

Re-emergence and global expansion of chikungunya virus: Climate change, vector adaptation, and urbanization

Farzand Ali^{1*}, and Dua E. Zahra²

¹Department of Haematology and Blood Bank, Shaikh Zayed Medical Complex, Lahore, Pakistan. ²Shaukat Khanum Memorial Cancer Hospital and research Center, Lahore, Pakistan

Abstract

Chikungunya Fever has re-emerged over the last two decades as one of the most important arboviral threats to global public health. Once considered a geographically restricted tropical disease, chikungunya virus (CHIKV) has expanded across Africa, Asia, Europe, and the Americas, driven by complex interactions among climate change, globalization, vector adaptation, urbanization, and increasing human mobility. The expansion of competent mosquito vectors, particularly *Aedes aegypti* and *Aedes albopictus*, has facilitated sustained transmission in regions previously unsuitable for CHIKV circulation. Climate-associated changes in temperature, rainfall, humidity, and extreme weather events have altered vector ecology and enhanced transmission potential in both tropical and temperate settings. Urbanization, population growth, inadequate sanitation, and expanding peri-urban settlements have further amplified mosquito breeding and human-vector contact. Additionally, adaptive viral mutations, including the E1-A226V mutation, have improved CHIKV fitness in the alternative vector *Aedes albopictus*, accelerating global spread. Recent outbreaks in Europe, the Americas, and parts of Asia demonstrate the increasing potential for autochthonous transmission outside traditional endemic zones. This review synthesizes current evidence regarding the epidemiological resurgence of CHIKV, emphasizing the interplay between environmental change, vector adaptation, and urbanization. The review also discusses future projections, surveillance challenges, integrated vector management, and the need for climate-informed public health preparedness. Understanding the multifactorial drivers of CHIKV emergence is critical for developing sustainable prevention and control strategies in an increasingly interconnected and warming world.

Keywords: chikungunya, CHIKV, climate, *Aedes aegypti*

1. Introduction

Chikungunya Fever is a mosquito-borne viral disease caused by chikungunya virus (CHIKV), an enveloped positive-sense single-stranded RNA virus belonging to the genus *Alphavirus* within the family *Togaviridae* [1]. The disease is characterized primarily by acute febrile illness, rash, myalgia, and debilitating polyarthralgia that may persist for months or years in some patients [2]. Although mortality is generally low, the disease imposes substantial morbidity and socioeconomic burden on affected populations [3].

CHIKV was first identified in Tanzania in 1952 following an outbreak in the Makonde Plateau [4]. For several decades, chikungunya remained largely confined to sporadic outbreaks in Africa and Asia. However, since the early 2000s, the epidemiology of CHIKV has changed dramatically, with explosive outbreaks occurring across multiple continents. Major epidemics in the Indian Ocean islands,

*Correspondence:

Farzand Ali (farzandali6184@gmail.com)

Received: 14-05-2026, **Accepted:** 09-07-2026, **Published:** 28-09-2026

How to cite: Ali F, and Zahra DE (2026) Re-emergence and global expansion of chikungunya virus: Climate change, vector adaptation, and urbanization. Global Virology Reports, 1(1): 7–17.

© The Author(s) (2026). This article is an open access article under the terms of the Creative Commons Attribution 4.0 License (<https://creativecommons.org/licenses/by/4.0/>)

Publisher's Note. IAA Academic Arena Ltd. remains neutral with regard to jurisdictional claims in published maps and institutional affiliations



India, Southeast Asia, Europe, and the Americas have transformed CHIKV into a major global public health concern [5]. The resurgence of CHIKV reflects the convergence of multiple ecological and anthropogenic drivers. Climate change has emerged as a critical factor influencing vector distribution, vector competence, and transmission dynamics [6]. Rising global temperatures, altered rainfall patterns, increasing humidity, and extreme weather events create favorable conditions for mosquito proliferation and viral replication [2]. Simultaneously, rapid urbanization and globalization have increased human exposure to mosquito vectors while facilitating international spread through travel and trade. A major turning point in CHIKV evolution was the emergence of adaptive mutations that enhanced transmission by *Aedes albopictus*, a vector capable of surviving in temperate climates [7]. This adaptation significantly expanded the ecological niche of CHIKV and contributed to outbreaks in regions previously considered low-risk, including parts of Europe and North America [8].

In addition to environmental and virological changes, urban growth has profoundly altered mosquito ecology. Expanding urban centers with inadequate waste management, poor water infrastructure, and high population density provide ideal breeding conditions for *Aedes* mosquitoes [9,10]. Urban heat islands and peri-urban sprawl further intensify transmission risk [11]. Given the increasing global burden of arboviral diseases, understanding the drivers of CHIKV emergence has become increasingly important. This narrative review examines the global expansion of CHIKV through the lenses of climate change, vector adaptation, and urbanization, while discussing implications for surveillance, prevention, and future public health preparedness.

2. Global epidemiology and re-emergence of CHIKV

Historically, CHIKV circulated primarily in sylvatic cycles involving non-human primates and forest-dwelling mosquitoes in Africa [12]. In Asia, however, urban transmission cycles involving humans and *Aedes* mosquitoes became established, enabling larger outbreaks in densely populated settings [1]. The modern resurgence of CHIKV began with the 2004 outbreak in Kenya, followed by major epidemics in the Indian Ocean region, particularly in Mauritius and Réunion [13]. The outbreak in Réunion Island between 2005 and 2006 represented a landmark event, affecting approximately one-third of the population and highlighting the epidemic potential of CHIKV [14]. During this outbreak, viral mutations associated with improved adaptation to *Ae. albopictus* were identified. Subsequently, India experienced massive outbreaks involving millions of suspected cases [15]. Southeast Asian countries including Thailand, Malaysia, and Indonesia also reported substantial transmission [16].

