ISSN 2096-7071 (Print)
ISSN 2096-3101 (Online)
CN 10-1629/R1

# CHINA CDC WEEKLY

Vol. 7 No. 49 Dec. 5, 2025

中国疾病预防控制中心周报




ISSN 2096-7071

China CDC Weekly

# Editorial Board



# Editorial Office



Cover Image: adapted from Canva, https://www.canva.cn/.

Editorial

# Letter from the New Editor-in-Chief

Jianwei Wang[1,#]

Six years of sustained progress, advancing steadily toward excellence. Since its establishment, *China CDC Weekly* (hereafter called *Weekly*) has remained steadfast in its founding mission, continuously innovating and moving forward with unwavering determination.

As the national public health journal, hosted by the Chinese Center for Disease Control and Prevention & Chinese Academy of Preventive Medicine, *Weekly* has sustained its commitment to core public health science, program, and values. By leveraging China's comprehensive CDC system, the journal rapidly disseminates first-hand surveillance data, insightful epidemiological analyses of infectious and chronic diseases, actionable investigation reports on public health emergencies, and cutting-edge scientific discoveries.

Throughout its six-year evolution, *Weekly* flourished through the dedicated efforts of successive editors-in-chief, editorial board members, staff, and countless authors and readers, supported by leadership at all levels. The journal has become an essential platform for timely, reliable, authoritative, and precise dissemination of public health information and for evidence-based recommendations to health professionals and the broader public. Through its academic leadership in public health practice, it has achieved an exemplary reputation in domestic and international public health communities.

*Weekly* has developed a robust multidimensional academic presence — it holds the distinction of dual indexing in Science Citation Index Expanded (SCIE) and Social Sciences Citation Index (SSCI) of the internationally renowned Web of Science, representing the only academic weekly journal in China's public health field to achieve this recognition while consistently maintaining its Q1 ranking. The journal is further indexed in prestigious domestic and international databases, including PubMed Central (PMC), Scopus, Chinese Science and Technology Core Journals, and the Chinese Science Citation Database (CSCD), thereby ensuring worldwide accessibility and maximizing the academic impact of its published research.

China's public health achievements constitute invaluable resources for global learning and local adaptation. Moving forward, guided by the Belt and Road Initiative and the Healthy China 2030 Blueprint, we will strengthen collaborative partnerships with international stakeholders to collectively address critical health challenges, including emerging and re-emerging infectious diseases, chronic disease prevention, climate change impact, food safety, occupational health hazards, and environmental health threats.

Looking ahead, we remain steadfast in our founding mission while embracing the principles of openness, collaboration, reform, and innovation. In partnership with all stakeholders, we are committed to elevating *Weekly* into an increasingly authoritative and influential flagship journal in the global public health arena. Through this platform, we will continue advancing international dissemination of China's public health expertise and insights, thereby contributing distinctive perspectives and substantive support to the advancement of the discipline worldwide.

**doi:** 10.46234/ccdcw2025.258

[#] Corresponding author: Jianwei Wang, wangjw@chinacdc.cn.

[1] Chinese Center for Disease Control and Prevention & Chinese Academy of Preventive Medicine, Beijing, China.



Submitted: November 29, 2025
Accepted: December 01, 2025
Issued: December 05, 2025

Jianwei Wang
Editor-in-Chief, Third Editorial Board, *China CDC Weekly*
Director General & President, Chinese Center for Disease Control and Prevention & Chinese Academy of Preventive Medicine
Academician, Chinese Academy of Engineering

Recommendation

# Boao Initiative of the 2025 Asia Pacific Congress on Public Health

The World Federation of Public Health Associations (WFPHA) Asia Pacific Regional Liaison Office,
The Chinese Preventive Medicine Association (CPMA)

## ABSTRACT

The 2025 Asia Pacific Congress on Public Health, held in Boao, China, in November 2025, released a transnational consensus and jointly issued the Boao Initiative by Chinese Preventive Medicine Association, World Federation of Public Health Associations, and other six associations from the Asia Pacific region. Centered on the core themes of equity, resilience, and innovation, the Initiative proposes a "Four-in-One" collaborative action plan to address the Asia Pacific region's severe public health challenges. These challenges include fragmented regional public health governance, widening health inequalities, increasing climate-health risks, and structural constraints on digital transformation. To tackle these issues, the "Four-in-One" plan includes four key components: 1) Strengthening regional governance and building joint prevention and control defenses; 2) Advancing health equity and protecting every life; 3) Enhancing health adaptation to climate change and building a resilient barrier; and 4) Leading digital innovation and empowering smart health systems. The initiative underscores the importance of transnational cooperation to build a comprehensive, inclusive, and sustainable public health framework. It reaffirms the Asia Pacific region's commitment to global health governance, advocating for shared responsibility to overcome disparities and foster resilience through innovation. Therefore, the Boao Initiative serves as a strategic roadmap for achieving equitable health outcomes and strengthening regional collaboration in public health.

Against the backdrop of a reshaping world order and profound transformation of the global health governance system in the post-pandemic era, the Asia-Pacific region, as one of the world's most densely populated and diverse areas in development, faces unprecedented public health challenges. To address this, the 2025 Asia Pacific Congress on Public Health (APCPH) was convened in Boao, Hainan Province of the People's Republic of China.

The Chinese Preventive Medicine Association (CPMA), in collaboration with the World Federation of Public Health Associations (WFPHA), the Public Health Association of New Zealand (PHANZ), the American Public Health Association (APHA), the Japan Public Health Association (JPHA), the Public Health Association of Australia (PHAA), the Vietnam Public Health Association (VPHA), and the Asia Pacific Alliance for the Control of Influenza (APACI), brought together global strategic leaders, policymakers, and academic authorities to discuss the future challenges and further collaborative action plan. Centered on the three core themes of "equity, resilience, and innovation," we build transnational consensus and jointly issue the following initiative:

## Acknowledging Four Severe Challenges Facing Asia-Pacific Public Health Systems

**Fragmentation of regional public health governance:** System coordination is sluggish, resulting in inefficient cross-border emergency response and resource integration, with the threat of cross-border transmission of infectious diseases being particularly pronounced.

**Widening health inequalities within the region:** Vulnerable groups face systemic barriers in universal health coverage (UHC), equitable access to vaccines, chronic disease management, and mental health services. Urban-rural and regional disparities are expanding, and the health needs of children, adolescents, and the elderly are especially urgent.

**Increasing climate-health risks:** Frequent extreme weather events pose a comprehensive impact on public health and healthcare systems by altering vector distribution, exacerbating air pollution, and threatening nutrition and food security through multiple pathways.

**Structural constraints on digital transformation:** Imbalances in regional information infrastructure, inadequate data governance mechanisms, and insufficient privacy protection capabilities severely limit the widespread adoption and application of innovative technologies such as artificial intelligence (AI) and telemedicine.

## Promoting a "Four-in-One" Collaborative Action Plan

To systematically address the aforementioned challenges, we advocate for the implementation of a comprehensive "Four-in-One" action plan:

**Strengthen regional governance and build joint prevention and control defenses:** Establish efficient cross-border infectious disease surveillance and early warning systems, focusing on enhancing joint prevention and control capabilities for acute respiratory infectious diseases like influenza. Strengthen cooperation in controlling vector-borne diseases and jointly safeguard regional biosafety. Strictly maintain the bottom line of food safety and advocate for balanced nutritional diets to ensure the "safety and well-being on people's tables." Vigorously promote the deep integration of medical and preventive services to solidify the grassroots "health gatekeeper" system.

**Advance health equity and protect every life:** Fully integrate chronic disease and mental health services into the basic public health service package. Promote the concept of active health for frail older adults to delay the decline of their intrinsic capacity. Drive the integration of comprehensive geriatric assessment into clinical practice to enhance the personalization of elder care. Optimize care models for vulnerable groups, such as those with disabilities or cognitive impairment, and deepen the integration of medical and elderly care services. Strengthen high-impact, cost-effective public health interventions, including tobacco control, oral health, mental health, and vaccination. Integrate Indigenous health services into community-led health systems to achieve equitable, localized, and sustainable public health outcomes.

**Enhance health adaptation to climate change and build a resilient health barrier:** Establish climate-health risk assessment mechanisms. Promote climate-appropriate health technologies. Accelerate the construction of climate-resilient health facilities and living environments to improve the core capacity of health systems to respond to extreme weather events.

**Lead digital innovation and empower smart health systems:** Develop regionally unified digital health ethics and data standards. Create multi-lingual, low-cost mobile health (mHealth) tools. Establish a regional validation and promotion mechanism for AI-assisted diagnostic technologies. Ensure that technological innovation is universally shared and does not exacerbate existing health inequalities.

## Mobilizing Regional Synergy to Drive Implementation

The Initiative systematically integrates comprehensive public health issues in the Asia-Pacific, from infectious to chronic diseases and mental health, from clinical medicine to health promotion, and from traditional threats to emerging challenges, while innovatively proposing the "Four-in-One" collaborative action path.

The Congress calls upon regional public health associations, international organizations, academia, industry, and civil society to strengthen collaboration to jointly push global health governance toward a more efficient and equitable direction, and to promote the reform and reinforcement of public health governance systems at national and regional levels. In the short term, initiate the construction of a regional health emergency network and climate-health assessment through transnational and cross-sectoral cooperation; In the long term, deeply integrate digital intelligence technology with regional collaborative governance mechanisms to continuously enhance the resilience and effectiveness of public health systems and health governance.

