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A constant contact community-based epidemiological investigation (C3EI) as part of malaria elimination demonstration project, Mandla district, Madhya Pradesh, India

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Abstract

Background In India, an increase in malaria cases by 21% (223,961 cases) has been reported between 2022 and 2023. Madhya Pradesh ranks 10th in malaria burden, with Mandla district selected for the Malaria Elimination Demonstration Project (MEDP) to demonstrate the feasibility of malaria elimination in a hard-to-reach, tribal-dominated, and hilly forested district. A Constant Contact Community-based Epidemiological Investigation (C3EI) was undertaken by continuous engagement with the community for real-time data collection, mapping of malaria cases, identification of risk factors, and monitoring of intervention outcomes designed to drive effective strategies for malaria elimination.

Methods The study mapped 1,143,126 individuals from 248,825 households in the year 2017 in Mandla district for constant contact surveillance. Fortnightly household visits were conducted to inquire about febrile episodes, with on-spot diagnosis and treatment. Data collection was done using the SOCH mobile application, and analysis using R.

Results The constant contact household surveillance revealed that out of 956,795 individuals, 230,780 (24.12%) unique individuals reported one or more febrile episodes, with a total of 322,577 febrile episodes and 490 malaria episodes (RDT positive). Males had a higher risk of malaria infection than females (OR = 2.62; $p < 0.0001$). The cumulative incidence of malaria was highest among children aged 5–15 years and pregnant women. Multiple episodes of malaria infections were more common in adults over 30 years. The incidence of malaria per 100,000 persons gradually declined from 26.13 in 2018 to 11.18 in 2020, with the highest incidence during the monsoon season.

Conclusion The C3EI presents a new strategy suitable for disease elimination programmes. Implementing C3EI-type longitudinal studies in elimination projects holds promise for generating data to expedite malaria elimination efforts because the unit of observation is a 'household'. Such a comprehensive approach allows identification in the gaps in case management for prompt interventions at the household-level.

Keywords Constant Contact Community based Epidemiological Investigation, Longitudinal malaria surveillance, Malaria elimination, MEDP

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Background

The World Health Organization (WHO) estimated 249 million malaria cases and 608,000 malaria deaths globally in the year 2022, of which countries in the WHO African region accounted for 94% of all malaria cases. The WHO South East Asia region has contributed about 2% to the global estimated malaria cases, with India contributing 66% and Indonesia contributing 22% of the estimated malaria cases in WHO SEA region [1].

Between 2000 and 2019, malaria deaths declined steadily from 864,000 in 2000 to 576,000 in 2019. In 2020, there was an increase of 55,000 malaria deaths to an estimated 631,000 partly as a result of the disruptions in access to malaria prevention and case management tools due to the COVID-19 pandemic; the challenges were navigated through normalization and optimization of malaria surveillance systems, which led to a marginal decline in 2021 to 610, 000 and further decline in 2022 [1].

In India, an increase in malaria cases by 21% (223,961 cases) has been reported between 2022 and 2023, and the number of high-burden districts has been modified from 24 to 32 [2, 3]. The highest malaria burden is concentrated in Odisha, followed by Jharkhand, Chhattisgarh, West Bengal, and Tripura. The state of Madhya Pradesh (MP) ranks number 10th. It is placed in category one with less than one malaria case per 1000 population in all the districts as per the National Strategic Plan for Malaria Elimination 2023–2027, which accounts for 1.92% of the total reported malaria cases in the country [3].

District Mandla in MP, a malaria-endemic and tribal-dominant district, was selected as the site for the Malaria Elimination Demonstration Project (MEDP) in a public–private-partnership mode by the Indian Council of Medical Research (ICMR), Government of MP, and the Foundation for Disease Elimination and Control of India (FDEC India), which is a not-for-profit CSR subsidiary of Sun Pharmaceutical Industries Ltd. The aim of the MEDP study was to demonstrate the feasibility of malaria elimination in a hard-to-reach, tribal-dominated, and hilly forested malaria-prone district by tracking each fever on a fortnightly basis and malarial episode at the household level [4].

Previous studies in the region have highlighted the unique socioeconomic and cultural factors contributing to malaria transmission, particularly in tribal populations and forested areas. A prior study has demonstrated that low literacy, poor hygiene, and cultural beliefs can act as barriers to effective malaria control and elimination [5]. Other studies in similar areas have shown the effectiveness of vector control measures and the role of community engagement in reducing malaria transmission [6, 7]. Building upon these findings, the C3EI approach aims to address these challenges by focusing on continuous household-level surveillance and engagement, which has been shown to improve the detection and treatment of cases in malaria-endemic areas [4, 8].

MEDP focused on improving the quality and timeliness of service delivery for existing interventions, with some context-specific modifications. These included connecting with the community for focused and sustained Information, Education and Communication (IEC) campaigns, engaging with the health care delivery workers in a continuous manner for training and capacity building, enhanced monitoring through review of real-time review of data, increased supervision, and greater accountability for service delivery quality, comprehensive tracking of individuals with febrile episodes, prompt testing, and guaranteed treatment compliance.

The project also emphasized optimizing vector control measures alongside periodic Mass Screening and Treatment (MSaT) and the molecular diagnosis of a subset of samples, which were carried out to check the burden of low-density malaria infections and asymptomatic cases [4].

As part of the Malaria Elimination Demonstration Project, this study presents here the results of the Constant Contact Community-based Epidemiological Investigation (C3EI). Unlike traditional cross-sectional studies, C3EI adopts a longitudinal approach, continuously monitoring malaria at the household level through fever surveillance. This enables the detection of trends, hotspots, and seasonality, thus informing targeted interventions at household levels and around the index households.

