Outbreak Reports

Early Detection and Response to the First Imported Case of Zika Virus Disease — Hainan Province, China, 2025

Xiangyu Yan[1,&]; Xiaoqing Fu[2,&]; Mingheng Wang[2]; Hao Yang[2]; Minghe Gu[3]; Jialin Liu[3]; Xianyi Zeng[2]; Qin Chen[2]; Lei Cui[4]; Xingqing Zhong[4]; Ling Zhang[4]; Jingjing Chen[4]; Yuming Jin[4]; Jian He[4]; Dapeng Yin[4]; Huiming Luo[4]; Tiejun Shui[5,#]; Yan Jin[4,#]

Summary

What is already known about this topic?

Zika virus (ZIKV) is primarily transmitted by *Aedes aegypti* and *Aedes albopictus*. The Zika epidemics in China were primarily imported cases.

What is added by this report?

This study documents the first laboratory-confirmed imported ZIKV case in Hainan Province, China. Phylogenetic analysis identified the Asian lineage, sharing 98.79% homology with a Thai strain.

What are the implications for public health practice?

This investigation highlighted the need to strengthen the patriotic health campaign, reducing local mosquito-borne transmission risk at the source. Multi-pathogen (dengue/chikungunya/Zika) testing of a single sample by Haikou Customs enabled Zika detection, while timely cross-department notification and coordinated response effectively enhanced outbreak containment.

ABSTRACT

Introduction: On September 2, 2025, a Singaporean national was reported Zika virus (ZIKV)-positive during inbound screening at Haikou Meilan Airport, Hainan Province, China. CDCs immediately launched epidemiological investigations, confirmatory laboratory testing, risk area delineation, and vector control measures.

Methods: Blood samples collected from the patient were tested for ZIKV nucleic acid using fluorescent quantitative polymerase chain reaction (PCR) technology. The complete viral genome sequence was obtained from the serum sample directly through a ZIKV-targeted sequencing with Oxford Nanopore. Phylogenetic analysis was conducted to determine the origin and genotype of the virus.

Results: Based on the patient's activity trajectory, the epidemic foci in Haikou City and Wenchang City were identified. The Breteau Indexes in the core areas were quickly reduced to below 5 within 5 days. Sequencing generated a 10,700-bp complete genome (ZIKA-HN/2025/China). Phylogenetic analysis revealed the Asian lineage, sharing 98.79% nucleotide homology with a Thailand strain (PP626399.1). No secondary cases were identified.

Conclusion: This imported case from Singapore was confirmed as the first ZIKV infection reported in Hainan Province. The climate and ecological conditions in Hainan required sustained suppression of mosquito density through source reduction under the patriotic health campaign. Multi-pathogen testing at ports, timely cross-department notification and coordination proved essential for early detection and effective containment.

On September 2, 2025, a Singaporean national of Chinese descent was reported Zika virus (ZIKV)-positive by Customs during inbound screening at Haikou Meilan Airport, Hainan Province, after arriving by air on September 1. Hainan CDC conducted epidemiological investigations, confirmatory testing, identified epidemic focus, and implemented health monitoring and mosquito vector control. Genetic sequencing revealed the ZIKV strain belonged to the Asian lineage. Timely control measures prevented local transmission.

INVESTIGATION AND RESULTS

On September 1, 2025, a 52-year-old male Singaporean national of Chinese descent traveled from Singapore to Haikou, entering through Haikou Meilan Airport at approximately 16:12. A whole blood sample was collected at the Customs and tested using the dengue-chikungunya-Zika triple assay kit with real-

Copyright © 2026 by Chinese Center for Disease Control and Prevention

time fluorescent PCR. At 15:30 on September 2, Customs notified Hainan Provincial CDC of a positive ZIKV nucleic acid result. Provincial CDC immediately deployed staff for investigation.

