

Preplanned Studies

Mapping of the Global Importation Risk of Malaria to China — Global, 2024

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Summary

What is already known about this topic?

China achieved World Health Organization certification for malaria elimination in 2021; however, the risk of local retransmission from imported malaria remains a primary challenge in the post-elimination era. While international trade is a critical driver of importation risk, current risk assessments are constrained by the lack of granular cross-border population mobility data.

What is added by this report?

This study introduces service trade volume as a proxy for population mobility. By integrating global malaria epidemiology, socioeconomic factors, and geographic resistance, an enhanced gravity model was developed to stratify global malaria importation risks. The findings revealed that *Plasmodium falciparum* importation risk exhibited pronounced geographic clustering, predominantly in sub-Saharan Africa. Conversely, *Plasmodium vivax* importation showed a distinct "connectivity-driven" pattern. Notably, low-endemicity countries geographically adjacent to China or sharing intensive trade relations (such as Republic of Korea, Thailand, and Vietnam) present substantial cryptic importation pressures, identifying them as pivotal surveillance targets in the post-elimination era.

What are the implications for public health practice?

The risk stratification matrix provides a scientific framework for tailoring surveillance strategies. For "high-endemicity, high-mobility" regions (such as specific African nations), priorities should focus on strengthening port-of-entry screening and post-arrival follow-up. For "low-endemicity, high-mobility" regions, heightened vigilance is required against cryptic importations driven by frequent commercial and economic exchanges. Public health strategies must move beyond analyses based solely on geographic proximity and incorporate economic connectivity metrics into active surveillance frameworks.

ABSTRACT

Introduction: This study aimed to assess the risk of global malaria importation into China, providing a scientific basis for surveillance in the post-elimination era.

Methods: A gravity model was constructed by integrating global malaria epidemiological data with national socioeconomic indicators. A multidimensional risk stratification framework was established to categorize importation risks into hierarchical tiers.

Results: This study showed that high-risk countries for *Plasmodium falciparum* (*P. falciparum*) importation are mainly in Africa, including Nigeria, Ethiopia, and Kenya. Severe local epidemics and intense population mobility increase cross-border risks. India, Vietnam, and Thailand also pose high risks via trade and personnel exchanges, whereas Zambia, Chad, and Guinea present long-term threats owing to high endemicity. High *Plasmodium vivax* (*P. vivax*) importation risks are concentrated in Pakistan, Afghanistan, and Myanmar, with high prevalence, geographical proximity, and close bilateral ties, causing superimposed risks. Low-incidence, high-mobility countries, such as India, Cambodia, and Thailand, may cause concealed importation.

Conclusion: Malaria importation risk is mainly driven by the local epidemic burden of source countries and population mobility. Low-endemic nations with geographic proximity or close trade may cause concealed malaria importation. Post-elimination surveillance should focus on high-burden African regions and hidden infections in highly connected areas.

China was once among the countries most severely burdened by malaria worldwide. Through the sustained efforts of the entire society, China has achieved remarkable milestones in malaria prevention

and control (1–2). Since 2017, the country has reported no indigenous malaria cases. China was officially certified malaria-free by the World Health Organization (WHO) in 2021 (3). However, malaria elimination is not the final goal. The risk of reestablishment from imported cases remains a primary challenge in China. The World Malaria Report 2025 noted a global surge to 282 million cases in 2024 (4). Simultaneously, burgeoning international trade and the "Belt and Road" Initiative have intensified cross-border movements for labor and business. This trend significantly heightens importation risks from endemic regions, posing a persistent threat to China's malaria-free status (5). However, the lack of granular real-time population mobility data creates a significant bottleneck for accurate risk assessment (6).

To bridge this "empirical gap" and overcome current data constraints, this study introduces bilateral service trade volume as a robust proxy for cross-border mobility (7). This approach leverages socioeconomic connectivity and the high synchronicity between trade flows and labor migration. By integrating these dynamic metrics into a gravity model, it characterizes economically driven movements more precisely, thereby providing a robust framework for quantifying importation risks.

Building on this methodological framework, this research stratifies the risk of malaria importation into China from globally endemic countries. By integrating multi-source and multi-channel data, including national malaria epidemiological records, international trade statistics, and diverse socioeconomic and demographic indicators, an augmented gravity model for global cross-border population mobility driven by international trade relations was developed. This model allows the analysis of population mobility patterns between China and other malaria-endemic nations, enabling a comprehensive assessment of the importation risk levels posed by these countries. The findings of this study provide a scientific foundation and methodological reference for malaria risk assessment in the context of normalized international exchange and increasing population mobility.

