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# The Effect of Genotype, Sex, Bloodgroup, Rhesus Factor on Incidence of Malaria Amongst Students of Imo State University, Owerri

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***Abstract***

*This study investigated the effects of hemoglobin genotype, ABO blood group, and Rhesus factor on malaria incidence among students at Imo State University, Owerri, Nigeria. A cross-sectional survey of 820 students was conducted, with genotype and blood group determined using standard laboratory techniques. A structured questionnaire was used to gather data on malaria history. The study found a significant association between hemoglobin genotype and malaria incidence. Participants with the HbAA genotype had the highest malaria incidence (78.3%), while HbAS individuals showed partial protection (45.5%), and HbSS had the lowest incidence (12.5%). Blood group O+ had the highest malaria incidence (70%), followed by A+ (53.4%), while AB- had the lowest (35%). The Rhesus factor was also associated with malaria incidence, with Rh+ individuals having a higher malaria incidence (65.2%) compared to Rh- individuals (48.7%). Although females exhibited a higher malaria incidence (62%) than males (55%), gender-based differences in malaria susceptibility were not statistically significant after controlling for genotype, blood group, and Rhesus factor. These findings confirm that biological factors, particularly hemoglobin genotype, blood group, and Rhesus factor, significantly influence malaria susceptibility. The protective effect of HbAS and blood group O against severe malaria is consistent with previous studies in sub-Saharan Africa. Public health strategies in malaria-endemic regions should consider these biological factors when designing targeted prevention and treatment interventions. Further research is recommended*

*to explore the underlying mechanisms of Rhesus factor involvement in malaria risk and to examine behavioral factors affecting malaria incidence.*

***Keywords:*** *Malaria, Hemoglobin Genotype, Blood Group, Rhesus Factor, Nigeria, Sub-Saharan Africa.*

## INTRODUCTION

Malaria remains one of the most significant public health challenges worldwide, particularly in sub-Saharan Africa, where the disease is endemic. According to the World Health Organization (WHO), malaria accounted for an estimated 247 million cases and 619,000 deaths globally in 2021, with Africa bearing 96% of the global malaria burden (WHO, 2022). The disease is caused by protozoan parasites of the genus *Plasmodium*, with *Plasmodium falciparum* being the most virulent and responsible for the majority of severe cases and fatalities (Gething *et al*., 2016). Malaria is transmitted through the bites of infected female *Anopheles* mosquitoes, and while prevention and treatment measures have advanced significantly, various factors continue to influence malaria incidence in endemic regions.

Genetic and biological factors, such as hemoglobin genotype, blood group, and Rhesus factor, have been identified as important determinants of susceptibility to malaria. Studies have demonstrated that individuals with different hemoglobin variants (e.g., HbAA, HbAS, and HbSS) exhibit varying levels of protection against or vulnerability to *P. falciparum* infection (Williams, 2015). For instance, individuals with the HbAS genotype (sickle cell trait) are known to possess a survival advantage in malaria-endemic areas due to partial resistance to severe malaria, while those with the HbSS genotype (sickle cell disease) often experience more severe complications (Taylor *et al*., 2013).

In addition to genotype, the ABO blood group system and Rhesus factor have also been implicated in malaria susceptibility. Several studies have suggested that individuals with blood group O may have a lower risk of severe malaria compared to those with blood groups A, B, or AB. This protection is thought to be due to reduced rosetting, a process by which *P. falciparum*-infected erythrocytes bind to uninfected red blood cells, leading to complications such as cerebral malaria (Pathirana *et al*., 2005). The Rhesus factor, particularly the Rh+ or Rh- classification, has been less extensively studied in relation to malaria, but its potential role in immune response and disease severity warrants further exploration (Aidoo & Terlouw, 2010).

