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Research article

Assessment of malaria transmission in Kenya using multilevel logistic regression

Dawit G. Ayele [a,*], Mohammed Omar Musa Mohammed [b], Ahmed Saied Rahama Abdallah [b], Gemechis A. Wacho [c]

[a] Center for Policy, Planning, and Evaluation (CPPE), DC Health, Washington DC, USA
[b] College of Business Administration in Hawtat Bani Tamim, Prince Sattam Bin Abdulaziz University, Al-Kharj, Saudi Arabia
[c] Psych Tech, Shady Grove Medical Center, Rockville, MD, USA

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ABSTRACT

Background: Kenya has a lower malaria incidence in comparison to other African malaria-endemic nations. Malaria is a significant public health concern in the country. The malaria indicator survey (MIS) data were analyzed using the logistic regression model. Nonetheless, independent data may be the cause of most MIS's hierarchical structure. This approach does not consider any association between data points within a cluster, as it assumes that the individual malaria statuses are independent of their causes. The approach may lead to biased analysis conclusions. The primary goal of this research is to determine the impact of sample enumeration areas (SEAs) and SEA features on individual malaria rapid diagnostic test (RDT) results. We are interested in identifying key factors influencing household members' malaria RDT findings or Kenya's malaria prevalence and assessing variation.

Methods: Our study utilized the robust 2020 Kenya National Malaria Indicator Surveys (KMIS) dataset, which is representative of the entire nation. This dataset, comprising 301 clusters (134 urban and 167 rural areas), was instrumental in applying several multilevel models, including random sample and sample Enumeration Area (SEA) effects. We also considered the weights used in the s survey design, which is used to adjust uneven probabilities of choice within clusters, further enhancing the reliability and relevance of our findings. The methods used in this study involved a rigorous analysis of the KMIS dataset, including applying multilevel models and considering survey design weights to ensure the robustness and strength of our results.

Results: This study's findings are significant and crucial in understanding the prevalence of malaria in Kenya. The findings reveal that factors such as region, place of residence, mosquito bed net use, water source location, wealth index, age, household size, and altitude are significantly associated with malaria's prevalence.

After accounting for these variables, systematic changes across SEAs accounted for approximately 47.1 % of the remaining variability in malaria occurrence in the study locations. In contrast, the remaining 52.9 % was projected to be unmeasured differences between individuals or family units. These findings provide a detailed explanation of the various processes that influence malaria prevalence in Kenya.

Conclusions: The study's multilevel logistic regression model, which includes random effects, identified two SEA-level and eight individual/household risk factors for malaria infection. Thus, increasing the availability of insecticide-treated bed nets is one crucial element that public health

* Corresponding author.
E-mail address: ejigmul@yahoo.com (D.G. Ayele).

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policymakers should consider. Furthermore, health planners can organize spatially targeted initiatives to prevent malaria transmission with the help of spatial clustering data.

1. Introduction

Malaria is one of the most challenging community health challenges worldwide. An estimated 241 million clinical episodes and 627,000 fatalities were attributed to malaria in 2020 worldwide [1]. In 2018, around 228 million malaria cases were reported worldwide, corresponding to the 251 million cases reported in 2010. Africa constituted 93 % of the cases, with Southeast Asia accounting for 3.4 % and the Eastern Mediterranean accounting for 2.1 % [2]. Worldwide, the number of malaria-endemic nations that reported less than 10,000 malaria cases climbed from 26 in 2000 to 46 in 2019 [3].

Malaria transmission occurs when the malaria parasite spreads from one infected person to another, usually through the female Anopheles mosquito bite. The parasite is spread to humans by an infected mosquito bite, and it can subsequently infect other mosquitoes during successive feedings. Preventing malaria transmission involves controlling mosquito populations, using insecticide-treated bed nets, and providing antimalarial drugs [4].

Kenya is predicted to see 10,700 deaths and 3.5 million new clinical practice cases annually; those living in western Kenya are especially susceptible to malaria. Comparably, 10,700 deaths and 3.5 million new clinical cases are reported in Kenya, with western Kenyans being the most vulnerable to malaria [5].

According to the World Health Organization's (WHO) Report 2019, Africa experienced the most significant decline in malaria-related mortality, with 533000 cases in 2010 and 380000 in 2018. According to the same study, the drop in malaria mortality rate was slower in 2016–2018 than from 2010 to 2015. The anticipated global malaria cases for 2018 were 228 million, down from 251 million in 2010 and 231 million in 2017 [3].