This study selected countries that reported indigenous malaria cases in 2024 as the research subjects to construct a multisource importation risk database. The data sources are as follows: malaria epidemiological data were obtained from the latest global dataset published in 2025 by the Malaria Atlas Project (MAP, <https://malariaatlas.org/>), from which the prevalence and incidence rates of *Plasmodium*

falciparum (*P. falciparum*) and *Plasmodium vivax* (*P. vivax*) for each endemic country in 2024 were extracted. The total import and export volumes of service trade between China and other countries in 2024 were collected from the World Trade Organization (WTO; <https://stats.wto.org/>). Data on gross domestic product (GDP) and total population for 2024 were retrieved from the World Bank database (<https://data.worldbank.org/>). Finally, the great-circle distance (distcap) between Beijing and the capitals of other nations was obtained from the GeoDist database of the Center d'Études Prospectives et d'Informations Internationales (CEPII, <http://www.cepii.fr/>).

Furthermore, considering the significant heterogeneity in biological characteristics and global geographical distribution among different *Plasmodium* species, this study further categorized the analyses by pathogen type. Independent importation risk assessment frameworks were constructed for *P. falciparum* and *P. vivax*, respectively, aiming to reveal the differentiated importation pressures exerted by various endemic sources from a more granular perspective.

Building on the traditional gravity model, this study develops a multifactor-driven simulation model for cross-border population flows by incorporating geospatial distance as an impedance factor and substituting traditional merchandise trade indicators with service trade volumes, which exhibit a higher degree of coupling with international personnel exchanges.

Due to the difficulty in acquiring global real-time population migration trajectory data, this study selected international service trade volume as a reliable proxy variable to reflect the structure of economically driven population mobility. Pearson correlation analysis based on paired data from 46 countries confirmed a significant positive correlation between the scale of service trade and migrant stocks, supporting the rationality and feasibility of this alternative indicator (the detailed validation process is provided in the [Supplementary Material](#), available at <https://weekly.chinacdc.cn>).

Based on the principles of the gravity model (8–10), the frequency of cross-border population mobility between countries is directly proportional to the economic scale and service trade intensity of the two nations and inversely proportional to the square of the physical distance between them:

$$M_{ij} \propto K \cdot \frac{G_i \cdot G_j \cdot T_{ij}^2}{D_{ij}^2} \quad (1)$$

M_{ij} : The frequency of population mobility between the home country (China) and partner country j ;

G_i, G_j : The GDP of the two countries, respectively;

T_{ij} : The total import and export volume of service trade between the two countries (serving as a proxy for economic ties highly correlated with human mobility);

D_{ij} : The physical distance between the capitals of the two countries, with its square term acting as the impedance coefficient;

K : The constant adjustment coefficient of the model.

The importation risks of *P. falciparum* and *P. vivax* were calculated by integrating population mobility frequency with the local disease burden as follows:

$$R_{ij} \propto M_{ij} \cdot P_j \cdot IR_j^2 \quad (2)$$

R_{ij} : Cross-border importation risk of a specific malaria species (*P. falciparum* or *P. vivax*);

IR_j : Local incidence rate of the corresponding malaria type in source country j ;

P_j : Total population of source country j .

To identify the driving patterns of malaria importation risk across countries, this study conducted a two-dimensional stratification based on the malaria burden in endemic countries and cross-border population mobility frequency. The annual malaria incidence (P) and cross-border mobility frequency (M) were selected as key indicators. Using the median values of these indicators as thresholds, all malaria-endemic countries were classified into four categories: the high-incidence–high-mobility category, the high-incidence–low-mobility category, the low-incidence–high-mobility category, and the low-incidence–low-mobility category. Based on this classification, stratified risk maps for *P. falciparum* and *P. vivax* importation were generated.

The results indicate that in 2024, a total of 78 countries reported indigenous *P. falciparum* cases, while 40 countries reported indigenous *P. vivax* cases. *P. falciparum* cases were predominantly distributed in Africa (57.7%) and Asia (20.5%); notably, African nations accounted for over 90% of the global incidence of *P. falciparum*, with Benin, the Democratic Republic of the Congo, and the Central African Republic identified as the most severely affected regions. In contrast, *P. vivax* cases were mainly distributed across Asia (52.5%) and the Americas (32.5%), with the highest epidemic intensities observed in the Solomon Islands and Papua New Guinea. Cross-border population mobility exists between China and the above-mentioned malaria-endemic countries. Among

P. falciparum-endemic countries, India, Indonesia, and Vietnam ranked among the top three in terms of the scale of cross-border population mobility with China. For *P. vivax*-endemic countries, Republic of Korea, India, and Indonesia occupied the top three positions.

