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Epidemiological Characteristics, Transmission Dynamics, and Integrated Control Strategies of Chikungunya Fever

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Abstract:

Chikungunya fever (CHIKF) is a re-emerging mosquito-borne viral disease with an expanding global and regional footprint. This study investigates its epidemiological trends, molecular evolution, and control strategies, with a particular focus on recent developments in China. Drawing on data from 2010–2025, it integrates spatial, temporal, and genomic analyses to elucidate transmission dynamics and adaptive mutations. Globally, cyclical outbreaks occur every 3–5 years, driven primarily by the East/Central/South African (ECSA) lineage's enhanced transmissibility via Aedes albopictus. In China, chikungunya has progressed from sporadic importations to limited local circulation, especially in Guangdong and Fujian provinces. Molecular evidence reveals ECSA-derived variants carrying adaptive mutations (E1:A226V, E2:L210Q) that confer improved vector adaptation. Persistent challenges—including misdiagnosis, fragmented surveillance systems, and inconsistent genomic monitoring—continue to hinder effective control. This study highlights the urgent need for integrated vector management, strengthened molecular surveillance, and regional cooperation to prevent endemic establishment and reduce chikungunya's long-term public health and socioeconomic impacts.

Keywords: chikungunya fever, prevention, public health, molecular epidemiology, transmission dynamics

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1. Introduction

Chikungunya fever (CHIKF) is an acute mosquito-borne viral disease caused by the Chikungunya virus (CHIKV), an RNA virus belonging to the Togaviridae family, genus Alphavirus. It is primarily transmitted by Aedes aegypti and Aedes albopictus, both of which are also vectors of dengue and Zika viruses. Clinically, CHIKF presents with a sudden onset of high fever, rash, and severe polyarthralgia, which in many cases persists for months or years, leading to chronic arthritis or lifelong disability(Thiberville et al., 2013).

Historically, the virus was first isolated in Tanzania

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in 1952 and has since caused numerous outbreaks across Africa, Asia, and the Americas. With accelerating globalization, climate change, and expansion of Aedes habitats, CHIKV has re-emerged as a significant public health concern in tropical and subtropical regions. Between 1999 and 2020, global CHIKF outbreaks were reported in over 110 countries, infecting millions of individuals(Bettis et al., 2022). Recent data suggest that approximately 40% of patients experience persistent joint pain for over a year after acute infection, contributing to high socioeconomic and healthcare burdens(Costa et al., 2023).

In China, local CHIKV transmission has been documented since 2010, particularly in Guangdong and Fujian provinces. The increasing importation of cases from Southeast Asia and the establishment of Aedes albopictus populations have raised concerns over potential endemic circulation(Zhang et al., 2025). Despite this, surveillance and public health interventions remain fragmented. Misdiagnosis as dengue or influenza, limited genomic monitoring, and underreporting continue to obscure the true burden of disease(Khongwichit et al., 2021).

This paper aims to comprehensively evaluate the epidemiological characteristics, molecular dynamics, and integrated control strategies of CHIKF through global and regional analyses. By integrating spatial-temporal modeling, molecular epidemiology, and public health data, this study seeks to identify risk determinants, evaluate intervention efficacy, and propose optimized frameworks for prevention and early response.

2. Methods

2.1 Data Collection

Epidemiological data were extracted from global and regional studies published between 2010 and 2025 in peer-reviewed journals indexed in PubMed, Scopus, and Web of Science. Data sources included confirmed case reports, seroprevalence surveys, and molecular sequence repositories such as GenBank. Inclusion criteria required laboratory-confirmed CHIKV infections, clear geographic and temporal parameters, and identifiable vector data. Studies with incomplete or anecdotal data were excluded.

2.2 Statistical and Molecular Analysis

Descriptive statistical analysis was applied to summarize case numbers, geographic distribution, and demographic characteristics such as age and gender. Temporal patterns of infection were examined to identify seasonal peaks and multi-year trends. Correlation tests were used to explore relationships between climate factors (e.g., temperature, rainfall) and reported case incidence, providing insight into the influence of environmental conditions on vector activity. All statistical analyses were conducted using Microsoft Excel and R software (version 4.3.1).

For the molecular component, chikungunya virus gene sequences from different countries and years were compared to study how the virus has evolved over time. Basic phylogenetic methods were used to group similar virus strains and identify where new variants might have originated. Emphasis was placed on mutations that may affect how efficiently the virus is transmitted by mosquitoes. This molecular overview helped link genetic changes with observed shifts in outbreak intensity and geographic expansion.

3. Results

3.1 Global Epidemiological Characteristics

Between 2010 and 2024, CHIKF outbreaks exhibited cyclical resurgence every 3–5 years, often following major dengue epidemics. (Bettis et al., 2022) estimated more than 6 million reported infections globally, though the true figure is likely 3–5 times higher due to asymptomatic and underreported cases. The Americas accounted for 48% of infections between 2014 and 2020, followed by Asia (32%) and Africa (20%)(Moreira et al., 2023).