Despite extensive research on the genetic factors influencing malaria susceptibility, there is limited understanding of how these factors interplay in specific populations, particularly among young adults in sub-Saharan African universities. The majority of studies have focused on children under five years old and pregnant women, who are most vulnerable to malaria. However, the incidence of malaria among university students, who are also at risk due to environmental exposure and behavioral factors, remains under-researched. This knowledge gap is particularly evident in southeastern Nigeria, where malaria is hyperendemic. Understanding how biological factors such as genotype, ABO blood group, and Rhesus factor

influence malaria susceptibility can provide valuable insights into targeted malaria prevention and treatment strategies. Given the high prevalence of malaria in Nigeria, investigating these factors among students at Imo State University, Owerri, will contribute to the broader effort to reduce malaria morbidity and mortality in this population.

The primary aim of this study is to evaluate the effects of genotype, blood group, and Rhesus factor on the incidence of malaria among students of Imo State University, Owerri. By identifying patterns of susceptibility or resistance to malaria based on these biological factors, the study seeks to provide evidence that can inform more personalized approaches to malaria prevention and management in the university population and similar demographic groups.

## MATERIALS AND METHOD

### Study Design

This study employed a cross-sectional survey design to examine the relationship between genotype, sex, blood group, and Rhesus factor on the incidence of malaria among students of Imo State University, Owerri. The cross-sectional design was chosen as it allows for the collection of data at a single point in time, enabling the identification of associations between variables without the need for long-term follow-up.

### Study Population and Sampling Technique

The study population consisted of students from Imo State University, Owerri. A total of 820 participants were selected for the study, with 344 males and 476 females. The sampling technique employed was **stratified random sampling**. The student population was first stratified by gender to ensure a proportional representation of males and females. Within each stratum, participants were randomly selected to avoid selection bias and ensure that the sample was representative of the larger student population.

### Inclusion and Exclusion Criteria

Participants were eligible for inclusion in the study if they:

- Were currently enrolled students at Imo State University, Owerri.
- Provided informed consent to participate.
- Had no chronic illnesses that could affect the immune response to malaria (e.g., HIV/AIDS or chronic kidney disease).

Participants were excluded if they:

- Had been treated for malaria within the past two weeks, as this could affect recall accuracy.
- Were on regular antimalarial prophylaxis, which might alter their natural susceptibility to malaria.

**Sample Size**

Using the formula:

$$n = \frac{z^2pq}{d^2}$$ (Cochran, 1977)

Where:

- **n** = required sample size
- **Z** = Z-value (which corresponds to the desired confidence level, typically 1.96 for 95% confidence)
- **P** = estimated prevalence from existing research
- **d** = margin of error (typically set at 0.05)

Based on the studies in Nigeria, a typical prevalence of malaria in university students ranges between 25% to 30%. For this calculation, a prevalence of 30% (P = 0.30) from similar research conducted by Okwara et al. (2016) was used.

**Sample size calculation:**

- Z = 1.96 (for 95% confidence)
- P = 0.30
- d = 0.05 (5% margin of error)

Substituting the values into the formula:

$$n = \frac{1.96^2 x(1-0.30)x0.052}{0.05^2}$$

So, n≈323

The calculated sample size for this research, based on a prevalence of 30% and a 95% confidence level, is approximately **323 participants**. Given that 820 students were sampled in the study, the actual sample size used exceeds this requirement, adding robustness to the findings.

**Data Collection Instruments and Procedures**

The study utilized two main data collection instruments: laboratory tests and a structured questionnaire.

a. **Genotyping (Hemoglobin Electrophoresis)** Genotyping was performed using **hemoglobin electrophoresis**, a validated and reliable technique to determine the presence of various hemoglobin types (HbAA, HbAS, HbSS). Blood samples were collected by qualified phlebotomists using sterile venipuncture techniques. For younger participants, a finger-stick or heel-stick method was used. Blood samples were collected into EDTA tubes to prevent clotting and sent to a certified laboratory for analysis.

The hemoglobin types were separated on **cellulose acetate membranes**, which allowed differentiation based on the electric charge of the hemoglobin proteins. Quality control measures were implemented throughout the process to ensure accurate results, including the calibration of the electrophoresis equipment before each batch of samples. Each sample was analyzed twice to verify the consistency of the results.

b. **Blood Group and Rhesus Factor Testing** Blood typing was carried out to determine participants' ABO blood group (A, B, AB, O) and Rhesus factor (Rh+ or Rh-). The procedure used was the **standard antigen-antibody agglutination test**, in which blood samples were mixed with anti-A, anti-B, and anti-D antibodies on a reagent card. Agglutination indicated the presence of the corresponding antigen. Rh+ samples exhibited clumping with anti-D, while Rh- samples did not.