This longitudinal investigation, which lasted from 2018 to 2020, has revealed significant insights into febrile and malarial episodes. The present study argues that this novel approach to disease surveillance is appropriate and applicable for malaria and other vector-borne disease elimination programmes.

Methods

Study area

Mandla is located between latitudes 22° 12’: 23° 22" 02’ N and longitudes 79° 59′ 23": 81° 44′ 22" E in the south-eastern part of the MP state, 44.44% forest covering area of a total geographical area of 8771 km^2. The district is divided into nine administrative blocks. Based on the 2011 census, the population was 1.05 million, projected to reach 1.23 million by 2022. About 58% of the population belongs to the indigenous tribal groups, mainly the *‘Gond’* and the *‘Baiga’*, who are classified as a Particularly Vulnerable Tribal Group (PVTG) and mainly confined to the eastern part of the district [9].

The topography of Mandla is characterized by hilly, forested, and highly undulating terrain, with narrow strips of cultivated plains along the valleys of rivers and streams. The eastern forest zone of the district comprises blocks of Mawai, Bichhiya, Ghughari and Mohgaon, are having densely forested areas of semi-deciduous sal (*Shorea robusta*) and deciduous teak (*Tectona grandis*) trees and bordering with Kanha tiger reserve national park [10]. The district experiences a tropical climate with rainfall primarily from the southwest monsoon. The higher elevation and abundance of forests moderate the summer temperatures compared to other parts of the state. The average annual rainfall is reported to be 1427.7 mm [11].

The district's villages are surrounded by perennial streams that provide breeding sites for *Anopheles culicifacies* and *Anopheles fluviatilis*, the primary vector responsible for malaria transmission in the area [7]. The malaria transmission dynamics in Mandla are seasonal, with *Plasmodium falciparum* and *Plasmodium vivax* being the predominant species [12].

Enumeration of the community surveillance cohort

The project staff that were trained and certified for treatment (minimum senior-secondary education) enumerated all individuals in the district during a household census as described in the study design of Malaria Elimination Demonstration Project [4]. Socio-demographic information, including gender, date of birth, caste, education, primary occupation, family income, and socio-economic indicator variables, were collected using a pre-tested structured interview schedule. Each household and individual received a unique identification representing the geographical location and family member sequence, starting with the head of the household (i.e. location-household-01 to n). A household or family was defined as a group of individuals related to each other by blood or marriage and sharing living space and kitchen.

Fever surveillance, diagnosis, and treatment

Fortnightly household visits were conducted to inquire about febrile episodes by trained Village Malaria Workers (VMWs) [4]. During these visits, VMWs collected information on clinical presentations related to malaria using an Android-based electronic family register and disease surveillance application developed by MEDP, known as the Solutions for Community Health-workers (SOCH) [13]. Suspected cases were diagnosed with malaria on the spot using Rapid Diagnostic Test kits (SD BIOLINE Malaria Ag P.f/P.v) for *P. falciparum* (HRP2) and *P. vivax* (pLDH). The positive cases were treated according to the modified National Drug Policy 2014 [14]. Treatment compliance was ensured by the direct observation method, and patients were tracked regularly until treatment completion and clinical recovery. The cases with severe illness and infected pregnant women were referred to the nearest health facility for better care and treatment. Cluster-level Malaria Field Coordinators (MFCs) randomly checked the VMW's visits to ensure service delivery and coverage quality.

Data management and analysis

Census records and fever surveillance data were entered into an Azure SQL Database with an ASP.net Web API. VMWs and MFCs used the front-end dashboard of the SOCH mobile application in the field to retrieve and input data during periodic household visits. All records underwent validation using pre-coded logical and consistency checks within the SOCH application before being uploaded to the web database server [13].

The census and fever surveillance datasets were exported to R and merged using an inner join SQL command. The age of individuals and months of the survey were grouped and numerically coded into categorical variables named age group and seasons, respectively. Households were categorized into different socioeconomic strata (SES) using a modified Kuppuswamy scale [15]. The nine blocks were classified into high and low malaria endemicity based on the five-year malaria prevalence data preceding 2017 from the Mandla District Malaria Office.

The frequency of fever and malaria episodes of study participants was tabulated for the three-year follow-up period (2018–2020). Cumulative incidence rates with 95% confidence intervals per 100,000 persons by category group were calculated. Univariate and multivariate mixed-effect logistic regression models estimated the association of malaria with independent factors such as age group, caste, pregnancy, season, endemicity, SES, and year. All statistical analyses were performed using R version 4.3.2 for Windows (R Project for Statistical Computing).

Results

The community surveillance cohort

The enumeration of the district population through household visits was conducted from June to August 2017. The field operations began in September 2017, and all RDT-positive malaria cases were treated per national guidelines and recorded. The study period of the present longitudinal analysis of constant contact epidemiological investigation was from January 2018 to December 2020. In this community cohort of 956,795 persons (study population) out of 1,143,126 total enumerated population were studied who were constantly available in the community cohort and were not infected at the entry point of the study. These subjects were followed up for three years and episodes of infection in the study population were analysed. This cohort was nearly equally split between males [480,850 (50.26%)] and females [475,945 (49.74%)].

