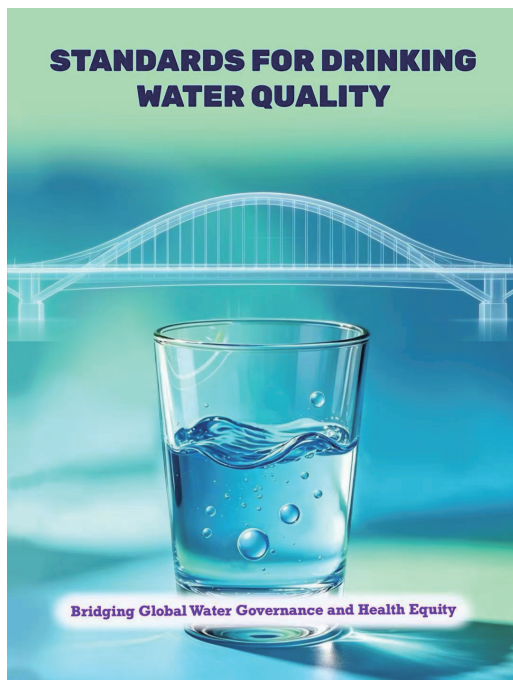


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Vital Surveillances

Epidemiological Characteristics of Imported Malaria Cases Along the China–Myanmar Border — Yunnan Province, China, 2021–2025

Chunli Ding^{1,*}; Yurong Zhang^{2,*}; Yaowu Zhou¹; Yulong Zhao¹; Zurui Lin^{1,†}; Zhigui Xia^{3,†}

ABSTRACT

Introduction: In this study, the epidemiological characteristics of imported malaria cases (IMCs) along the China–Myanmar border in Yunnan Province (CMBYP) between 2021 and 2025 were analyzed, to provide a scientific basis for formulating effective measures to control imported malaria, prevent re-transmission, and consolidate malaria elimination achievements.

Methods: Individual data were collected from the National Notifiable Disease Reporting System for 2021–2025. The temporal, spatial, and demographic distributions of malaria cases, along with *Plasmodium* species, case classification, source of infection, and timeliness of medical treatment, were analyzed to describe the epidemiological characteristics.

Results: A total of 1,602 IMCs were reported in the CMBYP, with *Plasmodium vivax* accounting for 98.50% (1,578/1,602) of the cases. Of these, 75.97% (1,217/1,602) originated in Myanmar. The number of cases peaked between May and July. Demographically, 75.09% (1,203/1,602) of the patients were male, with a male-to-female ratio of 3.02:1. All time intervals including those from onset to initial diagnosis and from the initial medical visit to malaria diagnosis were shorter in 2021–2022 than in 2023–2025. Additionally, 84.14% (1,348/1,602) of patients were correctly diagnosed at the initial medical visit.

Conclusion: Summer is a critical period for the prevention and control of imported malaria. Strengthening case surveillance and vector control is essential for preventing importation and introduced transmission. There was an increasing trend in the number of IMCs, suggesting a potentially increased risk of transmission. However, a comprehensive assessment requires integration of malaria epidemic

data from Myanmar. Malaria case surveillance is the core activity for malaria elimination, and for preventing the re-establishment of local malaria transmission.

Malaria is a severe threat to public health worldwide. The *World Malaria Report 2025* estimated that there were >280 million malaria cases and over 600,000 deaths worldwide in 2024 (1). Malaria, once highly prevalent in China, significantly endangers the health of the general population. After >70 years of sustained efforts, China eliminated malaria, and it was officially certified by the World Health Organization in 2021 (2). Nevertheless, the China–Myanmar border in Yunnan Province (CMBYP) remains the most challenging area for malaria control in China because of its unique geographical location, frequent cross-border movement, lack of natural border barriers, and an environment conducive to vector breeding and malaria transmission (3). To develop targeted prevention and control strategies, prevent introduced transmission, and sustain elimination achievements in border areas, the epidemiological characteristics of imported malaria cases (IMCs) along the CMBYP between 2021 and 2025 were analyzed.

METHODS

Individual malaria data from 18 counties (cities) along the CMBYP were collected via the National Notifiable Disease Reporting System (NNDRS) between 2021 and 2025. The temporal, spatial, and demographic distribution of malaria cases, together with data on *Plasmodium* species, case classification [indigenous^{*}, imported[†], or other

* Indigenous case: a malaria case that resulted in sustained local transmission over time (beyond the first generation), indicating an established transmission cycle.

† Imported case: a malaria infection acquired outside the area/country and diagnosed after entry/return; local mosquito transmission is not implied.

(relapse[§] or introduced[¶])] (4), source of infection, and timeliness of medical treatment, were analyzed to explore the characteristics of IMCs. Data from Hong Kong, Macao, and Taiwan were not included. Also, data from foreign nationals were included. Clinically diagnosed cases^{**} and confirmed cases^{††} were included in the analysis. The data were organized and analyzed using WPS (version 12.1.0.26895, Kingsoft Corp., Zhuhai, China) and SPSS (version 26.0, IBM Corp., New York, US). Time-interval data were compared using the Kruskal-Wallis H test, and annual variation was assessed using the chi-square (χ^2) test for trend, with $P < 0.05$ considered to be statistically significant. Anonymized routine surveillance data were used, and they were exempt from ethical review.

RESULTS

A total of 1,602 malaria cases within the CMBYP were recorded in the NNDRS between 2021 and 2025, all of which were IMCs. One death was reported in 2025^{§§}. The IMCs occurred predominantly among Chinese people ($n=1,410$, 88.01%). Among these, 1,601 (99.94%) were confirmed, and in one (0.06%) case there was a clinical diagnosis. The IMCs included *P. vivax* ($n=1,578$, 98.50%), *P. falciparum* ($n=20$, 1.25%), *P. ovale* ($n=3$, 0.19%), and *P. malariae* ($n=1$, 0.06%). Over the previous five years, except for a decrease in 2022, case numbers increased annually, with a statistically significant trend (χ^2 , 1,525.85; $P < 0.01$) (Figure 1).

The IMCs originated in 14 countries across two

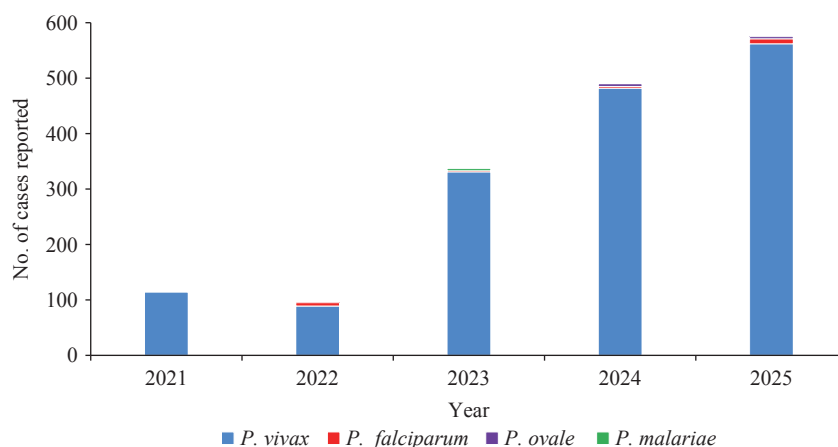


FIGURE 1. Imported malaria cases in counties along the China–Myanmar border in Yunnan Province (2021–2025).

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

TABLE 1. Distribution of regions of infection among the imported malaria cases reported along the China-Myanmar border in Yunnan Province (2021–2025).

Continent	Country	<i>P. vivax</i>	<i>P. falciparum</i>	<i>P. ovale</i>	<i>P. malariae</i>	Subtotal
Africa	12	1	17	3	1	22
Asia	2	1,577	3	0	0	1,580
Total	14	1,578	20	3	1	1,602

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

[§] Relapse case: a malaria case caused by reactivation of hypnozoites of previously acquired *P. vivax* or *P. ovale*.

[¶] Introduced case: a first generation, locally acquired malaria infection in which transmission occurs via local *Anopheles* mosquitoes infected after feeding on an imported case (i.e., the index infection is imported, but the subsequent case is locally transmitted).

^{**} Clinically diagnosed case: A cases with typical or atypical clinical symptoms, with a history of an overnight stay in malaria-endemic areas during the transmission season or a blood transfusion in the preceding 14 days.

^{††} Confirmed case: a clinically diagnosed case that is confirmed as positive by microscopy, rapid diagnostic test, or a polymerase chain reaction assay.

^{§§} This patient was infected with *P. falciparum*. The patient was in critical condition upon entry and developed multiple organ failure. On entering China from Myanmar, the patient immediately received antimalarial and symptomatic treatments. The patient died on the second day after entry.

TABLE 2. Distribution of imported malaria cases by counties along the China-Myanmar border in Yunnan Province (2021–2025).

County (city)	<i>P. vivax</i>	<i>P. falciparum</i>	<i>P. ovale</i>	<i>P. malariae</i>	Subtotal
Yingjiang	879	2	0	0	881
Tengchong	227	2	2	1	232
Longchuan	135	0	0	0	135
Ruili	127	0	0	0	127
Mangshi	81	5	1	0	87
Gengma	33	2	0	0	35
Cangyuan	34	0	0	0	34
Zhenkang	30	0	0	0	30
Longling	18	0	0	0	18
Mengla	2	5	0	0	7
Jinghong	3	2	0	0	5
Menglian	3	1	0	0	4
Lushui	3	1	0	0	4
Menghai	1	0	0	0	1
Fugong	1	0	0	0	1
Langcang	1	0	0	0	1
Total	1,578	20	3	1	1,602

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

continents (Asia and Africa). Of these, IMCs from Asia ($n=1,580$, 98.63%) originated in two countries (Myanmar and Laos), whereas IMCs from Africa ($n=22$, 1.37%) originated in 12 countries. Most IMCs originated in Myanmar ($n=1,217$, 75.97%) (Table 1).

Overall, 16 counties, except for Gongshan and Ximeng, reported IMCs. Yingjiang County ($n=881$, 54.99%), Tengchong City ($n=232$, 14.48%), Longchuan County ($n=135$, 8.43%), and Ruili City ($n=127$, 7.93%) had the highest numbers of IMCs. These four counties (cities) accounted for 85.83% (1,375/1,602) of all IMCs (Table 2).

The temporal distribution showed that IMCs were reported monthly between 2021 and 2025 (2–117 cases/month), peaking between May and July. Cases during these months accounted for 48.56% (778/1,602) of all cases. There were 1,203 (75.09%) IMCs in males and 399 (24.91%) in females, with a sex ratio of 3.02:1. The age at onset ranged from nine months to 87 years, mainly among adults aged 21–50 years ($n=1,022$, 63.80%). The travel purposes were labor ($n=659$, 52.93%), visiting relatives or friends ($n=297$, 23.61%), other purposes ($n=151$, 12.13%), business ($n=111$, 8.91%), tourism ($n=20$, 1.61%), and official business ($n=10$, 0.80%). Among cases with "other" travel purposes, the majority ($n=125$, 82.78%)

were Myanmar residents, primarily visiting relatives or for employment.

