Preplanned Studies

Spatiotemporal Dynamics of *Plasmodium vivax* at the Township Level in a High-Mobility Border Area — Yingjiang County, Yunnan Province, China, 2010–2024

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Summary

What is already known about this topic?

Yingjiang County, on the China–Myanmar border, reported the last indigenous malaria case in China, recorded the highest number of imported cases nationwide during the past 3 years.

What is added by this report?

This study is the first to analyze malaria's spatiotemporal landscape change before and after the last indigenous case along the China–Myanmar border at township level.

What are the implications for public health practice?

Fine-scale analyses of malaria hotspots along the border can identify challenges and update post-elimination surveillance and response strategies to consolidate malaria elimination efforts.

ABSTRACT

Introduction: In China, the areas adjacent to endemic countries remain vulnerable to imported *Plasmodium vivax* (*P. vivax*) after elimination. This study examined the long-term spatiotemporal and demographic changes of *P. vivax* in Yingjiang, a border county that reported China's last indigenous malaria case, to inform post-elimination surveillance.

Methods: The study analyzed 1,639 confirmed *P.vivax* cases from 2010 to 2024, comparing elimination (2010–2016) and post-elimination (2017–2024), and distinguishing imported from indigenous cases. Examining the impact of coronavirus disease 2019 (COVID-19), post-elimination phase divided into three sub-phases: pre-pandemic (2017–2019), intensive border control pandemic (2020–2022), and post-pandemic (2023–2024). Demographic, temporal, and spatial patterns were compared across phases using standard statistical and spatial methods.

Results: Overall, 94.1% of the cases were imported from 2010 to 2024. Intensive border control reduced imported cases by 28.4% but rebounded by 122.0% after policy relaxation. Cases remained predominantly male, while imported cases shifted toward older age groups and more diverse occupations. Spatial clusters persisted along the southern border, with clear seasonal peaks linked to cross-border movement.

Conclusion: Despite demographic shifts, malaria imports showed stable spatiotemporal patterns driven by persistent human mobility. Targeted surveillance of high-risk populations and hotspots, with efficient response and collaboration mechanisms, is critical for sustaining a malaria-free status.

Malaria remains a major global health challenge. Despite previous progress, the Greater Mekong Subregion (GMS) has experienced a resurgence, with 698,831 indigenous cases reported between 2021 and 2024 (*1*). While surveillance captures a portion of this, the World Health Organization (WHO) estimates the cases to reach 702,000 in 2024 alone in Myanmar, representing 95.5% of the subregional cases (*2*). Notably, a marked increase in cases was observed in Kachin State, which borders China. This resurgence has intensified the challenges of cross-border malaria importation (*3*).

China was certified malaria-free in 2021 (*4*). However, border areas in Yunnan Province remain vulnerable because of frequent cross-border population movements. In 2023, 334 imported malaria cases were reported in 18 border counties, representing a 122.7% increase compared with 2019. Yingjiang County, a major hotspot for imported malaria, accounts for 56.7% of imported cases in Yunnan and is nearly one-tenth nationally, characterized by complex terrain and intense cross-border mobility with historically high burden and the last indigenous case in China. Previous studies in this area have been limited by a lack of fine-scale spatial analysis and an insufficient assessment of the impact of coronavirus disease 2019 (COVID-19)-related border control policies. This study analyzed the epidemiological dynamics of *Plasmodium vivax* (*P. vivax*) in Yingjiang from 2010 to 2024, compared the elimination and post-elimination phases, and evaluated the impact of border control policies, thus providing evidence for targeted intervention strategies in border regions.

All laboratory-confirmed *P. vivax* cases reported in Yingjiang Country from January 1, 2010, to December 31, 2024 were included. Cases were classified according to the national guidelines as imported (infection acquired outside China) or indigenous (infection acquired locally). De-identified data, including sex, age, occupation, date of illness onset, case classification, and residential township, were extracted from the National Infectious Diseases Reporting Information System. Occupations were grouped into outdoor (farmers and other outdoor laborers), indoor, non-occupational (children, students, retirees, unemployed persons, or otherwise unspecified), and missing data groups (excluded from occupational analysis). The study period was divided into elimination (2010–2016) and post-elimination (2017–2024) phases[*], with further subdivisions into the pre-pandemic (2017–2019) of routine border control, pandemic (2020–2022) with intensive restrictions, and post-pandemic (2023–2024) of normalized management periods based on border management policies[†].

