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中国疾病预防控制中心周报 (英文)

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Vital Surveillances

Epidemiological Characteristics, Risk Factors, and Countermeasures of Imported Malaria — China, 2017–2024

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ABSTRACT

Introduction: This study aimed to analyze the epidemiological characteristics of imported malaria in China, identify transmission risks from the global malaria burden and China's international population exchanges, and propose a two-stage prevention and control strategy for overseas and post-entry periods of outbound personnel.

Methods: A descriptive epidemiological analysis was performed on the National Infectious Disease Surveillance Information System, including the number of patients with imported malaria, *Plasmodium* species distribution, spatiotemporal patterns, demographic characteristics, and countries of infection origin.

Results: Between 2017 and 2024, 16,571 patients with imported malaria, including 75 deaths, were reported, with a U-shaped temporal trend. The annual number of patients with imported malaria remained stable at 2,600–2,800 from 2017 to 2019, dropped to 798 in 2021, and rebounded to 3,155 in 2024. *Plasmodium falciparum* (10,593 patients) and *Plasmodium vivax* (3,288 patients) were the dominant species. *P. falciparum* was imported from Africa, whereas *P. vivax* was from Myanmar. Patients with imported malaria were distributed across China, with Yunnan, Guangdong, and Guangxi emerging as the top three provincial-level administrative divisions (PLADs). The high-risk population was male overseas laborers aged 30–59. Severe illness and fatality rates among individuals with imported malaria remained low with no upward trend.

Conclusion: The global malaria epidemic and China's international exchanges have increased the pressure on malaria importation. Strengthening multisectoral collaboration in health services for outbound personnel and improving targeted surveillance and treatment capacity in key post-entry areas are crucial to prevent severe illness, deaths, and secondary transmission and to consolidate China's

malaria elimination achievements.

China was certified malaria-free by the World Health Organization (WHO) in June 2021 after eliminating local mosquito-borne malaria transmission with no indigenous infections reported since 2017 (1). However, malaria remains a major global public health challenge, with the WHO reporting continuous growth in infections and deaths in recent years, especially in sub-Saharan Africa, where malaria transmission remains severe and uncontrolled. In 2024, the global infections exceeded 282 million, with an estimated 610,000 deaths, reflecting stagnant progress in elimination (2).

Meanwhile, China's opening-up and the Belt and Road Initiative have significantly expanded international population mobility, including overseas laborers, cross-border traders, and project personnel. This intensified international exchange has brought persistent and increasing import pressure on China, making imported malaria the main threat to its elimination achievements (3). Malaria vectors are still widely distributed in former endemic areas, especially in southern border provincial-level administrative divisions (PLADs), such as Yunnan (4). Delayed diagnosis and treatment of imported malaria infections increase severe illness and death risk, leading to introduced transmission if mosquito-borne transmission conditions are met (5).

In this context, analyzing the epidemiological characteristics of imported malaria in China from 2017 to 2024 based on national surveillance data is crucial for identifying key risk points, formulating scientific and targeted prevention strategies, and blocking reestablishment risk. This study aimed to systematically determine the temporal, spatial, and demographic distributions of imported malaria infections, providing evidence-based support for

national malaria surveillance and prevention.

completeness.

METHODS

Data Source

Surveillance data, including imported malaria infections in China from January 2017 to December 2024, were collected from the National Infectious Disease Surveillance Information System. An imported malaria infection was defined as contracted outside the country where the diagnosis was made, including Chinese residents infected overseas and repatriated and foreign nationals who entered China with malaria. Induced infection: traced to blood transfusion or parenteral inoculation of the parasite but not natural mosquito-borne transmission. Introduced infection: contracted locally, linked to an imported infection (first-generation local transmission). Clinical infection: suspected infection with consistent clinical and epidemiological features, without laboratory parasitological confirmation. The collected variables included the number of infections, *Plasmodium* species, patient age, sex, occupation, country of infection, and reporting PLAD in China. All data were reported and verified in accordance with relevant guidelines and regulations ("the National Malaria Elimination Action Plan (2010–2020)" and "the Management Measures for Preventing Re-establishment of Malaria Transmission"), ensuring data accuracy and

Statistical Analysis

Descriptive epidemiological methods were used to analyze the temporal trend, spatial distribution, population demographics, *Plasmodium* species distribution, and origin of imported malaria infections. The severity rate was calculated as the proportion of severe malaria infections among total reported imported infections. All statistical analyses and data visualizations were performed using R (version 4.5.1; R Foundation for Statistical Computing, Vienna, Austria).

RESULTS

China reported no indigenous malaria infections between January 2017 and December 2024. Besides 8 induced, 5 recurrent long incubation periods, and 4 introduced infections (in 2018), 16,571 imported infections, including 75 deaths, were reported. The epidemiological characteristics of imported infections showed distinct temporal, species, spatial, and population distribution regularities, with overall low severe infections and fatality rates.

Temporal Trend of Imported Infections, Severe Infection Rate and Fatality Rate

The number of patients with imported malaria in China presented a U-shaped trend over 8 years

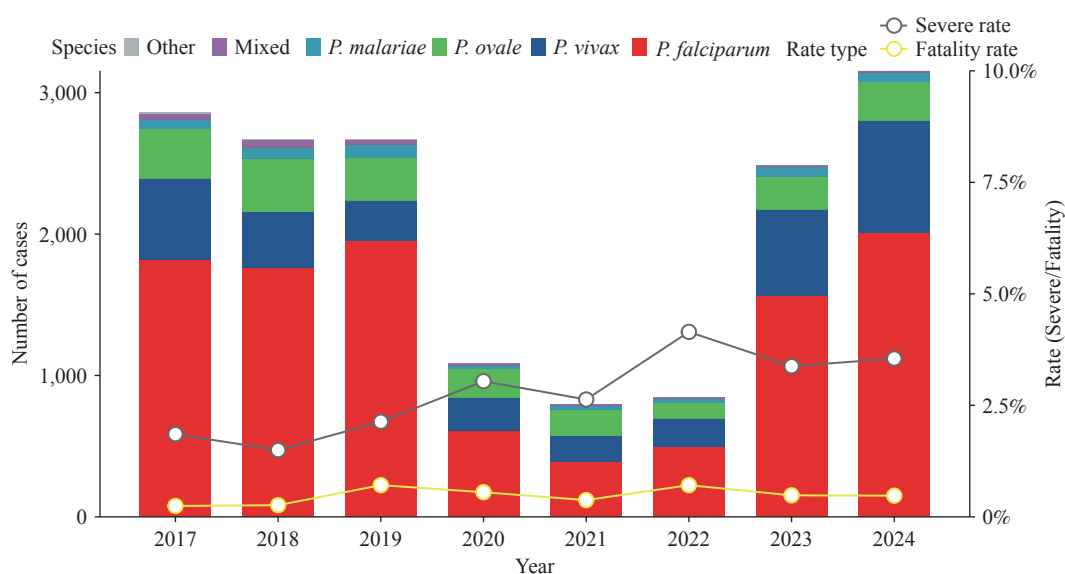


FIGURE 1. Temporal trends of imported malaria infections by *Plasmodium* species and in severe infection rate and fatality rate in China, 2017–2024.

(Figure 1). Annual infections were stable at 2600–2800 during 2017–2019, and subsequently dropped to 798 in 2021 (a 70.15% reduction from 2019). A rebound was observed, with the number of patients increasing to 3,155 in 2024, surpassing 2017–2019 levels. Severe imported malaria remained low at approximately 5% with no apparent upward trend; however, sporadic deaths were recorded each year, and most severe and fatal infections were caused by *Plasmodium falciparum*. From 2017 to 2024, 75 deaths were reported, with an average fatality rate of 0.45%. The number of deaths fluctuated, peaking at 19 in 2019 and dropping to 3 in 2021, then rising again (12 in 2023 and 15 in 2024).

Plasmodium Species Distribution

Imported malaria infections in China were dominated by two *Plasmodium* species: *P. falciparum* was the most prevalent species, followed by *P. vivax* (Figure 1). The total number of *P. falciparum* infections was 10,593 (63.92%), *P. vivax* 3288 (19.84%), *P. ovale* 2033 (12.27%), *P. malariae* 457 (2.76%), mixed infections 180 (1.09%), *P. knowlesi* 1, and 19 infections by clinical diagnosis in 2017–2019 (Table 1).

Geographic differentiation was evident in the species origin of the imported infections: *P. falciparum* was mainly from African countries, accounting for 75.27%

TABLE 1. Demographic characteristics of imported malaria infections in China, 2017–2024.

Characteristic	Number of patients	Proportion (%)
Sex		
Male	15,384	92.84
Female	1,187	7.16
Age group		
≤30 years	3,365	20.31
31–40 years	4,691	28.31
41–50 years	5,066	30.57
51–60 years	3,042	18.36
>60 years	407	2.46
Purpose of overseas travel		
Labor work	12,125	73.17
Business	1,495	9.02
Public affairs	761	4.59
Visiting relatives and friends	559	3.37
Tourism	240	1.45
Others/unknown	1,391	8.39
Region of travel		
Africa	13,941	84.13
Asia	2,444	14.75
Americas	42	0.25
Oceania	143	0.86
Species		
<i>P. falciparum</i>	10,593	63.92
<i>P. vivax</i>	3,288	19.84
<i>P. ovale</i>	2,033	12.27
<i>P. malariae</i>	457	2.76
Mixed infection	180	1.09
Clinical diagnosis	19	0.11
<i>P. knowlesi</i>	1	0.01

Abbreviation: *P. falciparum*=*Plasmodium falciparum*; *P. vivax*=*Plasmodium vivax*; *P. ovale*=*Plasmodium ovale*; *P. malariae*=*Plasmodium malariae*; *P. knowlesi*=*Plasmodium knowlesi*.

(10,490/13,936) of all malaria infections imported from Africa; *P. vivax* was predominantly from Asia, with Myanmar as the core origin, contributing 86.91% (2,019/2,323) of *P. vivax* infections from Asia.

Spatial Distribution of Imported Infections

Patients with imported malaria were distributed across China, showing substantial regional aggregation (Figure 2). Yunnan Province (2118 patients, 12.78%) had the highest number of patients with imported malaria, followed by Guangdong Province (1,534 patients, 9.22%) and Guangxi Zhuang Autonomous Region (1,308 patients, 7.89%). These high-incidence regions had frequent cross-border mobility (Yunnan, a border province) or many returnees (Guangdong, a coastal province). Other PLADs with high numbers of patients included Shandong, Henan, Sichuan, and Jiangsu, major labor export PLADs. In Yunnan Province, *P. vivax* comprised 89.42% (1,894 of 2,118) of the patients, unlike other PLADs where *P. falciparum* predominated.

Population Demographic Characteristics

Imported malaria infections showed a sex imbalance: male patients were 92.84% (15,384 patients) and female were 7.16% (1,187 patients) (Table 1). Infections were concentrated in the working-age population, with the 30–59 years old group accounting for over 79% of all patients. The 41–50 years old group was the largest (30.57%, 5,066 patients), followed by the 31–40 years old (28.31%, 4,691

patients), and 51–60 years old groups (18.36%, 3,042 patients) (Table 1). Age distribution across *Plasmodium* species showed no significant differences, with all species concentrated in the adult labor age group (Supplementary Figure S1, available at <https://weekly.chinacdc.cn/>). The ridgeline plot from 2017 to 2024 confirmed the concentration of patients in the 30–59 years old group, with no temporal shifts (Supplementary Figure S2, available at <https://weekly.chinacdc.cn/>).

Overseas labor was the primary travel purpose for confirmed patients, with laborers accounting for 73.17% (12,125 patients) of the total patients with imported infections, the core high-risk population. Other purposes included business (9.02%, 1,495 patients), public affairs (4.59%, 761 patients), visiting relatives and friends (3.37%, 559 patients), and tourism (1.45%, 240 patients); 8.39% (1,391 patients) were other or unknown (Table 1).

Geographical Origin of Overseas Travel

Africa was the primary source of imported malaria in China, accounting for 84.13% (13,941 patients) of the population. Asia was the second major source, contributing 14.75% (2,444 patients). The Americas and Oceania were minor sources, only 0.25% (42 patients) and 0.86% (143 patients), respectively (Table 1). Among African countries, Nigeria (2,001 patients), the Democratic Republic of the Congo (DR Congo, 1,940 patients) and Guinea (1,147 patients) were top sources; Myanmar was the main source in Asia, with 2,019 *P. vivax* infections, exceeding those of other Asian countries (Figure 3).

DISCUSSION

Given the ongoing global malaria burden and the intensification of China's international population mobility under the Belt and Road Initiative, imported malaria remains a challenge to China's malaria elimination achievements (6). Surveillance results from 2017 to 2024 show that imported malaria in China is characterized by *P. falciparum* dominance, African and Southeast Asian sources, border and coastal PLAD aggregation, and overseas labor predominance. The U-shaped trend of imported infections was associated with real-world events, with a sharp decline from 2020 to 2021 mainly caused by strict coronavirus disease 2019 (COVID-19) border controls and reduced travel, whereas the rebound since 2022 reflects the recovery of

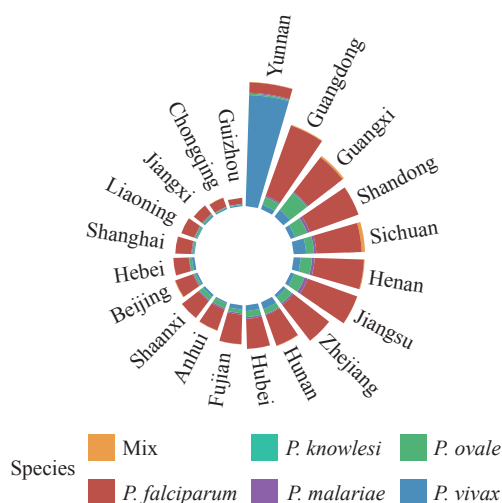


FIGURE 2. Spatial distribution of imported malaria infections in the top 20 PLADs of China, 2017–2024.

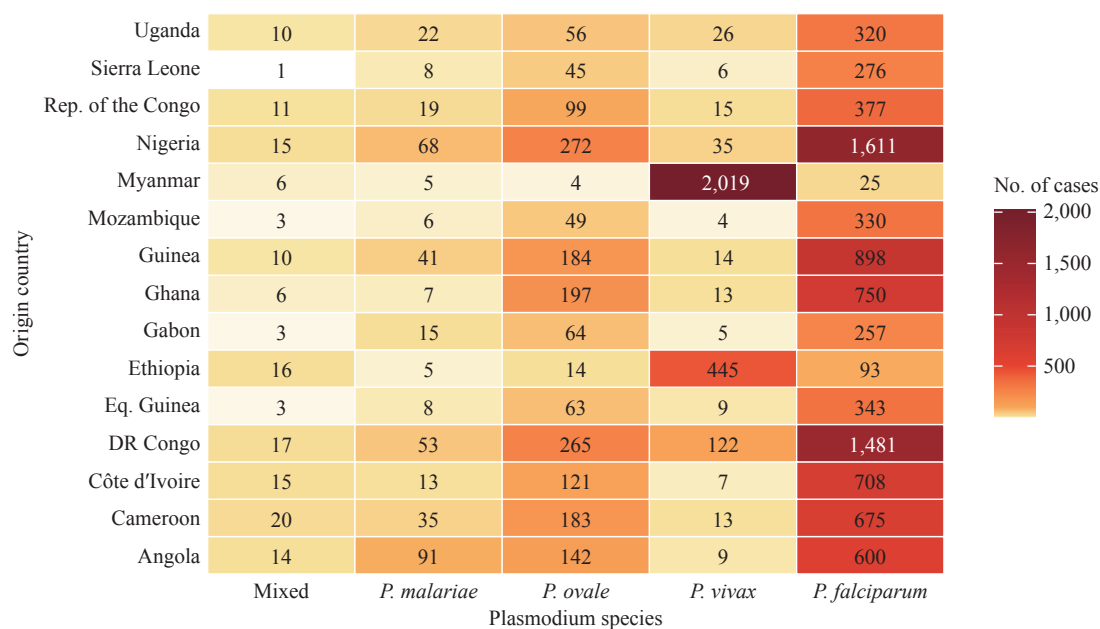


FIGURE 3. Distribution of *Plasmodium* species among imported malaria infections by major origin countries, 2017–2024.

international mobility and ongoing global malaria resurgence in endemic countries. Meanwhile, sporadic severe infections and deaths highlight gaps in imported malaria prevention and control. Based on the epidemiological characteristics and the full process of population outbound and entry, this study proposes a two-stage prevention and control strategy covering the overseas and post-entry periods, emphasizing multi-sector collaboration and precise intervention to establish a closed-loop management system.

