JEPIBIO
Journal of Epidemiology and Infection Biology

Review Article

Human Populations, Exposure Routes, and Health Outcomes in Chikungunya Virus Infection: A Rapid Review

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Date of Receiving: 02/10/2025
Date of Acceptance 28/11/2025
Date of Publishing 10/12/2025

ABSTRACT Chikungunya virus (CHIKV) is an arthropod-borne alphavirus with dominance including *Aedes aegypti* together with *Aedes albopictus* mosquitoes. It has experienced a spectacular geographic growth out of Africa to Asia, Europe and the Americas since 2004. It is a single stranded, positive RNA virus, which is classified into four major genotypes with each having far reaching and severe epidemic patterns. Current systematic review applied Population, Exposure, and Outcome (PEO) framework was applied to understand the CHIKV transmission globally. A Web of causation was developed to understand the causal factors across different levels. This disease shows U-shaped risk and key trends. The infection presents clinically with an acute high fever, rash and severe polyarthralgia that may continue over long periods, months or even years resulting in a high level of disability that is persistent and severe in a large percentage of infected persons. The proliferation of efficient vectors of the mosquito that is further enhanced by globalization, increased human mobility and climate change still supports the spread and the resurrection of the virus. Current study shows the urgent need to enhance surveillance, enhanced strategies to control the vectors and the process of creating specific antiviral therapies and effective vaccines.

KEYWORDS Chikungunya, *Aedes*, Viral infections, Vector borne, Mosquito

Introduction

Chikungunya virus (CHIKV) is an alphavirus in family of Togaviridae. Transmission of the disease is mainly through the bite of a folliculated Nile *Aedes aegypti* and *Aedes albopictus* mosquito causing a disease that is characterized by fever, rash and arthralgia. During massive rural epidemics, the human host is the principal amplifier ((Petersen and Powers, 2016; Bartholomeeusen *et al*, 2023). The initial outbreak of CHIKV was reported in Makonde Plateau in modern Tanzania in the period between 1952 and 1953 when it was first identified as a human pathogen (Silva and Dermody, 2017; Vairo *et al*, 2019)). Researchers identified four different lineages, one of which was the East/Central/South African (ECSA) genotype, and it is present in Africa with a distribution cycle of non-human primates. On the contrary, the Asian genotype is spread primarily in the cities of Southeast Asia ((Silva and Dermody, 2017; Wahid *et al*, 2017). Unlike in the past, over the last ten years, a rapid spread of CHIKV globally is directly associated with the ECSA lineage and its sub groups.

The spread of CHIKV in the world began with the outbreak of Kenya in 2004, and then to the islands of the Indian Ocean, and resulted in the great urban outbreaks. In certain regions, the rate of infection was more than a third of the population (Wahid *et al*, 2017). The Indian Ocean Lineage (IOL) is also an E. coli Interferon-stimulating antigen sublineage that originated during this outbreak (E1-A226V mutation) and became more transmissible (Cunha *et al*, 2020). The latter gave the virus increased infectiousness especially in Aedes albopictus mosquito and enabled it to be transmitted to new areas requiring temperate conditions like Italy (2007). In late 2013, on the Saint Martin Island, primarily due to the Asian descent, the virus was discovered in the Western Hemisphere and led to a massive outbreak. Approximately 45 countries of the Americas had registered over 2.9 million suspected and confirmed cases by mid-2016 (Wahid *et al*, 2017) (Yactayo *et al*, 2016). During this period, in Brazil the ECSA genotype first appeared in 2014, instantly becoming the most predominant, and putting Brazil in the spot of the most reported cases in the Americas (de Souza *et al*, 2023). As of today, CHIKV is spread across over 100 countries, exposing approximately 1.3 billion to the risk, and verifying the

importance of a severe and persisting health issue in question (Vairo *et al*, 2019; Bartholomeeusen *et al*, 2023).

CHIKV infection has a high morbidity as the adverse effects may be severe on health and the economy even after curing the acute illness effect. Although most of the acute stage of the disease does not last longer than 2 weeks, it is a disease with chronic sequelae, estimated 40 to greater than 60 percent of patients will develop permanent, debilitating rheumatologic problems, including chronic arthralgia and arthritis, which may last months or even years. Although the case-fatality rate is low (approximately 0.1), recent epidemics have disproved augmented mortality threats and drastic uncharacteristic functions, including neurological complications, such as encephalitis and Guillain-Barre syndrome, and myocarditis particularly in the neonates, aged, and individuals with a preexisting cardiac or metabolic condition. The morbidity is directly related, which causes immense socioeconomic impairments because of lower productivity and decreased living standards. The necessity of the increased research is further underlined by the fact that there are no licensed vaccines or specific antiviral therapies produced at the moment and the treatment is limited to the use of symptomatic treatment only. In addition, successful surveillance and clinical differentiation is also challenging because of the similarity in symptoms with the other arboviruses that are co-circulating in the area including dengue and Zika, which involves misdiagnosis and underreporting. Considering the ongoing growth and the impressive lack of standardized and evidence-based Clinical Management Guidelines on CHIKV, an extensive rapid review summarizing existing information on epidemiology and clinical presentation of the infection is highly justified to address the gap in knowledge and improve preparedness worldwide.

Methodology

The framework of the rapid review was limited to the Population, Exposure, and Outcome framework that described the key epidemiological and clinical aspects of the Chikungunya virus infection:

Population (P)

Research on human populations that live in or within the Chikungunya-infested or outbreak areas (Yactayo *et al*, 2016; Mourad *et al*, 2022; Bartholomeeusen *et al*, 2023). They involve patients in tropical and subtropical areas, tourists who visit them, and susceptible populations, e.g., the neonatal period, the older adult, pregnant women, and those with comorbid conditions (Vairo *et al*, 2019; Cunha *et al*, 2020; Bettis *et al*, 2022).

Exposure (E)

New infection with Chikungunya virus, which is mostly spread by biting the Aedes mosquitoes (Silva and Dermody, 2017; Wahid *et al*, 2017). It has entailed the urban transmission (human-mosquito-human) cycle and the sylvatic enzootic cycle(Silva and Dermody, 2017; Vairo *et al*, 2019) , whereas secondary causes encompass maternal-fetal and blood-transfusion routes (Constant *et al*, 2021).

Outcome (O)

Among the outcomes measured are acute clinical outcomes, the long-term effects, especially the presence of persistent arthralgia, overall morbidity, and the effects on the general population (Silva and Dermody, 2017; Wahid *et al*, 2017; Cunha *et al*, 2020; Bettis *et al*, 2022; Costa *et al*, 2023). The specific clinical outcomes under investigation are the severity of the disease, including neurological involvement and mortality among the high-risk groups (Vairo et al., 2019; Economopoulou et al., 2009) and long-term complications, including permanent rheumatologic complications (Ritz *et al*, 2015; Silva and Dermody, 2017). The potential broader health implication is the high level of economic burden in case of CHIKV (Costa *et al*, 2023; Simon *et al*, 2023).