The onset to initial diagnosis interval ranged from zero to 18 days [median, two days; interquartile range (IQR), three days], with 70.47% ($n=1,129$) of patients seeking care within three days of symptom onset. The initial visit to diagnosis interval ranged from zero to 10 days, with a median and IQR of zero days; 77.97% ($n=1,249$) of the cases were confirmed on the day of the initial consultation, and 89.45% ($n=1,433$) received a definitive diagnosis within two days. The diagnosis-to-reporting interval ranged from zero to four days (median, one day; IQR, one day), with almost all cases ($n=1,600$, 99.88%) reported within one day of diagnosis. The epidemiological survey completion interval ranged from zero to 239 days (median, two days; IQR, two days), with an 83.46% (1,337/1,602) completion rate within three days. Temporal trends across the five-year study period were assessed using the Kruskal–Wallis H test, which revealed statistically significant differences for all four intervals ($H=10.78$, 11.11, 71.39, and 466.36, respectively; all $P<0.05$). In addition, pairwise comparisons showed that all intervals were significantly shorter in 2021–2022 than in 2023–2025 ($U=125$, 742.50, 131,948.50, 115,313.00, and 123,525.00,

respectively; all $P < 0.01$).

Most patients ($n=1,348$, 84.14%) were diagnosed with malaria at their first visit, with the majority of the diagnoses being made at medical centers and CDCs at the county level or below ($n=1,297$, 96.22%). In contrast, 254 patients (15.86%) were initially diagnosed with other conditions, most frequently at township health centers or village clinics ($n=129$, 50.79%), followed by county-level medical centers or the CDC ($n=60$, 23.62%), and individual practitioners ($n=41$, 16.14%). Regarding reporting institutions, the IMCs were primarily reported by county-level medical institutions ($n=794$, 49.56%), township health centers ($n=649$, 40.51%), and prefecture-level medical institutions ($n=50$, 3.12%).

DISCUSSION

The predominance of *P. vivax* infections among IMCs in the CMBYP reflects the provincial case composition, but it diverges from the national profile. The high relapse potential of vivax malaria, together with the broad distribution of competent vectors and persistent control challenges, renders this region particularly vulnerable to introduced transmission following IMCs. The demographic distributions of sex and age were comparable to national figures (5–6). A distinct mid-year incidence peak, concurrent with maximal vector activity, underscores summer as a pivotal period for intervention. Reinforced case surveillance and vector control measures are imperative to prevent the re-establishment of local transmission. Notably, the majority of cases involved young to middle-aged males, with occupational labor and family visitation as the predominant travel motives. These observations suggest that targeted prevention strategies should be directed towards migrant workers returning from endemic areas and cross-border family visitors in the CMBYP, with an emphasis on improving malaria literacy and facilitating prompt medical consultation among these high-risk cohorts.

Over the 2021–2025 period, the accuracy of initial diagnoses for reported malaria cases was $>80\%$, closely aligning with the provincial mean. Initial misdiagnoses were most frequently documented at township health centers or village clinics, county-level medical facilities or CDCs, and individual practitioner offices. To reinforce malaria prevention and control in Yunnan Province, strategic priority should be assigned to

upgrading diagnostic capabilities at primary-level facilities and rectifying deficiencies in case diagnosis and treatment. Concurrently, structured training programs in malaria recognition and clinical management should be directed towards individual practitioners, with the goal of refining diagnostic judgment, and reducing the incidence of misdiagnosis and underdiagnosis.

The difference in the time intervals from onset to initial diagnosis and from initial diagnosis to definitive diagnosis is of great significance for public health (7). In the present study, it has been shown that the intervals between onset and initial diagnosis, and between initial diagnosis and confirmation, varied significantly across 2021–2025. Greater than 70% of the patients sought medical attention within three days of onset, and $>75\%$ were diagnosed on the day of the initial visit. These findings indicate that the diagnostic pathway in the CMBYP is efficient, facilitating early detection of cases, prompt administration of treatment, and effective interruption of transmission. The epidemiological investigation completion rate within three days was 83.46%, which is lower than that reported for Guangzhou City (8). The marked reduction in the three-day completion rate in 2023 was likely to be associated with the rollout of the new Parasitic Disease Prevention and Control Information Management System in September 2023. Additionally, the prolongation of all four time-intervals during 2023–2025, relative to 2021–2022, may reflect the combined effects of eased pandemic-related policies and decreased public vigilance towards fever-associated conditions in the post coronavirus disease 2019 era.

Yunnan Province is in the southwestern region of China, with a border of 4,060 km. It has 25 border counties in states (cities) bordering Myanmar, Laos, and Vietnam (3), including 18 counties bordering Myanmar. As a country with a high malaria burden, Myanmar has relatively poor public health infrastructure, slower economic development, and suitable conditions for malaria transmission. In 2024, the cumulative number of reported malaria cases increased by 238.04% compared to that in 2019, with cases mainly concentrated in the Thailand-Myanmar and China-Myanmar border areas (9). Since 2023, Yunnan Province has ranked first nationwide in reported malaria cases. From 2021 to 2025, 84% of malaria cases in the province originated from the CMBYP, with Yingjiang County, Tengchong City,

Longchuan County, and Ruili City reporting the highest numbers. Laiza and nearby areas in Myanmar, bordering Yingjiang County, were identified as the primary malaria hotspots in the border regions of Yunnan Province, China. The incidence rate of malaria in Kachin State in 2024 increased by 24.53 times compared with that in 2019, indicating a severe epidemic (10). A combination of these factors has led to a sustained and increasing risk of malaria transmission in the CMBYP.

To reduce imported malaria and prevent re-establishment of transmission, the "3+1" strategy was used to strengthen malaria surveillance, respond rapidly to imported malaria, and enhance cross-border collaboration with neighboring countries (11–12). To date, the province has achieved 10 consecutive years with no re-transmission of imported cases, and six consecutive years with no clustered cross-border imported malaria outbreak (13). However, after malaria elimination, some regions have shown declining attention towards malaria prevention and control (14). There is a perception that "malaria has specific therapeutics, rarely causes death, and will not lead to serious incidents" (15), resulting in insufficient staffing, funding, and material support for malaria control and prevention.

To further consolidate malaria elimination achievements in the China-Myanmar border areas, and to strengthen the foundations for preventing importation and transmission, all levels of government should establish "strictly preventing importation and transmission, consolidating malaria elimination achievements" as an annual work goal, and establish a normalized work mechanism; conversely, preferential support for border areas should be increased, with key guarantees in policy formulation, funding support, resource allocation, and other aspects, to support the prevention and control of introduced transmission. In addition, malaria case surveillance is the core activity for malaria elimination and prevention of the re-establishment of local malaria transmission, with laboratory diagnosis as the fundamental tool. This requires a medical-facility-based malaria case detection system supported by prompt CDC investigation and response, as well as effective communication and coordination across public and private hospitals, clinics, drug outlets, and pharmacies.

Conflict of interest: No conflicts of interest.

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Corresponding authors: Zurui Lin, linzurui@foxmail.com; Zhigui Xia, xiazg@nipd.chinacdc.cn.

¹ Yunnan Institute of Parasitic Diseases, Yunnan Provincial Key Laboratory of Vector-borne Diseases Control and Research, Kunming City, Yunnan Province, China; ² Yingjiang County Center for Disease Control and Prevention, Yingjiang County, Yunnan Province, China; ³ National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention (Chinese Center for Tropical Diseases Research), National Key Laboratory of Intelligent Tracking and Forecasting for Infectious Diseases, National Health Commission Key Laboratory of Parasite and Vector Biology, WHO Collaborating Center for Tropical Diseases, National Center for International Research on Tropical Diseases, Ministry of Science and Technology, Shanghai, China.

& Joint first authors.

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Preplanned Studies

Global Cross-Border Migration and Secondary Transmission Patterns of Lassa Fever — Global, 1969–2025

Zekun Wang^{1,†}; Na Zeng^{2,†}

Summary

What is already known about this topic?

Lassa fever has been increasingly transmitted from endemic West African regions via global migration; however, its macro-level transmission network and behavioral drivers remain uncharacterized.

What is added by this report?

We constructed a historical cross-border transmission network that revealed two distinct modes: air-travel-dependent intercontinental spread and land-dependent regional spread. Secondary human-to-human transmission is rare across all scenarios and relies critically on robust local infection prevention and control.

What are the implications for public health practice?

We recommend a shift from uniform border measures to precision- and scenario-based interventions. Enhancing targeted syndromic screening and local early warning capacities at the identified network hubs and bridge countries could optimize resource allocation and prevent outbreaks.

ABSTRACT

Introduction: Cross-border transmission of Lassa fever poses a growing global public health threat; however, its global transmission network and migration-related secondary transmission risks remain poorly understood.

Methods: We extracted data on historical cross-border transmission events (1969–2025) from the Global Infectious Diseases and Epidemiology Network database. Descriptive spatiotemporal and network analyses were utilized to characterize the transmission scenarios, transportation modes, and country-level transmission network community structures.

Results: We identified 57 cross-border transmission events, involving 84 migratory cases. Cross-border tours (61.4%, 35/57) drove intercontinental spread via air travel, while land travel characterized the West

African intracontinental spread. Secondary human-to-human transmission was rare across all scenarios and relied critically on robust local infection prevention and control. High-income nations served as frequent destinations for intercontinental case imports, likely reflecting the residents' travel exposure and strong detection capacities. West African nations acted as the primary endemic sources and vital structural bridges.

Conclusion: The global migration of Lassa fever cases was primarily driven by tours. Under robust infection prevention and control conditions, the risk of large-scale secondary outbreaks at import destinations can be effectively mitigated. Precision and scenario-based interventions, including targeted syndromic screening and enhanced local response capacities in critical hub and bridge countries, are vital for global containment.

Lassa fever poses a high risk of global dissemination and cross-border transmission has emerged as a major public health challenge. The potential for asymptomatic or mild transmission, estimated to account for approximately 80% of all infections during the 6–21-day incubation period, further complicates the detection and containment of Lassa fever (1), thereby increasing the risk of unnoticed cross-border transmission. Driven by increasing global mobility and international trade, Lassa fever was increasingly spread from traditionally endemic regions in West Africa to non-endemic areas. In July 2024, a chef returning from Guinea to Mianyang, Sichuan Province, China, presented with symptoms including high fever and hearing loss, and was subsequently confirmed to be infected with Lassa fever virus via nucleic acid testing and whole-genome sequencing (2).

Despite these growing threats, the global transmission network facilitating the cross-border spread of Lassa fever remains largely uninvestigated, as does the local secondary transmission following cross-

border migration. In this study, we used descriptive spatiotemporal and network analyses to characterize the cross-border migration patterns of Lassa fever and subsequent local transmission at the country level.

Cross-border transmission data were extracted from the Global Infectious Disease and Epidemiology Network (GIDEON) database (3) on July 12, 2025 (Supplementary Materials, available at <https://weekly.chinacdc.cn/>). We quantified cross-border transmission events and migratory and secondary cases, stratified by transmission and transportation modes. A country-level directed weighted network was constructed, where nodes represented countries, directed edges denoted case flows, and edge weights reflected the cumulative frequency of documented transmission events, analyzed via network density, node strength, and betweenness centrality (Supplementary Materials). The Louvain algorithm was used to identify the significant community structures (modularity, $Q > 0.300$). Statistical significance was set at a two-sided $P < 0.05$. All statistical analyses were performed using R (version 4.1.2; R Foundation for Statistical Computing, Vienna, Austria).

