

RESEARCH ARTICLE



Factors Associated with Malaria in Regions Implementing Case Based Surveillance in Mainland Tanzania, August 2021 to May 2022

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Abstract:

Introduction: A malaria case-based surveillance system (mCBS) was established in Kilimanjaro, Arusha, and Manyara regions in Tanzania following reports of very low parasite prevalence. The system aims to eliminate malaria by 2030, but had not been analyzed since its start. Our study used data from August 2021 to May 2022 to identify factors associated with malaria among contacts of local cases

Methods: This was a cross-sectional study that analyzed mCBS data collected between August 2021 and May 2022. The dataset included index cases and contacts information obtained through proactive and reactive case detection methods (pro-ACD and re-ACD respectively). Multivariate logistic regression was used to identify factors associated with malaria among contact cases. Statistical significance was tested at a 95% confidence interval and p-value ≤ 0.05

Results: From August 2021 to May 2022, 949 malaria cases were reported, with 63.8% being over 16 years old, median age 20 years. Most cases were local-introduced (96.5%), males accounting for 54.8%. Arusha region reported most cases (53%). Among 642 tested contacts, 51% were female, and only 3.7% tested positive. Factors associated with lower malaria positivity included, household size \geq six members (aOR = 0.11, 95% CI = 0.02 – 0.62), being afebrile past three days (aOR = 0.03, 95% CI = 0.01 – 0.14), having no history of contact with individuals on malaria treatment within past 28 days (aOR = 0.01, 95% CI = 0.004 – 0.04), as well as having no history of travel to malaria-endemic areas within past 28 days (aOR = 0.24, 95% CI = 0.06 – 0.92)

Conclusion: A history of contact with a household member treated for malaria or had travelled to an endemic area in past 28 days as well as a family size with fewer than three members are risk factors for malaria in regions implementing case-based surveillance in Tanzania

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1. BACKGROUND

Malaria remains to be a global disease of public health concern. In 2021, nearly 247 million malaria cases were reported worldwide, of which 95% of them (234 cases) were in Africa. Malaria-related deaths have reduced from 897,000 deaths in 2000 to 619,000 deaths in 2021 (1).

In Mainland Tanzania, the disease prevalence has declined from 18.1% in 2008 to 7.5% in 2017 (2), with the target of eliminating the disease by the year 2030 (3). However, there have been reports of uneven disease distribution among regions such that some regions, such as Kilimanjaro, Arusha,

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and Manyara, have been reporting a very low malaria prevalence of up to <1% (4, 5). These regions were categorised as regions under malaria elimination in Tanzania, and a malaria case-based surveillance (mCBS) system was therefore introduced in these regions as an interventional strategy to ensure that local malaria cases are eliminated.

The mCBS system determines whether an infection was acquired locally, the likely location of the infection, and whether Indigenous transmission leads to onward transmission. Through passive case detection (pro-ACD), local index malaria cases are identified. A reactive case detection (re-ACD) is then conducted in households of identified index cases, where every contact member is tested for malaria using a malaria rapid diagnostic test. Those found positive are treated and classified as either local Indigenous or locally introduced cases (6).

Nations such as China achieved zero Indigenous malaria cases, proving the effectiveness of a case-based surveillance system in contributing to the country's efforts to malaria elimination (7). In the context of Tanzania, since the implementation of mCBS in the year 2020, system data has never been analyzed for decision-making. We used the mCBS dataset collected from August 2021 to June 2022 to determine factors associated with malaria among household members of the identified index cases. The results of this analysis will help the National Malaria Control Program (NMCP) set up interventional priorities to attain disease elimination in the region by 2030.

2. METHODS

This was a cross-sectional study that used secondary data collected from the Malaria case-based surveillance (mCBS) system from August 2021 to May 2022. The dataset included both local malaria cases detected after passive case detection (pro-ACD), and contact cases recorded after reactive case detection (re-ACD) from health facilities in regions implementing case-based surveillance. The data were cleaned and analyzed using Stata (version 15). Bivariate and multivariate logistic regression was used to determine factors associated with malaria among household members of the identified index cases. Statistical significance was tested at 95% CI and p-value ≤ 0.05 .

2.1. Ethical Considerations

The Muhimbili University of Health and Allied Sciences granted permission to conduct the study. Approval to use the data was granted by the National Malaria Control Program (NMCP) in Dodoma, Tanzania. The data were kept confidential and never shared with any third party. Names and addresses of individuals in the dataset were not recorded during data collection.

3. RESULTS

3.1. Demographic Characteristics of Participants

A total of 2667 malaria cases were reported in the system from August 2021 to May 2022. Of these, 949 cases (35.5%) were reported as Local (index) cases. The majority of the index cases were over 16 years old, 63.8% (605/949). Males accounted for most of the index cases by 54.8% (520/949), and the median age of these cases was 20 years (IQR) = 10 - 31). Most of the index cases were classified as local-introduced cases 96.5% (916/949).