Inclusion and Exclusion Criteria

The search was narrowed down to those studies that were investigating the human effect of the Chikungunya virus (CHIKV) infection both primary research and secondary research (Mourad *et al*, 2022; Webb *et al*, 2022).

Inclusion Criteria

The studies raising primary data on CHIKV epidemiology, clinical presentation, methods of diagnosis, treatment strategy, preventive methods, and competence of vectors, as well as the economic consequences, likely to be included (Webb *et al*, 2022; Costa *et al*, 2023). The accepted study designs included observational research (cohort and cross-sectional), outbreak assessments, genomic research, and structured clinical management guidelines (CMGs), and no language restrictions were used.

Exclusion Criteria

The studies were filtered out when they were of pure secondary commentaries (e.g. opinion articles or non-systematic reviews without clear methodological rigor), addressed in vivo or animal models (except when they added data about vector competence or pathogenesis which also applies to human infection) or lacked methodological clarity in data collection to support quality assessment (Mourad *et al*, 2022; Costa *et al*, 2023)

Method of Data Extraction and Analysis

According to the PEO framework, data extraction included the variables that were associated with the disease incidence, the geographic patterns, the prevalence of particular viral genotypes, the clinical outcomes, therapeutic practices, and the economic burden (Costa *et al*, 2023).

Epidemiological and Descriptive Synthesis

Compiled case incidence, frequency of space, and seroprevalence data to describe the global geo-temporal incidence and heterogeneity of CHIKV infection (de Lima

Cavalcanti *et al*, 2022). The information lineage data were involved in narrative synthesis (Asian, ECSA, IOL) (Wahid *et al*, 2017).

Clinical-Guideline Quality

It was used to determine the rigor and clarity of CMGs in terms of their methodology (Webb *et al*, 2022). Recommendations that have been extracted concerned the supportive management, management of severe neurological and cardiovascular complications, and the management of chronic arthralgia (NSAIDs, corticosteroids, DMARDs) but they also recorded the inter-guideline discrepancies (Webb *et al*, 2022).

Juxtaposition of Morbidity and Economic Burden

Data on morbidity are severity, hospitalization, case-fatality ratio, long-term morbidity, and the economic impacts, including the cost-of-illness, productivity losses, DALYs, were summed to ascertain the overall health and socioeconomic burden (Yactayo *et al*, 2016; Costa *et al*, 2023).

Methodological Limitations

There are a number of limitations to the approach that led to a lack of specificity and comparative power of this rapid review, which were mostly due to the quality and access to source information. The actual percentage of CHIKV infection is probably underestimated because of poor surveillance strategies and misclassification of diagnosis, which is mainly caused by the clinical similarity between CHIKV and Dengue and Zika virus infections (Cunha *et al*, 2020; Khongwichit *et al*, 2021; Webb *et al*, 2022). Data on cases collected and nationally aggregated which include cases with confirmed, probable, and suspected areas of infection further undermine accuracy and mask subnational disparities(Khongwichit *et al*, 2021). In addition, the proportion of infections is estimated to range between 3 and 28% of asymptomatic infections that adds to a gross underreporting in symptom-based surveillance systems (Yactayo *et al*, 2016). The lack of valid, evidence-based research remains a thorn in the flesh of the standardization of the international clinical management strategies and treatment recommendations (Webb *et al*, 2022).

Results

The vast majority of the work produced by the greatest minds was published in cases of a big wave or spike of the virus. Nearly 39 percent of these articles discuss the movement of CHIKV in place and time. 33 percent of articles refer to care and test-needs (Wahid *et al*, 2017). The primary symptoms include high temperature, excessive pains in joints, and muscle pains(Vu *et al*, 2017; Vairo *et al*, 2019; Bettis *et al*, 2022). In most cases the sick time terminates after one or two weeks. Nevertheless, the concentration of a virus in the blood can be extremely high, over 10 9 bits per drop (Vairo *et al*, 2019). Doctors can hardly distinguish CHIKV with other insects such as Dengue and Zika since they have similar signs. This implies that the cases are not necessarily going to be viewed or narrated properly(Wahid *et al*, 2017; Cunha *et al*, 2020) Although the risk of fatality is low (approximately, 0.1%), new waves have demonstrated that the bug is able to trigger new and detrimental health injuries in the brain (such as brain swell, Guillain-Barré), or damage the entire body (such as heart, liver, and kidney failure) (Vairo *et al*, 2019; Cunha *et al*, 2020). Long-term effects are the important financial burden, which occurs in 40-60 percent of ill people (Silva and Dermody, 2017; Bartholomeeusen *et al*, 2023).
Once past the initial sick stage, most of them have sore joints, bad swelling, and poor joint movements. This might remain months or even years (Vairo *et al*, 2019; Bartholomeeusen *et al*, 2023). It is believed to be caused by the fact that the body continues to combats remains of the bug, which remain in the cells of the joints The following factors increase the risk of getting these long pains: old (over 40 -45 years), female, and having significant pain at initial sick (Vairo *et al*, 2019; de Souza *et al*, 2023). The risk has a U-shaped shape thus; it is most prevalent in the case of new babies and those who are old (65 and older) (Vairo *et al*, 2019; Cunha *et al*, 2020; de Lima Cavalcanti *et al*, 2022). There are other health problems that make the individuals more likely to become very ill or even die, such as sugar illness, heart problems, or a weak liver or kidneys. Fast, clear care is needed. Nevertheless, at this moment, the treatments of CHIKV are not obvious, are not equivalent and equal to the care short-term as well as long-term (Vu *et al*, 2017; Webb *et al*, 2022).

U-shaped risk and Key trends

Studies show a clear U-shaped risk pattern. Risk is highest at age extremes (Fig 1). Neonates are highly vulnerable (Vairo *et al*, 2019; Mourad *et al*, 2022). Their immune systems are not fully developed. Vertical transmission increases their risk. Elderly individuals also face high risk (Table 1). It is commonly observed that immunity lowers as age grows. Also, comorbidities enhance the severity of disease. Females demonstrate increased probability of chronic outcomes (Petersen and Powers, 2016; Silva and Dermody, 2017). Severe initial symptoms lead to long-term issues such as. chronic arthralgia. Many patients (around 40-60%) develop long-term joint pain.

