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Geographic Variation in *Plasmodium* Infection Intensity and Species Distribution among Children under Five: Evidence from Four Slums of Gombe State, Nigeria

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ABSTRACT

Background: Malaria transmission is geographically heterogeneous, even within small areas sharing similar climatic conditions. Understanding how infection intensity and *Plasmodium* species composition vary across communities is essential for rational targeting of malaria control resources. Objective: This study examined whether significant differences in malaria parasite seen (MPS) and *Plasmodium* species distribution exist across four communities among children under five years of age, between November 2024 to February 2026. Methods: A cross-sectional study enrolled 1,162 children under five from Dawaki (n = 272), Tabra Galdimari (n = 296), TudunHatsi (n = 294), and ZirinGaza (n = 300). Blood smear microscopy assessed parasite density (MPS) and identified *Plasmodium* species. Pearson chi-square tests and Cramer's V evaluated the association between study location and each infection outcome. Results: Highly significant associations were found between location and MPS ($\chi^2(9) = 344.76$, $p < .001$, $V = .314$) and location and *Plasmodium* species ($\chi^2(6) = 384.83$, $p < .001$, $V = .407$). Tudun Hatsi exhibited the highest moderate parasitaemia burden (92.9%) with no high-density infections, while Tabra Galdimari had the highest negativity rate (44.3%) and greatest proportion of high-density infections (6.4%). *P. malariae* was detected exclusively in Dawaki (25.0% of that site's sample)and absent from all other communities. Conclusion: Substantial and statistically meaningful geographic variation in malaria infection intensity and species composition exists across adjacent communities. These findings support site-specific malaria surveillance and targeted intervention strategies rather than uniform regional approaches.

Keywords: Geographic Variation; Malaria; *Plasmodium Falciparum*; *Plasmodium Malariae*; Community Epidemiology; Parasite Density; Children Under Five; Sub-Saharan Africa

INTRODUCTION

Malaria transmission is not uniform across endemic landscapes. Within distances of only a few kilometres, significant variations in parasite density, infection prevalence, and *Plasmodium* species composition can exist, driven by differences in vector ecology, housing quality, land use, proximity to water bodies, population immunity, and healthcare access (Bousema, *et al*, 2012; Stresman, 2010). This micro-geographic heterogeneity has important practical implications: interventions that are effective in one community may be insufficient or unnecessary in an adjacent one.

Despite growing recognition of malaria's spatial heterogeneity, many control programmes continue to rely on district- or region-level data to guide resource allocation. This approach risks both over-intervention in lower-burden areas and under-intervention in high-burden hotspots. The concept of malaria hotspotspatially defined areas of persistently high transmission has gained significant traction as a framework for precision malaria control (Bousema *et al*., 2012; Tusting*et al*., 2016). However, identifying such hotspots requires granular, community-level surveillance data that are often unavailable in resource-constrained settings.

Among the most important dimensions of geographic variation is *Plasmodium* species composition.*P. Falciparum* is the dominant malaria parasite across sub-Saharan Africa and is responsible for the majority of severe cases and death. However,*P. malariae* has a more focal distribution and is associated with distinct clinical outcomes, including quartan fever and malaria-associated nephropathy in chronically exposed children (Barsoum, 2000; Milner, 2018). Understanding the geographic boundaries of *P. malariae* transmission is therefore of both clinical and epidemiological relevance.

This study investigates the degree and nature of geographic variation in *Plasmodium* infection among 1,162 children aged 0–59 months across four communitiesDawaki, Tabra Galdimari, Tudun Hatsi, and Zirin Gaza, in Gombe State. Two key outcomes are examined: malaria parasite seen (MPS), as a measure of infection intensity, and *Plasmodium* species identified. By formally testing these associations and quantifying effect sizes, this paper seeks to generate actionable evidence for community-differentiated malaria control in this setting.

