Relative Abundance of Malaria Vector and Malaria Transmission in Keffi, Nasarawa State, Nigeria from 2019 To 2024

Attah, O. I.[1*]; Muhammed, A. O.[2]; Istifanus N.[3]

[1,2,3]Global Health and Inflectious Diseases and Control Institute, Nasarawa State University, Keffi.

Corresponding Author: Attah, O. I.[1*]

Abstract: This study assessed the relative abundance of malaria vectors and malaria transmission dynamics in Keffi, Nasarawa State, Nigeria, from 2019 to 2024. Malaria case data were obtained from the General Hospital, Keffi, while vector distribution and abundance data were sourced from the Presidential Malaria Initiative (PMI) Vector-Link database. Data were analysed using the chi-square test. A total of 53,077 Anopheles mosquitoes were collected during the study period. Anopheles gambiae sensu lato was the dominant vector, accounting for 83.2% of all collections, followed by Anopheles funestus (11.8%), while Anopheles nili was the least abundant (1.5%). Vector abundance varied significantly across the years ($p < 0.05$), with the highest collections recorded in 2024 (11,740) and 2021 (10,894), and the lowest in 2020 (3,418). Between 2019 and 2024, 6,650 patients were examined for malaria, of whom 4,084 tested positive, giving an overall prevalence of 61.4%. The highest malaria prevalence was recorded in 2023 (71.5%), followed by 2022 (69.0%), while the lowest prevalence occurred in 2020 (26.8%). Year-to-year variation in malaria prevalence was statistically significant ($p < 0.05$). A total of 15,272 Anopheles mosquitoes (An. Gambiae, An. Funestus, and An. Nili) were screened for Plasmodium species, with 2,013 found positive, yielding an overall sporozoite rate of 13.2%. Sporozoite rates differed significantly among vector species, with An. Gambiae showing the highest rate (14.6%), followed by An. Funestus (5.8%) and An. Nili (2.0%). Overall, malaria transmission in Keffi was primarily driven by Anopheles gambiae, with An. Funestus and An. Nili playing secondary roles. This study provides the first evidence of An. Nili contributing to malaria transmission in the area. The findings highlight the need for strengthened integrated vector management strategies, including indoor residual spraying, use of long-lasting insecticidal nets, and larval source management.

Keywords: *Malaria, Vector, Transmission.*

How to Cite: Attah, O. I.; Muhammed, A. O.; Istifanus N. (2026) Relative Abundance of Malaria Vector and Malaria Transmission in Keffi, Nasarawa State, Nigeria from 2019 To 2024. *International Journal of Innovative Science and Research Technology*, 11(1), 2634-2639. https://doi.org/10.38124/ijisrt/26jan1064

I. INTRODUCTION

Malaria is a mosquito-borne infectious disease that remains a major cause of morbidity and mortality in humans and other animals. In humans, the disease is caused by protozoan parasites of the genus *Plasmodium*, primarily *P. falciparum, P. malariae, P. ovale,* and *P. vivax*. Although less common, zoonotic transmission may occur when humans are infected with Plasmodium species that typically infect animals, such as *P. knowlesi* (WHO, 2013). Among these species, *P. falciparum* is the most virulent, owing to its high case-fatality rate, widespread resistance to antimalarial drugs, and predominance in highly endemic regions, particularly sub-Saharan Africa (Paton *et al.,* 2021). Malaria is transmitted mainly through the bite of an infected female Anopheles mosquito and accounts for approximately 80–90% of malaria-related morbidity and mortality worldwide (Alemu & Mama, 2016).

Malaria remains a leading cause of morbidity and mortality in many developing countries (Rumisha *et al.,* 2019; Romero *et al.,* 2021). The disease imposes substantial health, social, and economic burdens, particularly in tropical and subtropical regions. According to the World Health Organization (WHO, 2021), an estimated 241 million malaria cases and 627,000 malaria-related deaths were recorded globally in 2020 across 85 endemic countries. These figures represent increases of 6% in cases and 12% in deaths compared to 2019. The WHO African Region continues to bear the highest burden, accounting for approximately 228 million cases (95% of global cases), with Nigeria disproportionately affected, contributing about 27% of worldwide malaria cases and deaths (WHO, 2021).