We firmly believe that "equity, resilience, and innovation" are the core visions guiding the future of public health. The Asia-Pacific region must work hand in hand to jointly build a more comprehensive, inclusive, and sustainable public health system, making a more solid and profound contribution to the health and well-being of the region's people and to global health governance.

**This initiative is prepared by:**

**Xiaonong Zhou**

1. National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention (Chinese Center for Tropical Diseases Research); NHC Key Laboratory of Parasite and Vector Biology; WHO Collaborating Centre for Tropical Diseases; National Center for International Research on Tropical

Diseases, Ministry of Science and Technology, Shanghai, China;

2. School of Global Health, Chinese Center for Tropical Diseases Research, Shanghai Jiao Tong University School of Medicine, Shanghai, China.

**Minghui Ren**

3. China Centre for Health Development Studies, Peking University, Beijing, China;

4. Department of Global Health, School of Public Health, Peking University, Beijing, China.

November 29, 2025

Boao, Hainan Province of the People's Republic of China

**doi:** 10.46234/ccdcw2025.259



Submitted: November 29, 2025
Accepted: December 01, 2025
Issued: December 05, 2025

Preplanned Studies

# Outbreak of Chikungunya Virus with *Aedes albopictus*-Adaptive Mutations — Guangdong Province, China, 2025

Wenxiao Gong[1]; Dongli Wang[1]; Qianying Chen[1]; Shuting Zhong[1]; Xiaolu Shi[2,3,#]; Bo Peng[1,2,#]


## Summary

### What is already known about this topic?

The circulating strain in the recent Chikungunya fever outbreak in Guangdong Province belongs to the East/Central/South African (ECSA) genotype. However, the specific mutations in the viral genome remained unclear.

### What is added by this report?

This study conducted whole-genome sequencing of viral sequences from clinical samples. The results confirmed that the epidemic strain belongs to the Middle African Lineage (MAL) within the ECSA genotype, not the Indian Ocean Lineage (IOL). Further analysis of nucleotide mutations revealed several adaptive mutations compared with the S27 genomic sequence (NC_004162), such as E1-A226V, E2-L210Q, and E2-I211T.

### What are the implications for public health practice?

Based on previous genomic surveillance and pathogen studies, mutations like E1-A226V, E2-L210Q, and E2-I211T were generally considered characteristic of IOL within the ECSA genotype and are known to enhance viral replication and transmission efficiency in *Aedes albopictus* mosquitoes. This study identifies the circulating strain in Guangdong belongs to MAL, which is phylogenetically distinct from IOL, yet also carries these mutations. This suggests these may represent adaptive changes in the MAL strain to a new mosquito host. In Guangdong Province, *Ae. albopictus* is the predominant mosquito species, while the distribution of *Ae. aegypti* is relatively limited. The ecological predominance of *Ae. albopictus* likely serves as a key contributing factor facilitating the rapid importation and subsequent widespread dissemination of the current epidemic strain.

## ABSTRACT

**Introduction**: Chikungunya virus (CHIKV), transmitted by *Aedes aegypti* and *Aedes albopictus*, causes chikungunya fever. Since its 2005 re-emergence, it has become endemic in 119 countries across Africa, Asia, the Americas, Europe, and Oceania. An outbreak in China's Guangdong Province (July 2025) led to more than 15,000 cases by August 20, straining public health systems and highlighting the need to strengthen viral mutation surveillance. However, the precise genomic characteristics of this prevalent virus remain unknown, and this study aims to fill this critical knowledge gap through high-throughput sequencing technology.

**Methods**: This study collected two serum samples from this epidemic, extracting and sequencing total nucleic acids via an MGISEQ-G99 sequencer. Complete viral genomes were generated via a consensus reference assembly; they were phylogenetically analyzed and comparatively assessed to identify viral nucleotide variations and protein amino acid substitutions.

**Results**: Phylogenetic analysis confirmed that both research strains belong to the East/Central/South African genotype, clustering within the Middle African Lineage and sharing the highest identity with currently circulating CHIKV isolates from Réunion Island. The circulating strain carries adaptive mutation sites such as E1-A226V, E2-L210Q, and E2-I211T, significantly enhancing viral replication efficiency in *Ae. albopictus*.

**Conclusions:** Understanding viral etiology is essential for controlling outbreaks. The current epidemic strain carries mutations adaptive to *Ae. albopictus*, increasing transmission risk. Guangdong's mosquito population — predominantly *Ae. albopictus* with limited *Ae. aegypti* presence — facilitates efficient virus import and spread.


Chikungunya virus (CHIKV) is a single-stranded positive-sense RNA virus belonging to the genus *Alphavirus* of the family *Togaviridae*. As a significant mosquito-borne pathogen, CHIKV has spread to nearly all regions inhabited by *Ae. aegypti* and *Ae. albopictus* mosquitoes, facilitated by increasing

international travel (*1*). According to statistics from the World Health Organization, since the re-emergence of chikungunya fever in 2005, the virus has become endemic in 119 countries, affecting regions across Africa, Asia, islands in the Indian Ocean, the South Pacific islands, Europe, and the Americas (*2*).

The CHIKV genome is approximately 11,800 bases in length and consists of a 5' untranslated region (5' UTR), two open reading frames, and a 3' untranslated region (3' UTR). The two open reading frames encode two polyprotein precursors (CHIKVgp1 and CHIKVgp2). CHIKVgp1 is cleaved by the viral protease nsP2 into four nonstructural proteins (nsP1–nsP4), whereas host cell proteases process CHIKVgp2 into five structural proteins — the capsid protein (C), envelope glycoproteins (E1 and E2), and E3 and 6K proteins — which are involved in viral assembly and budding (*3*). During viral infection, the E2 protein serves as the primary target for neutralizing antibodies (*4*). The 3' UTR is a length polymorphism and contains functional RNA secondary structures (e.g., the stem-loop Y structure and repeated sequence elements), which play critical roles in host adaptation and viral replication (*5*).

Phylogenetic analysis of E1 gene sequences classified CHIKV into three genotypes: West African, Asian, and East/Central/South African (ECSA) (*6*). The re-emergence of CHIKV in Kenya in 2004 and its subsequent outbreak on Réunion Island in 2005 marked the emergence of the ECSA genotype as the dominant circulating lineage, during which adaptive mutations accumulated. Virological data indicate that the A226V substitution in the E1 envelope glycoprotein enhances CHIKV replication titers in *Aedes* mosquitoes, thereby increasing the transmission capacity of the mutant virus (*7*). The E2-L210Q and E2-I211T substitutions represent adaptive mutations that synergistically increase CHIKV transmission efficiency in *Ae. albopictus* mosquitoes. While E2-I211T (acquired circa 2004–2005) establishes a genetic background permissive for mosquito adaptation, E2-L210Q specifically augments midgut infectivity and viral dissemination, with both mutations exhibiting epistatic interactions with the key E1-A226V substitution (*8*). Since their initial detection in 2010, two novel mutations (E1-K211E and E2-V264A) have exhibited distinct genotypic distributions: E1-K211E is exclusively found in Asian lineages, whereas E2-V264A represents a unique cross-genotypic substitution. Functional studies have confirmed that the double mutant (E1-K211E + E2-V264A) in the background of E1-226A confers significantly enhanced transmission efficiency in *Ae. aegypti* (*9*).

Viral genomic surveillance activities have been driven by the rapid development of DNA sequencing technology and bioinformatics tools for genomic data analysis. These tools have allowed characterization of the genome and dispersal patterns of emerging and re-emerging pathogens. The 2025 large-scale Chikungunya fever outbreak in Shunde District, Foshan City, Guangdong Province, China, has drawn widespread attention (*10*). The release of the current epidemic strain's full genomic sequence and identification of critical mutation sites are essential for effective outbreak containment. Based on this knowledge gap, the present study aims to decode and obtain the complete genomic sequence of the circulating strain, enabling public health personnel to understand the genetic evolution and characteristics of the virus, thereby facilitating timely adjustments to control strategies.

On July 26, 2025, chikungunya virus infection was confirmed in two tourists who had entered Shenzhen from other Guangdong cities. This study immediately extracted nucleic acids from the samples and conducted meta-transcriptomic sequencing for molecular tracing of the viral origin. During the sequence assembly process, the La Réunion outbreak strain, UVE/CHIKV/2024/RE/CNR_79903 (GenBank: PV593524), was selected as the reference genome based on the optimal results from average nucleotide identity analysis. The 2 assembled viral genomes, designated GM01_ycj0728 and GM02_yzc0728, each comprised 11,713 bp with >99.7% coverage at a 30× sequencing depth.

Multiple sequence alignment and maximum-likelihood phylogenetic analyses (substitution model: GTR+F+I+G4; 1,000 bootstrap replicates) demonstrated that both strains clustered most closely with the UVE/CHIKV/2024/RE/CNR_79903 (GenBank: PV593524) and S30b03 (GenBank: PV685702) isolates from La Réunion (2024–2025). Together with the CAM/2016/Yaounde strain from Cameroon (GenBank: MT666072; sampled in 2021), these viruses were phylogenetically classified within the Central African lineage (Figure 1). Genomic comparison between the two viral strains analyzed in this study revealed no single-nucleotide polymorphisms.