All analyses were prespecified. Demographic differences were assessed using Pearson's chi-square or Fisher's exact tests for sex and occupation and the Wilcoxon rank-sum test for age (Table 1). Temporal

TABLE 1. Demographic characteristics of *P. vivax* cases in Yingjiang County (2010–2024).

Characteristic	Total (%)	No. of cases (%)		Statistics	P	No. of cases (%)		Statistics	P
		Imported	Indigenous			2010–2016	2017–2024		
Total	1,639	1,542	97			651	988		
Gender									
Male	1,170 (71.38)	1,106 (71.73)	64 (65.98)	χ^2=1.207	0.272	472 (72.50)	698 (70.65)	χ^2=0.574	0.449
Female	469 (28.62)	436 (28.27)	33 (34.02)			179 (27.50)	290 (29.35)		
Age (years)									
Median (IQR)	31 (21, 43)	31 (21, 43)	27 (15, 42)			29 (21, 40)	33 (21, 45)		
Age group (years)									
≤20	403 (24.59)	368 (23.87)	35 (36.08)	W=81,511	0.128	163 (25.04)	240 (24.29)	W=353,868	<0.005
21–30	414 (25.26)	394 (25.55)	20 (20.62)			201 (30.87)	213 (21.56)		
31–40	320 (19.52)	304 (19.72)	16 (16.50)			123 (18.90)	197 (19.94)		
41–50	264 (16.11)	256 (16.60)	8 (8.25)			94 (14.44)	170 (17.21)		
51–60	147 (8.97)	139 (9.01)	8 (8.25)			44 (6.76)	103 (10.42)		
>60	91 (5.55)	81 (5.25)	10 (10.30)			26 (3.99)	65 (6.58)		
Occupation									
Outdoors	1,289 (78.65)	1,222 (79.25)	67 (69.07)	Fisher's Exact Test	<0.005	538 (82.64)	751 (76.01)	χ^2=12.699	<0.005
Indoors	74 (4.51)	73 (4.73)	1 (1.03)			19 (2.92)	55 (5.57)		
Non-occupational	269 (16.41)	242 (15.69)	27 (27.84)			90 (13.83)	179 (18.12)		
Missing	7 (0.43)	5 (0.33)	2 (2.06)			4 (0.61)	3 (0.30)		

Abbreviation: *P. vivax=Plasmodium vivax*.

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[*] Using the 2016 last indigenous case as the temporal pivot.

[†] The classification of periods was based on national and provincial COVID-19 border control policies, including the implementation of strict entry restrictions (2020–2022) and subsequent normalization of border management (from 2023 onward). References: Yunnan Provincial COVID-19 Response Command. Announcement No. 15 on preventing overseas COVID-19 importation via land and water borders. 2020. Available at: https://www.nia.gov.cn/n741440/n741542/c1269375/content.html (Accessed: 02 April 2026). State Council of the People's Republic of China. Overall plan for implementing Class B management of COVID-19. 2022. Available at: https://www.gov.cn/xinwen/2022-12/27/content_5733739.htm?eqid=f65b0f820042236c0000000664598982 (Accessed: 02 April 2026).