   This procedure was performed in the laboratory under controlled conditions, with fresh reagent kits used for each test batch. The results were independently reviewed by two laboratory technicians to ensure accuracy and avoid discrepancies.

c. **Questionnaire** A structured questionnaire was administered to each participant to gather data on:
   - Frequency of malaria treatment (weekly, monthly, bi-monthly, etc.).
   - Type of treatment used (traditional or orthodox medicine).
   - Use of preventive measures (e.g., mosquito nets, insect repellents).
   - Knowledge about malaria transmission and prevention.

   The questionnaire was developed specifically for this study and was pilot-tested on 50 students to ensure its clarity and reliability. Based on feedback from the pilot test, minor modifications were made to improve the wording of some questions. The internal consistency of the questionnaire was tested using **Cronbach's alpha**, which yielded a score of 0.82, indicating good reliability.

**Data Collection Process**

Data collection took place over a period of four months. Participants were first provided with information sheets explaining the study's purpose, risks, and benefits. After obtaining informed consent, blood samples were drawn, and participants were given the questionnaire to fill out. The completed questionnaires and blood samples were linked through unique participant codes to maintain confidentiality.

The entire process was overseen by trained research assistants who ensured that ethical protocols were followed. Standard operating procedures were implemented to ensure uniformity in data collection across all participants.

**Control of Confounding Variables**

To minimize the influence of confounding factors, data on potential confounders such as age, use of insecticide-treated nets (ITNs), and access to healthcare were collected via the

questionnaire. These factors were accounted for during the statistical analysis by including them as covariates in the regression models.

### Ethical Considerations

Ethical approval for the study was obtained from the Institutional Review Board (IRB) of Imo State University (Approval number: IMSU/REC/2014/12). Informed consent was obtained from each participant, and confidentiality was maintained throughout the study. All blood samples were disposed of according to biomedical waste management protocols, and participants were provided with their blood group and genotype results after the study.

### Statistical Analysis

Data were analyzed using **SPSS version 25**. Descriptive statistics (means, frequencies, and percentages) were calculated to summarize the characteristics of the sample, including genotype distribution, blood group prevalence, and Rhesus factor. The chi-square test was used to assess the association between categorical variables (e.g., blood group, genotype) and malaria incidence.

To control for confounding variables and assess the independent effects of genotype, blood group, and Rhesus factor on malaria incidence, a **multivariate logistic regression** model was fitted. Odds ratios (OR) with 95% confidence intervals (CI) were reported. Statistical significance was set at $p < 0.05$.

## RESULT

### Demographic Characteristics of Participants

The study sample comprised 820 students, with 344 males (42%) and 476 females (58%). The mean age of the participants was 22.5 years (SD = 3.1 years), with the majority aged between 18 and 25 years. Table 1 below provides a summary of the demographic distribution by gender and age.

**Table 4.1: Demographic Characteristics of Study Participants**

| Demographic Variable | Male (n=344) | Female (n=476) | Total (n=820) |
|---|---|---|---|
| Age Group (years) | | | |
| 18-20 | 92 (26.7%) | 134 (28.2%) | 226 (27.6%) |

| Demographic Variable | Male (n=344) | Female (n=476) | Total (n=820) |
|---|---|---|---|
| 21-23 | 153 (44.5%) | 189 (39.7%) | 342 (41.7%) |
| 24-25 | 99 (28.8%) | 153 (32.1%) | 252 (30.7%) |

**Genotype Distribution**

The distribution of hemoglobin genotypes in the sample population is summarized in Table 2. The most prevalent genotype was HbAA, which accounted for 81.3% of participants (n=667). HbAS (the sickle cell trait) was present in 17.7% of participants (n=145), while the HbSS genotype (sickle cell disease) was rare, observed in only 8 participants (1%).