Table 1 Fever and malaria episodes in 36 months longitudinal community surveillance during 2018–2020

Episodes	Fever cases		Malaria positive		PF-PF			PV-PV			MIX-MIX			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
	nU	nF	nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
0	726,015																								
1	172,931	172,931	363	363	248	248		101	101		14	14													
2	39,797	79,594	52	104	33	66	296 (13–819)	16	32	205.4 (23–504)				2	4	90 (20–160)	1	2	130						
3	10,544	31,632	5	15	3	9	54 (45–59);180 (108–323)[a]													1	3	21;157	1	3	34;123
4	4137	16,548	2	8	1	4	59;349;535	1	4	77;121;144															
5+	3371	21,872						0	0																
Total	230,780	322,577	422	490	285	327		118	137		14	14		2	4		1	2		1	3		1	3	

nU Unique Persons, *nF* Total number of fever cases tested, *nM* Total malaria cases, *rMDI* Mean Days Interval (range), *PF P. falciparum*, *PV P. vivax*; MIX: *P. falciparum* + *P. vivax*

[a] The time interval between three episodes of 'Pf' infections was 54 days (range 45 to 59 days) from first to second infection in the same individual. It was 180 days (range 108–323 days) from first to third infection in the same individual. The mean days interval (range) interpretation should be done using this example for all Tables 1, 2, 3, 4, 5, 6

During the 72 household visits at 15-day intervals over the three-year longitudinal period of the present study, each participant was followed for a median of 37 times (IQR: 19, 55).

Fever and malarial episodes

Out of the 956,795 constant population of the community surveillance cohort, 230,780 individuals (24.12%) reported one or more febrile episodes during 2018–2020. There were a total of 322,577 febrile episodes, averaging 1.40 episodes per person during the study period. Over the three-year period of this study, a total of 490 (0.05%) malarial episodes were detected in 422 individuals, with an average of 1.16 episodes per person. Out of 322,577 fever cases, 145,717 (45.61%) were male, 178,860 (54.39%) were female, and out of 490 malaria cases, 303 (61.84%) were male, and 187 (38.16%) were female. In comparison to females, males reported lesser febrile events (OR = 0.68; 95% CI 0.67–0.69; $p < 0.0001$) but a higher risk of malaria infection (OR = 2.62; 95% CI 2.03 – 3.40; $p < 0.0001$).

Among the infected individuals, 86.02% (363/422) were diagnosed as a single episode, while 12.32% (52/422), 1.18% (5/422), and 0.47% (2/422) were diagnosed two, three, and four episodes of malaria, respectively. The day interval of the consecutive infections was calculated from the day of the first infection and considered as a constant zero-day. Mean days intervals between second, third and fourth malarial infections irrespective of malaria species were respectively 257 (range: 13–819), 164 (range: 108–323) and 339 (range: 144–535) days. The second repeated infection of *P. falciparum* was after 296 (range: 13–819) days, and of *P. vivax* was after 205 (range: 23–504) days. The third and fourth repeated infections of *P. falciparum* were after 180 (range: 108–323) and 535 days, respectively. The fourth repeated infection of *P. vivax* in a single case was after 144 days. The *Plasmodium* species was consistent across episodes, except in five individual cases where changes between *P. falciparum* and *P. vivax* infections were observed. Two cases (0.41%) of *P. falciparum* infection were turned into *P. vivax* during the second episode after 20 and 160 days. One case (0.20%) of mixed infection was reported as *P. vivax* after 130 days. One case (0.20%) of *P. falciparum* was reinfected or recrudescence with *P. falciparum* after 21 days and further reported with *P. vivax* after 157 days. One case (0.20%) of mixed infection (*P. falciparum* and *P. vivax*) was repeated with a mixed infection on 34th day and further reinfected or relapse of *P. vivax* after 123 days (Table 1).

Multiple episodes of malaria infections were found more in individuals over 30 years of age. Only two children less than five years old reported a second episode of malaria, of which one had a repeated episode of *P. falciparum* after 149 days, and another had repeated episodes of *P. vivax* after 40 days. Six children between five and 15 years of age group reported a second episode of malaria infection, three each for *P. falciparum* and *P. vivax* after 192 and 228 days, respectively. Further, the two episodes of malaria infection among the adult population of 15–30 years age group were in 15 persons [seven *P. falciparum* (374 days), seven *P. vivax* (243 days) and one *P. falciparum* to *P. vivax* (20 days)]. In 17 persons of 30–50 years of age group [14 *P. falciparum* (310 days), one *P. vivax* (504 days), one *P. falciparum* to *P. vivax* (160 days) and one mixed to *P. vivax* (130 days)] and above 50 years of age groups in 12 persons—8 *P. falciparum* (259 days), four *P. vivax* (89 days). Third and fourth malarial episodes were found among the 30–50 years and above 50 years of age groups (Table 2).

One woman was diagnosed with repeated *P. falciparum* infection in her two distinct pregnancies with 365 days intervals, and five non-pregnant women were reinfected with *P. falciparum* (four cases) after 252 days and *P. vivax* (one case) after 28 days. Another non-pregnant woman had a third episode of malaria infection where the first infection was mixed of *P. falciparum* and *P. vivax*, the second infection after the 34th day was mixed, and the third infection after 123 days was *P. vivax*; which could be a reinfection or a relapse. Additionally, six women presented second episodes of malaria infection, of which three were non-pregnant at the time of the first infection. During the second episode of infection (all *P. vivax)*, they were pregnant after 359 (range: 233–423) days, and the three pregnant women were reinfected after 323 (range: 20–819) days, by which time they were not pregnant anymore (Tables 3, 4).

None of the persons of the General Caste group had multiple episodes of malaria infection, and only two persons of the Scheduled Caste group were reinfected with one *P. falciparum* after 325 days and one *P. vivax* after 423 days. Amongst Other Backward Caste group, nine persons had a second episode of malaria (six *P. falciparum* after 187 days and three *P. vivax* after 40 days), and two persons had four episodes of malaria infection (*P. falciparum* after intervals of 59-349-535 days and *P. vivax* after intervals of 77-121-144 days).