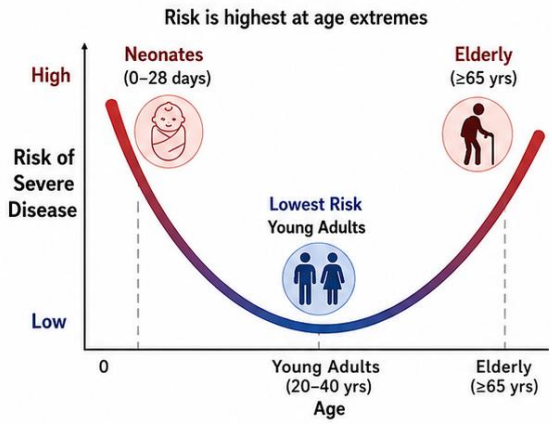

Fig. 1: U-shaped risk and Key trends associated with Chikungunya virus. It depicts that highest risk is at extreme ages.

Table 1: Populations affected due to Chikungunya virus extracted from published studies.

POPULATION EXPOSED	GROUPS	REFERENCES
General Population/Infected Individuals		(Bayrau *et al*, 2025; Dagnaw *et al*, 2025; Dai *et al*, 2025)
Vulnerable/High-Risk Human Subgroups	Severe disease, mortality, chronicity risk	(Fajardo *et al*, 2025; Menegale *et al*, 2025; Micheleto *et al*, 2025)
Specific Age Groups	Neonates, infants, children, adolescents, adults, elderly ≥65 years	(Dutra *et al*, 2024; Nagarajan *et al*, 2024; Nema *et al*, 2024; Orellano and Vezzani, 2024; Zerfu *et al*, 2024; Zini *et al*, 2024)
Pregnant Women /Mothers and Fetus /Neonates /Infants	Vertical/congenital transmission studies	(Fajardo *et al*, 2025; Micheleto *et al*, 2025)
Patients with Chronic Sequelae	Persistent arthralgia, arthritis, rheumatism, long-term complications	(Yang *et al*, 2025b; Gondim *et al*, 2026)
Patients with Atypical/Severe Disease	Neurological, cardiovascular, hepatic, renal complications, severe cases, critically ill patients	(Bayrau *et al*, 2025; Dagnaw *et al*, 2025; Dai *et al*, 2025; Fajardo *et al*, 2025)
Patients with Co-morbidities	Diabetes, hypertension, heart/liver/renal disease, HIV, pre-existing conditions	(Menegale *et al*, 2025; Micheleto *et al*, 2025; Gondim *et al*, 2026; Marques and Barratt-Boyes, 2026)
Geographical Populations in the Americas	Countries/regions mentioned in epidemiological studies	(Micheleto *et al*, 2025; Rosser *et al*, 2025; Shandhi *et al*, 2025; Marques and Barratt-Boyes, 2026)
Geographical Populations in Africa, Asia, Europe, Oceania	Countries/regions mentioned in epidemiological studies	(Auzenbergs *et al*, 2024; Cerqueira-Silva *et al*, 2024; Kronen *et al*, 2024; Pollett *et al*, 2024; Rosser *et al*, 2024)
Travelers/Returning Travelers	Epidemiological risk factor and surveillance target	(Auzenbergs *et al*, 2024; Cerqueira-Silva *et al*, 2024; Kronen *et al*, 2024; Pollett *et al*, 2024; Rosser *et al*, 2024)
Blood Donors/Blood Products	Surveillance/risk study	(Menegale *et al*, 2025; Micheleto *et al*, 2025; Rosser *et al*, 2025; Shandhi *et al*, 2025)
Non-human Primates (NHP) / Animals	Reservoirs and experimental models	(Menegale *et al*, 2025; Micheleto *et al*, 2025; Rosser *et al*, 2025; Shandhi *et al*, 2025)
Cell Lines / In Vitro Models	Fibroblasts, Macrophages, HEK cells	(Gato *et al*, 2024; McMahon *et al*, 2024; Yang *et al*, 2025a; Yang *et al*, 2025b; Gondim *et al*, 2026; Marques and Barratt-Boyes, 2026)
Occupational Groups	Laborers, students, cabin crew, pilots, military personnel	(Menegale *et al*, 2025; Micheleto *et al*, 2025; Rosser *et al*, 2025; Shandhi *et al*, 2025)

Associated exposure routes

Chikungunya virus infection is often associated with five major exposure categories (Table 2). Vector borne transmission especially mosquito-borne remains the biggest route of exposure. On the other hand, non-vector borne transmission such as maternal-fetal, transfusion-related, occupational, and potential sexual transmission also plays a significant role. Environmental factors such as travel, urban exposure, and co-circulation of CHIKV also further contribute to transmission risk. Therapeutic and prophylactic exposures primarily reflect vaccine candidates during clinical and experimental evaluation.

Table 2: Exposure reported in Chikungunya virus patients extracted from published studies.

EXPOSURE	Details	REFERNCES
Vector Borne Transmission	Mosquito-borne transmission Primary urban vector exposure	(Ritz *et al*, 2015; Petersen and Powers, 2016; Yactayo *et al*, 2016; Silva and Dermody, 2017; Vu *et al*, 2017)
Non-Vectorial Transmission	Maternal-fetal viraemic blood/blood products or blood transfusion Potential sexual transmission Accidental/Occupational transmission (e.g., needle prick, laboratory setting)	(Dai *et al*, 2025; Fajardo *et al*, 2025; Menegale *et al*, 2025; Micheleto *et al*, 2025; Rosser *et al*, 2025)
Environmental Risk Factors	Environmental factors Travel Exposure in uncontrolled urban environments Co-circulation or co-infection with other arboviruses	(de Souza *et al*, 2023; Simon *et al*, 2023; Shandhi *et al*, 2025; Yang *et al*, 2025a; Yang *et al*, 2025b; Gondim *et al*, 2026; Marques and Barratt-Boyes, 2026)
Therapeutic/ Prophylactic Exposure	Exposure to live-attenuated vaccine candidates virus-like particle (VLP) vaccine candidates viral vector vaccine candidates	(Auzenbergs *et al*, 2024; Cerqueira-Silva *et al*, 2024; Djamko Toko *et al*, 2024; Dutra *et al*, 2024; Nagarajan *et al*, 2024)
Viral Factors Affecting Transmission\ Efficiency	Exposure to ECSA/IOL lineage with the E1-A226V ECSA lineage with E1-K211E and E2-V264A mutation	(Pollett *et al*, 2024; Rosser *et al*, 2024; Zerfu *et al*, 2024; Zini *et al*, 2024; Bayrau *et al*, 2025)

Associated Outcomes

CHIKV infection is often associated with three major categories of clinical outcomes and range of clinical signs (Table 3). First, acute clinical disease is characterized by typical clinical signs including pyrexia, myalgia, gastrointestinal symptoms, and laboratory abnormalities. Second, a small proportion with acute disease progress to severe illness. Severe manifestations may include neurological, cardiovascular, and multi-organ complications. Such manifestations often require hospitalization and intensive care leading to occasional mortality. A small proportion of patients could experience chronic outcomes such as persistent arthralgia, arthritis, long-term neurological deficits, and reduced functional capacity.

