



Chikungunya outbreak in Africa: a review of the literature

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Introduction: The Chikungunya virus (CHIKV), transmitted via mosquitoes, exhibits clinical manifestations ranging from headaches, myalgia and arthralgia to debilitating systemic malfunctions. Endemic to Africa, CHIKV has seen an increase in cases since it was first recorded in 1950. There has recently been an outbreak in numerous African nations. The authors aim to review the history and epidemiology of CHIKV in Africa, current outbreaks, strategies adopted by governments and/or international organisations to mitigate such an outbreak, and future recommendations that can be employed.

Methodology: Data were collected from medical journals published on Pubmed and Google Scholar, and from the official World Health Organisation, African and United States of America's Centres for Disease Control and Prevention websites. All articles considering CHIKV in Africa, including epidemiology, aetiology, prevention and management, were sought after.

Results: Since 2015, the number of Chikungunya cases in Africa has increased, reaching the highest values ever recorded, especially in 2018 and 2019. Even though numerous vaccination and therapeutic intervention trials are still ongoing, no advancement has been made so far, including drug approval. Current management is supportive, with preventative measures, such as insecticides, repellents, mosquito nets and habitat avoidance, paramount to halting disease spread.

Conclusion: In light of the recent CHIKV outbreak in Africa, local and global attempts are re-emerging to mitigate the eruption of the case of the lack of vaccines and antivirals, controlling the virus may be an arduous feat. Improving risk assessment, laboratory detection and research facilities should be a priority.

Keywords: aetiology, Africa, CHIKF, Chikungunya virus, CHIKV, epidemiology, management, outbreak, prevention

Introduction

Chikungunya is a chronic mosquito-borne viral disease caused by the Chikungunya virus (CHIKV), identified as a member of positive-sense ribonucleic acid (+ssRNA) viruses known as *Togaviridae*. Chikungunya fever was first discovered in Africa

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HIGHLIGHTS

- Endemic to Africa, Chikungunya virus (CHIKV) has seen an increase in cases since it was first recorded in 1950. There has recently been an outbreak in numerous African nations.
- The virus reproduces inside the mosquito's mid-gut, where following dissemination to the Axillary tissues like salivary glands ensue. Compared to other mosquito-borne viruses, CHIKV can infect a new naïve host more quickly.
- A massive global effort and funding are needed to avoid future outbreaks. To start, each country, especially those where CHIKV is endemic, must employ an appropriate risk-assessment unit. Said responsibilities include surveillance of areas known to have the vector, detecting vector-attracting habitats and reporting back to the appropriate units.

among infected individuals over 68 years ago in 1953^[1]. Several clusters and sporadic cases of CHIKV outbreak, alongside the current re-occurrence of the virus in varying African nations, (Fig. 1) have been reported^[2–7] and also in other parts of the world. However, according to a study review of CHIKV outbreak between 1999 and 2020, 13 CHIKV outbreaks were reported from 11 African countries^[2–8] In Asia 53 CHIKV cases recorded in 15 countries^[8], which is higher than reported cases in Africa and in Oceania over 1700 suspected cases per 10 000 residency were reported by the Federated state of Micronesia^[9,10], and the