Malaria is a preventable and curable disease, yet it continues to impose a substantial global health burden. In 2015, an estimated 214 million new malaria cases and 438,000 malaria-related deaths were reported worldwide (WHO, 2015). By 2017, global cases increased to 231

ISSN No: -2456-2165 https://doi.org/10.38124/ijisrt/26jan1064

million, with 416,000 deaths recorded (WHO, 2019). A slight decline was observed in 2018, when 228 million cases and 405,000 deaths were reported globally (WHO, 2020). Children under five years of age were disproportionately affected, accounting for 272,000 deaths (67% of total malaria mortality) in 2018 alone (WHO, 2020). Sub-Saharan Africa bears the greatest burden, contributing approximately 93% of global malaria cases and 94% of malaria-related deaths (WHO, 2020).

Significant progress in malaria control was achieved between 2000 and 2015, with global incidence declining by 42% and malaria-related deaths by 66%, while Africa recorded reductions of 37% in incidence and 60% in mortality. These gains were largely attributed to the scale-up of effective vector control interventions, including insecticide-treated nets (ITNs) and indoor residual spraying (IRS) (WHO, 2015). However, progress has since plateaued, with malaria incidence remaining relatively unchanged between 2015 and 2018 (WHO, 2019). Sub-Saharan Africa continues to face challenges in implementing comprehensive and sustainable malaria elimination strategies (White, 2018; WHO, 2020). In contrast, malaria mortality declined substantially in other regions, with reductions of 72% in the Americas, 65% in the Western Pacific Region, 64% in the Eastern Mediterranean Region, and 49% in the South-East Asia Region since 2000 (WHO, 2015).

Limited access to healthcare, low levels of awareness, inadequate availability of intervention measures, poor socioeconomic conditions, and weak infrastructure are key drivers of the high malaria burden in sub-Saharan Africa (Sumbele *et al.*, 2024; Vorasan *et al.*, 2022). In response to the stagnation in malaria control progress observed between 2015 and 2017 following substantial gains made between 2000 and 2015, the “High Burden to High Impact” (HBHI) approach was launched in 2018. Implemented in 11 high-burden sub-Saharan African countries, HBHI is a country-led initiative supported by the World Health Organization (WHO), the Roll Back Malaria Partnership to End Malaria, and other global partners. The strategy emphasizes the strategic use of high-quality data to identify priority areas and deploy the most effective malaria control interventions for maximal impact, moving away from a uniform, “one-size-fits-all” approach (WHO, 2018). HBHI promotes the uptake of evidence-based public health measures aimed at reducing malaria-related deaths from a disease that is readily diagnosable, preventable, and treatable (WHO, 2020).

Despite global declines in malaria incidence and mortality, the disease remains a major public health challenge in Nigeria and other sub-Saharan African countries (Sumbele et al., 2024; Vorasan *et al.*, 2022). In Nigeria, malaria accounts for approximately 40% of outpatient visits and remains a leading cause of death, contributing to 29.3% of adult mortality and 30% of deaths among children under five years of age (Hassan et al., 2018). Malaria is also the primary cause of morbidity and mortality in Nigerian children under five, affecting over 60 million individuals approximately one-fifth of the national population (Guillebaud *et al.*, 2013). Notably, Nigeria accounted for about one-quarter of global malaria cases and recorded the highest estimated increase in cases in 2017 compared with 2016 (WHO, 2018).

This study is aimed at determining the relative abundance of malaria vectors and malaria transmission in Keffi, Nasarawa State, Nigeria, from 2019 to 2024.

