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Review Article

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Chikungunya fever outbreak: Addressing globle public health challenge through One Health approaches

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ABSTRACT

Since 2004, chikungunya fever (CHIKF), a neglected tropical disease, has emerged as a growing public health concern, with outbreaks reported in over 119 countries across Asia, Africa, the Americas, Europe, and Oceania. Currently, there is no specific antiviral treatment available for chikungunya virus (CHIKV) infection, highlighting an urgent need for innovative preventive strategies. In July 2025, an outbreak of CHIKF was reported in Foshan City, Guangdong Province, China, resulting in more than 7000 confirmed cases within a single month. This review aimed to examine the intricate interactions among etiology, epidemiological distribution, *Aedes* mosquito vectors, environmental factors (such as urbanization and climate change), and human behavioral patterns in disease transmission within the One Health framework, providing policymakers with actionable insights to bridge existing disciplinary gaps between human medicine, veterinary science, and environmental management in addressing the threat of arboviral diseases.

KEYWORDS: Chikungunya virus; Transmission; Mosquito-borne disease; One Health

1. Introduction

Chikungunya fever (CHIKF) is a mosquito-borne infectious disease characterized primarily by fever, rash, myalgia, and arthralgia, which caused by the chikungunya virus (CHIKV), transmitted by *Aedes* mosquitoes such as *Aedes aegypti* and *Aedes albopictus*[1]. CHIKV was first identified in Tanzania in 1952[2], and initially caused sporadic outbreaks in Africa and Asia until 2004, characterizing a sylvatic transmission cycle involving between *Aedes* mosquitoes and non-human primates[3]. Then, approximately 18.7 million cases have been reported across 119 countries worldwide between 2011 and 2020[4], with most of the burden in the Latin American and Caribbean region. The CHIKV infects approximately 3 million people annually, with an estimated 1.3 to 2.7 billion people currently residing in areas at risk of CHIKV transmission[5]. In 2023, more than 500 000 CHIKF cases were reported worldwide.The numbers remained high in 2024; when there were over 480 000 cases, resulting in 190 chikungunya-related deaths[6,7]. An outbreak of CHIKF was reported in Foshan City, Guangdong Province, China, in July 2025, and as of August 2, a total of 7528 cases have been reported[8]. CHIKF has evolved into a progressively more severe global public health issue.

Risk factors for the transmission of CHIKV encompass all conditions that facilitate its spread, such as elevated temperatures, precipitation, population density, and irrigation[9]. The intensification of the El Niño-Southern Oscillation, along with exacerbated high temperatures and heavy rainfall resulting from climate change, can trigger its epidemics[10]. It was advisable to adopt the One Health strategy to cope with these ecological pandemics[11]. Therefore, this review utilized the One Health framework to examine the complex interplay among etiology, epidemiological distribution, *Aedes*

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mosquito vectors, environmental factors, and human behavioral patterns in disease transmission, aiming to provide policymakers with actionable insights to bridge existing disciplinary gaps between human medicine, veterinary science, and environmental management in addressing the threat of arboviral diseases.

2. Etiology

The viral particle of CHIKV is spherical, enveloped, and measures 60-70 nm in diameter. The genome consists of a single-stranded positive-sense RNA approximately 11.8 kb in length, encoding three structural proteins (capsid protein C, envelope proteins E1 and E2) and four non-structural proteins (nsP1, nsP2, nsP3, nsP4[12]. Currently, three distinct lineages have been identified[1]: the West African genotype, the East/Central/South African (ECSA) genotype (including the Indian Ocean lineage) subtype, and the Asian genotype. Since the outbreak on Réunion Island, the ECSA lineage has accounted for the highest number of cases[13]. Whole genome sequencing of 190 cases in Foshan, and the genomic sequence analysis demonstrated high homology among these viral strains, which all belonged to the Central African Clade of the ECSA genotype[14].

3. Epidemiological distribution of CHIKV

3.1. Global spread of CHIKV

Occasional outbreaks have since occurred in Africa, Asia, and the Indian subcontinent, with the largest outbreak occurring on Réunion Island in the Indian Ocean, where around 35% of the island's 750 000 inhabitants were infected in 2005 and 2006[15]. Since then, the disease has spread to Europe in 2007, reaching the Americas via the Caribbean islands in 2013[16]. More recently, outbreaks have occurred in Brazil (2015), Kenya (2018), Sudan (2018), Congo (2019), and Chad (2020), Bangladesh (2024)[6,17].The range of affected countries in the Asia-Pacific region has steadily increased in the last 70 years[18].

From January 1 2025 to August 2 2025, over 500 000 confirmed cases have been reported across 20 countries and territories (Figure 1)[19]. France's overseas territories, such as Réunion Island accounted for the majority of infections, reporting over one-third of the population (885 700). South America represented significant secondary hotspots, with Brazil with over 198 000 cases. Within Asia, confirmed case numbers in China reached 7 530 as of August 2 2025. Although Bangladesh is also shown in Figure 1, systematic case reporting was unavailable; surveillance data among febrile individuals indicated an IgM seropositivity rate of approximately 71%. Between May 1 and July 22 2025, mainland France reported 871 autochthonous cases of CHIKF, as captured by the Global Incident Map surveillance system.