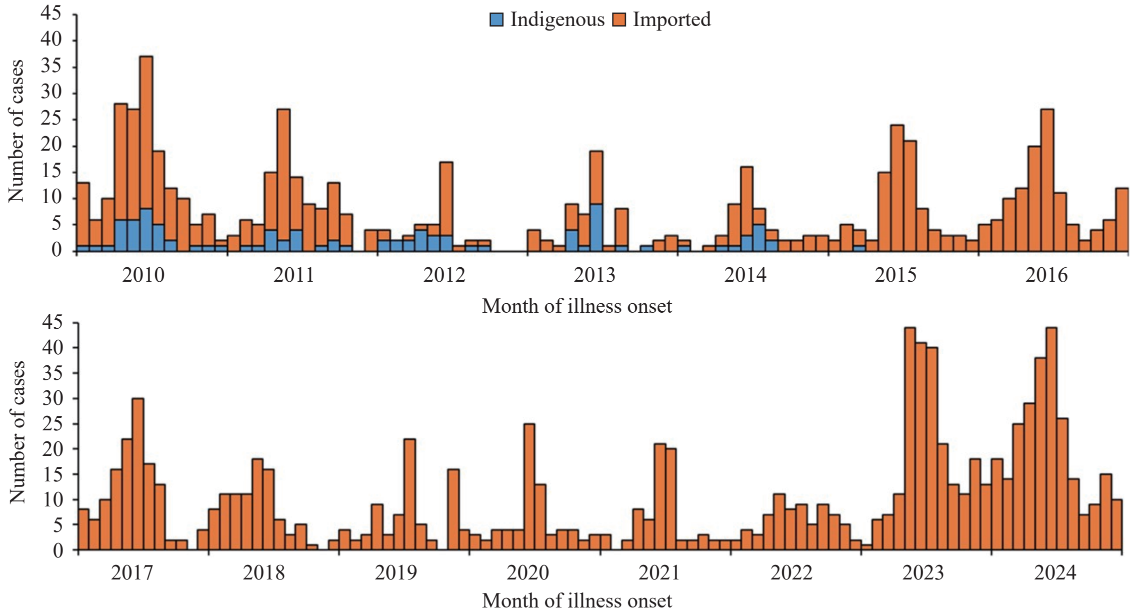

FIGURE 1. Temporal distribution of *Plasmodium vivax* cases in Yingjiang County, Yunnan Province, 2010−2024.