A total of 41 persons of the Scheduled Tribes ethnic group were found with second episodes of malaria infection, of which 26 were reinfected with *P. falciparum* after 320 days, 12 with *P. vivax* after 229 days, two *P. falciparum* to *P. vivax* after 90 days, and one mixed to *P. vivax* after 130 days. Another five Scheduled Tribes had third episodes of malarial infection, of which three from *P. falciparum* after 54 and 180-day intervals, one *P. falciparum* to again *P. falciparum* after 21 days, then *P. vivax* after

Table 2 Age group wise fever and malaria episodes in 36 months longitudinal community surveillance during 2018–2020

Age group (Population)	Episodes	Fever cases	Malaria positive		PF-PF			PV-PV			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
			nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
< 5 yrs (57,862)	1	29,329	15	15																		
	2	13,482	2	4	1	2	149	1	2	40												
	3	4,346																				
	4	1,820																				
	5+	2,430																				
5–15 yrs (59,645)	1	33,608	52	52																		
	2	6,078	6	12	3	6	192.3 (86–400)	3	6	228.3 (16–400)												
	3	1,604																				
	4	613																				
	5+	501																				
15–30 yrs (134,621)	1	60,268	95	95																		
	2	11,814	15	30	7	14	374.1 (13–794)	7	14	242.9 (28–503)	1	2	20									
	3	3,418																				
	4	1,341																				
	5+	1,536																				
30–50 yrs (199,845)	1	66,568	134	134																		
	2	15,715	17	34	14	28	310.4 (27–727)	1	2	504	1	2	160	1	2	130						
	3	5,052	3	9	1	3	59;109										1	3	21;157	1	3	34;123
	4	2,183	1	4	1	4	59;349;535															
	5+	2,306																				
> 50 yrs (504,822)	1	41,007	67	67																		
	2	10,760	12	24	8	16	259.5 (18–425)	4	8	89.5 (23–161)												
	3	3,632	2	6	2	6	51.5;215.5															
	4	1,551	1	4	1	4	77;121;144															
	5+	1,615																				

nU Unique Persons, *nF* Total number of fever cases tested, *nM* Total malaria cases, *rMDI* Mean Days Interval (range), *PF P. falciparum*, *PV P. vivax*, *MIX P. falciparum* + *P. vivax*

Table 3 Fever and malaria episodes among pregnant and non-pregnant women during 36 months of longitudinal community surveillance from 2018 to 2020

Pregnancy status (Population)	Episodes	Fever cases	Malaria positive		PF-PF			PV-PV			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
			nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
Non-Pregnant (92,338)	1	46,021	51	51																		
	2	11,973	5	10	4	8	252 (27–86)	1	2	28												
	3	3371	1	3																1	3	34;123
	4	2403																				
	5+	240																				
Pregnant (1160)	1	697	31	31																		
	2	122	1	2	1	2	365															
	3	43																				
	4	5																				
	5+	14																				

nU Unique persons, *nF* Total number of fever cases tested, *nM* Total malaria cases, *rMDI* Mean days interval (range), *PF P. falciparum*, *PV P. vivax*, *MIX P. falciparum + P. vivax*

Table 4 Malaria infections in the same individuals who were pregnant and Non-Pregnant during the 36 months of longitudinal community surveillance from 2018 to 2020

Sr. No	Pregnant	Non-pregnant	Days interval
1	MIX	PV	130
2	PF	PF	819
3	PF	PV	20
4	PV	PV	233
5	PV	PV	421
6	PV	PV	423

PF P. falciparum, *PV P. vivax*, *MIX P. falciparum + P. vivax*. The arrow showing direction from the initial infection to the subsequent second infection

157 days and one mixed to mixed after 34 days and then *P. vivax* after 123 days (Table 5).

Further analysis of repeated episodes of malaria infections between socioeconomic strata (SES) found that persons belonging to the higher socioeconomic status (SES) had a smaller number of repeated infections than those in the lower SES group except for one case of four times *P. falciparum* infections in the upper SES group (Table 6). The repeated episodes of malaria infections between years and seasons could not be presented appropriately because the particular individuals may be reinfected in consecutive months and years of the follow-up (Table 6).

Cumulative incidence (95% CI) of malaria (per 100,000 persons)

The cumulative incidence of fever (322,577/956,795) was 33,714.33 (33,619.60–33,809.15) per 100,000 persons with a cumulative malaria incidence of 51.21 [490/956795 (46.78–55.95)] per 100,000 persons (Table 1). The persons under the age group of 5–15 years were the most susceptible to malaria with a cumulative incidence of 107.30 (82.64–137.00), followed by 15–30 years [92.85 (77.30–110.62)], 30–50 years [90.57 (77.86–104.76)] and considerably low in < 5 years [32.84 (19.77–51.27)] and > 50 years of age [20.01 (16.30–24.31)] (Table 2). A total of 1,160 pregnancies were observed during the study period, and the cumulative incidence during pregnancy [3362.07 (2401.47–4567.59)] was about 44 folds higher than ever married non-pregnant women of the reproductive age group [75.81 (59.10–95.77)] (Tables 3, 4).

Persons belonging to the Scheduled Tribe community had the highest cumulative incidence [64.43 (58.04–71.34)] followed by Scheduled Caste [35.90 (23.85–51.88)], Other Backward Castes [31.00 (24.86–39.19)] and lowest in General Caste group [19.37 (5.28–49.59)] (Table 5). Further analysis of cumulative malaria incidence among the SES of the persons revealed that highest malaria incidence was among lower SES [104.09 (89.79–120.03)]. Followed by upper lower SES [53.62 (45.22–63.12)], lower middle SES [37.24 (30.87–44.53)], and upper SES [33.77 (21.41–50.67)]. The lowest incidence was in upper middle SES [12.04 (6.58–20.20)] (Table 6).