Between 1969 and 2025, 84 migratory cases were reported across 57 cross-border transmission events of Lassa fever worldwide, involving 22 countries, and resulting in 35 local secondary cases across three countries.

Global dissemination is inextricably linked to sociobehavioral scenarios. Tours [61.4%, 95% confidence interval (CI): 47.6%, 74.0%; 35/57] were the primary drivers of documented cross-border transmission events. Health-seeking behavior, military mobility, and agricultural mobility accounted for 15.8% (95% CI: 7.5%, 27.9%; 9/57), 8.8% (95% CI: 2.9%, 19.3%; 5/57) and 5.3% (95% CI: 1.1%, 14.6%; 3/57) of the events, respectively (Figure 1A). To further elucidate health-seeking behavior-driven pathways, compositional analysis revealed that medical personnel infections occurred in 55.6% of the nine health-seeking behavior-related events. Secondary transmission was generally rare across all mobility scenarios, indicating that imported cases escalated infrequently into widespread local outbreaks. Also, a significant difference in the number of cross-border transmission events between transportation modes was observed ($P = 0.002$) (Figure 1B). The negative binomial regression model confirmed a significantly increasing trend in the annual number of reported primary migratory cases (IRR=1.028, 95% CI: 1.007, 1.050, $P = 0.016$) (Supplementary Figure S1, available

at <https://weekly.chinacdc.cn/>).

The overall case fatality rate (CFR) among the documented migratory primary cases was 35.7% (95% CI: 25.6%, 46.9%). We observed no statistically significant differences in CFRs across distinct transmission scenarios ($P = 0.145$) or transportation modes ($P = 0.279$), although the subgroup estimates exhibited wide confidence intervals owing to the inherent sparsity of historical data (Supplementary Table S1, available at <https://weekly.chinacdc.cn/>).

The cross-border transmission network exhibited a highly structured hub-and-spoke architecture (density=0.067) (Figure 1C). The distributions for country in-degree (skewness=1.31), out-degree (skewness=1.68), in-strength (skewness=2.24), and out-strength (skewness=2.29) exhibited heavy right skewness (Figure 2), indicating that a minority of hub countries had a disproportionate influence on the Lassa fever global transmission trajectory. Sierra Leone, Nigeria, Liberia, and Burkina Faso functioned as primary outflow sources, exporting cases largely tied to health-seeking, military, and tourism activities. Conversely, high-income nations, such as Germany, the United Kingdom, and the United States, acted as primary intercontinental inflow destinations, consistently ranking at the top for both in-degree and in-strength metrics. This prominent inflow status likely reflects the residents' frequent travel to West Africa and their advanced diagnostic capacity to detect imported cases. Concurrently, neighboring West African countries, specifically Togo, Ghana, and Benin, also exhibited notable in-degree and in-strength rankings, highlighting frequent cross-border transmission events within endemic regions. Crucially, a subset of nodes, including Sierra Leone, Liberia, South Africa, Ghana, and Togo, exhibited the highest betweenness centrality (Figure 1C and 2), operating as vital structural bridges within the global transmission network, and marking them as critical hubs that could facilitate escalation from an endemic state to severe localized outbreaks or nosocomial clusters.

Distinct clustering patterns further elucidated these dynamics (modularity $Q = 0.362$), delineating four network communities, and revealing two primary modes of geographical spread (Figure 1C, Supplementary Table S2). Long-distance mode, characterized by intercontinental spread, was typified by Communities 1, 2, and 3 and predominantly utilized air travel. Air travel accounted for 50.0% (5/10), 69.2% (9/13), and 100.0% (5/5) of intra-community transmission events in communities 1, 2,

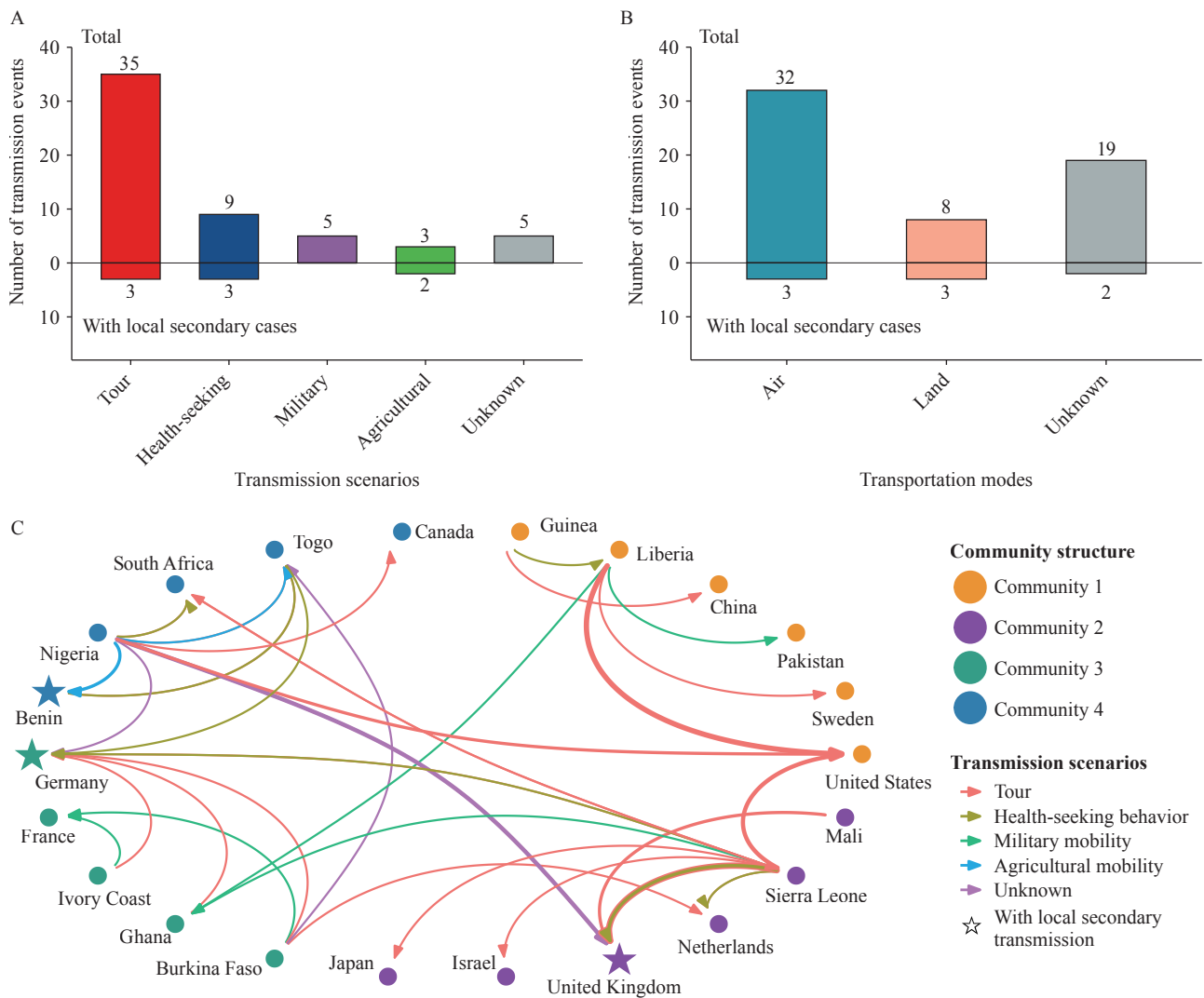


FIGURE 1. Global Lassa fever cross-border migration patterns. (A) Distribution of global Lassa fever migratory events by scenario; (B) Distribution of global Lassa fever migratory events by transportation mode; (C) Country-level directed weighted migration network for migratory events and clustering patterns detected using the Louvain algorithm.

and 3, respectively. This intercontinental mode was largely driven by tours; for instance, tours drove 80.0% (8/10) of the internal spread in Community 1, as well as 76.9% (10/13) and 60.0% (3/5) in Communities 2 and 3. Conversely, the short-distance mode was dominated by the intracontinental spread within West Africa, as typified by Community 4. This localized spread relied heavily on land travel, which constituted 50.0% (5/10) of its internal events (compared to only 10.0% for air travel).

DISCUSSION

The global spread of Lassa fever is a complex, dynamic, multifactorial process that relies heavily on human migration. Utilizing a transmission network

framework is essential for decoding the propagation dynamics. To the best of our knowledge, no previous study has analyzed the migration patterns and subsequent local secondary transmission of Lassa based on behavioral motivations from a global network perspective.

Our findings underscore the need to shift from one-size-fits-all border policies to precision and scenario-based interventions. The current landscape demands that countries assume different responsibilities based on their network roles. Primary source countries should prioritize upstream interventions such as rodent control and enhanced syndromic surveillance at primary care facilities (4). High-volume inflow countries could transition to active defense by deploying rapid metagenomic sequencing at aviation

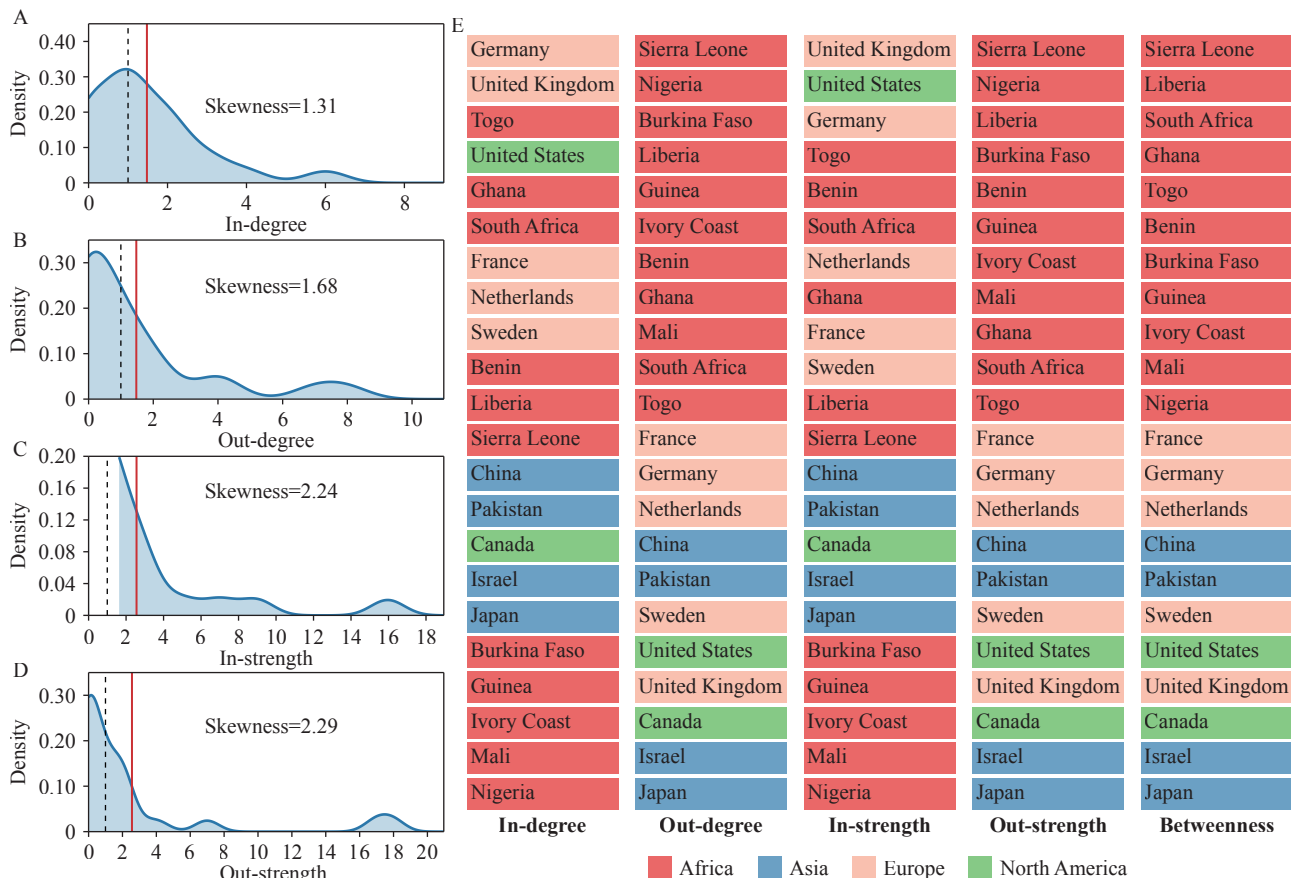


FIGURE 2. Distributions of countries' in-degree (A), out-degree (B), in-strength (C), out-strength (D), and betweenness centrality (E) in the global Lassa fever cross-border migration network.

