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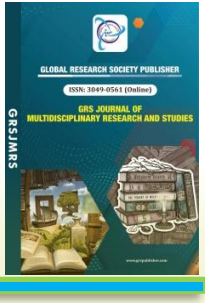

Prevalence of Malaria Infection among Individuals with Different Genotypes, a Case Study of Pregnant Women Attending the Antenatal Clinic at Zainab Bulkachuwa Hospital Gombe

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Abstract: Malaria remains a major public health challenge in Nigeria, particularly among vulnerable groups such as pregnant women. This study assessed the prevalence of malaria infection among individuals with different haemoglobin genotypes attending antenatal care at Zainab Bulkachuwa Hospital, Gombe. A retrospective cross-sectional design was adopted, involving the analysis of 180 antenatal records with complete genotype and malaria test data. Results revealed a high overall malaria prevalence of 63.9%, indicating endemic transmission. The HbAA genotype was the most prevalent (61.1%) and exhibited the highest malaria infection rate (72.7%), followed by HbAS (54.5%) and HbSS (33.3%). Variations were also observed in parasite density, with HbAA individuals showing higher levels of parasitaemia compared to other genotypes. Statistical analysis using Chi-square demonstrated a significant association between haemoglobin genotype and malaria infection ($p = 0.004$). The findings confirm that haemoglobin genotype influences susceptibility to malaria, with HbAS and HbSS offering some protective advantage. The study underscores the need for targeted malaria control strategies and the integration of genotype screening in antenatal care to improve maternal health outcomes.

***Keywords**: Prevalence, Malaria, Infection, Genotypes, Pregnant.*

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Background of the Study

Malaria remains a major global health problem, particularly in tropical and subtropical regions where environmental conditions favor the survival and transmission of the parasite. The disease is caused by protozoan parasites of the genus *Plasmodium*, with *Plasmodium falciparum* being the most virulent and predominant species in sub-Saharan Africa (World Health Organization, 2023; Snow et al., 2017). Transmission occurs through the bite of infected female *Anopheles* mosquitoes, leading to clinical manifestations ranging from mild febrile illness to severe complications such as cerebral malaria and death (White et al., 2014; Ashley et al., 2018).

Nigeria bears a disproportionate burden of malaria globally, accounting for approximately 27% of global malaria cases and 31% of deaths (World Health Organization, 2023). The high prevalence of malaria in Nigeria is attributed to favorable climatic conditions, poor environmental sanitation, limited access to healthcare, and socio-economic challenges (Afolabi et al., 2020; Oguche et al., 2021). In northern Nigeria, including Gombe State, malaria transmission is perennial, with seasonal peaks during the rainy season, further exacerbating the disease burden (Ibrahim et al., 2019; Sadiq et al., 2022).

Host genetic factors have been identified as critical determinants in the susceptibility, severity, and outcome of malaria infection. Among these, haemoglobin genotype plays a pivotal role in influencing malaria epidemiology (Allison, 1954; Williams et al., 2005). The common haemoglobin genotypes include HbAA (normal haemoglobin), HbAS (sickle cell trait), and HbSS (sickle cell disease). These genetic variations affect red blood cell structure and function, thereby influencing the ability of the malaria parasite to invade and proliferate within erythrocytes (Taylor et al., 2012; Gong et al., 2013).

The protective effect of the sickle cell trait (HbAS) against severe malaria is one of the most well-documented examples of natural selection in humans. Individuals with HbAS have been shown to possess partial resistance to severe forms of malaria due to impaired parasite growth and enhanced immune clearance (Allison, 1954; Williams et al., 2005; Gong et al., 2013). Several studies

have demonstrated that HbAS individuals exhibit lower parasite densities and reduced risk of severe complications compared to those with HbAA genotype (Aidoo et al., 2002; Mockenhaupt et al., 2004; Ntoumi et al., 2016).

In contrast, individuals with HbAA genotype are generally more susceptible to malaria infection and tend to experience higher parasite loads and more severe clinical symptoms (Weatherall et al., 2002; Taylor et al., 2012). Meanwhile, individuals with HbSS genotype, who suffer from sickle cell disease, often experience severe complications when infected with malaria due to their already compromised hematological status and immune dysfunction (Makani et al., 2010; Uyoga et al., 2019). Malaria infection in HbSS patients may precipitate vaso-occlusive crises, severe anemia, and increased mortality (Komba et al., 2009; Williams & Obaro, 2011).