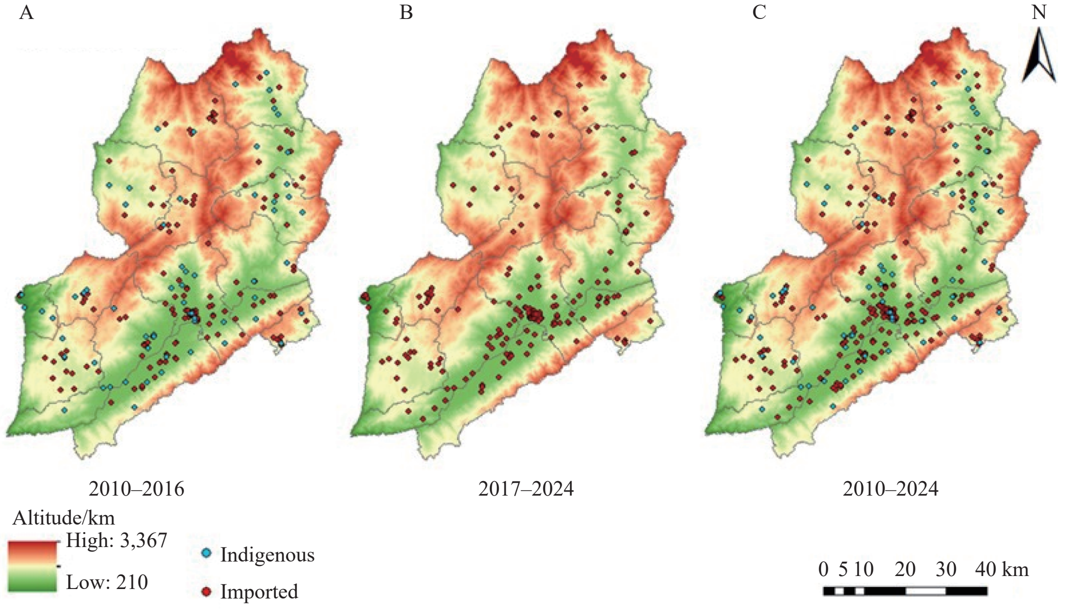

FIGURE 2. Spatial patterns of *Plasmodium vivax* cases in Yingjiang County during (A) 2010–2016, (B) 2017–2024, and (C) 2010–2024.
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seasonality (Figure 1) and spatial patterns were evaluated through monthly case counts and township-level incidence rates (Supplementary Table S1, available at http://weekly.chinacdc.cn/). Population denominators were based on 2016, 2024, and their means. Kernel density estimation (KDE) (5×5 km bandwidth) visualized case clustering (Figure 2, Supplementary Figures S1–S2, available at http://weekly.chinacdc.cn/). Statistical significance ($P<0.05$, two-sided) was determined using R software (version 4.3.1, R Core Team, Vienna, Austria) and ArcGIS software (version 10.8, Esri, Redlands, USA).

A total of 1,639 *P. vivax* cases were reported between 2010 and 2024, including 1,542 (94.1%) imported and 97 (5.9%) indigenous. During 2017–2024, 988 cases were reported, including: 299

pre-pandemic, 214 during pandemic, and 475 post-pandemic. The average annual cases increased by 33.3% in the post-elimination period than in the elimination period (93 *vs*. 124). During COVID-19, the average annual cases decreased by 25.26% during intensive border restriction, compared to pre-pandemic period (95 *vs*. 71), followed by a 235.21% rebound post-pandemic (71 *vs*. 238).

Males accounted for 71.4% of the cases, and no significant differences in sex distribution were observed between imported and indigenous cases (χ^2=1.207, *P*=0.272) or between elimination phases (χ^2=0.574, *P*=0.449). Among the imported cases, the median age increased significantly from 29 (IQR: 21, 40) years in the elimination period to 33 years (IQR: 21, 45) post-elimination (W=246,959, *P*<0.005), reflecting a shift toward the 31 to 60-year age group. While indigenous cases were younger (median: 27 years; IQR: 15, 42), with 36.1% aged ≤20.

Outdoor occupations accounted for 78.7% of cases; however, their proportion declined (85.0% to 76.0%), whereas the non-occupational groups increased (11.4% to 18.1%; χ^2=17.955, *P*<0.005) post-elimination among imported cases. In contrast, indigenous cases had more non-occupational groups (27.8% *vs*. 15.7%; Fisher's exact test, *P*<0.005).

Foreign cases accounted for 16.05% (263/1,639), with higher proportions observed in 2016–2017 and 2023–2024. These cases were clustered mainly in the low-altitude southern and central areas. During the pandemic, both the number and spatial extent of foreign cases markedly decreased, with clusters confined to the southern region.

Temporal analysis revealed clear seasonal peaks until 2016 with persisted local transmission (Figure 1) and a distinct "decline-stabilization-rebound" trend in annual incidence after 2016: incidence declined from 0.40 per 1,000 in 2017 to 0.23–0.24 per 1,000 during pandemic, and rebounded to 0.81 per 1,000 during post-pandemic. Since elimination, residual imported cases continue to exhibit seasonal peaks, particularly during 2023–2024, which is consistent with cross-border labor movement patterns.

Marked spatial heterogeneity was also observed. The incidence of imported malaria increased sharply in border townships, particularly in Nabang, where incidence rebounded from 19.17 per 1,000 during elimination to 171.60 per 1,000 after elimination. Tongbiguan (21.86 per 1,000) and Sudian Lisu Ethnic Township (6.45 per 1,000) remained high burden. In contrast, indigenous incidence was low (≤2.85 per 1,000) before elimination and disappeared thereafter. The spatial mapping revealed persistent cases along the southern border of Yingjiang County throughout the study period. KDE analysis confirmed persistent hotspots along the southern border, particularly in Nabang, Xima, and Taiping, across pandemic period (Supplementary Figures S1–S2).

DISCUSSION

This study demonstrated a clear epidemiological transition of *P. vivax* malaria in Yingjiang County following its elimination. A key finding was the fluctuating pattern of malaria with stable spatiotemporal distribution but evolving demographic characteristics. Case numbers fluctuated substantially across border control phases during the COVID-19 pandemic, while spatial distribution and seasonal patterns remained stable. This suggests that malaria importation in this setting is primarily driven by persistent human mobility and geographic connectivity, while border-control intervention temporarily mitigates the risk.