hubs during the tourism peak (5). Meanwhile, bridge countries hold the key to preventing regional endemic transmission from triggering severe cross-border healthcare-associated outbreaks; their focus may center on establishing robust screening protocols in international border trading zones and serving as regional epidemic information hubs (6).

The principal contribution of this study lies in its descriptive assessment of the local transmission risks associated with distinct migration pathways. While tours were the most frequent scenario for migratory case inflows, primarily driving intercontinental spread, agricultural mobility via land travel remained a critical localized pathway in West Africa. Agricultural workers inherently face high occupational exposure to rodent reservoirs and their excreta in source regions, leading to a high probability of primary zoonotic infections (7). However, our event-level analysis revealed that widespread secondary human-to-human transmission following these imports was exceedingly rare across all scenarios. Crucially, this rarity was highly conditional; it fundamentally relied on medical institutions and the

public in importing areas maintaining strong infection prevention awareness, enabling the standardized management of cases. This aligns with the epidemiological nature of Lassa fever; it is primarily a rodent-borne zoonosis in which humans act largely as dead-end hosts, and secondary transmission is typically restricted to close household contacts or healthcare settings lacking standard infection prevention and control (IPC) measures. Consequently, whether an imported case escalated into a secondary cluster was less dependent on the travel context itself and was overwhelmingly determined by the destination's local surveillance, early warning, and emergency response capacity. Although cross-border migration has facilitated viral export, the risk of establishing new natural endemic sites or triggering a true global pandemic remains low. To sustain this containment, global and regional public health apparatuses should prioritize these critical nodes by enhancing targeted syndromic screening, rapid diagnostic capabilities, and emergency preparedness, coupled with strict IPC adherence, at porous rural land crossings and

community clinics.

This study has some limitations. First, the reliance on the GIDEON database introduced reporting bias (underestimating cases in low-resource endemic regions) and ascertainment bias (disproportionately overdetecting imported cases in high-income nations). Furthermore, the 56-year span introduced temporal heterogeneity; the observed increasing trends likely reflected enhanced historical surveillance and diagnostics rather than a purely true epidemiological expansion. Second, the ultra-sparse nature of our network (density=0.067) made the topological metrics, particularly betweenness centrality, inherently unstable. Thus, identified structural "hubs" or "bridges" serve strictly as descriptive reflections of historical flows rather than robust predictive indicators. Finally, we utilized the aggregated static network-masked temporal evolution. Although dynamic network analysis is theoretically preferable, extreme data sparsity precludes this approach because stratifying limited events yields mathematically uninterpretable fragmented networks. Consequently, this network represents a cumulative historical overview, rather than an evolving temporal model.

This study highlighted that the global spread of Lassa fever operates through distinct behavior-driven network channels rather than through random dissemination. As widespread secondary transmission remains rare, public health strategies should shift from generalized border restrictions to precision and scenario-based interventions. Non-endemic destinations, including major aviation hubs and expanding trade partners such as China, should enhance port-of-entry syndromic screening and rapid diagnostics for high-risk inbound travelers, particularly returning expatriates and tourists. Concurrently, endemic nodes and structural bridge countries should strengthen their early warning systems, infection prevention protocols, and land border surveillance to promptly contain isolated importations.

Conflicts of interest: No conflicts of interest.

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Corresponding authors: Zekun Wang, wangzekun@wjw.beijing.gov.cn; Na Zeng, zengnapkufh@bjmu.edu.cn.

¹ Beijing Municipal Health Big Data and Policy Research Center, Beijing, China; ² Department of Infection Control, Peking University First Hospital, Beijing, China.

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SUPPLEMENTARY MATERIALS

MATERIALS AND METHODS

Data Collection

The socio-behavioral transmission scenarios driving cross-border transmission events were explicitly defined as follows: 1) Tour: Individuals crossing international borders for leisure, business, or non-medical occupational purposes (e.g., tourists, engineers, general aid workers, and diplomats) who contracted the virus in an endemic region and subsequently initiated a cross-border event (including returning to their home countries or being evacuated due to illness). 2) Health-seeking behavior: Cross-border movements specifically initiated for medical purposes post-infection. This category strictly comprises medical evacuations of infected healthcare personnel (e.g., foreign doctors and nurses with direct occupational exposure) and local residents of endemic regions crossing regional borders, specifically to seek better medical care. 3) Military mobility: Movement of armed forces, peacekeeping personnel, and military contractors across borders. 4) Agricultural mobility: The movement of seasonal agricultural workers, farmers, or livestock herders typically across land borders within the endemic West African region.

All data collection and extraction processes were independently conducted by two reviewers. The data extracted by the two reviewers were cross-checked at each stage. Discrepancies were resolved through discussion or consultation with a third reviewer to reach a final consensus.

Statistical Analyses

First, we quantified the number of documented transmission events, migratory primary cases, and local secondary cases, stratified by cross-border transmission scenarios and modes of transportation. To appropriately quantify the uncertainty in our descriptive exploratory analysis, 95% confidence intervals (CIs) for the proportions were calculated using the exact binomial (Clopper–Pearson) method. Missing data were not imputed to prevent artificial bias. Differences in case counts across transmission scenarios and modes of transportation were evaluated using the Kruskal–Wallis H test. When significant, this was followed by Dunn's post-hoc test with the Benjamini–Hochberg false discovery rate (FDR) correction for multiple comparisons. Furthermore, owing to the inherent sparsity of the subgroup data, we compared case fatality rates (CFRs) across different scenarios and transportation modes using Fisher's exact test.

We utilized a negative binomial regression model to assess temporal trends while accounting for the overdispersed and zero-inflated nature of the long-term historical count data. The annual count of reported primary migratory

SUPPLEMENTARY TABLE S1. Case fatality rates of primary migratory Lassa fever cases by transmission and transportation mode.

Characteristics	Total migratory cases	Total deaths	CFR (%)	95% CI (%)	P
Overall	84	30	35.7	25.6–46.9	
Scenarios					0.145
Tour	39	19	48.7	32.4–65.2	
Health-seeking behavior	9	3	33.3	7.5–70.1	
Military mobility	21	4	19	5.4–41.9	
Agricultural mobility	10	2	20	2.5–55.6	
Unknown	5	2	40	5.3–85.3	
Transportation modes					0.279
Air	34	14	41.2	24.6–59.3	
Land	15	7	46.7	21.3–73.4	
Mixed air and land	2	1	50.0	1.3–98.7	
Unknown	33	8	24.2	11.1–42.3	

Note: 95% CIs were calculated using the exact binomial (Clopper–Pearson) method. P-values were derived using the Fisher's exact test. Abbreviation: CFR=case fatality rate; CI=confidence interval.

SUPPLEMENTARY TABLE S2. Flow of Lassa fever within and between communities by scenario and transportation mode.

Characteristics	Community 1 (n, %)		Community 2 (n, %)		Community 3 (n, %)		Community 4 (n, %)	
	Inter-community	Outflow to others	Inter-community	Outflow to others	Inter-community	Outflow to others	Inter-community	Outflow to others
Total	10 (100)	2 (100)	13 (100)	8 (100)	5 (100)	2 (100)	10 (100)	11 (100)
Scenarios								
Tour	8 (80.0)	1 (50.0)	10 (76.9)	6 (75.0)	3 (60.0)	1 (50.0)	5 (50.0)	5 (45.5)
Health-seeking behavior	1 (10.0)	0 (0.0)	3 (23.1)	1 (12.5)	0 (0.0)	0 (0.0)	2 (20.0)	2 (18.2)
Military mobility	1 (10.0)	1 (50.0)	0 (0.0)	1 (12.5)	2 (40.0)	0 (0.0)	0 (0.0)	0 (0.0)
Agricultural mobility	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	3 (30.0)	0 (0.0)
Unknown	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (50.0)	0 (0.0)	4 (36.4)
Transportation modes								
Air	5 (50.0)	2 (100.0)	9 (69.2)	4 (50.0)	5 (100.0)	1 (50.0)	1 (10.0)	8 (72.7)
Land	2 (20.0)	0 (0.0)	0 (0.0)	1 (12.5)	0 (0.0)	0 (0.0)	5 (50.0)	0 (0.0)
Unknown	3 (30.0)	0 (0.0)	4 (30.8)	3 (37.5)	0 (0.0)	1 (50.0)	4 (40.0)	3 (27.3)

Note: Intercommunity: migratory case flow within each community; outflow to others: migratory case flow to other communities.

cases was modeled as the dependent variable, with the year of reporting as the independent continuous variable. Incidence rate ratios (IRRs) and 95% *CI*s were calculated to quantify trends.