Epidemiological investigation showed the patient (a business owner) had no discomfort symptoms in the past month. Upon arrival, his temperature was 37.3 °C at screening and 37.4 °C on follow-up. On the afternoon of September 2, his temperature was 37.1 °C. He had no rash, joint pain, or conjunctivitis. No other passengers on the same flight showed ZIKV-related symptoms during routine screenings, so they did not receive testing or control measures.

During the two-day stay, his activities covered Haikou and Wenchang cities. On September 1, he returned directly to his cousin's home in Jinling Yaju Community, Longhua District, Haikou, and did not go out. At 8:51 on September 2, he had breakfast at Restaurant A, then drove to Wenchang. In Wenchang, his activity trajectory was as follows: from 10:30–10:50, he was at Wenchang Government Affairs Center; from 11:15–13:00, in his hometown in Nanpo Village; at 13:27, he had lunch at Restaurant B; at around 14:00, he returned to Haikou, arriving at his cousin's home at approximately 15:30, and did not go out again. He flew back to Singapore at 23:50 on September 3. No new cases emerged.

In terms of laboratory testing, provincial CDC re-tested the original sample, and reported ZIKV-positive [cycle threshold (Ct): 35] at 20:30 on September 2. Longhua District CDC re-collected his blood sample, and provincial CDC reported ZIKV-positive (Ct: 36) at 22:00. Detection was performed using fluorescent quantitative PCR (Jiangsu Bioperfectus kit, batch T202507013).

A 10,700-bp genome sequence was directly obtained from the serum sample (*ZIKA-HN/2025/China*) using Oxford Nanopore targeted sequencing for Zika (*1*–*4*). Basic Local Alignment Search Tool (BLAST) analysis showed 98.79% similarity to GenBank PP626399.1 (2017). Genetic evolution analysis showed that the virus belongs to the Asian lineage (Figure 1).

PUBLIC HEALTH RESPONSE

The patient was confirmed with ZIKV infection on the evening of September 2. Haiken Community Health Service Center in Longhua District reported the case as required. Municipal and district CDCs promptly conducted epidemiological investigations and delineated risk areas. The patient was guided to implement home-based quarantine with mosquito precautions because he planned to return to Singapore on September 3 and refused to go to medical institutions. The patient's residence was equipped with window screens, door screens, and mosquito nets, providing necessary conditions for home-based mosquito prevention and isolation. On September 3, under CDC guidance, he wore long clothing and boarded his flight back to Singapore (Figure 2A).

Provincial CDC conducted a rapid risk assessment. As a Class I dengue-endemic area nationally, Hainan has a climate similar to Southeast Asia, with higher *Aedes* density and wider distribution than other provincial-level administrative divisions (PLADs), posing greater localized transmission risk. Delayed or inadequate response could lead to secondary cases or wider outbreaks.

Based on the patient's activity trajectory, his residence building in Jinling Yaju Community in Haikou and Nanpo Village in Wenchang were designated as epidemic foci. A 200-meter radius from each epidemic focus was designated as the core zone, and an outer 200-meter radius as the alert zone. Because the patient spent short periods at the Government Affairs Center and the two restaurants, and not during the peak period of *Aedes* mosquito activity, these locations were not classified as epidemic foci but rather as risk sites. Health monitoring and education were strengthened in core zones, alert zones, risk sites, and other key sites (construction sites, urban villages, fringe areas), ensuring symptomatic individuals would promptly visit fever clinics. Medical institutions citywide enhanced surveillance and screening of febrile patients with suspected symptoms, emphasizing travel history to epidemic areas. Technical training for medical staff was strengthened to improve differential diagnosis of dengue, chikungunya, and Zika, as well as awareness of reporting. A multi-disease co-prevention approach was implemented to enhance surveillance sensitivity (Figure 2A).