Between 2010 and 2018, the worldwide malaria mortality toll decreased to 405,000 cases. According to the 2019 World Health Organization (WHO) report, Africa significantly reduced malaria-related fatalities, dropping the number of cases from 533,000 in 2010 to 380,000 in 2018. However, the same study notes that malaria mortality decreased in 2016–2018 compared to 2010–2015. Incidences of malaria were predicted to have reduced from 251,000,000 in 2010 and 231,000,000in 2017 to 228,000,000 worldwide in 2018 [6].

Africa contributed to 95 % of infections related to malaria and 96 % of malaria-related fatalities in 2020. An estimated 80 % of all malaria-related fatalities in the Third World were caused by children under the age of five [6]. The incidence of malaria for children under the age of five has generally declined in the East African region, but it remains high. The prevalence rates in Burundi, for instance, were 22 % in 2013 and 27 % in 2016–2017; in Kenya, 5 % in 2015; in Rwanda, 2 % in 2015 and 7 % in 2017; in Tanzania, 14 % in 2016 and 7 % in 2017; in South Sudan, 32 % in 2017; in Sudan, 5.9 % in 2017; in Ethiopia, 0.6 % in 2015; and in Uganda, 19 % in 2015 and 30.3 % in 2016 according to recent studies [7–14]. As per the Nigeria Malaria Indicator Survey 2015, malaria prevalence was reported to be 45 % using Random Diagnostic Test (RDT) and 27 % using Microscopy [15]. A recent study demonstrated a substantial correlation between the President's Malaria Initiative and the heightened implementation of measures to control malaria. This, in turn, resulted in a decrease in the number of deaths among children under the age of five in Sub-Saharan Africa [16]. A study conducted in Ethiopia revealed that individual-level factors related to malaria included frequent or current trips to rural areas, with an occurrence proportion of 12.96, and having an indoor job, with an incidence rate ratio of 0.37. Furthermore, adult malaria risk was found to be correlated with low amounts of vegetation within the household complex, with an incidence rate ratio of 0.27; a tidy compound, with an incidence rate ratio of 0.29; household use of preventive measures, with an incidence rate ratio of 0.31, and the number of children aged 5–9 years in the household, with an incidence rate ratio of 1.66 [17]. The incidence of malaria among youngsters was 8.7 %. Sleeping under long-lasting insecticide-treated nets was correlated with a smaller risk of malaria. In contrast, children who spent the night outside or in homes with standing water in the compound had a higher risk of contracting the disease [18]. The incidence of malaria was 14 %, with a significant rate when comparing youngsters between the ages of 5 and 9 to other age groups, 15.6 %. The findings revealed that gender, household size, and the presence of bed nets were correlated with malaria [19]. A more serious problem of contracting malaria was linked to certain factors, including children under the age of five and between 5 and 9 years old and homes with holes [20]. Age groups had significantly different malaria prevalence rates, although gender and location did not. Significant correlations between malaria and being 12 years of age or older, having a poor household income, not utilizing insecticide-treated nets (ITNs), and not having a toilet in the home were found in the multilevel findings [21]. Research in Nigeria indicated that malaria prevalence depends on socio-economic status and risk factors facilitating transmission [22]. The incidence of severe anemia was higher in children who tested positive for malaria (87.6 %) and 67.4 % for RDT and Microscopy, respectively, than in children who were not anemic (RDT = 31.6 %, Microscopy = 12.9 %) [23]. The study's results indicated a strong association between malaria and factors such as residing in Forest Guinean areas, living in rural areas, and having splenomegaly [24]. Research by Ayele et al. identified strong positive associations between Malaria RDT and socio-economic, demographic, and geographic factors [25]. It has been discovered that the prevalence of malaria increases in countryside areas compared to town areas, rises with the age of the child, and falls with increasing household socio-economic position and higher levels of mother's education [26]. According to reports, five thousand three hundred eighty-two malaria cases were reported in Saudi Arabia in 2016 [27]. Furthermore, a study conducted in Ethiopia found that education, the original place of residence of migrant laborers, visits, sleeping outside, and bed-net application were correlated with the prevalence of malaria [28]. Compared to children who did not sleep beneath insecticide-treated mosquito nets (ITNs), children who did so had a higher chance of being protected from malaria infection [29]. Males living in rural areas were found to be at a greater risk