MATERIALS AND METHODS

Study Area

This study was carried out in Gombe Metropolis, the capital of Gombe State, located in the northeastern geopolitical zone of Nigeria. Gombe Metropoliscovers an area of 52 SquareKilometres the projected population of Gombe State in 2023 is 573,000 with density of 79 Square Kilometres hectares (UN), 2023 world population prospects). About 20% of the population of Gombe State live in Gombe City. Its

geographical coordinates range between latitude 10° 14' 30'' N and 10° 19' 30'' N and longitude 11° 7' 30'' E and 11° 13' 30'' E (Satellite image of Gombe State 2014). Gombe is mainly inhabited by Fulani, Bolewa, Tera, Tangale, Hausa, Kanuri, Waja and Tula people. There are eleven Local Government Areas in Gombe State namely:Billiri, Kaltungo, Shongom, Balanga, Akko, YelmatuDeba, Kwami, Dukku, Funakaye, Nafada and Gombe LGA's. There are five slums identified in Gombe Metropolis namely: Ziringaza, Tudunhatsi, Taura, Dawaki and Tabra. These urban settlements are inhabited by the urban poor, located in parts of the city where health services and other social services are not accessible. The environment is characterized by inadequate housing, poor sanitation, unsafe drinking water, heap of solid waste, blocked drainage and stagnant waters, which exposure to the risk of infectous diseases. Gombe City is situated at the heart of north east and this made it a popular resting spot for travelers and traders.

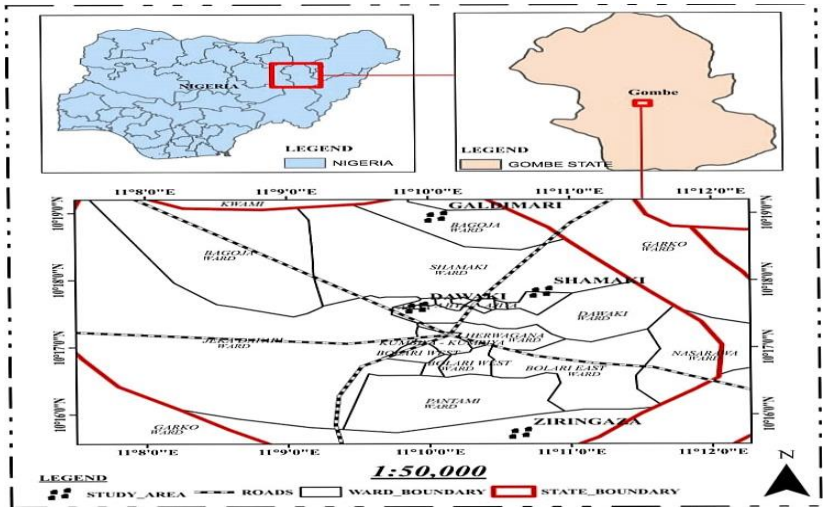

Figure 1: Map of Gombe State showing the study areas

Ethical Consideration

Ethical clearance to carry out this study was granted by the Health research ethics committee of Gombe State Ministry of Health and was assigned reference numberMOH/ADM/621/V.1/559. Approval was also obtained from Gombe State Primary Health Care Development Agency (GSPHCDA) with reference number GSPHCDA/ADM/44/VOL.1, to secure permission for sample collection within designated health care facilities.

Informed Consent Form

Informed consent was obtained from the parents/ guardians of the participating children and permission was sought from the community leader known as Hakimi. The form was written in English but were translated in Hausa language during administration. Participation was voluntary, and parents were informed that they could decline or withdraw their children at any time without penalty. Consent was then documented before any sample was collected.

Study Design

This was a cross-sectional study conducted across four communities in a malaria-endemic setting: Dawaki, Tabra TudunHatsi, and ZirinGaza. It was conducted at the household level and health facilities located near the slum areas. Data was collected using interview –administered questionnaire, Blood sample collections and analysis.

Sample Size Estimation

Sample size were calculated using Daniel (2013), formula for one sample size determination Formula

$$N = \frac{Z^2 P (1-P)}{d2}$$

Where N= minimum sample size

Z= Z-Score for the desired confidence level, which is 1.95

P=Prevalence of malaria in children under five, which is 23 %(NDHS) express as decimal, P=0.23.

d= level of precision which is 0.05.