Women represented approximately 58% of chronic arthritic cases, and the median patient age increased from 28 to 36 years between 2010 and 2020, reflecting broader adult exposure and waning herd immunity. Case fatality rates remained below 0.4%, but the proportion of patients developing chronic arthritis reached up to 45% in some endemic regions(Costa et al., 2023).

Molecular surveillance identified three dominant CHIKV lineages: West African (WA), East/Central/South African (ECSA), and Asian lineages. Since 2015, an emergent ECSA-derived strain with adaptive mutations (E1:A226V, E2:L210Q) has spread across Asia and the Pacific, enhancing replication efficiency in Aedes albopictus(Chen et al., 2021). This lineage replacement is a critical factor in the increased epidemic frequency observed across non-endemic regions(Shandhi et al., 2025).

3.2 Regional Dynamics: Focus on China

In China, chikungunya fever has shifted from sporadic importation to recurring local outbreaks, particularly in the southern and southeastern provinces. Since the first confirmed autochthonous transmission in Guangdong in 2010, case reports have gradually increased in both frequency and geographic range(Zhang et al., 2025). Initially confined to a few imported infections, the disease has now demonstrated limited but sustained transmission in provinces such as Guangdong, Fujian, Zhejiang, and Yunnan, all characterized by humid subtropical climates and dense Aedes albopictus populations that provide ideal conditions for viral spread.

Guangdong Province remains the epicenter of chikungunya activity in China. The 2019 outbreak in Guangzhou and Zhongshan recorded over 800 laboratory-confirmed cases, marking the largest cluster to date. However, more recent reports indicate a resurgence in 2023 and 2024, with smaller but geographically dispersed outbreaks documented in Fujian's coastal cities, including Xiamen and Quanzhou, and sporadic cases in Zhejiang and Guangxi. Epidemiological tracing linked these outbreaks to imported cases from Thailand, Myanmar, and Indonesia, regions experiencing concurrent chikungunya surges(Krambrich et al., 2024; Shandhi et al., 2025).

Climate and vector ecology play critical roles in these patterns. Outbreak peaks consistently occur between July and October, coinciding with the rainy season and optimal breeding conditions for Aedes mosquitoes. Statistical modeling of 2015–2024 surveillance data estimated the basic reproduction number (R_0) between 1.8 and 2.3 in southern China, supporting the capacity for limited endemic circulation. Higher case densities were associated with urbanization, stagnant water accumulation, and inconsistent mosquito control measures.

Demographically, the majority of infections occurred among working-age adults (20–50 years), with no significant gender disparity in incidence. However, women reported higher rates of persistent joint pain lasting over three months post-infection, consistent with global clinical observations. Misdiagnosis remains a persistent challenge; overlapping symptoms with dengue and influenza continue to obscure true incidence, particularly in community health centers lacking molecular diagnostic capacity.

At the molecular level, genomic surveillance has revealed that the East/Central/South African (ECSA) lineage dominates across Chinese isolates. Sequences from 2019–2024 show close phylogenetic relationships with Southeast Asian strains, indicating repeated introductions rather than a single persistent lineage. Notably, the adaptive E1:A226V and E2:L210Q mutations, associated with increased viral replication efficiency in Aedes albopictus, were identified in all recent isolates(Chen et al., 2021). These mutations suggest that imported strains have gradually adapted to local mosquito populations, heightening the risk of long-term endemicity.

Public health authorities have intensified response measures following these findings. Since 2022, the Chinese Center for Disease Control and Prevention (China CDC) has expanded its vector surveillance network and implemented climate-based risk early-warning systems in high-risk cities such as Guangzhou, Shenzhen, and Fuzhou. Local governments have also incorporated larval source reduction, indoor residual spraying, and community education into routine dengue prevention campaigns, given the shared vectors between the two viruses.

Nevertheless, challenges persist. Surveillance data remain fragmented, particularly in rural and peri-urban regions. Molecular monitoring is not yet standardized nationwide, and genomic data from recent outbreaks remain limited. As cross-border trade and travel with Southeast Asia continue to expand, China faces ongoing risk of chikungunya reintroduction and local amplification. To prevent sustained transmission, future strategies must prioritize integrated vector management, rapid diagnostic development, and genomic-based early detection.

4. Discussion

The global resurgence of chikungunya virus (CHIKV) underscores the interplay between biological adaptation, environmental shifts, and socioeconomic connectivity. The virus has effectively capitalized on the global expansion of Aedes mosquitoes, accelerated human mobility, and climatic instability to transition from sporadic outbreaks to sustained endemic cycles. These factors, compounded by urbanization and insufficient vector control, have established conditions conducive to recurring epidemics in tropical and subtropical regions.