Subgroup analysis across the COVID-19-related border control phases further support this interpretation. During period of intensive border restrictions, although residual cases persisted because of staggered implementation of controls, porous nature of border regions, and essential movement, the overall reduction was substantial, confirming the role of border restrictions as a temporary "scale suppressor." However, following the relaxation of restrictions, the number of cases rebounded rapidly, while their spatiotemporal characteristics remained unchanged. This indicates that short-term interventions only temporarily reduce the intensity of malaria importation.

The demographics of the mobile population reflect the increasing complexity of imported malaria cases. A gradual shift toward older age groups and an increase in nontraditional occupations suggest the diversification of mobile populations. Foreign cases accounted for notable proportion of cases and showed distinct demographic shifts, with a wide distribution across multiple townships, posing additional challenges for surveillance and case management. Meanwhile, persistent vector receptivity sustains local transmission risk. In high-risk border townships (e.g., Nabang, Tongbiguan, and Xima), *Anopheles minimus* (*An. minimus*), a highly efficient *P.vivax* vector, remains dominant at notable densities, enabling imported cases to seed onward transmission.

These findings are consistent with studies on GMS, where spatial heterogeneity and human mobility are key determinants of transmission (*5*). The rebound observed after COVID-19-related restrictions aligns with patterns reported in similar border settings and may reflect increased transmission pressure in neighboring regions of Myanmar, particularly in Kachin State (*6*). Although border control measures temporarily reduce the number of cases, structural risk factors are not addressed, leaving border regions vulnerable even after elimination. This pattern corresponds to the evolving objectives of malaria elimination: reducing transmission, achieving malaria elimination, and preventing reestablishment of transmission (*7*).

However, there are several challenges. First, sustained spatial clustering along border townships highlight entrenched geographic vulnerability. Second, increased heterogeneity of mobile populations complicates risk identification and reduces effectiveness of traditional occupational interventions. Third, strong seasonality of imported cases requires temporally targeted surveillance and response. Finally, reliance on passive surveillance may underestimate asymptomatic infections and obscure residual transmission.

To address these challenges, a "source-vector-host" framework is required. Surveillance should be strengthened in high-risk border areas through proactive case detection (*8*), entry screening, and follow-up of mobile populations, with enhanced cross-border collaboration, including information sharing and synchronizing responses. Vector control should be prioritized in hotspots where *An. minimus* predominates and aligns with seasonal transmission patterns, supported by sustained entomological surveillance and rapid focal responses. For mobile populations, grid-based management and multisectoral coordination should be strengthened to improve registration, health monitoring, health education, and timely diagnosis among cross-border travelers (*9*). Incorporating molecular surveillance approaches such as Capture and Ligation Probe-PCR (CLIP-PCR) may further improve the detection of low-density and asymptomatic infections. Rapid cross-border response mechanisms are essential to enable joint investigation and prompt containment of importation-related transmission (*10*).

This study has several limitations. First, passive surveillance may have underestimated the asymptomatic infections. Second, occupational classification limits detailed risk assessment. Third, potential misclassification of case origins cannot be entirely excluded. Finally, limited entomological data constrained the assessment of transmission potential and the relationship between vector dynamics and imported case patterns.

In conclusion, although intensive border control effectively reduced the *P. vivax* importation, it did not alter spatiotemporal patterns. The rapid resurgence of cases following policy relaxation highlights the ongoing vulnerability of border regions. Sustaining, targeting, and coordinating efforts are essential to prevent the potential re-establishment of malaria transmission along borders.

Conflicts of interest: No conflicts of interest.

Ethical statement: This analysis used de-identified routine surveillance data collected as part of public health practices. Ethical review and informed consent were waived in accordance with the applicable institutional and national regulations for public health surveillance.