of acquiring malaria illness [30]. Additionally, the research by Tadesse et al. displayed a significant correlation between age groups and living in rural areas with malaria [31]. The study revealed that individuals with access to drinking water, who have access to a toilet, and who live in larger living areas have a reduced probability of the risk of malaria. Additionally, it was found that applying anti-mosquito spray to the house's walls and utilizing malaria nets were efficient control techniques. Ayele et al., in 2012 and 2013 study findings, indicated that gender and age were significantly associated with malaria [32,33]. Furthermore, it was discovered that one way to lower the danger of malaria was to apply anti-malaria medicines around the home.

When examining data on malaria status, the basic binary logistic regression model has been used extensively. However, this model does not consider any association between observations within a cluster, as it assumes that an individual's malaria status is independent and depends only on the variables. As a result, it could produce conclusions and findings that are skewed. Additionally, this approach disregards the data's hierarchical structure and hinders investigating the relationship between particular cluster features and the individual outcome. The intra-policymakers in the healthcare industry may find helpful information from cluster correlation. Multilevel models split the total separate variance into variance attributable to the clusters and the remaining individual-level variation, then utilize cluster-specific random effects to account for the data's dependency [34–37]. Multilevel models describe the clustered formation of the data, allowing for the examination of factors contributing to differences within and between clusters. They also enable precise estimation of standard errors and more accurate inferential inferences.

Researchers can utilize multilevel logistic regression models to address the clustered nature of the data, examine the factors contributing to distinctions within and between clusters, and determine the variables that can predict differences at individual and cluster levels. These studies included the Community as a cluster and found that Community-level impacts were significant. In their multilevel analyses, the studies conducted in Cambodia and Peru also included homes as a cluster. The latter demonstrated the significance of risk factors at the household level in accounting for variations in infection prevalence between homes and communities. The former documented variations in malaria occurrence between communities that were impacted by household and individual variables, and it evaluated risk factors in models tailored to a particular community. However, the variations in random household-level influences were insufficiently minor [34,37].

The primary purpose of this study is to quantify the variance factor of sample enumeration areas (SEAs) and SEA attributes on unique malaria rapid diagnostic test (RDT) outcomes. We are interested in determining essential elements that impact household members' malaria RDT results or Kenya's malaria prevalence and assessing the variation. We can quantify these parameters' differences and compare malaria prevalence across multiple SEAs with different features. The article compared malaria RDT results to malaria incidence. It treated the survey sample enumeration area (SEA) as a cluster, and both SEA and cluster were used interchangeably [32,38,39].

Malaria transmission research in Kenya is important for various reasons, including the public health effect, economic burden, regional and global implications, climate change impact, intervention assessment, vector biology and resistance, and health system strengthening. Researchers and public health officials may get significant insights about malaria transmission in Kenya, which can then be used to influence evidence-based policies, interventions, and resource allocation to battle malaria successfully and enhance the health and well-being of the community. The study's goal is to measure malaria transmission in Kenya.

2. Materials and methods

2.1. Study data

The survey used in this study was acquired from the 2020 Kenya Malaria Indicator Survey (KMIS). The survey was created, sponsored, and administered following Kenya's Vision 2030 goals, AID's Effectiveness criteria, and the United States Agency for International Development's Journey to Self-Reliance mandate. As the implementing agency for the 2020 KMIS, the Health Ministry worked with the National Malaria Program Division (DNMP) and the Kenya National Bureau of Statistics (KNBS) to plan and carry out data collection and investigation while upholding a high standard of data excellence and distributing the survey outcomes. The World Health Organization (WHO), the United States President's Malaria Initiative (PMI), ICF, the Medical Research Institute of Kenya (KEMRI), and the United Nations Children's Fund (UNICEF) were among the organizations and partners with which this was carried out in cooperation [8]. The data used for this study can be accessed from the DHS program.