On the other hand, of 949 index cases, 642 household/contact members were tested for malaria during re-ACD. The majority of the contacts, 57.6% (370/642), were over 16 years old. Females were most of the reported contacts by 51% (327/642) and had a median age of 20 years old (IQR 95 = 7- 34). Of the 642 contacts, only 24 cases (3.7%) had a positive malaria rapid test. Most of the malaria-positive contacts were classified as local – indigenous 58.3% (14/24). Arusha region had the most index cases, 53% (504/949), and contact members, and 73% (472/642) (Table 1).

Table 1. Characteristics of index and contact cases reported from regions implementing mCBS from August 2021 to May 2022.

Characteristic	Index cases		Contact members	
	Frequency (N)	Percentage (%)	Frequency (N)	Percentage (%)
Age (years)				
≤5	167	17.6	115	17.9
6 – 15	177	18.7	157	24.5
≥16	605	63.8	370	57.6
Region				
Kilimanjaro	153	16.1	31	4.8
Arusha	504	53.1	472	73.5
Manyara	292	31.8	139	21.7
Sex				
Male	520	54.8	315	49.1
Female	429	45.2	327	50.9
Malaria Rapid Test Results				
Positive	949	100	24	3.7
Negative	0	0	618	96.3
Local Case Category				
Indigenous	33	3.5	14	58.3
Introduced	916	96.5	10	41.7

3.2. Risk Factors Associated with Malaria Infection among Family Members Identified through Reactive Case Detection

Factors such as age, sex, family size, history of fever in the past three days before re-ACD, history of contact with a person treated for malaria in the same household in the past 28 days, as well as the history of travel to a malaria endemic area in the past 28 days, were analyzed to assess their association with testing positive for malaria among contact cases

Multivariate analysis showed that the odds of a positive malaria rapid test decreased with an increase in family size such that households whose family size was over members had 81% lower odds of having a positive malaria rapid test compared to households with a family size of less than three members (aOR = 0.19, 95% CI = 0.05 – 0.72). Similarly, household members who had a history of contact with a household member who had been treated for malaria in the past 28 days had 2.6 times the odds of having a positive malaria rapid test compared to those who had not contacted household members known to have been on malaria treatment (aOR = 2.60, 95% CI 113 = 1.11 – 6.06). On the other hand, household members who had a history of travel to malaria- endemic areas in the past 28 days had about four times the odds of testing positive for malaria compared to those who hadn't travelled (aOR = 3.67, 95% CI = 1.47 – 9.20) (Table 2).

4. DISCUSSION

Tanzania is among malaria endemic countries in the world with malaria prevalence varying within and among its regions. The burden of malaria varies from as low as <1% in the highlands to as high as 24% along the Lake and Western zones of the country. As an interventional strategy toward disease elimination in the country by the year 2030, malaria case-based surveillance was introduced in regions that consistently reported a disease prevalence of <1%.

Table 2. Bivariate and Multivariate Logistic regression analysis of factors associated with malaria infection identified through reactive case detection

Characteristics	Malaria rapid test results		Bivariate analysis	Multivariable analysis		
	Positive N (%)	Negative N (%)	cOR*(95% CI)	p-value	aOR*(95% CI)	p-value
Age (Years)						
≤ 5	6 (5.2)	109 (94.8)	1.6 (0.60 – 4.48)	0.33		
6 – 15	6 (3.8)	151 (96.2)	1.2 (0.44 – 3.22)	0.74		
≥16	12 (3.2)	358 (96.8)	1			
Sex						
Male	8 (2.5)	307 (97.5)	0.51 (0.21 – 1.20)	0.12	0.46 (0.19 – 1.12)	0.09
Female	16 (4.9)	311 (95.1)	1			
Family Size						
≤ 3	9 (7.1)	117 (92.9)	1			
4 - 5	12 (4.1)	280 (95.9)	0.56 (0.23 – 1.36)	0.20	0.66(0.27 – 1.66)	0.38
≥6	3 (1.3)	221 (98.7)	0.18 (0.05 – 0.66)	0.01	0.19(0.05 – 0.72)	0.02
History of Fever Three Days Prior re-ACD						
Yes	11 (4.1)	257 (95.9)	1.19 (0.52 - 2.70)	0.68		
No	13 (3.5)	361 (96.5)	1			
Contact with a Family Member Treated for Malaria Last 28 Days						
Yes	14 (5.9)	224 (94.1)	2.46(1.08 -5.63)	0.03	2.60 (1.11 - 6.06)	0.03
No	10 (2.5)	394 (97.5)	1			
History of Travel to a Malaria-Endemic Area Past 28 Days						
Yes	8 (9.2)	79 (90.8)	3.41 (1.41 – 8.23)	<0.01	3.67 (1.47– 9.20)	<0.01
No	16 (2.9)	539 (97.1)	1			