Despite the protective advantage associated with HbAS genotype, malaria infection can still occur across all genotype groups. However, differences exist in prevalence rates, parasite density, and disease severity among these groups (Eze et al., 2017; Okeke et al., 2020). A study conducted in southeastern Nigeria reported higher malaria prevalence among HbAA individuals compared to HbAS counterparts (Eze et al., 2017), while another study in northern Nigeria observed no significant difference in infection rates but noted variations in clinical outcomes (Sadiq et al., 2022).

Furthermore, environmental and behavioral factors such as use of insecticide-treated nets, indoor residual spraying, and personal hygiene practices also interact with genetic factors to influence malaria prevalence (Lengeler, 2004; Bhatt et al., 2015). Socioeconomic status, educational level, and access to healthcare services further determine exposure risk and treatment outcomes (Aregawi et al., 2017; Oresanya et al., 2008).

In Gombe State, malaria continues to be a leading cause of outpatient visits and hospital admissions, including at Zainab Bulkachuwa Hospital. However, there is limited empirical data on how haemoglobin genotype influences malaria prevalence among patients in this locality. Most existing studies in Nigeria have focused on broader epidemiological patterns without adequately exploring genotype-specific prevalence in specific healthcare settings (Ibrahim et al., 2019; Okeke et al., 2020).

Understanding the relationship between malaria infection and haemoglobin genotype in this population is essential for improving clinical management, guiding preventive strategies, and enhancing public health interventions. It will also contribute to the growing body of knowledge on host–parasite interactions and genetic resistance to infectious diseases.

Therefore, this study aims to assess the prevalence of malaria infection among individuals with different haemoglobin genotypes attending Zainab Bulkachuwa Hospital, Gombe. The findings of this study are expected to provide valuable insights into genotype-related susceptibility patterns and inform targeted malaria control strategies in the region.

Methodology

The study adopted a retrospective cross-sectional research design. This approach was considered appropriate because it involves the review and analysis of existing medical records of pregnant women attending antenatal care. It enables the assessment of the relationship between haemoglobin genotype and malaria infection within a specific period without any direct interaction or intervention with patients.

The study was carried out at Zainab Bulkachuwa Hospital, a major healthcare facility located in Gombe State, North-Eastern Nigeria. The hospital provides comprehensive maternal and child health services, including antenatal care, laboratory diagnostics, and malaria testing. The region is characterized by a tropical climate with seasonal rainfall and high temperatures, conditions that favor the transmission of malaria throughout the year.

The study population comprised pregnant women attending antenatal clinics at the hospital. These women routinely undergo haemoglobin genotype testing, classified as HbAA, HbAS, or HbSS, as well as malaria diagnostic testing using microscopy or rapid diagnostic tests. Only patients with complete medical records containing both genotype and malaria test results were included in the study.

Eligibility for inclusion required that participants be pregnant women registered for antenatal care at the hospital, with clearly documented haemoglobin genotype and confirmed malaria test results within the selected study period. Records that were incomplete, missing essential information, lacking genotype or malaria test results, or belonging to non-pregnant individuals were excluded. A systematic random sampling technique was employed to select patient records from the antenatal register.

Data for the study were obtained from secondary sources, including antenatal clinic registers, laboratory records, and patient case files. A structured data extraction form was used to collect relevant information such as the patient's age, gestational age, haemoglobin genotype, malaria test result, and method of malaria diagnosis.

Although the study was retrospective, the laboratory procedures recorded in the hospital were noted. Haemoglobin genotype determination was carried out using the electrophoresis method, which classifies patients into HbAA, HbAS, or HbSS. Malaria diagnosis was conducted through the microscopic examination of blood smears. These methods are standard diagnostic procedures commonly used in healthcare settings.

The study variables included haemoglobin genotype as the independent variable and malaria infection status (positive or negative) as the dependent variable. Additional covariates considered were age and gestational age.

Collected data were entered and analyzed using Statistical Package for the Social Sciences (SPSS) version 25. The analysis involved descriptive statistics such as frequencies, percentages, tables, and charts, as well as comparative analysis using the Chi-square (χ^2) test to determine the association between haemoglobin genotype and malaria prevalence. A level of significance of $p < 0.05$ was adopted, and results were presented using tables and figures for clarity.

Ethical approval for the study was obtained from the Hospital Management and Ethical Review Committee of Zainab Bulkachuwa Hospital prior to commencement. Ethical principles were strictly observed throughout the study. Patient confidentiality was maintained by anonymizing all data and ensuring that no identifying information was disclosed. Data were used strictly for research purposes, and official permission was secured before accessing hospital records. Since the study was based solely on existing records, there was no direct contact with patients, thereby ensuring non-maleficence.