One of the most significant epidemiological milestones occurred in 2007 when autochthonous transmission was documented in Italy [17]. This outbreak demonstrated that CHIKV transmission could occur in temperate European regions where competent vectors had become established. Similar local transmission events were later documented in France and other European countries [18]. The introduction of CHIKV into the Americas in 2013 marked another major turning point [19]. Beginning in the Caribbean island of Saint Martin, the virus rapidly spread across North, Central, and South America [19]. Within a few years, millions of cases were reported throughout the Western Hemisphere. The scale and speed of spread reflected the widespread presence of *Aedes* vectors, high human mobility, and immunologically naïve populations [20]. Recent years have witnessed continuing expansion into previously unaffected regions, including parts of China and temperate Europe. Current evidence indicates that CHIKV transmission has now been reported in over 100 countries, placing billions of people at risk [21].

3. Climate change and CHIKV expansion

Climate change is among the most influential drivers of emerging vector-borne diseases. Mosquito vectors are highly sensitive to environmental conditions, particularly temperature [22]. Temperature affects mosquito survival, feeding behavior, development rate, biting frequency, and viral replication. Warmer temperatures shorten the extrinsic incubation period of CHIKV within mosquitoes, allowing vectors to become infectious more rapidly [23]. Increased temperatures may also enhance mosquito reproduction and biting activity, thereby increasing transmission efficiency. However,

excessively high temperatures may reduce mosquito survival, suggesting that climate effects are nonlinear and region-specific [24].

Climate modeling studies predict a substantial expansion of CHIKV-suitable areas under future warming scenarios [25]. Consequently, regions in Europe, East Asia, North America, and higher-altitude tropical zones are expected to become increasingly favorable for transmission. Several models project northward shifts of *Ae. albopictus* distribution into temperate regions during the twenty-first century [26].

Rainfall patterns strongly influence mosquito breeding habitats. Moderate rainfall can increase the availability of water-filled containers and stagnant water, supporting larval development [27]. Conversely, drought conditions may paradoxically increase transmission in urban settings where water storage practices create artificial breeding sites. Humidity also influences mosquito longevity and activity [28]. High humidity improves vector survival and increases the probability of successful transmission. Climate change-associated shifts in precipitation and humidity patterns may therefore alter seasonal transmission dynamics [29].

Extreme weather events such as floods, cyclones, and heatwaves further complicate vector ecology. Flooding can create new breeding habitats, whereas post-disaster population displacement and weakened public health infrastructure may facilitate outbreaks [30].

The spread of *Ae. albopictus* into Europe provides one of the clearest examples of climate-driven vector expansion. Originally native to Asia, this mosquito has colonized large areas of Europe and North America through global trade and favorable climatic conditions [31]. Its tolerance for cooler climates enables CHIKV transmission in regions previously considered unsuitable. Climate suitability models suggest increasing transmission potential across southern and central Europe [32]. Seasonal outbreaks may become more frequent as warming temperatures extend mosquito activity periods [32].

Similarly, the climate-driven expansion of vector habitats in East Asia and parts of China raises significant concerns regarding future endemic establishment. Global modeling studies indicate that billions more individuals may become exposed to CHIKV transmission risk under future climate scenarios [26]. Table 1 summarizes major drivers contributing to CHIKV re-emergence and global expansion.

4. Vector adaptation and viral evolution

The primary vectors of CHIKV are *Aedes aegypti* and *Aedes albopictus*. *Ae. aegypti* is traditionally regarded as the principal urban vector because of its close association with humans, preference for human blood meals, and adaptation to urban environments [33]. However, *Ae. albopictus* has emerged as a critically important vector in the global expansion of CHIKV. This species possesses several ecological advantages, including tolerance for cooler temperatures, ecological flexibility, and ability to thrive in peri-urban and rural settings [34]. The global spread of *Ae. albopictus* has been facilitated by international trade, especially the movement of used tires and ornamental plants [35].

A major factor contributing to the resurgence of CHIKV was the emergence of adaptive mutations that enhanced viral fitness in *Ae. albopictus*. The most notable mutation, E1-A226V, emerged during the Réunion Island outbreak and significantly improved transmission efficiency in *Ae. albopictus* mosquitoes [36]. This adaptation increased the epidemic potential of CHIKV by enabling transmission in regions where *Ae. aegypti* populations were limited but *Ae. albopictus* was abundant [37]. The mutation represented a striking example of how viral evolution can alter vector specificity and expand geographic range. Additional mutations affecting viral infectivity, dissemination, and transmission have also been identified [38]. Continued viral evolution raises concern regarding the emergence of strains with enhanced epidemic capacity or altered pathogenicity [38].

Urban ecosystems favor the proliferation of *Aedes* mosquitoes. Artificial containers, discarded plastics, water storage tanks, clogged drainage systems, and poor sanitation provide ideal breeding habitats [39]. Urban heat islands may further enhance mosquito development and survival. Unlike many rural mosquito species, *Ae. aegypti* thrives in densely populated human settlements [40]. The close proximity of humans facilitates rapid transmission cycles and explosive outbreaks. Urban adaptation therefore represents a central feature of modern CHIKV epidemiology [41].

