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Research Article

Forecasting Malaria Elimination: A Regression-Based Time Series Analysis of Malaria Cases in Odisha, India

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I N F O

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A B S T R A C T

Introduction: Malaria remains a significant public health challenge, particularly in tropical and subtropical regions, where it contributes considerably to global morbidity and mortality.This study aims to analyze the incidence of *Plasmodium falciparum* and *Plasmodium vivax* malaria cases from 2010 to 2024 in Kalahandi district using regression-based time series forecasting models to evaluate progress toward malaria elimination.

Materials and Methods: Secondary data on malaria incidence were collected from the National Centre for Vector Borne Diseases Control(NCVBDC) and the National Centre for Vector Borne Diseases Control (NCVBDC). Using Microsoft Excel and SPSS, linear regression and polynomial regression models were applied to evaluate temporal trends and forecast future caseloads of *P. falciparum* and *P. vivax*. Model performance was assessed using R^2 and RMSE values.

Results: From 2010 to 2024, there was a significant reduction in the number of *P. falciparum* and *P. vivax* cases in Kalahandi. Regression analysis indicated a strong negative trend in malaria incidence, with linear and polynomial models showing high R^2 values, suggesting good model fit. Forecasts indicate that if current trends continue, malaria cases may reach elimination targets in the near future.

Conclusion: The application of regression-based time series forecasting reveals encouraging trends toward malaria elimination in Kalahandi. Continued investment in surveillance, vector control, and targeted interventions in high-risk populations is essential to sustain and accelerate progress. The methodology demonstrated in this study can be replicated in other high-burden districts to guide data-driven public health planning and policy.

Keywords: Malaria, *P. falciparum*, *P. vivax*, Forecasting, Regression Analysis

Introduction

Malaria remains a significant public health challenge, particularly in tropical and subtropical regions, where it contributes considerably to global morbidity and mortality. The disease is caused by *Plasmodium* parasites and transmitted through the bites of infected female *Anopheles* mosquitoes. Among the major species, *Plasmodium falciparum* is responsible for the most severe cases and the highest mortality rates, while *P. vivax*, *P. ovale*, *P. malariae*, and *P. stephensi*also contribute to the disease burdendue to its ability to relapse and sustain transmission over time.[1-5] In recent years, intensified malaria control efforts—including vector control strategies, improved diagnostic facilities, and expanded access to antimalarial treatment—have led to a decline in malaria incidence in several endemic regions.[6] However, achieving malaria elimination requires a comprehensive understanding of temporal trends and predictive analysis of future transmission. Time series analysis, a statistical approach for evaluating disease incidence over time, has proven to be an essential tool in assessing malaria trends and informing policy interventions.[7]

Malaria Burden in India

India remains one of the 11 high malaria burden countries globally, contributing significantly to the disease's worldwide impact, alongside Sub-Saharan African nations before 2024.[7-9]After achieving over an 80% decline in cases between 2015 and 2023, India has shifted from high burden country now.Despite a remarkable reduction in malaria cases—by 28% from 2017 to 2018—the disease continues to affect millions.In 2019, *P. falciparum* accounted for 63.1% of malaria cases, while *P. vivax* was responsible for 36.9%. [10,11] Seasonal variations significantly influence malaria transmission, with peak incidence occurring from July to October, coinciding with monsoon-driven increases in mosquito breeding sites. This pattern is consistent with findings from other Indian settings. [10,12,13]Approximately 95% of India's population resides in malaria-endemic areas, with 80% of reported malaria cases concentrated in tribal, hilly, and hard-to-reach regions.[14,5] Odisha is India's most vulnerable state to vector-borne diseases, and within it, the Kalahandi, Bolangir and Koraput district(KBK)experiences a disproportionately high malaria burden.[15-17]