Malaria prevention overseas reduces infection risk for outbound personnel in malaria-endemic areas by targeting high-risk population, overseas laborers, and conducting joint interventions with health, commerce, foreign affairs, and labor departments (7–8). Pre-departure health education and prevention guidance should be strengthened by establishing a training system for outbound laborers visiting malaria-endemic areas, focusing on malaria transmission routes, symptoms, preventive measures, and early treatment (9). On-site health services and medical support in overseas projects must be promoted by constructing medical and health service points in Chinese-funded projects in malaria-endemic areas; equipping professional medical personnel with complete diagnosis, treatment equipment, and drugs; and providing timely diagnosis and treatment for personnel with fever and other symptoms to avoid delayed treatment. Cooperation between Chinese overseas medical institutions and local health departments should be strengthened to share epidemic information,

diagnoses, and treatment resources. Regular health monitoring and early warning should be conducted by temperature monitoring and symptom screening for outbound personnel in malaria-endemic areas, establishing a symptom reporting mechanism, and conducting rapid malaria testing for personnel with fever to achieve early detection and treatment, reducing the risk of severe illness and cross-border transmission.

The core of malaria prevention and control post-entry is blocking local secondary transmission from imported infections. The key is to focus on important PLADs (border and coastal areas) and populations (overseas laborers returning from malaria-endemic areas) to improve surveillance sensitivity. In China, a sensitive nationwide surveillance system should be maintained for timely detection, reporting, and investigation of all imported infections. Strengthening laboratory capacity for species identification and confirmation of *Plasmodium* infections is critical to reduce misdiagnosis and delayed treatment. Integrated monitoring covering patient detection, epidemiological investigation, vector surveillance, and response should be implemented to block potential secondary transmission and sustain a malaria-free status.

Targeted post-entry surveillance and screening should be strengthened by establishing a health declaration and malaria screening system for returnees from malaria-endemic areas, especially overseas laborers from Nigeria, the DR Congo, Myanmar, and other high-risk countries; conducting voluntary malaria testing at ports and designated medical institutions;

and monitoring for 30 days after entry for high-risk groups to detect patients with latent infection in a timely manner. This system should rely on facility-based malaria infection detection, supported by rapid investigation and public health responses from local Centers for Disease Control and Prevention.

Malaria diagnosis and treatment capacity of medical institutions in key areas should be improved by strengthening the training of medical staff in primary and secondary medical institutions in border PLADs such as Yunnan and coastal PLADs such as Guangdong and Shandong, improving early identification, differential diagnosis, standardized treatment of malaria, and equipping (10–11). Rapid diagnostic tests and first-line anti-malarial drugs are used to ensure imported infections are diagnosed and treated first (12). Severe malaria rescue capacity and emergency response should be enhanced by establishing a hierarchical rescue system for severe malaria, designating tertiary hospitals in each PLAD as designated hospitals for severe malaria rescue, equipping professional rescue teams, and complete rescue equipment (13). For confirmed imported infections, focus disposal in surrounding areas should be conducted to reduce the risk of local secondary transmission (14–15).

This study has certain limitations. First, the data are based on reported infections in the national infectious disease surveillance system, and some asymptomatic or mild imported infections may be underreported due to lack of medical treatment, mainly attributed to the high mobility of high-risk populations and their possible possession of anti-malarial drugs obtained overseas, leading to underestimation of the actual number of imported infections; Second, a comprehensive semi-quantitative and quantitative assessment of secondary transmission risk of imported malaria in key PLADs was not conducted, which involves integration and systematic analysis of multisource heterogeneous data, including vector distribution and primary medical care capacity. This exceeds the research scope and data acquisition limits and will be the focus of follow-up research. Third, the surveillance data lacked follow-up information on some patients with imported infections, limiting in-depth analysis of the latent period and transmission risk of different *Plasmodium* species.

The 8-year surveillance results from 2017 to 2024 confirm that China's malaria elimination achievement is stable and sustainable; however, increasing importation pressure indicates that malaria prevention

and control work cannot be relaxed. The two-stage prevention and control strategy proposed for overseas and post-entry periods aligns with the epidemiological characteristics of imported malaria in China and the actual needs of international population mobility, and has important guiding significance for consolidating malaria elimination achievements. In the context of the ongoing global malaria burden and the deepening of the Belt and Road Initiative, malaria prevention and control in China has shifted from original elimination of local transmission to prevention of imported infections and secondary transmission. The surveillance results provide a scientific basis for revising national malaria prevention and control technical guidelines, and help optimize allocation of public health resources in key areas and populations.

China should maintain a sensitive malaria surveillance system, optimize detection and follow-up of at-risk populations, strengthen multi-sector and cross-regional collaboration (e.g., coordination between health and labor departments for pre-departure training, and between border PLADs for cross-regional infection tracking), and implement two-stage precise prevention and control measures comprehensively. Simultaneously, deepening international cooperation with malaria-endemic countries in epidemic information sharing, joint vector control, and drug resistance monitoring is crucial for reducing the global malaria burden. Only through such a comprehensive approach can China alleviate the import pressure of malaria and consolidate its malaria elimination achievements long term.

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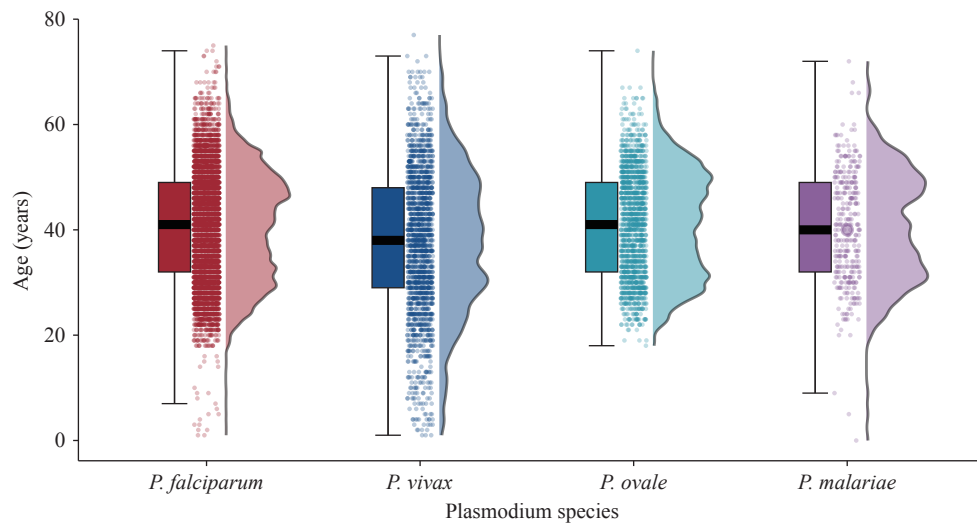
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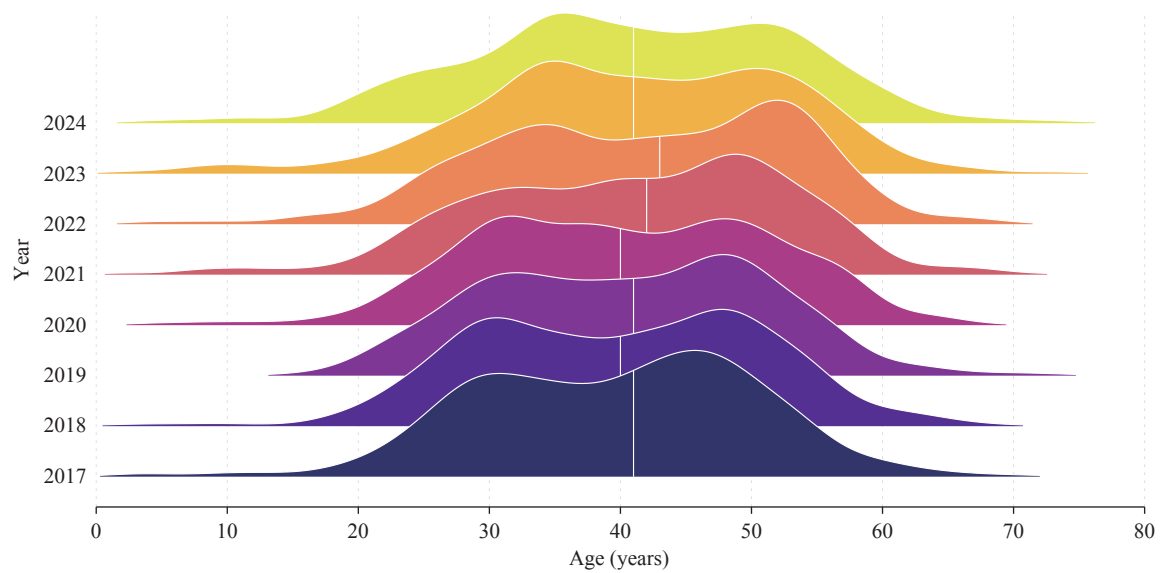
REFERENCES

1. Zhou XN. China declared malaria-free: a milestone in the world malaria eradication and Chinese public health. *Infect Dis Poverty* 2021;10(1):98. <https://doi.org/10.1186/s40249-021-00882-9>.
2. World Health Organization. World malaria report 2025: addressing the threat of antimalarial drug resistance. 2025. <https://www.who.int/publications/i/item/9789240117822>. [2025-12-4].
3. Yi B Y, Xia Z G. Risk factors for imported severe malaria cases — China, 2019-2023. *China CDC Wkly* 2025;7(18):602 – 8. <https://doi.org/10.46234/ccdcw2025.100>.
4. Zheng DS, Tian P, Yan GY, Lin ZR, Zhou HN, Liu XB, et al. Stratified vector control and proactive cross border collaboration for sustaining malaria elimination in Yunnan, China. *BMJ* 2025;389:e082300. <https://doi.org/10.1136/bmj-2024-082300>.
5. Zhang T, Wang DQ, Qian YJ, Ruan W, Liu Y, Xia J, et al. Profile and determinants of delayed care-seeking and diagnosis among patients with imported malaria: a retrospective study in China, 2014-2021. *Infect Dis Poverty* 2022;11(1):125. <https://doi.org/10.1186/s40249-022-01050-3>.
6. Yang S, Li RY, Yan SN, Yang HY, Cao ZY, Zhang L, et al. Risk assessment of imported malaria in China: a machine learning perspective. *BMC Public Health* 2024;24(1):865. <https://doi.org/10.1186/s12889-024-17929-9>.
7. Wang Y, Fang F, Li CY, Wang JJ, Lu GY, Huang YZ. Understanding international travelers' intentions to adopt protective behaviors against malaria during staying abroad: insights from a study of Chinese international travelers. *Global Health* 2025;21(1):39. <https://doi.org/10.1186/s12992-025-01132-5>.
8. Naing C, Whittaker MA, Tanner M. Inter-sectoral approaches for the prevention and control of malaria among the mobile and migrant populations: a scoping review. *Malar J* 2018;17(1):430. <https://doi.org/10.1186/s12936-018-2562-4>.
9. Zhang T, Xu X, Liu BW, Wang DQ, Ye XG, Jiang JJ, et al. Establishing and applying an adaptive framework for imported malaria: a field practice in Anhui Province, China from 2012 to 2022. *BMC Public Health* 2024;24(1):695. <https://doi.org/10.1186/s12889-024-18239-w>.
10. Yin JH, Zhang L, Yi BY, Zhou SS, Xia ZG. Regional heterogeneity of malaria healthcare seeking and diagnosis in China (2017-2022): implications in preventing re-establishment of malaria transmission. *J Infect Public Health* 2025;18(1):102601. <https://doi.org/10.1016/j.jiph.2024.102601>.
11. Yan H, Li M, Xia ZG, Yin JH. Competency of malaria laboratory diagnosis at national and provincial levels at the beginning of malaria post-elimination phase, China. *Malar J* 2024;23(1):58. <https://doi.org/10.1186/s12936-024-04883-5>.
12. Li WD, Zhang XZ, Feng J, Zhang T, Xu X, Jiang JJ, et al. Evaluation of the combination of rapid diagnostic tests and microscopy for imported malaria surveillance in Anhui Province, China. *Acta Trop* 2021;222:106042. <https://doi.org/10.1016/j.actatropica.2021.106042>.
13. Zhang L, Tu H, Zhou SS, Xia ZG, Feng J. Malaria deaths — China, 2011-2020. *China CDC Wkly* 2021;3(17):360 – 5. <https://doi.org/10.46234/ccdcw2021.098>.
14. Borton D. Preventing malaria spread in the US. *Nursing* 2024;54(3):21 – 8. <https://doi.org/10.1097/01.NURSE.0001006264.42321.ff>.
15. Yi BY, Zhang L, Yin JH, Zhou SS, Xia ZG. 1-3-7 surveillance and response approach in malaria elimination: China's practice and global adaptations. *Malar J* 2023;22(1):152. <https://doi.org/10.1186/s12936-023-04580-9>.

SUPPLEMENTARY MATERIAL



SUPPLEMENTARY FIGURE S1. Age distribution profiles of imported malaria infections by *Plasmodium* species in China, 2017–2024.



SUPPLEMENTARY FIGURE S2. Temporal evolution of age distribution for imported malaria infections in China, 2017–2024.

Vital Surveillances

Five-Year Immune Recovery After ART Initiation Among PLWH Aged ≥ 15 Years with Baseline Immunosuppression — China, 2013–2024

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Lieyu Huang²; Nana Liu²; Zhihang Peng³; Yan Zhao^{1,*}

ABSTRACT

Introduction: Although antiretroviral therapy (ART) suppresses human immunodeficiency virus (HIV) replication in most people living with HIV (PLWH), 10%–40% show inadequate CD4 reconstitution despite sustained virologic suppression, increasing risks of AIDS- and non-AIDS-related events. Prior studies have suggested that immunological nonresponse (INR) is particularly common among individuals starting ART with immunosuppression. In China, real-world evidence for long-term immune recovery in immunosuppressed PLWH remains limited.

Methods: Immunosuppression was defined as a baseline CD4 < 350 cells/ μ L at ART initiation. At year 5, INR was defined as CD4 < 350 cells/ μ L and favorable immune recovery as CD4 $\geq$ 500 cells/ μ L. From China's National ART Cohort, we included PLWH (aged ≥ 15 years; baseline CD4 < 350 cells/ μ L) initiating ART during 2013–2019 who achieved year-5 virologic suppression (≤ 50 copies/mL). We described 5-year CD4 changes and examined factors associated with year-5 immune outcomes.

Results: Among 315,109 participants, the median CD4 count increased from 199 cells/ μ L at baseline to 424 cells/ μ L over 5 years of ART. At year 5, 111,899 (35.5%) had CD4 $\geq$ 500 cells/ μ L (favorable immune recovery). In contrast, 109,344 (34.7%) patients had a CD4 < 350 cells/ μ L and were classified as having INR. Lower baseline CD4 counts, older age, male sex, heterosexual or injection drug transmission, HBsAg positivity, anti-HCV positivity, and delayed ART initiation were associated with higher odds of INR. Compared to continuous non-nucleoside reverse transcriptase inhibitor (NNRTI)-based therapy, continuous protease inhibitor (PI)- and integrase strand transfer inhibitor (INSTI)-based therapies, and switching from NNRTI- to INSTI-based regimens showed higher odds of favorable immune recovery.

Conclusions: Among PLWH who initiated ART with immunosuppression and achieved virologic suppression at 5 years, most experienced immune recovery; however, approximately one-third remained INR. Early diagnosis, timely ART initiation, and targeted long-term immunological monitoring are required for populations at increased risk of suboptimal immune recovery.

The Joint United Nations Programme on HIV/AIDS (UNAIDS) set the "95–95–95" targets, underscoring antiretroviral therapy (ART) as a cornerstone of human immunodeficiency virus (HIV) control. However, immune recovery after ART remains heterogeneous, and even among people living with HIV (PLWH) with sustained virologic suppression, an estimated 10%–40% do not achieve favorable CD4 recovery and consequently face elevated risks of AIDS- and non-AIDS-related events (1–2). In China, free ART has been available since 2004 under the "Four Frees and One Care" policy, and ART coverage and virologic suppression rates have exceeded 90% in recent years (3). Nevertheless, a substantial proportion of PLWH continue to initiate ART late, and real-world evidence of long-term immune recovery and its determinants in this population remains limited. Therefore, immune recovery at 5 years after ART initiation was assessed, and factors associated with immunological nonresponse (INR) (CD4 < 350 cells/ μ L) and favorable immune recovery (CD4 $\geq$ 500 cells/ μ L) were examined among PLWH in China with immunosuppression at ART initiation (2).