Table 1. Major drivers contributing to the re-emergence and global expansion of CHIKV

Driver	Mechanism contributing to CHIKV expansion	Examples/implications
Climate change	Increased temperature accelerates mosquito development and viral replication; altered rainfall creates breeding habitats	Expansion of <i>Aedes</i> mosquitoes into temperate regions
Rising global temperatures	Shortened extrinsic incubation period enhances transmission efficiency	Increased seasonal transmission in Europe and East Asia
Urbanization	Dense human populations increase mosquito–human contact	Large outbreaks in rapidly growing cities
Poor sanitation and water storage	Creation of artificial breeding sites for <i>Aedes</i> mosquitoes	Informal settlements with inadequate infrastructure
Globalization and travel	Rapid movement of viremic individuals across continents	Introduction of CHIKV into Europe and the Americas
International trade	Spread of mosquito vectors through shipping and transportation	Dissemination of <i>Ae. albopictus</i> via used tires
Vector adaptation	Enhanced vector competence increases transmission efficiency	Adaptation of CHIKV to <i>Ae. albopictus</i>
Viral evolution	Mutations improve infectivity and ecological fitness	E1-A226V mutation during Réunion outbreak
Human behavioral factors	Water storage and waste accumulation support mosquito breeding	Increased household vector density
Weak vector surveillance	Delayed outbreak detection and response	Sustained local transmission before intervention
Inadequate public health infrastructure	Reduced vector control effectiveness	Recurrent outbreaks in resource-limited settings
Climate-related disasters	Flooding and displacement increase exposure risk	Post-cyclone and post-flood outbreaks

5. Urbanization and human mobility

Urbanization has dramatically reshaped the epidemiology of arboviral diseases, particularly in low- and middle-income countries where rapid population growth has severely outpaced municipal infrastructure development [42]. This lag in expansion leads to informal, densely populated settlements characterized by inadequate sanitation, poor drainage, and unreliable water supplies. Such environments compel residents to store water manually, creating ideal artificial breeding conditions that maximize human-vector contact and fuel sustained viral transmission [39]. Compounding this issue, rapid peri-urban expansion produces highly fragmented landscapes that blur the boundaries between expanding human habitats and native vector ecosystems [43]. Furthermore, the development of urban heat islands exacerbates transmission dynamics, as elevated city temperatures accelerate mosquito larval development, boost adult survival rates, and significantly prolong active seasonal transmission windows [40].

Modern globalization has significantly accelerated the international dissemination of CHIKV. International air travel facilitates the rapid movement of viremic individuals across continents within hours, enabling infected travelers to introduce the virus into new regions where competent vectors are

already established [41,44]. The expansion of CHIKV into Europe and the Americas clearly illustrates the profound role of this travel-associated importation. Once the virus is introduced, localized transmission can rapidly occur if underlying environmental conditions are favorable enough to sustain vector activity [45]. Beyond human movement, global trade has contributed heavily to vector dissemination. The intercontinental spread of *Ae. albopictus* driven by the transportation of used tires and ornamental plants demonstrates how commercial activities can unintentionally facilitate invasive vector establishment worldwide [46].

The emergence of CHIKV in temperate regions represents one of the most concerning developments in contemporary arbovirology, fundamentally shifting its historical restriction from tropical climates to a global public health threat [47]. Outbreaks in Italy and France demonstrated that imported cases can seed sustained local transmission where *Ae. albopictus* populations are established, a paradigm shift driven by warming temperatures, increased vector survival, and extended mosquito activity seasons alongside globalization, urbanization, and international travel [48]. As mathematical models predict increasing suitability for seasonal summer epidemics across Europe, North America, and East Asia under future climate scenarios, public health systems in these newly exposed temperate countries face severe diagnostic and surveillance challenges, where a lack of clinical familiarity can lead to misdiagnoses with dengue, influenza, or rheumatologic conditions and critically delay outbreak detection [26,49].

6. Surveillance and public health challenges

Diagnosing CHIKV infections remains exceptionally difficult in co-endemic regions because it shares core clinical features (such as acute fever, rash, and debilitating arthralgia) with dengue and Zika viruses [50]. While standard laboratory diagnosis relies on reverse transcription-polymerase chain reaction (RT-PCR), viral isolation, and serological assays, widespread resource limitations often hinder diagnostic capacity in the most heavily affected areas [51,52]. This diagnostic challenge underscores an urgent need for multiplex diagnostic tools capable of simultaneously distinguishing co-circulating arboviruses [51]. To overcome these limitations, effective public health strategies must implement integrated surveillance frameworks that monitor both human cases and vector populations [53]. Modern climate-informed surveillance systems—which synthesize meteorological, ecological, and epidemiological data via geographic information systems (GIS) and predictive modeling—are increasingly vital to mapping emerging risk areas, identifying transmission hotspots, and guiding targeted vector control interventions before outbreaks escalate [54,55].

When these preventative measures fail, large-scale CHIKV outbreaks can rapidly overwhelm local healthcare systems due to the sudden surge of acute, highly symptomatic cases [56]. The public health impact is further compounded by the long-term healthcare burden of chronic chikungunya-associated arthralgia, which can persist in patients for months or even years [57]. Beyond the immediate strain on medical infrastructure, the broader economic consequences of these epidemics are devastating to affected regions. Communities frequently face staggering healthcare expenditures, severe productivity losses, a sharp decline in tourism, and a significantly reduced workforce capacity, demonstrating that CHIKV is both a profound medical crisis and a major socio-economic disruptor [58,59].