Tribal communities, residing in remote natural settings, often lack access to modern healthcare services. These populations face challenges such as poverty, illiteracy, and economic backwardness, making them particularly vulnerable to malaria and other infectious diseases.[15,18] While several countries in the WHO South-East Asia (SEA) region have successfully eliminated malaria—such as the Maldives and Sri Lanka—others, including Thailand, Timor-Leste, Bhutan, and Nepal, are working towards elimination by 2025 under the "E2025" initiative.[19,20] The Asia Pacific region, which aims to eliminate malaria by 2030, continues to report high case numbers, particularly in Papua New Guinea and the Solomon Islands, where the Annual Parasitic Incidence (API) remains high at 65 and 119, respectively.[19, 20]The WHO's Global Technical Strategy for Malaria 2016–2030 has set ambitious targets to reduce malaria cases by at least 90% and achieve zero indigenous malaria cases by 2030.[19, 21]

Geographic Variation in Malaria Transmission

Malaria transmission patterns vary significantly across different regions due to ecological and climatic factors affecting the distribution of *Anopheles* mosquitoes and *Plasmodium* species. High-transmission zones in India include Odisha, Jharkhand, Chhattisgarh, Maharashtra, Madhya Pradesh, West Bengal, and Uttar Pradesh.[22] The diverse geography and climate of India create favorable environments for malaria parasites and their vectors, facilitating persistent transmission in several endemic regions.[23]

Prompt and accurate diagnosis is critical for effective malaria management. Malaria remains a potential medical emergency, and delays in diagnosis and treatment are among the leading causes of malaria-related deaths worldwide.[15] The global malaria burden has driven the development of advanced diagnostic strategies, particularly in resource-limited settings where malaria continues to impose a substantial health and economic burden.[24-26]

In regions where malaria is not endemic, healthcare providers may overlook malaria as a differential diagnosis, leading to misdiagnoses and treatment delays. Laboratory-based malaria diagnosis includes various methods such as conventional microscopy (thin and thick peripheral blood smears), quantitative buffy coat (QBC) technique, and rapid diagnostic tests (RDTs) like OptiMAL, ICT, ParaHIT-f, ParaScreen, SD Bioline, and Paracheck. [24,26-36] Molecular diagnostic techniques, particularly polymerase chain reaction (PCR), have enhanced malaria detection accuracy.[27-36]To tackle emerging and persisting challenges, WHO introduced the Global Technical Strategy for Malaria 2016–2030 (GTS 2016–2030), which outlines the most ambitious malaria reduction targets since the elimination era over 60 years ago. The strategy aims to reduce malaria incidence and mortality rates by at least 90% and achieve elimination in at least 35 countries by 2030. However, achieving these goals requires substantial financial investments—estimated at $8.7 billion annually by 2030—far beyond the current global funding levels. [37]

As malaria remains a significant health threat, sustained investment, strengthened surveillance, and innovative public health strategies will be essential for malaria control

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and elimination efforts. This study contributes to the growing body of evidence on malaria epidemiology and aims to support data-driven policymaking to accelerate malaria elimination in India.This study applies time series regression modeling to analyze malaria incidence patterns in Kalahandi district, focusing on infections caused by *P. falciparum* and *P. vivax*. Using data spanning from 2010 to 2024, we assess the statistical significance of temporal changes, evaluate the goodness-of-fit of different regression models, and project the potential trajectory of malaria incidence. By employing rigorous statistical methods, this study provides insights into the effectiveness of existing malaria control measures and the feasibility of achieving malaria elimination by 2030, in alignment with WHO's global targets.[38,39]

Materials and Methods

Data Collection

The study analyzed year-wise malaria cases due to *Plasmodium falciparum* and *Plasmodium vivax* in the study area. The data were obtained from blood sample testing records spanning from 2010 to 2024. The dataset included the total number of blood samples tested, as well as the number of positive cases for *P. falciparum*, *P. vivax*, and overall malaria infections.

Time Series Analysis

Time series regression analysis was employed to assess the trends in malaria cases. First- to fourth-degree polynomial regression models were fitted to the malaria incidence data using Microsoft Excel. The regression equations were derived to estimate the temporal trends for *P. falciparum*, *P. vivax*, and total malaria cases.