METHODS

Data Sources

Study data were derived from the National ART

Cohort in China and extracted from the National Free Antiretroviral Treatment Information System, which is maintained by the China Centers for Disease Control and Prevention and quality-controlled under the National Quality Assurance Program. This system has been described in detail in previously published studies (4). Because China's 2012 treatment guidelines expanded free ART eligibility to patients with CD4 <350 cells/ μ L, this study included persons aged ≥ 15 years who initiated ART during 2013–2019 and were followed through June 30, 2025, ensuring that all participants had the opportunity to complete 5 years of follow-up (60 months after ART initiation; ± 6 months). PLWH initiating ART with immunosuppression (baseline CD4 <350 cells/ μ L) (5) were included if they had a year-5 CD4 measurement and two consecutive viral load measurements ≤ 50 copies/mL (1).

Definitions

Initiation of ART with immunosuppression was defined as baseline CD4 <350 cells/ μ L (5). Baseline CD4 count was defined as the CD4 measurement obtained within 30 days before ART initiation and was categorized as <100, 100–199, and 200–349 cells/ μ L. Follow-up CD4 counts at years 1–5 were ascertained within predefined windows (12 $\times$ N months after ART initiation, ± 6 months), selecting the measurement closest to 12 $\times$ N months. Virologic suppression was defined as two consecutive viral load measurements ≤ 50 copies/mL before the year-5 CD4 date (1). Among PLWH with virologic suppression at year 5, immunological non-response (INR) was defined as a CD4 <350 cells/ μ L at year 5 (1). Favorable immune recovery was defined as a CD4 ≥ 500 cells/ μ L at year 5 (2).

Study Design

This study was a retrospective cohort study. Baseline variables included sex, age at ART initiation, marital status, route of HIV transmission, time from HIV diagnosis to ART initiation, baseline CD4 count, hepatitis B surface antigen (HBsAg) status, anti-HCV serostatus, and ART regimen. To describe immune recovery, baseline characteristics were summarized as counts (percentages), and baseline and year-5 CD4 counts were reported as medians with interquartile ranges (IQR). CD4 at year 5 was categorized as <200, 200–349, 350–499, and ≥ 500 cells/ μ L, and frequencies (percentages) were calculated overall and

across baseline subgroups. The distribution of CD4 categories at baseline and each annual follow-up throughout year 5 was summarized using 100% stacked bar charts. Median CD4 trajectories from years 1 to 5 were also plotted, stratified by baseline CD4 category (<100, 100–199, 200–349 cells/ μ L) and age group (15–30, 31–45, 46–60, ≥ 61 years). Finally, among PLWH with virologic suppression at year 5, determinants of INR (CD4 <350 cells/ μ L) and favorable immune recovery (CD4 ≥ 500 cells/ μ L) were evaluated.

Statistical Analysis

Group differences in the year-5 CD4 categories were assessed using the chi-square test. Factors associated with INR and favorable immune recovery at year 5 were examined using univariable logistic regression, and variables with $P < 0.05$ and clinical relevance were included in multivariable logistic regression models. The results are presented as adjusted odds ratios (aORs) with 95% confidence intervals (CIs). Analyses were conducted in R (version 4.4.3; R Foundation for Statistical Computing, Vienna, Austria), and two-sided $P < 0.05$ indicated statistical significance.

RESULTS

Cohort Characteristics and Year-5 CD4 Distribution

Among the 460,161 participants with a baseline CD4 <350 cells/ μ L, 71,048 (15%) died before the year-5 assessment window and 22,553 (5%) had no CD4 measurement within the year-5 window. Among those with an available year-5 CD4 result, 315,109 (86%) achieved virological suppression and were included in the final analysis. A total of 315,109 participants were included, of whom 241,028 (76.5%) were male. Heterosexual contact was the most frequently reported route of HIV transmission (194,373; 61.7%). At baseline, CD4 cell counts of <100, 100–199, and 200–349 cells/ μ L were observed in 79,436 (25.2%), 79,028 (25.1%), and 156,645 (49.7%) participants, respectively. At year 5 after ART initiation, the median CD4 cell count was 424 cells/ μ L (IQR: 300, 570) and CD4 categories of <200, 200–349, 350–499, and ≥ 500 cells/ μ L accounted for 28,107 (8.9%), 81,237 (25.8%), 93,866 (29.8%), and 111,899 (35.5%) participants, respectively (Table 1).

Across follow-up, the proportion of PLWH with CD4 <350 cells/ μ L decreased from 100% at baseline

TABLE 1. Year-5 CD4 cell count distribution by selected characteristics among PLWH initiating ART with baseline CD4<350 cells/ μ L and virologic suppression at year 5 in China, 2013–2024 (N=315,109).

Variable	Total n (%)	CD4 at baseline, cells/ μ L median (IQR)	CD4 at year 5, cells/ μ L median (IQR)	CD4 count at year 5 (cells/ μ L)				P
				<200	200–349	350–499	$\geq$ 500	
				n (%)	n (%)	n (%)	n (%)	
Gender								<0.01
Male	241,028 (76.5)	196 (92, 273)	418 (294, 564)	23,070 (9.6)	63,478 (26.3)	71,124 (29.5)	83,356 (34.6)	
Female	74,081 (23.5)	205 (116, 275)	442 (321, 587)	5,037 (6.8)	17,759 (24.0)	22,742 (30.7)	28,543 (38.5)	
Age at ART initiation (years)								<0.01
15–30	83,222 (26.4)	230 (137, 292)	489 (368, 632)	3,093 (3.7)	14,750 (17.7)	25,900 (31.1)	39,479 (47.4)	
31–45	111,090 (35.3)	191 (84, 270)	432 (311, 577)	8,547 (7.7)	27,800 (25.0)	33,790 (30.4)	40,953 (36.9)	
46–60	82,578 (26.2)	180 (84, 259)	386 (269, 528)	9,857 (11.9)	25,031 (30.3)	23,821 (28.9)	23,869 (28.9)	
$\geq$ 61	38,219 (12.1)	185 (108, 256)	335 (234, 464)	6,610 (17.3)	13,656 (35.7)	10,355 (27.1)	7,598 (19.9)	
Marital status								<0.01
Unmarried	94,463 (30.0)	217 (111, 286)	471 (348, 615)	4,952 (5.2)	18,919 (20.0)	29,071 (30.8)	41,521 (44.0)	
Married or with partner	167,031 (53.0)	191 (95, 267)	404 (284, 548)	17,134 (10.3)	47,032 (28.2)	49,316 (29.5)	53,549 (32.1)	
Divorced or widowed	53,615 (17.0)	189 (94, 267)	400 (278, 545)	6,021 (11.2)	15,286 (28.5)	15,479 (28.9)	16,829 (31.4)	
Route of transmission								<0.01
Heterosexual transmission	194,373 (61.7)	189 (92, 267)	405 (284, 550)	20,508 (10.6)	54,276 (27.9)	56,839 (29.2)	62,750 (32.3)	
MSM transmission	90,701 (28.8)	219 (120, 286)	469 (348, 609)	4,403 (4.9)	18,449 (20.3)	28,430 (31.3)	39,419 (43.5)	
Injection drug use	9,961 (3.2)	207 (122, 276)	387 (262, 533)	1,313 (13.2)	2,922 (29.3)	2,744 (27.6)	2,982 (29.9)	
Other	20,074 (6.4)	179 (74, 265)	414 (290, 559)	1,883 (9.4)	5,590 (27.9)	5,853 (29.2)	6,748 (33.6)	
Time from HIV diagnosis to ART initiation (days)								<0.01
0–6	39,490 (12.5)	179 (80, 260)	410 (289, 558)	3,863 (9.8)	10,824 (27.4)	11,551 (29.3)	13,252 (33.6)	
7–30	130,583 (41.4)	186 (84, 264)	420 (297, 564)	11,816 (9.1)	34,514 (26.4)	39,033 (29.9)	45,220 (34.6)	
31–360	98,503 (31.3)	211 (114, 280)	424 (302, 567)	8,748 (8.9)	25,159 (25.5)	29,705 (30.2)	34,891 (35.4)	
>360	46,533 (14.8)	221 (126, 288)	447 (317, 599)	3,680 (7.9)	10,740 (23.1)	13,577 (29.2)	18,536 (39.8)	
Baseline CD4 count (cells/ μ L)								<0.01
0–99	79,436 (25.2)	38 (17, 67)	310 (217, 431)	16,257 (20.5)	31,006 (39.0)	19,455 (24.5)	12,718 (16.0)	
100–199	79,028 (25.1)	155 (129, 178)	382 (282, 504)	7,135 (9.0)	25,939 (32.8)	25,716 (32.5)	20,238 (25.6)	
200–349	156,645 (49.7)	274 (237, 310)	502 (385, 643)	4,715 (3.0)	24,292 (15.5)	48,695 (31.1)	78,943 (50.4)	
HBsAg								<0.01
Positive	22,746 (7.2)	187 (89, 265)	403 (285, 545)	2,290 (10.1)	6,530 (28.7)	6,750 (29.7)	7,176 (31.5)	
Negative	220,808 (70.1)	201 (102, 275)	429 (305, 575)	18,893 (8.6)	55,628 (25.2)	65,978 (29.9)	80,309 (36.4)	
Missing/Unknown	71,555 (22.7)	193 (89, 272)	416 (293, 562)	6,924 (9.7)	19,079 (26.7)	21,138 (29.5)	24,414 (34.1)	

Continued

Variable	Total n (%)	CD4 at baseline, cells/μL	CD4 at year 5, cells/μL	CD4 count at year 5 (cells/μL)				P
				<200	200–349	350–499	≥500	
		median (IQR)	median (IQR)	n (%)	n (%)	n (%)	n (%)	
Anti-HCV								<0.01
Positive	13,400 (4.3)	198 (111, 272)	400 (275, 548)	1,560 (11.6)	3,775 (28.2)	3,786 (28.3)	4,279 (31.9)	
Negative	226,906 (72.0)	200 (101, 274)	429 (305, 574)	19,209 (8.5)	57,405 (25.3)	67,961 (30.0)	82,331 (36.3)	
Missing/Unknown	74,803 (23.7)	194 (89, 272)	415 (292, 560)	7,338 (9.8)	20,057 (26.8)	22,119 (29.6)	25,289 (33.8)	
ART Regimen								<0.01
Continuous NNRTI-based	296,787 (94.2)	201 (103, 275)	423 (300, 568)	26,457 (8.9)	76,835 (25.9)	88,676 (29.9)	104,819 (35.3)	
Continuous PI-based	12,546 (4.0)	163 (54, 258)	449 (313, 606)	1,091 (8.7)	2,866 (22.8)	3,504 (27.9)	5,085 (40.5)	
Continuous INSTI-based	3,435 (1.1)	93 (24, 215)	425 (297, 578)	293 (8.5)	906 (26.4)	1,008 (29.3)	1,228 (35.7)	
Switched from NNRTI to INSTI	1,090 (0.3)	53 (18, 159)	382 (272, 519)	134 (12.3)	319 (29.3)	330 (30.3)	307 (28.2)	
Switched from NNRTI to PI	1,251 (0.4)	192 (83, 271)	422 (290, 579)	132 (10.6)	311 (24.9)	348 (27.8)	460 (36.8)	
Total	315,109 (100)	199 (99, 273)	424 (300, 570)	28,107 (8.9)	81,237 (25.8)	93,866 (29.8)	111,899 (35.5)	

Note: *P* values were obtained from chi-square tests comparing the distribution of year-5 CD4 categories across the subgroups.

Abbreviation: HIV=human immunodeficiency virus; PLWH=people living with HIV; ART=antiretroviral therapy; IQR=interquartile range; HBsAg=hepatitis B surface antigen; anti-HCV=antibody to hepatitis C virus; MSM=men who have sex with men; NNRTI=non-nucleoside reverse transcriptase inhibitor; PI=protease inhibitor; INSTI=integrase strand transfer inhibitor.

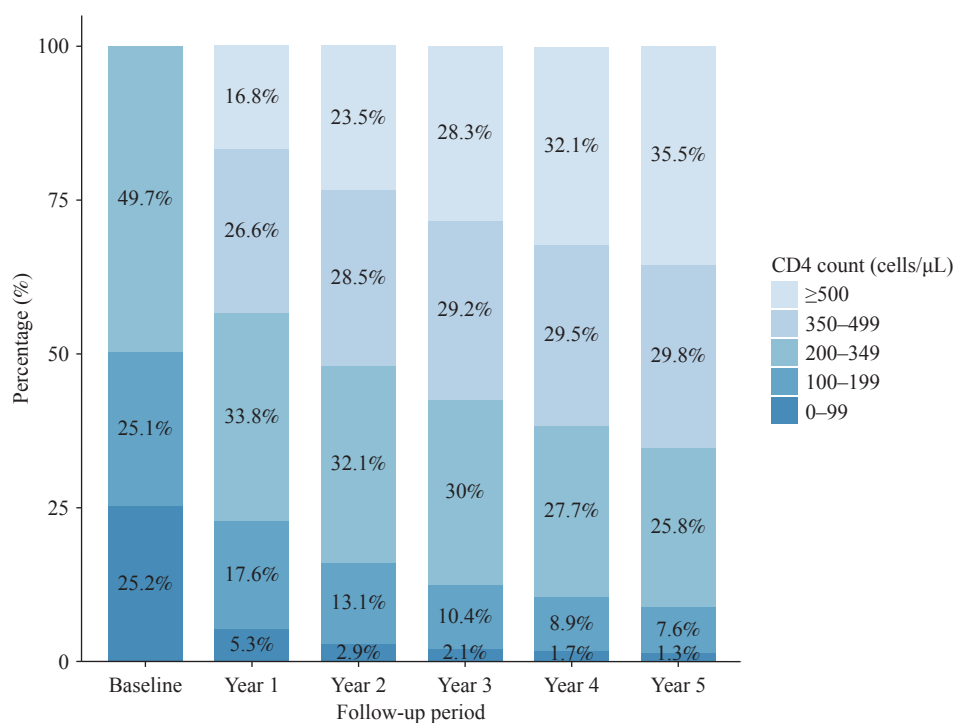


FIGURE 1. Distribution of CD4 cell count categories from baseline to year 5 after ART initiation among PLWH with baseline CD4 <350 cells/μL and virologic suppression at year 5 in China, 2013–2024 (N=315,109).

Note: Bars show 100% stacked percentages at baseline and 1–5 years after ART initiation. Virologic suppression was defined as two consecutive viral load measurements ≤50 copies/mL before the year-5 CD4 date.

Abbreviation: HIV=human immunodeficiency virus; PLWH=people living with HIV; ART=antiretroviral therapy.

to 56.5% at year 1, 48.0% at year 2, 42.5% at year 3, 38.4% at year 4, and 34.7% at year 5 (Figure 1). At year 5, 35.5% had CD4 $\geq$ 500 cells/ μ L (favorable immune recovery) (Figure 1). In the line plots of median CD4 count, the largest year-to-year increase occurred between baseline and year 1 across all groups (Figure 2). For example, the median CD4 count increased by 142 cells/ μ L from baseline to year 1 in the baseline CD4 200–349 cells/ μ L group and by 144 cells/ μ L in the 15–30 years old age group (Figure 2).

Factors Associated with Immune Recovery at Year 5

In multivariable analyses, compared with baseline CD4 200–349 cells/ μ L, baseline CD4 100–199 cells/ μ L and <100 cells/ μ L were associated with higher odds of INR (aOR=2.99 and 6.64, respectively). They were also associated with lower odds of achieving CD4 $\geq$ 500 cells/ μ L (aOR=0.36 and 0.19, respectively) (Table 2). Age at ART initiation showed a dose–response pattern. Compared with those aged 15–30 years, older age groups had higher odds of INR (31–45 years: aOR=1.33; 46–60 years: aOR=2.04; $\geq$ 61 years: aOR=3.49). In parallel, the odds of achieving CD4 $\geq$ 500 cells/ μ L decreased with age (aOR=0.83, 0.58, and 0.33, respectively). Compared with females,

males had higher odds of INR (aOR=1.49; 95% CI: 1.46, 1.52) (Table 2).