The incidence of malaria gradually declined over the years. In the year 2018, the malaria incidence was 26.13 (22.99–29.58), which was about a 47% decline during 2019 [13.90 (11.64–16.47)] and further about 20% decline during 2020 [11.18 (9.16–13.51)]. Monsoon months (July – September) [18.60 (15.97–21.55)] and spring (January – March) [14.32 (12.02–16.93)] were higher malarious seasons than winter (October – December) [10.35 (8.41–12.60)] and summer (April – June) [7.94 (6.26–9.94)] (Table 7).

Block-wise data revealed the highest incidence in Mawai, followed by Mohgaon and Bichhiya, with Mandla, Bijadandi, and Narayanganj reporting the lowest (Fig. 1). A total of 114 malaria cases were reported from the 369,379 persons residing in low malaria endemic areas of the district, and 376 cases were reported from the 587,416 persons residing in high malaria endemic areas. The cumulative incidence of malaria in low and high endemic blocks was 30.87 (95% CI 25.47–37.09) and 64.01 (95% CI 57.70–70.82), respectively.

There was a significant annual decrease in malaria incidence from 26.13 in 2018 (95% CI 22.99–29.58) to 13.90 in 2019 (95% CI 11.64–16.47) and 11.18 in 2020 (95% CI 9.16 – 13.51) ($p < 0.0001$). The season wise analysis of malaria incidence showed that the highest incidence was during the monsoon season (July–September) [66.54 (95% CI 57.13–77.06)] and the lowest in the summer (April–June) [37.08 (95% CI 29.22–46.41)] (Table 7).

Factors associated with malaria

Univariate and multivariate logistic regression model revealed that the incidence of malaria was highest among 5–15 years of age group (crude OR = 1.68; $p < 0.0001$ and adjusted OR = 2.23; $p = 0.007$) followed by 15–30 years (crude OR = 1.53; $p < 0.0001$ and adjusted OR = 1.23; $p = 0.001$) and 30–50 years of age group (crude OR = 1.51; $p < 0.0001$ and adjusted OR = 1.21; $p = 0.001$) in reference to adults more than 50 years of age. During pregnancy, the risk of malaria was about 45 times higher than ever in married non-pregnant women of the reproductive age group (crude OR = 45.86 and adjusted OR = 45.00; $p < 0.0001$). Scheduled Tribes were the highly susceptible group to malaria infection (crude OR = 3.33; $p = 0.017$ and adjusted OR = 1.02; $p = 0.037$). The population of lower SES showed a significantly higher risk of malaria in the univariate model, but this factor was not found

Table 5 Fever and malaria episodes among caste groups in 36 months longitudinal community surveillance during 2018 – 2020

Caste group (Population)	Episodes	Fever cases	Malaria positive		PF-PF			PV-PV			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
			nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
GENERAL (20,650)	1	4,608	4	4																		
	2	1,870																				
	3	518																				
	4	260																				
	5+	322																				
OBC (283,895)	1	68,148	62	62																		
	2	17,327	9	18	6	12	186.7 (13–424)	3	6	39.7 (28–63)												
	3	5,601	0	0																		
	4	2,350	2	8	1	4	59; 349; 535	1	4	77; 121; 144												
	5+	2,650																				
SC (78,001)	1	19,321	24	24																		
	2	5,589	2	4	1	2	325	1	2	423												
	3	1,765																				
	4	733																				
	5+	950																				
ST (574,249)	1	1,38,703	273	273																		
	2	33,063	41	82	26	52	320.1 (18–819)	12	24	228.7 (16–504)	2	4	90	1	2	130 (20–160)						
	3	10,168	5	15	3	9	54;180 (45–59; 108–323)										1	3	21; 157	1	3	34; 123
	4	4,165																				
	5+	4,466																				

nU Unique Persons, *nF* Total number of fever cases tested, *nM* Total malaria cases, *rMDI* Mean Days Interval (range), *PF P. falciparum*, *PV P. vivax*, *MIX P. falciparum + P. vivax*, *OBC* Other Backward Caste, *SC* Scheduled Caste, *ST* Scheduled tribe

Table 6 Fever and malaria episodes among socioeconomic strata in 36 months of longitudinal community surveillance from 2018 to 2020

SES Group (Population)	Episodes	Fever cases	Malaria positive		PF-PF			PV-PV			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
			nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
Lower (181,567)	1	81,131	136	136																		
	2	15,042	23	46	14	28	295.4 (88–794)	8	16	175.6 (23–421)				1	2	130						
	3	4,706	1	3	1	3	59;109															
	4	1,775	1	4				1	4	77;121;144												
	5+	1,564																				
Upper lower (268,559)	1	61,081	105	105																		
	2	11,429	15	30	10	20	220.7 (13–495)	4	8	106 (16–233)	1	2	20									
	3	3,621	3	9	1	3	58;108										1	3	21; 157	1	3	34; 123
	4	1,372																				
	5+	1,261																				
Lower middle (322,257)	1	54,643	91	91																		
	2	11,128	13	26	9	18	380.6 (27–819)	3	6	345 (28–504)	1	2	160									
	3	3,700	1	3	1	3	45; 323															
	4	1,503																				
	5+	1,522																				
Upper middle (116,309)	1	13,034	14	14																		
	2	2,188																				
	3	670																				
	4	269																				
	5+	274																				
Upper (68,103)	1	20,891	17	17																		
	2	18,062	1	2				1	2	423												
	3	5,355																				
	4	2,589	1	4	1	4	59; 349; 535															
	5+	3,767																				

nU Unique Persons, *nF* Total number of fever cases tested, *nM* Total malaria cases, *rMDI* Mean Days Interval (range), *PF P. falciparum*, *PV P. vivax*, *MIX P. falciparum + P. vivax*