Figure 1 presents the stratification results for *P. falciparum* and *P. vivax* importation risk. For *P. falciparum*, endemic countries exhibited a multimodal distribution. China maintains varying levels of population mobility with high-incidence countries; even countries with relatively low mobility still pose considerable risks of imported cases. Moreover, high-frequency population mobility further amplifies importation risk. For *P. vivax*, most endemic countries are concentrated in low-incidence ranges, and high-risk clustering is less pronounced. Countries with relatively higher incidence tend to have lower mobility with China, resulting in weaker aggregation of high-risk areas. Instead, risk is characterized by a "low-incidence–high-mobility" pattern, reflecting concealed importation risks.

Through a stratified analysis of *P. falciparum*-endemic countries (Table 1), the risk distribution presented distinct regional clustering and heterogeneous driving factors.

The high-incidence, high-mobility group comprises 14 countries dominated by high-burden African nations, including Nigeria, Ethiopia, and Kenya. These regions experience severe malaria transmission and intense cross-border population mobility. With a high endemic burden and close economic and trade ties with China, they serve as the core priority areas for *falciparum* malaria importation prevention.

The low-incidence, high-mobility group comprises 24 countries, including India, Southeast Asian nations (Vietnam, Thailand, and the Philippines), and Latin American countries (Brazil, Colombia, and Peru). Despite the low local *P. falciparum* transmission intensity, their geographical proximity and close service trade links drive frequent population exchanges, leading to heightened cross-border importation risks.

The high-incidence, low-mobility group comprises 24 African countries, including Zambia, Chad, and Guinea. Limited bilateral service trade and low population connectivity with China cannot offset their extremely high local endemicity; occasional cross-border movement may even trigger importation, forming a persistent latent threat to *P. falciparum* introduction.

The low-incidence–low-mobility group is represented by Bolivia and other regions. Both malaria

burden and cross-border connectivity remain at low levels, with currently controllable importation risks. Nevertheless, expanding bilateral trade in the future may bring emerging potential risks that require continuous attention.

Stratified analysis of *P. vivax*-endemic countries (Table 2) revealed that the risk drivers were linked to geographic proximity and economic connectivity.

The high-incidence, high-mobility group comprises eight countries, including Pakistan, Afghanistan, and

Myanmar. These nations are highly endemic for *P. vivax* and have frequent population exchanges with China. Notably, Myanmar, Pakistan, and Afghanistan, owing to their geographic proximity and close bilateral economic, trade, and diplomatic ties, impose dual *P. vivax* importation pressure, making them the most critical regions for China's current control efforts.

The low-incidence, high-mobility group includes 12 countries (India, Republic of Korea, Cambodia, and Thailand). Despite the low local *P. vivax* annual