The CHIKV genome encodes four nonstructural and five structural proteins. While nonstructural proteins are not incorporated into mature virions,

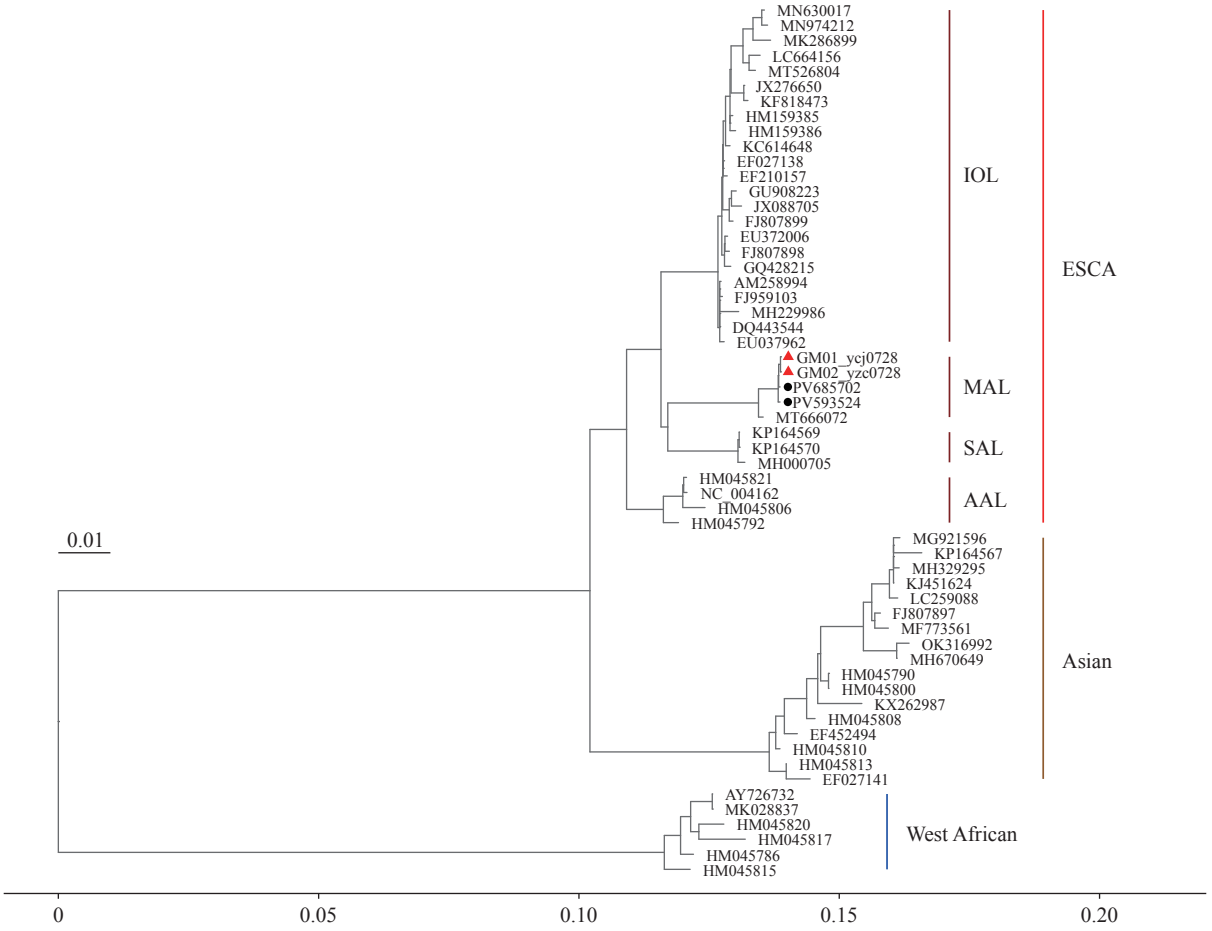


FIGURE 1. Maximum-likelihood phylogenetic analysis of Chikungunya virus based on whole-genome nucleotide sequences.
Note: The tree was inferred with IQ-TREE (version 2.1.2) using the GTR+F+I+G4 model and 1,000 bootstrap replicates, and it was rooted using the O'nyong-nyong virus as outgroup. Scale bar represents the average number of nucleotide substitutions per site. This analysis involved 57 nucleotide sequences. Red triangles denote the viral strains characterized in this study, whereas black circles represent the predominant circulating strains identified in La Réunion during 2024–2025.
Abbreviation: ECSA=East/Central/South Africa genotype; IOL=Indian Ocean Lineage; MAL=Middle African Lineage; SAL=South American Lineage; AAL=African/Asian Lineages.

structural proteins serve as critical targets for host humoral immune responses and represent the primary antigenic components in most vaccine formulations (*4*). Consequently, this study focused specifically on analyzing amino acid variation sites within these structural proteins. Genomic analysis revealed that both the GM01_ycj0728 and GM02_yzc0728 strains harbored several critical mutations, including E1-A226V, as well as the E2-L210Q and E2-I211T substitutions (Table 1).

The E1-A226V mutation was first identified in 2005 and has been demonstrated to significantly increase CHIKV adaptation and replication competence in *Ae. albopictus* mosquitoes, although it is not considered the sole determinant of the virus's high transmission efficiency (*7*,*11*). Notably, the additional acquisition of E1-K211E and E2-V264A mutations synergistically amplified CHIKV replication efficiency in *Ae. aegypti*, yielding exponential increases in viral load compared with the single E1-A226V variant (*9*). The sequences revealed only the E1-A226V mutation in both isolates, lacking the E1-K211E/E2-V264A combination. While E2-L210Q/I211T mutations synergize with E1-A226V to enhance *Ae. albopictus*-specific adaptation, this epistatic interaction has no significant effect on CHIKV performance in *Ae. aegypti* or standard vertebrate cell cultures (*9*). In Guangdong Province, *Ae. albopictus* serves as the predominant mosquito species, while the distribution of *Ae. aegypti* remains relatively limited. This ecological predominance of *Ae. albopictus* may represent a key contributing factor in the rapid import and subsequent

TABLE 1. Non-synonymous mutations in the structural polyprotein of Chikungunya virus.

| Protein | Protein position | Viruses | | | |
|---|---|---|---|---|---|
| | | NC_004162 | PV593524 | GM01_ycj0728 | GM02_yzc0728 |
| C | 23 | P | P | P | P |
| C | 27 | V | V | V | V |
| C | **63** | **K** | **R** | **R** | **R** |
| C | 73 | K | K | K | K |
| E3 | **23** | **A** | **T** | **T** | **T** |
| E2 | **57** | **G** | **K** | **K** | **K** |
| E2 | 60 | D | D | D | D |
| E2 | **74** | **I** | **T** | **T** | **T** |
| E2 | **79** | **G** | **E** | **E** | **E** |
| E2 | **160** | **N** | **T** | **T** | **T** |
| E2 | **164** | **A** | **T** | **T** | **T** |
| E2 | **181** | **L** | **M** | **M** | **M** |
| E2 | **194** | **S** | **G** | **G** | **G** |
| E2 | 198 | R | R | R | R |
| E2 | 205 | G | G | G | G |
| E2 | **210** | **L** | **Q** | **Q** | **Q** |
| E2 | **211** | **I** | **T** | **T** | **T** |
| E2 | 233 | K | K | K | K |
| E2 | 252 | K | K | K | K |
| E2 | 264 | V | V | V | V |
| E2 | **267** | **M** | **R** | **R** | **R** |
| E2 | **299** | **S** | **N** | **N** | **N** |
| E2 | 312 | T | T | T | T |
| E2 | **344** | **A** | **T** | **T** | **T** |
| E2 | 375 | S | S | S | S |
| E2 | 386 | V | V | V | V |
| 6K | 8 | V | V | V | V |
| 6K | **54** | **I** | **V** | **V** | **V** |
| E1 | 98 | A | A | A | A |
| E1 | 211 | K | K | K | K |
| E1 | **226** | **A** | **V** | **V** | **V** |
| E1 | **269** | **M** | **V** | **V** | **V** |
| E1 | 284 | D | D | D | D |
| E1 | **317** | **I** | **V** | **V** | **V** |
| E1 | **322** | **V** | **A** | **A** | **A** |

Note: Bold text in the chart indicates amino acid positions where mutations were detected.

widespread dissemination of the current epidemic.

## DISCUSSION

CHIKV is a significant mosquito-borne pathogen that has undergone sustained transmission in all global regions inhabited by *Aedes* mosquitoes since 2005. Notably, the acquisition of adaptive mutations has increased the epidemic potential through increased transmissibility (*12*). In this study, it was confirmed that the circulating virus carries adaptive mutation sites

such as E1-A226V, E2-L210Q, and E2-I211T, which have been demonstrated to significantly enhance viral replication efficiency in *Ae. albopictus*.

This study performed whole-genome sequencing of viral sequences from clinical samples, establishing a robust framework for CHIKV genomic surveillance and single-nucleotide polymorphism analysis. Specifically, meta-transcriptomic sequencing is recommended for emerging epidemic strains, as this method overcomes 3' UTR amplification failures associated with primer-based whole-genome amplification approaches, thereby significantly increasing the likelihood of obtaining complete genomes. Second, during genome assembly, the selection of reference sequences should be guided by average nucleotide identity analysis — a strategy critical for ensuring the accuracy of CHIKV genome reconstruction. This approach addresses technical challenges such as the 3' UTR gaps observed in consensus sequences when suboptimal references are used (e.g., the S27 genomic sequence in this study). Third, based on prior epidemiological and virological experimental data, this study identified 35 amino acid sites within structural proteins as high-priority surveillance targets, enabling efficient large-scale identification of critical mutations in genomic datasets.

The findings of this study are subject to at least two limitations. First, although genomic evolution was analyzed through average nucleotide identity and phylogenetic reconstruction, further investigations into 3' UTR polymorphisms and short repetitive sequence elements would provide deeper insights into CHIKV adaptive evolution. Second, while high-frequency mutation sites in structural proteins are prioritized for surveillance, the biological significance of low-frequency mutations in nonstructural proteins remains to be elucidated.