For environmental vector control, rapid adult mosquito elimination and breeding site clearance were carried out in core zones, alert zones, and risk sites. Using the Breteau Index (BI) to monitor *Aedes* mosquito larvae and the human-baited double net trap method to monitor adult mosquitoes, emergency vector monitoring was conducted daily within core zones until mosquito density reached a safe level, then twice weekly until the outbreak ended. In core zones, adult mosquito density decreased to a safe level (0.9

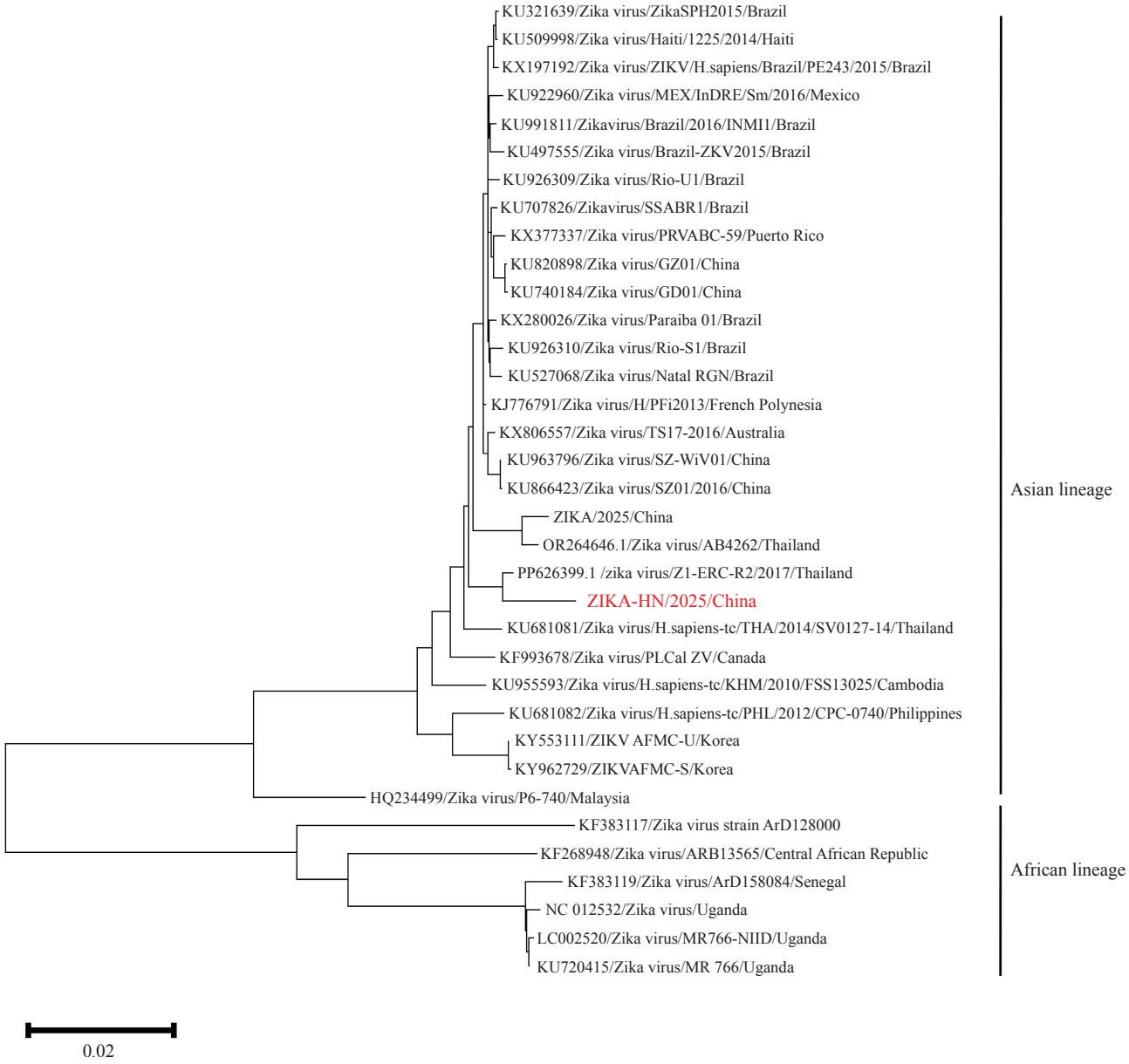


FIGURE 1. Phylogenetic tree of ZIKV whole-genome sequence.
Abbreviation: ZIKV=Zika virus.