To plug into formular:

$$N = \frac{(1.96)2x0.23(1-0.23)}{(0.05)2}$$

$$N = \frac{3.8416x0.23x0.77}{0.0025}$$

$$N = \frac{068034}{0.0025}$$

N= 272

Adjusted sample size after 5% non- response Rate: 272x (1+0.05) =286

Thus, 286 participants to be recruited per site, given an overall total of 1,144 for the 4 slums.

Study Population

Gombe State has five slums, among which four were selected due to financial constraint. Childrenunder the age of five attending health facilities or participating in community-based malaria screening within each study site were included. A total of 1,162 children were enrolled across the four sites. The minimum calculated sample size was 286 participant per sites, giving a total of 1,144 participants across the four sites. During field data collection, 1,162 eligible participants were ultimately enrolled. The additional 18 participants resulted from the field implementation process, where eligible participants who met the inclusion criteria were encountered and consented to participate.

Samples and Sampling Techniques

Multi-Stage sampling method was used to select study participant and areas to be studied.

First Stage

Four out of five slums in Gombe were selected by simple random sampling using ballot method.

Second Stage
The household was selected through systematic sampling method using the National Immunization plus Days micro-planning as a sample frame.

Third Stage
In each household, respondent were selected using inclusive and exclusive criteria.

Inclusive Criteria
The eligible households are those that have children under the age of five residing in the selected slum communities, whose parents filled informed consent for participation in the study.
Exclusive Criteria
The household without children of the required age was excluded. Those whose parent, did not provide the consent. The under five children, who were severely ill and required immediate emergency intervention. Also children who had received anti-malarial treatment within the period of data collection were excluded

Parasitological Examination of Blood Sample
A total of 1,162 blood samples were collected. It was analyzed within 3-4 hours after collection. A Thick and thin smear was prepared on a glass slide and labeled accordingly as recommended by (Cheesebrough, 2010) to determine the positive slides and parasites densities. The prepared slide was air dried and stained with Giemsa and examined microscopically using 100x oil immersion objective lens to observe *Plasmodium* parasite. Parasite density was determined by counting against 200 leucocytes, the parasitaemia was graded 1000/u as mild(+), 1000-9,999/u as moderate(++), or 10000/u as severe(+++) (Rogerson *et al*.,2000)

Plasmodium Species Identification
Positive thin smearswere examined for species morphology and classified as *P. malariae* or *P. falciparum.* No mixed infections or other species were identified.

Statistical Analysis
Pearson chi-square (χ^2) test was used to assess the association between study location and each outcome (MPS; *Plasmodium* species). Effect size was estimated using Cramer's V, interpreted as small (0.10–0.29), moderate (0.30–0.49), or large (≥ 0.50) following Cohen (1988). All analyses were conducted at $\alpha = 0.05$. Post-hoc inspection of standardized residuals was used to identify which specific location-category combinations drove significant associations. Analyses were conducted using SPSS version 28.0

RESULTS AND DISCUSSION

Overview of Infection by Location
Table 1 presents the overall sample distribution across the four study sites. Participant counts were broadly comparable: Dawaki (23.4%), Tabra Galdimari (25.5%), Tudun Hatsi (25.3%), and Zirin Gaza (25.8%). Despite this roughly equal representation, the four communities showed markedly different infection profiles, as detailed in the sections below.

Table 1: Sample Distribution by Study Location (N = 1,162)

Location	n	% of Total Sample
Dawaki	272	23.4
Tabra Galdimari	296	25.5
Tudun Hatsi	294	25.3
Zirin Gaza	300	25.8
Total	1,162	100.0

Note. Near-equal distribution across sites supports inter-site comparability.