Subsequently, a country-level directed weighted network was constructed to characterize the historical migration patterns. In this network, nodes represent individual countries and the directed edges denote the direction of cross-border transmission flows. To strictly align with a transmission-event-level framework and minimize the disproportionate impact of clustered individual cases originating from single outbreaks, the edge weight between any two nodes was defined as the cumulative frequency of documented independent transmission events traveling from the origin country to the destination country, rather than the raw count of individual migratory cases. The following summary statistics and methods were used to characterize the global Lassa fever transmission network:

1) Node strength quantifies a node's overall connectivity by calculating the sum of the weights attached to its edges. In the context of global disease spread, the node degree and strength indicate the diversity of a country's travel partners and the total volume of imported/exported transmission events, respectively. It was defined as,

$$S_i = \sum_{j=1, j \neq i}^n w_{ij} + w_{ji} \quad (1)$$

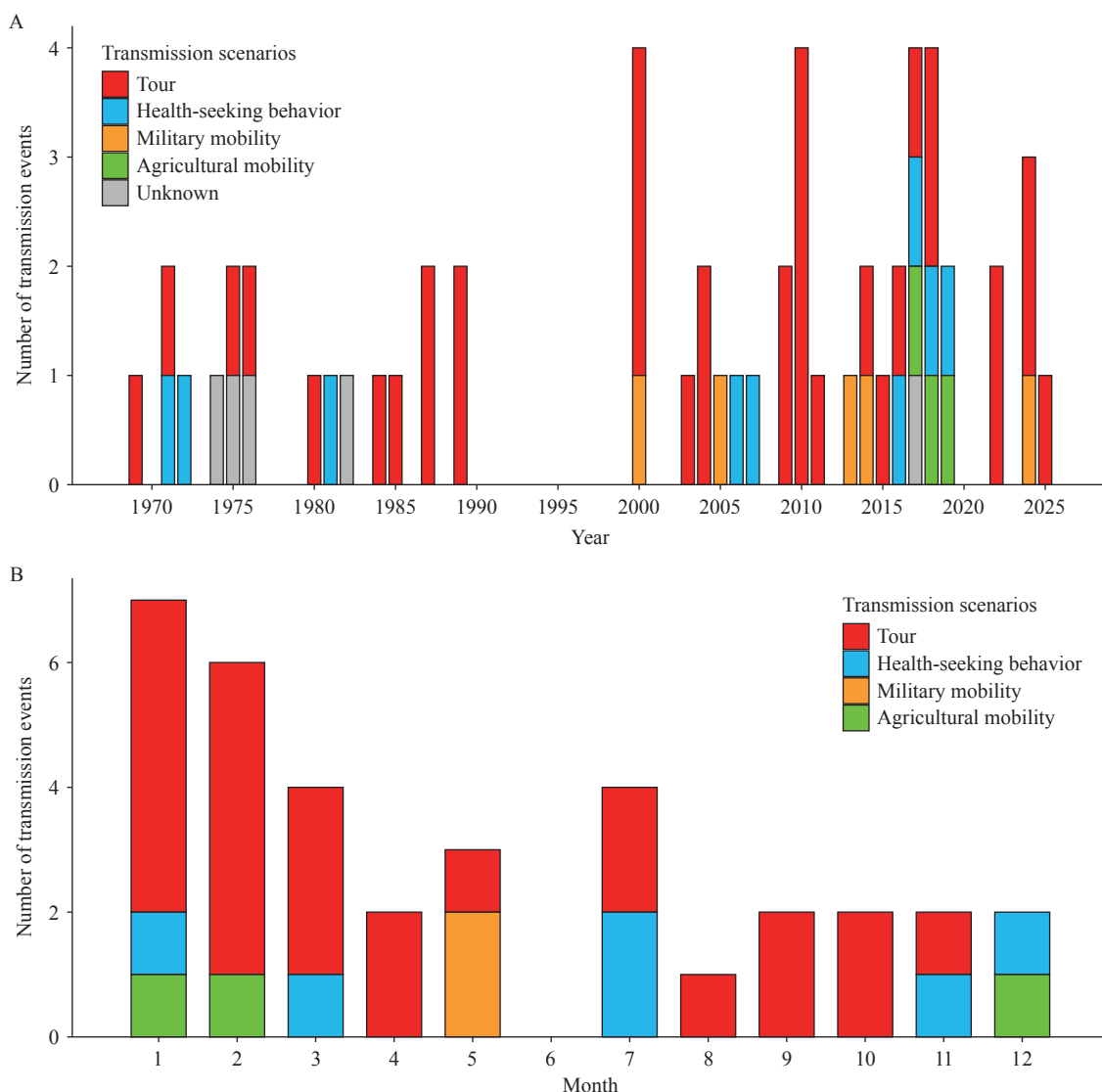
where n is the number of countries in the network, w_{ij} is the weight of the directed edge from country i to j , and w_{ji} is the weight of the directed edge from country j to i . Node strength is categorized into in-strength and out-strength in directed networks. In-strength represents the total weight of the incoming edges, reflecting the country's risk as a destination for imported Lassa fever. Out-strength corresponds to the total weight of the outgoing edges, indicating the country's potential to export Lassa fever.

2) Node betweenness is the number of shortest directed paths (i.e., the path between two nodes that minimizes the sum of the weights along the path) between all pairs of country nodes passing through an intermediary node, indicating the country's role as a bridge in the network. In public health terms, betweenness centrality identifies structural bridge countries that act as critical bottlenecks connecting different regional transmission corridors. The betweenness centrality of a country node is defined as

$$B_i = \frac{1}{(n-1)(n-2)} \sum_{j=1, j \neq i}^n \sum_{k=1, k \neq i \neq j}^n \frac{g_{ik}(i)}{g_{jk}} \quad (2)$$

where n is the number of countries in the network, $g_{ik}(i)$ is the number of shortest paths from countries j to k passing through country i , and g_{jk} is the total number of shortest paths between countries j and k .

3) Network density describes the proportion of existing directed edges relative to the maximum possible number of edges in a network. In a directed network, the maximum number of edges is $n(n-1)$, where n is the number of countries. A high network density implies strong connectivity, which may facilitate the global spread of Lassa fever.



SUPPLEMENTARY FIGURE S1. Temporal trends of Lassa fever transmission events by scenarios. (A) Annual number of transmission events. (B) Monthly number of transmission events.

In contrast, a low density suggests limited direct connections and an ultrasparse architecture. It is defined as:

$$D = \frac{E}{n(n-1)} \quad (3)$$

where E represents the number of existing directed edges in the network, and n is the number of countries.

4) Community detection was applied to identify the underlying structural clusters in the global Lassa fever migration network. We employed the Louvain algorithm, which is a hierarchical clustering method that optimizes modularity by iteratively merging countries and communities, to detect potential community structure in the network. The modularity Q of a network is calculated as:

$$Q = \sum_c \left[\frac{W_{C,in}}{2W_{tot}} - \gamma \left(\frac{W_{C,con}}{2W_{tot}} \right)^2 \right] \quad (4)$$

where $W_{C,in}$ is the total weight of the edges within community C , $W_{C,con}$ is the total weight of the edges connecting community C to other communities, and W_{tot} is the sum of all edge weights in the network. A modularity Q value exceeding 0.3 indicates significant community structures.

A two-sided $P < 0.05$ was considered statistically significant. All statistical analyses and mapping were performed using R (version 4.1.2; R Foundation for Statistical Computing, Vienna, Austria).

Outbreak Reports

A Foodborne Disease Outbreak Caused by *Salmonella enterica* Serovar Braenderup (ST311) — Yangjiang City, Guangdong Province, China, July 2025

Huaying Ao¹; Zhenhui Huang¹; Jiajun Liu²; Tongqi Huang³; Lin Liu⁴; Chenglong Ye¹; Ping Gan²; Yihuo Huang¹; Zhuliang Chen¹; Xianju Lin¹; Ruogu Chen¹; Ruidan Zhu⁵; Yijing Chen¹; Jian Wen²; Junhua Liang²; Qiong Huang²; Zhiting Liu^{2,†}

Summary

What is already known about this topic?

Salmonella is a major foodborne pathogen, and eggs are established vehicles for common serotypes such as Enteritidis. However, rare serotypes like Braenderup are infrequently identified in outbreaks, partly due to limited routine surveillance and the low resolution of conventional typing methods.

What is added by this report?

This report documents a point-source outbreak of *Salmonella* Braenderup ST311 involving 130 cases (attack rate 19.2%, median incubation 17 hours). Sandwich consumption was strongly associated [corrected odds ratio=1,626.7 (Haldane-Anscombe correction); 95% confidence interval: 81.7, 32,360; $P<0.0001$]. The outbreak strain was isolated from 34 patients, leftover sandwiches, and raw eggs, with cgMLST allelic differences of 0–1. Whole-Genome Sequencing (WGS) linked it to 32 historical sporadic cases and one food isolate, indicating persistent local circulation.

What are the implications for public health practice?

Eggs can harbor rare outbreak-prone serotypes. Bakeries must separate raw/cooked materials and ensure hand hygiene. WGS was critical for early detection and traceback in this event.

control study ascertained the suspected food vehicle.

Results: Among 676 graduation ceremony attendees, 130 probable cases were identified. A case control study conducted among attendees confirmed that sandwich consumption was significantly associated with illness [corrected odds ratio=1,626.7 (Haldane-Anscombe correction); 95% confidence interval: 81.7, 32,360.0; $P<0.0001$], with 100% (96/96) of cases and only 9.4% (3/32) of controls reporting sandwich consumption, epidemiologically implicating bakery-produced sandwiches served during the event as the vehicle. WGS revealed clonal relatedness among *Salmonella* Braenderup sequence type 311 (ST311) isolates from 34 patients, one leftover sandwich, and one egg sample from the implicated bakery, with core genome multilocus sequence typing allelic differences of 0–1. The outbreak strain showed high genetic homology with 32 sporadic case isolates and one food isolate detected in Yangjiang since 2019, suggesting a persistent contamination source.

Conclusion: *Salmonella* Braenderup (ST311) caused this outbreak. Cross-contamination from eggs used in other bakery products was the most likely mechanism. The investigation highlights the emerging risk of eggs as vehicles for rare *Salmonella* serotypes and the significance of WGS-based surveillance in linking sporadic cases to point-source outbreaks.

ABSTRACT

Introduction: In July 2025, Yangjiang CDC received reports of five children from the same kindergarten with vomiting, abdominal pain, diarrhea, and fever, suggesting a foodborne outbreak.

Methods: A multi-agency team used epidemiology and Whole-Genome Sequencing (WGS) to identify the cause, source, and transmission chain. A case

On July 27, 2025, at 22:04, Yangjiang CDC was notified by Yangjiang People's Hospital that five children from TLB Kindergarten had presented to the fever clinic with vomiting, abdominal pain, diarrhea, and fever, raising suspicion of a foodborne outbreak. Municipal and district CDCs immediately initiated a field investigation. As cases accumulated, a provincial emergency response was activated, and a joint

investigation team was formed at provincial, municipal, and county levels. This study identified the cause and risk factors to inform prevention and control.

INVESTIGATION AND RESULTS

Epidemiological Investigation

On July 26, 2025, from 14:00 to 18:00, TLB Kindergarten held a joint graduation ceremony for its Jiangcheng and Yangdong campuses at M Hotel in Jiangcheng District. A total of 676 persons attended: 231 children, 35 staff, and 410 family members. At around 16:00, a uniform afternoon snack — commercially packaged M brand milk and sandwiches produced by AEQ Bakery — was provided to the children. Out of the total of 300 sandwiches, 231 were distributed to children, and the remaining 69 were consumed by on-site staff and family members. Some

children also shared their sandwiches with their family members.

Case Definitions

Probable Case: An individual who attended the TLB Kindergarten graduation ceremony at M Hotel on July 26, 2025, or a family member of an attendee, presenting with fever (axillary temperature $\geq 37.3\text{ }^{\circ}\text{C}$) and diarrhea (≥ 3 episodes/24 hours with altered stool consistency) with onset on or after July 26, 2025.