**Ethical statement**: Approved by The Ethics Committee of Shenzhen Center for Disease Control and Prevention, China (approval number: SZCDC-IRB2024033).

**Conflicts of interest**: No conflicts of interest.

**Funding:** Supported by Shenzhen Medical Research Fund (B2404002), Sanming Project of Medicine in Shenzhen (SZSM202211023), and Shenzhen Science and Technology Program (SYSPG2024121117392 1049, SGDX20240115113259001).

**doi:** 10.46234/ccdcw2025.260

[#] Corresponding authors: Bo Peng, pb18@163.com; Xiaolu Shi, shixiaolu831@163.com.

[1] Shenzhen Guangming District Center for Disease Control and Prevention, Shenzhen City, Guangdong Province, China; [2] Microbiology Laboratory, Shenzhen Center for Disease Control and Prevention, Shenzhen City, Guangdong Province, China; [3] School of Public Health, Southern Medical University, Guangzhou City, Guangdong Province, China.



Submitted: September 25, 2025
Accepted: November 27, 2025
Issued: December 05, 2025

## REFERENCES

1. Weaver SC, Forrester NL. Chikungunya: evolutionary history and recent epidemic spread. Antiviral Res 2015;120:32 – 9. https://doi.org/10.1016/j.antiviral.2015.04.016.
2. Feng Y, Chang FF, Yang Y, Lu HZ. From dengue to chikungunya: Guangdong as a sentinel for arboviral threats in East Asia. Biosci Trends 2025;19(4):368 – 73. https://doi.org/10.5582/bst.2025.01228.
3. Freppel W, Silva LA, Stapleford KA, Herrero LJ. Pathogenicity and virulence of chikungunya virus. Virulence 2024;15(1):2396484. https://doi.org/10.1080/21505594.2024.2396484.
4. Powers AM. Vaccine and therapeutic options to control chikungunya virus. Clin Microbiol Rev 2018;31(1):e00104 – 16. https://doi.org/10.1128/CMR.00104-16.
5. Bardossy ES, Volpe S, Alvarez DE, Filomatori CV. A conserved Y-shaped RNA structure in the 3'UTR of chikungunya virus genome as a host-specialized element that modulates viral replication and evolution. PLoS Pathog 2023;19(5):e1011352. https://doi.org/10.1371/journal.ppat.1011352.
6. Powers AM, Tesh R, Weaver S, Brault A. Re-emergence of Chikungunya and O'nyong-nyong viruses: evidence for distinct geographical lineages and distant evolutionary relationships. J Gen Virol 2000;81(Pt 2):471-9. http://dx.doi.org/10.1099/0022-1317-81-2-471.
7. Tsetsarkin KA, Vanlandingham DL, McGee CE, Higgs S. A single mutation in chikungunya virus affects vector specificity and epidemic potential. PLoS Pathog 2007;3(12):e201. https://doi.org/10.1371/journal.ppat.0030201.
8. Tsetsarkin KA, Weaver SC. Sequential adaptive mutations enhance efficient vector switching by Chikungunya virus and its epidemic emergence. PLoS Pathog 2011;7(12):e1002412. https://doi.org/10.1371/journal.ppat.1002412.
9. Agarwal A, Sharma AK, Sukumaran D, Parida M, Dash PK. Two novel epistatic mutations (E1:K211E and E2:V264A) in structural proteins of Chikungunya virus enhance fitness in *Aedes aegypti*. Virology 2016;497:59 – 68. https://doi.org/10.1016/j.virol.2016.06.025.
10. Li YH, Jiang SY, Zhang M, Li Y, He JF, Yang ZF, et al. An outbreak of chikungunya fever in China — Foshan city, Guangdong province, China, July 2025. China CDC Wkly 2025;7(32):1064 – 5. https://doi.org/10.46234/ccdcw2025.172.
11. Fortuna C, Toma L, Remoli ME, Amendola A, Severini F, Boccolini D, et al. Vector competence of *Aedes albopictus* for the Indian Ocean lineage (IOL) chikungunya viruses of the 2007 and 2017 outbreaks in Italy: a comparison between strains with and without the E1:A226V mutation. Euro Surveill 2018;23(22):1800246. https://doi.org/10.2807/1560-7917.ES.2018.23.22.1800246.
12. Burt FJ, Chen WQ, Miner JJ, Lenschow DJ, Merits A, Schnettler E, et al. Chikungunya virus: an update on the biology and pathogenesis of this emerging pathogen. Lancet Infect Dis 2017;17(4):e107 – 17. https://doi.org/10.1016/S1473-3099(16)30385-1.

Outbreak Reports

# The First Imported Case of Chikungunya Virus Infection — Anhui Province, China, 2025

Liangzi Guo[1,&]; Jun He[2,&]; Sai Hou[3]; Ziqing Yuan[4]; Junling Yu[3]; Zhaoqian Meng[1]; Guoxia Guo[1]; Xialian Gao[1]; Huaibiao Li[1]; Lei Gong[3]; Yinxu Hou[3]; Jialin Zhang[3]; Xiuzhi Chen[3]; Yujie Feng[3]; Xiaofeng Lyu[3]; Tuantuan Li[4]; Ge Bu[1,#]; Jiabing Wu[3,#]

**Summary**

**What is already known about this topic?**

Since China's first imported Chikungunya fever (CHIKF) case in 2008, 16 provinces have reported cases, primarily imported from endemic areas in Southeast Asia, South Asia, and Africa. Most of China, including Anhui Province, is non-endemic; Anhui had no cases prior to August 2025.

**What is added by this report?**

This report documents the first laboratory-confirmed imported case of Chikungunya virus (CHIKV) infection in Anhui Province and presents the complete viral genome sequence. Comprehensive clinical documentation characterizes the patient's symptoms in detail, including fever, arthralgia, and cutaneous manifestations, thereby addressing a critical gap in the regional clinical profile of CHIKV infection. Comparative analysis of real-time fluorescent quantitative polymerase chain reaction (qPCR) and Enzyme-Linked Immunosorbent Assay (ELISA) results demonstrated that nucleic acid testing provides superior sensitivity during the acute phase of infection.

**What are the implications for public health practice?**

This case underscores China's escalating CHIKF risk. Key implications are: 1) Establishing a cross-regional surveillance network is vital for enhanced case and vector detection sensitivity; 2) In non-endemic areas, strengthening public health education on CHIKV risks is essential for imported disease control. Effectively reducing the burden of vector-borne diseases requires strengthened international cooperation, multi-sectoral collaboration, and innovative technologies.

## ABSTRACT

**Introduction:** On August 11, 2025, a suspected Chikungunya virus (CHIKV) case traveled from Foshan to Fuyang Xiguan Airport, Anhui Province. After symptom reporting on August 12, local CDC launched epidemiological investigations, laboratory testing, and control measures.

**Methods:** We collected serial blood samples throughout the patient's hospitalization and documented the complete clinical progression from admission to discharge. Real-time fluorescent quantitative polymerase chain reaction (qPCR) was employed to detect CHIKV nucleic acid, while Enzyme-Linked Immunosorbent Assay (ELISA) was used to test for CHIKV IgG and IgM antibodies. MinION nanopore sequencing was performed on blood samples to obtain the complete viral genome sequence. Phylogenetic analyses were subsequently constructed to determine the origin, genotype, and mutation profile of this imported case.

**Results:** The qPCR analysis confirmed CHIKV presence in the patient's serum samples. ELISA detected CHIKV IgG and IgM antibodies in blood samples collected on the fifth and ninth days after illness onset, respectively. Nanopore sequencing successfully generated the complete CHIKV genome sequence. Phylogenetic analysis demonstrated that the strain belonged to the East-Central-South-African lineage, consistent with the genotype identified from 190 cases in the local clustered Chikungunya fever (CHIKF) outbreak that occurred in Guangdong Province in July 2025. The strain showed 99.964% nucleotide identity (4 differential loci) with strain PX216392.1 detected in the current epidemic, and 99.9556% identity (5 differential loci) with PX236189.1.

**Conclusion:** This is Anhui's first imported CHIKV case, linked to the Guangdong outbreak. No local transmission or CHIKV-positive vector mosquitoes were detected.

Chikungunya fever (CHIKF), caused by Chikungunya virus (CHIKV) represents a mosquito-

borne arboviral disease that has emerged as a significant global public health threat (*1*). The clinical presentation typically manifests as an acute febrile illness accompanied by high fever, severe polyarthralgia, myalgia, rash, and headache (*2*). CHIKV has been classified into four distinct genotypes: East-Central-South African (ECSA), West African (WA), Asian (AL), and Indian Ocean Lineages (IOL), with the ECSA genotype demonstrating the highest virulence and most widespread global distribution (*3*). This represents the first detection of CHIKV in a migrant worker returning to Anhui Province, necessitating comprehensive entomological surveillance, systematic case screening, and targeted public health education in the region.

## INVESTIGATION AND RESULTS

### Epidemiological Investigation

On August 11, 2025, a 52-year-old female patient returned to Anhui Province from Shunde District, Foshan City, Guangdong Province. Prior to departure, she had developed joint pain, fever, and scattered erythematous maculopapules on her trunk. The patient had been residing in an urban village area in Foshan characterized by high mosquito density. Despite this environmental exposure, no colleagues or family members contracted CHIKV infection, and the patient denied experiencing recent mosquito bites. She was admitted to Fuyang Second People's Hospital on August 12.