The 2020 KMIS was designed to present estimations of fundamental malaria factors for the country. The study considered a two-stage stratified cluster sample plan. The survey used the same household master sample frame from the fifth program for the National Sample Survey and Evaluation (NASSEP V). The Bureau of Statistics (KNBS) employed the framework to carry out household-based sample surveys in Kenya between 2012 and 2020. Clusters created from areas of enumeration (EAs) served as the main units of sampling created during the 2009 Census. "EAs" refers to the smallest geographic regions used for population census. The counties of Nairobi and Mombasa are urban. Ninety-two sample strata were produced by stratifying the 5360 clusters in the frame within each of the 47 counties. The stratified cluster sampling design was employed for the two-stage survey. In the first selection phase, 301 clusters (134 and 167 for urban and rural, respectively) were picked from the master frame by using a probability selection procedure. In the next stage, a roster of the sampled clusters' households was used, and systematic random sampling was applied to randomly choose a set number of thirty households per cluster [40].

2.2. Response and explanatory variables

This study's explanatory factors predicted whether a person had malaria illness (i.e., confirmed positive for malaria, with one

representing positive and zero representing negative). The independent factors incorporated to substantiate the effects of malaria RDTs are categorized as individual (and household) features and SEA or cluster features. Age and sex with household setting factors were used as individual-level characteristics. Previous studies were used to select household background variables. Therefore, this study includes region, place of residence, sex, mosquito bed net, children under five slept under mosquito bed net last night, location of the source for water, wealth Index, insecticide-treated Net (ITN), and altitude. A SEA level attributes are region, place of residence, and altitude. Sampling weights for the level-1 survey design are included in the data from the malaria indicator survey.

3. Statistical methods

3.1. Multilevel logistic regression model with random effects

The incidence of malaria may change depending on the climate or the availability of public health facilities in various geographic areas. We may utilize random effects to integrate these unknown changes into the model. Furthermore, residents of the same SEA may be more similar to one another than those of different SEAs since they have identical ecosystems, access to local public health services, and other traits that may influence malaria RDT results.

Moreover, there is a correlation between the malaria condition of those living in the same family unit. These demonstrate intra-class correlation, which measures how similar the malaria status of patients in the same cluster is to one another. This study applied the SEA-specific random effects multilevel logistic regression model to measure the change in a malaria RDT outcome explained by the SEA variances and to account for the intra-class correlation.

Let Y_{ij} represent the malaria indicator of the ith individual in the jth Sample Enumeration Area defined by RDT with probability, π_{ijk}, where $Y_{ij} = 1$ represents the persons with positive tested results, while $Y_{ij} = 0$ represents those who tested negative for malaria. The random effect multilevel logistic regression model for the indicator Y_{ij} is denoted by

$$\eta_{ij} = g\left(\mu_{ij}\right) = X_{ij}'\beta + Z_j'\alpha + b_j, i = 1, \ldots, n_j; j = 1, \ldots, m. \tag{1}$$

g(.) is the link function, $X_{ij} = (1, X_{1ij}, \ldots, X_{pij})$ is a vector of p covariates, or explanatory factors, based on the i individual, and $Z_j = (z_{1j}, \ldots, Z_{qi})$ is a vector of q explanatory variables determined on the j cluster, β and $\boldsymbol{a}$ are a vector of fixed regression factors and b_i is a random effect. Here, b_i is independently and normally distributed with mean zero and variance σ_b^2, i.e., $b_j \sim N(0, \sigma_b^2)$. The conditional expectation $\mu ij = \boldsymbol{E(Y_{ij}|X_{ij}, Z_i, b_j)}$ is the relationship between the linear predictor and the conditional distribution, Y_{ij} is established using a link function [34,41,51].

3.2. Sampling weights

The data considered for this analysis contains general level-1 weighting that considers level-2 design effects. The sample weights consider the probability associated with different population sizes in the enumeration areas. The multilevel regression model can be extended by incorporating a pseudo-maximum-likelihood technique to accommodate weights at multiple levels. Survey data derived from multistage sampling can be analyzed with great benefit from this technique. Furthermore, survey weights are frequently adjusted in these sample designs to consider post-stratification, non-response adjustments, and unequal sampling probabilities [41,52–54].