Geographic Variation in Malaria Parasite Seen (MPS)
A highly significant and moderate-strength association was found between study location and MPS (χ^2 (9, N = 1162) = 344.76, p < .001, Cramer's V = .314). Table 2 presents MPS distribution disaggregated by location.
*TudunHats*i exhibited the most concentrated infection pattern: 92.9% of children had moderate-density infections (++), 7.1% were negative, and no low-density (+) or high-density (+++) infections were recorded. This remarkably uniform moderate burden suggests a stable, high-transmission environment with consistent exposure across the community.
Dawaki showed a predominantly moderate infection profile (68.0%), with a notable proportion of low-density infections (25.7%) and no high-density cases. The absence of high-density infections alongside the high rate of low-density positivity may reflect a population with some degree of acquired or partial immunity, or a setting with moderate vector pressure.
ZirinGaza presented a more dispersed profile: 52.3% moderate, 29.0% negative, 15.3% low density, and 3.3% high density. This distribution suggests heterogeneous exposure within the community, possibly due to variation in household-level protective factors.
Tabra Galdimari was the most epidemiologically distinct site. It recorded the highest negativity rate (44.3%) of all four communities, yet simultaneously the highest rate of high-density infection (6.4%). This bimodal pattern where many children are uninfected but those who are infected tend toward higher parasitaemia may indicate focal, intense transmission affecting a subset of the community, or seasonal effects on infection timing.

Table 2: Distribution of Malaria Parasite Seen by Location (N = 1,162)

Location	NIL (%)	(+) Low (%)	(++) Moderate (%)	(+++) High (%)	Total (n)
Dawaki	6.3	25.7	68.0	0.0	272
Tabra Galdimari	44.3	20.9	28.4	6.4	296
Tudun Hatsi	7.1	0.0	92.9	0.0	294
Zirin Gaza	29.0	15.3	52.3	3.3	300
Total	22.0	15.3	60.2	2.5	1,162

Note. Row percentages shown. $\chi^2(9) = 344.755$, $p < .001$, Cramer's V = .314 (moderate effect).

Geographic Variation in Plasmodium Species Identified

An even stronger association was observed between location and Plasmodium species ($\chi^2(6, N = 1162) = 384.83$, $p < .001$, Cramer's V = .407), approaching the threshold of a large effect. Table 3 presents species distribution by site.

The most striking finding was the exclusive presence of P. malariae in Dawaki, where it accounted for 25.0% of that site's sample. P. malariae was entirely absent from Tabra Galdimari, Tudun Hatsi, and Zirin Gaza. This binary geographic boundary present in one community and absent in three represents a highly localized species distribution that warrants specific investigation. P. falciparum was the sole species in the remaining three sites among positive cases.

Among the three P. falciparum-only sites, Tudun Hatsi had the highest P. falciparum positivity rate (92.9%), followed by Zirin Gaza (71.0%) and Tabra Galdimari (55.7%). These differences mirror the MPS findings and reinforce the interpretation that Tudun Hatsi has the highest active transmission burden of the four communities. P. falciparum prevalence in Dawaki, where *P. malariae* is accounted for, was 68.8% comparable to ZirinGaza.

Table 3: Plasmodium Species Identified by Location (N = 1,162)

Location	NIL (%)	P. malariae (%)	P. falciparum (%)	Total (n)
Dawaki	6.3	25.0	68.8	272
Tabra Galdimari	44.3	0.0	55.7	296
Tudun Hatsi	7.1	0.0	92.9	294
Zirin Gaza	29.0	0.0	71.0	300
Total	22.0	5.9	72.1	1,162

Note. Row percentages shown. χ^2 (6) = 384.830, $p < .001$, Cramer's V = .407 (moderate-large effect).

Summary of Inferential Statistics

Table 4: Summary of Chi-Square Test Results: Location vs Infection Outcomes

Hypothesis	χ^2 Value	df	p	Decision	Cramer's V	Effect Size
H_{01}: Location vs. MPS	344.755	9	< .001	Reject H_0	.314	Moderate
H_{02}: Location vs. Species	384.830	6	< .001	Reject H_0	.407	Moderate–Large

Note. All hypotheses tested at $\alpha = 0.05$.