II. MATERIALS AND METHOD

➢ *Study Area*

This study was conducted in selected communities within Nasarawa State, North-Central Nigeria. The state lies within the Guinea savanna vegetation zone and is characterized by a tropical climate. Mean annual temperatures range between 27°C and 33°C, while relative humidity varies from approximately 65% to 80%. Nasarawa State is bordered by Kaduna and Plateau States to the north, Benue State to the south, the Federal Capital Territory (FCT) to the west, and Kogi State to the east.

ISSN No: -2456-2165 https://doi.org/10.38124/ijisrt/26jan1064

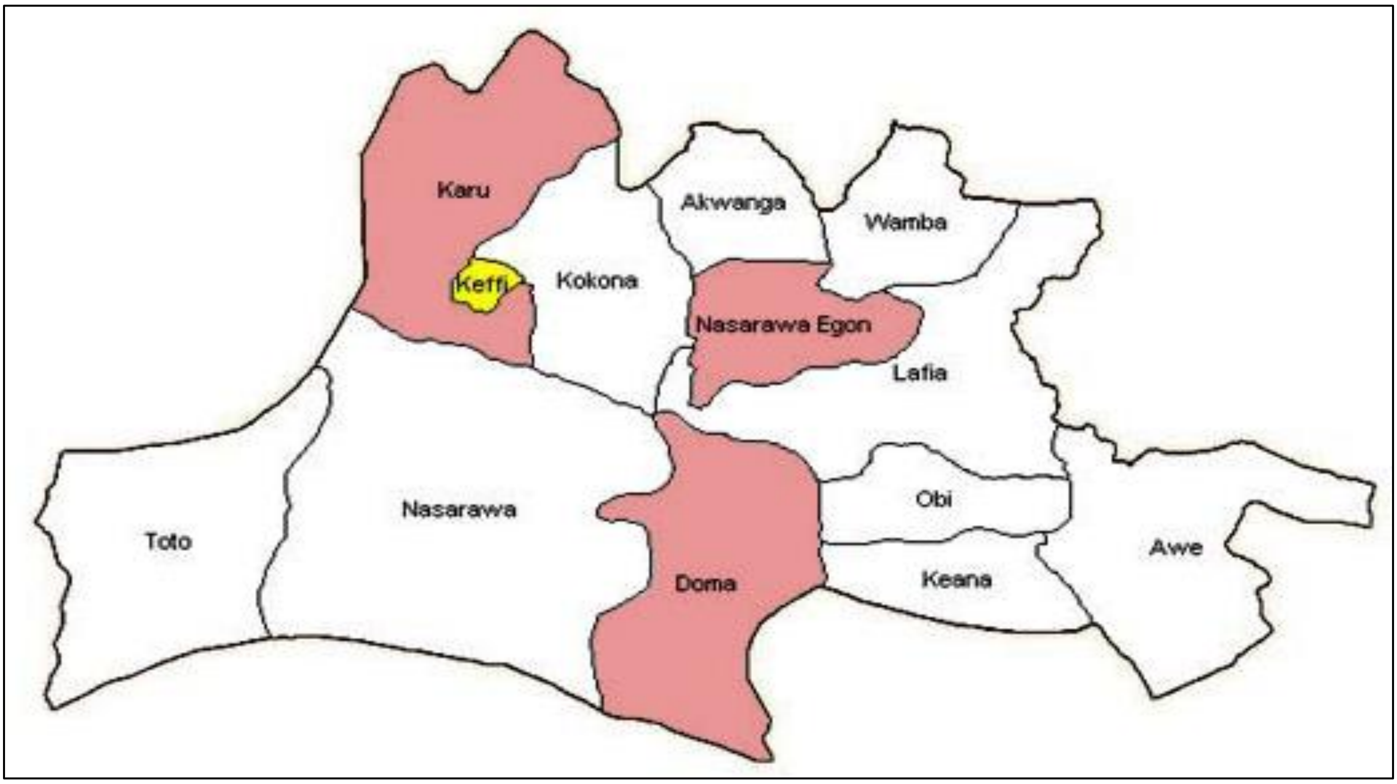

Fig 1 Map of Nasarawa State Showing the Study Sites.