3.2. CHIKF cases in China

The first indigenous CHIKF case in China was identified in Xishuangbanna, Yunnan Province, in 1987, with the virus isolated from the patient's blood[20]. Subsequently, since 2008, imported CHIKF cases have been detected multiple times in Guangdong, Zhejiang, and Yunnan province[21–23]. Notably, in 2010, a

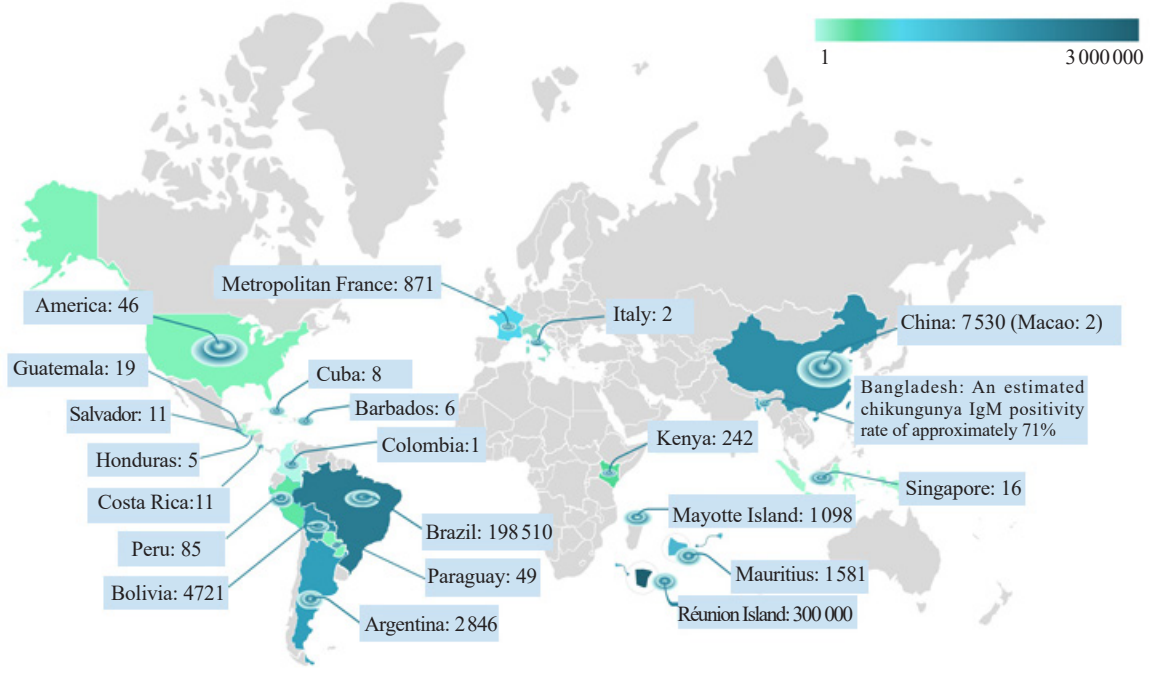


Figure 1. Chikungunya cases reported worldwide in 2025. Note: Case counts were compiled from both official public health authorities and non-official sources.

cluster outbreak involving 91 suspected cases and 10 confirmed cases occurred in Wanjiang Xincun Community, Dongguan City, Guangdong Province, breaking the long-standing pattern characterized primarily by sporadic imported cases[24]. In August 2017, Quzhou People's Hospital in Zhejiang Province treated one imported CHIKF case from Bangladesh, resulting in a total of four reported cases[22]. Furthermore, on July 8, 2025, a locally transmitted CHIKF outbreak triggered by an imported case was detected in Shunde District, Foshan City, Guangdong Province[25].

4. One Health approach for CHIKF prevention and control

The rapid spread of CHIKF on a global scale exhibited a pronounced trend of geographical expansion, with the distinction between traditional endemic regions (Africa, South Asia) and newly emerging endemic regions (Europe, Americas) becoming increasingly indistinct. This spatial diffusion pattern underscored the inadequacy of conventional epidemiological descriptions, necessitating a deconstruction of the complex interdependencies among humans, animals, and ecosystems through the lens of the "One Health" framework. Accumulating evidence suggests that the transmission dynamics of CHIKV are fundamentally shaped by three key interfaces: 1) host-adaptive mutations in *Aedes* (*Ae*.) *albopictus* and *Ae*. *aegypti*; 2) synergistic environmental pressures arising from urbanization and climate change; and 3) cross-border human behaviors, including travel patterns and water storage practices.