Table 7 Year and season-wise fever and malaria episodes in 36-month longitudinal community surveillance from 2018 to 2020

Year/Seasons	Episodes	Fever cases	Malaria positive		PF-PF			PV-PV			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
			nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
2018	1	84,948	222	222																		
	2	14,608	14	28	11	22	67.2 (13–149)	2	4	34 (28–40)	1	2	20									
	3	7,249																				
	4	2,263																				
	5+	2,784																				
2019	1	1,04,512	86	86																		
	2	30,146	19	38	10	20	189.4 (45–325)	8	16	67.9 (23–161)				1	2	130						
	3	7,541	3	9	2	6	58.5;108.5													1	3	34;123
	4	3,554																				
	5+	3,693																				
2020	1	41,320	107	107																		
	2	13,095																				
	3	3,262																				
	4	1,691																				
	5+	1,911																				
Jul-Sep (Monsoon)	1	77,612	166	166																		
	2	19,320	6	12	2	4	386.5 (27–746)	4	8	316.7 (23–423)												
	3	5,380																				
	4	2,443																				
	5+	2,297																				
Oct-Dec (Winter)	1	49,377	81	81																		
	2	15,938	9	18	5	10	173 (13–727)	3	6	56 (28–77)				1	2	123						
	3	6,788																				
	4	2,510																				
	5+	3,161																				
Jan-Mar (Spring)	1	60,190	129	129																		
	2	13,136	4	8	2	4	336 (323–349)	1	2	144	1	2	20									
	3	3,606																				
	4	1,498																				
	5+	1,707																				

Table 7 (continued)

Year/Seasons	Episodes	Fever cases	Malaria positive		PF-PF			PV-PV			PF-PV			MIX-PV			PF-PF-PV			MIX-MIX-PV		
			nU	nM	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI	nU	nM	rMDI
Apr-Jun (Summer)	1	43,601	74	74																		
	2	9,455	1	2	1	2	56															
	3	2,278																				
	4	1,057																				
	5+	1,223																				

The repeated episodes of malaria infections between years and seasons could not be presented appropriately due to the particular individuals may reinfected in consecutive months and years of the followup

nU Unique Persons, *nF* Total number of fever cases tested, *nM* Total malaria cases, *rMDI* Mean Days Interval (range), *PF P. falciparum*, *PV P. vivax, MIX P. falciparum + P. vivax*

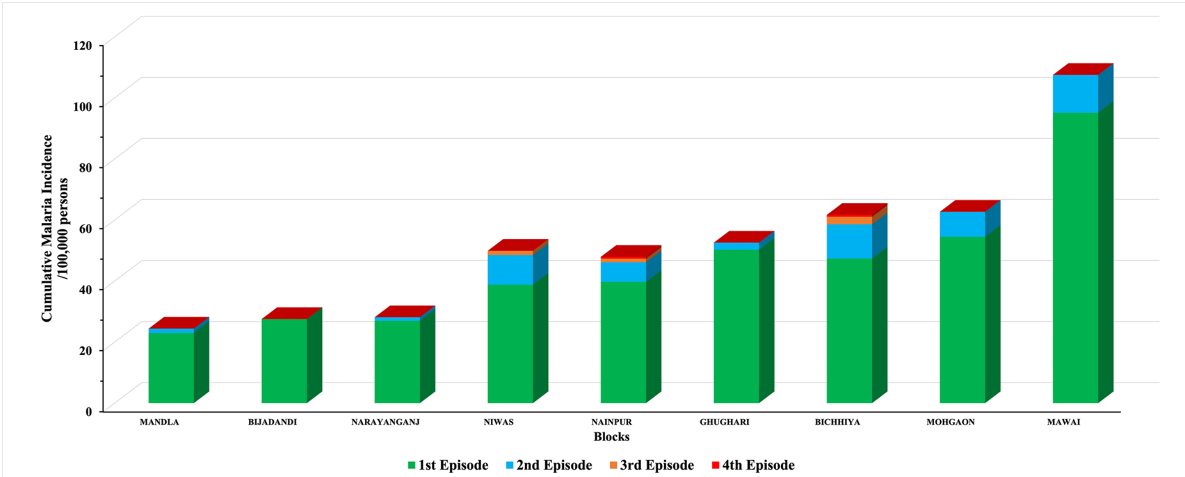

Fig. 1 Cumulative malaria incidence and episodes of malaria infection in blocks of district Mandla

significant in the multivariate model (crude OR = 3.08; $p < 0.0001$ and adjusted OR = 1.05; $p = 0.905$).

Those residing in high endemic areas were likely at greater risk of malarial infection than those in low endemic areas (crude OR = 2.07; $p < 0.0001$ and adjusted OR = 1.60; $p = 0.036$). The decrease in malaria incidence was statistically significant for 2019 (crude OR = 0.53; $p < 0.0001$ and adjusted OR = 0.20; $p < 0.0001$) and 2020 (crude OR = 0.43; $p < 0.0001$ and adjusted OR = 0.48; $p = 0.007$). The monsoon months were highly malarious season than summer (crude OR = 2.34; $p < 0.0001$ and adjusted OR = 1.71; $p = 0.007$) (Table 8).

Discussion

Implementation of C3EI type of longitudinal studies in elimination projects holds promise for generating data that would expedite malaria elimination efforts. This study design in the Mandla district has revealed patterns and risk factors of malaria distinct from the region and most likely reflects broader trends in malaria epidemiology within India.