7. Prevention and control strategies

Because no universally available antiviral therapy currently exists for CHIKV infection, prevention strategies remain heavily dependent on effective vector control measures [60]. Integrated vector management has therefore become a cornerstone of CHIKV prevention, combining environmental, biological, chemical, and community-based approaches to reduce mosquito populations and interrupt transmission cycles [61]. Control efforts focus primarily on reducing breeding habitats through elimination of stagnant water sources, improved household water storage practices, proper waste disposal, and environmental sanitation [62]. Additional interventions such as larviciding and insecticide spraying may further reduce vector density during outbreaks, while community education programs play an essential role in promoting public awareness and encouraging sustained participation

in mosquito control activities [62]. Nevertheless, conventional vector control strategies continue to face important challenges, including the emergence of insecticide resistance, high operational costs, logistical constraints, and concerns regarding long-term sustainability [63].

In recent years, climate-informed public health approaches have gained increasing attention as an essential component of CHIKV prevention and preparedness. Since climatic factors strongly influence mosquito ecology and transmission dynamics, integrating meteorological data into surveillance systems may improve outbreak prediction and enable earlier implementation of preventive interventions [64]. Early warning systems that incorporate climate forecasts, vector surveillance, and epidemiological monitoring can help identify high-risk regions before large-scale outbreaks occur [65]. Effective preparedness also requires close collaboration among public health authorities, meteorological agencies, environmental scientists, and urban planners to ensure coordinated responses to emerging transmission threats [66]. Furthermore, urban planning strategies should incorporate vector control considerations, including improved drainage infrastructure, efficient waste management systems, and housing designs that minimize human exposure to mosquito vectors [64].

Recent advances in vaccine development represent a promising milestone in the long-term prevention of CHIKV infection. Multiple vaccine platforms, including live-attenuated vaccines, virus-like particle vaccines, and mRNA-based vaccines, are currently under investigation or approaching regulatory implementation [59]. Vaccination may become increasingly important as climate change and globalization expand transmission into immunologically naïve populations and previously unaffected regions [25]. However, several challenges remain, including ensuring equitable vaccine access, monitoring long-term safety and effectiveness, and establishing cost-effective immunization strategies for endemic and outbreak-prone settings [67]. In addition to vaccines, innovative vector control technologies such as genetically modified mosquitoes and *Wolbachia*-based interventions are emerging as potential complementary tools for reducing transmission [13]. Together, these integrated preventive strategies may significantly strengthen global preparedness against the continuing expansion of CHIKV [13].

8. Future perspectives

The future epidemiology of CHIKV infection will likely be influenced by the complex interplay between climate change, rapid urbanization, globalization, demographic transitions, and ongoing viral evolution. Current evidence suggests that CHIKV will continue to expand into new ecological and geographical regions over the coming decades, particularly as environmental conditions become increasingly favorable for mosquito vector survival and transmission [68]. Climate projections indicate a growing suitability for CHIKV transmission in temperate regions, especially in parts of Europe and East Asia, where warming temperatures may extend mosquito activity and breeding seasons [69]. At the same time, rapid urban population growth in tropical and subtropical regions may intensify epidemic potential by increasing human density, expanding peri-urban settlements, and creating additional mosquito breeding habitats [39]. Aging populations may also contribute to a greater burden of severe disease manifestations and chronic chikungunya-associated complications [70].

Future research efforts should therefore focus on improving understanding of viral adaptation mechanisms, identifying correlates of protective immunity, developing more accurate climate-health predictive models, and advancing the discovery of effective antiviral therapies and vaccines [71]. Strengthening integrated surveillance systems that combine epidemiological, entomological, environmental, and climatic data will also be essential for early outbreak detection and timely public health response. In addition, there is increasing recognition that CHIKV should be addressed through a One Health approach that acknowledges the interconnectedness of human, animal, and environmental health [72]. Such multidisciplinary collaboration may enhance preparedness and provide more sustainable strategies for mitigating the expanding global threat posed by CHIKV [72].

9. Conclusion

The re-emergence and global expansion of CHIKV infection illustrate the profound impact of environmental change, viral evolution, urbanization, and globalization on the epidemiology of

infectious diseases in the modern era. Climate change has significantly altered the ecological distribution and seasonal activity of mosquito vectors, particularly *Ae. aegypti* and *Ae. albopictus*, thereby increasing the potential for CHIKV transmission in both tropical and temperate regions. At the same time, rapid urbanization, population growth, inadequate sanitation, and expanding international travel have intensified human-vector interactions and facilitated the rapid dissemination of the virus across continents. The emergence of adaptive viral mutations, especially those enhancing transmission efficiency in *Ae. albopictus*, has further accelerated the establishment of CHIKV in previously unaffected regions. Collectively, these factors have transformed CHIKV from a relatively localized tropical infection into a major global public health concern. Additionally, the increasing burden of CHIKV highlights the urgent need for comprehensive and integrated prevention strategies involving vector control, climate-informed surveillance systems, improved urban planning, vaccine development, and international collaboration. Future preparedness efforts must also recognize the growing influence of climate variability and global interconnectedness on arboviral disease emergence. Without sustained and coordinated intervention, CHIKV may continue expanding into new ecological niches and establish endemic transmission in additional regions, posing substantial clinical, economic, and public health challenges worldwide. Addressing this evolving threat will require multidisciplinary collaboration integrating virology, epidemiology, entomology, climate science, urban health, and public policy within a broader One Health framework.