On the evening of July 26, attendees developed fever, diarrhea, and vomiting; the index case developed symptoms at 20:00. The incubation period ranged 4–49 hours, with a median of 17 hours. A total of 130 probable cases were identified: 67 males and 63 females, including 109 children and 21 family members or staff. Specifically, among these 21 cases, 7 were adults and 14 were children not enrolled in the kindergarten. The median age was five years, with an

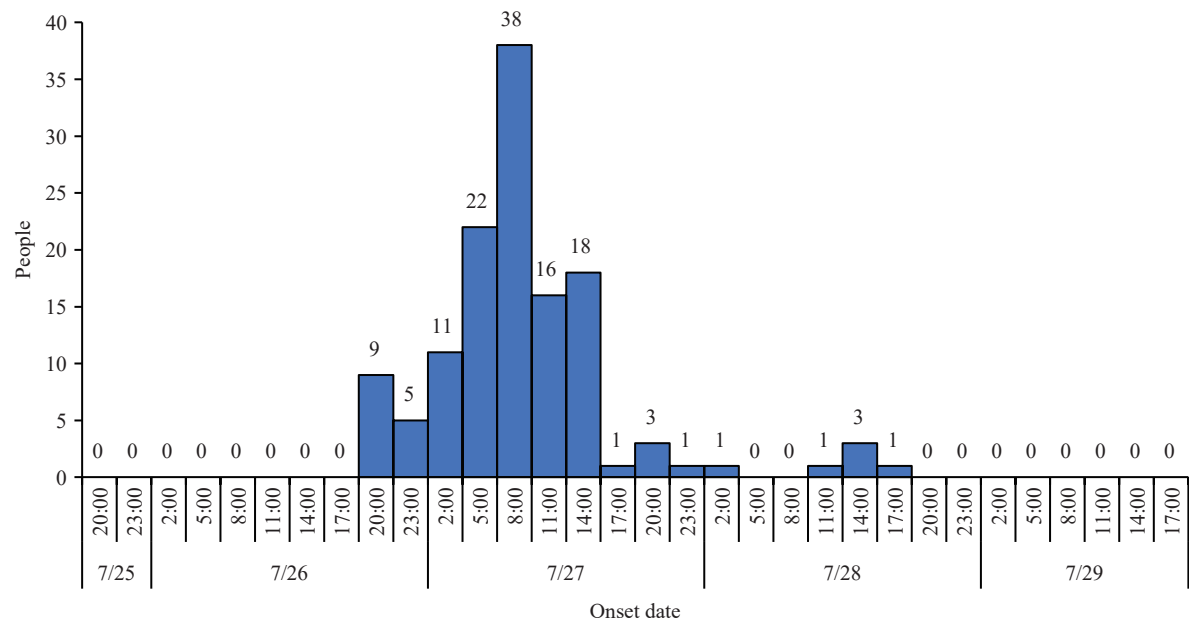


FIGURE 1. Epidemic curve of onset dates for suspect cases ($n=130$) of *Salmonella* Braenderup infection, Yangjiang City, Guangdong Province, China, July 2025.

TABLE 1. Attack rates among children by kindergarten campus and class, Yangjiang City, 2025.

Variable	Group	Cases (<i>n</i>)	Total (<i>N</i>)	Attack rate (%)	χ^2	<i>P</i>
Campus	TLB Jiangcheng Campus	75	155	48.39	0.27	0.602
	TLB Yangdong Campus	34	76	44.74		
Class	Preschool classroom	29	53	54.72	2.00	0.573
	Senior	43	94	45.74		
	Middle	26	56	46.43		
	Junior	11	28	39.29		

age range of 1–43 years. The overall attack rate was 19.2% (130/676). The epidemic curve exhibited a typical point-source pattern, with symptom onset concentrated on July 26–27 (Figure 1). No severe cases or deaths were reported. The attack rates of children in the two campuses were similar: 48.4% (75/155) and 44.7% (34/76) for the Jiangcheng and Yangdong campuses, respectively ($\chi^2=0.27$, $P=0.602$). The differences in attack rates among different classes was statistically insignificant (Table 1).

Food Hygiene Investigation

The afternoon snack on July 26 was the only common meal exposure among all attendees. Commercially packaged milk was excluded because of its wide distribution; contamination would have caused a geographically widespread outbreak. Based on the initial finding of *Salmonella* in five laboratory-confirmed cases, sandwiches became the focus of investigation.

The 180 m² AEQ Bakery (Hongfeng Town, Yangdong District) has food-processing and storage rooms, but no dedicated cleaning and disinfection area or video surveillance. Both pastry chefs denied any recent illness. Hygiene was poor: visible stains on refrigerators and ovens, uncovered food inside refrigerators, disorganized utensils, and mixed storage of raw eggs, opened meat floss, and cooked foods. In the week before the event, the bakery sold 50–150 pastries daily. On July 26, it produced 300 sandwiches — all sold to TLB Kindergarten. Sandwiches were made of bread slices, salad dressing, ham slices, and meat floss. Bread slices were prepared one day in advance and stored at room temperature. Pastry chefs did not wear gloves during dough preparation and baking (Figure 2).

Case-control Study

A case-control study was conducted among all graduation attendees, from whom 96 case-patients and 32 controls were randomly selected. The control group ($n=32$) was smaller than the case group ($n=96$) because of staffing and time constraints during the field investigation. All 96 case-patients (100%, 96/96), but only three controls (9.4%, 3/32) reported sandwich consumption, which was significantly associated with the illness [corrected odds ratio (OR)=1,626.7 (Haldane-Anscombe correction); 95% confidence interval (CI): 81.7, 32,360.0; $P<0.0001$]. Because of a zero cell in the 2×2 table, we applied the Haldane-Anscombe correction (adding 0.5 to each cell) to

obtain a finite odds ratio estimate. This confirmed sandwiches as the vehicle.

Laboratory and Whole-Genome Sequencing Analysis

Microbiological testing was performed according to the national standard (GB 4789.4-2024). Anal swabs from suspected cases, leftover food (sandwiches and milk), and bakery ingredients and environmental samples were collected. Swabs were plated on selective media; suspected colonies were identified by matrix-assisted laser desorption ionization time-of-flight mass spectrometry and serotyped using specific Cell (O) antigen and flagella (H) antigen antisera from Statens Serum Institut, Denmark. Representative isolates underwent Whole-Genome Sequencing (WGS). DNA was extracted using the Magen Hipure Bacterial DNA Kit, and paired-end sequencing of 2×150 base pairs was performed on an Illumina HiSeq 2000 platform. Data analysis yielded multilocus sequence typing, resistance genes, and virulence factors. Sequencing results were compared with a historical *Salmonella* allele database to determine homology with prior cases.

No *Salmonella* was isolated from environmental samples or food handler anal swabs. *Salmonella* Braenderup was isolated from patient specimens, leftover sandwiches, and raw egg samples from the bakery. WGS confirmed high genetic homology among isolates from 34 patients, one leftover sandwich, and one egg sample. Traceback identified the eggs as originating from L Farm in Gaozhou City, supplied by TM Food Co., Ltd. Although eggs were not a direct ingredient of the sandwiches, they were used in pastries produced concurrently at the bakery, strongly suggesting cross-contamination.

All outbreak-related isolates were ST311. Core genome multilocus sequence typing (cgMLST) showed that 15 human isolates and one sandwich isolate clustered together with zero allelic differences; they differed by only one allele from the egg isolate. Notably, the outbreak strain was genetically highly homologous to 32 sporadic case isolates and one food isolate reported in Yangjiang from 2019 until just before this outbreak, suggesting a common source (Figure 3).

PUBLIC HEALTH RESPONSE

Based on these findings, public health measures were implemented: enforcing strict separation of raw and cooked materials, ordering the implicated bakery to

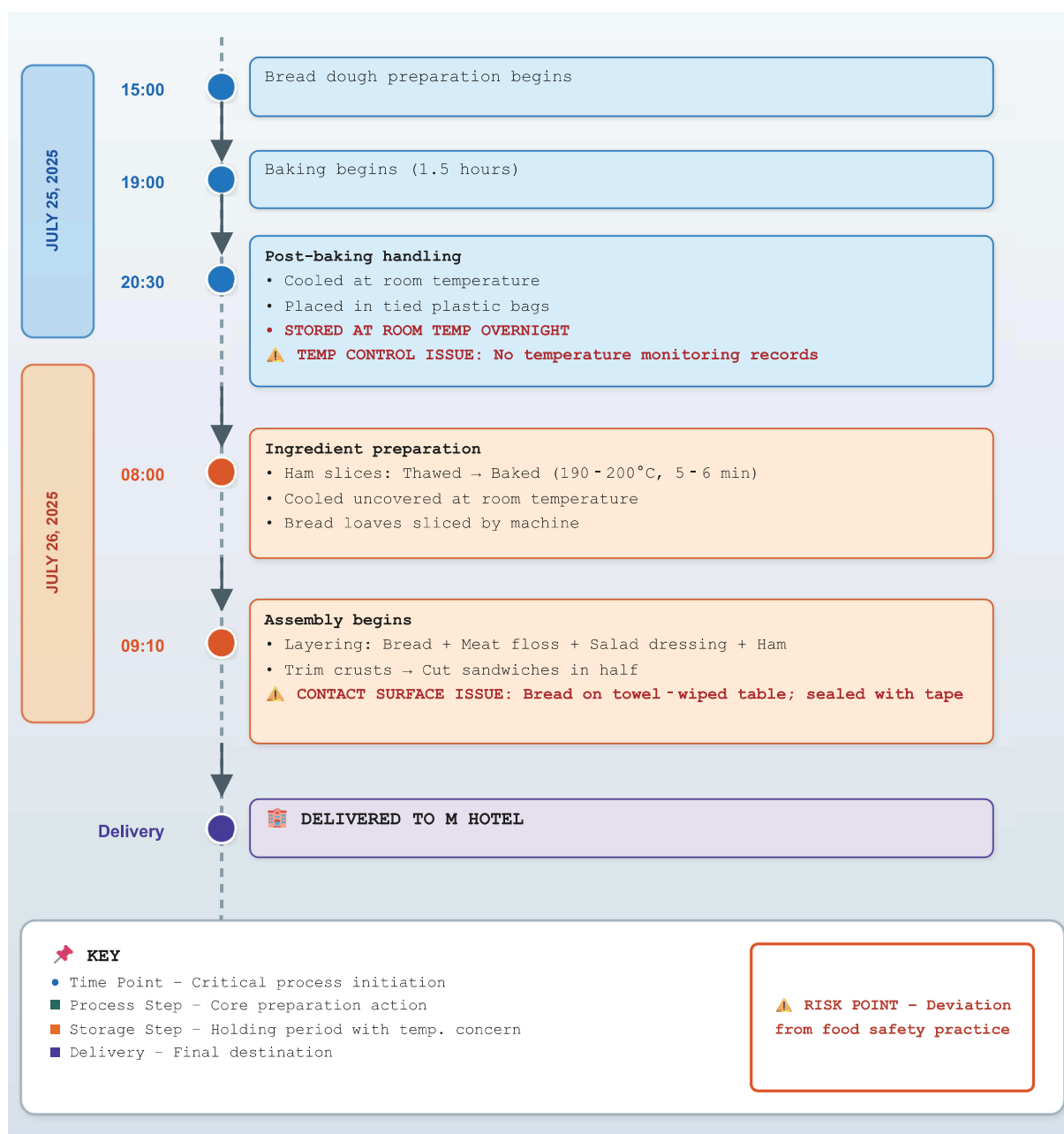


FIGURE 2. Timeline of sandwich preparation, storage, and transportation in a foodborne disease outbreak investigation, Yangjiang, China, July 2025.

suspend operations for rectification, strengthening food procurement supervision in kindergartens, and integrating genomic surveillance for early detection and traceback of persistent contamination sources by rare *Salmonella* serotypes.