Table 3: Outcomes reported due to Chikungunya virus extracted from published studies.

OUTCCOME	Signs and Symptoms	REFERENCES
Acute Disease (Typical Symptoms)	Abrupt onset of high fever, Myalgia, Gastrointestinal symptoms, Laboratory abnormalities High risk for severe illness	(Chang *et al*, 2024; de Castro *et al*, 2024; Djamko Toko *et al*, 2024; Earnest *et al*, 2024)
Severe/Atypical Manifestations	High risk for severe illness, leading to hospitalization, Neurological Complications, Cardiovascular Complications, Organ/System Failure, Other Atypical Symptoms, Mortality	(Amaral *et al*, 2024; Cerqueira-Silva *et al*, 2024; Chang *et al*, 2024; Djamko Toko *et al*, 2024; Paixao *et al*, 2024; Verani *et al*, 2024)
Chronic Sequelae (Post-CHIKV Syndrome)	Persistent Arthralgia/Arthritis, Persistent joint pain, Chronic neurological or neurocognitive deficits, Reduced functional capacity, Socioeconomic Burden	(Amaral *et al*, 2024; Cavalcante *et al*, 2024; Chang *et al*, 2024; Djamko Toko *et al*, 2024; Faria *et al*, 2024; Verani *et al*, 2024)

Web of causation

Chikungunya virus infection is driven by a complex interconnected network of events. This network includes environmental, ecological, viral, and host-related determinants which indicates CHIKV is a multi-factorial disease (Fig. 2). Distal, proximal, and immediate factors are the 3 types of determinants which further interacts and lead to outcomes. Distal determinants majorly include suitable conditions for disease emergence such as global, socioeconomics, environmental factors etc. These determinants enhance vector habitats, increase human mobility, and limit outbreak detection and control. These upstream drivers collectively influence proximal determinants, where vector expansion, viral adaptation, overlapping urban and sylvatic transmission cycles. Lack of immunity in population promotes susceptibility and helps rapid transmission during outbreaks. These processes lead to immediate causal factors such as infected mosquito bites, alternative transmission routes, high viremia, and host-related risk factors. Immediate causal factors act in a synergistic way rather than independently. Transmission potential is increased during high viremic episodes. On the other hand, disease severity is modified by host characteristics. Alternative transmission routes may cause sporadic infections during reduced mosquito transmission spans.

The combined effect of these interconnected pathways determines disease spread and clinical outcomes. The convergence of these pathways determines the spectrum of clinical outcomes i.e. uncomplicated febrile illness leading to severe multisystem disease and chronic sequelae. These severe outcomes generate a huge socioeconomic burden through long-term disability, productivity loss, increased healthcare utilization, and pressure on already weak health systems.

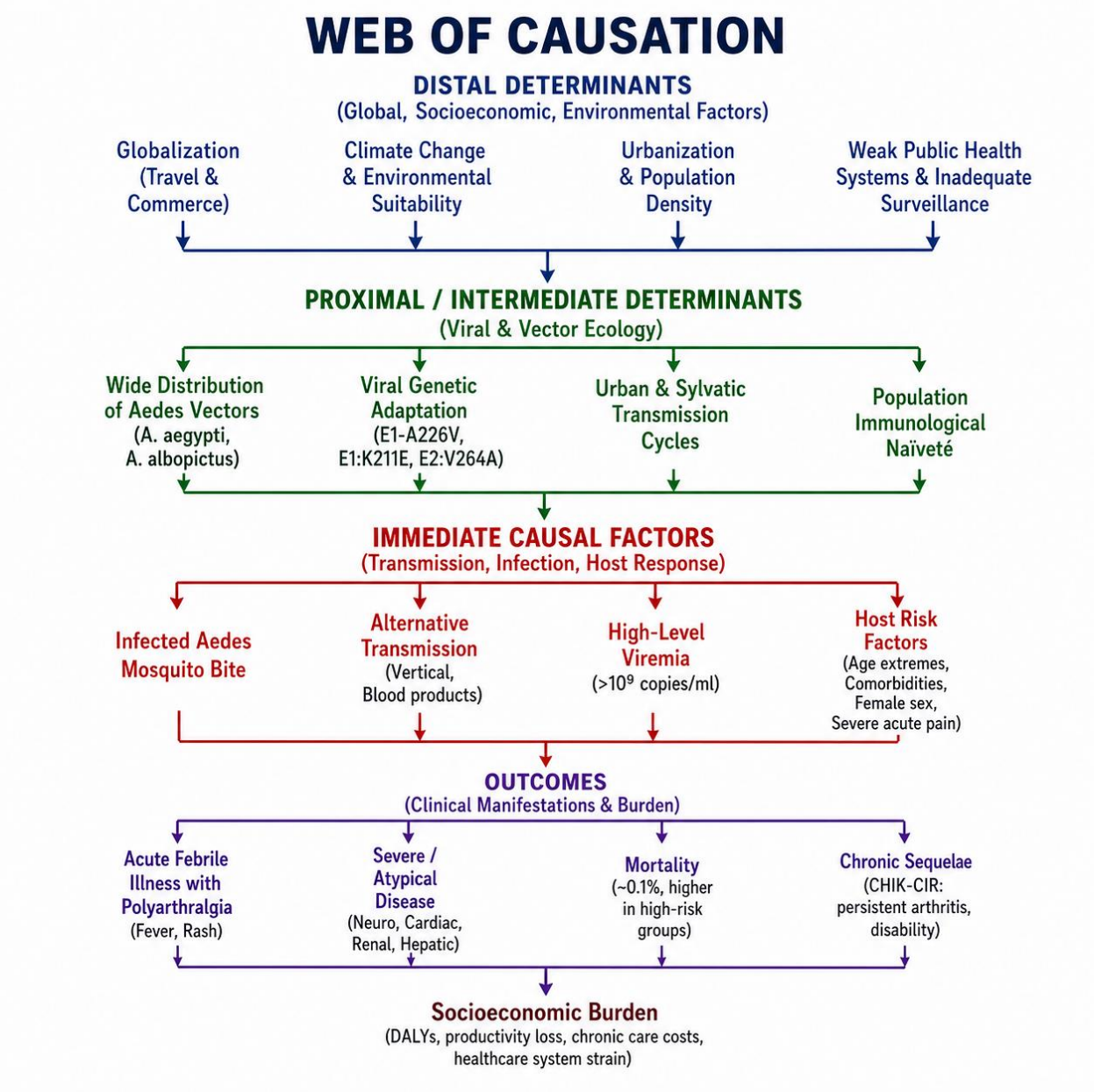

Fig. 2 Web of causation describing the outcome, immediate causal factors associated with CHIKV.