- *Research Design*

This study adopted a retrospective survey design, which enabled the use of existing data to achieve a comprehensive understanding of the study subject under natural conditions (Nasiru, 2015).

- *Information Sources and Search Strategies*

Data on the transmission of malaria was collected from General Hospital Keffi, Nasarawa State, and data on the distribution and abundance of malaria vectors was sourced from the database of the Presidential Malaria Initiative VectorLink, Keffi, Nasarawa State.

- *Statistical Analysis*

Malaria prevalence and vector abundance were expressed as percentages. All data were entered and analysed using SPSS version 25.0 for Windows. Descriptive statistics, including frequencies and tables, were generated, while comparisons between categorical variables were performed using the chi-square test. Statistical significance was set at $p \leq 0.05$.

III. RESULTS

- *Relative Abundance of Malaria Vector in Keffi Nasarawa State Collected by PMI from 2019 to 2024.*

A total of 53,077 Anopheles mosquitoes collected by the Presidential Malaria Initiative (PMI) in Keffi between 2019 and 2024 are presented in Table 1. Anopheles gambiae sensu lato was the predominant malaria vector, accounting for 83.2% (44,160/53,077) of all collections. This was followed by Anopheles funestus, which comprised 11.8% (6,239/53,077), while Anopheles nili was the least abundant species, representing 1.5% (767/53,077). The relative abundance and species composition of malaria vectors varied across the study years. However, An. gambiae consistently predominated, contributing more than 70% of the annual collections in most years, followed by An. funestus, with An. nili remaining the least represented species. The highest number of malaria vectors was recorded in 2024 (11,740), followed by 2021 (10,894), whereas the lowest number was observed in 2020 (3,418). Statistical analysis revealed a significant difference in the relative abundance of malaria vectors collected in Keffi during the study period ($p < 0.05$).

Table 1 Relative Abundance of Malaria Vector in Keffi Nasarawa State Collected by PMI from 2019 to 2024.

Year	*An. gambiae* s.l	*An. funestus* s.l	*An. nili* s.l	Other *Anopheles* spp.	Total (%)
2019	6,778	941	197	359	8,276 (15.6)
2020	3,051	208	28	131	3,418 (6.4)
2021	8,962	1,354	139	439	10,894 (20.5)
2022	8,465	1,102	201	386	10,154 (19.1)
2023	9,729	1,421	108	482	11,740 (22.1)
2024	7,175	1,213	94	114	8,596 (16.0)
Total (%)	44,160 (83.2)	6,239 (11.8)	767 (1.5)	1911 (3.6)	53,077 (100)

Source: PMI 2024 Survey

F = 48,606

P-value = 0.0004

➢ *Yearly Distribution of Malaria Transmission in Keffi, Nasarawa State, Using Data Collected from General Hospital Keffi.*

Table 2 presents the prevalence of malaria parasite infection among patients examined at General Hospital Keffi between 2019 and 2024. A total of 6,650 patients were screened during the six-year period, of whom 4,084 tested positive, resulting in an overall prevalence of 61.4%. The highest malaria prevalence was recorded in 2023 (71.5%), followed by 2022 (69.0%), while the lowest prevalence was observed in 2020 (26.8%). Chi-square analysis indicated a statistically significant difference in malaria prevalence across the study years ($p < 0.05$).

➢ *Entomological Factors in Relation to Malaria Transmission in Keffi Nasarawa State Collected by PMI from 2019 to 2024.*

A total of 18,199 Anopheles mosquitoes were dissected to determine parous rates, yielding an overall parous rate of 83.9%. Species-specific parous rates were 83.3% for Anopheles gambiae, 88.9% for Anopheles funestus, and 87.2% for Anopheles nili. Additionally, 15,272 Anopheles mosquitoes (An. gambiae, An. funestus, and An. nili) were analysed for the presence of Plasmodium species, of which 2,013 were positive, resulting in an overall sporozoite rate of 13.2%. Sporozoite rates varied significantly among vector species, with An. gambiae recording the highest rate (14.6%), followed by An. funestus (5.8%) and An. nili (2.0%). These findings are presented in Table 3.