Compared with continuous non-nucleoside reverse transcriptase inhibitor (NNRTI)-based therapy, continuous protease inhibitor (PI)-based therapy was associated with higher odds of achieving favorable immune recovery (CD4 $\geq$ 500 cells/ μ L) (aOR=1.54; 95% CI: 1.48, 1.60). A similar association was observed for continuous integrase strand transfer inhibitor (INSTI)-based therapy (aOR=1.42; 95% CI: 1.32, 1.54). Switching from an NNRTI-based regimen to an INSTI-based regimen was also associated with higher odds of CD4 $\geq$ 500 cells/ μ L (aOR=1.23; 95% CI: 1.07, 1.42) (Table 2). In addition, injection drug use, HBsAg/anti-HCV positivity, and delayed ART initiation were independently associated with higher INR odds (Table 2).

DISCUSSION

The objectives of ART include both sustained virological suppression and immune reconstitution, with the overarching aim of improving long-term survival and quality of life (1). Prior studies have shown that INR signifies persistent immune dysfunction and is associated with an increased risk of

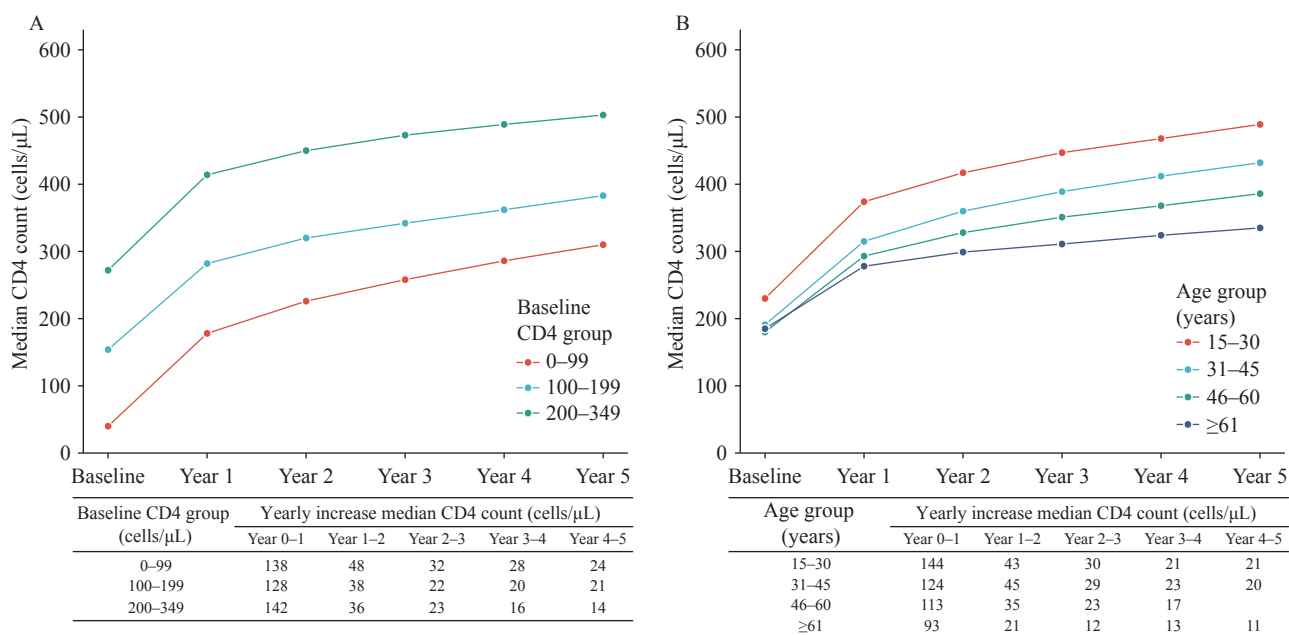


FIGURE 2. Median CD4 cell count trajectories from baseline to year 5 after ART initiation, stratified by (A) baseline CD4 category and (B) age at ART initiation, among PLWH with baseline CD4 <350 cells/ μ L and virologic suppression at year 5 — China, 2013–2024 (N=315,109).

Note: Panel A groups: 0–99, 100–199, and 200–349 cells/ μ L. Panel B groups: 15–30, 31–45, 46–60, and $\geq$ 61 years. Abbreviation: HIV=human immunodeficiency virus; PLWH=people living with HIV; ART=antiretroviral therapy.

TABLE 2. Multivariable factors associated with immunological non-response (INR; CD4<350 cells/ μ L) and favorable immune recovery (CD4 $\geq$ 500 cells/ μ L) at year 5 among PLWH initiating ART with baseline CD4<350 cells/ μ L and virologic suppression at year 5 in China, 2013–2024 (N=315,109).

Variable	CD4 $\geq$ 500 (cells/ μ L)		CD4<350 (cells/ μ L)	
	Adjusted OR (95% CI)	P	Adjusted OR (95% CI)	P
Gender				
Female	1.00 (Reference)		1.00 (Reference)	
Male	0.73 (0.72, 0.75)	<0.01	1.49 (1.46, 1.52)	<0.01
Age at ART initiation (years)				
15–30	1.00 (Reference)		1.00 (Reference)	
31–45	0.83 (0.81, 0.85)	<0.01	1.33 (1.30, 1.36)	<0.01
46–60	0.58 (0.57, 0.60)	<0.01	2.04 (1.98, 2.09)	<0.01
$\geq$ 61	0.33 (0.32, 0.34)	<0.01	3.49 (3.37, 3.61)	<0.01
Marital Status				
Unmarried	1.00 (Reference)		1.00 (Reference)	
Married or with partner	0.89 (0.87, 0.91)	<0.01	1.13 (1.10, 1.16)	<0.01
Divorced or widowed	0.91 (0.89, 0.94)	<0.01	1.14 (1.11, 1.17)	<0.01
Route of Transmission				
MSM transmission	1.00 (Reference)		1.00 (Reference)	
Injection drug use	0.59 (0.56, 0.63)	<0.01	2.07 (1.96, 2.19)	<0.01
Heterosexual transmission	0.81 (0.79, 0.83)	<0.01	1.38 (1.35, 1.41)	<0.01
Other	0.90 (0.87, 0.93)	<0.01	1.25 (1.21, 1.30)	<0.01
Time from HIV diagnosis to ART initiation (days)				
0–6	1.00 (Reference)		1.00 (Reference)	
7–30	0.98 (0.95, 1.00)	0.07	1.00 (0.97, 1.02)	0.77
31–360	0.87 (0.84, 0.89)	<0.01	1.14 (1.11, 1.17)	<0.01
>360	0.98 (0.95, 1.01)	0.17	1.07 (1.04, 1.10)	<0.01
Baseline CD4 cell count (cells/ μ L)				
200–349	1.00 (Reference)		1.00 (Reference)	
0–99	0.19 (0.18, 0.19)	<0.01	6.64 (6.50, 6.77)	<0.01
100–199	0.36 (0.35, 0.36)	<0.01	2.99 (2.93, 3.05)	<0.01
HBsAg				
Negative	1.00 (Reference)		1.00 (Reference)	
Positive	0.85 (0.83, 0.88)	<0.01	1.18 (1.14, 1.21)	<0.01
Missing/unknown	1.03 (1.00, 1.07)	0.04	0.97 (0.94, 0.99)	<0.01
Anti-HCV				
Negative	1.00 (Reference)		1.00 (Reference)	
Positive	0.91 (0.87, 0.95)	<0.01	1.14 (1.09, 1.20)	<0.01
Missing/unknown	0.93 (0.91, 0.96)	<0.01	1.08 (1.05, 1.12)	<0.01
ART Regimen				
Continuous NNRTI-based	1.00 (Reference)		1.00 (Reference)	
Continuous PI-based	1.54 (1.48, 1.60)	<0.01	0.66 (0.63, 0.69)	<0.01
Continuous INSTI-based	1.42 (1.32, 1.54)	<0.01	0.70 (0.65, 0.76)	<0.01
Switch from NNRTI to INSTI	1.23 (1.07, 1.42)	<0.01	0.76 (0.67, 0.87)	<0.01
Switch from NNRTI to PI	1.05 (0.93, 1.20)	0.41	1.02 (0.90, 1.16)	0.76

Abbreviation: HIV=human immunodeficiency virus; aOR=adjusted odds ratio; CI=confidence interval; INR=immunological nonresponse; PLWH=people living with HIV; ART=antiretroviral therapy; HBsAg=hepatitis B surface antigen; anti-HCV=antibody to hepatitis C virus; MSM=men who have sex with men; NNRTI=non-nucleoside reverse transcriptase inhibitor; PI=protease inhibitor; INSTI=integrase strand transfer inhibitor.

opportunistic infections, malignancies, and non-AIDS comorbidities, translating into two- to three-fold higher morbidity and mortality than those observed among immunological responders (2,6). By contrast, achieving favorable immune recovery ($CD4 \geq 500$ cells/ μ L) is associated with morbidity and mortality approaching those of HIV-negative individuals (2). In this large real-world cohort study from China, with over 5 years of follow-up, median CD4 cell counts increased steadily, and the CD4 distribution shifted from lower to higher strata, consistent with previous findings (6). Nevertheless, heterogeneity in immune reconstitution persisted despite virological suppression. The analysis showed that 35.5% of participants achieved ≥ 500 cells/ μ L (favorable immune recovery) and 34.7% met criteria for immunological non-response (INR). These proportions were generally comparable to those reported in previous studies (32.9% and 36.1%, respectively) (7). In multivariable analysis, baseline CD4 count was the strongest predictor of achieving $CD4 \geq 500$ cells/ μ L at year 5, consistent with reports from other settings. In a national laboratory-based analysis from South Africa, among PLWH who initiated ART with baseline $CD4 < 50$ cells/ μ L, 71% of participants did not recover to $CD4 \geq 200$ cells/ μ L by 12 months, and 39% of them did not reach this threshold during follow-up (8). Late ART initiation indicates advanced immune injury and is characterized by persistent immune activation and aberrant inflammation. Among people with a low baseline CD4 count, these abnormalities may not be fully resolved even after achieving virological suppression with ART. Individuals who initiate ART late often have a lower frequency of naïve $CD4^+$ T cells and a higher proportion of effector memory T cells. This pattern suggests a reduced pool for expansion and replenishment, thereby limiting the magnitude of subsequent $CD4^+$ T-cell recovery (2). Together, these findings support the current recommendations for the early diagnosis of HIV and prompt initiation of ART before profound CD4 depletion to maximize long-term immune recovery.

Older age at the time of ART initiation is associated not only with a reduced likelihood of achieving $CD4 \geq 500$ cells/ μ L but also with an increased risk of remaining at $CD4$ counts < 350 cells/ μ L and is consistent with established evidence (9–10). This impaired CD4 recovery persists despite effective virological suppression and is largely attributed to age-related thymic involution, which limits the production of naïve T cells. This immunological deficit

may be further exacerbated by suboptimal treatment adherence in older PLWH (9). Supporting this, the Polish cohort data demonstrated significantly better immune reconstitution when ART was initiated before the age of 35 (10). These findings underscore the urgent need for targeted strategies for older populations, including the promotion of early HIV diagnosis, timely ART initiation, and enhanced support in areas such as nutrition and comorbidity management.

The findings showed that PI- or INSTI-based regimens, as well as switching from an NNRTI-based to an INSTI-based regimen, were associated with higher odds of achieving favorable immune recovery ($CD4 \geq 500$ cells/ μ L). These associations are supported by previous studies. Protease inhibitors have been reported to suppress $CD4^+$ T-cell apoptosis by targeting the mitochondrial permeability transition pore complex (PTPC), independent of their antiviral effects on HIV replication (11–12). Other studies have shown that INSTIs are associated with better immune recovery, particularly in patients with advanced disease (13–14). In the analysis, the association appeared slightly stronger for PI-based than for INSTI-based therapy (aOR=1.54; 95% CI: 1.48, 1.60 vs. aOR=1.42; 95% CI: 1.32, 1.54). Because the study required at least 5 years of continuous treatment, INSTI-based regimens were uncommon in this cohort, and INSTI exposure may have been too limited to fully capture the potential immunologic benefits.

This study has several limitations. First, this observational study was subject to residual confounding from unmeasured factors, such as ART adherence, socioeconomic status, and nutritional status. Second, requiring CD4 measurements at both baseline and year 5 excluded participants who died or were lost to follow-up before 5 years, likely leading to an overestimation of CD4 recovery due to healthy survivor bias. Third, INSTI-based regimens were uncommon in this cohort, limiting the statistical power to evaluate the association between regimen class and immune recovery.

In summary, among PLWH with baseline $CD4 < 350$ cells/ μ L who achieved virologic suppression at year 5, most experienced substantial immune recovery; however, a considerable proportion remained in INR, highlighting marked heterogeneity in long-term immune reconstitution. These findings support the strengthening of early HIV diagnosis and timely ART initiation before a substantial CD4 decline. They also suggest the importance of risk-stratified long-term

immunologic monitoring and individualized management for patients at an increased risk of suboptimal immune recovery, including older individuals, those with low baseline CD4 counts, delayed ART initiation, HBsAg-positive or anti-HCV-positive status, and certain transmission groups. Additionally, integrated care and follow-up may improve long-term immune outcomes (15–16).

Conflicts of interest: No conflicts of interest.

Ethical statement: Approved by the Ethics Committee of the National Center for AIDS/STD Control and Prevention and the Chinese Center for Disease Control and Prevention (Approval No: KX230601731). The need for informed consent was waived because this study used routinely collected and deidentified data.

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REFERENCES

1. Acquired Immunodeficiency Syndrome Professional Group, Society of Infectious Diseases, Chinese Medical Association, Chinese Center for Disease Control and Prevention. Chinese guidelines for the diagnosis and treatment of human immunodeficiency virus infection/acquired immunodeficiency syndrome (2024 edition). *Infect Dis Immun* 2025;5(1):4 – 27. <https://doi.org/10.1097/ID9.0000000000000152>.
2. Yang XD, Su B, Zhang X, Liu Y, Wu H, Zhang T. Incomplete immune reconstitution in HIV/AIDS patients on antiretroviral therapy: challenges of immunological non-responders. *J Leukoc Biol* 2020;107(4):597 – 612. <https://doi.org/10.1002/JLB.4MR1019-189R>.
3. Wei L, Jia HL, Geng YX, Dou ZH, Zhao DC, Gan XM, et al. Trends in life expectancy of HIV-infected patients receiving antiretroviral therapy — China, 2013–2023. *China CDC Wkly* 2025;7(24):838–42. <http://dx.doi.org/10.46234/ccdcw2025.136>.
4. Mao YR, Wu ZY, Poundstone K, Wang CH, Qin QQ, Ma Y. Development of a unified web-based national HIV/AIDS information system in China. *Int J Epidemiol* 2010;39(S2):ii79–9. <http://dx.doi.org/10.1093/ije/dyq213>.
5. Arbaeen AF, Iqbal MS, Alsafi R, Almasmoum H, Qadhi A, Alharbi W, et al. Immuno-hematological profiles of HIV-positive patients stratified by CD4⁺ T-cell counts: toward identifying a surrogate hematological marker for immune suppression severity. *Diagnostics* 2025;15(23):2976. <https://doi.org/10.3390/diagnostics15232976>.
6. Liu JY, Wang LF, Hou YY, Zhao Y, Dou ZH, Ma Y, et al. Immune restoration in HIV-1-infected patients after 12 years of antiretroviral therapy: a real-world observational study. *Emerg Microbes Infect* 2020;9(1):2550 – 61. <https://doi.org/10.1080/22221751.2020.1840928>.
7. Chen LY, Liu CH, Kang S, Du LY, Ma FH, Li CM, et al. Determinants of suboptimal immune recovery among a Chinese Yi ethnicity population with sustained HIV suppression. *BMC Infect Dis* 2022;22(1):137. <https://doi.org/10.1186/s12879-022-07113-y>.
8. Kufa T, Shubber Z, MacLeod W, Takuva S, Carmona S, Bor J, et al. CD4 count recovery and associated factors among individuals enrolled in the South African antiretroviral therapy programme: an analysis of national laboratory based data. *PLoS One* 2019;14(5):e0217742. <https://doi.org/10.1371/journal.pone.0217742>.
9. Chen JX, Titanji K, Sheth AN, Gandhi R, McMahon D, Ofotokun I, et al. The effect of age on CD4⁺ T-cell recovery in HIV-suppressed adult participants: a sub-study from AIDS Clinical Trial Group (ACTG) A5321 and the Bone Loss and Immune Reconstitution (BLIR) study. *Immun Ageing* 2022;19(1):4. <https://doi.org/10.1186/s12979-021-00260-x>.
10. Lembas A, Załęski A, Mikuła T, Dyda T, Stańczak W, Wiercińska-Drapała A. Evaluation of clinical biomarkers related to CD4 recovery in HIV-infected patients – 5-year observation. *Viruses* 2022;14(10):2287. <https://doi.org/10.3390/v14102287>.
11. Marin RC, Behl T, Negrut N, Bungau S. Management of antiretroviral therapy with boosted protease inhibitors—darunavir/ritonavir or darunavir/cobicistat. *Biomedicines* 2021;9(3):313. <https://doi.org/10.3390/biomedicines9030313>.
12. Phenix BN, Lum JJ, Nie ZL, Sanchez-Dardon J, Badley AD. Antiapoptotic mechanism of HIV protease inhibitors: preventing mitochondrial transmembrane potential loss. *Blood* 2001;98(4):1078 – 85. <https://doi.org/10.1182/blood.v98.4.1078>.
13. Bono V, Marchetti GC. Immunological recovery with BIC/FTC/TAF: CD4 T-cell count and CD4/CD8 ratio as markers of response. *New Microbiol* 2025;48(1):1–4. <https://pubmed.ncbi.nlm.nih.gov/40314675/>.
14. Alzate-Angel JC, Loaiza JD, Perdomo-Celis F, Hernandez JC, Galindo-Orrego X, Mantilla-Suárez M, et al. Benefits of INSTI-based regimens in a real-world setting of people living with HIV-1 in Colombia. *Int J Microbiol* 2025;2025:9081023. <https://doi.org/10.1155/ijm/9081023>.
15. Zhao Y, Wu ZY, McGoogan JM, Sha YY, Zhao DC, Ma Y, et al. Nationwide cohort study of antiretroviral therapy timing: treatment dropout and virological failure in China, 2011–2015. *Clin Infect Dis* 2019;68(1):43 – 50. <https://doi.org/10.1093/cid/ciy400>.
16. Chen DL, Chen QH, Lin MZ. Retrospective analysis of factors influencing immunologic failure among people living with HIV on antiretroviral therapy. *AIDS Care* 2025;37(9):1475 – 81. <https://doi.org/10.1080/09540121.2025.2534541>.