The Fuyang CDC conducted qPCR testing on blood samples collected from both the patient and her family members. The patient's sample tested positive for CHIKV, whereas all family members tested negative. On August 25, 2025, nucleic acid testing returned negative results (Table 1). According to the Diagnosis and Treatment Protocol for Chikungunya Fever (2025 Edition), isolation may be discontinued when body temperature normalizes for more than 24 hours with negative nucleic acid testing, or when the disease course exceeds 7 days. Following these criteria, the patient was discharged.

### Laboratory Test of the Patient

The CDC performed etiological and serological testing for CHIKV, while Fuyang No.2 People's Hospital conducted general laboratory examinations of the patient.

Upon admission, the patient exhibited elevated C-reactive protein (CRP) and serum amyloid A (SAA) levels, accompanied by abnormal liver function indicators. Following symptomatic treatment, all laboratory parameters improved and returned to normal ranges by discharge (Table 2).

TABLE 1. Laboratory test results of blood samples from the first imported case of Chikungunya virus infection in Anhui Province.

| Time | CHIKV tested by qPCR (Ct value) |
|---|---|
| August 12, 2025 | (+) 24.00 |
| August 13, 2025 | (+) 23.00 |
| August 15, 2025 | (+) 33.30 |
| August 19, 2025 | (+) 36.00 |
| August 22, 2025 | (+) 37.00 |
| August 25, 2025 | (–) |

Note: "+" indicates a positive result, defined as an amplification curve displaying a characteristic S-shape with a Ct value ≤35; "–" indicates a negative result, with Ct value >38 or no detection. Suspected positive results show a typical S-shaped amplification curve with 35< Ct value ≤38, requiring retesting. If retest results are consistent, the sample is classified as positive; if the Ct value >38 or remains undetected, the sample is classified as negative. LOD: 500 copies/mL.

Abbreviation: CHIKV=chikungunya virus; qPCR=quantitative polymerase chain reaction; LOD=limit of detection; Ct value=cycle threshold value.

CHIKV viral RNA was extracted from patient samples using a nucleic acid extraction and purification kit (Xi'an Tianlong Technology Co., Ltd., No.T183). PCR amplification was performed using a CHIKV nucleic acid detection kit employing the fluorescent PCR method [Fantasia Biopharma (Zhejiang) Co., Ltd., No.RFKNT027]. Primer sequences are presented in Table 3. Gene amplification was conducted using the SLAN 96S instrument (Shanghai Hongshi Medical Technology Co., Ltd.).

Viral amplification was performed using the CHIKV Whole Genome Capture Kit (BAIYITECH, Hangzhou, China; No. BK-CHIKV024). Amplified products underwent sequencing on a MinION Mk1B Nanopore sequencer (Oxford Nanopore Technologies, Oxford, UK). Sequencing libraries were prepared using the Sample Library Prepsystem (BJSLB-240, Hangzhou BAIYI Technology Co., Ltd., Hangzhou, China) in combination with the multiple samples DNA Library Prep Kit for Ligation Sequencing (BAIJU, Hangzhou, China; No. K024) and Ligation Sequencing Kit (ONT, UK; No. SQK-LSK110) with R9.4.1 flow cells. Data analysis was conducted using the BAIYI MicroGeno Platform (V 5.4.2, Hangzhou Baiyi Technology Co., Ltd.). Raw sequencing data underwent quality control using NanoPlot (V 1.30.07)

TABLE 2. Serial laboratory findings during hospitalization from the first imported case of Chikungunya virus infection in Anhui Province.

| Laboratory test item | August 12 | August 13 | August 15 | August 19 | August 22 | August 25 | Reference range |
|---|---|---|---|---|---|---|---|
| TP (Biuret method) (g/L) | 61.7↓ | 62.2↓ | 63.8↓ | 70.2 | 71 | 74.5 | 65–85 |
| ALB (BGM) (g/L) | 37.8↓ | 38.6↓ | 37.7↓ | 41.3 | 42.1 | 45.5 | 40–55 |
| GLOB (g/L) | 23.9 | 23.6 | 26.1 | 28.9 | 28.9 | 29 | 20–40 |
| A/G | 1.6 | 1.6 | 1.4 | 1.4 | 1.5 | 1.6 | 1.2–2.4 |
| PA (mg/mL) | 17.9↓ | 16.6↓ | 18.4 | 23.7 | 27.2 | 30.3 | 18–35 |
| ALT (U/L) | 12 | 14 | 10 | 13 | 24 | 26 | 0–40 |
| AST (U/L) | 18 | 15 | 13 | 32 | 54 | 24 | 0–35 |
| AST/ALT ratio | 1.5 | 1.07 | 1.3 | 2.46 | 2.25 | 0.92 | 0.8–1.5 |
| γ-GT (U/L) | 15 | 13 | 14 | 27 | 31 | 20 | 0–45 |
| ALP (U/L) | 38↓ | 45↓ | 39↓ | 30↓ | Undetected | 58 | 0–135 |
| TB (μmol/L) | 7.9 | 8.9 | 5.2 | 7.8 | 6.5 | 9.6 | 0–21 |
| DB (μmol/L) | 3.0 | 2.8 | 1.6 | 4.5 | 3.1 | 2.3 | 0–8.0 |
| IB (μmol/L) | 4.9 | 6.1 | 3.6 | 3.3 | 3.4 | 7.3 | 0–13 |
| BUN (mmol/L) | 6.4 | 4.0 | 4.9 | 4.3 | 4.8 | 4.7 | 2.6–7.5 |
| Creatinine (sarcosine oxidase method) (μmol/L) | 52 | 46 | 48 | 46 | 47 | 90 | 35–115 |
| UA (μmol/L) | 191 | 207 | 224 | 215 | 234 | 300 | 155–357 |
| CRP (mg/L) | 16.6↑ | 16.7↑ | 9.1↑ | 2.5 | 0.7 | 2.1 | 0–6 |
| SAA (mg/L) | 277.8↑ | 348.6↑ | 338.1↑ | 13.8↑ | 3.9 | Undetected | 0–10 |

Note: ↑ means the detected value is below the upper limit of the normal reference interval; ↓ means the detected value is below the lower limit of the normal reference interval.
Abbreviation: TP=total protein; ALB(BGM)=albumin (bromocresol green method); GLOB=globulin; A/G=albumin/globulin ratio; PA=prealbumin; ALT=alanine aminotransferase; AST=aspartate aminotransferase; γ-GT=γ-glutamyl transferase; ALP=alkaline phosphatase; TB=total bilirubin; DB=direct bilirubin; IB=indirect bilirubin; BUN=blood urea nitrogen; Cr=creatinine (sarcosine oxidase method); UA=uric acid; CRP=C-reactive protein; SAA=serum amyloid A.

TABLE 3. The nucleotide sequences of primers and probes used in the CHIKV nucleic acid PCR detection kit.

| Primer/probe name | Sequence (5'-3') |
|---|---|
| CHIKV-F (Forward) | TTTAGCCGTAATGAGCRTCGG |
| CHIKV-PB (Probe) | FAM-TGCCCACACTGTGA-MGB |
| CHIKV-R (Reverse) | CCGTGTTCGGGATCACTGTTA |

Abbreviations: CHIKV=chikungunya virus; PCR=polymerase chain reaction.

(Coster et al., 2018), followed by filtering of low-quality reads using Filtlong (V 0.2.08). The filtered clean data were aligned to the Chikungunya reference genome using minimap2 (V 2.2210) (Li, 2018).

CHIKV IgM and IgG antibodies were detected using an Enzyme-Linked Immunosorbent Assay (ELISA) Kit (Shanghai Baipeng Biotechnology Co., Ltd., No.BP04933, No.BP04932). CHIKV IgM antibodies first appeared in the patient's serum on the fifth day after symptom onset. IgG antibodies emerged later than IgM antibodies, and both antibody types maintained high titers throughout the subsequent monitoring period (Figure 1).

## PUBLIC HEALTH RESPONSE

Following laboratory confirmation of CHIKV infection, the Anhui Provincial CDC, Fuyang CDC, and Yingquan CDC implemented comprehensive coordinated control measures. The patient received treatment in a mosquito-proof isolation ward at Fuyang Second People's Hospital (also designated as Fuyang Infectious Disease Prevention and Control Hospital), while exposed individuals were monitored at home under strict mosquito prevention protocols. Using the patient's current residence as the epicenter, three distinct surveillance zones were established: a core zone, alert zone, and monitoring zone. After case confirmation, CDCs conducted comprehensive vector surveillance in the surrounding environment and dispatched professional technical personnel to implement full-scale mosquito elimination and disinfection operations in areas adjacent to the patient's residence. Emergency mosquito vector control measures — including rapid adult mosquito eradication, breeding site management, case isolation

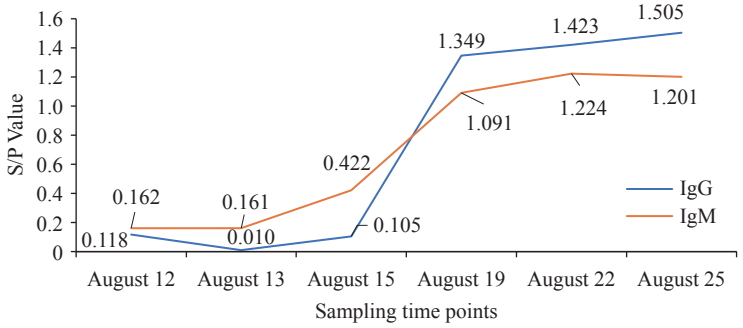


FIGURE 1. ELISA test results for CHIKV IgG and IgM antibodies in the patient's serum.
Note: The x-axis represents sampling time points, while the y-axis displays S/P values. Samples with S/P values ≥0.2 are classified as positive; samples with S/P values <0.2 are classified as negative. S/P=(Optical Density value of the sample to be tested−Optical Density value of the negative control)/(Optical Density value of the positive control−Optical Density value of the negative control).
Abbreviation: CHIKV=chikungunya virus; ELISA=enzyme-linked immunosorbent assay.

and treatment, and comprehensive health education — successfully contained the spread of the epidemic. As shown in Table 4, the Breteau Index (BI) was monitored daily for three consecutive days at sampling sites in core and alert zones following case confirmation. After the BI dropped below 5, surveillance was conducted twice weekly for three consecutive weeks. Following implementation of these systematic emergency mosquito vector control measures, the BI in the core zone plummeted from 83.1 to 0, while that in the alert zone also decreased to 0. No adult mosquitoes or evidence of local transmission were detected during this period.