If the sampling weights connected to level-1 units are high, variance component estimators may become biased [34]. Consequently, the weights were rescaled using two procedures, referred to as method 1 and method 2, to correct them and reduce bias [33–35]. Let $n_j^{(1)}$ refer to level-1 units in the level-2 unit j and w_{ij} consider the weight of the ith level-1 in level-2 unit j. In order to guarantee that the total of the updated sample weights equals the intended cluster size, Method 1 modifies the sample weights.

$$\sum_{i=1}^{n_j^{(1)}} \lambda w_{i/j} = \frac{\left(\sum_{i=1}^{n_j^{(1)}} w_{i/j}\right)^2}{\sum_{i=1}^{n_j^{(1)}} \lambda w_{i/j}^2} \tag{2}$$

where λ is the factor of scale and given as

$$\lambda = \frac{\sum_{i=1}^{n_j^{(1)}} w_{i/j}}{\sum_{i=1}^{n_j^{(1)}} \lambda w_{i/j}^2} \tag{3}$$

In contrast, Method 2 adjusts the weights so that the cluster sample size equals the new weights' total. So that the scale factor is

$$\lambda = \frac{n_j^{(1)}}{\sum_{i=1}^{n_j^{(1)}} w_{i/j}}$$

We did not assign a weight to level 2 in the analysis because there is no defined weight for it in the study data. Scaling level 2 wt, as Rabe-Hesketh and Skrondal [41] suggested, has a minimal practical impact. The weighted analysis results for the two scaling approaches' fixed and random effect variances were nearly equal at two decimal places [38]. Despite the significant differences in the results obtained from these methods, we derived the same conclusions based on the characteristics of households and clusters in each model we used. For brevity, we have provided the results from scaling method one in this report [42].

Odds ratios can be used to interpret the fixed parameters of the models M1 and M2 based on population averages and subject specifics. When considering the unobserved SEA impact, the odds ratios from these models provide estimates of relationships specific to SEA or clusters. For covariates at the individual or household level, their interpretations make sense. SAS's PROC GLIMMIX fits all multilevel logistic regression models with random effects. PROC GLIMMIX in SAS utilizes the weights provided in the dataset for analysis. Hence, the scaled weights must be present in the dataset.

4. Results

In this research, 11587 individuals were examined for malaria illness. Using rapid diagnostic testing, 10,397 (89.7 %) of these people tested negative for malaria. The malaria RDT test revealed that 5 % of the people in the Coast, 1 % in the Northeast, 2 % in the Rift Valley, 24 % in the Western, 16 % in Nyana, and 2 % in Nairobi were positive (Table 1). The respondent's mean (SD) age, household size, sleeping room size, person who used LLIN net, number of persons who used net, and median altitude were 24.3 (20.1), 5.5(2.8), 2.1(1.1), 0.39(0.5), 2.5(1.9), 2.1(0.9), and 1359(634.6), respectively.

In the study, around 66.1 % of people resided in rural regions, while 33.9 % lived in urban areas. Mosquito nets were used by the majority of the studied homes in the research area (69.6 %), with insecticide-treated mosquito nets accounting for about 88.5 %. About 78.8 % of the sampled households had a water source, whereas outside their living area, 15.7 % and 5.5 % of them had water locations in their yards/plots and dwellings, respectively. 47.65 percent of children under five who were part of the examined populations spent the previous night sleeping under mosquito bed nets. In addition, 15.3 % of kids under five said they had never spent the night before sleeping beneath a mosquito net. The wealth index used in this survey indicates a household's wealth level is coherent with the methods of expenses and earnings. 51, 20.5, and 28.4 % of the selected families fell into the low, middle, and richest (or highest) wealth quintiles, respectively (Table 1).

Table 1
Chi-square testing and descriptive statistics Between malaria RDT and covariates.

Indicator		Result of malaria rapid test					Chi-square
		Negative		Positive		Total	
		Number	%	Number	%	Number	
Region	Coast	1335	95.02	70	4.98	1405	<0.0001
	North Eastern	497	100.00	0	0.00	497	
	Eastern	1371	99.20	11	0.80	1382	
	Central	517	100.00	0	0.00	517	
	Rift Valley	2336	97.66	56	2.34	2392	
	Western	1934	76.05	609	23.95	2543	
	Nyanza	2352	84.15	443	15.85	2795	
	Nairobi	55	98.21	1	1.79	56	
Type of place of residence	Urban	3726	94.88	201	5.12	3927	<0.0001
	Rural	6671	87.09	989	12.91	7660	
Sex of household member	Male	5118	89.37	609	10.63	5727	0.202
	Female	5279	90.09	581	9.91	5860	
Has mosquito bed net for sleeping	No	3281	93.00	247	7.00	3528	<0.0001
	Yes	7116	88.30	943	11.70	8059	
Children under 5 slept under mosquito bed net last night	No	1100	87.44	158	12.56	1258	<0.0001
	All children	3485	89.20	422	10.80	3907	
	Some children	624	88.39	82	11.61	706	
	No net in household	2187	93.50	152	6.50	2339	
Location of source for water	In own dwelling	451	88.78	57	11.22	508	0.079
	In own yard/plot	1312	89.74	150	10.26	1462	
	Elsewhere	6424	87.70	901	12.30	7325	
Wealth Index	Poor	5159	87.23	755	12.77	5914	<0.0001
	Middle	2116	88.68	270	11.32	2386	
	Rich	3122	94.98	165	5.02	3287	
Insecticide-Treated Net (ITN)	No, don't know	593	97.85	13	2.15	606	<0.0001
	Yes	4155	88.78	525	11.22	4680	