Goodness of Fit Evaluation

The goodness of fit for each regression model was determined by calculating the percentage of variance explained by the model. The R-squared values were computed for each polynomial degree to assess how well the model predictions aligned with observed data.

Statistical Significance Testing

The statistical significance of the fitted regression models was evaluated using Analysis of Variance (ANOVA). The F-test was applied to compare successive polynomial models and determine whether increasing the polynomial degree significantly improved model performance.

Correlation Analysis

To examine overall trends in malaria incidence, Pearson's correlation coefficient was calculated between time (years) and malaria cases. The statistical significance of the correlation coefficients was assessed at the 0.01 and 0.05 significance levels to determine whether the observed decreasing trend was statistically meaningful.

Software and Tools

All statistical analyses, including regression modeling, calculation of confidence intervals, ANOVA, and correlation analysis, were performed using Microsoft Excel 2007 software.

Results

Table 1 offers a yearly overview from 2010 to 2024 of blood samples screened for malaria in Kalahandi, alongside confirmed positives for*P. falciparum*,*P. vivax*, and combined totals, revealing an overall drop despite some yearly ups and downs.. Prediction up to 2030 of malaria cases was done in table 2. Table 3 lists polynomial equations up to fourth order for*P. falciparum*,P*. vivax*, and total infections, plus fit percentages that climb notably for higher degrees, peaking near 70%. The statistical significances of the regression equations and successive increase of their degrees were estimated by analysis of variance (ANOVA) using 'F; test. The test results of infection by *Plasmodium falciparum*, *Plasmodium vivax* and total malaria cases are presented in Tables 4 – 6 respectively.

Table 1.Year-Wise Blood Samples Tested for Detection of Malaria

Year	Number of blood samples tested	*Plasmodium falciparum*	*Plasmodium vivax*	Total
2010	256191	23332	3389	26721
2011	240715	18497	2435	20932
2012	264662	17369	1706	19075
2013	286591	18553	1567	20120
2014	314450	26709	2826	29535
2015	319753	28227	3512	31739
2016	362899	39463	5453	44916
2017	314236	26404	4861	31265
2018	318893	7290	1406	8696
2019	338933	5493	533	6026

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2020	299439	10017	560	10577
2021	346635	4646	518	5164
2022	375950	3387	543	3930
2023	424814	6370	1173	7543
2024	420453	10120	2875	12995

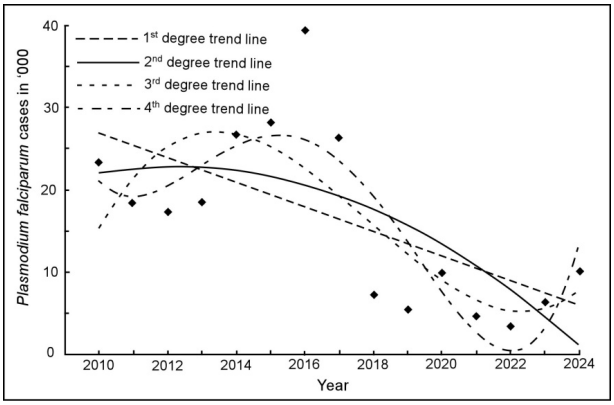

Figure 1.Time Series Regression Lines Fitted to the Cases Infected by *Plasmodium Falciparum*

Table 2.Year Wise Prediction of Malaria Cases After 1st Degree Equation

Year	Total malaria 1st degree equation =31658-1630*R20
2010	30028*
2011	28398*
2012	26768*
2013	25138*
2014	23508*
2015	21878*
2016	20248*
2017	18618*
2018	16988*
2019	15358*
2020	13728*
2021	12098*
2022	10468*
2023	8838*
2024	7208*
2025	5578*
2026	3948*
2027	2318*
2028	688*
2029	-942*
2030	-2572*