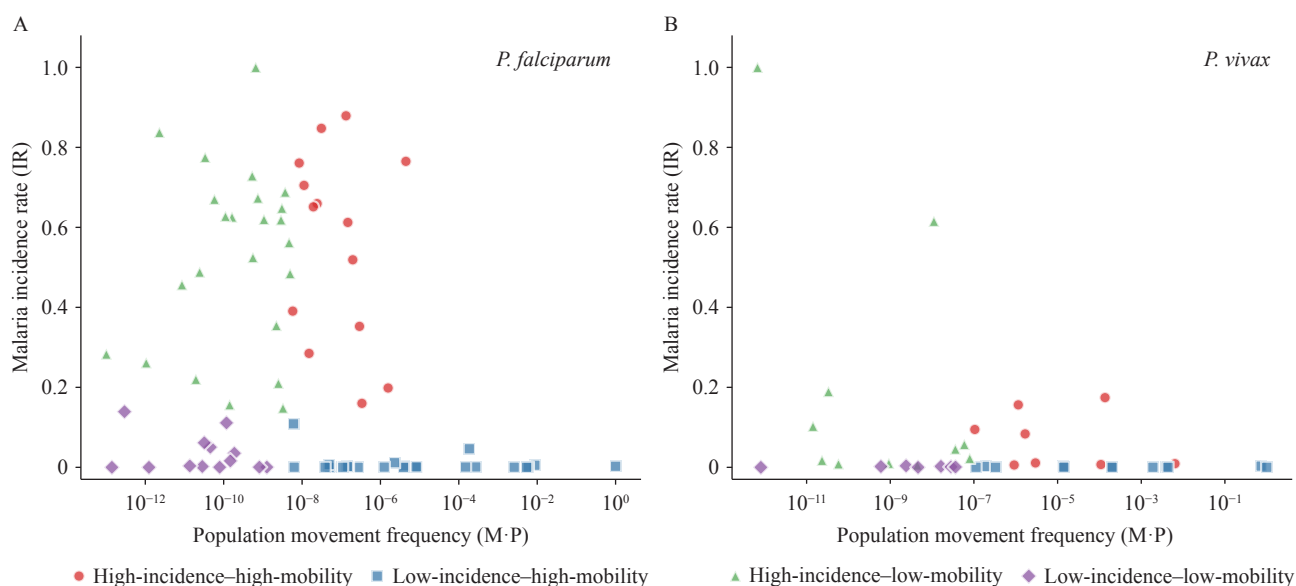


FIGURE 1. Global stratification of malaria importation risk to China. (A) Global stratification of *P. falciparum* importation risk; (B) Global stratification of *P. vivax* importation risk.

Abbreviation: *P. falciparum*=*Plasmodium falciparum*; *P. vivax*=*Plasmodium vivax*.

TABLE 1. Stratification of *P. falciparum*-endemic countries by importation risk to China, 2024.

Mobility Frequency	High Incidence Rate (High IR)	Low Incidence Rate (Low IR)
High Mobility Frequency	Nigeria, Ethiopia, Kenya, Tanzania, Ghana, Angola, Sudan, Democratic Republic of the Congo, Uganda, Côte d'Ivoire, Papua New Guinea, Cameroon, Mozambique, Senegal	India, Indonesia, Vietnam, Thailand, Philippines, Bangladesh, Pakistan, Brazil, Iran, South Africa, Colombia, Nepal, Myanmar, Peru, Cambodia, Oman, Afghanistan, Panama, Dominican Republic, Ecuador, Venezuela, Laos, Costa Rica, Yemen
Low Mobility Frequency	Zambia, Chad, Guinea, Somalia, Mali, Congo, Zimbabwe, Madagascar, Malawi, Niger, Benin, Gabon, Burkina Faso, Togo, Mauritania, Equatorial Guinea, Burundi, Sierra Leone, Liberia, Djibouti, Gambia, Central African Republic, Solomon Islands, Guinea-Bissau	Bolivia, Honduras, Namibia, Haiti, Rwanda, Nicaragua, Guyana, Eritrea, Botswana, Eswatini, Timor-Leste, Comoros, Vanuatu, Sao Tome and Principe

TABLE 2. Stratification of *P. vivax*-endemic countries by importation risk to China, 2024.

Mobility Frequency	High Incidence Rate (High IR)	Low Incidence Rate (Low IR)
High Mobility Frequency	Pakistan, Ethiopia, Afghanistan, Myanmar, Colombia, Indonesia, Brazil, Peru	India, Cambodia, North Korea, Bangladesh, Thailand, Iran, Oman, Philippines, Republic of Korea, Vietnam, Nepal, Mexico
Low Mobility Frequency	Solomon Islands, Papua New Guinea, Guyana, Djibouti, Vanuatu, Sudan, Venezuela, Panama, Eritrea, Bolivia, Nicaragua, Yemen	Somalia, Guatemala, Honduras, Laos, Ecuador, Costa Rica, Timor-Leste

incidence, weak geographic barriers and their status as key trade partners of China amplify the risks through spatial proximity. This highlights that, for *P. vivax* control, East and Southeast Asian countries with a low endemic burden but intense cross-border movement are prone to concealed malaria importation (10).

The high-incidence, low-mobility group mainly consists of 12 countries (e.g., the Solomon Islands and Papua New Guinea). Geographical distance and limited trade linkages mean that their importation risk is primarily driven by the local epidemiological burden. With a large infected population and a high risk of infected individuals entering China, targeted screening of specific returning groups is required.

The low-incidence–low-mobility group (e.g., Laos and Somalia) has low endemicity and mobility, resulting in relatively limited importation pressure.

The top 20 high-risk countries were identified based on the importation risks calculated using the model (Table 3). The top five countries for *P. falciparum* are India, Nigeria, Pakistan, Indonesia, and Sudan. These nations consistently ranked among the primary source

locations of imported *P. falciparum* malaria in China's national surveillance records, confirming the reliability of the model in capturing high-burden risk sources.