Discussion

Magnitude of Geographic Variation

The effect sizes observed in this study (V = .314 for MPS; V = .407 for species) are among the most notable findings, indicating that geographic location is a substantively meaningful predictor of both infection intensity and species composition not merely a statistically significant one. A Cramer's V of .407 for species distribution approaches the threshold of a large effect, meaning that knowing a child's community provides meaningful predictive information about whether they will test positive for *P. malariae* or *P. falciparum*.

This level of geographic heterogeneity within a relatively contained study area is consistent with findings from spatially disaggregated malaria studies elsewhere in sub-Saharan Africa, which have demonstrated that community-level variation can rival or exceed variation explained by individual-level risk factors such as age and sex (Bousema*et al*, 2012; Gaudart*et al.*,2006). The implication is that treating these four communities as a single epidemiological unit for planning purposes would obscure critical differences in burden and species risk.

Tudun Hatsi: A High-Transmission Hotspot

TudunHatsi stands out as the community with the highest and most concentrated malaria burden. This near-universal moderate parasitaemia pattern is characteristic of high, perennial transmission in which virtually all children in the community are chronically exposed and infected, but where some degree of partial immunity may be attenuating progression to high-density disease (Langhorne *et al*., 2008). This profile warrants immediate prioritization for malaria control. Universal distribution of insecticide-treated bed nets (ITNs), indoor residual spraying (IRS), and community-level chemoprevention should be considered for TudunHatsi. The absence of high-density infections may be masking a significant burden of malaria-attributable anaemia, growth faltering, and cognitive impairment in this communityconditions associated with chronic moderate parasitaemia in young children (Crawley, 2004).

Tabra Galdimari: Focal High-Density Transmission

Tabra Galdimari presents a paradoxical profile having the highest negativity rate (44.3%) occuring alongside the highest proportion of high-density infections (6.4%). This finding suggests considerable heterogeneity in malaria transmission within the community, with infection concentrated among a subset of children rather than being uniformly distributed across the population. The observation is consistent with the findings of Oyibo, *et al.,* (2023*),* who demonstrated geographical variation in malaria parasite density among children under the age of five in Nigeria. Their nationwide analysis found that parasite densities were generally higher in northern Nigeria and that areas with higher malaria prevalence tended to have higher parasite densities. However, the present findings adds an important micro-geographical dimension, because the variation observed in Tabra occurred within a single urban-slum setting rather than between geopolitical zones or States. The relatively high proportion of children with high parasite density despite the high malaria –negativity, also differ from the pattern that might be expected in uniformly high transmission community. Oyibo, *et al*., (2023), reported a positive association between community malaria prevalence and parasite density at the State level., suggesting that higher prevalence accompanies greater parasite burden.

The contrasting pattern may indicate localized transmission hotspots, where particular household experience greater exposure to infected mosquito while others remain uninfected or cleared infection. Differences in proximity to breeding sites, housing conditions may contribute to this heterogeneity.

The Exclusive Presence of P. malariae in Dawaki

P. malariae's complete confinement to Dawaki where it accounted for 25.0% of the local samples, are the single most striking geographic finding in this study. This sharp spatial

boundary is unlikely to be a statistical artifact given the sample size and the strength of the association (V = .407). Several explanations merit investigation.

First, *P. malariae* is known to require a specific subset of *Anopheles* vector species for efficient transmission, and its geographic distribution may reflect local differences in vector community composition (Milner, 2018). If Dawaki hosts a vector species capable of transmitting both *P. falciparum* and *P. malariae*, while neighbouring communities' dominant vectors are less permissive to *P. malariae*, this could explain the observed distribution.

Second, human genetic factors including polymorphisms in red blood cell antigens to which *P. malariae* binds may differ between communities if they have distinct ethnic compositions or migration histories (Mueller *et al.,* 2009).

Third, the possibility of a locally persistent animal reservoir (primates are known hosts of a closely related parasite, *P. brasilianum*) warrants consideration if Dawaki is proximate to relevant wildlife habitats.