Data availability

All data are included in the manuscript.

Ethical approval

Not applicable.

Authors' contribution

FA and DEZ: conceptualized and designed the study, conducted literature search and synthesis, preparation of original draft, critical review, and editing.

Acknowledgments

None.

Funding

None.

Competing interests

The authors declare that they have no competing interests.

Informed consent statement

Not applicable.

Declaration of generative AI and AI-assisted technologies in the manuscript preparation process

During the preparation of this manuscript, the authors used ChatGPT (OpenAI) to improve grammar, language clarity, and presentation. The authors reviewed and edited all AI-assisted content and take full responsibility for the accuracy, integrity, and final content of the manuscript.

References

- [1] Silva LA, Dermody TS. Chikungunya virus: epidemiology, replication, disease mechanisms, and prospective intervention strategies. *J Clin Invest* 2017;127:737–49. <https://doi.org/10.1172/JCI84417>
- [2] da Cunha R V., Trinta KS. Chikungunya virus: Clinical aspects and treatment - A review. *Mem Inst Oswaldo Cruz* 2017;112:523–31. <https://doi.org/10.1590/0074-02760170044>
- [3] Pedí VD, de França GVA, Rodrigues VB, Duailibe FT, Santos MTP, de Oliveira MRF. Burden of chikungunya fever and its economic and social impacts worldwide: a systematic review. *Trop Med Int Health* 2025;30:865–92. <https://doi.org/10.1111/tmi.70012>
- [4] Simon F, Javelle E, Oliver M, Leparcoffart I, Marimoutou C. Chikungunya virus infection. *Curr Infect Dis Rep* 2011;13:218–28. <https://doi.org/10.1007/s11908-011-0180-1>
- [5] Khongwichit S, Chansaenroj J, Chirathaworn C, Poovorawan Y. Chikungunya virus infection: molecular biology, clinical characteristics, and epidemiology in Asian countries. *J Biomed Sci* 2021;28:1–17. <https://doi.org/10.1186/s12929-021-00778-8>

- [6] de Lima Cavalcanti TYV, Pereira MR, de Paula SO, Franca RF de O. A review on chikungunya virus epidemiology, pathogenesis and current vaccine development. *Viruses* 2022;14:1–20. <https://doi.org/10.3390/v14050969>
- [7] Schwameis M, Buchtele N, Wadowski PP, Schoergenhofer C, Jilma B. Chikungunya vaccines in development. *Hum Vaccin Immunother* 2016;12:716–31. <https://doi.org/10.1080/21645515.2015.1101197>
- [8] Higgs S, Vanlandingham D. Chikungunya virus and its mosquito vectors. *Vector Borne and Zoonotic Diseases* 2015;15:1–10. <https://doi.org/10.1089/vbz.2014.1745>
- [9] Kraemer MUG, Sinka ME, Duda KA, Mylne AQN, Shearer FM, Barker CM, et al. The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. albopictus*. *Elife* 2015;4:e08347. <https://doi.org/10.7554/eLife.08347>
- [10] Gubler DJ. Dengue, urbanization and globalization: the unholy trinity of the 21(st) century. *Trop Med Health* 2011;39:3–11. <https://doi.org/10.2149/tmh.2011-S05>
- [11] Eisen L, Moore CG. *Aedes* (*Stegomyia*) *aegypti* in the continental United States: a vector at the cool margin of its geographic range. *J Med Entomol* 2013;50:467–78. <https://doi.org/10.1603/me12245>
- [12] Weaver SC, Chen R, Diallo M. Chikungunya virus: Role of vectors in emergence from enzootic cycles. *Annu Rev Entomol* 2020;65:313–32. <https://doi.org/10.1146/annurev-ento-011019-025207>
- [13] Abdelnabi R, Neyts J, Delang L. Chikungunya virus infections: time to act, time to treat. *Curr Opin Virol* 2017;24:25–30. <https://doi.org/10.1016/j.coviro.2017.03.016>
- [14] Soumahoro M-K, Boelle P-Y, Gaüzere B-A, Atsou K, Pelat C, Lambert B, et al. The Chikungunya epidemic on La Réunion Island in 2005-2006: a cost-of-illness study. *PLoS Negl Trop Dis* 2011;5:e1197. <https://doi.org/10.1371/journal.pntd.0001197>
- [15] Vairo F, Haider N, Kock R, Ntoumi F, Ippolito G, Zumla A. Chikungunya: epidemiology, pathogenesis, clinical features, management, and prevention. *Infect Dis Clin North Am* 2019;33:1003–25. <https://doi.org/10.1016/j.idc.2019.08.006>
- [16] Bettis AA, L'Azou Jackson M, Yoon I-K, Breugelmans JG, Goios A, Gubler DJ, et al. The global epidemiology of chikungunya from 1999 to 2020: A systematic literature review to inform the development and introduction of vaccines. *PLoS Negl Trop Dis* 2022;16:e0010069. <https://doi.org/10.1371/journal.pntd.0010069>
- [17] Caputo B, Russo G, Manica M, Vairo F, Poletti P, Guzzetta G, et al. A comparative analysis of the 2007 and 2017 Italian chikungunya outbreaks and implication for public health response. *PLoS Negl Trop Dis* 2020;14:1–12. <https://doi.org/10.1371/journal.pntd.0008159>
- [18] Silva Jr. JVJ, Ludwig-Begall LF, Oliveira-Filho EF de, Oliveira RAS, Durães-Carvalho R, Lopes TRR, et al. A scoping review of Chikungunya virus infection: epidemiology, clinical characteristics, viral co-circulation complications, and control. *Acta Trop* 2018;188:213–24. <https://doi.org/10.1016/j.actatropica.2018.09.003>
- [19] Bartholomeeusen K, Daniel M, LaBeaud DA, Gasque P, Peeling RW, Stephenson KE, et al. Chikungunya fever. *Nat Rev Dis Primers* 2024;9:1–48. <https://doi.org/10.1038/s41572-023-00429-2>
- [20] Wimalasiri-yapa BMCR, Stassen L, Huang X, Hafner LM, Hu W, Devine GJ, et al. Chikungunya virus in Asia – Pacific : a systematic review. *Emerg Microbes Infect* 2019;8:70–9. <https://doi.org/10.1080/22221751.2018.1559708>
- [21] Schmidt C, Schnierle BS. Chikungunya vaccine candidates: current landscape and future prospects. *Drug Des Devel Ther* 2022;16:3663–73. <https://doi.org/10.2147/DDDT.S366112>
- [22] Thomson M, Stanberry LR. Climate change and vectorborne diseases. *N Engl J Med* 2022;387:1969–78. <https://doi.org/10.1056/NEJMr2200092>
- [23] Onyango MG, Bialosuknia SM, Payne AF, Mathias N, Kuo L, Vigneron A, et al. Increased temperatures reduce the vectorial capacity of *Aedes* mosquitoes for Zika virus. *Emerg Microbes Infect* 2020;9:67–77. <https://doi.org/10.1080/22221751.2019.1707125>
- [24] Liu Z, Zhang Q, Li L, He J, Guo J, Wang Z, et al. The effect of temperature on dengue virus transmission by *Aedes* mosquitoes. *Front Cell Infect Microbiol* 2023;13:1242173. <https://doi.org/10.3389/fcimb.2023.1242173>
- [25] Abbasi E. The impact of climate change on travel-related vector-borne diseases: A case study on dengue virus transmission. *Travel Med Infect Dis* 2025;65:102841. <https://doi.org/10.1016/j.tmaid.2025.102841>
- [26] Ryan SJ, Carlson CJ, Mordecai EA, Johnson LR. Global expansion and redistribution of *Aedes*-borne virus transmission risk with climate change. *PLoS Negl Trop Dis* 2019;13:e0007213. <https://doi.org/10.1371/journal.pntd.0007213>
- [27] Dharmamuthuraja D, Rohini PD, Lakshmi MI, Isvaran K, Ghosh SK, Ishtiaq F. Determinants of *Aedes* mosquito larval ecology in a heterogeneous urban environment- a longitudinal study in Bengaluru, India. *PLoS Negl Trop Dis* 2023;17:e0011702. <https://doi.org/10.1371/journal.pntd.0011702>