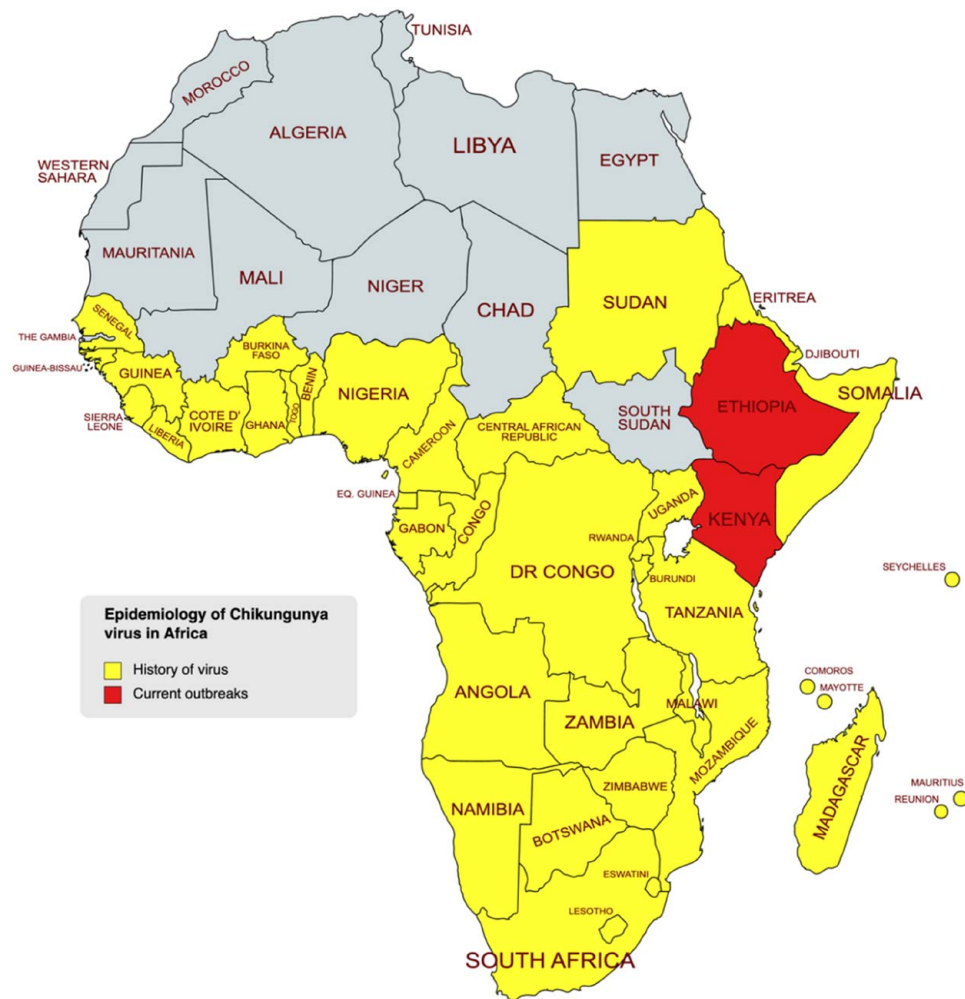


Figure 1. Geographical representation of the spread of the CHIKV virus over time and the current outbreak in domains of Africa. CHIKV, Chikungunya virus.

study revealed that Americas and Caribbean recorded 25 cases in 16 countries and 5 outbreak of CHIKV were reported in Europe between 1999 and 2020^[81] (Table 1).

Chikungunya is an acute disease that may cause neurological deformity (i.e. stooped posture) in infected individuals^[19], as well as various joint issues (i.e. arthralgia lasting more than 2–3 years)^[20–22], dermatological manifestations, myalgia and fever, all common prodromal symptoms^[23,24]. The transmission of CHIKV to humans is mainly facilitated by environmental factors, the infestation of flavivirus family-infected mosquitoes (i.e. *Aedes albopictus* and *Aedes aegypti*), and topographic widespread and sylvatic monkey cyclic transmissions, directly and indirectly, responsible for periodic disease outbreaks and re-emergence in Africa^[25–28]. CHIKV genomic content is approximated to be 11.89 kb with encoded properties of four non-structural proteins (NsP1-4) which enhance viral multiplication and CHIKV pathogenesis^[29]. CHIKV genotypes are frequently classified into three groups: West African, East/Central and South African (ECSA) and Asian.

Despite continued efforts to create suitable and efficient Chikungunya fever vaccinations^[30,31], there is no current recommended curative or therapy for Chikungunya. This review,

thereby, discussed the Chikungunya outbreak in Africa by reviewing the epidemiology and associated issues in combating Chikungunya. We also highlight Chikungunya in Africa and ongoing efforts alongside novel and strategic recommendations being made for the future.

Epidemiology and outbreak of CHIKV in Africa

In some nations, including Africa, Indonesia, the Southern United States, India and the West Indies, weakening polyarthralgia and fever became more common in the eighteenth and nineteenth centuries. Although, CHIKV could not be accurately associated with said outbreaks before the virus advent in the mid-1950s^[32,33]. Previous incidents before the virus's discovery may have been caused by the virus itself or another virus that was already found in the afflicted areas, such as the o'nyong'nyong virus in Africa which exhibits similar clinical manifestations^[34].