4.1. Multilevel models result

Before fitting the models M1 and M2, the variables to be included in the study were selected using the stepwise variable choice process. Moreover, multicollinearity among the selected variables was tested using the variance inflation factors (VIF), with variables having a VIF more significant than five being excluded. After removing the implausible components, the variables for the final M1 and M2 models were chosen using the Akaike Information Criteria (AIC), the Bayesian Information Criteria (BIC), and likelihood ratio tests.

Therefore, for models M1 and M2, the following variables were chosen: wealth index, region, type of habitation, sex of a household member, has a mosquito bed net, under-five children slept using bed net last night, wealth index, insecticide-treated net (ITN), and altitude. Model 2 contains the random effect in addition to the fixed effects. These models incorporate the study's design effect. Fit statistics show that the multilevel versions of M1 and M2 significantly outperform the logistic regression models (Table 2). This suggests that the multilevel models were chosen for the research data instead of the logistic regression models.

The asymptotic chi-square mixed distribution [2.09 test statistic produces 329.01, 210.19, and 107.87, respectively, for testing against the models Mo, M1, and M2, with a p-value <0.0001 in each test. The null hypothesis states that no cluster-specific random effects should be included in the model and is strongly supported to be rejected when the test statistic is substantial or the p-value is incredibly small. These findings suggest that the model has to consider the SEA (cluster) random effects.

The estimated intercept Model M0 was −1.073 (with a standard error of 1.145), and the estimated variance of the sample enumeration (SEA) specific random effects was 4.041 (with a standard error of 0.695). The fact that the random effect of the SEA was equal to zero on the logit scale indicated the probability that a resident of any SEA in the research's study regions would be discovered to have malaria. It should be noted that the average SEA-forecasted probability of a person who has malaria may differ from the average SEA-exact probability of malaria infection due to the possibility of an intercept component that does not equal zero.

Table 2 displays the fit statistics or model choice criteria for the fitted Mo, M1, and M2. The results of these criteria point to M2 as the best model to fit the data. Consequently, we exclusively publish results based on M2 in the following sections.

The computed regression coefficients for model M2's with a 95 % confidence interval are shown in Table 3. Exponential estimations were utilized to calculate malaria patients' odds ratio (OR) compared to a suitable reference group.

The findings in Table 3 demonstrate that the likelihood of malaria infection among residents in the study area was significantly correlated with eight of the fifteen individual/household characteristics, region, place of residence, under-five children sleeping under a bed net the previous night, location of the water source, wealth index, age of household members, family size, and altitude. Moreover, the two SEA-level factors, region and altitude, were also statistically significant.

Table 3 indicates that the likelihood of positive malaria was 2.053 times greater for residents of rural regions than those who lived in urban areas (OR = 2.053, 95 % CI: 1.268, 2.870). According to Table 3's findings, a person's age rose with the probability of contracting malaria (OR = 1.080 with 95 % Cl: 1.045, 1.117). For all under-five who slept under a bed net the previous night, the OR of positive malaria result was 1.328 with 95 % Cl (1.086, 2.052), compared to certain other children. These 95 % confidence intervals indicate that as a person matures, the likelihood of a positive malaria RDT result greatly decreases since they do not include one. All under five children who slept under a bed net the previous night differed significantly from some other children. In the research location, however, there was a lower risk of malaria infection for some children under five who had spent the previous night sleeping under a mosquito bed net. Individuals who had access to a water source in their home had a 0.831-fold lower chance of having malaria than those who did not (95 % Cl: 0.457, 0.809). The positive malaria RDT result rose with the number of household members (OR = 1.156, 95 %: 1.042, 1.282). The odds of getting malaria were 2.422 times greater for low-income households than for wealthy households (OR = 2.422, 95 % Cl: 1.665, 3.521). In a similar vein, the odds of having malaria were 1.875 times higher for residents of middle-class homes than for those in wealthy households (OR = 1.875, 95 % CI: 1.268, 2.773). Additionally, Table 3 data showed that as cluster altitude climbed, the chances of malaria risk dropped (OR = 0.995 with 95 % Cl: 0.924, 0.998).