*Predicted values on the basis of first-degree equation

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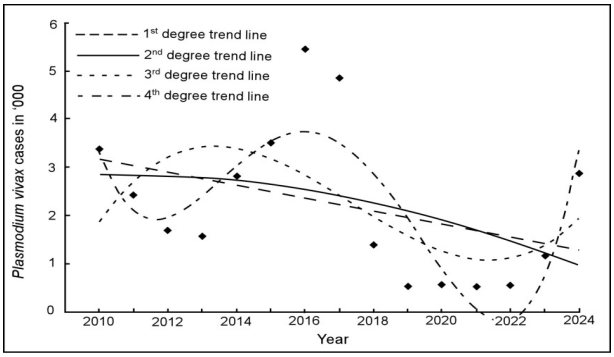

Figure 2.Time Series Regression Lines Fitted to the Cases Infected by *Plasmodium Vivax*

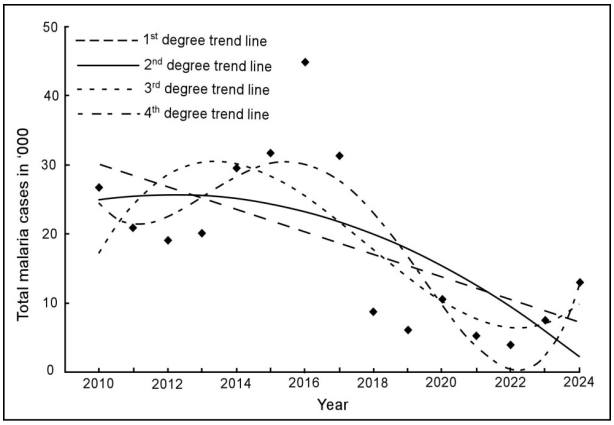

Figure 3.Time Series Regression Lines Fitted to the Total Malaria Cases

Table 3.Time Series Equations, 95% Confidence Intervals and Goodness of Fit of Equations

Degree	Time series equation with 95% confidence equation	Goodness of fit (%)
Plasmodium falciparum		
First-degree	$y = 28349 – 1494x$ (±16014.69)	38.40
Second-degree	$y = 21172 + 1038x - 158.3x^2$ (±15159.93)	44.80
Third-degree	$y = 6111 + 10796x - 1634.x^2 + 61.52x^3$ (±13319.96)	58.10
Fourth-degree	$y = 28147 - 10618x + 3948x^2 - 469x^3 + 16.58x^4$ (±11086.91)	71.00
Plasmodium vivax		
First-degree	$y = 3309 - 135.6x$ (±2766.78)	14.60
Second-degree	$y = 2839 + 30.11x -10.36x^2$ (±2748.36)	15.90
Third-degree	$y = 624.8 + 1464x - 227.4x^2 + 9.046x^3$ (±2524.65)	29.30
Fourth-degree	$y = 6263 - 4014x + 1201x^2 – 126.7x^3 + 4.242x^4$ (±1669.51)	68.30
Total malaria cases		
First-degree	$y = 31658 -1630x$ (±18560.43)	35.60
Second-degree	$y = 24011 + 1068.x -168.6x^2$ (±17735.57)	41.20
Third-degree	$y = 6736 + 12261x - 1862x^2 + 70.57x^3$ (±15581.19)	54.90
Fourth-degree	$y = 34410 - 14632x + 5149x^2 - 595.8x^3 + 20.82x^4$ (±12324.00)	70.60

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Table 4.Completed Analysis of Variance (Anova) for Significance of *Plasmodium Falciparum* Cases