Note: *cOR = Crude Odds Ratio, aOR = Adjusted Odds Ratio

Our study investigated factors associated with malaria infection in regions implementing Case Based Surveillance in Tanzania from August 2021 to May 2022. The findings suggest that having a history of contact with a household member who had been on malaria treatment in the past 28 days as well as having a history of travel in a malaria endemic area within the past 28 days, are significantly associated with increased odds of malaria positivity, whereas having a family size of more than 6 members is significantly associated with reduced odds of malaria positivity.

We observed significantly higher odds of having a positive malaria test in individuals with a history of contact with a person previously treated for malaria in the past 28 days. Similar findings have been reported by previous literature (8–11). This concern may have been contributed by either delay in obtaining a malaria treatment or non-adherence to antimalarial drugs, which may have all contributed to increased risk of disease transmission from index cases to contacts. Increased malaria infectivity has been reported by individuals who had delayed or had not adhered to malaria treatment (12). These factors may have made these individuals act as reservoirs for the ongoing transmission of malaria parasites from one individual to another in the household. The lack of index case data on drug adherence and schedules from this dataset provides a setback to making comparisons with other studies.

Furthermore, our analysis showed that a history of travel to the malaria-endemic area in the past 28 days before re-ACD was significantly associated with an increased risk of having a positive malaria test. These

results are congruent with the findings reported from a meta-analysis study that reported travel as a key risk factor for malaria transmission in pre-elimination settings (13). Similarly, our results are also similar to previous literature (14–16). Being regions of potential tourism interest, Kilimanjaro, Arusha, and Manyara regions are likely to be visited by different individuals across the world who might be potential sources of the infection. However, the use of ultra-sensitive diagnostic tests such as loop-mediated isothermal amplification polymerase chain reaction has been suggested as an alternative approach to early detection of travel-associated malaria at key border entry points (17).

Surprisingly, our analysis has revealed that the higher the family size of more than 6 members, the lower the risk of malaria infection. This finding is contrary to what has been reported by other literature on an increased risk of malaria infection with increasing family size (18–20). Other studies have found no significant association between family size and risk of malaria transmission (21, 22). However, households with larger family sizes have been associated with having good knowledge and positive attitudes about malaria (23). Therefore, households with large family sizes, are more likely to use their good knowledge engaging in malaria prevention practices enough to cover a large area of house surroundings during cleaning.

CONCLUSION

Having a history of contact with a family member treated for malaria or had traveled to a malaria-endemic area in the last 28 days, as well as having a family size of fewer than three members, were risk factors for positive malaria rapid tests among contacts of index cases in the Kilimanjaro, Arusha, and Manyara regions under malaria surveillance. Enhancing community engagement in malaria elimination programs could accelerate progress in these regions.

AUTHORS' CONTRIBUTIONS

The author confirms sole responsibility for the following: study conception and design, data collection, analysis and interpretation of results, and manuscript preparation.

CONSENT FOR PUBLICATION

Not applicable.

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CONFLICT OF INTEREST

The author confirms that this article's content has no conflict of interest.

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REFERENCES

- [1] World Health Organization. World Malaria Report 2022 [Internet]. Available from: www.who.int/teams/global-malaria-programme/reports/world-malaria-report-2022
- [2] Ministry of Health, Community Development, Gender, Elderly and Children (MoHCDGEC) (Tanzania Mainland), Ministry of Health (Zanzibar), National Bureau of Statistics, Office of the Chief Government Statistician, Dar es Salaam. Tanzania Malaria Indicator Survey. 2017.
- [3] National Malaria Control Program, Dodoma, Tanzania. Malaria Surveillance Bulletin. 2020.
- [4] Thawer SG, Chacky F, Runge M, Reaves E, Mandike R, Lazaro S, et al. Sub-national stratification of malaria risk in mainland Tanzania: A simplified assembly of survey and routine data. *Malar J* [Internet]. 2020; 19(1):1–12. Available from: <https://doi.org/10.1186/s12936-020-03250-4>