Comparative Insights regarding regions and risk groups

CHIKV burden varies among geographic regions and countries. Some regions report higher morbidity than others. The Americas reported a high disease burden as compared to other continents. South Asia also reported frequent outbreaks in suitable seasons. A few countries from Africa remain heavily affected continuously. Due to climatic conditions, these regions strongly favour mosquito breeding and survival which enhances disease transmission. Additionally, urban density in these countries also increases transmission risk. Climatic conditions such as temperate regions show fewer outbreaks as compared to tropical. However, due to global warming and climate change outbreaks still occur in Europe and other temperate regions.

Discussion

Following the outbreak of the Chikungunya virus (CHIKV) in East Africa in 2004 that made it a significant issue of concern globally, the virus has resurfaced very fast and has spread to other geographical locations(Wahid *et al*, 2017) . The new type of the old-scale outbreaks have been facilitated by globalization, climate changes, and above all development of viruses, which has rendered endemic merely an intermittent event (Wahid *et al*, 2017; Bartholomeeusen *et al*, 2023). During the research, the mutations that influence their capacity to infect their cells in wild-type organisms were detected. The CHIKV has been identified to fit genetic mutations to aid the greatest infectivity in various hosts. This mutation occurs in one of the residues that aid in infectivity in the vectors such as Aedes albopictus.

This caused the virus to reach large scale dissemination thereafter entered the Western Hemisphere as early as in 2013. There is an estimate that 1.3 billion people in the

whole world can become infected (Vairo *et al*, 2019). It is disturbing the extent to which the danger is prevalent. According to a study in 2023, the biggest issue economically and socially is as a result of this chronic inflammatory rheumatism that occurs in about 40 percent of the cases. It lingers over months, and even years. It is believed that aspect adds to it and makes it even worse, as it does not subside easily. Subsequent waves occurred in locations with prior infections, not only in localities with increased mosquitoes (de Souza *et al*, 2023). The localized immunity to previous outbreaks leaves some individuals vulnerable and continues the virus transmission. In Asia, there are places that have had CHIKV linger decades and this implies that there are varying levels of immunity in those locations. Until vaccines or antivirals are developed, only supportive care was offered for CHIKV, which is a significant deficit in the management of the health and monetary burden of the illness in the world (Silva and Dermody, 2017; de Souza *et al*, 2023; Simon *et al*, 2023). In addition, there are just inadequate sound clinical guidelines available were weak method-wise and non-agreeing on treatments (Vu *et al*, 2017; Webb *et al*, 2022). Also, with CHIKV, dengue and Zika transmitted by the same Aedes mosquitoes, it confounds surveillance and labs there (Vu *et al*, 2017).

The absence of cohesive approaches toward the chronic issues or high-risk populations continues to pose a threat to the patients all around (Webb *et al*, 2022). Like this overlap in diagnosis is a relief to complicate everything. In order to resolve the problems, we should have more effective surveillance in endemic areas, using both genomic and long-term data to obtain real incidence rates and prevent the problem of underreporting (Constant *et al*, 2021). The randomized trials would place acute and chronic symptom standards, particularly the persisting joint pains, in a clinical setting. Similarly, assessing the dosing of corticosteroid, or whether DMARDs such as methotrexate are safe in the long-term in patients with post-CHIKV arthropathy(Webb *et al*, 2022). The spread of vectors is increasing with changing climate and the virus as they changed. It is unclear entirely but with vaccines soon, markers of immune protection may better target vulnerable individuals. That could aid in setting priorities of those who are protected first (Paixao *et al*, 2018; Bettis *et al*, 2022; Webb *et al*, 2022; Bartholomeeusen *et al*, 2023).

CHIKV has propagated rapidly on the globe. This transmission is attributed to the modifications in the bug, increase of travel, and the alteration in weather. There are now 1.3 billion people who can fall ill. Majority of the individuals become healthy within a short period; however, others remain ill. Pain & bad health can last. This is not good to old individuals, small children, and sick people. No shot or drug to this purpose is made. It is not obvious how to assist people. Physicians have tenuous regulations that they give consideration to sick people. This bug is like Dengue & Zika. Thus, it is not easy to say which one people possess. Such bugs make it difficult to verify and monitor sickness. To rectify this, there must be an addition of another watch on the bug and the home of the bug. Vigorous experimentation should be conducted to identify the most appropriate method of taking care of sick individuals. The work should be vigorous in such a way that good solutions are produced to ensure that the risk of those who may fall ill is kept down.

Declaration of Competing Interest

The authors declare that they have no competing or conflict of interests.

Author Contributions

ENC: Conceptualization, formal analysis, Writing—initial draft. **SHG:** Writing—review and editing. All authors have read and agreed to the published version of the manuscript.

References

1. Amaral, J. K., G. Lucena, and R. T. Schoen. (2024). *Chikungunya Arthritis Treatment with Methotrexate and Dexamethasone: A Randomized, Double-blind, Placebo-controlled Trial*. Curr Rheumatol Rev 20(3):337-346. doi: 10.2174/0115733971278715231208114037
2. Auzenbergs, M., C. Maure, H. Kang, A. Clark, O. Brady, S. Sahastrabuddhe, and K. Abbas. (2024). *Programmatic considerations and evidence gaps for chikungunya vaccine introduction in countries at risk of chikungunya outbreaks: Stakeholder analysis*. PLoS Negl Trop Dis 18(4):e0012075. doi: 10.1371/journal.pntd.0012075
3. Bartholomeeusen, K., M. Daniel, D. A. LaBeaud, P. Gasque, R. W. Peeling, K. E. Stephenson, L. F. Ng, and K. K. Ariën. (2023). *Chikungunya fever*. Nature Reviews Disease Primers 9(1):17.
4. Bayrau, B. A., C. Ichura, A. Tariq, C. A. Winter, J. S. Amugongo, V. A. Okuta, L. W. Mwambingu, K. O. Ogamba, K. N. Shaita, C. O. Ronga, P. Chebii, S. L. Malumbo, O. K. Godana, Z. J. Jembe, C. M. Ng'ang'a, M. M. Mshahame, E. Buyukcangaz, E. Migliore, D. Bisanzio, B. Ndenga, F. Mutuku, and A. D. LaBeaud. (2025). *Risk factors associated with dengue and chikungunya seroprevalence and seroconversion among urban populations in western and coastal Kenya*. PLoS Negl Trop Dis 19(11):e0013740. doi: 10.1371/journal.pntd.0013740
5. Bettis, A. A., M. L'Azou Jackson, I.-K. Yoon, J. G. Breugelmans, A. Goios, D. J. Gubler, and A. M. Powers. (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. doi: 10.1371/journal.pntd.0010069
6. Cavalcante, A. F. L., J. Holanda, J. O. S. Passos, J. M. Pereira de Oliveira, E. Morya, A. H. Okano, M. Bikson, and R. Pegado. (2024). *Anodal tDCS over the motor cortex improves pain but not physical function in chronic chikungunya arthritis: Randomized controlled trial*. Ann Phys Rehabil Med 67(4):101826. doi: 10.1016/j.rehab.2024.101826
7. Cerqueira-Silva, T., J. M. Pescarini, L. L. Cardim, C. Leyrat, H. Whitaker, C. A. Antunes de Brito, E. B. Brickley, M. Barral-Netto, M. L. Barreto, M. G. Teixeira, V. S. Boaventura, and E. S. Paixao. (2024). *Risk of death following chikungunya virus disease in the 100 Million Brazilian Cohort, 2015-18: a matched cohort study and self-controlled case series*. Lancet Infect Dis 24(5):504-513. doi: 10.1016/S1473-3099(23)00739-9

