

Preplanned Studies

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

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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,

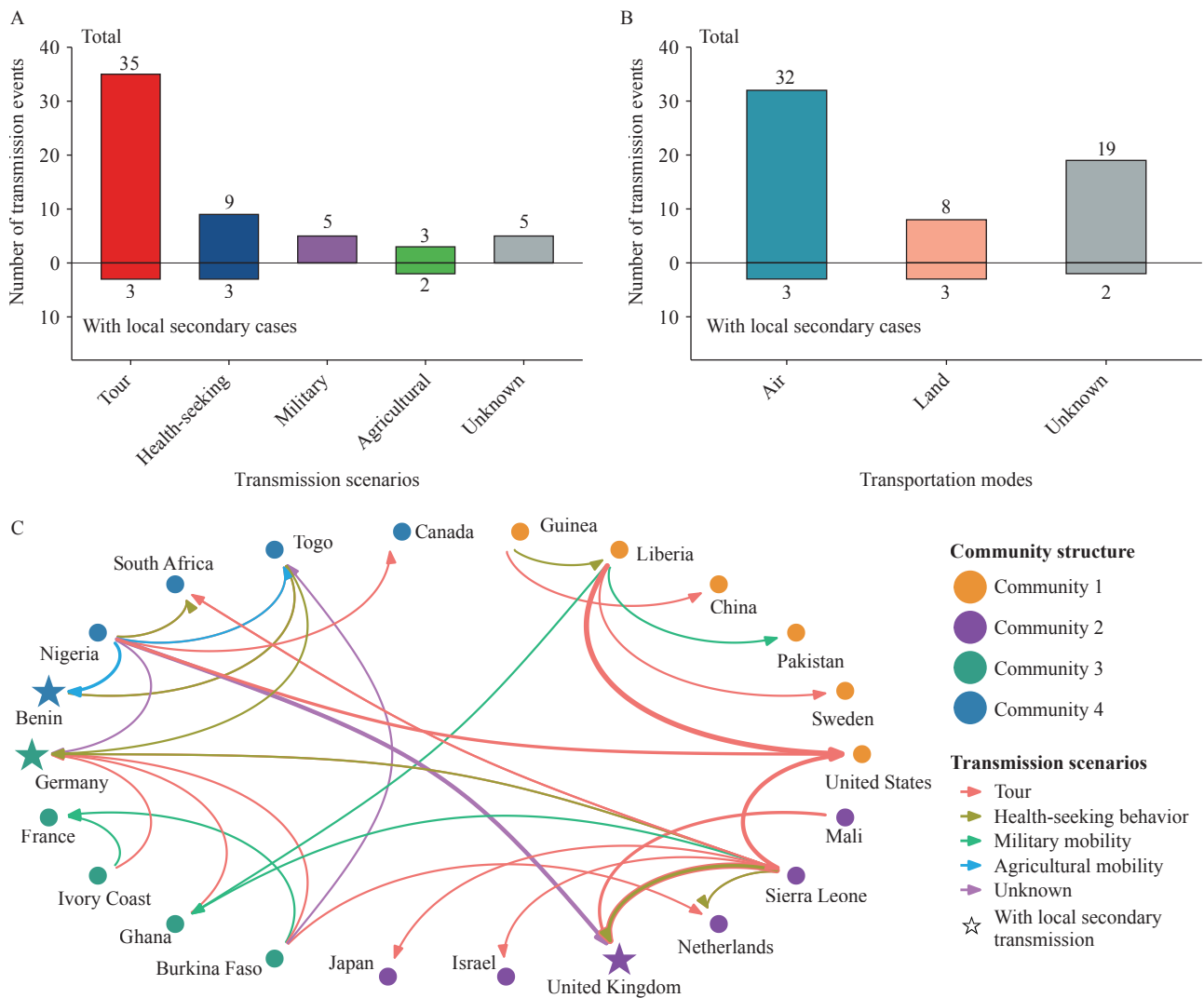


FIGURE 1. Global Lassa fever cross-border migration patterns. (A) Distribution of global Lassa fever migratory events by scenario; (B) Distribution of global Lassa fever migratory events by transportation mode; (C) Country-level directed weighted migration network for migratory events and clustering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