Source of variation	Sum of squares	Degrees of freedom	Mean squares	F-test result
First-degree regression (CSS_{R1})	624970080	1	624970080	$F_1 = 8.113^*$ ($F_{\upsilon1=1, \upsilon2=13, \alpha=0.05} = 4.67$)§
First-degree deviation (CSS_{D1})	1001420132	13	77032317.88	
Second-degree regression (CSS_{R2})	729015845.4	2	364507922.7	$F_2 = 4.874^*$ ($F_{\upsilon1=2, \upsilon2=12, \alpha=0.05} = 3.89$)§
Second-degree deviation (CSS_{D2})	897374367	12	74781197.25	
Added by second-degree (CSS_{R2-1})	104045765.4	1	104045765.4	$F_{2-1} = 1.391$ ($F_{\upsilon1=1, \upsilon2=12, \alpha=0.05} = 4.75$)§
Third-degree regression (CSS_{R3})	933626596.2	3	311208865.4	$F_3 = 4.942^*$ ($F_{\upsilon1=3, \upsilon2=11, \alpha=0.05} = 3.59$)§
Third-degree deviation (CSS_{D3})	692763616.2	11	62978510.57	
Added by third-degree (CSS_{R3-2})	204610750.8	1	204610750.8	$F_{3-2} = 3.249$ ($F_{\upsilon1=1, \upsilon2=11, \alpha=0.05} = 4.84$)§
Fourth-degree regression (CSS_{R4})	1146435360	4	286608839.9	$F_4 = 5.972^*$ ($F_{\upsilon1=4, \upsilon2=10, \alpha=0.05} = 4.38$)§
Fourth-degree deviation (CSS_{D4})	479954852.7	10	47995485.27	
Added by fourth-degree (CSS_{R4-3})	212808763.6	1	212808763.6	$F_{4-3} = 4.434$ ($F_{\upsilon1=1, \upsilon2=10, \alpha=0.05} = 4.96$)§
Total variation (CSS_T)	1626390212	14	-	-

*Significant F value, §Critical values of F are given within brackets

Table 5.Completed Analysis of Variance (ANOVA) for Significance of *Plasmodium vivax* cases

Source of variation	Sum of squares	Degrees of freedom	Mean squares	F-test result
First-degree regression (CSS_{R1})	5148460.80	1	5148460.80	$F_1 = 2.239$ ($F_{\upsilon1=1, \upsilon2=13, \alpha=0.05} = 4.67$)§
First-degree deviation (CSS_{D1})	29890227.60	13	2299248.28	
Second-degree regression (CSS_{R2})	5595028.68	2	2797514.34	$F_2 = 1.138$ ($F_{\upsilon1=2, \upsilon2=12, \alpha=0.05} = 3.89$)§
Second-degree deviation (CSS_{D2})	29493473.44	12	2457789.45	
Added by second-degree (CSS_{R2-1})	446567.88	1	446567.88	$F_{2-1} = 0.182$ ($F_{\upsilon1=1, \upsilon2=12, \alpha=0.05} = 4.75$)§
Third-degree regression (CSS_{R3})	10260488.77	3	3420162.92	$F_3 = 1.512$ ($F_{\upsilon1=3, \upsilon2=11, \alpha=0.05} = 3.59$)§
Third-degree deviation (CSS_{D3})	24887589.93	11	2262508.18	
Added by third-degree (CSS_{R3-2})	4665460.09	1	4665460.09	$F_{3-2} = 2.062$ ($F_{\upsilon1=1, \upsilon2=11, \alpha=0.05} = 4.84$)§
Fourth-degree regression (CSS_{R4})	23881686.92	4	5970421.73	$F_4 = 5.486^*$ ($F_{\upsilon1=4, \upsilon2=10, \alpha=0.05} = 4.38$)§
Fourth-degree deviation (CSS_{D4})	10883154.90	10	1088315.49	
Added by fourth-degree (CSS_{R4-3})	13621198.15	1	13621198.15	$F_{4-3} = 12.516^*$ ($F_{\upsilon1=1, \upsilon2=10, \alpha=0.05} = 4.96$)§
Total variation (CSS_T)	35065376.40	14		

*Significant F value, §Critical values of F are given within brackets

Table 6.Completed Analysis of Variance (ANOVA) for Significance of Total malariacases