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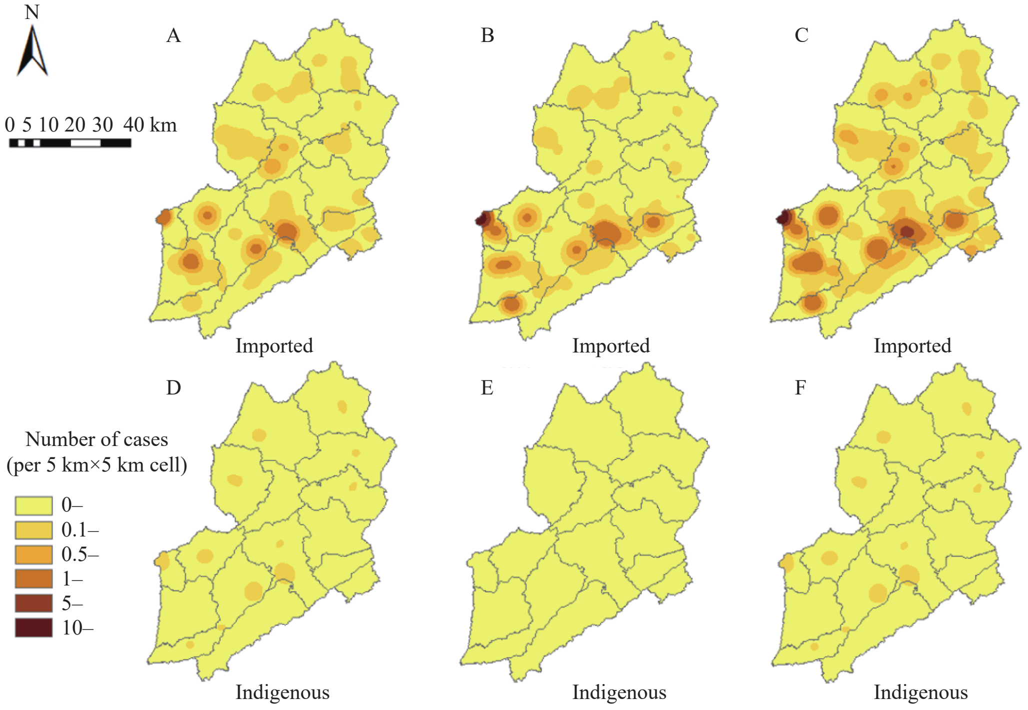
SUPPLEMENTARY MATERIAL

SUPPLEMENTARY TABLE S1. Incidence of imported and indigenous *Plasmodium vivax* malaria at the township level in Yingjiang County, 2010–2024.

Township	Incidence (‰)				
	2010–2016 (Imported)	2017–2024 (Imported)	2010–2016 (Indigenous)	2010–2024 (Imported)	2010–2024 (Indigenous)
Pingyuan Town	1.08	2.05	0.18	3.14	0.18
Jiucheng Town	0.82	1.91	0.13	2.73	0.13
Nabang Town	19.17	171.60	2.85	156.12	3.50
Nongzhang Town	0.41	0.71	0.12	1.09	0.13
Zhanxi Town	0.46	0.26	0.17	0.70	0.16
Machang Town	3.40	1.73	0.58	5.13	0.58
Xima Town	2.88	2.97	0.41	5.84	0.41
Taiping Town	1.81	3.25	0.43	5.03	0.44
Xincheng Town	0.51	0.70	0.10	1.21	0.11
Yousongling Township	1.32	0.88	0.23	2.21	0.24
Mangzhang Township	1.23	0.85	0.74	2.08	0.75
Zhina Township	1.20	0.42	0.49	1.62	0.49
Sudian Lisu Ethnic Township	2.65	3.85	0.69	6.45	0.72
Mengnong Township	4.42	0.90	0.20	5.79	0.22
Tongbiguan Township	11.10	10.74	0.43	21.86	0.46

Note: The incidence was calculated per 1,000 population. Imported cases: 2010–2016 using the 2016 township population, and 2017–2024 using the 2024 population. Indigenous cases (2010–2016): the 2016 population. Overall 2010–2024 incidence: mean of the 2016 and 2024 populations.