For *P. vivax*, the leading positions were occupied by India, Pakistan, Indonesia, Ethiopia, and Myanmar, followed closely by nations characterized by intense human movement, such as Thailand and Republic of Korea. Notably, despite their low local indigenous incidence, Republic of Korea and Thailand were included among the top 15 priority countries, driven by their frequent service trade activities and strong geographic connectivity with China. This alignment with historical importation patterns from East and Southeast Asia further validates the model's unique capability to detect concealed risks driven primarily by population mobility frequency.

DISCUSSION

This study developed a multidimensional risk assessment model for imported malaria by integrating service trade data, geographic resistance factors,

TABLE 3. Top 20 priority countries for malaria importation risk to China.

Rank	<i>P. falciparum</i>	Risk Category	<i>P. vivax</i>	Risk Category
1	India	Category II (Low-High)	India	Category II (Low-High)
2	Nigeria	Category I (High-High)	Pakistan	Category I (High-High)
3	Pakistan	Category II (Low-High)	Indonesia	Category I (High-High)
4	Indonesia	Category II (Low-High)	Ethiopia	Category I (High-High)
5	Sudan	Category I (High-High)	Myanmar	Category I (High-High)
6	Ethiopia	Category I (High-High)	Thailand	Category II (Low-High)
7	Angola	Category I (High-High)	Republic of Korea	Category II (Low-High)
8	Ghana	Category I (High-High)	Brazil	Category I (High-High)
9	Tanzania	Category I (High-High)	Papua New Guinea	Category III (High-Low)
10	Democratic Republic of the Congo	Category I (High-High)	Afghanistan	Category I (High-High)
11	Uganda	Category I (High-High)	Bangladesh	Category II (Low-High)
12	Kenya	Category I (High-High)	Colombia	Category II (Low-High)
13	Côte d'Ivoire	Category I (High-High)	Sudan	Category III (High-Low)
14	Cameroon	Category I (High-High)	Venezuela	Category III (High-Low)
15	Mozambique	Category I (High-High)	DPRK	Category II (Low-High)
16	Guinea	Category III (High-Low)	Panama	Category III (High-Low)
17	Chad	Category III (High-Low)	Philippines	Category II (Low-High)
18	Mali	Category III (High-Low)	Peru	Category I (High-High)
19	Papua New Guinea	Category I (High-High)	Vietnam	Category II (Low-High)
20	Zambia	Category III (High-Low)	Guyana	Category III (High-Low)

Abbreviation: DPRK=Democratic People's Republic of Korea; *P. falciparum*=*Plasmodium falciparum*; *P. vivax*=*Plasmodium vivax*.

epidemiological data, and socioeconomic indicators. The model stratified the global importation risk of *P. falciparum* and *P. vivax* into China.

The findings revealed regional clustering of *P. falciparum* importation risk, primarily in sub-Saharan Africa and parts of South Asia. High endemicity in source countries is the dominant risk driver, whereas population mobility modulates the actual importation risk under high-transmission scenarios. Strengthening quarantine and surveillance along high-mobility China–Africa routes remains critical (11).

In contrast, *P. vivax* importation risk is predominantly "connectivity-driven," with major risks arising in Asia and the Americas. Notably, countries such as Republic of Korea, Thailand, and Vietnam, despite their low endemicity, pose non-negligible risks due to their geographic proximity and high connectivity. Minor fluctuations in local transmission may lead to importation through frequent travel, creating "concealed importation pressure" (12–13).

The use of service trade volume as a proxy for population mobility proved effective. For example, increased trade connections with Latin American countries such as Brazil and Peru have elevated importation risks. These findings suggest that public health strategies should move beyond approaches based solely on geographic distance and incorporate economic connectivity into surveillance systems.

However, the model relies primarily on official service trade statistics and has a limited capacity to capture informal cross-border movements, such as small-scale border trade along the China–Myanmar border (11). Future research should integrate multi-source data to improve predictive accuracy and address complex border dynamics, ultimately enhancing the global malaria importation risk assessment framework.