## DISCUSSION

The global epidemiology of CHIKV has evolved dramatically in recent decades. Originally confined to tropical and subtropical regions, CHIKV has expanded into temperate countries due to global warming and increased human mobility. Most patients develop fever, joint pain, and rash, while some experience neurological complications or death. On October 3, 2025, the World Health Organization (WHO) issued a critical warning, noting that CHIKV has been detected in 119 countries and regions worldwide. From January to September 2025, 263,592 suspected and 181,679 confirmed CHIKV disease cases and 155 CHIKV disease-related deaths have been reported globally, making epidemic control increasingly challenging worldwide (*4*).

In July 2025, an imported CHIKV outbreak emerged in Shunde District, Foshan City, Guangdong Province, China (*5*). Guangdong subsequently experienced China's largest locally clustered outbreak originating from imported cases. By September 13, cumulative confirmed cases reached 10,873, demonstrating CHIKV's significant local transmission potential in China (*6*). On August 11, 2025, Fuyang CDC identified a suspected case in an individual returning from Shunde District. Laboratory testing confirmed CHIKV infection, marking the first imported CHIKF case in Anhui Province. Phylogenetic analysis confirmed that the strain belonged to the East/Central/South African (ECSA) genotype (Figure 2).

Epidemiological investigation and molecular tracing confirmed this case as an imported infection acquired in Foshan City, with symptom development occurring before the patient's return to Anhui Province. The 52-year-old female patient developed symptoms on August 11 and returned from Shunde District — the CHIKV outbreak epicenter in Guangdong Province — on the same day. On August 12, the patient's family contacted the local CDC to report her residence history in the epidemic area. The Fuyang CDC responded immediately by arranging urgent treatment and organizing comprehensive epidemiological investigations, pathogen testing, environmental monitoring, and surveillance activities. Through timely intervention, this imported case did not result in local transmission. Although two vaccines have been approved (with IXCHIQ suspended by the U.S. Food and Drug Administration on August 22, 2025), no vaccine has achieved widespread global implementation to date. Personal mosquito prevention therefore remains the primary strategy for CHIKF prevention in most areas (*7*). Following CDC prevention and control measures, virus transmission risk in both core epidemic and warning zones

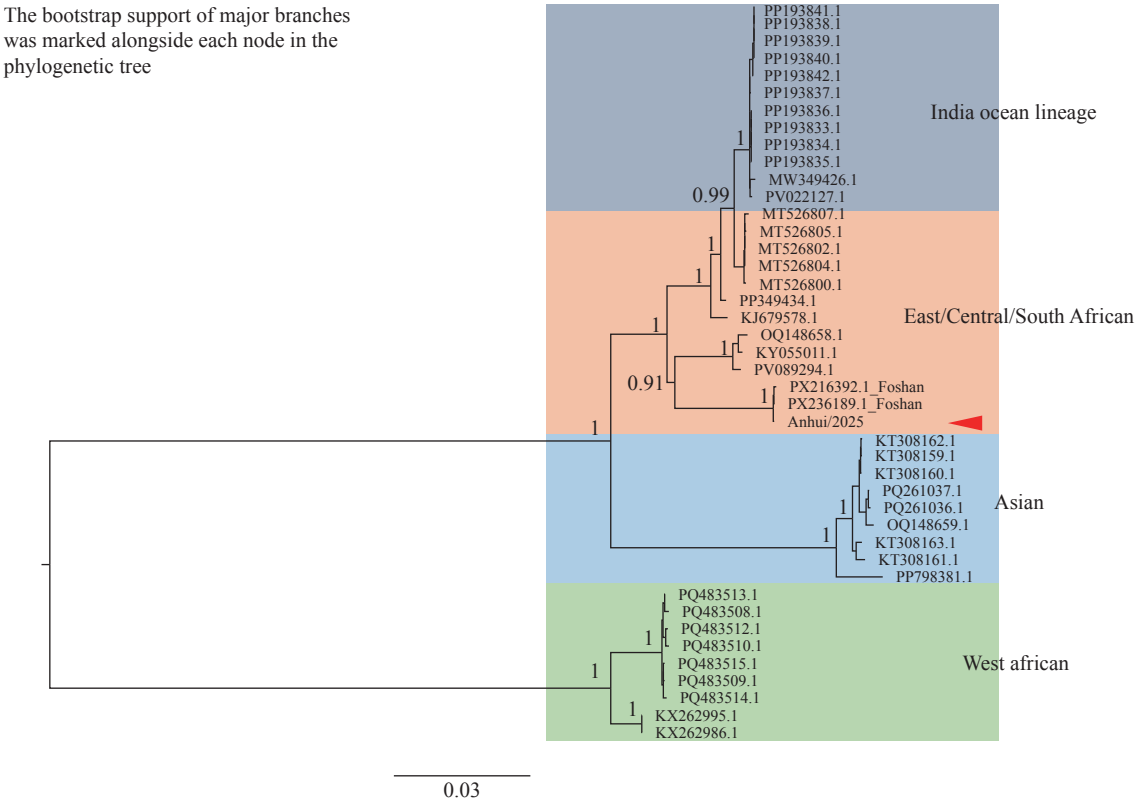


FIGURE 2. Phylogenetic analysis of Anhui|China|August-2025 CHIKV whole-genome sequences using the neighbor-joining method.
Note: Anhui2025 represents the viral strain isolated from the first imported CHIKV case detected in Anhui Province.
Abbreviation: CHIKV=chikungunya virus.

decreased to safe levels (indicators below 5) within 3 days (Table 4). The confirmation and isolation of the patient within 2 days of symptom onset underscores that collective vigilance at the family and individual levels is essential for achieving early detection, diagnosis, and treatment of imported cases. Zhao Jin et al. (*8*) similarly emphasized that early diagnosis and evidence-based prevention measures are crucial for effective CHIKF control.

The patient exhibited characteristic CHIKF manifestations: fever, rash, and joint pain. Joint pain emerged first at onset, primarily affecting the interphalangeal joints of both hands and knee joints, followed by fever. Scattered erythematous maculopapules appeared on the extremities without obvious pruritus, resolving 10 days after symptom onset. These clinical features align with CHIKF symptoms reported in both domestic and international literature (*9*–*10*).

Comparison with an imported CHIKF case detected in Haikou City, Hainan Province on July 28, 2025, revealed that both patients presented with mild symptoms and were confirmed by CHIKV nucleic acid testing in the early stage of illness (*11*). Nevertheless, the case in this study exhibited the classic CHIKF triad symptoms at an early stage, whereas the Haikou case first developed a rash and fever without joint pain, followed by myalgia on the third day after onset. Regarding the genotypic distribution of CHIKV detected in China (*12*), the epidemic strains are predominantly of the ECSA genotype, followed by the Asian genotype — our sequencing results are consistent with this epidemic pattern.

Clinical laboratory results obtained on the admission day (second day after symptom onset) revealed elevated CRP and SAA levels (Table 5), indicating an acute inflammatory response. This finding aligns with the viremia and systemic inflammation characteristic of CHIKV infection, representing typical laboratory manifestations during the acute phase (*13*). Among liver and kidney function indicators, total protein (biuret method), albumin (bromocresol green method), prealbumin, and alkaline phosphatase levels fell below normal ranges (*14*). This pattern suggests that CHIKV infection may induce hepatocellular damage, warranting further investigation. The patient's

TABLE 4. Chikungunya fever emergency mosquito surveillance data.

| Time | Areas | Household visits | Number of indoor and outdoor water-holding containers | Number of positive containers | BI |
|---|---|---|---|---|---|
| August 13, 2025 | Core zones | 71 | 235 | 59 | 83.1 |
| | Alert zones | 69 | 178 | 42 | 60.9 |
| | Monitoring zones | – | – | – | – |
| August 14, 2025 | Core zones | 72 | 16 | 7 | 9.72 |
| | Alert zones | 95 | 83 | 8 | 8.42 |
| | Monitoring zones | – | – | – | – |
| August 15, 2025 | Core zones | 76 | 8 | 3 | 3.95 |
| | Alert zones | 101 | 37 | 4 | 3.96 |
| | Monitoring zones | – | – | – | – |
| August 20, 2025 | Core zones | 93 | 15 | 0 | 0 |
| | Alert zones | – | – | – | – |
| | Monitoring zones | – | – | – | – |
| August 22, 2025 | Core zones | 105 | 3 | 0 | 0 |
| | Alert zones | 103 | 13 | 0 | 0 |
| | Monitoring zones | – | – | – | – |
| August 26, 2025 | Core zones | 109 | 14 | 0 | 0 |
| | Alert zones | – | – | – | – |
| | Monitoring zones | 61 | 17 | 1 | 1.64 |
| August 29, 2025 | Core zones | 106 | 11 | 0 | 0 |
| | Alert zones | 99 | 5 | 0 | 0 |
| | Monitoring zones | – | – | – | – |
| September 1, 2025 | Core zones | 104 | 10 | 0 | 0 |
| | Alert zones | 96 | 8 | 0 | 0 |
| | Monitoring zones | 56 | 6 | 0 | 0 |