SUPPLEMENTARY FIGURE S1. Kernel density of indigenous and imported malaria cases by years in Yingjiang County, Yunnan Province, China. (A) Kernel density estimation of indigenous malaria cases during 2010–2016; (B) Kernel density estimation of indigenous malaria cases during 2017–2024; (C) Kernel density estimation of indigenous malaria cases during 2010–2024; (D) Kernel density estimation of imported malaria cases during 2010–2016; (E) Kernel density estimation of imported malaria cases during 2017–2024; (F) Kernel density estimation of imported malaria cases during 2010–2024.
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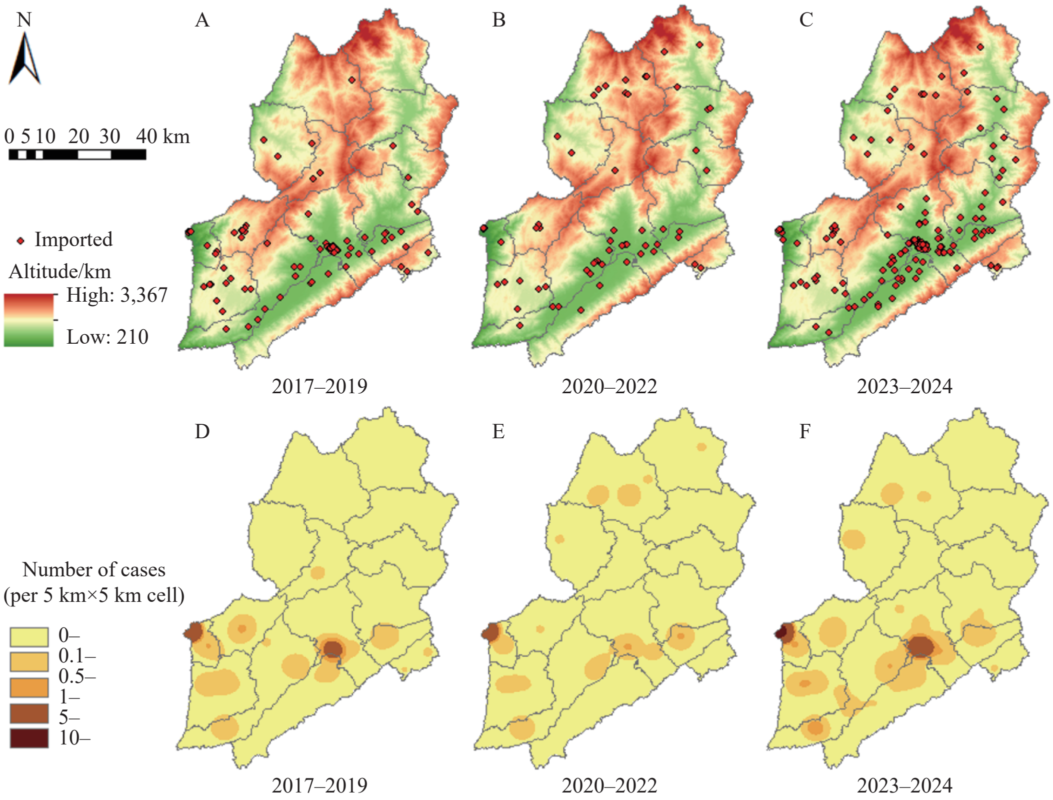

SUPPLEMENTARY FIGURE S2. Spatial distribution and kernel density estimation of imported *Plasmodium vivax* cases in Yingjiang County, Yunnan Province, China, stratified by different border control phases. (A) Spatial distribution of imported *P. vivax* cases during 2017–2019; (B) Spatial distribution of imported *P. vivax* cases during 2020–2022; (C) Spatial distribution of imported *P. vivax* cases during 2023–2024; (D) Kernel density estimation of imported *P. vivax* cases during 2017–2019; (E) Kernel density estimation of imported *P. vivax* cases during 2020–2022; (F) Kernel density estimation of imported *P. vivax* cases during 2023–2024.
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