- [5] Ministry of Health, Community Development, Gender, Elderly and Children, Dodoma Tanzania. National Malaria Strategic Plan. 2020.
- [6] National Malaria Control Programme, Tanzania. Malaria case-based surveillance reference manual. 2020.
- [7] Feng J, Zhang L, Huang F, Yin JH, Tu H, Xia ZG, et al. Ready for malaria elimination: Zero indigenous case reported in the People's Republic of China. *Malar J* [Internet]. 2018; 17(1):1–13. Available from: <https://doi.org/10.1186/s12936-018-2444-9>
- [8] Temu EA, Coleman M, Abilio AP, Kleinschmidt I. High prevalence of malaria in Zambezia, Mozambique: The protective effect of IRS versus increased risks due to pig-keeping and house construction. *PLoS One*. 2012; 7(2).
- [9] Khatib RA, Chaki PP, Wang DQ, Mlacha YP, Mihayo MG, Gavana T, et al. Epidemiological characterization of malaria in rural southern Tanzania following China- Tanzania pilot joint malaria control baseline survey. *Malar J* [Internet]. 2018; 17(1):1–14. Available from: <https://doi.org/10.1186/s12936-018-2446-7>
- [10] West PA, Protopopoff N, Rowland M, Cumming E, Rand A, Drakeley C, et al. Malaria Risk Factors in North West Tanzania: The Effect of Spraying, Nets and Wealth. *PLoS One*. 2013; 8(6).
- [11] Carlucci JG, Blevins Peratikos M, Cherry CB, Lopez ML, Green AF, González-Calvo L, et al. Prevalence and determinants of malaria among children in Zambézia Province, Mozambique. *Malar J*. 2017; 16(1):1–13.
- [12] Challenger JD, Gonçalves BP, Bradley J, Bruxvoort K, Tiono AB, Drakeley C, et al. How delayed and non-adherent treatment contribute to onward transmission of malaria: a modelling study. *BMJ Glob Heal*. 2019; 1–11.
- [13] Ahmed S, Reithinger R, Kaptoge SK, Ngondi JM. Travel is a key risk factor for malaria transmission in pre-elimination settings in Sub-Saharan Africa: A review of the literature and meta-analysis. *Am J Trop Med Hyg*. 2020; 103(4):1380–7.
- [14] Abdalal SA, Yukich J, Andrinopoulos K, Alghanmi M, Wakid MH. Livelihood activities, human mobility, and risk of malaria infection in elimination settings: a case – control study. *Malar J* [Internet]. 2023; 1–11. Available from: <https://doi.org/10.1186/s12936-023-04470-0>
- [15] Alemu K, Worku A, Berhane Y, Kumie A. Men Traveling Away from Home Are More Likely to Bring Malaria into High Altitude Villages, Northwest Ethiopia. 2014; 9(4):1–7.
- [16] Yukich JO, Taylor C, Eisele TP, Reithinger R, Nauhassenay H, Berhane Y, et al. Travel history and malaria infection risk in a low-transmission setting in Ethiopia: a case control study. 2013; 1–9.
- [17] Mkali HR, Reaves EJ, Lalji SM, Al-mafazy AW, Joseph JJ, Ali AS, et al. Risk factors associated with malaria infection identified through reactive case detection in Zanzibar, 2012–2019. *Malar J* [Internet]. 2021; 20(1):1–10. Available from: <https://doi.org/10.1186/s12936-021-04025-1>
- [18] Mohan I, Kodali NK, Chellappan S, Karuppusamy B, Behera SK, Natarajan G, et al. Socio-economic and household determinants of malaria in adults aged 45 and above: analysis of longitudinal ageing survey in India, 2017 – 2018. *Malar J* [Internet]. 2021; 1–9. Available from: <https://doi.org/10.1186/s12936-021-03840-w>
- [19] Tesfaye A, Teshome T. Prevalence and Associated Factors of Malaria Infection among Outpatients Visiting Shewa Robit Health Center, Northcentral Ethiopia. *J Trop Med*. 2022.
- [20] Guerra M, Sousa B De, Mabale NN, Berzosa P, Arez AP. Malaria determining risk factors at the household level in two rural villages of mainland Equatorial Guinea. *Malar J* [Internet]. 2018; 1–10. Available from: <https://doi.org/10.1186/s12936-018-2354-x>
- [21] Odeyemi A, Olasinde Y, Ojewuyi A, Ala O. Malaria Parasitaemia and its Associated Factors among Febrile Children in a Tertiary Hospital in Southwest Nigeria. *West Afr J Med*. 2022 ;(May).
- [22] Gunathilaka N, Abeyewickreme W, Hapugoda M, Wickremasinghe R. Determination of demographic, epidemiological, and socio-economic determinants and their potential impact on malaria transmission in Mannar and Trincomalee districts of Sri Lanka. *Malar J*. 2016; 1–11.
- [23] Dejazmach Z, Alemu G, Yimer M, Tegegne B, Getaneh A. Prevalence of Malaria and Associated Knowledge, Attitude , and Practice among Suspected Patients in Bahir Dar Zuria District , Northwest Ethiopia. 2021.