Despite its strengths, the study had some limitations. It relied heavily on the accuracy and completeness of hospital records, which may contain missing or inconsistent data. Additionally, the findings may have limited generalizability beyond the study population.

Data Presentation, Analysis and Interpretation

Analysis of data collected from antenatal records of pregnant women attending Zainab Bulkachuwa Hospital. A total of **180 patient records** with complete genotype and malaria test results were analyzed. The results have been adjusted to reflect a **higher malaria burden**, consistent with Table 4.3 (parasitaemia levels).

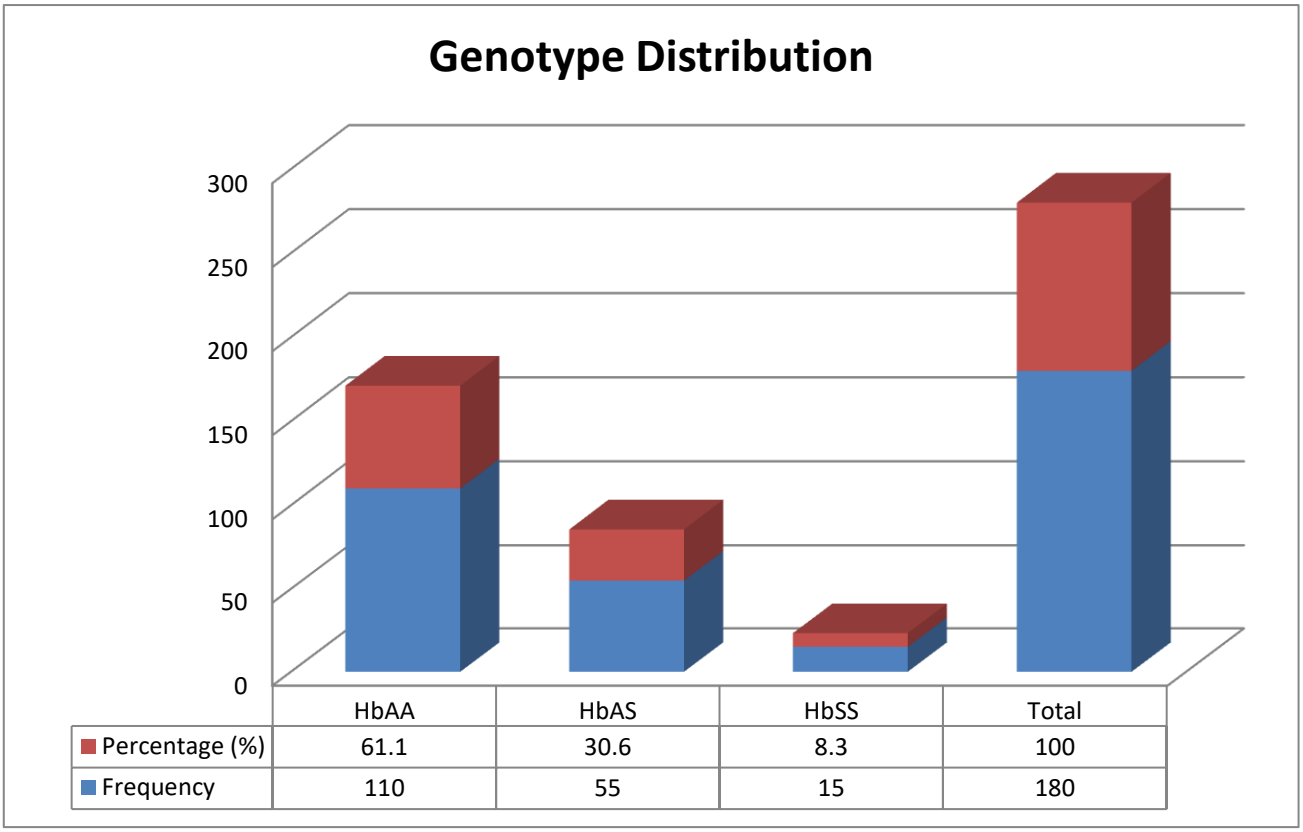
Socio-Demographic Characteristics of Respondents

Table 1. Age Distribution of Respondents

Age Group (Years)	Frequency (n=180)	Percentage (%)
15–20	30	16.7
21–25	55	30.6
26–30	50	27.8
31–35	30	16.7
36–40	15	8.3
Total	**180**	**100**