Model M2 has an estimated between-SEA variance of 2.484, equivalent to a VPC of 0.471. After adjusting for twelve confounders and two enumeration area factors, systematic differences between SEAs accounted for 47.1 % of the residual variance in malaria RDT results. The remaining 52.9 % came from unmeasured differences between individuals or families.

5. Discussion

Evaluating malaria transmission in Kenya involves analyzing disease prevalence, mosquito population, climate, and control methods. Malaria is widespread in various parts of Kenya, with transmission levels differing across regions and seasons. Variables like temperature, rainfall, and altitude impact the distribution and severity of malaria transmission. The presence of Anopheles mosquitoes, the primary carriers of malaria, significantly influences the disease's spread. Assessing malaria transmission in Kenya includes conducting surveys to determine disease prevalence, monitoring mosquito populations, and gauging the effectiveness of control measures

Table 2
Model diagnosis for the three models.

Fit Statistics	Fitted models		
	M0	M1	M2
−2 Log Likelihood	1374.43	1416.62	1459.88
AIC (smaller is better)	1446.43	1470.62	1507.88
BIC (smaller is better)	1576.63	1567.44	1592.3

Table 3
Model M2 odds ratio estimates with 95 % confidence intervals.

Effect	OR	95 % Wald Confidence Limits		P-Value
Region (Ref. Western)				
Central	0.000	0.000	1.524	0.985
Coast	0.134	0.073	0.247	**<0.0001**
Eastern	0.015	0.002	0.110	**0.014**
Nairobi	0.000	0.000	1.025	0.998
North Eastern	0.000	0.000	1.105	0.981
Nyanza	0.691	0.529	0.904	**0.016**
Rift Valley	0.077	0.039	0.153	**0.045**
Type of place of residence (Ref. Urban)				
Rural	2.053	1.468	2.870	**<0.0001**
Gender (Ref. male)				
Female	0.904	0.711	1.150	0.092
Children under 5 slept under mosquito bed net last night (Ref. Some children)				
All children vs Some children	1.328	1.086	2.052	**0.032**
No	0.847	0.443	1.618	0.674
Location of source for water (Ref. Elsewhere)				
In own yard/plot	0.748	0.526	0.964	**0.014**
In own dwelling	0.831	0.457	0.809	**0.020**
Wealth index (Ref. rich)				
Poor	2.422	1.665	3.521	**<0.0001**
Middle	1.875	1.268	2.773	**0.004**
Insecticide-Treated Net (ITN) (Ref. No, don't know)				
Yes	0.825	0.254	2.687	0.167
Cluster altitude in meters	0.995	0.924	0.998	**<0.0001**
Number of rooms used for sleeping	0.968	0.847	1.107	0.634
Age of household members	1.080	1.045	1.117	**<0.0001**
Number of persons who slept under this net	1.141	0.038	1.253	0.374
Person slept under an LLIN net	0.051	0.005	0.807	0.450
Number of household members	1.156	1.042	1.282	**0.006**
Number of children 14 and under (de jure)	0.905	0.795	1.030	0.067
Variance of random effects				
σ_b^2	**2.484 (0.537)**			
VPC or ICC	**0.471**			
Median Odd ratio	**4.575**			

like bed nets treated with pesticides and spraying anti-malaria and the availability of prompt and efficient medical care. In summary, evaluating malaria transmission in Kenya involves monitoring multiple factors to comprehend the disease's dynamics and guide targeted interventions to reduce malaria transmission and its impact [43,44].

This research explained the relationship between individual's age and gender and the results of their malaria RDT, revealing that their exposure to malaria problems dramatically reduces with increasing age. The findings on age are consistent with those of other researchers [45–47]. Household characteristics, particularly socio-economic factors such as insecticide-treated bed nets and the principal water source, were substantially related to malaria infection among household members.