per trap-hour) within 3 days. BI in Jinling Yaju Community was 5 on September 2, and 12 in Nanpo Village on September 3; both dropped below 5 within 5 days. Community staff mobilized residents for environmental sanitation improvements. Pest control operators received enhanced guidance and oversight. Municipal and district CDCs promptly fed back monitoring results and control recommendations to community staff to effectively guide epidemic prevention and control work. Mosquito-borne emergency monitoring continued for 24 consecutive days, with no secondary cases detected, and the outbreak was declared concluded (Figure 2A).

DISCUSSION

All ZIKV cases in China have been imported, with no local secondary transmission. The first imported case in Chinese mainland was reported in Jiangxi in February 2016 (*5*), followed by cases in Zhejiang, Guangdong, and other PLADs, showing a sporadic trend with main sources initially from South America (e.g., Venezuela) (*6*). As cross-border travel increased, the source shifted to Southeast Asia. Recently, Yunnan (2019) (*7*), Shandong (2025) (*8*), and Sichuan (2026) (*9*) reported imported cases from Myanmar, Thailand,

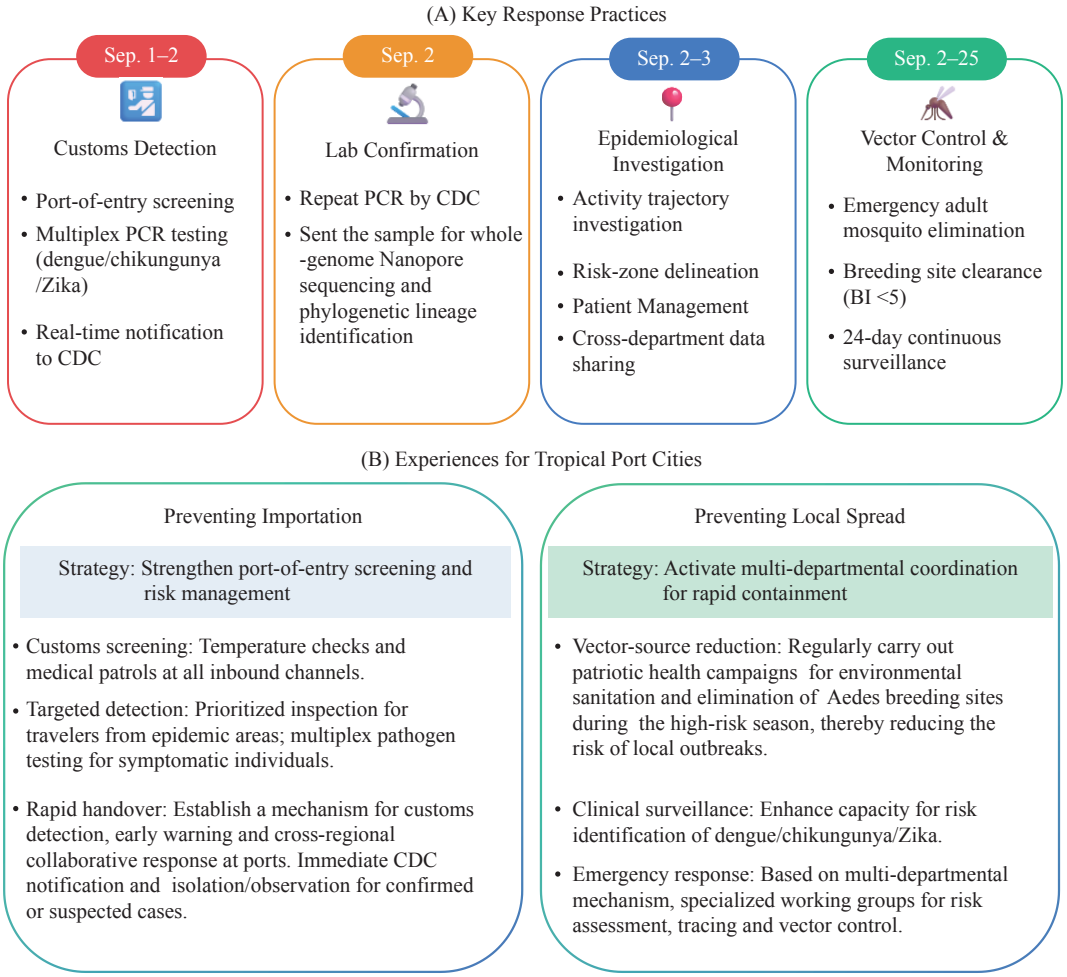


FIGURE 2. Key response practices and experiences for tropical port cities. (A) Key response practices. (B) Experiences for tropical port cities.
Abbreviation: BI=Breteau Index; PCR=polymerase chain reaction.

and Malaysia, respectively, with the Asian lineage predominating.

As Hainan's first ZIKV case, the case was imported from Singapore. Singapore experienced a minor Zika peak from 2023–2025 (30 cases in 2023, 13 in 2024, 16 in 2025) (*6*). In 2025, except one local case, most were imported from Southeast Asia (15 cases), explaining the strong homology between this study's virus sequence and the Thai strain (*10*). Compared with recent imported cases in Shandong (*8*) and Sichuan (*9*), despite different countries of origin, all sequences showed strong homology with the Thai strain, indicating the primary importation risk source and priorities for pathogen surveillance.