Vital Surveillances

Epidemiological Characteristics and Spatiotemporal Cluster Analysis of Multidrug-Resistant and Rifampicin-Resistant Tuberculosis Among Older People — China, 2019–2025

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ABSTRACT

Introduction: Multidrug- and rifampicin-resistant tuberculosis (MDR/RR-TB) in older individuals remains a significant public health challenge in China. This study evaluated the epidemiological characteristics and spatiotemporal patterns of MDR/RR-TB in individuals aged ≥ 65 years in China between 2019 and 2025.

Methods: Data were obtained from the China Information System for Disease Control and Prevention (CISDCP). Spatiotemporal distribution and demographic characteristics of MDR/RR-TB cases in China were analyzed using descriptive epidemiological methods. Global Moran's I and local indicators of spatial association were employed to assess spatial clustering, and spatiotemporal scanning was performed using the SaTScan software to detect high-risk clusters.

Results: From 2019 to 2025, 21,569 patients with MDR/RR-TB aged ≥ 65 years were registered across 31 provincial-level administrative divisions nationwide [1.72% of all pulmonary tuberculosis (PTB) in older patients]. The notification rate of MDR/RR TB among older people declined in 2022 and then rebounded in 2025. The proportion of MDR/RR-TB among older patients with PTB increased. The patients were predominantly male (73.3%) in the 65–69-year age group. Of the cases, 46.0% were retreated, and 83.3% underwent molecular diagnostic testing. Heilongjiang and Gansu were persistent high-high cluster areas, whereas Xinjiang presented the highest risk. Spatiotemporal scanning identified significant clusters in Xinjiang, the three northeastern provinces, Chongqing-Guizhou, and Ningxia-Shaanxi-Gansu.

Conclusions: The proportion of MDR/RR-TB among older patients with PTB in China increased significantly. The clusters were mainly located in the central-western and northeastern regions. We recommend strengthening drug resistance surveillance,

expanding molecular testing coverage in high-risk areas, and optimizing treatment strategies for retreated patients.

China is among the countries with the highest burden of drug-resistant tuberculosis globally. In 2024, newly diagnosed multidrug-resistant and rifampicin-resistant tuberculosis (MDR/RR-TB) cases in China will account for approximately 7.1% of the global total and rank second worldwide (1). China's population is rapidly aging. In 2024, the number of people aged ≥ 65 years reached 220 million (15.6% of the total population), making China a veritable aging society. Older adults are particularly vulnerable to TB because of their declining immune function, multiple comorbidities, and prior *Mycobacterium tuberculosis* infections (2). MDR/RR-TB poses even greater challenges for this population, including complex treatment regimens, a high incidence of adverse reactions, and poor outcomes (3).

Previous studies have focused primarily on MDR/RR-TB in the general population or in specific regions (4–6), with limited nationwide research on the epidemiological patterns and spatiotemporal distribution of drug-resistant tuberculosis in older patients. Thus, this study analyzed the epidemiological characteristics, spatial distribution, and spatiotemporal clustering of MDR/RR-TB among older adults in China from 2019 to 2025.

METHODS

Data Source

Data on older patients with MDR/RR-TB from 31 provincial-level administrative divisions (PLADs) in China (2019–2025) were obtained from the China Information System for Disease Control and Prevention (CISDCP). All personal identifiers were

removed to ensure anonymity and only aggregated provincial data were used. Data on age, sex, residence, treatment history, drug sensitivity diagnostic type, and drug sensitivity testing methods were collected. All cases were diagnosed according to the Chinese national health industry standard, "Diagnosis for Pulmonary Tuberculosis (WS 288-2017)" (7). As the study involved the analysis of de-identified secondary surveillance data, ethical approval and informed consent were waived in accordance with national regulations. Detailed information on the data reporting specifications, quality control, data cleaning, and drug resistance detection methods is provided in Supplementary Material (available at <https://weekly.chinacdc.cn/>).

Global Moran's *I* and local indicators of spatial association (LISA) were used to evaluate spatial autocorrelation. The LISA results were classified into -high, -low, high-, and -low, with statistical significance assessed at $P < 0.05$ after 999 permutations. For spatiotemporal cluster detection, we performed a retrospective scan using SaTScan (version 10.2.5; Martin Kulldorff, Boston, MA, USA) based on a discrete Poisson model. The maximum spatial cluster size was set to 50% of the at-risk population and the maximum temporal cluster size was set to 50% of the study period. Statistical significance was assessed using 999 Monte Carlo replications, and clusters with $P < 0.05$ were considered statistically significant. All statistical analyses were performed using the R (version 4.2.1; R Foundation, Vienna, Austria). Spatial mapping was conducted using the ArcGIS Desktop software (version 10.8; Esri, Redlands, California, USA).

RESULTS

Sociodemographic Characteristics

From 2019 to 2025, 21,569 older patients with MDR/RR-TB were registered among the 31 PLADs in China. The population comprised 15,817 men (73.3%) and 5,752 women (26.7%), with a male-to-female ratio of 2.7:1. The mean age was 71.5 ± 6.6 years, with the largest proportion of cases (41.0%) occurring in the 65–69-year age group, followed by the 70–74-year age group (29.6%), 75–79-year age group (17.6%), and ≥ 80 -year age group (11.7%).

Most cases (90.5%) involved local residents, whereas the migrant population accounted for only 9.5%. Nearly half of patients (46.0%) had a history of prior

tuberculosis treatment. Molecular diagnostics were the primary method for detecting rifampicin resistance, which was used in 83.3% of cases (Table 1).

Temporal Trends

Between 2019 and 2022, the registration rate for pulmonary tuberculosis (PTB) among older individuals (≥ 65 years) in China declined significantly from 114.46 to 79.98 per 100,000 (average annual decline, 11.26%). Over the same period, the registration rate of MDR/RR-TB in this population decreased from 1.79 to 1.14 per 100,000 people (average annual decline, 13.96%). From 2023 to 2025, both rates rebounded. The PTB registration rate increased to 90.68 per 100,000 (average annual decline, 0.61%) over the full period. By contrast, the MDR/RR-TB registration rate increased to 1.79 per 100,000 (average annual growth rate, 4.16%) (Figure 1A).

The proportion of MDR/RR-TB among older patients with PTB declined from 1.57% to 1.43% between 2019 and 2022, then increased to 1.97% in 2025, representing a 25.7% increase from the 2019 level (Figure 1B).

TABLE 1. General characteristics of registered MDR/RR-TB cases among adults aged ≥ 65 years in PLADs in China (2019–2025).

Characteristic	Total (N=21,569), n (%)
Age (years)	
65–69	8,854 (41.0)
70–74	6,382 (29.6)
75–79	3,806 (17.6)
≥ 80	2,527 (11.7)
Sex	
Male	15,817 (73.3)
Female	5,752 (26.7)
Residence	
Local	19,524 (90.5)
Migrant	2,045 (9.5)
Treatment history	
New	11,657 (54.0)
Retreated	9,912 (46.0)
Drug sensitivity diagnostic type	
Molecular	17,971 (83.3)
Phenotypic	3,598 (16.7)

Abbreviation: MDR/RR-TB=multidrug-resistant and rifampicin-resistant tuberculosis; PLADs=provincial-level administrative division.

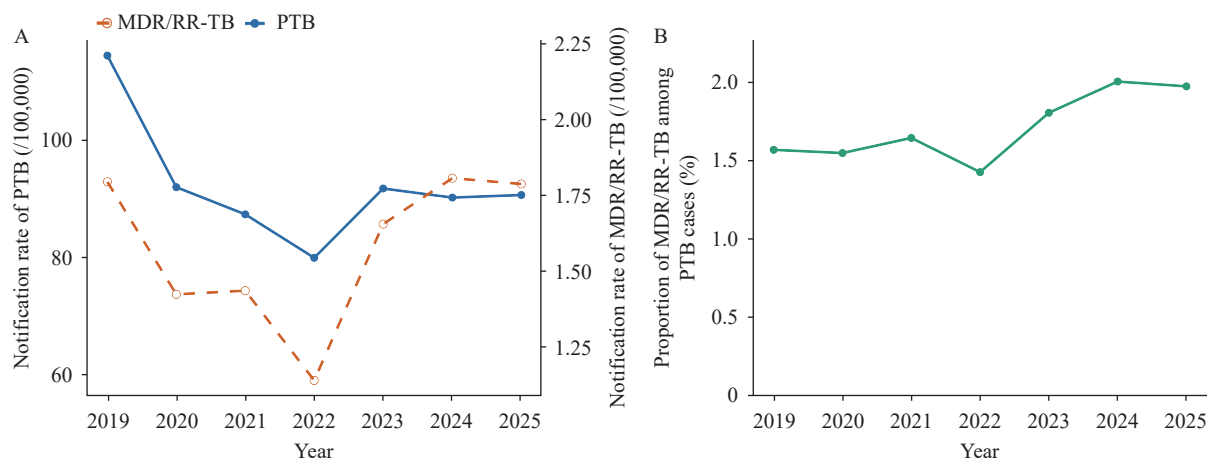


FIGURE 1. Registration trend of PTB and MDR/RR-TB among adults aged ≥ 65 years in PLADs in China (2019–2025). (A) Notification rate of PTB and MDR/RR-TB; (B) MDR/RR-TB proportion in notified PTB cases.

Note: In panel A, the left y-axis (blue) shows the notification rate of PTB per 100,000 population aged ≥ 65 years; the right y-axis (orange) shows the notification rate of MDR/RR-TB per 100,000 population aged ≥ 65 years. Solid lines with filled circles represent PTB and dashed lines with open circles represent MDR/RR-TB. The notification rate was calculated as follows: (notified cases in a given year/mid-year population aged ≥ 65 years) $\times 100,000$. In panel B, the solid line with filled circles indicates the proportion of MDR/RR-TB among notified PTB cases, calculated as (notified MDR/RR-TB cases $\div$ notified PTB cases) $\times 100\%$.

Abbreviation: PTB=pulmonary tuberculosis; MDR/RR-TB=multidrug- and rifampicin-resistant tuberculosis; PLADs=provincial-level administrative divisions; TB=tuberculosis.

Spatial Analysis

From 2019 to 2025, provincial MDR/RR-TB notification rates exhibited marked spatial heterogeneity and temporal dynamics. Global Moran's I values ranged from 0.058 to 0.486 across years, with significant positive spatial autocorrelation detected in all years, except 2022 ($P=0.195$) (all $P<0.05$) (Table 2).

LISA analysis revealed that high-high clusters were primarily distributed in Heilongjiang Province (persisting throughout 2019–2025) and Gansu Province (2019, 2020, 2021, 2023, 2024, and 2025), with further expansion to Xinjiang, Xizang, and Qinghai in 2020. Low-high clusters were observed in Sichuan (2020), Xizang (2021), Anhui (2023), Qinghai (2024), and Inner Mongolia (2025). The low-low clusters included multiple central-eastern provinces, including Jiangsu, Anhui, Shandong, Henan, Hebei, and Zhejiang (Table 2). In addition, Anhui Province exhibited a high-low clustering pattern in 2022.

Spatiotemporal Cluster Analysis

The SaTScan spatiotemporal scanning analysis identified 10 statistically significant high-rate clusters from 2019 to 2025 (Table 3). The cluster with the highest relative risk was Xinjiang [2019–2021, relative risk (RR)=7.92], followed by another cluster in

Xinjiang (2023–2024, $RR=7.45$). The three northeastern provinces had two clusters (2023–2025, $RR=2.51$; 2019–2021, $RR=1.89$). Chongqing and Guizhou formed a cluster (2023–2025, $RR=2.28$), whereas Chongqing alone constituted a cluster (2019–2021, $RR=2.13$). The Ningxia-Shaanxi-Gansu region has two clusters (2024–2025, $RR=1.72$; 2019–2020, $RR=1.49$). Jiangxi (2024–2025, $RR=1.49$) and Anhui (2023–2024, $RR=1.34$) were identified as clusters (Table 3).

DISCUSSION

The proportion of MDR/RR-TB among PTB cases increased from 1.57% to 1.97%, with notification rates declining more slowly than those of PTB. MDR/RR-TB exhibited distinct spatiotemporal clustering: Heilongjiang and Gansu were persistent high-burden areas, Xinjiang presented the highest risk, the three northeastern provinces showed recurrent clustering, and Anhui and other eastern provinces emerged as hotspots.

Temporal trend analysis revealed that the notification rates for both PTB and MDR/RR-TB among older adults declined rapidly from 2019 to 2022. Although China launched the "Action Plan to Stop Tuberculosis (2019–2022)," prioritizing drug-resistant tuberculosis and emphasized enhanced

TABLE 2. Global and local spatial autocorrelation of MDR/RR-TB notification rates among adults aged ≥ 65 years in PLADs in China (2019–2025).

Year	Global aggregation analysis			Localized areas of aggregation			
	Moran's <i>I</i>	Z	P	High–high agglomeration	High–low agglomeration	Low–high agglomeration	Low–low agglomeration
2019	0.058	2.016	0.044	Gansu Heilongjiang Xinjiang Xizang Qinghai			Jiangsu Anhui Jiangsu Anhui
2020	0.486	4.965	<0.001	Gansu Heilongjiang Gansu Heilongjiang		Sichuan	Shandong Henan Hebei
2021	0.220	2.409	0.016	Gansu Heilongjiang	Anhui	Xizang	Henan Hebei
2022	0.108	1.294	0.195	Heilongjiang			Shanxi Hebei
2023	0.174	2.205	0.027	Heilongjiang			Hebei
2024	0.104	1.469	0.142	Heilongjiang			
2025	0.375	3.531	<0.001	Heilongjiang Jilin		Inner Mongolia	Jiangsu Anhui Shandong

Abbreviation: MDR/RR-TB=multidrug-resistant and rifampicin-resistant tuberculosis; PLADs=provincial-level administrative divisions.

TABLE 3. Spatiotemporal clusters of MDR/RR-TB notification rates among adults aged ≥ 65 years in PLADs in China (2019–2025).