8. Chang, A. Y., S. Simmens, H. Watson, R. L. Amdur, A. Siqueira, A. Proctor, S. Tritsch, C. A. Herrera Gomez, L. Encinales, A. Sucerquia Hernandez, J. Forero-Mejia, A. Jaller, J. J. Jaller, J. K. Amaral, I. Heckler, G. L. Simon, L. Moreland, A. Cadena, and G. S. Firestein. (2024). *Development of a Chikungunya Arthritis Disease Activity Score (CHIK-DAS) Based on a Prospective Cohort Study*. J Cell Immunol 6(6):236-246. doi: 10.33696/immunology.6.211
9. Constant, L. E., B. F. Rajsfus, P. H. Carneiro, T. Sisnande, R. Mohana-Borges, and D. Allonso. (2021). *Overview on chikungunya virus infection: from epidemiology to state-of-the-art experimental models*. Frontiers in microbiology 12:744164.
10. Costa, L. B., F. K. d. A. Barreto, M. C. A. Barreto, T. H. P. d. Santos, M. d. M. O. d. Andrade, L. A. B. G. Farias, A. R. R. d. Freitas, M. J. Martinez, and L. P. d. G. Cavalcanti. (2023). *Epidemiology and Economic Burden of Chikungunya: A Systematic Literature Review*. Tropical Medicine and Infectious Disease 8(6):301.
11. Cunha, M. S., P. A. Costa, I. A. Correa, M. R. De Souza, P. T. Calil, G. P. D. Da Silva, S. M. Costa, V. W. P. Fonseca, and L. J. da Costa. (2020). *Chikungunya virus: an emergent arbovirus to the South American continent and a continuous threat to the world*. Frontiers in microbiology 11:1297.
12. Dagnaw, G. G., A. T. Gessese, S. L. Abey, A. B. Bitew, K. Berrie, and H. Dejene. (2025). *Seroprevalence and risk factors of Chikungunya in Ethiopia: a systematic review and meta-analysis*. Front Public Health 13:1538911. doi: 10.3389/fpubh.2025.1538911
13. Dai, Z., Y. Chen, Y. Jiang, Y. Wu, B. Jin, Y. Xu, J. Xu, F. Tao, and X. Hu. (2025). *Global Assessment of current and future chikungunya virus transmission risk using optimized maxent modeling*. Acta Trop 269:107756. doi: 10.1016/j.actatropica.2025.107756
14. de Castro, A. S., C. H. N. Costa, D. L. Costa, A. B. Ibiapina, C. O. da Silva, J. O. Costa, F. S. Tajra, and C. V. M. Abdala. (2024). *[Evidence map of chikungunya treatmentsMapa de la evidencia sobre el tratamiento del chikunguna]*. Rev Panam Salud Publica 48:e99. doi: 10.26633/RPSP.2024.99
15. de Lima Cavalcanti, T. Y. V., M. R. Pereira, S. O. de Paula, and R. F. d. O. Franca. (2022). *A Review on Chikungunya Virus Epidemiology, Pathogenesis and Current Vaccine Development*. Viruses 14(5):969.
16. de Souza, W. M., S. T. de Lima, L. M. S. Mello, D. S. Candido, L. Buss, C. Whittaker, I. M. Claro, N. Chandradeva, F. Granja, and R. de Jesus. (2023). *Spatiotemporal dynamics and recurrence of chikungunya virus in Brazil: an epidemiological study*. The Lancet Microbe 4(5):e319-e329.
17. Djamko Toko, L. P., B. R. Galani Tietcheu, I. D. Tembar, P. D. Chuisseu Djamen, and N. Njintang Yanou. (2024). *Seroprevalence and biochemical parameters among patients with Chikungunya in Adamaoua region, Cameroon: A cross-sectional study*. Public Health Chall 3(1):e157. doi: 10.1002/puh2.157
18. Dutra, J. I. S., M. C. Souza, C. A. A. Lins, and A. C. Q. Medeiros. (2024). *Impact of chronic illness caused by chikungunya fever on quality of life and functionality*. Einstein (Sao Paulo) 22:eAO0562. doi: 10.31744/einstein_journal/2024AO0562
19. Earnest, J. T., O. D. Kirstein, A. C. Mendoza, G. A. Barrera-Fuentes, H. Puerta-Guardo, M. Parra-Cardena, K. Yam-Trujillo, M. H. Collins, N. Pavia-Ruz, G. Ayora-Talavera, G. Gonzalez-Olvera, A. Medina-Barreiro, W. Bibiano-Marin, A. Lenhart, M. E. Halloran, I. Longini, N. Dean, L. A. Waller, A. M. Crisp, F. Correa-Morales, J. Palacio-Vargas, P. Granja-Perez, S. Villanueva, H. Delfin-Gonzalez, H. Gomez-Dantes, P. Manrique-Saide, and G. M. Vazquez-Prokopec. (2024). *The TIRS trial: Enrollment procedures and baseline characterization of a pediatric cohort to quantify the epidemiologic impact of targeted indoor residual spraying on Aedes-borne viruses in Merida, Mexico*. PLoS One 19(9):e0310480. doi: 10.1371/journal.pone.0310480
20. Fajardo, T. C. G., A. C. Quadros Junior, C. A. L. Pinto, G. R. D. Santos, A. Silva, D. T. Catalan, A. Bertozzi, R. E. Gazeta, A. F. Moron, S. D. Passos, G. Jundiai Zika Cohort, A. S. Mello, A. Soriano-Arandes, A. Alarcon, A. Garcia-Alix, A. B. D. Silva, D. F. Ventura, D. B. L. Oliveira, D. S. Tambalo, D. D. S. Lima, D. T. Fujiwara, E. L. Durigon, E. R. Bagne, F. G. Velasco, L. C. P. Baran, F. N. Arita, F. D. M. Hernandez, J. P. G. Almeida, K. R. Camandulli, L. P. Castro, M. B. Machado, M. Zatz, M. M. D. Rodrigues, M. F. V. Rizzo, M. A. Farrao, M. N. B. Leite, N. Florence Filho, P. C. Loiola, R. Prestes, R. C. A. Dezena, S. H. A. Bonon, S. Vranjac, S. Rosemberg, S. G. P. Sarmento, S. S. Witkinchi, T. G. Souza, V. C. M. Pandini, and V. P. Paiva. (2025). *Serology survey of chikungunya virus in high-risk pregnant women and placental tissue findings*. Rev Inst Med Trop Sao Paulo 67:e43. doi: 10.1590/S1678-9946202567043
21. Faria, B. S., L. B. da Silva, C. F. R. Avelar, P. A. S. de Morais, and A. A. Bentes. (2024). *Vertical transmission of chikungunya virus: a worldwide concern*. Braz J Infect Dis 28(3):103747. doi: 10.1016/j.bjid.2024.103747
22. Gato, R., Z. Menendez, M. Rodriguez, G. Gutierrez-Bugallo, and M. Del Carmen Marquetti. (2024). *Advancing the art of mosquito control: the journey of the sterile insect technique against Aedes aegypti in Cuba*. Infect Dis Poverty 13(1):61. doi: 10.1186/s40249-024-01224-1
23. Gondim, A., L. Schultz, X. Huo, and S. Ruan. (2026). *Quantifying the risk of long-term chikungunya persistence in Miami-Dade county*. Math Biosci 392:109597. doi: 10.1016/j.mbs.2025.109597
24. Khongwichit, S., J. Chansaenroj, C. Chirathaworn, and Y. Poovorawan. (2021). *Chikungunya virus infection: molecular biology, clinical characteristics, and epidemiology in Asian countries*. Journal of Biomedical Science 28(1):84.
25. Kronen, J., M. Leuchner, and T. Kupper. (2024). *Zika and Chikungunya in Europe 2100 - A GIS based model for risk estimation*. Travel Med Infect Dis 60:102737. doi: 10.1016/j.tmaid.2024.102737
26. Marques, E. T. A., and S. Barratt-Boyes. (2026). *Chikungunya adolescent vaccination and the distinct risk-benefit landscapes*. Lancet Infect Dis 26(4):333-334. doi: 10.1016/S1473-3099(25)00680-2
27. McMahon, R., S. Toepfer, N. Sattler, M. Schneider, M. Narciso-Abraham, S. Hadl, R. Hochreiter, K. Kosulin, R. Mader, O. Zoihsl, N. Wressnigg, K. Dubischar, V.