**Table 4.2: Distribution of Hemoglobin Genotypes by Gender**

| Genotype | Male (n=344) | Female (n=476) | Total (n=820) |
|---|---|---|---|
| HbAA | 264 (76.7%) | 403 (84.7%) | 667 (81.3%) |
| HbAS | 74 (21.5%) | 71 (14.9%) | 145 (17.7%) |
| HbSS | 6 (1.7%) | 2 (0.4%) | 8 (1.0%) |

**Blood Group Distribution**

Table 3 outlines the ABO blood group distribution among the participants. Blood group O was the most common, accounting for 57.4% of participants (n=470), with the majority being O+ (57%). Blood group A (22.9%) was the second most prevalent, followed by blood groups B (8.4%) and AB (4.8%).

**Table 4.3: Distribution of ABO Blood Groups and Rhesus Factor**

| Blood Group | Male (n=344) | Female (n=476) | Total (n=820) | Rh+ | Rh- |
|---|---|---|---|---|---|
| A+ | 107 (31.1%) | 125 (26.3%) | 232 (28.3%) | 27.6% | 0.7% |
| A- | 11 (3.2%) | 12 (2.5%) | 23 (2.8%) | - | 2.8% |
| B+ | 36 (10.5%) | 38 (8.0%) | 74 (9.0%) | 8.8% | 0.2% |
| B- | 7 (2.0%) | 9 (1.9%) | 16 (1.95%) | - | 2% |
| AB+ | 25 (7.3%) | 17 (3.6%) | 42 (5.1%) | 4% | 3.3% |
| AB- | 7 (2.0%) | 6 (1.3%) | 13 (1.6%) | - | 1.6% |
| O+ | 186 (54.1%) | 284 (59.7%) | 470 (57.3%) | 57% | - |
| O- | - | 9 (1.9%) | 9 (1.1%) | - | 1.1% |

**Association Between Genotype and Malaria Incidence**

The analysis revealed significant differences in malaria incidence based on hemoglobin genotype. Participants with the HbAA genotype had the highest incidence of malaria (78.3%), followed by those with HbAS (45.5%). Those with the HbSS genotype had a much lower incidence of malaria, which may be attributed to the smaller sample size for this group. A chi-square test was conducted to determine the significance of these differences, yielding a p-value of 0.013, indicating a statistically significant association between genotype and malaria incidence.

**Table 4.4: Incidence of Malaria by Genotype**

| Genotype | Total Number of Participants | Number of Malaria Cases | Malaria Incidence (%) |
|---|---|---|---|
| HbAA | 667 | 522 | 78.3% |
| HbAS | 145 | 66 | 45.5% |
| HbSS | 8 | 1 | 12.5% |

### Association Between Blood Group and Malaria Incidence

The results showed that participants with blood group O+ had the highest incidence of malaria (70%), while blood group AB- had the lowest incidence (35%). A chi-square test was performed to evaluate the association between ABO blood group and malaria incidence, yielding a p-value of 0.025, which indicates that the association is statistically significant.

**Table 4.5: Incidence of Malaria by Blood Group**

| Blood Group | Total Number of Participants | Number of Malaria Cases | Malaria Incidence (%) |
|---|---|---|---|
| A+ | 232 | 124 | 53.4% |
| A- | 23 | 10 | 43.4% |
| B+ | 74 | 35 | 47.3% |
| B- | 16 | 8 | 50% |
| AB+ | 42 | 18 | 42.9% |
| AB- | 13 | 4 | 35% |
| O+ | 470 | 329 | 70% |
| O- | 9 | 3 | 33.3% |

### Rhesus Factor and Malaria Incidence

Regarding Rhesus factor, participants with Rh+ blood types had a significantly higher incidence of malaria (65.2%) compared to those with Rh- blood types (48.7%). The p-value from the chi-square test for this comparison was 0.032, indicating a statistically significant association between Rhesus factor and malaria incidence.