Table 2 Yearly Distribution of Malaria Transmission in Keffi, Nasarawa State, Using Data Collected from General Hospital Keffi.

Year	No. Examined	No. Positive	No. Negative	% Prevalence
2019	1,371	720	651	52.5
2020	392	105	287	26.8
2021	1,542	941	601	61.0
2022	1,121	753	368	67.2
2023	1,012	698	314	69.0
2024	1,212	867	345	71.5
Total (%)	6,650	4,084	2,566	61.4

$\chi 2 = 23.945$

P-value = 0.0005

Table 3 Entomological Factors in Relation to Malaria Transmission in Keffi Nasarawa State Collected by PMI from 2019 to 2024.

Parameter	*An. gambiae* s.l	*An. funestus* s.l	*An. nili* s.l	Other *Anopheles* spp.	Total (%)
Total mosquitoes collected (%)	44,160 (83.2)	6,239 (11.8)	767 (1.5)	1911 (3.6)	53,077 (100)
Total dissected	15,567	2,142	169	321	18,199
Parity rate (95% CI), Total parous	83.3 (83.0–83.6), 12,967	88.9 (88.2–89.5), 1904	87.2 (86.4–87.9),147	79.2 (76.4–81.9), 254	83.9 (81.4–84.6), 15272
Total tested for sporozoites	12,967	1,904	147	254	15,272
Number of sporozoite positive	1,893	110	3	7	2,013
Overall sporozoite rate %	14.6	5.8	2.0	2.8	13.2
Mean density in rainy season [95% CI]	24.9 [22.5–27.3]	3.6 [3.1–4.2]	0.2 [0.1–.2]	0.7 [0.5–1.0]	32.6 [29.0–35.8]
Mean density in dry season [95% CI]	7.0 [5.7–8.3]	0.15 [0.10–0.20]	0	-	7.2 [5.8–8.4]

IV. DISCUSSION

This study demonstrates a high abundance of mosquito species and sustained malaria transmission in Keffi, Nasarawa State. A high level of mosquito diversity, comprising six genera, was recorded in the study area. The observed diversity and abundance of mosquito fauna are likely attributable to favourable environmental conditions that support mosquito development and survival (Brooks *et al.*, 2022).

Analysis of the annual malaria transmission pattern revealed the involvement of three major African *Anopheles* vectors *Anopheles gambiae, Anopheles funestus*, and *Anopheles nili* in sustaining malaria transmission in Keffi. Anopheles gambiae was identified as the primary vector, recording the highest sporozoite rate (14.6%), which indicates a high level of Plasmodium infection and underscores its dominant role in malaria transmission within the area. The infection rates observed in An. gambiae in this study are comparable to those reported by Oyewole *et al.*

(2009). However, the concurrent involvement of An. funestus and An. nili contrasts with more recent findings suggesting that malaria transmission in similar settings is predominantly driven by An. gambiae alone (Adja *et al.,* 2021). Nonetheless, all vector species implicated in this study have previously been reported as malaria vectors in Nigeria (Onyido *et al.,* 2018; Ombugadu *et al.,* 2020; Madara *et al.,* 2023).

The high relative abundance of mosquito species observed in the study area is also consistent with the presence of diverse and suitable breeding habitats (Minakawa & Jam, 2021). These habitats ranged from temporary ground pools to large, permanent water bodies distributed across the study locations. Furthermore, the high prevalence of malaria infection recorded in Keffi may be attributed to the endemic nature of malaria in Nigeria, including Nasarawa State, where sustained transmission continues to pose a significant public health challenge.

This study showed that malaria vector species composition, abundance, and transmission intensity in Keffi varied significantly with season. *Anopheles gambiae* was present throughout the year but occurred at very low densities during the dry season, becoming highly abundant during the rainy season. This seasonal pattern is consistent with the ecology of *An. gambiae,* whose larval habitats increase in availability and productivity during periods of rainfall and decline markedly in the dry season (Mourou *et al.*, 2021).