Buerger, S. Eder-Lingelbach, and J. C. Jaramillo. (2024). *Antibody persistence and safety of a live-attenuated chikungunya virus vaccine up to 2 years after single-dose administration in adults in the USA: a single-arm, multicentre, phase 3b study*. Lancet Infect Dis 24(12):1383-1392. doi: 10.1016/S1473-3099(24)00357-8

28. Menegale, F., M. Manica, M. Del Manso, A. Bella, A. Zardini, A. Gobbi, A. D. Mignuoli, G. Mattei, F. Vairo, L. Vezzosi, F. Russo, F. Ferraro, F. Maraglino, A. T. Palamara, g. Dengue risk assessment working, P. Poletti, P. Pezzotti, S. Merler, and F. Riccardo. (2025). *Risk assessment and perspectives of local transmission of chikungunya and dengue in Italy, a European forerunner*. Nat Commun 16(1):6237. doi: 10.1038/s41467-025-61109-1
29. Micheleto, J. P. C., K. A. Melo, F. C. S. Veloso, S. B. Kassar, and M. J. C. Oliveira. (2025). *Risk factors for mortality in patients with chikungunya: A systematic review and meta-analysis*. Trop Med Int Health 30(4):235-245. doi: 10.1111/tmi.14088
30. Mourad, O., L. Makhani, and L. H. Chen. (2022). *Chikungunya: an emerging public health concern*. Current infectious disease reports 24(12):217-228.
31. Nagarajan, R., L. Ayyasamy, P. Ganeshkumar, S. Velusamy, and M. Murhekar. (2024). *Seropositivity of Chikungunya in Hospital Setting, India: A Systematic Review and Meta-Analysis*. Indian J Community Med 49(6):805-811. doi: 10.4103/ijcm.ijcm_63_24
32. Nema, S., D. Kale, R. Jain, A. Halder, M. Shrivastava, D. Vaishnav, A. K. Yadav, D. Namdeo, and D. Biswas. (2024). *A Pilot Seroprevalence Study Suggests Silent Zika virus Transmission in Bhopal Region of Central India*. Indian J Public Health 68(2):163-166. doi: 10.4103/ijph.ijph_1098_23
33. Orellano, P., and D. Vezzani. (2024). *[Observations on the dengue vaccination strategy in Argentina]*. Medicina (B Aires) 84(4):734-740.
34. Paixao, E. S., T. Cerqueira-Silva, P. T. V. Florentino, O. Carroll, N. Sanchez Clemente, D. A. Lawlor, R. C. Ribeiro Silva, L. C. Rodrigues, L. Smeeth, and M. L. Barreto. (2024). *A nationwide longitudinal investigation on the role of prenatal exposure to infectious diseases on the onset of chronic conditions in children and adolescents in Brazil*. Wellcome Open Res 9:320. doi: 10.12688/wellcomeopenres.22430.2
35. Paixao, E. S., L. C. Rodrigues, M. d. C. N. Costa, M. Itaparica, F. Barreto, P. Gerardin, and M. G. Teixeira. (2018). *Chikungunya chronic disease: a systematic review and meta-analysis*. Transactions of the Royal Society of Tropical Medicine and Hygiene 112(7):301-316.
36. Petersen, L. R., and A. M. Powers. (2016). *Chikungunya: epidemiology*. F1000Research 5:F1000 Faculty Rev-1082.
37. Pollett, S., H. C. Hsieh, D. Lu, M. Grance, S. Richard, G. Nowak, C. Lanteri, D. Tribble, and T. Burgess. (2024). *The risk and risk factors of chikungunya virus infection and rheumatological sequelae in a cohort of U.S. Military Health System beneficiaries: Implications for the vaccine era*. PLoS Negl Trop Dis 18(8):e0011810. doi: 10.1371/journal.pntd.0011810
38. Ritz, N., M. Hufnagel, and P. Gérardin. (2015). *Chikungunya in children*. The Pediatric infectious disease journal 34(7):789-791.
39. Rosser, J. I., J. J. Openshaw, A. Lin, R. R. Taruc, A. Tela, N. Tamodding, N. P. E. Abdullah, M. Amiruddin, E. Buyukcangaz, S. F. Barker, A. Turagabeci, Ansariadi, K. Leder, I. Wahid, and R. Consortium. (2025). *Seroprevalence, incidence estimates, and environmental risk factors for dengue, chikungunya, and Zika infection amongst children living in informal urban settlements in Indonesia and Fiji*. BMC Infect Dis 25(1):51. doi: 10.1186/s12879-024-10315-1
40. Rosser, J. I., J. J. Openshaw, A. Lin, R. R. Taruc, A. Tela, N. Tamodding, N. P. E. Abdullah, M. Amiruddin, E. Buyukcangaz, S. F. Barker, A. Turagabeci, A. Ansariadi, K. Leder, and I. Wahid. (2024). *Seroprevalence, incidence estimates, and environmental risk factors for dengue, chikungunya, and Zika infection amongst children living in informal urban settlements in Indonesia and Fiji*. Res Sq doi: 10.21203/rs.3.rs-5141509/v1