The eastern densely forested blocks, such as Mawai, Mohgaon, Bichhiya and Ghughri, were reported as the most malarious blocks in the district. The *'Baiga'*, a Particularly Vulnerable Tribal Group (PVTG) tribal population, is primarily confined in these blocks. Low levels of literacy, poor habitats and hygiene, cultural beliefs, taboos and practices and residing in scattered hamlets may provide a higher risk of malaria diseases among the '*Baiga*' community. This finding is in agreement with previous studies, which have identified cultural beliefs and practices as potential barriers to the optimal utilization of formal healthcare services [16, 17].

The findings of this study underscore the considerably heightened risk of malaria among pregnant women, who were observed to be at approximately 45 times greater risk than their non-pregnant counterparts. This is consistent with previous health facility-based studies across various regions in India, including north-western, eastern, and central parts, which have also reported increased susceptibility to malaria among pregnant women [5, 18–22].

In the MEDP study, every pregnant woman diagnosed with malaria was promptly referred to the closest health facility and received treatment under strict medical supervision. Vigilant monitoring was maintained throughout their pregnancy, including regular usage of LLINs (if eligible), culminating in recording health outcomes post-delivery. This meticulous follow-up protocol was pivotal in ensuring no adverse birth outcomes were reported, demonstrating the effectiveness of proactive and comprehensive healthcare interventions for this vulnerable population.

The substantial decrease in malaria cases reported in the district of Mandla, when compared to both the state of Madhya Pradesh and national averages, is noteworthy [23]. This success can be attributed to the MEDP's rigorous approaches, including the longitudinal tracking of each individual at household-level during robust disease surveillance [13, 24], optimal utilization of vector control measures [6, 7], community mobilization [25], capacity building of healthcare providers [26–28], MSaT [29], molecular diagnosis of asymptomatic and low-density infections [30], monitoring and evaluation by internal and external review of real-time data [13, 31], accountability for quality-service-delivery [4, 32]. These methods align with the systems outlined in global studies that

Table 8 Univariate and multivariate logistic regression to estimate the association of malaria incidence with independent variables of the community surveillance cohort

Independent Factors	Univariate				Multivariate			
	cOR	95% CI		P value	aOR	95% CI		P value
		Lower	Upper			Lower	Upper	
Age Group								
> 50 yrs	Reference				Reference			
30–50 yrs	1.51	1.27	1.75	< 0.0001	1.21	1.04	7.17	0.001
15–30 yrs	1.53	1.27	1.8	< 0.0001	1.23	1.09	6.54	0.001
5–15 yrs	1.68	1.37	1.99	< 0.0001	2.23	1.12	12.59	0.007
< 5 yrs	0.49	0.005	0.98	0.048	Omitted			
Pregnancy status								
No-pregnant	Reference				Reference			
Pregnant	45.86	30.86	68.14	< 0.0001	45.00	28.62	70.75	< 0.0001
Caste group								
General	Reference				Reference			
OBC	1.6	0.59	4.36	0.358	0.36	0.20	0.64	< 0.0001
SC	1.85	0.65	5.28	0.248	0.24	0.07	0.76	0.015
ST	3.33	1.24	8.91	0.017	1.02	1.00	3.17	0.037
SES Group								
Upper	Reference				Reference			
Upper Middle	0.36	0.18	0.69	0.002	Omitted			
Lower Middle	1.1	0.70	1.72	0.668	1.69	0.72	3.94	0.227
Upper Lower	1.59	1.02	2.47	0.039	1.28	0.56	2.92	0.564
Lower	3.08	2.00	4.75	< 0.0001	1.05	0.45	2.45	0.905
Year of survey								
2018	Reference				Reference			
2019	0.53	0.43	0.66	< 0.0001	0.20	0.12	0.33	< 0.0001
2020	0.43	0.34	0.54	< 0.0001	0.48	0.28	0.82	0.007
Seasons								
Summer (Apr-Jun)	Reference				Reference			
Spring (Jan-Mar)	1.8	1.36	2.39	< 0.0001	0.97	0.48	1.94	0.928
Winter (Oct-Dec)	1.3	0.97	1.76	0.083	0.57	0.27	1.19	0.136
Monsoon (Jul-Sep)	2.34	1.79	3.06	< 0.0001	1.71	1.09	3.14	0.007
Endemicity								
Low	Reference				Reference			
HIGH	2.07	1.68	2.56	< 0.0001	1.60	1.03	2.49	0.036
Constant					0.06	0.01	0.67	0.022

CI Confidence interval, *cOR* Crude odds ratio, *aOR* Adjusted odds ratio, *OBC* Other backward caste, *SC* Scheduled caste, *ST* Scheduled Tribe, *SES* Socioeconomic strata

advocate for robust surveillance to inform malaria elimination strategies [33, 34].

Recently, the WHO published its 2023 guidelines for malaria and gave conditional recommendations against Mass Testing and Treatment (MTaT) due to limited evidence of benefits on malaria prevalence and incidence [35]. MTaT involves simultaneously testing all the individuals and treating all positive malaria cases in a defined area. However, the WHO recommendation notes that MTaT may be appropriate in exceptional cases, such as very low transmission or post-elimination settings [35]. In MEDP Mandla, MSaT (Mass Screening and Treatment—which is similar to MTaT) was performed in the defined areas using Cluster-Combination Approaches (CCA) in the target areas based on endemicity (low and high API) and accessibility (hard to reach and forest areas) to ascertain its impact on achieving elimination of indigenous malaria transmission. The coverage of the population using MSaT increased from 74% in 2017 to 82.6% in 2019 [24]. The findings were published to provide high-quality evidence to help the national malaria programmes and the WHO make context-specific policy decisions for implementing MTaT [29].