Similarly, *Anopheles funestus* densities declined during the dry season. While this trend aligns with expectations for *An. gambiae,* it contrasts with reports from other savannah settings where *An. funestus* typically peaks during the dry season (Soma *et al.*, 2020). The larvae of An. funestus are commonly associated with large, permanent or semi-permanent freshwater bodies such as swamps, ponds, and lake margins, particularly those with emergent vegetation (Soma *et al.*, 2020). In the present study area, natural swamps and marshes constitute the primary breeding habitats, and their extent is largely rainfall-dependent, which likely explains the reduced *An. funestus* density observed during the dry season. Despite its low density, the relatively high sporozoite rate recorded for *An. funestus* suggests that this species plays an important role in sustaining malaria transmission during the dry season.

Anopheles nili was also detected during the rainy season, although at consistently low densities, indicating a minor role in transmission within the study area.

Overall, 15,272 *Anopheles* mosquitoes (*An. gambiae, An. funestus,* and *An. nili*) were analysed for *Plasmodium* species, of which 2,013 were infected, yielding an overall sporozoite rate of 13.2%. Species-specific sporozoite rates differed significantly, with *An. gambiae* recording the highest rate (14.6%), followed by *An. funestus* (5.8%) and *An. nili* (2.0%). These values are higher than those reported by Awolola et al. (2013) in south-western Nigeria, who documented sporozoite rates of 5.6%, 2.9%, and 1.8% for the respective species, suggesting comparatively higher transmission intensity in the present study area.

V. CONCLUSION

Malaria transmission in Keffi was predominantly driven by Anopheles gambiae, with the An. funestus group and An. nili complex contributing to a lesser extent. This study provides the first evidence of *An. nili* acting as a secondary malaria vector in the area. Despite widespread use of long-lasting insecticidal nets (LLINs), entomological indicators of malaria transmission remained high, highlighting the urgent need for additional and complementary vector control strategies to strengthen existing malaria control efforts.

RECOMMENDATIONS

- Breeding sites should be effectively managed through targeted larviciding to reduce mosquito larval populations, alongside sustained use of long-lasting insecticidal nets (LLINs) to minimize human vector contact.
- Continuous surveillance and accurate identification of vector species should be prioritized in Nasarawa State and beyond, as this is essential for understanding malaria epidemiology and transmission dynamics in specific settings.
- Furthermore, an integrated vector management (IVM) approach should be strengthened to limit vector distribution and proliferation. This should include a combination of indoor residual spraying (IRS), widespread use of LLINs, and environmentally appropriate larval source management.

REFERENCES

[1]. Adja, A. M., Zoh, D. D., Sagna, A. B., Kpan, D. M. S., Guindo-Coulibaly, N., and Yapi A, (2021). Diversity of *Anopheles gambiae* sl, Giles (Diptera: Culicidae) larval habitats in urban areas and malaria transmission in Bouaké Côte d'Ivoire. *Vector-Borne Zoonotic Diseases*; 21:593–601.

[2]. Alemu G, and Mama M. (2016): Assessing ABO/Rh blood group frequency and association with asymptomatic Malaria among blood donors attending Arba Minch blood bank,. *Malaria Research and Treatment*. 2016:8043768

[3]. Brooks, M. E., Kristensen, K., van, Benthem, K. J., Magnusson, A. Berg, C. W., and Nielsen, A. (2022). glmmTMB balances speed and fexibility among packages for zero-infated generalized linear mixed modeling. *Rational Journal*; 9:378–400.

[4]. Guillebaud, J., Mahamadou, A., Zamanka, H., Katzelma, M., Arzika, I., Ibrahim, M. L., and Fandeur, T. (2013). Epidemiology of malaria in an area of seasonal transmission in Nigeria and implications for the design of a seasonal malaria chemoprevention strategy. *Malaria journal*, 12(1), 379

[5]. Madara, A. A., Abdulraheem, N. O., and Elkanah, S. O. (2023) Relative Abundance of Adult Mosquitoes in University of Abuja Main Campus, Abuja FCT, Nigeria. *Nigerian Journal of Parasitology* 34(2): 79-84.