DISCUSSION

This report describes a point-source outbreak of *Salmonella* Braenderup ST311, with a complete chain of evidence from patients to the common food

vehicle — sandwiches, and to the contaminated ingredient — eggs, as established by WGS. *Salmonella* remains a leading cause of foodborne disease worldwide, and its vehicles have expanded from traditional animal-derived products to agricultural commodities (1–3). *Salmonella* Braenderup is common in Europe and the Americas, associated with both agricultural and animal-derived foods (4–5), but is rare in China. In Guangdong Province, ST311 has become a locally dominant sequence type, but previous cases were sporadic with diverse suspected foods, rendering

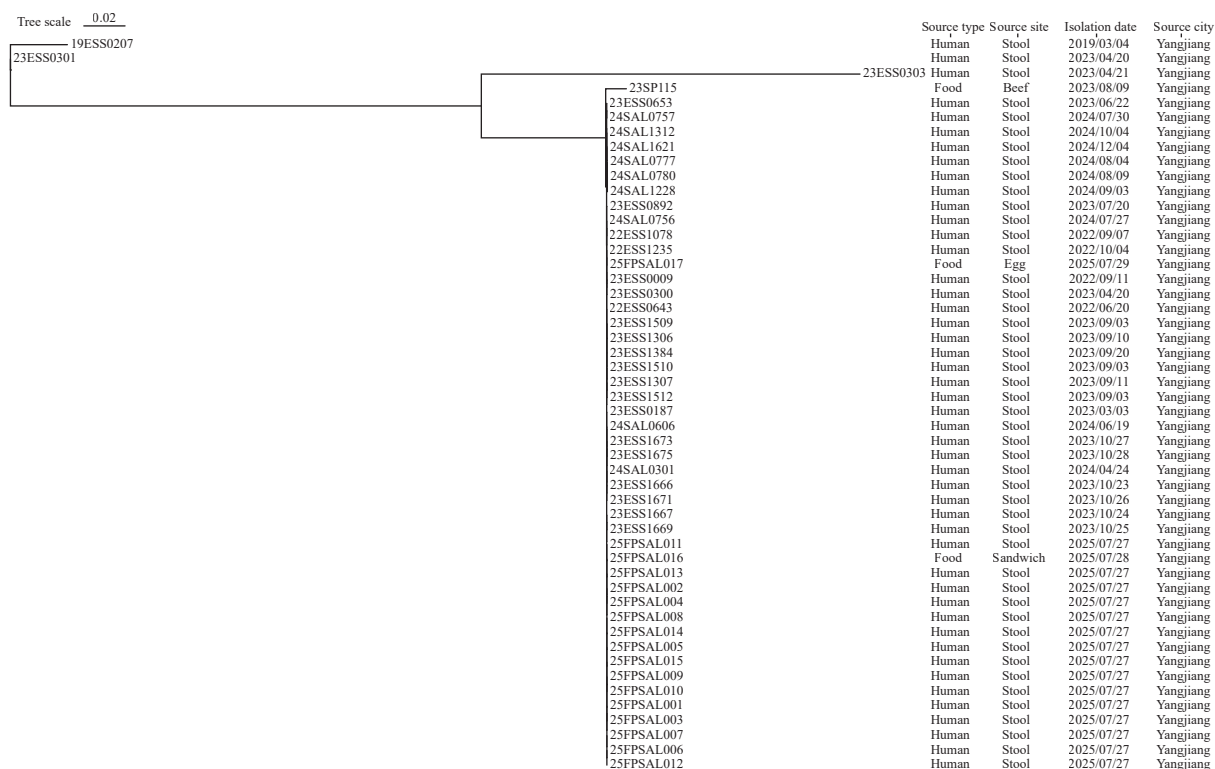


FIGURE 3. Cluster analysis of *Salmonella* Braenderup isolates from outbreak and historical passive surveillance based on cgMLST.

Abbreviation: cgMLST=core genome multilocus sequence typing

traceback difficult.

This outbreak demonstrates that eggs can transmit not only common serotypes such as *Salmonella* Enteritidis, which is responsible for approximately 92% of egg-associated outbreaks globally (6), but also rare serotypes like *Salmonella* Braenderup ST311. The typical incubation period for salmonellosis ranges 6–72 hours (2); however, the outbreak index case had an incubation period of merely 4 hours. This unusually rapid onset is likely attributable to a combination of host- and exposure-related factors: the affected child's immature immune system, lower gastric acidity, and reduced physiological resistance may have accelerated disease progression, while children who consumed contaminated sandwiches may have received a higher bacterial load relative to body weight, further shortening the incubation period (7). Isolation of the outbreak strain from pasteurized egg contents suggests that surface disinfection of eggshells alone may not prevent internal contamination (8–10). The affected population was predominantly young children, who are more susceptible to *Salmonella* infection and at higher risk for severe disease. This highlights the significance of prioritizing pasteurized egg products and promoting staff training in group meal settings

such as kindergartens. Additionally, it demonstrates the critical role of WGS in responding to outbreaks caused by rare serotypes. The ability of WGS to link outbreak strains to historical sporadic cases transcends simple matching, revealing that seemingly isolated sporadic cases are often clues to a persistent, hidden source. This changes outbreak thinking: rare serotypes are not random accidents but signals of long-term endemic circulation.

In summary, this outbreak shows that eggs can serve as vehicles for rare *Salmonella* serotypes with epidemic potential. The genetic relatedness between the outbreak strain and historical sporadic isolates indicates that this serotype has become endemic in the local area. Effective hygiene management in food establishments — separation of raw and cooked materials, hand hygiene, glove use, etc. — is essential for preventing cross-contamination. Integrating genomic surveillance into layer farming and egg processing will facilitate early detection and control of emerging serotypes.

This study has a few limitations. First, shortage of resources for on-site epidemiological investigation restricted complete interviews with all 676 attendees, yielding a relatively small control group in the case

control study, which may have somewhat reduced the statistical power. Nevertheless, the significant association between exposure (consumption of sandwiches) and illness ($OR=\infty$, $P<0.0001$) supports the robustness of this finding. Second, despite a thorough investigation among all kindergarten children and staff, we could not ascertain the total number of adults and children among all family attendees (including those who did not become ill) because of the large number of family attendees and the small number of sandwiches consumed. Moreover, sandwiches were primarily distributed to children; few adults were actually exposed. Consequently, we were unable to determine the attack rates separately for children and adults, nor perform a meaningful age-stratified comparison. Nonetheless, the consistently high attack rates among children across the two campuses (48.4%, Jiangcheng; 44.7%, Yangdong) strongly implicate sandwiches as the primary vehicle.

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* Corresponding author: Zhiting Liu, liuzhiting6@163.com.

¹ Yangjiang Municipal Center for Disease Control and Prevention, Yangjiang City, Guangdong Province, China; ² Guangdong Provincial Center for Disease Control and Prevention, Guangzhou City, Guangdong Province, China; ³ Yangjiang Inspection and Testing Center, Yangjiang City, Guangdong Province, China; ⁴ Baiyun District Center for Disease Control and Prevention, Guangzhou City, Guangdong Province, China; ⁵ Jiangcheng District Center for Disease Control and Prevention, Yangjiang City, Guangdong Province, China.

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Commentary

Release of the English Version of China's Standards for Drinking Water Quality: Bridging Evidence and Global Health Equity

Bixiong Ye¹; Xiaoyuan Yao¹; Lan Zhang^{1,*}; Xiaoming Shi^{2,*}

ABSTRACT

To eliminate language barriers to international water cooperation, the official English language version of China's *Standards for Drinking Water Quality (GB 5749-2022)* was released in December 2025. Compiled under national translation specifications, this authoritative edition ensures accurate communication of content. A comparative analysis with international standards demonstrates that *GB 5749-2022* balances global harmonization and localized adaptation in accordance with China's hydrogeological and public health conditions. The English version effectively eliminates technical ambiguities in transnational water projects and strengthens China's voice in global water governance. Nonetheless, challenges remain, including cross-lingual interpretations issues and gaps in the coverage of emerging contaminants such as per- and polyfluoroalkyl substances (PFAS). This article proposes optimizing interpretative documents, establishing dynamic updating mechanisms, constructing equitable cooperation platforms, and improving multi-dimensional evaluation systems. It aims to facilitate the global application of China's drinking water criteria, provide references for developing countries, and contribute to equitable global public health governance.

In recent years, China has actively engaged in extensive cooperation and exchanges with numerous countries and international organizations in the drinking water sector, where water quality serves as a core pillar of public health and technical collaboration (1–2). As the benchmark for national drinking water safety, authoritative foreign-language versions of China's drinking water standards have become essential for promoting the internationalization of China's water-related products, technologies, and scientific achievements. Furthermore, they serve as a critical

foundation for advancing the export of water services and facilitating international trade in the water sector. Consequently, the official foreign language translation and standardization of these national standards is a strategic imperative.

Adhering to the Standardization Administration of China (SAC) guidelines, the National Disease Control and Prevention Administration spearheaded the meticulous translation, expert review, and technical verification of the English version of the *Standards for Drinking Water Quality (GB 5749–2022)* (3). This effort strictly conformed to *Guidelines for Standardization—Part 10: General Rules for English Translation (GB/T 20000.10–2016)* (4) and *Part 11: Format and Presentation Requirements (GB/T 20000.11–2016)* (5). Following a rigorous approval process, the official English edition was formally promulgated on December 9, 2025, by the State Administration for Market Regulation and SAC (6). It is the first official English version of China's drinking water hygiene standards, marking a milestone in the internationalization of its public health standards.

Breaking Down Information Barriers:

From "Unreadable" to "Benchmarkable"

Complete and authoritative translation Earlier unofficial translations, characterized by fragmented excerpts and non-standard renditions, frequently exhibited omitted parameters, terminological inconsistencies, and inaccurate limit values. These deficiencies led to misinterpretations of China's water quality benchmarks, analytical methodologies, and oversight mechanisms (7), limiting global comprehension of its risk-based drinking water safety system.

In contrast, the official English version reproduces the full text of the national standard verbatim, covering all 55 reference indicators in Appendix A alongside detailed technical specifications and compliance criteria. With no content omission nor deviations from the original intent, it eliminates ambiguities and

transforms it to a transparent, globally benchmarkable technical instrument.

High international comparability with global mainstream standards The release of the English version enables direct global access to China's water quality limits and regulatory provisions, supporting direct benchmarking against the World Health Organization (WHO) *Guidelines for Drinking-water Quality*, the U.S. *National Primary Drinking Water Regulations*, the EU *Drinking Water Directive*, and Japan's *Drinking Water Quality Standards* (Table 1).

Comparative analysis indicates a high degree of congruence between *GB 5749–2022* and international benchmarks across most indicators, reflecting China's convergence with global paradigms in water safety governance (8). Furthermore, the standard incorporates region-specific parameters and limits reflecting China's distinct hydrogeochemical, epidemiologic, and socio-economic conditions. This demonstrates a science-based approach that reconciles international best practices with domestic public health priorities. Such a dual emphasis on harmonization and contextual adaptation reinforces the standard's scientific robustness and practical applicability.