- [28] Schmidt CA, Comeau G, Monaghan AJ, Williamson DJ, Ernst KC. Effects of desiccation stress on adult female longevity in *Aedes aegypti* and *Ae. albopictus* (Diptera: Culicidae): results of a systematic review and pooled survival analysis. *Parasit Vectors* 2018;11:267. <https://doi.org/10.1186/s13071-018-2808-6>
- [29] Abbasi E. Climate change and vector-borne disease transmission: the role of insect behavioral and physiological adaptations. *Integr Org Biol* 2025;7:obaf011. <https://doi.org/10.1093/iob/obaf011>
- [30] Cann KF, Thomas DR, Salmon RL, Wyn-Jones AP, Kay D. Extreme water-related weather events and waterborne disease. *Epidemiol Infect* 2013;141:671–86. <https://doi.org/10.1017/S0950268812001653>
- [31] Benedict MQ, Levine RS, Hawley WA, Lounibos LP. Spread of the tiger: global risk of invasion by the mosquito *Aedes albopictus*. *Vector Borne Zoonotic Dis* 2007;7:76–85. <https://doi.org/10.1089/vbz.2006.0562>
- [32] Fischer D, Thomas SM, Niemitz F, Reineking B, Beierkuhnlein C. Projection of climatic suitability for *Aedes albopictus* Skuse (Culicidae) in Europe under climate change conditions. *Glob Planet Change* 2011;78:54–64. <https://doi.org/10.1016/j.gloplacha.2011.05.008>
- [33] Powell JR, Tabachnick WJ. History of domestication and spread of *Aedes aegypti* - a review. *Mem Inst Oswaldo Cruz* 2013;108 Suppl 1:11–7. <https://doi.org/10.1590/0074-0276130395>
- [34] Bonizzoni M, Gasperi G, Chen X, James AA. The invasive mosquito species *Aedes albopictus*: current knowledge and future perspectives. *Trends Parasitol* 2013;29:460–8. <https://doi.org/10.1016/j.pt.2013.07.003>
- [35] Zahouli JBZ, Koudou BG, Müller P, Malone D, Tano Y, Utzinger J. Effect of land-use changes on the abundance, distribution, and host-seeking behavior of *Aedes arbovirus* vectors in oil palm-dominated landscapes, southeastern Côte d'Ivoire. *PLoS One* 2017;12:1–26. <https://doi.org/10.1371/journal.pone.0189082>
- [36] Zhao T, Chen T, Zhang J, Li C, Qin C. Chikungunya virus: current situation and future challenges. *Biosaf Health* 2025;7:348–56. <https://doi.org/10.1016/j.bsheal.2025.10.001>
- [37] Gong W, Wang D, Chen Q, Zhong S, Shi X, Peng B. Outbreak of chikungunya virus with *Aedes albopictus*-adaptive mutations - Guangdong province, China, 2025. *China CDC Wkly* 2025;7:1528–32. <https://doi.org/10.46234/ccdcw2025.260>
- [38] Ning X, Xia B, Wang J, Gao R, Ren H. Host-adaptive mutations in Chikungunya virus genome. *Virulence* 2024;15:2401985. <https://doi.org/10.1080/21505594.2024.2401985>
- [39] Kolimenakis A, Heinz S, Wilson ML, Winkler V, Yakob L, Michaelakis A, et al. The role of urbanisation in the spread of *Aedes* mosquitoes and the diseases they transmit-A systematic review. *PLoS Negl Trop Dis* 2021;15:e0009631. <https://doi.org/10.1371/journal.pntd.0009631>
- [40] Sureshkumar S, Shekhar S. Impact of urban heat island effect on dengue incidence: a remote sensing approach using thermal and high-resolution optical imagery. *BMC Public Health* 2025;25:2914. <https://doi.org/10.1186/s12889-025-23763-4>
- [41] Yip SSW, Charm CYC, Ng KS, Lam SC. Chikungunya fever: a re-emerging mosquito-borne threat demanding proactive prevention strategies in Asia. *Front Public Health* 2026;14:1–6. <https://doi.org/10.3389/fpubh.2026.1745145>
- [42] Bastaraud A, Cecchi P, Handschumacher P, Altmann M, Jambou R. Urbanization and waterborne pathogen emergence in low-income countries: Where and how to conduct surveys? *Int J Environ Res Public Health* 2020;17:1–19. <https://doi.org/10.3390/ijerph17020480>
- [43] Haddad NM, Brudvig LA, Clobert J, Davies KF, Gonzalez A, Holt RD, et al. Habitat fragmentation and its lasting impact on Earth's ecosystems. *Sci Adv* 2015;1:e1500052. <https://doi.org/10.1126/sciadv.1500052>
- [44] Kiarash Aghayan S, Moghadas hosseinzadeh F. The impact of traveling on infectious diseases transmission with a focus on air travel: a narrative review. *Int J Travel Med Glob Health* 2025;13:33–41. <https://doi.org/10.30491/ijtmgh.2024.485399.1439>
- [45] Vega-Rúa A, Lourenço-De-Oliveira R, Mousson L, Vazeille M, Fuchs S, Yébakima A, et al. Chikungunya virus transmission potential by local *Aedes* mosquitoes in the Americas and Europe. *PLoS Negl Trop Dis* 2015;9:1–18. <https://doi.org/10.1371/journal.pntd.0003780>
- [46] Swan T, Russell TL, Staunton KM, Field MA, Ritchie SA, Burkot TR. A literature review of dispersal pathways of *Aedes albopictus* across different spatial scales: implications for vector surveillance. *Parasit Vectors* 2022;15:303. <https://doi.org/10.1186/s13071-022-05413-5>
- [47] Radici A, Hammami P, Cannet A, L'Ambert G, Lacour G, Fournet F, et al. *Aedes albopictus* is rapidly invading its climatic niche in France: wider implications for biting nuisance and arbovirus control in western Europe. *Glob Chang Biol* 2025;31:e70414. <https://doi.org/10.1111/gcb.70414>