Source of variation	Sum of squares	Degrees of freedom	Mean squares	F-test result
First-degree regression (CSS_{R1})	743932000	1	743932000	$F_1 = 7.190^*$ ($F_{\upsilon1=1, \upsilon2=13, \alpha=0.05} = 4.67$)§
First-degree deviation (CSS_{D1})	1345102358	13	103469412.1	
Second-degree regression (CSS_{R2})	860833485.1	2	430416742.6	$F_2 = 4.205^*$ ($F_{\upsilon1=2, \upsilon2=12, \alpha=0.05} = 3.89$)§
Second-degree deviation (CSS_{D2})	1228200872	12	102350072.7	

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Added by second-degree (CSS_{R2-1})	116901485.1	1	116901485.1	F_{2-1} = 1.142 ($F_{\upsilon1=1, \upsilon2=12, \alpha=0.05}$ = 4.75)§
Third-degree regression (CSS_{R3})	1141094961	3	380364987	F_3 = 4.414* ($F_{\upsilon1=3, \upsilon2=11, \alpha=0.05}$ = 3.59)§
Third-degree deviation (CSS_{D3})	947939396.7	11	86176308.79	
Added by third-degree (CSS_{R3-2})	280261475.8	1	280261475.8	F_{3-2} = 3.252 ($F_{\upsilon1=1, \upsilon2=11, \alpha=0.05}$ = 4.84)§
Fourth-degree regression (CSS_{R4})	1495996552	4	373999137.9	F_4 = 6.306* ($F_{\upsilon1=4, \upsilon2=10, \alpha=0.05}$ = 4.38)§
Fourth-degree deviation (CSS_{D4})	593037806.1	10	59303780.61	
Added by fourth-degree (CSS_{R4-3})	354901590.6	1	354901590.6	F_{4-3} = 5.984* ($F_{\upsilon1=1, \upsilon2=10, \alpha=0.05}$ = 4.96)§
Total variation (CSS_T)	2089034358	14		

*Significant F value, §Critical values of F are given within brackets

Discussion

The goodness of fit of time series lines in case of people infected by *Plasmodium falciparum* are substantial, varying from 38.40 to 71.00 percentages (Table 3). The 'F' test results indicate the statistical significance of all the four degree equations (Table 4), but the increases of degrees are not significant. This is corroborated by significant negative correlation coefficient of -0.62 at 0.01 significance level, which indicate gradual decrease of the infection by *Plasmodium falciparum* with time.

In case of *Plasmodium vivax*,the goodness of fit forfirst-, second- and third-degree lines are comparatively less (Table 3) and the 'F' test results suggest statistical insignificance of these three lines (Table 5). The fourth-degree line, for which the goodness of fit is 68.32%, is statistically significant. This line shows alternate decreasing and increasing trends with time (Fig. 2) and its correlation coefficient with time is -0.38. This decreasing trend is not statistically significant at 0.05 significance level (0.437).

When the malaria infection by both *Plasmodium falciparum* and *Plasmodium vivax* are taken into consideration, the time series lines with goodness of fit ranging from 35.60 to 70.60% (Table 3) become statistically significant (Table 6). The negative correlation coefficient of -0.60 is also significant at 0.01 significance level. This suggests gradual decrease of the infection by malaria parasites. With the current rate of decrease,it is expected that the malaria will be completely eradicated by 2030 from the study area.The present study reveals a sustained decline in malaria incidence in Kalahandi district over the study period, particularly for *Plasmodium falciparum*, which demonstrates a statistically significant downward trend. This reduction reflects the cumulative impact of ongoing malaria control strategies and is consistent with broader epidemiological patterns reported across endemic regions. [8,20] The strong model fit and significant negative correlation observed in this study further validate the reliability of the declining trajectory.

When interpreted in a global context, these findings show similarities with countries that have successfully eliminated malaria. Nations such as Sri Lanka and the Maldives achieved malaria-free certification through comprehensive strategies involving strengthened surveillance, timely diagnosis, effective vector control, and sustained political commitment.[7,21] Comparable approaches have also contributed to substantial malaria reduction across several countries in the WHO South-East Asia region, reinforcing the importance of targeted and evidence-driven interventions. The trends observed in Kalahandi suggest that the district is progressing along a similar pathway toward elimination.