Clinically, the 25.0% *P. malariae* prevalence in Dawaki has direct implications. *P. malariae* is associated with nephrotic syndrome in children through immune complex deposition in the glomeruli (Barsoum, 2000). Clinicians and community health workers in Dawaki should be alert to renal complications in children with chronic or recurrent malaria, and diagnostic protocols should explicitly screen for *P. malariae* rather than defaulting to *P. falciparum*-only rapid diagnostic tests.

ZirinGaza: *Moderate Heterogeneous Burden*

Zirin Gaza's infection profile of 9.0% negative, 15.3% low density, 52.3% moderate and 3.3% high density suggests a moderately endemic community with more within-site heterogeneity than Tudun Hatsi. This pattern could reflect a mixture of protected and unprotected households, or temporal variation in transmission intensity. With 71.0% *P. falciparum* positivity overall, Zirin Gaza carries a significant burden and should not be deprioritised in favour of the more dramatically profiled Tudun Hatsi or Dawaki. The findings is comparable with evidence from southwestern Nigeria, were a study of children under the age of five in peri-urban communities reported a 71.7% prevalence of *P. falciparum* and a mean parasite density of 1,857 parasite/ul Awosolu, *et al*., (2021). The study also found particularly high prevalence and parasite density among under five children and identified stagnant water around homes as an important risk factors. However, the distribution of parasite density categories in Ziringaza differs from findings from other Nigerian populations. Hospital based study in southeastern Nigeria, only 22.6% of malaria positive children had light parasitaemia,where 77.4% had heavy parasitaemia Nwaneli, *et al*., (2020). The authors reported that under five children have the highest meanparasite density. In, contrast, the predominance of moderate density infections and low of high density infection in this area may indicate that most infected children were experiencing established but comparatively less intense infections at the time of sampling. The predominance of P. falciparum in Ziringaza, therefore agrees with the broader Nigerian epidemiological pattern, while the parasite density categories demonstrate the additional value of examining malaria at the community and micro-geographical level.

Implications for Malaria Control Policy

The findings of this study have three clear policy implications. First, malaria surveillance and programme planning in this setting should operate at the community level rather than the district level. The four communities studied show distinct enough profiles to warrant differentiated responses rather than a uniform approach. Second, Tudun Hatsi requires immediate scale-up of universal prevention, while Tabra Galdimari requires investigation of intra-community heterogeneity before intervention design. Third, Dawaki requires *P. malariae*-aware clinical protocols, entomological investigation, and potentially enhanced diagnostic capacity.

These findings also support the broader global call for precision malaria control using high-resolution spatial data to target interventions where they are most needed (Tusting*et al.,* 2016; WHO, 2023). Investment in community-level surveillance capacity is a prerequisite for this approach and should be reflected in national malaria programme budgets.

Limitations

Several limitations apply to this study. As a cross-sectional design, it captures infection at a single time point and cannot account for seasonal variation in transmission. Entomological data on vector species composition and density were not collected alongside clinical data, limiting mechanistic interpretation of geographic patterns. Community-level covariates housing quality, proximity to water, bed net coverage, and socioeconomic status are not systematically recorded, preventing formal mediation analysis of the geographic associations observed. Future studies coupling parasitological survey data with environmental, entomological, and household-level data would substantially advance understanding of why these communities differ.

CONCLUSION

This study demonstrates substantial, statistically significant, and epidemiologically meaningful geographic variation in *Plasmodium* infection intensity and species distribution across four adjacent communities. Tudun Hatsi emerges as the highest-burden site, characterized by near-universal moderate-density *P. falciparum* infection. Tabra Galdimari presents a paradoxical profile of high negativity alongside the greatest proportion of high-density infections. Most strikingly, *P. malariae* was detected exclusively in Dawaki entirely absent from all other communities a finding with significant clinical and entomological implications. These results make a compelling case for community-differentiated malaria surveillance and control, and highlight the risk of obscuring actionable local patterns through district-level aggregation.

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