- [48] Cunha MS, Costa PAG, Correa IA, de Souza MRM, Calil PT, da Silva GPD, et al. Chikungunya virus: an emergent arbovirus to the South American continent and a continuous threat to the world. *Front Microbiol* 2020;11:1297. <https://doi.org/10.3389/fmicb.2020.01297>
- [49] Gizaw Z, Salubi E, Pietroniro A, Schuster-Wallace CJ. Impacts of climate change on water-related mosquito-borne diseases in temperate regions: A systematic review of literature and meta-analysis. *Acta Trop* 2024;258:107324. <https://doi.org/10.1016/j.actatropica.2024.107324>
- [50] Rueda JC, Peláez-Ballestas I, Angarita J-I, Santos AM, Pinzon C, Saldarriaga E-L, et al. Clinical diagnosis of chikungunya infection: an essential aid in a primary care setting where serological confirmation is not available. *Trop Med Infect Dis* 2023;8. <https://doi.org/10.3390/tropicalmed8040213>
- [51] Varghese J, De Silva I, Millar DS. Latest advances in arbovirus diagnostics. *Microorganisms* 2023;11. <https://doi.org/10.3390/microorganisms11051159>
- [52] Kerkhof K, Falconi-Agapito F, Van Esbroeck M, Talledo M, Ariën KK. Reliable serological diagnostic tests for arboviruses: feasible or utopia? *Trends Microbiol* 2020;28:276–92. <https://doi.org/10.1016/j.tim.2019.11.005>
- [53] Esser HJ, Mögling R, Cleton NB, van der Jeugd H, Sprong H, Stroo A, et al. Risk factors associated with sustained circulation of six zoonotic arboviruses: a systematic review for selection of surveillance sites in non-endemic areas. *Parasit Vectors* 2019;12:265. <https://doi.org/10.1186/s13071-019-3515-7>
- [54] de Lima CL, da Silva ACG, Moreno GMM, Cordeiro da Silva C, Musah A, Aldosery A, et al. Temporal and spatiotemporal arboviruses forecasting by machine learning: a systematic review. *Front Public Health* 2022;10:900077. <https://doi.org/10.3389/fpubh.2022.900077>
- [55] Lim A-Y, Jafari Y, Caldwell JM, Clapham HE, Gaythorpe KAM, Hussain-Alkhateeb L, et al. A systematic review of the data, methods and environmental covariates used to map Aedes-borne arbovirus transmission risk. *BMC Infect Dis* 2023;23:708. <https://doi.org/10.1186/s12879-023-08717-8>
- [56] Pialoux G, Gaüzère B-A, Jauréguiberry S, Strobel M. Chikungunya, an epidemic arbovirolosis. *Lancet Infect Dis* 2007;7:319–27. [https://doi.org/10.1016/S1473-3099\(07\)70107-X](https://doi.org/10.1016/S1473-3099(07)70107-X)
- [57] Soumahoro M-K, Gérardin P, Boëlle P-Y, Perrau J, Fianu A, Pouchot J, et al. Impact of Chikungunya virus infection on health status and quality of life: a retrospective cohort study. *PLoS One* 2009;4:e7800. <https://doi.org/10.1371/journal.pone.0007800>
- [58] Costa LB, Barreto FK de A, Barreto MCA, Santos THP dos, Andrade M de MO de, Farias LABG, et al. Epidemiology and economic burden of chikungunya: a systematic literature review. *Trop Med Infect Dis* 2023;8:1–17. <https://doi.org/10.3390/tropicalmed8060301>
- [59] DeFilippis VR. Chikungunya virus vaccines: platforms, progress, and challenges. *Curr Top Microbiol Immunol* 2022;435:81–106. https://doi.org/10.1007/82_2019_175
- [60] WHO. Guidelines for prevention and control of Chikungunya fever 2009. <https://www.who.int/publications/i/item/guidelines-for-prevention-and-control-of-chikungunya-fever> (accessed May 25, 2026).
- [61] Wilson AL, Courtenay O, Kelly-Hope LA, Scott TW, Takken W, Torr SJ, et al. The importance of vector control for the control and elimination of vector-borne diseases. *PLoS Negl Trop Dis* 2020;14:1–31. <https://doi.org/10.1371/journal.pntd.0007831>
- [62] MOH. Updates in vector control in Malaysia – what is new? 2022. <https://nih.gov.my/covid-19/component/content/article/88-slides/237-12-02-2022-updates-in-vector-control-in-malaysia-what-is-new-by-dr-norhayati-mokhtar?Itemid=437> (accessed January 2, 2026).
- [63] Moyes CL, Vontas J, Martins AJ, Ng LC, Koo SY, Dusfour I, et al. Contemporary status of insecticide resistance in the major Aedes vectors of arboviruses infecting humans. *PLoS Negl Trop Dis* 2017;11:e0005625. <https://doi.org/10.1371/journal.pntd.0005625>
- [64] Rocklöv J, Dubrow R. Climate change: an enduring challenge for vector-borne disease prevention and control. *Nat Immunol* 2020;21:479–83. <https://doi.org/10.1038/s41590-020-0648-y>
- [65] Lowe R, Coelho CA, Barcellos C, Carvalho MS, Catão RDC, Coelho GE, et al. Evaluating probabilistic dengue risk forecasts from a prototype early warning system for Brazil. *Elife* 2016;5. <https://doi.org/10.7554/eLife.11285>
- [66] WHO. Handbook for integrated vector management 2012. <https://www.who.int/publications/i/item/9789241502801> (accessed May 25, 2026).
- [67] Rodrigues CMC, Plotkin SA. Impact of vaccines; health, economic and social perspectives. *Front Microbiol* 2020;11:1526. <https://doi.org/10.3389/fmicb.2020.01526>