41. Shandhi, S. S., S. Malaker, M. Shahriar, and R. Anjum. (2025). *Chikungunya virus: from genetic adaptation to pandemic risk and prevention*. Ther Adv Infect Dis 12:20499361251371110. doi: 10.1177/20499361251371110
42. Silva, L. A., and T. S. Dermody. (2017). *Chikungunya virus: epidemiology, replication, disease mechanisms, and prospective intervention strategies*. The Journal of clinical investigation 127(3):737-749.
43. Simon, F., E. Caumes, T. Jelinek, R. Lopez-Velez, R. Steffen, and L. H. Chen. (2023). *Chikungunya: risks for travellers*. Journal of Travel Medicine 30(2):taad008.
44. Vairo, F., N. Haider, R. Kock, F. Ntoumi, G. Ippolito, and A. Zumla. (2019). *Chikungunya: epidemiology, pathogenesis, clinical features, management, and prevention*. Infectious Disease Clinics 33(4):1003-1025.
45. Verani, J. R., E. N. Eno, E. A. Hunsperger, P. Munyua, E. Osoro, D. Marwanga, G. Bigogo, D. Amon, M. Ochieng, P. Etau, V. Bandika, V. Zimbulu, J. Kiogora, J. W. Burton, E. Okunga, A. M. Samuels, K. Njenga, J. M. Montgomery, and M. A. Widdowson. (2024). *Acute febrile illness in Kenya: Clinical characteristics and pathogens detected among patients hospitalized with fever, 2017-2019*. PLoS One 19(8):e0305700. doi: 10.1371/journal.pone.0305700
46. Vu, D. M., D. Jungkind, and A. D. LaBeaud. (2017). *Chikungunya virus*. Clinics in laboratory medicine 37(2):371.
47. Wahid, B., A. Ali, S. Rafique, and M. Idrees. (2017). *Global expansion of chikungunya virus: mapping the 64-year history*. International journal of infectious diseases 58:69-76.
48. Webb, E., M. Michelen, I. Rigby, A. Dagens, D. Dahmash, V. Cheng, R. Joseph, S. Lipworth, E. Harriss, and E. Cai. (2022). *An evaluation of global Chikungunya clinical management guidelines: A systematic review*. EClinicalMedicine 54
49. Yactayo, S., J. E. Staples, V. Millot, L. Cibrelus, and P. Ramon-Pardo. (2016). *Epidemiology of Chikungunya in the Americas*. The Journal of infectious diseases 214(suppl_5):S441-S445.
50. Yang, S., Z. Wan, L. Zhan, H. Zhang, Y. Lin, Z. Weng, X. Wang, Z. Su, and X. Yu. (2025a). *Validation of*

China's 2025 high-risk criteria in RT-PCR-confirmed chikungunya inpatients: a single-centre retrospective cohort. BMC Infect Dis 25(1):1798. doi: 10.1186/s12879-025-12421-0

51. Yang, Y. F., Y. B. Qiu, Q. Xu, R. C. Gao, T. Tang, Y. Tian, Y. H. Wang, S. H. Lin, Y. D. Shi, L. T. Chen, Y. Zhang, J. Ma, C. L. Lv, G. L. Wang, H. F. Pan, W. Liu, and L. Q. Fang. (2025b). *Mapping the global risk of chikungunya virus endemicity and autochthonous transmission following importation*. Travel Med Infect Dis 67:102892. doi: 10.1016/j.tmaid.2025.102892
52. Zerfu, B., T. Kassa, G. Mamo, and M. Legesse. (2024). *Knowledge, attitude, and practices of the community about Chikungunya in selected Districts of Afar Region, Northeast Ethiopia; its implications for controlling the disease: a community-based quantitative and qualitative cross-sectional study*. BMC Public Health 24(1):3441. doi: 10.1186/s12889-024-20987-8
53. Zini, N., M. H. T. Avila, N. M. Cezarotti, M. C. P. Parra, C. A. Banho, L. Sacchetto, A. F. Negri, E. Araujo, C. Bittar, B. Milhin, V. Miranda Hernandes, K. R. Dutra, L. A. Trigo, L. Cecilio da Rocha, R. Alves da Silva, G. Celestino Dutra da Silva, T. Fernanda Pereira Dos Santos, B. de Carvalho Marques, A. Lopes Dos Santos, M. T. Augusto, N. F. B. Mistrao, M. R. Ribeiro, T. M. Pinheiro, T. Maria Izabel Lopes Dos Santos, C. M. S. Avilla, V. Bernardi, C. Freitas, F. A. Gandolfi, H. C. Ferraz Junior, G. C. Perim, M. C. Gomes, P. H. C. Garcia, R. S. Rocha, T. M. Galvao, E. A. Favaro, S. N. Scamardi, K. S. Rogovski, R. L. Peixoto, L. Benfatti, L. T. Cruz, P. P. F. Chama, M. T. Oliveira, A. S. A. Watanabe, A. C. B. Terzian, A. de Freitas Versiani, M. R. Dibo, F. Chiaravalotti-Neto, S. C. Weaver, C. F. Estofolete, N. Vasilakis, and M. L. Nogueira. (2024). *Cryptic circulation of chikungunya virus in Sao Jose do Rio Preto, Brazil, 2015-2019*. PLoS Negl Trop Dis 18(3):e0012013. doi: 10.1371/journal.pntd.0012013