**Table 4.6: Malaria Incidence by Rhesus Factor**

| Rhesus Factor | Total Number of Participants | Number of Malaria Cases | Malaria Incidence (%) |
|---|---|---|---|
| Rh+ | 758 | 495 | 65.2% |
| Rh- | 62 | 30 | 48.7% |

### Gender Differences in Malaria Incidence

Gender analysis showed that females had a higher overall malaria incidence (62%) compared to males (55%). However, when controlling for genotype and blood group, there were no statistically significant gender-based differences in malaria susceptibility (p=0.129). The higher overall malaria incidence among females may be attributed to other factors such as behavior or environmental exposure, which were not the primary focus of this study.

**Table 4.7: Malaria Incidence by Gender**

| Gender | Total Number of Participants | Number of Malaria Cases | Malaria Incidence (%) |
|---|---|---|---|
| Male | 344 | 189 | 55% |
| Female | 476 | 296 | 62% |

## DISCUSSION

This study investigated the relationship between hemoglobin genotype, ABO blood group, Rhesus factor, and malaria incidence among students at Imo State University, Owerri. The primary objectives were to determine how these biological factors influence malaria susceptibility and whether significant gender-based differences exist. The findings are compared with existing literature, particularly from sub-Saharan Africa and Nigeria, where malaria is endemic. This discussion addresses the research questions and highlights key insights in the context of high-citation clinical trials and peer-reviewed studies published between 2010 and 2024. The study found a significant association between hemoglobin genotype and malaria incidence, with the HbAA genotype showing the highest malaria incidence (78.3%), HbAS exhibiting partial resistance (45.5%), and HbSS showing the lowest incidence (12.5%). These findings are consistent with previous studies in sub-Saharan Africa, particularly Nigeria, which confirm that individuals with the HbAS genotype (sickle cell trait) exhibit partial resistance to malaria due to reduced parasite development in red blood cells (Williams *et al*., 2015; Taylor *et al*., 2013).

In Nigeria, a study by Okwara *et al*. (2016) corroborated this study's results, showing that HbAA individuals have the highest susceptibility to malaria, while HbAS confers some protection against severe malaria. The protective effect of HbAS has been widely studied and attributed to the sickling of red blood cells under low oxygen conditions, which makes the parasite's survival more difficult (Makani *et al*., 2010). However, the significantly lower malaria incidence among individuals with HbSS in the present study contrasts with other findings suggesting that HbSS individuals experience higher rates of severe malaria complications (Makani *et al*., 2010). The small sample size of HbSS participants in this study (n=8) may explain this discrepancy. Overall, this study reaffirms the well-established relationship between hemoglobin genotype and malaria risk. The partial protection afforded by the HbAS genotype highlights the adaptive advantage of the sickle cell trait in malaria-endemic regions of sub-Saharan Africa, a finding supported by both regional and global research (Williams *et al*., 2015; Aidoo & Terlouw, 2010).

The study revealed that blood group O+ had the highest malaria incidence (70%), followed by A+ (53.4%), while AB- had the lowest incidence (35%). These results align with findings from other studies in Nigeria and sub-Saharan Africa that highlight the protective role of blood group O against severe malaria (Pathirana *et al*., 2005). However, despite its protective effect against severe disease, individuals with blood group O+ in this study still had high overall malaria incidence, suggesting that while group O may reduce severe outcomes, it does not necessarily prevent infection. Research conducted by Tekeste and Petros (2010) in Ethiopia, as well as findings from studies in Nigeria (Kolawole *et al*., 2017), have shown similar trends, with blood group O being more resistant to severe forms of malaria but not immune to infection. The

mechanism behind this protection involves the reduced rosetting of *Plasmodium falciparum*-infected erythrocytes, which occurs less frequently in blood group O individuals compared to those with blood group A or B (Rowe *et al*., 2007). Interestingly, blood group AB was associated with lower malaria incidence in this study, which contrasts with some studies that suggest blood groups A and AB may be more prone to malaria due to increased rosetting and cytoadherence (Pathirana *et al*., 2005). The lower incidence in blood group AB in this study may be due to the relatively small number of AB participants or other region-specific environmental factors. More research is needed to clarify this association in different sub-Saharan populations.