- [68] Wang S, Liu Y, Wang Y, Zhou L, Liu J. Global and regional burden of chikungunya from 2004 to 2024: a worldwide observational study. *J Glob Health* 2026;16:4055. <https://doi.org/10.7189/jogh.16.04055>
- [69] Caminade C, Medlock JM, Ducheyne E, McIntyre KM, Leach S, Baylis M, et al. Suitability of european climate for the Asian tiger mosquito *Aedes albopictus*: recent trends and future scenarios. *J R Soc Interface* 2012;9:2708–17. <https://doi.org/10.1098/rsif.2012.0138>
- [70] Badawi A, Ryoo SG, Vasileva D, Yaghoubi S. Prevalence of chronic comorbidities in chikungunya: a systematic review and meta-analysis. *Int J Infect Dis* 2018;67:107–13. <https://doi.org/10.1016/j.ijid.2017.12.018>
- [71] Freppel W, Silva LA, Stapleford KA, Herrero LJ. Pathogenicity and virulence of chikungunya virus. *Virulence* 2024;15:2396484. <https://doi.org/10.1080/21505594.2024.2396484>
- [72] Guo C, Mishra N, Aouacheria A, Pham CT, Asiedu EK, Long Y, et al. A One Health perspective on the 2025 chikungunya outbreak in Guangdong province, China. *HLife* 2025;3:618–20. <https://doi.org/10.1016/j.hlife.2025.09.007>