The epidemic control provided a model for multiplex pathogen joint testing and coordinated emergency management in tropical ports and other high-risk border areas (Figure 2B). The patient in Hainan had an insidious onset with inconspicuous symptoms, posing risk of cryptic transmission and local spread. Therefore, disease surveillance awareness and timely result notification of Meilan Airport Customs were crucial for early detection. Multiplex nucleic acid testing with different fluorescent dyes enabled simultaneous detection of multiple targets, reducing laboratory workload and turnaround time versus single-target assays. Furthermore, the multi-departmental coordination mechanism was also important. After the outbreak, Haikou activated its emergency response mechanism, established an on-site command center, and launched a joint epidemiological investigation by public security, public health, and information technology teams. Seven task forces — information, patriotic health and disinfection, environmental improvement, household screening, environmental monitoring, source tracing, and supervision and education — ensured seamless operation. To build a second defense line beyond the

border, stronger international epidemic intelligence and risk assessment, closer Customs coordination, screening of inbound travelers from key areas, and post-entry health monitoring are essential.

Successful containment of this imported epidemic also benefited from timely emergency response measures, including scientifically defining risk zones, classified and graded epidemic management, and emergency vector mosquito monitoring and control. Since 2024, Hainan has conducted a three-year patriotic health special campaign, implemented ledger management of mosquito breeding sites and carry out breeding site inspections, dynamically clearing mosquito breeding grounds. Continuously suppressing *Aedes* vector density during the high-risk season for mosquito-borne infectious diseases and reducing the risk of local outbreaks can provide practical reference for other PLADs in China that face the risk of local mosquito-borne diseases transmission (Figure 2B). Since the Hainan Free Trade Port closed its customs operations on December 18, 2025, economic, trade, and personnel exchanges with Southeast Asian countries have become increasingly frequent, raising the risk of importing mosquito-borne infectious diseases. Therefore, multiplex pathogen testing for strengthening port-of-entry detection, and multi-departmental coordination mechanism for rapid containment should remain a long-term priority.

Conflicts of interest: No conflicts of interest.

Ethical statement: Approval by the Ethics Committee of Hainan Center for Disease Control and Prevention, China (approval number: 2025005).