Cluster number	PLADs (location IDs)	Time (year)	Number of MDR/RR-TB cases	Expected cases	RR	LLR	P
1	Xinjiang	2019–2021	816	106.49	7.92	964.025	<0.001
3	Jilin Liaoning Heilongjiang	2023–2025	2,062	871.73	2.51	619.914	<0.001
1	Xinjiang	2023–2024	451	61.66	7.45	511.592	<0.001
2	Chongqing Guizhou Jilin	2023–2025	1,115	503.30	2.28	284.167	<0.001
3	Liaoning Heilongjiang	2019–2021	1,354	740.10	1.89	213.101	<0.001
1	Chongqing	2019–2021	483	229.78	2.13	107.109	<0.001
3	Ningxia Shaanxi Gansu	2024–2025	541	317.98	1.72	65.661	<0.001
3	Ningxia Shaanxi Gansu	2019–2020	389	262.05	1.49	27.099	<0.001
1	Jiangxi	2024–2025	283	190.87	1.49	19.530	<0.001
1	Anhui	2023–2024	402	302.22	1.34	15.143	<0.001

Abbreviation: RR=relative risk; LLR=log likelihood ratio; MDR/RR-TB=multidrug-resistant and rifampicin-resistant tuberculosis; PLADs=provincial-level administrative divisions.

screening, the coronavirus disease 2019 (COVID-19) pandemic (2020–2022) severely disrupted timely medical consultations for individuals with suspected TB cases, resulting in a substantial decline in case detection, especially among older individuals (8). After the pandemic ended in 2023, notification rates for both conditions rebounded, with MDR/RR-TB recovering faster than PTB, resulting in an approximately 25% increase in the proportion of MDR/RR-TB among older patients with tuberculosis

compared to 2019. Although molecular diagnostics have been increasingly used since 2019 (Supplementary Table S1, available at <https://weekly.chinacdc.cn/>), their detection effect was masked during the pandemic owing to reduced healthcare access. This divergence may be attributed to post-pandemic recovery of diagnostic services that led to catch-up detection of previously missed MDR/RR-TB cases and pandemic-related treatment interruptions that likely increased acquired resistance among retreatment

patients. Although PTB detection has stabilized, the number of MDR/RR-TB cases has continued to increase, suggesting differing transmission dynamics between drug-resistant and drug-sensitive TB. Therefore, TB control efforts should prioritize older patients with MDR/RR-TB, focusing on standardized management and drug resistance screening, especially among retreatment patients.

Of the older patients with MDR/RR-TB, 73.3% were male, and 41.0% were aged 65–69 years, consistent with data reported in China (9). A higher proportion of men may be linked to increased exposure to *M. tuberculosis* (10), whereas the predominance of the 65–69-year age group may reflect an elevated risk of latent infection reactivation and a higher prevalence of comorbidities such as diabetes (11–12). Molecular diagnostics accounted for 83.3% of the detections, highlighting the significant role of technologies such as GeneXpert MTB/RIF in identifying drug-resistant cases (13).

Drug resistance in tuberculosis is clinically classified into primary resistance, which is more common among new patients, and acquired resistance, which is typically observed in retreatment cases. In this study, 54.0% of the older patients with MDR/RR-TB were new cases, whereas 46.0% were retreatment cases. The high proportion of new cases suggests the substantial burden of primary resistance in this population. However, without molecular epidemiological data, determining whether this reflects recent transmission, endogenous reactivation, or reinfection remains challenging, especially considering the high latent infection rate in the older population. Meanwhile, 46.0% of the patients were retreated, indicating that treatment failure or improper treatment remains significant (14–15). Therefore, prevention and control require strengthening early and rapid screening of all newly diagnosed patients to ensure timely initiation of appropriate treatment, while simultaneously enhancing standardized retreatment regimens and case management to improve adherence and prevent further development of acquired resistance.

The spatial distribution of MDR/RR-TB notification rates showed significant clustering. Heilongjiang and Gansu were persistent high-high cluster areas. In Heilongjiang, the contributing factors may include a cold climate, prolonged indoor gatherings, a high proportion of the older population, limited primary-level detection capacity, and the ongoing transmission of resistant strains. This clustering is partly attributable to a substantial burden

of retreatment cases, among which 61.5% of patients with MDR/RR-TB had received retreatment and 60.3% had experienced non-standard hospitalization (16). In Gansu, economic underdevelopment, uneven healthcare distribution, and poverty are likely contributors. In 2020, high-high clusters extended westward to Xinjiang, Xizang, and Qinghai, which were likely influenced by the pandemic. During its early phase, the western regions, which were less affected by strict control measures, maintained relatively stable case detection rates, resulting in higher notification rates than regions with more significant declines. Xinjiang exhibited the highest risk ($RR=7.92$), which was attributable to its heavy baseline burden and active screening strategies (17). The three northeastern provinces formed clusters in both 2019–2021 and 2023–2025, with the latter potentially linked to release of accumulated cases and ongoing transmission. Other regions (Chongqing, Guizhou, Ningxia, Shaanxi, Gansu, Jiangxi, and Anhui) also exhibited clustering, although at a lower risk. Multiple central-eastern provinces exhibited low-low clustering, forming a stable low-burden belt associated with better economic development and healthcare accessibility (18).

This study has some limitations. Passive surveillance may result in under-reporting or diagnostic delays. In addition, provincial-level analysis could not identify intra-provincial clusters; prefecture-level analysis was limited by low case counts and was therefore not conducted, as the results would be unstable. Future studies should address prefecture-level heterogeneity within hotspot provinces as data accumulate.

A shifting epidemiological landscape of MDR/RR-TB was observed among older individuals in China. Following the COVID-19 pandemic, notification rates rebounded rapidly, and drug resistance proportions continued to increase, with significant clustering in the central-western and northeastern regions. Current risk patterns included persistent high-high clusters in Heilongjiang and Gansu, extremely high risk in Xinjiang, recurrent clustering in the three northeastern provinces, and emerging hotspots in the eastern provinces. Therefore, we recommend implementing differentiated control strategies within a risk-stratified framework, investigating the drivers of sustained transmission, developing region-specific action plans, and adopting tailored measures (enhanced surveillance, active screening, and optimized treatment) for different cluster types. These strategies emphasize moving beyond a "one-size-fits-all" model to address the complex heterogeneity of MDR/RR-TB across spatial,

temporal, and demographic dimensions.

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REFERENCES

- World Health Organization. Global tuberculosis report 2025. Geneva: World Health Organization; 2025. <https://www.who.int/publications/item/9789240116924>.
- Liu HC, Zou LP, Yu JJ, Zhu QD, Yang S, Kang WL, et al. Treatment outcomes and associated influencing factors among elderly patients with rifampicin-resistant tuberculosis: a multicenter, retrospective, cohort study in China. *BMC Infect Dis* 2025;25(1):1086. <https://doi.org/10.1186/s12879-025-11491-4>.
- Dheda K, Gumbo T, Gandhi NR, Murray M, Theron G, Udwadia Z, et al. Global control of tuberculosis: from extensively drug-resistant to untreatable tuberculosis. *Lancet Respir Med* 2014;2(4):321 – 38. [https://doi.org/10.1016/S2213-2600\(14\)70031-1](https://doi.org/10.1016/S2213-2600(14)70031-1).
- Su W, Ruan YZ, Li T, Du X, Jiang JW, Li RZ. Characteristics of rifampicin-resistant tuberculosis detection in China, 2015–2019. *Infect Dis Poverty* 2021;10(1):99. <https://doi.org/10.1186/s40249-021-00883-8>.
- Xian SL, Yu Y, Chen J, Wu B, Wu CG, Fan J, et al. Spatiotemporal distribution and time-series analysis of rifampicin-resistant tuberculosis in Chongqing Municipality, China. *Public Health* 2025;242:165 – 71. <https://doi.org/10.1016/j.puhe.2025.03.002>.
- Wang Y, Chen HJ, Liao L, Lu XL, Zhang AH. Time trend prediction and spatial-temporal analysis of multidrug-resistant tuberculosis in Guizhou Province, China, during 2014–2020. *BMC Infect Dis* 2022;22(1):525. <https://doi.org/10.1186/s12879-022-07499-9>.
- National Health Commission of the People's Republic of China. WS 288-2017 Diagnosis for pulmonary tuberculosis. Beijing: Standards Press of China, 2017. <http://www.nhc.gov.cn/wjw/s9491/201712/a452586fd21d4018b0ebc00b89c06254.shtml>. [2026-4-14]. (In Chinese).
- Li T, Du X, Kang JJ, Luo D, Liu XQ, Zhao YL. Patient, diagnosis, and treatment delays among tuberculosis patients before and during COVID-19 epidemic — China, 2018–2022. *China CDC Wkly* 2023;5(12):259 – 65. <https://doi.org/10.46234/ccdcw2023.047>.
- Liu YS, Fan MK, Li YH, Kang JJ, A Y, Yan TX, et al. Patient delay in the diagnosis of pulmonary tuberculosis in the elderly — China, 2015–2023. *China CDC Wkly* 2024;6(42):1075 – 9. <https://doi.org/10.46234/ccdcw2024.221>.
- Rickman HM, Phiri MD, Feasey HRA, Krutikov M, Shao H, Horton KC, et al. Sex differences in the risk of *Mycobacterium tuberculosis* infection: a systematic review and meta-analysis of population-based immunoreactivity surveys. *Lancet Public Health* 2025;10(7):e588 – 98. [https://doi.org/10.1016/S2468-2667\(25\)00120-3](https://doi.org/10.1016/S2468-2667(25)00120-3).
- Wang X, Song Y, Li N, Huo JY, Wang BB, Jiang X, et al. Elderly patients with tuberculosis combined with diabetes mellitus: a comprehensive analysis of lymphocyte subpopulation dynamics, clinical features, drug resistance and disease regression. *Int J Gen Med* 2025;18: 1271 – 82. <https://doi.org/10.2147/IJGM.S502996>.
- Romero-Rodríguez DP, Díaz-Alvarado CA, Rocha-González HI, Juárez E. Control of *Mycobacterium tuberculosis* infection in the elderly: is there a role for epigenetic reprogramming reversal? *Biofactors* 2025;51(1): e2151. <http://dx.doi.org/10.1002/biof.2151>.
- Steyn J, Williams J, Naufal F, Limberis J, Grobbelaar M, Ismail N, et al. Bedaquiline resistance in patients with Xpert MTB/RIF ultra-tested rifampicin-resistant tuberculosis in the Western Cape, South Africa: a prospective study. *Lancet Microbe* 2026;7(3):101293. <https://doi.org/10.1016/j.lanmic.2025.101293>.
- Wang XY, Shang AQ, Chen HW, Li J, Jiang Y, Wang LL, et al. Global, regional, and national disease burden of multidrug-resistant tuberculosis without extensive drug resistance, 1990–2021: Findings from the Global Burden of Disease Study 2021. *Drug Resist Updat*. 2025; 82:101265. <http://doi.org/10.1016/j.drug.2025.101265>.
- Nair SA, Raizada N, Sachdeva KS, Denkinger C, Schumacher S, Dewan P, et al. Factors associated with tuberculosis and rifampicin-resistant tuberculosis amongst symptomatic patients in India: a retrospective analysis. *PLoS One* 2016;11(2):e0150054. <https://doi.org/10.1371/journal.pone.0150054>.
- Li D, Wang JL, Ji BY, Cui JY, Pan XL, Fan CL, et al. Persistently high prevalence of primary resistance and multidrug resistance of tuberculosis in Heilongjiang Province, China. *BMC Infect Dis* 2016;16(1):516. <https://doi.org/10.1186/s12879-016-1848-9>.
- Zhang Y, Wang XQ, Liu NQ, Wang SL, Wang XM, Cao MQ. Intervention effect of new tuberculosis control model on tuberculosis incidence in Xinjiang. *Infect Drug Resist* 2023;16:7485 – 96. <https://doi.org/10.2147/IDR.S441899>.
- Lv HL, Chen H, Zhang XL, Li X, Liu LS, Dang CX, et al. Analyzing factors affecting tuberculosis incidence in various mainland Chinese economic regions and predicting trends: a comprehensive regression study. *BMC Public Health* 2025;25(1):3282. <https://doi.org/10.1186/s12889-025-24575-2>.

SUPPLEMENTARY MATERIAL

Data Reporting Specifications, Data Cleaning, Quality Control, and Drug Resistance Detection Methods

Data reporting and management: Designated institutions are required to complete case registration within 24 hours of diagnosis and enter follow-up and treatment outcome data within 48 h. The China Information System for Disease Control and Prevention (CISDCP) incorporates automated logic checks and duplication detection to ensure data integrity.

Data cleaning and quality control: Laboratory quality control strictly adheres to the guidelines outlined in China's "National Technical Specifications for Tuberculosis Prevention and Control" (2020 edition). For data cleaning, records with the following issues were excluded to ensure accuracy and consistency:

1. Identification of non-tuberculous mycobacteria (NTM) cases.
2. Contradictory drug susceptibility testing (DST) results, such as cases labeled "sensitive" despite evidence of resistance.
3. Cases exhibiting isoniazid monoresistance were excluded to focus on MDR/RR-TB.

Drug resistance detection methods: According to the National Tuberculosis Control Program (NTP), rifampicin drug susceptibility testing (DST) is universally recommended for all patients with bacteriologically confirmed pulmonary tuberculosis.

The primary detection methods were as follows:

1. Molecular diagnostic methods for rapid detection include GeneXpert MTB/RIF and line probe assays.
2. Phenotypic DST methods, including the proportion method and absolute concentration method, performed on *Mycobacterium tuberculosis* strains isolated from culture.

In China, DST coverage among patients with bacteriologically confirmed TB increased from 81.8% in 2019 to over 90% during 2020–2025, reflecting substantial improvement in detection capacity.

Molecular biology testing includes rapid molecular diagnostics such as GeneXpert MTB/RIF and line probe assays. Traditional phenotypic DST refers to culture-based methods such as the proportion method and absolute concentration method. Molecular testing proportion (%) = (molecular biology testing / total DST) × 100%.

SUPPLEMENTARY TABLE S1. Annual drug susceptibility testing methods for MDR/RR-TB cases among older individuals aged ≥65 years in China (2019–2025).

Year	Molecular biology testing (n)	Traditional phenotypic DST (n)	Total DST (n)	Molecular testing proportion (%)
2019	2029	935	2,964	68.45
2020	1,850	666	2,516	73.53
2021	2,069	674	2,743	75.43
2022	1,851	405	2,256	82.05
2023	2,960	452	3,412	86.75
2024	3,514	305	3,819	92.01
2025	3,665	194	3,859	94.97

Abbreviation: DST=drug susceptibility testing; MDR/RR-TB=multidrug- and rifampicin-resistant tuberculosis.

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.

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.

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

Malaria remains a major global health challenge. Despite previous progress, the Greater Mekong Sub-region (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 County 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)	$\chi^2=1.207$	0.272	472 (72.50)	698 (70.65)	$\chi^2=0.574$	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)	$\chi^2=12.699$	<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*.

* 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).

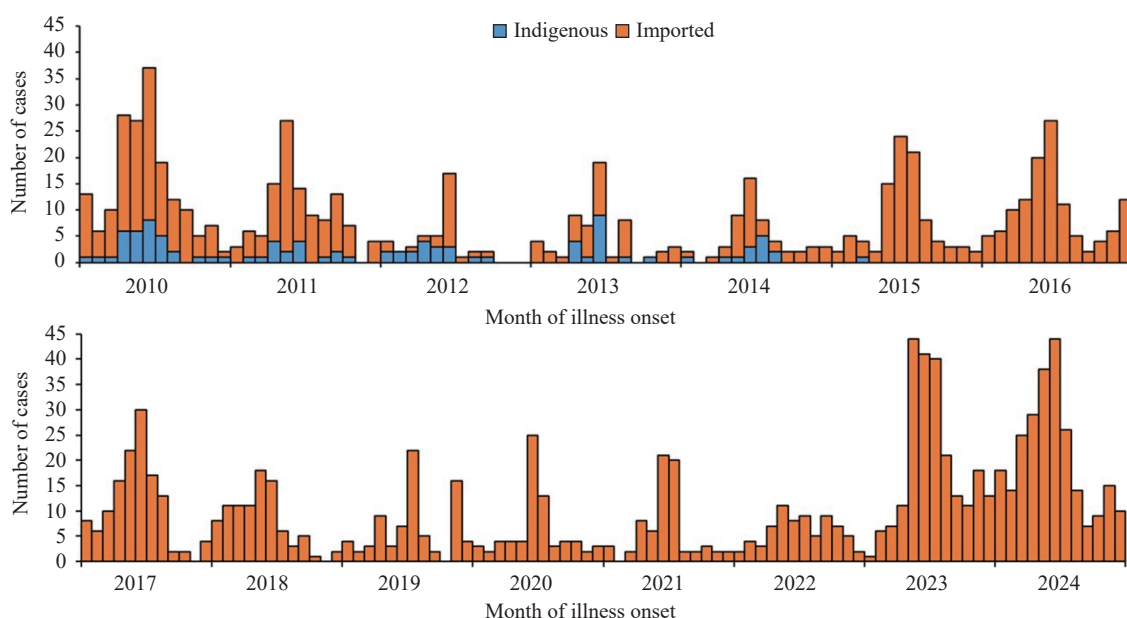


FIGURE 1. Temporal distribution of *Plasmodium vivax* cases in Yingjiang County, Yunnan Province, 2010–2024.