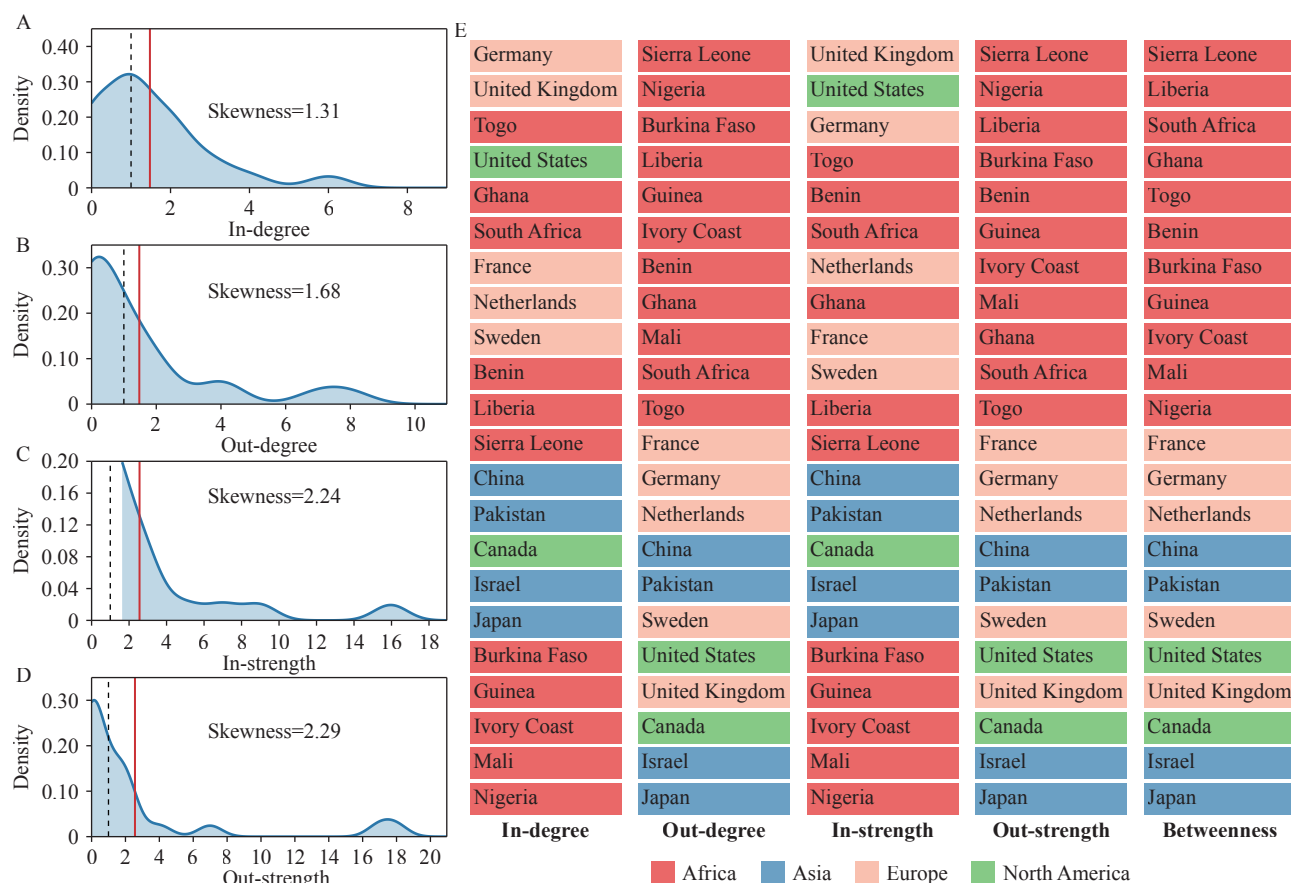


FIGURE 2. Distributions of countries' in-degree (A), out-degree (B), in-strength (C), out-strength (D), and betweenness centrality (E) in the global Lassa fever cross-border migration network.

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.

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REFERENCES

- Ogundele GO, Jolayemi KO, Bello S. Lassa fever in West Africa: a systematic review and meta-analysis of attack rates, case fatality rates and risk factors. *BMC Public Health* 2025;25(1):2948. <https://doi.org/10.1186/s12889-025-24377-6>.
- Zhou YN, Wang JB, Cao RR, Yang Y, Feng YL, Tang C, et al. The biological characteristics and mouse model of Lassa virus from the first imported case in China. *MedComm* 2025;6(8):e70315. <https://doi.org/10.1002/mco2.70315>.
- Yu VL, Edberg SC. Global Infectious Diseases and Epidemiology Network (GIDEON): a world wide Web-based program for diagnosis and informatics in infectious diseases. *Clin Infect Dis* 2005;40(1):123 – 6. <https://doi.org/10.1086/426549>.
- Taboe HB, Pilyugin SS, Ngonghala CN. Revealing hidden drivers of Lassa fever through a model-informed approach for reproducing and predicting disease dynamics and guiding control strategies. *Sci Rep* 2025;15(1):33786. <https://doi.org/10.1038/s41598-025-01176-y>.
- Allison R, Pai A, Sibal B, Sookoo R, Anderson SR. A systematic review of contact tracing interventions for international arrivals by air, sea, or land. *Travel Med Infect Dis* 2025;68:102924. <https://doi.org/10.1016/j.tmaid.2025.102924>.
- Ma J. Study of epidemic spreading in multi-community networks with bridge nodes [dissertation]. Boston, USA: Boston University; 2022. <https://hdl.handle.net/2144/45297>.
- Eskew EA, Bird BH, Ghersi BM, Bangura J, Basinski AJ, Amara E, et al. Reservoir displacement by an invasive rodent reduces Lassa virus zoonotic spillover risk. *Nat Commun* 2024;15(1):3589. <https://doi.org/10.1038/s41467-024-47991-1>.