At the national level, India has made considerable progress in reducing malaria burden over the past decade. This decline has been attributed to intensified vector control measures, improved diagnostic coverage, and programmatic interventions under national malaria control initiatives. [10,20]Odisha, historically recognized as a high-burden state, has shown marked improvement following the implementation of targeted strategies such as the DAMaN programme, which emphasized mass screening, treatment, and vector control in high-risk populations .[5,17] The declining trends identified in the present study are consistent with these programmatic achievements and highlight the effectiveness of focused interventions in endemic and hard-to-reach regions.

However, species-specific differences remain an important consideration. While *P. falciparum* exhibits a consistent and statistically significant decline, the trend for *P. vivax* appears less stable, with periodic fluctuations and weaker statistical association. This observation aligns with existing evidence indicating that *P. vivax* is more difficult to eliminate due to its ability to relapse and persist in low-transmission settings [2,6] Therefore, elimination strategies

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must incorporate species-specific approaches, including radical treatment and enhanced case surveillance, to address residual transmission.

From a policy perspective, the findings of this study are in agreement with the targets outlined in the WHO Global Technical Strategy for Malaria 2016–2030, which aims for a substantial reduction in malaria incidence and progression toward elimination. [7,21]The projected decline based on regression models suggests that, if current interventions are maintained, malaria elimination in the study area may be achievable within the proposed timeline. Similar forecasting studies have also emphasized the importance of sustained intervention coverage and adaptive public health strategies in achieving elimination goals.[6,20]

Despite the encouraging progress, certain challenges continue to pose risks to malaria elimination. Persistent transmission in tribal and forested regions, limited healthcare accessibility, and socio-economic vulnerabilities may hinder sustained control efforts .[16,18] Strengthening surveillance systems, integrating environmental and climatic determinants into predictive models, and enhancing community participation are essential to maintain progress. Additionally, continuous monitoring and localized response mechanisms will be crucial to prevent resurgence and ensure long-term success.

In summary, the findings of this study indicate substantial progress in malaria reduction in Kalahandi and provide supportive evidence for the feasibility of achieving elimination targets. The results underscore the importance of sustained, targeted, and data-driven interventions, while also highlighting the need for adaptive strategies to address remaining challenges in malaria control and elimination.

In 1993, Brazil, in collaboration with the Pan-American Health Organization (PAHO), introduced an innovative approach that focused primarily on directing control measures toward municipalities identified as high-risk areas. [40] In 1993, Brazil, in collaboration with the Pan-American Health Organization (PAHO), introduced an innovative approach that focused primarily on directing control measures toward municipalities identified as high-risk areas.[40]

Conclusion

The results of this study indicate a statistically significant decline in malaria cases caused by *Plasmodium falciparum* and *Plasmodium vivax* over the analyzed period. The regression models demonstrate strong goodness of fit, particularly for *P. falciparum*, suggesting a consistent downward trend. Although the trend for *P. vivax* exhibits some fluctuations, the overall decrease in total malaria cases supports the effectiveness of ongoing malaria control efforts.

The significant negative correlation coefficients for malaria cases highlight the progress made in malaria reduction through improved surveillance, early diagnosis, and vector control measures. The time series analysis further suggests that, if the current rate of decline persists, malaria elimination in the study area may be feasible by 2030, aligning with WHO's global malaria elimination targets.

However, achieving this goal will require sustained efforts, including continued investment in malaria prevention, enhanced healthcare accessibility,Usereal-time surveillance systems for early outbreak signals, Expand mobile health units and outreach services and strengthened community engagement. Future studies incorporating additional environmental and socioeconomic factors could provide a more comprehensive understanding of malaria dynamics and further improve predictive models for malaria elimination.

Data availability statement

The data supporting the findings of this study are available from the corresponding author upon request.

Authors contribution

SP and SRP provide the resources for the study. SP and NK performed the study.SG and RNH did the analysis and reviewed the article.

Conflict of Interest: None

Source of Funding: None

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