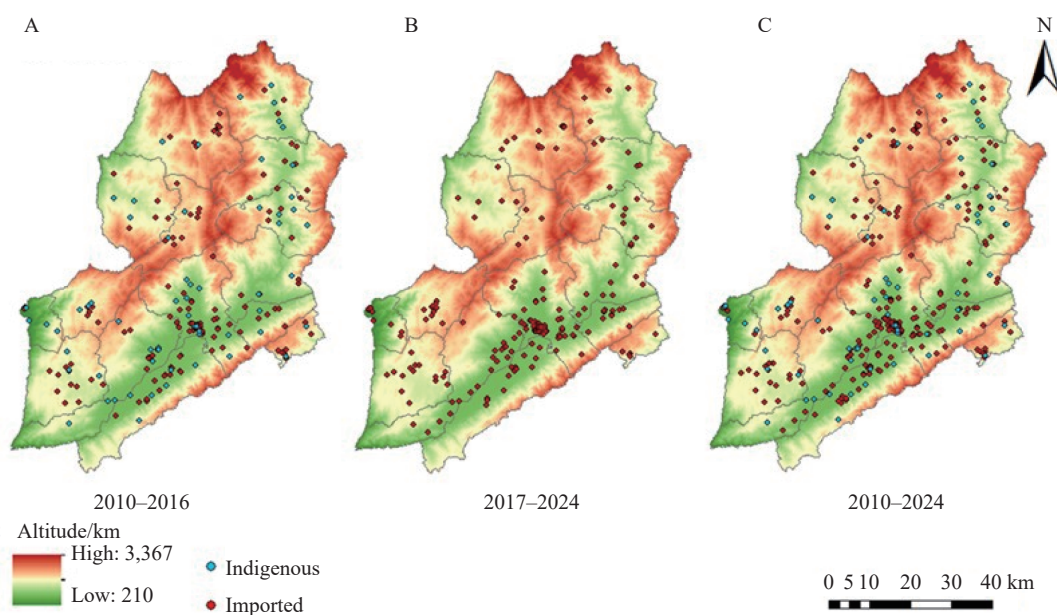


FIGURE 2. Spatial patterns of *Plasmodium vivax* cases in Yingjiang County during (A) 2010–2016, (B) 2017–2024, and (C) 2010–2024.

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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 [\[weekly.chinacdc.cn/\]\(http://weekly.chinacdc.cn/\)\). Statistical significance \(\$P<0.05\$, two-sided\) was determined using R software \(version 4.3.1, R Core Team, Vienna, Austria\) and ArcGIS software \(version 10.8, Esri, Redlands, USA\).](http://</p>
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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 ($\chi^2=1.207$, $P=0.272$) or between elimination phases ($\chi^2=0.574$, $P=0.449$). 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%; $\chi^2=17.955$, $P<0.005$) 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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REFERENCES

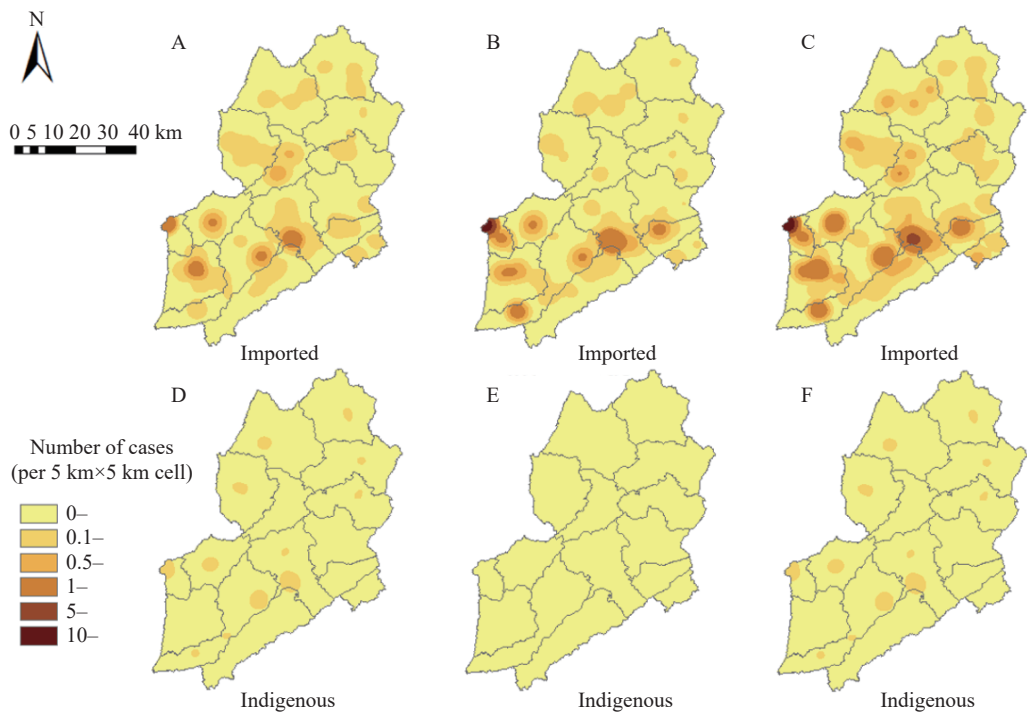
1. APLMA. Elimination in the greater mekong subregion. 2026. <https://www.aplma.org/blog/elimination-in-the-greater-mekong-subregion>. [2026-4-2].
2. World Health Organization. World malaria report 2025: addressing the threat of antimalarial drug resistance. Geneva: World Health Organization; 2025. <https://www.who.int/publications/i/item/9789240117822>.
3. Zhu Y, Restrepo AC, Wang HB, Mills DJ, Liang RR, Liu ZB, et al. Malaria cases in China acquired through international travel, 2013–2022. *J Travel Med* 2024;31(8):taae056. <https://doi.org/10.1093/jtm/taae056>.
4. Yin JH, Zhang L, Yi BY, Zhou SS, Xia ZG. Imported malaria from land bordering countries in China: a challenge in preventing the reestablishment of malaria transmission. *Travel Med Infect Dis* 2023;53:102575. <https://doi.org/10.1016/j.tmaid.2023.102575>.
5. Manzoni G, Try R, Guintran JO, Christiansen-Jucht C, Jacoby E, Sovannaroeth S, et al. Progress towards malaria elimination in the Greater Mekong Subregion: perspectives from the World Health Organization. *Malar J* 2024;23(1):64. <https://doi.org/10.1186/s12936-024-04851-z>.
6. Tian P, Li SG, Zhou YW, Lin ZR, Sun XD, Guo XR, et al. Cooperative sentinel surveillance of malaria in Laiza and nearby areas of Myanmar and importation threat monitoring — China, 2019–2023. *China CDC Wkly* 2024;6(17):378 – 82. <https://doi.org/10.46234/ccdcw2024.073>.
7. Li QL, Liu T, Lv KY, Liao FL, Wang JG, Tu YY, et al. Malaria: past, present, and future. *Signal Transduct Target Ther* 2025;10(1):188. <https://doi.org/10.1038/s41392-025-02246-3>.
8. Lai SJ, Sun JL, Ruktanonchai NW, Zhou S, Yu JX, Routledge I, et al. Changing epidemiology and challenges of malaria in China towards elimination. *Malar J* 2019;18(1):107. <https://doi.org/10.1186/s12936-019-2736-8>.
9. Lu SN, Ding W, Wang JZ, Yin SQ, Li SG, Zhou XW, et al. Application of an innovative grid-based surveillance strategy to ensure elimination and prevent reintroduction of malaria in high-risk border communities in China. *BMC Public Health* 2022;22(1):1347. <https://doi.org/10.1186/s12889-022-13753-1>.
10. Yang S, Li RY, Yan SN, Yang HY, Cao ZY, Zhang L, et al. Risk assessment of imported malaria in China: a machine learning perspective. *BMC Public Health* 2024;24(1):865. <https://doi.org/10.1186/s12889-024-17929-9>.

SUPPLEMENTARY MATERIAL

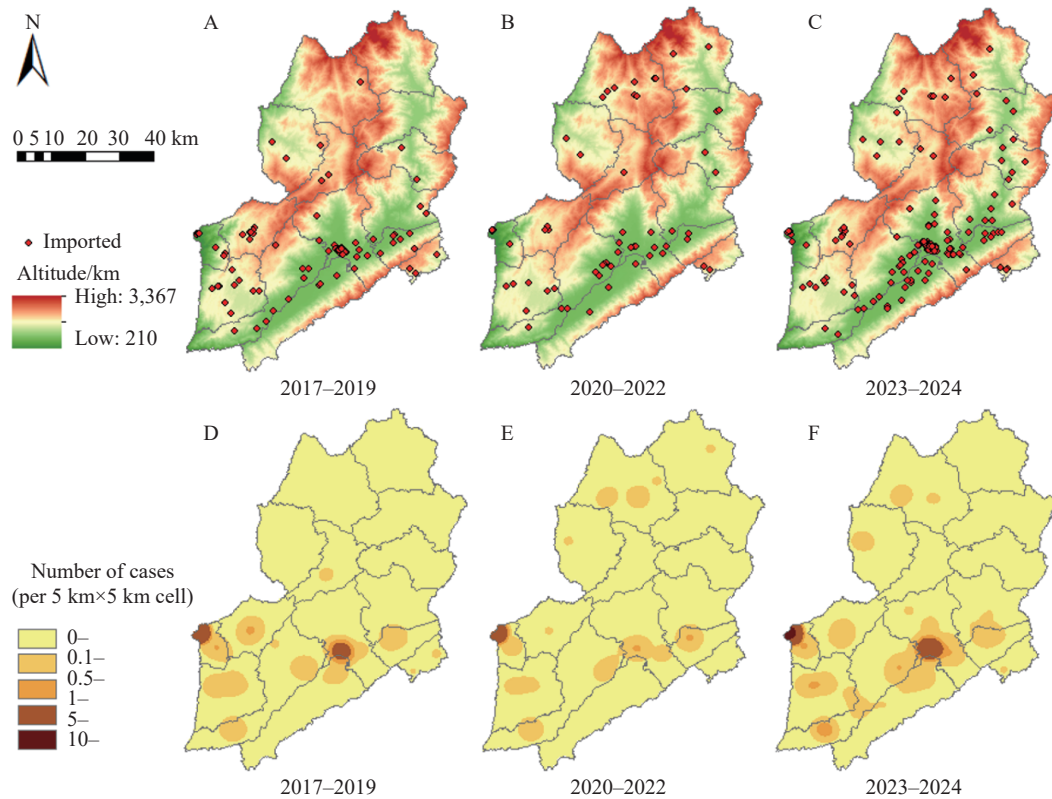
SUPPLEMENTARY TABLE S1. Incidence of imported and indigenous *Plasmodium vivax* malaria at the township level in Yingjiang County, 2010–2024.

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. Map approval number: 德 S(2026)3 号.



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.

Map approval number: 德 S(2026)3 号.

Preplanned Studies

Distribution and Ecological Habitat Characteristics of *Biomphalaria straminea* — Shenzhen City, Guangdong Province, China, August–December 2023

Qian Lu^{1,2,3,4}; Xuesen He^{2,*}; Yinjun He³; Panjue Chen³; Shitong Gao⁴; Daokui Fang⁴; Changqing Tu²; Yuan Li⁴

Summary

What is already known about this topic?

Biomphalaria straminea (*B. straminea*) is an invasive snail and a key intermediate host of *Schistosoma mansoni* (*S. mansoni*), which was previously widespread in Shenzhen's major rivers.

What is added by this report?

In contrast to historical records, no live snails were detected in rivers or reservoirs, whereas stable populations persisted in agricultural areas. Infested habitats show eutrophication and higher levels of Ca^{2+} , HCO_3^- , and PO_4^{3-} . All the samples tested negative for *S. mansoni*.

What are the implications for public health practice?

B. straminea shows apparent redistribution into agricultural environments, increasing spatial overlap with human activities and raising a theoretical transmission risk of *S. mansoni*. Surveillance and control efforts should prioritize agricultural ecosystems over urban waterways.

established in agricultural areas. Infested habitats had heavy organic deposition and significantly higher Ca^{2+} , HCO_3^- , and PO_4^{3-} levels than snail-free areas ($P < 0.05$). Molecular testing of 64 snail samples confirmed the absence of *S. mansoni* infection.

Conclusion: This survey revealed an apparent redistribution of *B. straminea* in Shenzhen, where the snail is apparently absent from urban rivers but has colonized polluted agricultural waters. Although the samples tested negative, dense colonization of this competent host in agricultural landscapes with frequent human-water contact enables potential local transmission if the pathogen is introduced. Future monitoring and control efforts should prioritize agricultural ecosystems.

ABSTRACT

Introduction: *Biomphalaria straminea* (*B. straminea*) is an intermediate host of *Schistosoma mansoni* (*S. mansoni*), and its distribution in Shenzhen threatens public health. This study aimed to investigate the distribution patterns and ecological habitat characteristics of *B. straminea* to inform public health prevention and control strategies.

Methods: Sampling was conducted across major natural water systems (rivers and reservoirs) and vegetable-planting areas in Shenzhen. Species were identified using morphological and molecular methods. *S. mansoni* infection and water quality were analyzed to compare infested and snail-free habitats.

Results: No live *B. straminea* were detected in major rivers or reservoirs. Instead, stable populations were

Schistosoma mansoni (*S. mansoni*) is a global public health threat, with 54 million annual infections worldwide. Its transmission range is determined by the dispersal of its intermediate host, *Biomphalaria straminea* (*B. straminea*) (1–2). In China, while *Schistosoma japonicum* is under control, increased exchange and trade with schistosomiasis-endemic regions under the Belt and Road Initiative have made imported *S. mansoni* control increasingly critical (3). Multiple imported cases were reported in China, predominantly among travelers and workers returning from *S. mansoni* endemic regions (4), indicating a persistent cross-border introduction risk. Systematic surveillance and early warning for imported *S. mansoni* remain insufficient in China, and control capacity needs further improvement. As a major port city, Shenzhen faces introduction risks from frequent cross-border personnel, trade, and ballast water (5).

Since 1981, *B. straminea* has spread to Dongguan, Huizhou, and other Pearl River Delta cities (2). Systematic historical surveillance has documented the widespread distribution of the snail in Shenzhen's

major urban rivers and reservoir flood channels during 2012–2013, with multiple high-density breeding populations detected in these lotic river habitats (6–7). Previous studies mainly focused on its distribution and dispersal, with limited analysis of its adaptive mechanisms, environmental drivers, and niche dynamics across habitats. In recent years, river restoration and channel-hardening projects in Shenzhen have drastically altered its original habitats. However, its response to these changes and the colonization of new habitats remain unclear. Therefore, this study aimed to assess these ecological changes to inform public health strategies.

This study was conducted from August to December 2023 in Shenzhen, a coastal city in southern China. Shenzhen has a subtropical monsoon climate (annual mean temperature about 23 °C, abundant rainfall) and extensive river networks. Surveys covered diverse freshwater habitats in Shenzhen, including major rivers, reservoirs, and agricultural sites. Sampling points were established at the upper, middle, and lower reaches of waterways to ensure geographical representation.

Targeting stagnant waters and aquatic vegetation, we searched within 20–50 m of each site. Snails were collected using dip nets and hand-picking and then transported to the laboratory in ventilated containers with moist gauze. For molecular analysis, 20 mg of soft tissue was dissected and preserved in absolute ethanol at –80 °C. Surface water samples were collected from 12 sites using portable samplers for water quality analysis (Supplementary Table S1, available at <https://weekly.chinacdc.cn/>), with the sampling basis following the Technical Specifications for Environmental Quality Monitoring of Surface Water (HJ 91.2-2022). Statistical analyses were performed using R (version 4.3.1, R Foundation for Statistical Computing, Vienna, Austria). Differences between snail-infested and snail-free habitats were analyzed using the Mann-Whitney U test. The significance level was set at $\alpha=0.05$, and $P<0.05$ was considered statistically significant.