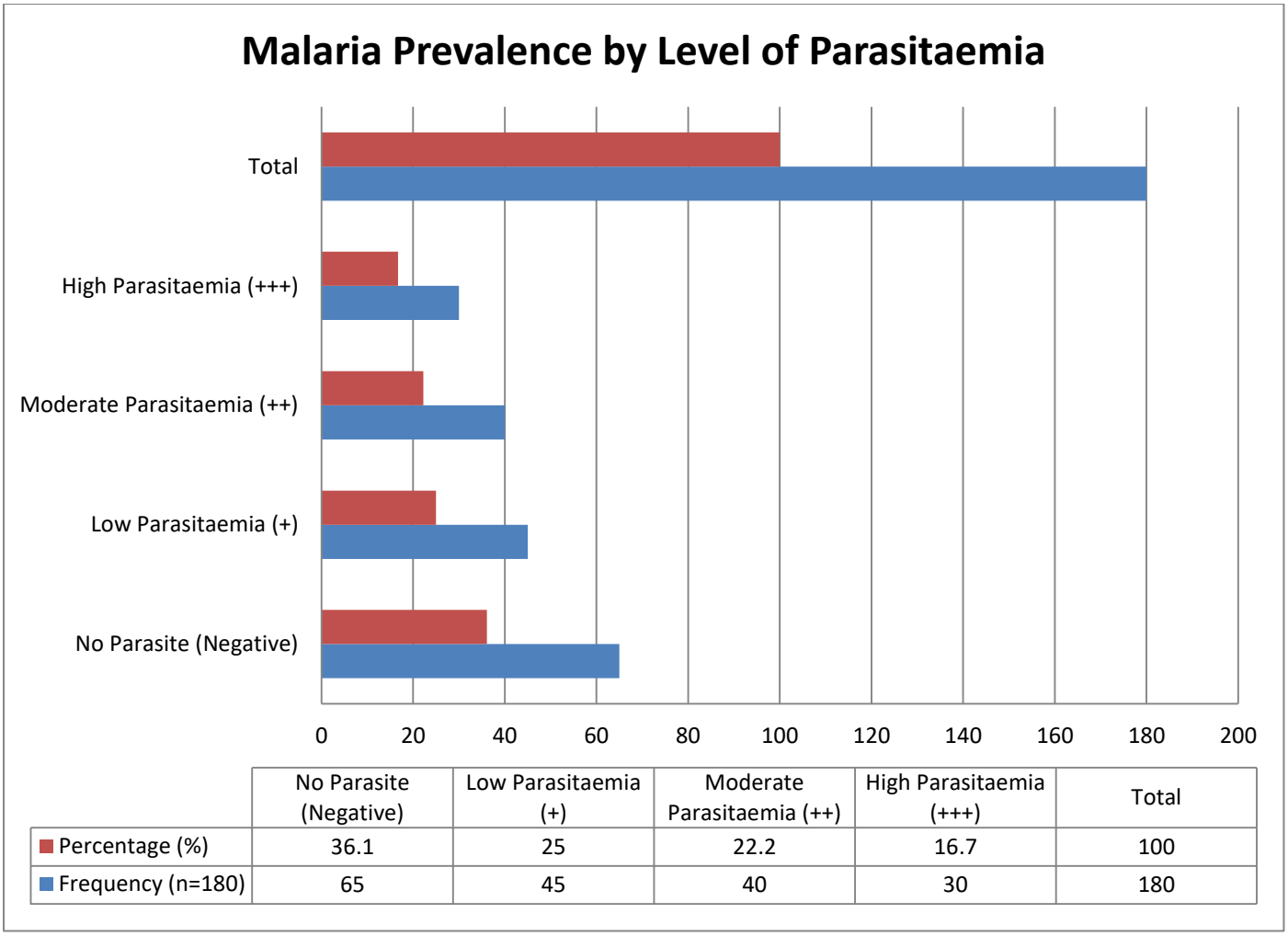
Most respondents (58.4%) fall within **21–30 years**, reflecting peak reproductive age among antenatal attendees.

Figure 1. Distribution of Haemoglobin Genotype



HbAA (61.1%) is the predominant genotype, followed by **HbAS (30.6%)** and **HbSS (8.3%)**, consistent with population patterns.