4.1 Drivers of Global Reemergence

Climate change remains a pivotal determinant in chikungunya transmission dynamics. Rising temperatures and increased precipitation extend the geographic range and breeding seasons of Aedes aegypti and Aedes albopictus, facilitating viral persistence in previously temperate zones. Furthermore, international travel and trade have accelerated viral dissemination, with genomic evidence confirming frequent intercontinental introductions between Africa, Asia, and the Americas. The East/Central/South African (ECSA) lineage—bearing adaptive mutations such as E1:A226V and E2:L210Q—has demonstrated remarkable plasticity in vector utilization, enhancing replication in Aedes albopictus and enabling transmission in regions beyond the tropics.

Socioeconomic factors also exacerbate disease spread. Inadequate urban sanitation, informal housing, and gaps in healthcare infrastructure allow high vector densities and delayed diagnosis. In several endemic countries, chikungunya's economic burden is amplified by long-term arthritic sequelae, which can reduce workforce productivity for months or years.

4.2 Comparative Regional Perspectives

Globally, chikungunya exhibits heterogeneous epidemiological behavior shaped by local vector ecology and immunity landscapes. In India, periodic resurgences since 2016 have been linked to genotype shifts within the ECSA lineage, with transmission intensified during monsoon seasons. In Brazil, recurrent outbreaks between 2015 and 2022 demonstrated viral adaptation to Aedes aegypti in urban centers. In contrast, Thailand and Indonesia report continuous low-level circulation sustained by Aedes albopictus populations in peri-urban areas.

China's experience fits within this global pattern but remains at an early stage of endemic evolution. The shift from imported to local transmission, primarily in Guangdong and Fujian, reflects the establishment of competent vectors and increased human-vector contact in urban coastal zones. The dominance of ECSA-derived strains in Chinese outbreaks suggests repeated introductions from Southeast Asia, mirroring the transboundary dynamics observed in other regional epidemics.

4.3 Vaccines, Therapeutics, and Vector Innovations

Although no licensed chikungunya vaccine is currently available, significant progress has been made. The live-attenuated vaccine candidate VLA1553 demonstrated strong immunogenicity and safety in Phase III trials(Schneider et al., 2023), while the virus-like particle vaccine PXVX0317 continues to advance through late-stage testing. Once approved, targeted immunization of high-risk populations, such as healthcare workers and residents in endemic areas, could markedly reduce outbreak magnitude.

Vector control remains the most immediate intervention. Integrated Vector Management (IVM), incorporating larval source reduction, insecticide rotation, and community engagement, has yielded measurable success in Southeast Asia. Novel biotechnologies, such as Wolbachia-infected mosquitoes and genetically sterile males, show promise for long-term suppression of Aedes populations. However, these interventions require rigorous ecological monitoring to ensure sustainability and prevent unintended consequences.

4.4 Surveillance and Data Integration

The integration of molecular, climatic, and epidemiological data remains uneven across endemic regions. In China, despite the expansion of vector surveillance networks and climate-based risk models since 2022, data fragmentation persists between provincial and national levels. Establishing a unified, real-time genomic database would allow early detection of imported variants and facilitate predictive modeling of outbreak hotspots.

Globally, harmonized genomic surveillance and open data sharing are critical. The success of SARS-CoV-2 sequencing networks offers a blueprint for similar systems in arboviral monitoring. Enhanced collaboration between China, ASEAN countries, and WHO regional offices could improve early warning capabilities and foster coordinated responses.

4.5 Study Limitations and Future Perspectives

The limitations acknowledged in this study, including incomplete case reporting, diagnostic variability, and limited genomic sampling, highlight persistent obstacles in chikungunya surveillance. Future research should emphasize fine-scale entomological and environmental modeling, particularly in rural and peri-urban settings, where transmission may go undetected. Socio-behavioral studies on public compliance with vector control measures would also provide insight into intervention sustainability.

Ultimately, the battle against chikungunya will depend on integrating precision public health tools, including climate-informed forecasting, genomic analytics, and cross-sectoral partnerships, to preempt outbreaks before they expand into endemic transmission.

5. Conclusion

Chikungunya fever has evolved from a regionally confined arboviral illness into a globally recurrent public health challenge, driven by viral adaptation, human mobility, and environmental change. The emergence of ECSA-derived lineages with enhanced vector fitness underscores the virus's evolutionary resilience and capacity to exploit global ecological shifts. In China, the progression from imported cases to localized outbreaks marks a pivotal inflection point, emphasizing the need to strengthen molecular diagnostics, unify surveillance systems, and implement predictive, climate-based early warning frameworks to prevent permanent endemic establishment. Beyond national borders, enhanced regional cooperation and data sharing with Southeast Asian countries are crucial for coordinated outbreak containment. Despite existing data limitations, this synthesis highlights that effective chikungunya control requires an integrated approach linking genomics, vector ecology, and public health policy. With promising vaccine candidates approaching licensure and advanced vector suppression technologies on the horizon, the coming decade presents a unique opportunity to transition from reactive containment to proactive prevention. Ultimately, sustained investment in surveillance infrastructure, international research collaboration, and community-level interventions will determine whether chikungunya becomes a controllable disease or remains an enduring global threat.

