.4) |
| Female | 141 | 25(17.7) |
| Total | 300 | 51(17.0) |

$\chi^2$=0.101; p=0.751

Table 5: Malaria prevalence by education level

| Education | Malaria Parasitemia | |
|---|---|---|
| | No. Examined | No. Infected (%) |
| No. formal education | 169 | 28(16.6) |
| Primary | 99 | 16(16.2) |
| Secondary | 16 | 5(31.2) |
| Tertiary | 16 | 2(12.5) |
| Total | 300 | 51(17.0) |

$\chi^2$=2.604; p=0.457 NS" (not significant)

Table 6: Distribution of malaria in relation to occupation among patients attending health facilities in Yola south and Yola North

| Occupation | Malaria Parasitemia | |
|---|---|---|
| | No. Examined | No. Infected (%) |
| Students | 180 | 30(16.7) |
| Farmer | 77 | 13(16.9) |
| Civil servants | 29 | 4(13.8) |
| Others | 14 | 4(28.6) |
| Total | 300 | 51(17.0) |

$\chi^2$=1.555; p=0.670

## 4. Discussion

The findings of this study revealed a malaria prevalence of 17.0% among patients attending health facilities in Yola North and Yola South, with a slightly higher prevalence in Yola North (18.7%) compared to Yola South (15.3%). However, the difference was not statistically significant (p = 0.442), suggesting similar malaria transmission patterns across both locations. The prevalence observed in this study is lower than those reported Akinyele *et al*. (2021) who found a 27.3% malaria prevalence among febrile patients in Southwest Nigeria, while Okonko *et al.* (2022) recorded 32.5% in a rural community in Northern Nigeria. The relatively lower prevalence in this study may be attributed to improved malaria control interventions, including the use of insecticide-treated nets (ITNs), antimalarial prophylaxis, and increased public awareness of malaria prevention measures.

A significant association (p = 0.000) was observed between hemoglobin genotype and malaria parasitemia, with SS and SC genotypes exhibiting the highest prevalence (66.7% each), while individuals with AS (sickle cell trait) had the lowest prevalence (5.9%). This supports previous findings by Ofori *et al.* (2020) in Ghana, where AS individuals had a malaria prevalence of 6.8%, compared to 63.4% in SS individuals. The protective effect of the AS genotype against malaria has been well documented, as *Plasmodium falciparum* struggles to thrive in red blood cells with abnormal hemoglobin structure as also reported by Williams *et al*. (2021). On the other hand, individuals with sickle cell disease (SS and SC genotypes) tend to have a compromised immune response, leading to increased susceptibility to malaria infection (Taylor *et al*., 2019).

Regarding age distribution, the highest malaria prevalence was recorded in the 15–24 years' age group (23.0%), while the lowest was among those aged 25–34 years (6.7%). However, the association was not statistically significant (p = 0.088). Similar findings were reported by Yusuf *et al.* (2020), who found that young adults had higher malaria prevalence due to increased outdoor exposure and lower acquired immunity compared to older adults. However, some studies, such as Bassey *et al*. (2018), have reported that children under five years have the highest malaria burden due to undeveloped immunity and higher susceptibility to severe malaria. The discrepancy between studies may be due to differences in study populations, geographical variations, and malaria transmission intensity.

The study also examined gender differences in malaria prevalence. While females had a slightly higher prevalence (17.7%) compared to males (16.4%), the difference was not statistically significant (p = 0.751). This aligns with findings by Ademola *et al.* (2022), who reported no significant gender differences in malaria prevalence, indicating that exposure to malaria is more dependent on environmental and behavioral factors rather than biological sex. However, other studies, such as Kumar *et al.* (2019), have suggested that men may have a higher risk due to increased outdoor activities and occupational exposure to mosquito breeding sites.

The highest prevalence was observed among individuals with secondary education (31.2%), while those with tertiary education had the lowest prevalence (12.5%). However, the association was not statistically significant (p = 0.457). These findings support those of Eze *et al.* (2021), who reported that malaria prevalence tends to decrease with higher educational attainment, likely due to better knowledge of malaria prevention strategies, increased economic capacity to afford healthcare, and improved living conditions.

Occupation was another factor considered in this study, with malaria prevalence being highest among workers (28.6%), followed by farmers (16.9%), while civil servants had the lowest prevalence (13.8%). However, the association between malaria prevalence and occupation was not statistically significant (p = 0.670). These findings contrast with those of Adebayo *et al.* (2020), who found that farmers had the highest malaria prevalence due to frequent exposure to mosquito breeding sites and limited access to healthcare facilities. The relatively lower prevalence among farmers in this study could be attributed to better malaria control practices and improved agricultural work conditions in the study area.

## 4. Conclusion

This study highlights a moderate malaria prevalence (17.0%) in Yola North and Yola South, with a significant relationship between hemoglobin genotype and malaria susceptibility. Individuals with SS and SC genotypes were the most vulnerable, while those with AS had the lowest risk, supporting the protective effect of sickle cell trait against malaria. Other demographic factors such as age, gender, education, and occupation did not show statistically significant associations with malaria prevalence. Compared to previous studies, the prevalence in this study appears lower, likely due to improved malaria control measures and better access to healthcare services. However, the persistence of malaria cases despite these interventions suggests the need for continuous surveillance, strengthened malaria control programs, and targeted interventions for high-risk groups, particularly individuals with sickle cell disease.

## 5. Recommendations

The following recommendations are made from the result of this study;

1.Specialized malaria prevention programs such as prophylactic antimalarial treatment, increased access to insecticide-treated nets (ITNs), and regular health check-ups should be implemented for individuals with SS and SC to reduce their vulnerability.

2. Continuous surveillance, community-based vector control measures, and improved access to rapid diagnostic testing (RDTs) and effective treatment should be prioritized to further reduce malaria burden.

3. Health authorities should intensify malaria awareness campaigns in schools, workplaces, and rural communities, emphasizing proper use of ITNs, environmental sanitation, and early treatment-seeking behavior.

4. Given that malaria transmission is largely influenced by environmental factors, government and community leaders should support large-scale indoor residual spraying (IRS), drainage of stagnant water, and proper waste disposal to reduce mosquito breeding sites and lower transmission rates.

5. The significant association between hemoglobin genotype and malaria prevalence calls for further molecular studies to explore the mechanisms behind malaria resistance in AS individuals and increased susceptibility in SS and SC individuals.

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