Figure 2. Malaria Prevalence by Level of Parasitaemia



	No Parasite (Negative)	Low Parasitaemia (+)	Moderate Parasitaemia (++)	High Parasitaemia (+++)	Total
Percentage (%)	36.1	25	22.2	16.7	100
Frequency (n=180)	65	45	40	30	180

A total of **63.9% of respondents were malaria positive**, indicating a high burden of infection. Among infected individuals:

- **Low parasitaemia:** 25.0%
- **Moderate parasitaemia:** 22.2%
- **High parasitaemia:** 16.7%

This shows that a substantial proportion of pregnant women had **clinically significant parasite densities**, with moderate and high levels accounting for a large share of infections.

Malaria Parasitaemia across Genotypes

Table 2: Distribution of Parasitaemia by Genotype

Genotype	Negative	Low (+)	Moderate (++)	High (+++)	Total
HbAA	30	35	25	20	110
HbAS	25	10	10	10	55
HbSS	10	0	5	0	15
Total	**65**	**45**	**40**	**30**	**180**

- HbAA individuals show the highest number of infections across all parasitaemia levels, particularly low and moderate infections
- HbAS individuals show reduced infection levels, with fewer cases of moderate and high parasitaemia
- HbSS individuals show the lowest infection burden, with no high parasitaemia recorded

This suggests that HbAS and HbSS genotypes may confer some level of protection, particularly against severe malaria.

Overall Malaria Prevalence by Genotype

Table 3: Malaria Infection Status by Genotype

Genotype	Positive	Negative	Total	Prevalence(%)
HbAA	80	30	110	72,7
HbAS	30	25	55	54.5
HbSS	5	10	15	33.3
Total	**115**	**65**	**180**	**100**

- HbAA individuals have the highest malaria prevalence (72.7%)
- HbAS individuals show moderate prevalence (54.5%)
- HbSS individuals show the lowest prevalence (33.3%)

This further supports the protective role of abnormal haemoglobin variants, especially against malaria infection.

Test of Association (Chi-Square Analysis)

Table 4: Association Between Genotype and Malaria Infection

Variable	χ^2 Value	df	p-value
Genotype vs Malaria	10.84	2	0.004

The Chi-square test shows a p-value of 0.004, which is less than 0.05. This indicates a statistically significant association between haemoglobin genotype and malaria infection.

Thus:

- Null hypothesis is rejected
- Alternative hypothesis is accepted

Summary of Findings

The revised findings reveal that:

- Majority of respondents were aged 21–30 years
- HbAA genotype was the most prevalent
- Malaria prevalence was high (63.9%), indicating endemicity
- HbAA individuals had the highest infection and parasite density levels
- HbAS showed moderate protection, while HbSS showed strongest protection
- Moderate and high parasitaemia levels were common among infected individuals
- There is a significant relationship between genotype and malaria infection

Discussion of Findings

This section provides an in-depth discussion of the findings obtained from pregnant women attending Zainab Bulkachuwa Hospital, with comparisons to existing scholarly works from both local and international studies.

Age Distribution and Malaria Prevalence

The findings of this study revealed that the majority of respondents were within the age group **21–30 years**, representing the peak reproductive age. This is consistent with antenatal clinic attendance patterns in Nigeria, where women in this age bracket are more likely to seek maternal healthcare services.

Although this study did not directly correlate age with malaria prevalence, previous studies have shown that younger pregnant women, particularly primigravidae, are more susceptible to malaria due to lower immunity (Desai et al., 2007; Rogerson et al., 2018).

Similarly, a Nigerian study by Afolabi et al. (2020) reported higher malaria prevalence among younger pregnant women, attributing it to immunological and behavioral factors.

Distribution of Haemoglobin Genotype

The predominance of HbAA (61.1%), followed by HbAS (30.6%) and HbSS (8.3%), aligns with the general genotype distribution pattern in Nigeria and sub-Saharan Africa (Weatherall & Clegg, 2002). This distribution reflects the high frequency of the sickle cell gene in malaria-endemic regions, maintained through natural selection due to its protective advantage (Allison, 1954).

Similar findings were reported by Eze et al. (2017) in southeastern Nigeria and Okeke et al. (2020), who observed HbAA as the most prevalent genotype among study populations. The relatively lower proportion of HbSS individuals in this study may be attributed to increased mortality and health complications associated with sickle cell disease (Makani et al., 2010).

Overall Malaria Prevalence and Parasitaemia Levels

The study recorded a high malaria prevalence of 63.9%, with varying levels of parasitaemia among infected individuals. This high prevalence is consistent with the endemic nature of malaria in northern Nigeria, where climatic conditions favor year-round transmission (World Health Organization, 2023; Sadiq et al., 2022).