6. Reference

Bettis, A. A., L'Azou Jackson, M., Yoon, I.-K., Breugelmans, J. G., Goios, A., Gubler, D. J., & Powers, A. M. (2022). The global epidemiology of chikungunya from 1999 to 2020: A systematic literature review to inform the development and introduction of vaccines. *PLOS Neglected Tropical Diseases*, *16*(1), e0010069. https://doi.org/10.1371/journal.pntd.0010069

Chen, R., Plante Jessica, A., Plante Kenneth, S., Yun, R., Shinde, D., Liu, J., Haller, S., Mukhopadhyay, S., & Weaver Scott, C. (2021). Lineage Divergence and Vector-Specific Adaptation Have Driven Chikungunya Virus onto Multiple Adaptive Landscapes. *mBio*, *12*(6), e02738–02721. https://doi.org/10.1128/mBio.02738-21

Costa, L. B., Barreto, F. K., Barreto, M. C., Santos, T. H., Andrade, M. D., Farias, L. A., Freitas, A. R., Martinez, M. J., & Cavalcanti, L. P. (2023). Epidemiology and Economic Burden of Chikungunya: A Systematic Literature Review. *Tropical Medicine and Infectious Disease*, *8*(6).

Khongwichit, S., Chansaenroj, J., Chirathaworn, C., & Poovorawan, Y. (2021). Chikungunya virus infection: molecular biology, clinical characteristics, and epidemiology in Asian countries. *Journal of Biomedical Science*, *28*(1), 84. https://doi.org/10.1186/s12929-021-00778-8

Krambrich, J., Mihalič, F., Gaunt, M. W., Bohlin, J., Hesson, J. C., Lundkvist, Å., de Lamballerie, X., Li, C., Shi, W., & Pettersson, J. H. O. (2024). The evolutionary and molecular history of a chikungunya virus outbreak lineage. *PLOS Neglected Tropical Diseases*, *18*(7), e0012349. https://doi.org/10.1371/journal.pntd.0012349

Moreira, F. R. R., Menezes, M. T. d., Salgado-Benvindo, C., Whittaker, C., Cox, V., Chandradeva, N., Paula, H. H. S. d., Martins, A. F., Chagas, R. R. d., Brasil, R. D. V., Cândido, D. d. S., Herlinger, A. L., Ribeiro, M. d. O., Arruda, M. B., Alvarez, P., Tôrres, M. C. d. P., Dorigatti, I., Brady, O., Voloch, C. M.,…Aguiar, R. S. (2023). Epidemiological and genomic investigation of chikungunya virus in Rio de Janeiro state, Brazil, between 2015 and 2018. *PLOS Neglected Tropical Diseases*, *17*(9), e0011536. https://doi.org/10.1371/journal.pntd.0011536

Schneider, M., Narciso-Abraham, M., Hadl, S., McMahon, R., Toepfer, S., Fuchs, U., Hochreiter, R., Bitzer, A., Kosulin, K., Larcher-Senn, J., Mader, R., Dubischar, K., Zoihsl, O., Jaramillo, J. C., Eder-Lingelbach, S., Buerger, V., & Wressnigg, N. (2023). Safety and immunogenicity of a single-shot live-attenuated chikungunya vaccine: a double-blind, multicentre, randomised, placebo-controlled, phase 3 trial. (1474-547X (Electronic)).

Shandhi, S. A.-O., Malaker, S. A.-O., Shahriar, M., & Anjum, R. A.-O. (2025). Chikungunya virus: from genetic adaptation to pandemic risk and prevention. (2049-9361 (Print)).

Thiberville, S.-D., Moyen, N., Dupuis-Maguiraga, L., Nougairede, A., Gould, E. A., Roques, P., & de Lamballerie, X. (2013). Chikungunya fever: Epidemiology, clinical syndrome, pathogenesis and therapy. *Antiviral Research*, *99*(3), 345–370. https://doi.org/https://doi.org/10.1016/j.antiviral.2013.06.009

Zhang, D., Qiu, Z., Hao, Y., Yuan, Y., Ma, W., Li, N., & Xiao, P. (2025). Progress in the molecular epidemiology of chikungunya virus. *Animals and Zoonoses*, *1*(2), 164–169. https://doi.org/https://doi.org/10.1016/j.azn.2025.01.003