The present study highlighted a substantial prevalence of fever in the community, with a minimal proportion attributable to malaria, underscoring a broader public health challenge beyond the scope of malaria control and elimination efforts. This disparity highlights the presence of other febrile illnesses that contribute significantly to the health burden. In South India, a review of diagnostic tools for Acute Febrile Illness (AFI) found that besides malaria, diseases like dengue, scrub typhus, typhoid, and leptospirosis are commonly tested for and identified as causes of AFI [36].

The convergence of environmental and social determinants, such as water quality and healthcare accessibility, further exacerbates the incidence of these febrile illnesses. Addressing this multifaceted health issue demands an integrated disease surveillance system that extends beyond malaria, incorporating robust laboratory diagnostics, healthcare worker training in syndromic management, and heightened community awareness. Such an approach ensures a comprehensive public health strategy capable of addressing the diverse causes of fever in the community and improving overall health outcomes.

Furthermore, the recent data from the National Centre for Vector Borne Diseases Control (NCVBDC) has reported an increase in malaria cases, from 176,522 in 2021 to 223,961 in 2022 (21.18%). In a state-wise breakdown, this increase was primarily contributed by Odisha (43.36%) and Jharkhand (38.4%), both of which are tribal-dominated states. This surge may be attributed to a confluence of factors, including the increase due to the newly introduced Integrated Health Information Platform (IHIP) for near real-time data reporting and better compliance due to mandatory private sector reporting of malaria [3, 37].

The implementation of the C3EI analysis strategy demonstrates significant potential in improving the timeliness of interventions and enhancing surveillance accuracy. However, it is important to consider the feasibility of this approach, particularly in terms of cost. Compared to conventional surveillance methods, C3EI uses the same frequency of active surveillance as per the national guidelines. While no direct cost analysis was conducted in this study, the authors argue that with optimized operational accountability and monitoring of the existing malaria workers, similar results can be achieved with no or little additional costs. A model for malaria elimination with existing local infrastructure using learnings from MEDP Mandla has been published [8, 32].

The C3EI approach has several notable strengths and weaknesses. One of its key strengths is the ability to collect real-time data through continuous engagement with the community, allowing for prompt interventions and better tracking of malaria cases. By focusing on household-level surveillance, C3EI can identify cases for prompt treatment, therefore enhancing the case management capacity in the target areas. Its longitudinal design further enhances the understanding of malaria trends, hotspots, and seasonality, which is crucial for refining elimination strategies. Additionally, the approach fosters strong community engagement, improving compliance with malaria interventions and ensuring comprehensive monitoring of febrile and confirmed malaria cases. However, the complexity of managing large volumes of real-time data may present challenges for some programmes, particularly in areas with limited digital infrastructure.

The present study has demonstrated a significant risk of malaria infections in select populations characterized by hard-to-reach areas, forest cover, varying socio-economic status, and different seasons. The selective, focused, and targeted interventions in these high-risk areas will be critical in eliminating indigenous malaria from the country by 2027.

Conclusion

The Constant Contact Community-based Epidemiological Investigation (C3EI) presents a new surveillance strategy suitable for disease elimination programmes. The study design emphasizes community engagement, longitudinal monitoring, and data-driven decision-making at the household level. This model's potential applicability to other high-endemic, tribal-dominated regions holds promise for contributing to India's goal of achieving zero malaria by 2027, as committed by the national programme. The implications of these findings are that by harnessing the power of real-time longitudinal data analytics, C3EI offers a promising approach towards achieving malaria elimination goals on a global scale.

Abbreviations

MEDP	Malaria Elimination Demonstration Project
C3EI	Constant Contact Community-based Epidemiological Investigation
SOCH	Solutions for Community Health-workers
RDT	Rapid Diagnostic Test
WHO	World Health Organization
MP	Madhya Pradesh
ICMR	Indian Council of Medical Research
FDEC	Foundation for Disease Elimination and Control
CSR	Corporate Social Responsibility
IEC	Information, Education and Communication
MSaT	Mass Screening and Treatment
PVTG	Particularly Vulnerable Tribal Group
VMWs	Village Malaria Workers
HRP_2	Histidine Rich Protein $_2$

pLDH	Plasmodium Lactate Dehydrogenase
MFCs	Malaria Field Coordinators
SES	Socioeconomic strata
IQR	Inter Quartile Range
OR	Odds Ratio
CI	Confidence Interval
LLIN	Long Lasting Insecticidal Net
MTaT	Mass Testing and Treatment
CCA	Cluster-Combination Approaches
AFI	Acute Febrile Illness
NCVBDC	National Center for Vector Borne Diseases Control
IHIP	Integrated Health Information Platform

Author contributions
AAL, MPS, HR conceptualized the study; RSS, SN helped with the data collection; MPS analysed the data; HR and MPS developed the manuscript; PKB, ARA, HJ, SN and AAL critically reviewed and edited the manuscript; All authors read and approved the final manuscript.

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Availability of data and materials
We have reported all the findings in this manuscript. The hardcopy data is stored at MEDP Office in Jabalpur, Madhya Pradesh, and Indian Council of Medical Research-National Institute of Research in Tribal Health (ICMR-NIRTH), Jabalpur, Madhya Pradesh. Softcopy data is available on the project server of MEDP hosted by Microsoft Azure. If anyone wants to review or use the data, they should contact: Dr. Altaf A. Lal, Project Director – Malaria Elimination Demonstration Project, Mandla Foundation for Disease Elimination and Control of India, Mumbai, Maharashtra, India. No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate
The project was approved by the Institutional Ethical Clearance (IEC) Committee of the Indian Council of Medical Research-National Institute of Research in Tribal Health (ICMR-NIRTH), Jabalpur bearing reference no. 201701/10.

Consent for publication
All authors have given their consent for publication.

Competing interests
The authors declare no competing interests.

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