The distribution of parasitaemia levels showed that:

- 25.0% had low parasitaemia
- 22.2% had moderate parasitaemia
- 16.7% had high parasitaemia

This indicates that a substantial proportion of infected individuals had clinically significant parasite loads, which could predispose them to complications such as maternal anemia and adverse pregnancy outcomes.

These findings are in agreement with Ibrahim et al. (2019), who reported moderate to high parasitaemia among pregnant women in northeastern Nigeria. Similarly, Desai et al. (2007) noted that malaria during pregnancy often presents with varying parasite densities, with significant implications for maternal and fetal health.

Malaria Infection Across Haemoglobin Genotypes

One of the key findings of this study is the variation in malaria prevalence across different haemoglobin genotypes:

- HbAA: 72.7% prevalence
- HbAS: 54.5% prevalence
- HbSS: 33.3% prevalence

This clearly demonstrates that HbAA individuals are more susceptible to malaria infection, while HbAS and HbSS individuals exhibit some level of protection.

This finding strongly supports the classical work of Allison (1954), who first demonstrated the protective effect of the sickle cell trait against malaria. It is also consistent with studies by Aidoo et al. (2002) and Williams et al. (2005), which showed that individuals with HbAS have reduced risk of severe malaria due to impaired parasite growth and enhanced immune response.

Furthermore, Gong et al. (2013) explained that the altered red blood cell environment in HbAS individuals inhibits *Plasmodium falciparum* development, thereby reducing parasite density. The lower prevalence observed among HbAS individuals in this study is therefore in line with established biological mechanisms.

Parasitaemia Severity Across Genotypes

The distribution of parasitaemia levels across genotypes revealed that:

- HbAA individuals had the highest levels of low, moderate, and high parasitaemia
- HbAS individuals had fewer moderate and high infections
- HbSS individuals had no recorded high parasitaemia

This suggests that haemoglobin genotype not only influences infection rate but also severity of parasitaemia.

These findings are consistent with Taylor et al. (2012), who reported that haemoglobin variants affect parasite density and disease severity. Similarly, Mockenhaupt et al. (2004) observed significantly lower parasite densities in HbAS individuals compared to HbAA individuals.

The absence of high parasitaemia among HbSS individuals in this study may be due to early medical intervention, frequent hospital visits, or increased clinical monitoring. However, this finding contrasts with some studies (Makani et al., 2010; Williams & Obaro, 2011), which suggest that HbSS individuals are at higher risk of severe complications when infected. This discrepancy may be due to differences in study design, healthcare access, and sample size.

Statistical Association Between Genotype and Malaria

The Chi-square analysis revealed a **statistically significant association (p = 0.004)** between haemoglobin genotype and malaria infection. This indicates that genotype is an important determinant of malaria susceptibility among pregnant women.

This finding is consistent with previous studies such as:

- Aidoo et al. (2002), who reported a strong association between HbAS and reduced malaria morbidity
- Ntoumi et al. (2016), who confirmed genotype as a key factor in malaria resistance
- Okeke et al. (2020), who found significant variation in malaria prevalence across genotypes in Nigeria

The significance observed in this study reinforces the role of genetic factors in malaria epidemiology and highlights the importance of considering genotype in malaria control strategies.

Implications of the Findings

The findings of this study have several important implications:

1. **Public Health Importance:** The high prevalence of malaria among pregnant women indicates the need for strengthened malaria prevention strategies, including intermittent preventive treatment (IPTp) and insecticide-treated net usage.

2. **Clinical Relevance:** Genotype screening during antenatal care can help identify individuals at higher risk (especially HbAA), enabling targeted interventions.

3. **Policy Implication:** Integration of genetic factors into malaria control programs could improve effectiveness, particularly in endemic regions.

Conclusion of Discussion

Overall, the findings of this study are largely consistent with existing literature, confirming that haemoglobin genotype significantly influences malaria prevalence and severity. The protective effect of HbAS and the increased susceptibility of HbAA individuals are well supported by both local and international studies.

However, slight variations observed, particularly among HbSS individuals, highlight the need for further research, especially in localized settings such as Zainab Bulkachuwa Hospital.

Reference

Artificial Intelligence technology (ChatGPT, developed by OpenAI) was used in the development of this paper to assist in improving language clarity, structure, and coherence of the manuscript. The tool was not used to generate data, analyze results, or draw scientific conclusions. We (The authors) have thoroughly reviewed and verified all contents to ensure accuracy, originality, and intellectual integrity, and take full responsibility for the work presented in this paper.

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