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SUPPLEMENTARY MATERIAL

Mapping the Risks of Imported Infectious Diseases by Exploring the International Service Trade Dataset

The scientific assessment of importation risk is predicated on the acquisition of high-quality cross-border population mobility data. Quantifying human movement is fundamental for identifying the risks of cross-border malaria transmission (1). On a global scale, however, obtaining high-frequency, real-time microtrajectories of cross-border migration remains constrained by significant technical challenges and privacy restrictions. This "empirical gap" in cross-border mobility persists as a primary obstacle to risk assessment modeling (2–3), as incomplete or biased mobility data can substantially undermine the predictive accuracy of cross-border disease transmission models (4). To address this data bottleneck, scholars have proposed utilizing quantifiable structural data, such as census records and socioeconomic connectivity indicators, as proxy measures for population movement — an approach whose efficacy has been validated in spatial malaria forecasting (5–6). Building on this paradigm, this study introduces bilateral service trade volume as a proxy variable for inferring cross-border mobility frequency, a choice that is supported by robust theoretical and empirical evidence.

First, a significant statistical correlation exists between service trade volume and labor migration flows. Research indicates that the inflection points of international trade and cross-border population flows are highly synchronized, suggesting that trade data (particularly for labor-intensive sectors) serve as effective indicators for characterizing population mobility (7). Theoretical frameworks further reveal that the scale and characteristics of labor exports are not randomly distributed but are deeply embedded within shifts in international trade structures (8). Given that imported malaria cases in China are highly concentrated among mobile populations, service trade volume can identify high-risk groups with specific exposure profiles more precisely than conventional data sources. This approach serves as an indirect proxy for total entry–exit aggregates by characterizing "structural cross-border mobility" driven by service trade relations. Furthermore, numerous studies have emphasized that during the malaria elimination phase, economically driven labor migration constitutes the primary source of imported malaria (9–10).

Second, coupling macroeconomic indicators with the dynamic characteristics of infectious disease epidemics has emerged as a cutting-edge trend in interdisciplinary research. Existing studies have incorporated economic indicators as key covariates in mapping vector-borne diseases (11). Such "epidemiological-macroeconomic models" (12) represent a novel direction in public health forecasting and early warning systems. Empirical research has also confirmed that economic activity possesses robust quantitative explanatory power regarding population mobility and the associated health risks (13–14).

Finally, the integration of multi-source data into gravity model construction has been extensively validated. Utilizing gravity models to quantify connectivity between nations is a well-established approach for assessing the risk of transnational disease diffusion (15). In quantitative assessments of cross-border risk, gravity models built upon socioeconomic connectivity indicators have demonstrated significant predictive value (16). Recent studies further demonstrate that in complex public health contexts, integrating multi-source socioeconomic data (e.g., trade indicators and mobility proxies) can effectively correct biases inherent in single data sources, thereby substantially enhancing the reliability of spatiotemporal transmission models (17–18).

This study focuses on the risk of malaria importation from endemic countries worldwide. By integrating multi-source data, including malaria surveillance, service trade, and socioeconomic metrics, a global cross-border mobility gravity model driven by international trade relations was constructed. This model aims to quantitatively analyze mobility patterns between China and malaria-endemic nations and, subsequently, evaluate importation risk levels from major endemic source countries.

The application of this interdisciplinary index and model offers a novel alternative for establishing risk assessment systems in environments that lack empirical mobility data. The results of this study not only provide a scientific basis for monitoring imported malaria risk as international exchanges normalize but also establish a robust methodological foundation for developing early warning mechanisms for various imported infectious diseases.

Statistical Validation of Service Trade Volume as a Proxy for Population Mobility

Data Selection and Sample Processing In this study, paired data for malaria-endemic countries were obtained by

cross-referencing the World Trade Organization Service Trade Database with the International Migrant Stock Database of the United Nations Department of Economic and Social Affairs. After excluding cases with missing values for the key variables, a final set of 46 valid country samples was included in the empirical analysis.

Methodology Pearson's correlation analysis was used to examine the association between total service trade volume (imports and exports) and international migrant stocks. This analysis aims to evaluate the validity of trade metrics as proxy variables for population mobility.

Statistical Results Correlation Coefficient: A significant positive correlation was observed between service trade volume and international migrant stocks, with a correlation coefficient of $r=0.57$. Significance Level: $P<0.05$, indicating statistical significance.

Interpretation of Results The result of $r=0.57$ demonstrates that the expansion of trade volume and the growth of population mobility exhibit high spatial synchronicity. This statistically significant association further validates the scientific rationale for incorporating service trade volume into the gravity model. Compared with static population stock data, trade indicators not only reflect fundamental population distribution characteristics but also more sensitively characterize dynamic population movements driven by economic and trade activities. Consequently, this approach provides more timely proxy data support for the construction of cross-border population mobility models.

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