ISSN No: -2456-2165 https://doi.org/10.38124/ijisrt/26jan1064

[6]. Minakawa, N. G. and Jam, G. (2021). Relationship between occurrence of *Anopheles* S.I. (Diptera: Cullicidae) and size and stability of larvae habitat *medical journal of Entomology*, 42, 295-300.

[7]. Mourou, J-R., Cofnet, T., Jarjaval, F., Cotteaux, C., Pradines, E., and Godefroy, L., (2022). Malaria transmission in Libreville: results of a one-year survey. *Malaria Journal*; 11:40.

[8]. Ombugadu A, Ekawu RA, Pam VA, Odey SA, Igboanugo SI, *et al*. (2020). Feeding Behaviour of Mosquito Species in Mararraba-Akunza, Lafia Local Government Area, Nasarawa State, Nigeria. Biomedical *Journal of Scientific & Technical Research 25*(1): 18742-18752.

[9]. Onyido, A.E., Ezeani, A.C., Irikannu, K.C., Umeaneto, P.U., Egbuche, C.M., Chikezie, F.M. and Ugha, C.N. (2020). Anthropophilic mosquito species prevalence in Nibo community, Awka South Local Government Area, Anambra State, Southeastern, Nigeria. *Ewemen Journal of Epidemiology and Clinical Medicine*, 2(1): 14 – 20.

[10]. Paton, R. S., Kamau, A., Akech, S., Agweyu, A., Ogero, M., Mwandawiro, C. and Snow, R. W. (2021). Malaria infection and severe disease risks in Africa. *Science*, 373(6557), 926-931.

[11]. Romero, M., Leiba, E., Carrion-Nessi, F.S., Diana, C., Nobrega, F., Kaid-Bay, S., *et al.* (2021) Malaria in pregnancy complications in Southern Venezuala. *Malaria Journal*, 20:186.

[12]. Rumisha, S. F., Shayo, E. H., and Mboera, L. E. (2019). Spatiotemporal prevalence of malaria and anaemia in relation to agroecosystems in Mvomero district, Tanzania. *Malaria Journal*, 18(1), 1-14.

[13]. Soma DD, Zogo BM, Somé A, Tchiekoi BN, de Hien DF, S, Pooda HS, (2020). *Anopheles* bionomics, insecticide resistance and malaria transmission in southwest Burkina Faso: a pre-intervention study. PLoS ONE.;15: e0236920.

[14]. Sumbele, I. U. N., Sama, S. O., Kimbi, H. K., and Taiwe, G. S. (2024). Malaria, moderate to severe anemia, and malaria-anemia in children at presentation to hospital in the Mount Cameroon area: a cross-sectional study. *Anemia*.

[15]. Vorasan, N., Pan-Ngum, W., Jittamala, P., Maneeboonyang, W., Rukmanee, P., and Lawpoolsri, S. (2022). Long-term impact of childhood malaria infection on school performance among school children in a malaria endemic area along the Thai–Myanmar border. *Malaria Journal*, 14(1), 401.

[16]. World Health Organization (2013) Malaria control in humanitarian emergencies: an inter-agency field handbook – 2nd edition.

[17]. World Health Organization. (2015). Malaria fact sheet: World malaria report 2015. https://www.who.int/malaria/media/world-malaria-report-2015/en/.

[18]. World Health Organization. (2019). Malaria: Key facts. https://www.who.int/newsroom/fact-sheets/detail/malaria.

[19]. World Health Organization. (2021). World malaria day: WHO launches effort to stamp out malaria in 25 more countries by 2025. https://www.who.int/news/item/21-04- 2021-world-malaria-day-who-launches-effort-to-stamp-out-malaria-in-25-morecountries-by-2025.