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,

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

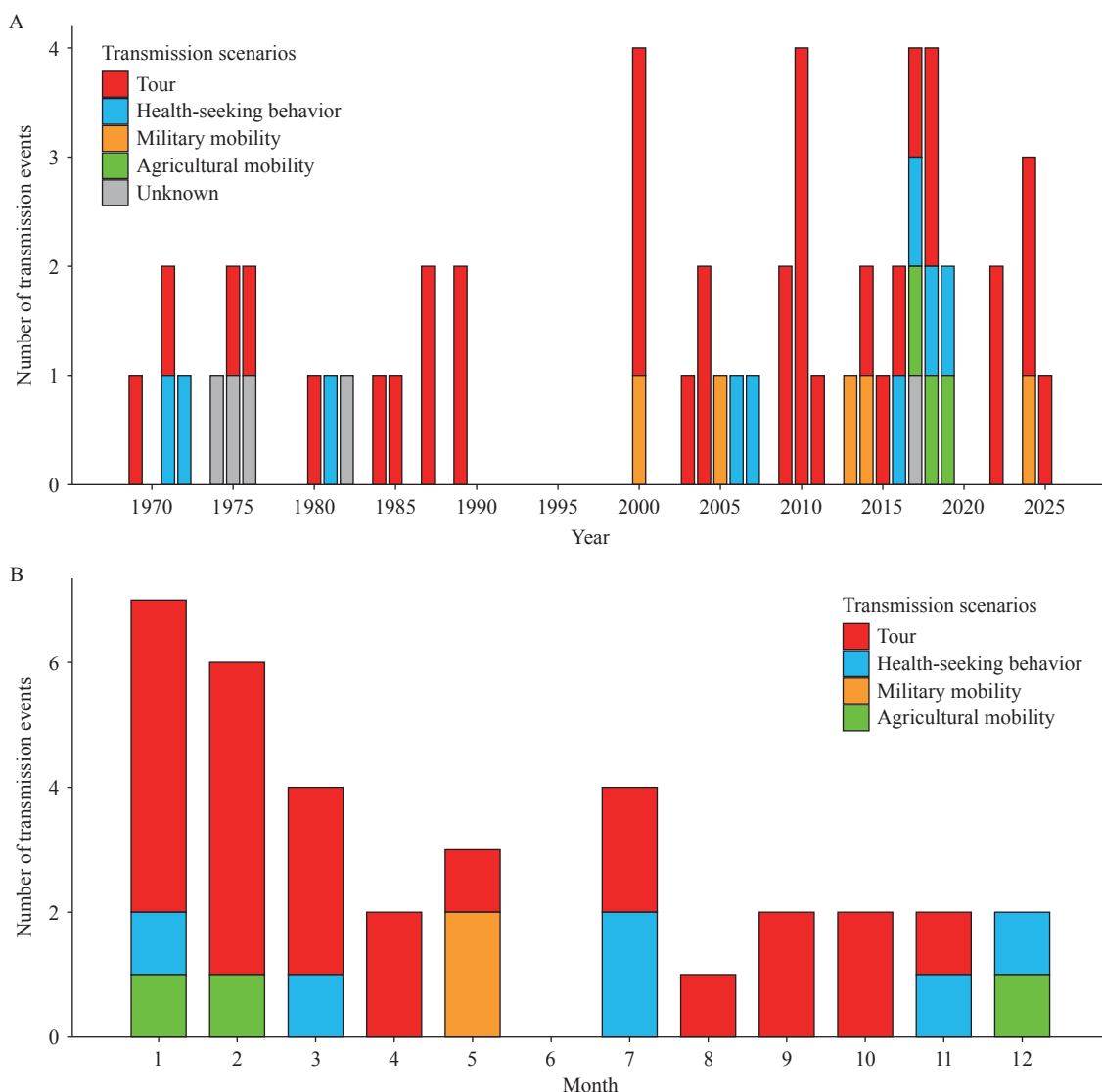
where n is the number of countries in the network, w_{ij} is the weight of the directed edge from country i to j , and w_{ji} is the weight of the directed edge from country j to i . Node strength is categorized into in-strength and out-strength in directed networks. In-strength represents the total 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).