Note: The BI survey represents a standardized methodology for rapidly assessing *Aedes* mosquito density, the primary vector for CHIKV transmission. "-" means undetected.Using BI values as the primary indicator for evaluating *Aedes* mosquito density, the classification system encompasses four distinct grades: high density (BI>20), medium density (10<BI≤20), low density (5<BI≤10), and acceptable control levels meeting prevention requirements (BI≤5).
Abbreviation: BI=breteau index; CHIKV=chikungunya virus.

hematological profile demonstrated increased neutrophil percentage alongside decreased lymphocyte and eosinophil percentages, with reduced absolute lymphocyte and eosinophil counts. White blood cell and platelet counts remained within normal limits (Table 5). These characteristics align with hematological findings reported in previous CHIKV outbreaks (*13*–*15*). Comparison of nucleic acid and antibody test results revealed that during early CHIKV infection, RNA detection provides superior sensitivity compared to antibody detection. However, as the disease progresses, viral RNA disappears rapidly while serum antibodies gradually emerge and persist long-term (*16*–*19*). Real-time PCR represents a more reliable method for detecting acute-phase cases, whereas antibody detection better suits determining previous viral exposure. The selection of CHIKV detection methods should be determined based on research objectives and sample collection timing. These laboratory indicators comprehensively confirm the patient's acute CHIKV infection across four dimensions: viral presence (positive nucleic acid), inflammatory response (elevated inflammatory markers), organ function impact (reduced liver-related proteins), and immune cell changes (abnormal complete blood count). They provide multiple lines of evidence for clinical diagnosis and serve as reference indicators for formulating treatment plans and monitoring patient condition.

The patient demonstrated mild symptoms and achieved favorable outcomes with symptomatic treatment. However, this single-case report has

TABLE 5. Baseline Laboratory Results on Admission from the first imported case of Chikungunya virus infection in Anhui Province.

| Laboratory test item | August 13 | Results tips | Reference range |
|---|---|---|---|
| TP (Biuret method) (g/L) | 62.2 | ↓ | 65–85 |
| ALB (BCG) (g/L) | 38.6 | ↓ | 40–55 |
| GLOB (g/L) | 23.6 | | 20–40 |
| A/G | 1.6 | | 1.2–2.4 |
| PA (mg/mL) | 16.6 | ↓ | 18–35 |
| ALT (U/L) | 14 | | 0–40 |
| AST (U/L) | 15 | | 0–35 |
| AST/ALT Ratio | 1.07 | | 0.8–1.5 |
| γ-GT (U/L) | 13 | | 0–45 |
| ALP (U/L) | 45 | ↓ | 50–135 |
| TB (μmol/L) | 8.9 | | 0–21 |
| DB (μmol/L) | 2.8 | | 0–8.0 |
| IB (μmol/L) | 6.1 | | 0–13 |
| BUN (μmol/L) | 4 | | 2.6–7.5 |
| Creatinine (Sarcosine Oxidase Method) (μmol/L) | 46 | | 35–115 |
| UA (μmol/L) | 207 | | 155–357 |
| ECC (mL/min) | 152.61 | ↑ | 80–120 |
| Glu (mmol/L) | 4.16 | | 3.89–6.11 |
| K (mmol/L) | 3.39 | ↓ | 3.5–5.3 |
| Na (mmol/L) | 137.8 | | 137–147 |
| Cl (mmol/L) | 104.2 | | 99–110 |
| Ca (mmol/L) | 2.09 | | 2.03–2.67 |
| CRP (mg/L) | 16.7 | ↑ | 0–6 |
| SAA (mg/L) | 348 | ↑ | 0–10 |
| WBC ($\times 10^9$/L) | 3.68 | | 3.5–9.5 |
| NP (%) | 80.4 | ↑ | 40–75 |
| LP (%) | 12.8 | ↓ | 20–50 |
| MP (%) | 6.4 | | 3–10 |
| EP (%) | 0.1 | ↓ | 0.4–8.0 |
| BP (%) | 0.3 | | 0–1 |
| ANC ($\times 10^9$/L) | 2.96 | | 1.8–6.3 |
| ALC ($\times 10^9$/L) | 0.47 | ↓ | 1.1–3.2 |
| AMC ($\times 10^9$/L) | 0.24 | | 0.1–0.6 |
| AEC ($\times 10^9$/L) | 0.00 | ↓ | 0.02–0.52 |
| ABC ($\times 10^9$/L) | 0.01 | | 0–0.06 |
| RBC ($\times 10^{12}$/L) | 4 | | 3.8–5.1 |
| Hb (g/L) | 117 | | 115–150 |
| Hct (%) | 35.8 | | 35–45 |
| MCV (fL) | 90.4 | | 82–100 |
| MCH (pg) | 29.6 | | 27–34 |
| MCHC (g/L) | 327 | | 316–354 |
| RDW-CV (%) | 12.8 | | 11.6–16 |

Continued

| Laboratory test item | August 13 | Results tips | Reference range |
|---|---|---|---|
| PLT (×$10^9$/L) | 137 | | 125–350 |
| MPV (fL) | 11.4 | | 6–13 |
| PDW (%) | 16.3 | | 9–18 |
| P-LCR (%) | 36.2 | | 17.5–42.3 |
| PCT (%) | 0.157 | | 0.114–0.282 |

Note: "↓" means the detected value is above the lower limit of the normal reference interval;"↑"means the detected value exceeds the upper limit of the normal reference interval.

Abbreviation: TP=total protein; ALB=albumin; GLOB=globulin; A/G=albumin/globulin ratio; PA=prealbumin; ALT=alanine aminotransferase; AST=aspartate aminotransferase; γ-GT=γ-glutamyl transferase; ALP=alkaline phosphatase; TB=total bilirubin; DB=direct bilirubin; IB=indirect bilirubin; BUN=blood urea nitrogen; UA=uric acid; ECC=endogenous creatinine clearance; Glu=glucose; K=potassium; Na=sodium; Cl=chloride; Ca=calcium; CRP=C-reactive protein; SAA=serum amyloid A; WBC=white blood cell; NP=neutrophil percentage; LP=lymphocyte percentage; MP=monocyte percentage; EP=eosinophil percentage; BP=basophil percentage; ANC=absolute neutrophil count; ALC=absolute lymphocyte count; AMC=absolute monocyte count; AEC=absolute eosinophil count; ABC=absolute basophil count; RBC=red blood cell; Hb=hemoglobin; Hct=hematocrit; MCV=mean corpuscular volume; MCH=mean corpuscular hemoglobin; MCHC=mean corpuscular hemoglobin concentration; RDW-CV=red blood cell distribution width-coefficient of variation; PLT=platelet count; MPV=mean platelet volume; PDW=platelet distribution width; P-LCR=platelet large platelet ratio; PCT=platelet crit.

inherent limitations. The sample size precludes generalization regarding disease characteristics such as incidence rates, clinical manifestation diversity, and prognostic variability across the broader patient population. Furthermore, the absence of a control group prevents conclusions regarding clinical variation or transmission efficiency of chikungunya fever among local vector populations in Anhui Province. Future studies incorporating larger case series will be necessary to validate these preliminary findings and establish more robust epidemiological patterns.

This first imported CHIKF case in Anhui Province highlights China's increasing vulnerability to imported infections and the growing risk of local transmission. The successful prevention of secondary transmission can be attributed to two critical factors: prompt patient reporting and a robust regional surveillance system equipped with advanced diagnostic capabilities. Together, these elements enabled the "early detection, rapid response, and immediate isolation" framework essential for effective disease control.

This incident demonstrates the urgent need to strengthen infectious disease surveillance systems targeting returning migrant workers. Effective prevention and control strategies should focus on three core areas: source control, transmission interruption, and protection of vulnerable populations. Interdepartmental coordination between port health authorities, local CDCs, and hospitals requires enhancement through several mechanisms. For instance, health declarations and vector screening should be strengthened for individuals arriving from affected areas at entry ports. Mandatory CHIKV screening should be implemented for travelers from WHO-designated high-risk areas, and joint vector control drills should be conducted within 24 hours of case reporting. These findings provide valuable guidance for managing similar imported infectious disease threats throughout China.

**Conflicts of interest**: No conflicts of interest.

**Ethical statement**: Approved by The Ethics Committee of Anhui Center for Disease Control and Prevention, China (approval number SL2024-73003-01).

**Funding:** Supported by the Anhui Provincial Health Science and Technology Project (AHWJ2024Aa20203 and AHWJ2024Aa20208), the Key Health Research Program of Anhui Province in 2024 (AHWJ2024Aa10092), and the Peak Discipline Project from the School of Public Health, Anhui Medical University (Collaborative Education Innovation Project) (2024GWXTYRZ005).

**doi:** 10.46234/ccdcw2025.261

[#] Corresponding authors: Jiabing Wu, wjb0386@ahcdc.com.cn; Ge Bu, fycdcbuge@163.com.

[1] Fuyang Center for Disease Control and Prevention, Fuyang City, Anhui Province, China; [2] Department of Microbiology Laboratory, Anhui Provincial Academy of Preventive Medicine, Hefei City, Anhui Province, China; [3] Anhui Provincial Center for Disease Control and Prevention, Hefei City, Anhui Province, China; [4] Fuyang Second People's Hospital, Fuyang City, Anhui Province, China.