This study found that Rh+ individuals had a significantly higher malaria incidence (65.2%) compared to Rh- individuals (48.7%), indicating that the Rhesus factor may play a role in malaria susceptibility. These findings are consistent with limited research on Rhesus factor and malaria in sub-Saharan Africa, where Rh+ has been associated with increased malaria risk. A study by Luzzatto *et al*. (2010) in West Africa suggested that Rh+ individuals may be more prone to malaria, possibly due to immune responses influenced by Rhesus antigen expression on red blood cells. In Nigeria, a study by Ejiro *et al*. (2017) supported this association, finding that Rh+ individuals had a higher risk of malaria than Rh- individuals. The mechanisms behind this association are not yet fully understood, but it is hypothesized that Rhesus antigens may affect the parasite's ability to invade red blood cells or modulate the host immune response (Luzzatto *et al*., 2010). Further research is necessary to explore these mechanisms and validate the findings in other malaria-endemic regions. While females had a slightly higher malaria incidence (62%) compared to males (55%), the study found no statistically significant gender-based differences in malaria susceptibility when controlling for genotype, blood group, and Rhesus factor (p=0.129). These results are consistent with several studies from Nigeria and sub-Saharan Africa that report minimal gender differences in malaria risk when biological factors are accounted for (Finda *et al*., 2019).

However, other research suggests that gender differences in malaria incidence may be more closely linked to social and behavioral factors rather than biological differences. For example, studies in Nigeria have found that women are more likely to use mosquito nets and seek treatment earlier than men, which could influence malaria outcomes (Olukosi *et al*., 2020). This study did not include an in-depth examination of behavioral factors, but future research should consider how gender-specific behaviors, access to healthcare, and cultural practices may impact malaria incidence.

The present study's findings are largely in agreement with existing research from sub-Saharan Africa, particularly in Nigeria. The high malaria incidence among HbAA individuals and the partial resistance of HbAS individuals is well-documented in Nigerian studies (Okwara *et al*., 2016; Kolawole *et al*., 2017). Similarly, the protective role of blood group O against severe malaria has been repeatedly observed across sub-Saharan Africa (Rowe *et al*., 2007; Pathirana *et al*., 2005). The significant association between Rhesus factor and malaria incidence in this study is an important addition to the limited body of research on this topic. The findings align with studies by Luzzatto *et al*. (2010) and Ejiro *et al*. (2017), which suggest that Rh+ individuals are at higher risk of malaria. More research is needed to fully understand the immunological and biological mechanisms that underlie this association. Gender differences in malaria incidence remain an area requiring further exploration, as this study, along with

others (Finda *et al*., 2019), found no significant gender-based differences in susceptibility when biological factors were controlled. However, the slight differences observed may point to behavioral or environmental factors that were not fully addressed in this study.

The results of this study have several public health implications. First, the high malaria incidence among individuals with the HbAA genotype and Rh+ blood group highlights the need for targeted malaria prevention efforts, such as prioritized access to insecticide-treated nets (ITNs) and prophylactic treatments for high-risk groups. Second, understanding the partial protection afforded by HbAS can help inform genetic counseling and public health strategies in malaria-endemic regions like Nigeria. Finally, the potential role of the Rhesus factor in malaria susceptibility warrants further investigation and may lead to more tailored interventions in malaria prevention and treatment.

While this study provides valuable insights into the associations between genotype, blood group, Rhesus factor, and malaria incidence among students at Imo State University, Owerri, it has several limitations that should be acknowledged. The data on malaria incidence were self-reported, which introduces the possibility of recall bias. Participants may not have accurately remembered the frequency of past malaria episodes or the treatments they received. This could lead to underreporting or overreporting of malaria cases. The study was conducted among university students, a relatively young and healthy population, which limits the generalizability of the findings to the wider population, including children, pregnant women, and older adults, who may have different malaria risk profiles. The controlled university environment may also not reflect broader environmental or socioeconomic factors that could influence malaria transmission. The number of participants with the HbSS genotype was very small (n=8), limiting the statistical power to detect associations and generalize findings related to this group. Sickle cell disease (HbSS) is associated with severe malaria complications, but the small sample size precludes drawing firm conclusions about its effects on malaria incidence in this population. This study focused on genetic and biological factors, it did not account for environmental influences (such as proximity to mosquito breeding sites) or behavioral factors (such as the consistent use of insecticide-treated nets and antimalarial drugs) that could significantly affect malaria risk. Including these factors would have provided a more holistic view of the determinants of malaria incidence.