Strategic Value for Cross-Border Cooperation and Health Diplomacy

Addressing the "Contractual Ambiguity" pain point in cross-border engineering projects Relevant policies underscore that the absence of authoritative English regulatory documents drive normative discrepancies in international water safety planning and implementation (13). In Belt and Road partner regions, particularly Southeast Asia and Africa, water supply projects undertaken by Chinese enterprises are situated within complex epidemiological and climatic contexts. Historically, fragmented standards have created contractual ambiguities and technical barriers in overseas engineering practices (14).

As the sole authoritative text available for formal citation, the English version of *GB 5749–2022* provides unified, unambiguous technical criteria for international water supply projects. It directly addresses the "contractual ambiguity" pain point, lowers technical negotiation costs, accelerates project delivery, and mitigates compliance risks across the full lifecycle from design to operation and maintenance.

Serving as a "rule carrier" of health diplomacy The standard transcends routine technical documentation; it constitutes critical soft infrastructure for China's participation in global health governance and international development cooperation. As a global public good featuring both scientific rigor and contextual adaptability, the English version translates policy commitments into actionable tools. It can be disseminated via multilateral and bilateral mechanisms including the Lancang-Mekong Cooperation Mechanism (15), the China - Association of Southeast Asian Nations (ASEAN) Public Health Cooperation Initiative (16), and the Forum on China-Africa Cooperation water supply programs (17), offering a replicable "Chinese approach" for partner countries revising their national drinking water regulations.

It further supports the overseas transfer and localization of China's proven expertise in water pollution control, centralized rural water-supply management, and water quality monitoring network, advancing technology transfer and institutional capacity building in recipient countries. This marks a strategic upgrade in China's foreign cooperation, from exporting infrastructure and products to exporting normative standards and governance philosophy (18), strengthening its influence in global health governance.

Challenges in Implementation and Interpretation

Terminology differences and context-dependent interpretation barriers The precise interpretation of

TABLE 1. Comparative analysis of *GB 5749–2022* and major international drinking water standards (Unit: number of parameters).

Comparison category	WHO (9)	USA (10)	EU (11)	Japan (12)
Identical limit values	41	17	19	23
Stricter limits in <i>GB 5749-2022</i>	15	26	2	6
Less stringent limits in <i>GB 5749-2022</i>	1	16	11	20
Indicators not listed or non-comparable	40	38	65	48

Note: Number of parameters in each category when *GB 5749–2022* is benchmarked against the corresponding international standard. "Non-comparable" refers to parameters whose divergent definitions, units, or testing methods prevent direct comparison.

Abbreviation: GB=guobiao (Chinese national standard); WHO=world health organization; USA=United States of America; EU=European Union.

specialized terminology constitutes a central challenge to the standard's global dissemination. Concepts specific to China's regulatory framework, such as "regular indicators" and "expanded indicators," diverge substantively from international classification systems. These include the U.S. distinction between primary and secondary drinking water regulations (10). Japan's approach features a tripartite categorization comprising water quality standard items, targeted management items, and items under consideration (12). Although the translation strictly adheres to *GB/T 20000.10–2016* to ensure semantic fidelity (4), such structural disparities cannot be reconciled through lexical equivalence alone.

The current absence of support for bilingual interpretation guidelines and application manuals creates a risk of misinterpretation among international users unfamiliar with China's regulatory context. Clarifications on indicator classification logic, monitoring frequencies, and application scenarios are needed to bridge the gap between translation and implementation.

Insufficient regulation of emerging contaminants restricts global adaptability Regulatory gap persists regarding fast-evolving emerging contaminants. The 97 indicators included in *GB 5749–2022* do not cover substances of growing global concern, including PFAS, microplastics, cyanobacterial toxins, and novel organic pesticides. For example, the U.S. Environmental Protection Agency (U.S. EPA) sets a stringent limit of 4.0 ng/L for perfluorooctanoic acid (PFOA) and perfluorooctanesulfonic acid (PFOS) given their carcinogenicity and developmental toxicity (19); the latest WHO guidelines also introduce limits for cylindrospermopsin and saxitoxin (9). The exclusion of these contaminants creates notable divergence from

international best practices.

During the compilation of *GB 5749–2022*, the drafting committee reviewed relevant international research but opted not to include these indicators, citing the limited detection capacity of domestic institutions and the high upgrade costs for water treatment facilities (20). While this prudent approach ensures short-term feasibility, it weakens the standard's alignment with the frontier of global regulatory science. A dynamic annual review mechanism should be established. As toxicological evidence and detection technologies advance, emerging contaminants should be added and existing limits revised.

Call for Global Participation: Building a Community of Water Security

Establish equal international standard cooperation mechanisms

This article advocates the global adoption of the English version of *GB 5749–2022* as an authoritative reference, addressing the need for enhanced transboundary water cooperation underscored by UN-Water and other multilateral frameworks (21). However, securing genuine global recognition necessitates more than unilateral promulgation; it hinges upon the establishment of equitable, open, and mutually beneficial dialogue mechanisms.

China will take a proactive role in leading deeper engagement with the International Organization for Standardization (ISO), WHO, and regional standard-setting bodies, establishing regular mechanisms for standard mutual recognition and technical consultation to replace one-way "export" with reciprocal exchange (Table 2). Parallel efforts will focus on joint verification pilots in Belt and Road partner countries. These pilots will explore implementation

TABLE 2. Standard internationalization roadmap.

Phase	Core Action	Key Tools / Mechanisms	Expected Outcome
Phase 1: mechanism establishment	High-level engagement with ISO, WHO, and regional bodies.	Memorandum of understanding, joint working groups, dialogue platforms.	A formal platform for standard mutual recognition.
Phase 2: technical adaptation	Joint verification pilots in Belt and Road partner countries.	Water quality baseline surveys, technological adaptability assessments.	Localized implementation plans tailored to specific regional needs ("one country, one policy") (22).
Phase 3: efficacy assessment	Establishing a transnational health impact monitoring system.	Epidemiological data analysis, water treatment efficacy evaluation.	Evidence-based reports demonstrating tangible public health improvements.
Phase 4: global adoption	Integration into regional/global technical guidelines.	Academic promotion, multilateral development banks procurement integration, policy briefs.	Transition from a "national document" to a "globally adopted public good."

Abbreviation: ISO=international organization for standardization; WHO=world health organization.

pathways tailored to local water quality, epidemiological profiles, and treatment capacities. Ultimately, the standard will be transformed into a global public good for drinking water safety.

Optimizing the multi-dimensional global impact evaluation system Evaluation of the English version's global influence must be evidence- and outcome-based. Reliance on bibliometric indicators (e.g., downloads, citation counts) only captures superficial academic attention and fails to reflect the standard's practical value in global public health governance. A multi-dimensional, quantifiable framework integrating academic recognition, practical applicability, and public health benefits is urgently needed (23).

Core indicators should track the standard's real-world performance. First, they should measure adoption and citation by international organizations and partner countries. Second, they should assess its technical contribution to cross-border water projects. Third, they should monitor reductions in waterborne disease incidence. Fourth, they should evaluate improvements in water treatment efficiency and water quality compliance rates. Finally, they should gauge international stakeholder awareness and acceptance of China's drinking water standards. This outcome-oriented system shifts focus from dissemination scale to governance efficacy and from academic impact to tangible public health gains (24). Continuous empirical assessment can enhance the global credibility and leadership of China's drinking water standards, supporting Chinese contributions to global water security governance.

CONCLUSION

The release of the English version of *GB 5749–2022* represents a paradigm shift in leveraging technical standards to advance global health equity. This development has prompted the strategic prioritization of English translations for other critical Chinese public health standards with international implications. Priority should be assigned to those governing food safety and quarantine protocols. These areas play a crucial role in international trade, travel, and collaborative health security. By presenting its science-based regulatory framework in a globally accessible language, China not only provides a replicable model for global water governance, particularly for developing countries, but also underscores that the ultimate value of these standards lies not merely in textual accuracy but in delivering tangible improvements in drinking

water safety worldwide. Therefore, this release is not the end of China's standard internationalization but an invitation for global collaboration. By adopting science-based and equitable approaches, countries can work together to achieve safe drinking water for all and strengthen global health governance.

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Corresponding authors: Lan Zhang, zhanglan@nieh.chinacdc.cn; Xiaoming Shi, shixm@chinacdc.cn.

¹ National Institute of Environmental Health, Chinese Center for Disease Control and Prevention, Beijing, China; ² Chinese Center for Disease Control and Prevention, Beijing, China.

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Notifiable Infectious Diseases Reports

Reported Cases and Deaths of National Notifiable Infectious Diseases — China, May 2026*

Diseases	Cases	Deaths
Plague	0	0
Cholera	2	0
COVID-19	21,861	1
SARS-CoV	0	0
Acquired immune deficiency syndrome [†]	3,833	1,454
Hepatitis	131,378	194
Hepatitis A	1,238	0
Hepatitis B	111,588	35
Hepatitis C	15,036	157
Hepatitis D	27	0
Hepatitis E	2,928	2
Other hepatitis	561	0
Poliomyelitis	0	0
Human infection with noval influenza virus	3	1
Measles	78	0
Epidemic hemorrhagic fever	364	4
Rabies	20	19
Japanese encephalitis	1	0
Dengue	222	0
Monkey pox [§]	86	0
Chikungunya fever	35	0
Severe fever with thrombocytopenia syndrome	900	33
Anthrax	13	0
Dysentery	2,626	0
Tuberculosis	57,225	167
Typhoid fever and paratyphoid fever	376	0
Meningococcal meningitis	14	1
Pertussis	769	0
Diphtheria	0	0
Neonatal tetanus	2	0
Scarlet fever	2,057	0
Brucellosis	6,748	0
Gonorrhea	11,243	0
Syphilis	57,027	2
Leptospirosis	21	0
Schistosomiasis	1	0
Malaria	406	0

Continued

Diseases	Cases	Deaths
Influenza	514,726	2
Mumps	7,748	0
Rubella	44	0
Acute hemorrhagic conjunctivitis	1,846	0
Leprosy	34	0
Typhus	113	0
Kala azar	32	0
Echinococcosis	340	1
Filariasis	0	0
Hand, foot and mouth disease	114,376	0
Infectious diarrhea [†]	155,958	0
Total	1,092,528	1,879

* According to the National Bureau of Disease Control and Prevention.

[†] The number of deaths of Acquired immune deficiency syndrome (AIDS) is the number of all-cause deaths reported in the month by cumulative reported AIDS patients..

[§] Since September 20, 2023, Monkey pox was included in the management of Class B infectious diseases.

[¶] Infectious diarrhea excludes cholera, dysentery, typhoid fever and paratyphoid fever.

The number of cases and cause-specific deaths refer to data recorded in National Notifiable Disease Reporting System in China, which includes both clinically-diagnosed cases and laboratory-confirmed cases. Only reported cases of the 31 provincial-level administrative divisions in the Chinese mainland are included in the table, whereas data of Hong Kong Special Administrative Region, Macau Special Administrative Region, and Taiwan, China are not included. Monthly statistics are calculated without annual verification, which were usually conducted in February of the next year for de-duplication and verification of reported cases in annual statistics. Therefore, 12-month cases could not be added together directly to calculate the cumulative cases because the individual information might be verified via National Notifiable Disease Reporting System according to information verification or field investigations by local CDCs.

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Jianwei Wang

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