[&] Joint first authors.



Submitted: September 15, 2025
Accepted: December 01, 2025
Issued: December 05, 2025

## REFERENCES


1. Shiferaw B, Lam P, Tuthill S, Choudhry H, Syed S, Ahmed S, et al. The Chikungunya epidemic: a look at five cases. IDCases 2015;2(4):89 – 91. https://doi.org/10.1016/j.idcr.2015.08.004.
2. Webb E, Michelen M, Rigby I, Dagens A, Dahmash D, Cheng V, et al. An evaluation of global Chikungunya clinical management guidelines: a systematic review. eClinicalMedicine 2022;54:101672. https://doi.org/10.1016/j.eclinm.2022.101672.
3. Calvez E, Bounmany P, Somlor S, Xaybounsou T, Viengphouthong S, Keosenhom S, et al. Multiple Chikungunya virus introductions in Lao PDR from 2014 to 2020. PLoS One 2022;17(7):e0271439. https://doi.org/10.1371/journal.pone.0271439.
4. World Health Organization. Disease outbreak news; Chikungunya virus disease-global situation. 2025. https://www.who.int/emergencies/disease-outbreak-news/item/2025-DON581. [2025-10-3].
5. Li YH, Jiang SY, Zhang M, Li Y, He JF, Yang ZF, et al. An outbreak of Chikungunya fever in China - Foshan City, Guangdong Province, China, July 2025. China CDC Wkly 2025;7(32):1064 – 5. https://doi.org/10.46234/ccdcw2025.172.
6. Guangdong Provincial Center for Disease Control and Prevention. Guangdong Province Chikungunya fever surveillance information (August 3-9, 2025). 2025. https://cdcp.gd.gov.cn/ywdt/zdzt/yfjkkyr/yqxx/content/post_4756601.html. [2025-8-18]. (In Chinese).
7. Chen LH, Fritzer A, Hochreiter R, Dubischar K, Meyer S. From bench to clinic: the development of VLA1553/IXCHIQ, a live-attenuated Chikungunya vaccine. J Travel Med 2024;31(7):taae123. https://doi.org/10.1093/jtm/taae123.
8. Zhao J, Liu RC, Chen SL, Chen TM. A model for evaluation of key measures for control of Chikungunya fever outbreak in China. Chin J Epidemiol 2015;36(11):1253 – 7. https://doi.org/10.3760/cma.j.issn.0254-6450.2015.11.014.
9. Lin BL, Xie DY, Zhai JQ, Huang YB, Gao ZL. Investigation of confirmed cases with Chikungunya fever in Dongguan. J Sun Yat-Sen Univ (Med Sci) 2011;32(2):208 – 12. https://doi.org/10.13471/j.cnki.j.sun.yat-sen.univ(med.sci).2011.0038.
10. Zhai JQ, Li HC, Lin BL, Chen GX, Huang YB, Yin SC. Clinical features of inpatients in the first Chikungunya fever epidemic in China. Chin J Infect Dis 2011;29(6):344 – 7. https://doi.org/10.3760/cma.j.issn.1000-6680.2011.06.007.
11. Shan YY, Chen YS, Huang JM, Wu B. The first imported case of Chikungunya fever reported in Haikou City, Hainan Province. China Trop Med 2025;1-5. https://link.cnki.net/urlid/46.1064.R.20250814.1138.002. [2025-11-27]. (In Chinese).
12. Ning XH, Yu CY, Cheng ZM, Gao R, Tang HL, Xia BH, et al. Genotype distribution and transmission risk of Chikungunya virus detected in China. Chin J Vector Biol Control 2025;36(5):557 – 67. https://doi.org/10.11853/j.issn.1003.8280.2025.05.001.
13. Borgherini G, Poubeau P, Staikowsky F, Lory M, Moullec NL, Becquart JP, et al. Outbreak of Chikungunya on reunion island: early clinical and laboratory features in 157 adult patients. Clin Infect Dis 2007;44(11):1401 – 7. https://doi.org/10.1086/517537.
14. Zhang M, Chen PH, Huang ZY, Zhong XG, Chen WF, Zeng YM, et al. Clinical characteristics of 81 laboratory-confirmed Chikungunya fever cases. Chin J Clin Infect Dis 2011;4(4):239 – 41. https://doi.org/10.3760/cma.j.issn.1674-2397.2011.04.013.
15. Danis-Lozano R, Díaz-González EE, del Carmen Trujillo-Murillo K, Caballero-Sosa S, Sepúlveda-Delgado J, Malo-García IR, et al. Clinical characterization of acute and convalescent illness of confirmed Chikungunya cases from Chiapas, S. Mexico: a cross sectional study. PLoS One 2017;12(10):e0186923. https://doi.org/10.1371/journal.pone.0186923.
16. Chua CL, Sam IC, Chiam CW, Chan YF. The neutralizing role of IgM during early Chikungunya virus infection. PLoS One 2017;12(2):e0171989. https://doi.org/10.1371/journal.pone.0171989.
17. Chelluboina S, Robin S, Aswathyraj S, Arunkumar G. Persistence of antibody response in Chikungunya. VirusDisease 2019;30(3):469 – 73. https://doi.org/10.1007/s13337-019-00534-5.
18. Wan SC, Zhang X, Cong X, Liu Y, Huang S, Zhou MY, et al. Viral load dynamics of chikungunya virus in human specimens - Foshan City, Guangdong Province, China, 2025. China CDC Wkly 2025;7(33):1067 – 72. https://doi.org/10.46234/ccdcw2025.182.
19. Prince HE, Seaton BL, Matud JL, Batterman HJ. Chikungunya virus RNA and antibody testing at a national reference laboratory since the emergence of Chikungunya virus in the Americas. Clin Vaccine Immunol 2015;22(3):291 – 7. https://doi.org/10.1128/CVI.00720-14.

Notifiable Infectious Diseases Reports

# Reported Cases and Deaths of National Notifiable Infectious Diseases — China, October 2025*

| Diseases | Cases | Deaths |
|---|---|---|
| Plague | 0 | 0 |
| Cholera | 3 | 0 |
| COVID-19 | 18,704 | 3 |
| SARS-CoV | 0 | 0 |
| Acquired immune deficiency syndrome† | 3,749 | 1,532 |
| Hepatitis | 116,746 | 247 |
| Hepatitis A | 1,036 | 0 |
| Hepatitis B | 99,645 | 42 |
| Hepatitis C | 13,170 | 205 |
| Hepatitis D | 16 | 0 |
| Hepatitis E | 2,333 | 0 |
| Other hepatitis | 546 | 0 |
| Poliomyelitis | 0 | 0 |
| Human infection with noval influenza virus | 5 | 0 |
| Measles | 65 | 0 |
| Epidemic hemorrhagic fever | 233 | 0 |
| Rabies | 22 | 22 |
| Japanese encephalitis | 21 | 1 |
| Dengue | 3,727 | 0 |
| Monkey pox§ | 71 | 0 |
| Anthrax | 34 | 0 |
| Dysentery | 2,501 | 0 |
| Tuberculosis | 50,265 | 240 |
| Typhoid fever and paratyphoid fever | 511 | 0 |
| Meningococcal meningitis | 9 | 0 |
| Pertussis | 893 | 0 |
| Diphtheria | 0 | 0 |
| Neonatal tetanus | 0 | 0 |
| Scarlet fever | 2,073 | 0 |
| Brucellosis | 3,298 | 0 |
| Gonorrhea | 10,003 | 1 |
| Syphilis | 50,354 | 7 |
| Leptospirosis | 169 | 0 |
| Schistosomiasis | 0 | 0 |
| Malaria | 331 | 1 |
| Influenza | 427,083 | 0 |
| Mumps | 7,093 | 0 |

Continued

| Diseases | Cases | Deaths |
|---|---|---|
| Rubella | 53 | 0 |
| Acute hemorrhagic conjunctivitis | 1,790 | 0 |
| Leprosy | 14 | 0 |
| Typhus | 165 | 0 |
| Kala azar | 25 | 0 |
| Echinococcosis | 242 | 0 |
| Filariasis | 0 | 0 |
| Hand, foot and mouth disease | 378,738 | 0 |
| Infectious diarrhea[¶] | 112,656 | 0 |
| **Total** | 1,191,646 | 2,054 |

* 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.

**doi:** 10.46234/ccdcw2025.255



Submitted: November 24, 2025
Accepted: November 26, 2025
Issued: December 05, 2025

# Youth Editorial Board

Indexed by Science Citation Index Expanded (SCIE), Social Sciences Citation Index (SSCI), PubMed Central (PMC), Scopus, Chinese Scientific and Technical Papers and Citations, and Chinese Science Citation Database (CSCD)



The inauguration of *China CDC Weekly* is in part supported by Project for Enhancing International Impact of China STM Journals Category D (PIIJ2-D-04-(2018)) of China Association for Science and Technology (CAST).

CCDC weekly

*Vol. 7 No. 49 Dec. 5, 2025*

**Responsible Authority**
National Disease Control and Prevention Administration

**Sponsor**
Chinese Center for Disease Control and Prevention

**Editing and Publishing**
China CDC Weekly Editorial Office
No.155 Changbai Road, Changping District, Beijing, China
Tel: 86-10-63150501, 63150701
Email: weekly@chinacdc.cn

**CSSN**
ISSN 2096-7071 (Print)
ISSN 2096-3101 (Online)
CN 10-1629/R1