Acknowledgements: Supported by Hainan Provincial Natural Science Foundation of China (326MS0423), and National Natural Science Foundation of China (72604287).

doi: 10.46234/ccdcw2026.201

[#] Corresponding authors: Tiejun Shui, shuitiejunynjkedu@163.com; Yan Jin, jinyanfangyi@sina.com.

[1] School of Disaster and Emergency Medicine, Tianjin University, Tianjin, China; [2] Haikou Center for Disease Control and Prevention, Haikou City, Hainan Province, China; [3] School of Medicine, Tianjin University, Tianjin, China; [4] Hainan Provincial Center for Disease Control and Prevention (Hainan Academy of Preventive Medicine), Haikou City, Hainan Province, China; [5] Yunnan Center for Disease Control and Prevention, Kunming City, Yunnan Province, China.
[&] Joint first authors.

Copyright © 2026 by Chinese Center for Disease Control and Prevention & Chinese Academy of Preventive Medicine. All content is distributed under a Creative Commons Attribution Non Commercial License 4.0 (CC BY-NC).

Submitted: June 28, 2026
Accepted: September 25, 2026
Issued: October 02, 2026

REFERENCES

1. Gu SH, Song DH, Lee D, Jang J, Kim MY, Jung J, et al. Whole-genome sequence analysis of Zika virus, amplified from urine of traveler from the Philippines. Virus Genes 2017;53(6):918 – 21. https://doi.org/10.1007/s11262-017-1500-9.
2. Khongwichit S, Chuchaona W, Vongpunsawad S, Poovorawan Y. Molecular epidemiology, clinical analysis, and genetic characterization of Zika virus infections in Thailand (2020-2023). Sci Rep 2023;13(1):21030. https://doi.org/10.1038/s41598-023-48508-4.
3. Rajaiah P, Gupta B, Mayilsamy M. ZIKA virus, an emerging arbovirus in India: a glimpse of global genetic lineages. Microorganisms 2025;13(3):544. https://doi.org/10.3390/microorganisms13030544.
4. Zadra N, Rizzoli A, Rota-Stabelli O. Comprehensive phylogenomic analysis of Zika virus: insights into its origin, past evolutionary dynamics, and global spread. Virus Res 2024;350:199490. https://doi.org/10.1016/j.virusres.2024.199490.
5. Liao Y, Zeng ZL, Hu GL, Yang JP, Yuan H, Li JH, et al. Survey of the first case of Zika virus disease in the mainland of China. Chin J Epidemiol 2016;37(5):593 – 6. https://doi.org/10.3760/cma.j.issn.0254-6450.2016.05.001.
6. Wang YL, Zhang XY, Ren RQ, Li C, Xiang NJ, Tu WX, et al. Epidemiological and clinical characteristics of 25 imported Zika cases in mainland China. Chin J Vector Biol Control 2017;28(6):535 – 7. https://doi.org/10.11853/j.issn.1003.8280.2017.06.005.
7. Zhao DN, Li HC, Zhang HJ, Shi J, Guo JW, Yang L, et al. Dengue virus, chikungunya virus, and Zika virus infections in febrile cases in Gengma county, Yunnan province, in 2019. Dis Surveill 2024;39(6):711 – 7. https://doi.org/10.3784/jbjc.202305040194.
8. Zhang S, Wu JL, Wang D, Song JD, Li Y, Yin CH, et al. The first imported case of Zika virus infection - Shandong Province, China, 2025. China CDC Wkly 2025;7(30):1004 – 8. https://doi.org/10.46234/ccdcw2025.169.
9. Hu LW, Tian LB, Yan K, Zhang S, Xie WJ, Feng J, et al. An imported case of dengue/Zika coinfection - Sichuan Province, China, 2026. China CDC Wkly 2026;8(13):394 – 8. https://doi.org/10.46234/ccdcw2026.063.
10. Communicable Diseases Agency. Weekly infectious diseases bulletin 2025. 2026. https://www.cda.gov.sg/resources/weekly-infectious-diseases-bulletin-2025/. [2026-1-8].