All the collected specimens were black morphotypes, measuring 4–12 mm in diameter and 1–3 mm in height. The shells were dextral and discoid, with four rapidly expanding whorls and a typical horseshoe-shaped aperture. The flattened dorsal, deeply concave apex, and prominent umbilicus matched the taxonomic description of *B. straminea*.

Field surveys showed significant differences in *B. straminea* distribution across Shenzhen's main water

systems. No live *B. straminea* were found in Shenzhen's main rivers or the Shenzhen Reservoir flood channel, with only a few empty shells discovered at some sites. In contrast, the snail was prolifically breeding in the vegetable-planting areas of Longgang and Pingshan, forming stable communities (Table 1).

The environmental characteristics differed significantly between snail-infested and snail-free habitats (Table 2). In snail-free rivers and reservoirs, water was odorless, clear, or slightly turbid, with minimal humus and debris. However, snail-present vegetable areas had stagnant, shallow, turbid, and malodorous water, with heavy humus deposits and dense vegetation covering the water surface.

Water quality analysis showed that snail-infested waters had high hardness and eutrophication (Table 3). Specifically, Ca^{2+} , Mg^{2+} , HCO_3^- , and PO_4^{3-} concentrations were significantly higher in snail-infested areas ($P<0.05$). Mean Ca^{2+} reached 132.23 mg/L in snail-infested areas, compared with 31.38 mg/L in snail-free areas. Similarly, HCO_3^- and PO_4^{3-} differed markedly, with snail-infested values being significantly higher. Moreover, PO_4^{3-} in snail-infested areas severely exceeded the surface water standard (total phosphorus ≤ 0.1 mg/L), indicating heavy organic pollution. In contrast, pH, Na^+ , Cl^- , DO, and $\text{NH}_3\text{-N}$ showed no significant differences ($P>0.05$). These results confirm that *B. straminea* prefers calcium-rich, eutrophic, and polluted stagnant waters. All the 64 samples tested negative for *S. mansoni* by PCR. Molecular evidence confirmed that none of the *B. straminea* samples harbored *S. mansoni*.

DISCUSSION

Historical surveys consistently recorded widespread *B. straminea* populations in Shenzhen's urban rivers and reservoir flood channels (6–7). In contrast, our survey found no live snails in these habitats. Compared with historical data, this cross-sectional survey suggests an indicative spatial distribution shift of *B. straminea* in Shenzhen. Their apparent absence from urban rivers aligns with riverbed hardening and restoration that eliminated the organic-rich substrates essential for their survival (8). In addition, we observed that *B. straminea* has invaded agricultural irrigation systems with stagnant, calcium-rich water. This environment favors shell calcification and population establishment (9) and increases the likelihood of schistosomes being close to agricultural areas with frequent human activities.

Although this study adopted a cross-sectional design

TABLE 1. Distribution survey of *Biomphalaria straminea* in Shenzhen.

Water system	Location	<i>B. straminea</i>	Other freshwater snails
Longgang River	Puluobei Middle Bridge	Not found	<i>P. striatulus</i> , <i>B. aeruginosa</i>
	Ailian New Bridge	Shells present	<i>P. canaliculata</i>
	Longcheng Blvd Viaduct	Shells present	<i>P. canaliculata</i> , <i>P. striatulus</i>
	Shihuw Community Park	Not found	<i>B. aeruginosa</i>
	Xinsheng Kindergarten	Few shells	<i>C. chinensis</i>
	Longyuan	Shells present	<i>Bithynia</i> sp.
Dasha River	Shenzhen University Lihu Campus	Not found	<i>P. striatulus</i>
	Nanshan Talent Apt. Riverside	Not found	<i>S. quadrata</i>
	Dasha River Park	Not found	None
	Binhai Shahexi Viaduct	Shells present	<i>C. chinensis</i> , <i>P. canaliculata</i>
Guanlan River	Yousong Waterfront Park	Not found	<i>P. striatulus</i> , <i>Bithynia</i> sp
	Guanlan River Artificial Wetland	Not found	<i>C. chinensis</i>
	Guanhu Culture, Art & Sports Center	Shells present	<i>B. aeruginosa</i> , <i>Bithynia</i> sp
	Guanlan River Overhead Bridge	Not found	<i>P. canaliculata</i> , <i>P. striatulus</i>
	Miaoxi New Village	Shells present	<i>P. striatulus</i>
	Guihua Riverside Park	Shells present	<i>P. striatulus</i>
Shenzhen Reservoir	Discharge Channel 1	Shells present	<i>P. striatulus</i> , <i>Bithynia</i> sp.
	Discharge Channel 2	Not found	<i>P. striatulus</i> , <i>Bithynia</i> sp.
Vegetable-Planting Areas	Pingshi Liuwu Vegetable Field	Live individuals dominant	<i>P. striatulus</i> , <i>C. chinensis</i> , <i>P. canaliculata</i>
	Hutian Rd. Liulian Bridge Field	Live individuals dominant	<i>P. striatulus</i> , <i>C. chinensis</i> , <i>P. canaliculata</i>
	Next to Agri-Tech Industry Park	Live individuals dominant	<i>C. chinensis</i>

and lacked data from neighboring cities, it demonstrated that environmental changes have reshaped the distribution of *B. straminea*. Notably, as a key international hub, Shenzhen has frequent cross-border exchanges with *S. mansoni* endemic areas (10), which may elevate the probability of pathogen introduction. Although no infected snails were found and no epidemiological linkage exists between imported cases and local agricultural settings, if *S. mansoni* is introduced into these agricultural landscapes, the co-occurrence of the pathogen, a competent intermediate host, and human water contact could form a biologically plausible transmission cycle. The current situation of "snails without schistosomes" provides a valuable opportunity for disrupting potential transmission chains. Prevention and control efforts should focus on vector control, pathogen surveillance, and protection of high-risk populations.

Implications for public health arising from the apparent redistribution of *B. straminea* into agricultural ecosystems necessitate a strategic adjustment of schistosomiasis control in Shenzhen. Prevention efforts should focus on the irrigation networks; for example,

dredging sediment and controlling Ca^{2+} and PO_4^{3-} levels to reduce eutrophication can disrupt snail breeding habitats and reduce reliance on chemical molluscicides. Routine malacological surveys should be linked with active stool screening for high-risk groups, including agricultural workers and laborers returning from endemic areas, to enable timely response through the existing reporting mechanisms. In addition, health education targeting farming communities and a joint prevention framework involving Shenzhen, Dongguan, and Huizhou are essential for bridging surveillance gaps and reducing the risk of a localized *S. mansoni* outbreak across shared watersheds.

Conflicts of interest: No conflicts of interest.

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TABLE 2. Physical and sensory characteristics of biomphalaria straminea survey sites.

Location	Odor	Transparency	Water flow	Organic matter	Floating debris
Longgang River					
Puluobei Middle Bridge	None	Turbid	Relatively fast	Low	Small amount
Ailian New Bridge	None	Clear	Slow	Low	None
Longcheng Blvd Viaduct	None	Clear	Relatively fast	Low	None
Shihuw Community Park	None	Clear	Slow	Low	None
Xinsheng Kindergarten	None	Clear	Slow	Low	None
Longyuan	None	Clear	Slow	Low	None
Dasha River					
Shenzhen University Lihu Campus	None	Clear	Slow	Low	None
Ecological Corridor Children's Park	None	Clear	Slow	Low	None
Dasha River Park	None	Clear	Slow	Low	None
Binhai Shahevi Viaduct	None	Clear	Relatively fast	Low	None
Guanlan River					
Yousong Waterfront Park	None	Clear	Slow	Low	None
Guanlan River Artificial Wetland	None	Clear	Slow	Low	None
Guanhu Culture, Art & Sports Center	None	Clear	Slow	Low	None
Guanlan River Overhead Bridge	None	Clear	Relatively fast	Low	None
Miaoxi New Village	None	Clear	Slow	Low	None
Guihua Riverside Park	None	Clear	Slow	Low	None
Shenzhen Reservoir					
Discharge Channel 1	Foul odor	Heavily polluted	Relatively fast	Relatively high	Present
Discharge Channel 2	None	Turbid	Slow	Relatively high	Present
Vegetable-Planting Areas					
Pingdi Liuwu Vegetable Field	None	Turbid	Stagnant	Relatively high	Relatively high
Hutian Rd. Liulian Vegetable Field	None	Turbid	Stagnant	Relatively high	Relatively high
Shenzhen Pingshan Agri-Tech Park Side	Foul odor	Turbid	Stagnant	Relatively high	Relatively high

TABLE 3. Water chemistry characteristics of biomphalaria straminea survey sites.

Variable	Sites with Snails	Sites without Snails	Mann-whitney U (W/U)	P
	Median (Q1–Q3)	Median (Q1–Q3)		
Ca ²⁺ (mg/L)	109.00 (96.22–145.00)	33.70 (28.18–37.35)	0.0	0.004
Mg ²⁺ (mg/L)	16.90 (15.38–21.83)	3.95 (3.30–7.24)	3.0	0.028
Na ⁺ (mg/L)	32.05 (23.92–38.23)	34.55 (8.95–57.78)	16.0	1.000
HCO ₃ ³⁻ (mg/L)	292.00 (238.5–322.00)	68.50 (65.75–80.00)	2.0	0.016
CO ₃ ²⁻ (mg/L)	<5 (LOD)	<5 (LOD)	NA	NA
Cl ⁻ (mg/L)	74.55 (59.75–81.50)	79.10 (48.38–134.00)	19.0	0.683
PO ₄ ³⁻ (mg/L)	0.42 (0.35–1.31)	0.05 (0.045–0.083)	3.0	0.033
pH	6.90 (6.65–7.53)	7.45 (7.18–7.53)	21.5	0.394
DO (mg/L)	8.97 (8.20–9.73)	7.42 (6.97–7.62)	5.0	0.074
NH ₃ -N (mg/L)	0.92 (0.37–7.075)	0.44 (0.30–1.14)	13.0	0.683

Abbreviation: Q1=25th percentile; Q3=75th percentile; LOD=limit of detection; NA=not available.

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REFERENCES

1. da Trindade MAO, Fonseca ÁLS, Dias IHL, de Sousa SRM, Enk MJ, Lima KVB, et al. Geospatial analysis and prevalence of *Schistosoma mansoni* and soil-transmitted helminth infections in an endemic area in eastern Brazilian Amazon. *Trop Med Int Health* 2024;29(6):507 – 17. <https://doi.org/10.1111/tmi.13993>.
2. Habib MR, Guo YH, Lv S, Gu WB, Li XH, Zhou XN. Predicting the spatial distribution of *Biomphalaria straminea*, a potential intermediate host for *Schistosoma mansoni*, in China. *Geospat Health* 2016;11(3): 453. <https://doi.org/10.4081/gh.2016.453>.
3. Yang Y, Cheng WT, Wu XY, Huang SY, Deng ZH, Zeng X, et al. Prediction of the potential global distribution for *Biomphalaria straminea*, an intermediate host for *Schistosoma mansoni*. *PLoS Negl Trop Dis* 2018;12(5):e0006548. <https://doi.org/10.1371/journal.pntd.0006548>.
4. Wang L, Wu XY, Li XL, Zheng XY, Wang F, Qi ZQ, et al. Imported schistosomiasis: a new public health challenge for China. *Front Med* 2020;7:553487. <https://doi.org/10.3389/fmed.2020.553487>.
5. Qu YY, Kong Y, Li Z, Zhu EY. Pursue the coordinated development of port-city economic construction and ecological environment: a case of the eight major ports in China. *Ocean Coastal Manage* 2023;242: 106694. <https://doi.org/10.1016/j.ocecoaman.2023.106694>.
6. Huang SY, Zhang QM, Li XH, Deng ZH. Distribution and schistosomiasis transmission risks of *Biomphalaria straminea* in Inland China. *Chin J Schisto Control*, 2014;26(3):235-7. <https://www.zgxfz.com/CN/Y2014/V26/I3/235>. (In Chinese).
7. Gao ST, Li XH, Huang SY, Xie X, Mei SJ, Ruan CW, et al. Primary investigation of distribution and ecological environment of *Biomphalaria straminea* in Dasha and Guanlan Rivers in Shenzhen areas. *China Trop Med* 2013;13(3):313-4. <https://www.cntropmed.com/CN/Y2013/V13/I3/313>. (In Chinese).
8. Fu L, Dong XY, Shen HL, Zhu TS, Sun FF. River ecosystem health assessment in rapid urbanization regions (Shenzhen, China) under the guidance of bioremediation objectives. *Water* 2023;15(21):3859. <https://doi.org/10.3390/w15213859>.
9. Wang JY, Zhong JY, Zhu YH, Zheng HZ, Ma QM, Qian YC, et al. *Biomphalaria* snails release immune proteins in aquaculture water that influence egg production and development. *Sci Rep* 2025;15(1):41431. <https://doi.org/10.1038/s41598-025-26479-y>.
10. Lin DT, Zeng X, Sanogo B, He P, Xiang SY, Du SL, et al. The potential risk of *Schistosoma mansoni* transmission by the invasive freshwater snail *Biomphalaria straminea* in South China. *PLoS Negl Trop Dis* 2020;14(6):e0008310. <https://doi.org/10.1371/journal.pntd.0008310>.

SUPPLEMENTARY MATERIAL

Analytical Methods, Instruments, and Detection Limits for Water Quality

SUPPLEMENTARY TABLE S1. Test methods, analytical instruments, and detection limits.

Test item	Test standard (method) and number (including year)	Analytical instrument model	Detection limit	Unit
Ca ²⁺	Determination of 32 Elements in Water by Inductively Coupled Plasma Optical Emission Spectrometry HJ 776-2015	Inductively Coupled Plasma Optical Emission Spectrometer (Avio 200)	0.02	mg/L
Mg ²⁺	Determination of 32 Elements in Water by Inductively Coupled Plasma Optical Emission Spectrometry HJ 776-2015	Inductively Coupled Plasma Optical Emission Spectrometer (Avio 200)	0.003	mg/L
Na ⁺	Determination of 32 Elements in Water by Inductively Coupled Plasma Optical Emission Spectrometry HJ 776-2015	Inductively Coupled Plasma Optical Emission Spectrometer (Avio 200)	0.12	mg/L
HCO ₃ ⁻	Acid-Base Indicator Titration Method 3.1.12.1, <i>Standard Methods for the Examination of Water and Wastewater</i> (Fourth Edition, Supplemented Version, 2002), State Environmental Protection Administration of China	Stoppered Burette (Dual-Purpose Acid-Base Burette)	5	mg/L
CO ₃ ²⁻	Acid-Base Indicator Titration Method 3.1.12.1, <i>Standard Methods for the Examination of Water and Wastewater</i> (Fourth Edition, Supplemented Version, 2002), State Environmental Protection Administration of China	Stoppered Burette (Dual-Purpose Acid-Base Burette)	5	mg/L
Cl ⁻	Determination of Inorganic Anions in Water (F ⁻ , Cl ⁻ , NO ₂ ⁻ , Br ⁻ , NO ₃ ⁻ , PO ₄ ³⁻ , SO ₃ ²⁻ , SO ₄ ²⁻) by Ion Chromatography HJ 84-2016	Ion Chromatograph (ICS-90)	0.007	mg/L
PO ₄ ³⁻	Determination of Total Phosphorus in Water by Ammonium Molybdate Spectrophotometry GB/T 11893-1989	UV-Visible Spectrophotometer (Blue star A)	0.01	mg/L
pH	Determination of pH Value in Water by Electrode Method HJ 1147-2020	Portable pH/Electrical Conductivity/Dissolved Oxygen Meter (SX836)	Dimensionless	—
DO	Determination of Dissolved Oxygen in Water by Electrochemical Probe Method HJ 506-2009	Portable pH/Electrical Conductivity/Dissolved Oxygen Meter (SX836)	—	mg/L
NH ₃ -N	Determination of Ammonia Nitrogen in Water by Nessler's Reagent Spectrophotometry HJ 535-2000	UV-Visible Spectrophotometer (Blue star A)	0.025	mg/L

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