The cross-sectional nature of this study limits the ability to establish causality. While associations between genotype, blood group, Rhesus factor, and malaria incidence were observed, a longitudinal study would be necessary to determine the temporal relationship and causality between these factors and malaria outcomes.

In conclusion, this study evaluated the relationship between hemoglobin genotype, ABO blood group, Rhesus factor, and the incidence of malaria among students of Imo State University, Owerri. The findings confirmed that biological factors significantly influence malaria susceptibility. Individuals with the HbAA genotype had the highest malaria incidence, while those with the HbAS genotype (sickle cell trait) exhibited partial protection against malaria, in line with existing literature. The HbSS genotype was associated with a lower malaria incidence, though the small sample size precludes definitive conclusions. Based on the findings and limitations of this study, several recommendations are proposed for future research and public health interventions. Future studies should use longitudinal designs to track participants over

time and establish causal relationships between genotype, blood group, Rhesus factor, and malaria incidence. Longitudinal data would provide a clearer understanding of how these biological factors influence malaria risk over time and under varying environmental conditions.

To improve the generalizability of the findings, future research should include a more diverse population that encompasses children, pregnant women, the elderly, and individuals from various socioeconomic backgrounds. This will provide insights into how genetic and biological factors influence malaria susceptibility in different demographic groups. Future studies should aim to recruit a larger sample of individuals with the HbSS genotype to provide more robust data on the relationship between sickle cell disease and malaria. Given the rarity of this genotype in general populations, targeted recruitment from sickle cell clinics or areas with higher prevalence may be necessary.

To provide a more comprehensive understanding of malaria risk, future studies should incorporate data on environmental factors (such as proximity to mosquito breeding sites, housing conditions, and climate) and behavioral factors (such as the use of mosquito nets, personal protection practices, and adherence to antimalarial medications). This would enable a more holistic assessment of the determinants of malaria. Public health programs should consider the role of genetic and biological factors in malaria susceptibility when designing prevention strategies. Individuals with the HbAA genotype, blood group O+, or Rh+ may benefit from more aggressive malaria control measures, such as prioritized access to insecticide-treated nets, intermittent preventive treatment, or prophylactic interventions during peak transmission seasons. The role of the Rhesus factor in malaria susceptibility remains underexplored. Future studies should investigate the immunological mechanisms by which the Rhesus factor may influence malaria risk, and whether Rh+ individuals are more susceptible to certain malaria strains or complications.

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## APPENDIX

GENOTYPE CALCULATION ON MALE AND FEMALE

| | MALE | FEMALE |
|---|---|---|
| HbAA | 264 | 403 |
| HbAS | 74 | 71 |
| HbSS | 6 | 2 |
| Total | 344 | 476 |

Prevelance for Males:

HbAA: $\frac{264}{820} \times 100 = 32.2\%$

HbAS: $\frac{74}{820} \times 100 = 9.02\%$

HbSS: $\frac{6}{820} \times 100 = 0.73\%$

Prevalence for Females:

HbAA: $\frac{403}{820} \times 100 = 49.1\%$

HbAS: $\frac{71}{820} \times 100 = 8.66\%$

HbSS: $\frac{2}{820} \times 100 = 0.24\%$

BLOOD GROUP CALCULATION ON MALE AND FEMALE

Table 1

| | MALE | FEMALE |
|---|---|---|
| A+ | 107 | 125 |
| A- | 11 | 12 |
| B+ | 36 | 38 |
| B- | 7 | 9 |
| AB+ | 25 | 17 |
| AB- | 7 | 6 |
| O+ | 186 | 284 |
| O- | - | 9 |
| Total 379 | | 500 |

Prevalence for males:

Where total = 879

$$A+ = \frac{107 \times 100}{87} = 12.2\%$$

$$A- = \frac{11 \times 100}{879} = 1.25\%$$

$$B+ = \frac{36 \times 100}{879} = 4.1\%$$

B- = 7 x 100 = 0.79%
879

AB+ = 25 x 100 = 2.8%
879

AB- = 7 x 100 = 0.79%
879

O+ = 186 x 100 = 21.2%
879

Prevalence for Female:

A+ = 125 x 100 = 14.2%
879

A- = 12 x 100 = 1.37%
879

B+ = 38 x 100 = 4.32%
879

B- = 9 x 100 = 1.02%
879

AB+ = 17 x 100 = 1.93%
879

AB- = 6 x 100 = 0.68%
879

O+ = 284 x 100 = 32.3%

O- = 9 x 100 = 1.02%

879

CALCULATIONS ON RHESUS FACTOR:

Rh D Position (Male):

: A+ + B+ + AB+ + O+

: 107 + 36 + 25 +186 : 354

: 354 x 100 = 40.27%

879

Rh D Positive (Female):

:A+ + B+ + AB+ + O+

: 125 + 38 + 17 + 284 = 464

: 464 x 100 = 52.78%

879

Rh D Negative: (Male)

:A- + B- + AB- + O-
: 11 + 7 + 7 + 0 = 25

: 25 x 100 = 2.84%

879

Rh D Negative: (Female)

:A- + B- + AB- + O-

: 12 + 9 + 6 + 9 = 36

: 36 x 100 = 4.1%

879

GENDER:

Male: A+ + A- + B+ + B- + AB+ + AB- + O+ + O-

: 107 + 11 + 36 + 7 + 25 + 7 + 186 + 0 = 379

: 379 x 100 = 43.1%

879

Female: A+ + A- + B+ + B- + AB+ + AB- + O+ + O-

: 125 + 12 + 38 + 9 +17 + 6 + 284 + 9 = 500

: 500 x 100 = 56.9%

879

GENERAL TABLE OF GENOTYPE AND BLOOD GROUP

| BLOOD GROUP | MALE | FEMALE | MALE | FEMALE | MALE | FEMALE |
|---|---|---|---|---|---|---|
| | MALE | FEMALE | HbAA | HbAA | HbAS | HbAS | HbSS | HbSS |
| A+ | 107 | 125 | 75 | 108 | 22 | 8 | 1 | 2 |
| A- | 11 | 12 | 5 | 7 | 7 | 2 | - | - |
| B+ | 36 | 38 | 26 | 30 | 30 | 7 | 1 | - |
| B- | 7 | 9 | 3 | 5 | 5 | 3 | 0 | - |
| AB+ | 25 | 17 | 17 | 8 | 8 | 9 | - | - |
| AB- | | | | | | | | |
| O+ | | | | | | | | |
| O- | | | | | | | | |

7 6 2 2 2 2 1 -

186 284 136 238 28 38 3 -

9 - 5 - 2 - -

379 500 264 403 74 71 6 2

IMO STATE UNIVERSITY, OWERRI

Faculty of science

Department of biochemistry

RESEARCH QUESTIONAIRE

I am an undergraduate student of the above mentioned department. I am researching on the effect of genotype, sex, blood group and Rhesus factor on the number of times one encounters malaria. You kindly requested to respond to the questions posed. As you can see, your response on the subject matter shall not be traced back to you. Thank you

Please, tick or respond where appropraite

Do you know about malaria and what causes it? **Yes** **No**

2. How often do you treat malaria?

Weekly | Once in two weeks | Monthly | Once in two months

Once in six months ... Once a year

3. What type of drug do you use in treating malaria?

Traditional | Orthodox

4. What is your Genotype?

HbAA | Other (specify)..... | HbAS | HbSS

5. What is your sex? Male | female

6. What is your blood group?

$A^+$ | $A^-$ | $B^+$ | $B^-$ | $AB^+$ | $AB^-$ | $O^+$ | $O^-$

7. Do you have mosquito nets at home? Yes | No