4.1. Host–adaptive of CHIKV

Humans and non-human primates are the primary reservoirs for CHIKV. Prior to 2005, *Ae*. *aegypti* was the primary vector. Subsequently, *Ae*. *albopictus* has become the most common vector. This shift is likely attributable to a mutation (E1-A226V) in the viral envelope protein gene, enhancing the virus's ability to replicate efficiently in *Ae*. *albopictus*[26] and transmit the virus to humans. *Ae*. *albopictus* has a broader global distribution, including parts of Europe and the United States. Therefore, after this adaptation, CHIKV has been transmitted to more than 100 countries worldwide between 2014 and 2019[1].

Therefore, the primary prevention is the avoidance of mosquito bites. Potential measures include: reducing time of outdoor exposure (mosquitoes can transmit infection throughout the day, not just at dusk or dawn); wearing long sleeves; consistent use of repellents containing DEET (30% to 50%), picaridin, IR3535, oil of lemon eucalyptus, or para-menthane-diol; use of ermethrin on clothing; decreasing conditions in or around the household that may favour the breeding of larvae (such as removing containers that hold water); use of mosquito nets and air conditioning; and redoubling efforts while travelling in endemic areas[27]. The Public Health Department of California has extensive guidelines for mosquito surveillance, detection, and eradication that could be used by local health departments[28].

4.2. Environmental factors favouring breeding of mosquitoes

Environmental monitoring is an important aspect of detecting CHIKV within the One Health framework. The virus can be present in the environment, especially in areas where the mosquito vectors breed. It is expected that as climate change progresses, warmer and drier environments will facilitate the expansion of the vectors into areas previously considered too cold to guarantee their survival[29]. In a study in Mozambique, water samples from the Infulene River were tested for the presence of arboviruses, including CHIKV[30]. CHIKV was detectable in 98% of the samples, highlighting the potential of environmental surveillance as a tool for assessing the circulation of the virus in non-sewered settings. A study estimating the drivers of autochthonous transmission in the Americas found significant relationships between CHIKV transmission and climatic factors, with transmission being correlated with linear and quadratic terms for temperature and precipitation[31]. In addition to natural conditions, overgrown household bushes, blocked drains, potholes, waste motor tyres, and rubbish dumps may increase the density of mosquito larvae. Use of mosquito nets, air conditioning, and insecticides reduces the prevalence of larvae[27].

Ae. *aegypti* is predominantly a container-breeding species, primarily reproducing in artificial containers and receptacles. Therefore, all water storage units such as tanks, cisterns, barrels, and trash containers should be securely covered with tightly fitting lids. Discarded items like old tires, tin cans, buckets, drums, and bottles should be removed, as they can accumulate water and serve as breeding sites for mosquitoes. In ornamental garden ponds or water tanks, the introduction of larvivorous fish, such as Gambusia or guppies, is recommended. If water containers cannot be emptied on a daily or weekly basis, appropriate larvicidal treatments may be applied to prevent mosquito breeding.

4.3. Human behavioral factors

4.3.1. Travel to or residence in endemic area

Although locally transmitted cases have been reported in the US and Europe, it is still expected that the bulk of cases in industrialised countries will be from returning travellers. A travel history to, or residence in, an endemic area within the 15 days prior to onset of infection should prompt suspicion. Housing and sanitary conditions outside developed countries may favour exposure to mosquito bites[32]. The spread of CHIKV in the Americas was likely facilitated by increased travel and trade, as well as the presence of suitable mosquito vectors[33]. In Panama, the introduction and spread of the virus were associated with travelers from Haiti and the Dominican Republic, and phylogenetic analysis showed that the circulating strains belonged to the Asian lineage[34].

Travelers are advised to avoid areas with active CHIKF outbreaks. Moreover, outbreaks of chikungunya driven by human movement highlight the need for multisectoral strategies in preventing and controlling the disease, comprising doctors, experts in public health and social sciences, virologists, immunologists, entomologists, and pathologists, along with representatives from sectors like tourism, economy, law, and agriculture.

4.3.2. Outdoor exposure

The longer time spent outdoors, the higher the likelihood of being exposed to mosquito bites. In a study of more than 500 people in an endemic area, spending 8 or more hours outdoors increased the risk of both asymptomatic and symptomatic infection with CHIKV[35].

Thus, this suggested to reduce outdoor activities, and wear long-sleeved shirts and full-length pants when outdoors.

5. Conlusions

The outbreak of CHIKF in China and its reemergence across multiple countries has elevated the risk of a global pandemic. This review highlights that implementing a One Health strategy-involving continuous surveillance of mosquito vectors, and human populations, coupled with environmental interventions and targeted mosquito control measures-may effectively mitigated the risk of human infection.

Conflict of interest statement

The authors declare that there is no conflict of interest.

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Data availability statement

The data supporting the findings of this study are available from the corresponding author upon request.

Authors' contributions

Liang WJ and Zhao DT conceptulized the study and wrote the original draft; Liang WJ, Zhao DT, Zhang RG, and Lu JH reviewed and edited the manuscript. All authors have read and agreed to the published version of the manuscript.

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