Contrary to findings published in the malaria literature, the current investigation found no positive correlation between malaria prevalence in the study locations and mosquito nets treated with insecticides used at home. This connection was not statistically significant, though. Having a mosquito net reduces the risk of contracting malaria. This might be because the nets are distributed in areas where the disease is widespread, or perhaps a mosquito bit a household member or individual while the net was not in use, either during the day or at night.

To lessen the impact of malaria, the government should regularly distribute insect repellent (IRS) to homes, mosquito nets to families outside of malaria hotspots and to the population at risk, and more information on the benefits of these tools. There is a clear negative correlation between altitude and positive malaria RDT results; among individuals living in the survey regions, the probability of contracting malaria dropped as median altitude climbed. This is consistent with research done in Ghana [48], Ethiopia [33,49] and Uganda [50]. In addition to identifying major risk variables correlated with the risk of malaria, the research enabled us to measure heterogeneity in the odds ratio scale using data from pairs of randomly chosen people from distinct SEAs. The SEA-level variance decreased when SEA-level components were added to the fitted models in addition to the twelve covariates. This demonstrates how considering these factors lessens some significant variability at the SEA level (level 2). According to SEA-level variance, the results indicate that while some flexibility is considerable at the SEA level, it is not explained by SEA-level features or variables incorporated into the model. Our findings suggest the necessity for additional SEA-level factors to clarify the SEA's unpredictability. Additionally, because malaria-affected regions occur in the spatial patterns of SEAs' random effects, individual/household and SEA characteristics could not explain all SEA-level heterogeneities in malaria prevalence in the study sites. Because malaria incidence varies geographically, authorities need to keep a close eye on both newly emerging and existing malaria-affected regions and implement targeted health interventions to stop the disease from spreading, particularly in settings with limited resources.

6. Conclusion

In the current study, we used multilevel logistic regression with random impacts to evaluate the influence of various causes of heterogeneity and correlations between malaria RDT effects. Our models not only helped us assess the variation but also helped us pinpoint important risk factors linked to malaria infection. It is necessary that public health officials not only extend access to clean drinking water but also address other critical challenges. They also need to organize the provision of mosquito nets, indoor residual spray (IRS), and advice on how often to reapply insect repellent to interior walls. The studies also show that malaria infection rates vary by geography. As a result, inhabitants in malaria-infested regions should be given additional attention.

One of the study's limitations is that meteorological elements are not currently included in the research. The prevalence of malaria is mostly influenced by meteorological variables such as temperature, humidity, and rainfall. Malaria spreads in tropical and subtropical regions where Anopheles mosquitoes thrive and proliferate and where malaria parasites can finish their life cycle in mosquitoes. In the next phase of the study, climatic parameters will be included, and their relationships will be investigated.

CRediT authorship contribution statement

Dawit G. Ayele: Writing – review & editing, Writing – original draft, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Mohammed Omar Musa Mohammed:** Writing – review & editing, Resources, Methodology, Data curation, Conceptualization. **Ahmed Saied Rahama Abdallah:** Writing – review & editing, Methodology, Formal analysis, Data curation, Conceptualization. **Gemechis A. Wacho:** Writing – review & editing, Writing – original draft, Methodology, Conceptualization.

Informed consent

Informed consent was obtained from all individual participants included in the study.

Availability of data and materials

The data can be obtained by requesting the DHS program using the following website: https://www.dhsprogram.com/data/dataset_admin/login_main.cfm. Register and request the datasets.

Ethics approval and consent to participate

The protocol for the 2020 KMIS was approved by the Kenyatta National Hospital/University of Nairobi Scientific and Ethics Review Committee and the institutional review board at ICF. The risks and benefits of participation in the survey were explained to respondents. Informed consent was provided by eligible respondents before administering the Household or 'Woman's Questionnaire. Before collecting blood samples for malaria and anemia testing, informed consent was requested from parents or guardians of children.

Consent for publication

The article does not contain any individual details, and consent for publication is not applicable.

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Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:Mohammed Omar Musa Mohammed reports financial support was provided by Prince Sattam bin Abdulaziz University College of Business Administration. Ahmed Saied Rahama Abdallah reports a relationship with Prince Sattam bin Abdulaziz University College of Business Administration that includes: employment. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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