Since the advent of CHIKV, multiple minor incidences of the virus have occurred in Africa^[34]. Recent cases, which started as far back as 2004, have affected many areas in Africa alongside other continents. Between 1952 and 1953, Chikungunya was

Table 1
Chikungunya virus outbreak across the globe [2–7,11–18]

Region/country	Affected area	Year of outbreak
Africa		
Cameroon	West (Yaoundé and Douala)	2006
Democratic Republic of Congo	North-west (Kinshasa)	1999–2000, 2010, 2018–2020
Ethiopia	East (Dire Dawa)	2019
Gabon	North-west (Libreville and Surroundings)	2006–2007
	South-east (Franceville and Surrounding)	2010
	West – Central (Lambaréné)	2020–2021
La Reunion	La Reunion	2005–2006
Madagascar	East (Toamasina)	2006
Mayotte	Mayotte	2005–2006
Republic of Congo	South (Brazzaville)	2011
	West (Diosso)	2019
	South (Bouenza)	2019
	West (Kouilou river region)	2019
Sudan	East (Kassala)	2015
	East (Kassala), Khartoum, Northern states, and South Darfur	2018
Senegal	South-east (Kédougou)	2009
	South-east (Kédougou)	2015
Sierra Leone	South (Bo)	2012–2013
Kenya	Lamu County	2004–2005
	East County	2016
	Mombasa County	2018 and 2022
America and Caribbean		
Barbados	Southwest (Bridgetown)	2014
Brazil	North (Amapá)	2014–2015
	North-east (Sergipe)	2014–2016
	North-east (Feira de Santana and Riachão do Jacuípe, Bahia)	2015
	South-east (Rio de Janeiro)	2015–2016
	North-east (Ceará)	2015–2017
	North-east (Ceará)	2017–2022
	North-east (Piauí)	2016–2017
	North-east (Salvador, Bahia)	2017
	North-east (Alagoas, Amazonas, Bahia, Ceará, Distrito Federal)	2023
	South region of Brazil	2023
Argentina	North (Buenos Aires Province)	2016, 2023
Bolivia	—	2015, 2022, 2023
Paraguay	Amambay	2015–2016, 2018, 2022, 2023
Colombia	North (Corozal and Ovejas, Sucre)	2014–2015
	North (Piedecuesta, Santander)	2014–2015
	Colombia	2015, 2023
Dominica	Dominica	2013–2014
Dominican Republic	South-east (La Romana)	2014
Grenada	Grenada	2014
Haiti	West	2014
Honduras	Honduras	2015
Martinique and Guadeloupe	Martinique and Guadeloupe	2013–2015
Mexico	South (Chiapas)	2014
	South-east (Yucatan)	2015–2016
Nicaragua	West (Managua)	2014–2016
Puerto Rico	Puerto Rico	2014
Saint Martin/Sint Maarten	Saint Martin/Sint Maarten	2013–2014
Suriname	North (Paramaribo and Commewijne)	2014–2015
U.S. Virgin Islands	U.S. Virgin Islands	2014–2015

Table 1
(Continued)

Region/country	Affected area	Year of outbreak
Venezuela	North (Aragua)-	2014, 2023
Uruguay	North-west (Paysandú)	2023
Peru	Peru	2017, 2020 and 2023
Asia		
Bangladesh	Bangladesh (Shibganj, Char Kusahi, Gopalpur)	2011–2012
	East (Dhaka)	2017
Bhutan	Southwest (Samtse, Chukha and Thimphu)	2012
Cambodia	South (Trapeang Roka, Kampong Speu)	2012
	Cambodia (Nationwide)	2020
China	South	2010
	Quzhou Zhejiang Province	2017
India	East (West Bengal)	2014–2015
	North-east (Assam)	2015
	West (Pune, Maharashtra)	2016
	North (Delhi)	2016
	Central (Madhya Pradesh)	2016–2018
	India (Nationwide) but Karnataka is most affected cross the country	2019–2022
Indonesia	North-west (Sei Suka, North Sumatra)	2013
	North-west (Sumatra)	2014–2015
	South (Bali)	2015–2019
Lao PDR	South (Champassak)	2012
Malaysia	Malaysia	2010–2011
	Tanjung Sepat	2017–2019
	Malaysia	2023
Nepal	South (Terai)	2013–2015
Pakistan	Rawalpind	2016–2017
Philippines	Philippines	2010–2011
	North (San Pablo, Laguna)	2012
	Central (Cebu)	2012–2014
	Calabarzon region	2021
	Metro manila, Central Luzon, Calabarzon and northern Mindanao	2023
Thailand	West	2010–2011
	North-east (Bueng Kan)	2013
	Nationwide	2021–2023
Vietnam	Vietnam	2010–2011
Yemen	West (Al-Hudaydah)	2010–2012
Europe		
Italy	Central (Lazio)	2017
France	Provence- Alpes-côte d'Azur	2010
	Montpellier	2014
	Provence- Alpes-côte d'Azur	2017

isolated initially following the original epidemic in Tanzania. There was a very high transmission of the virus in many African countries^[35] (Table 2). Following the outbreak in said countries, the spread of Chikungunya ceased between 1999 and 2000, when ~50 000 individuals in Kinshasa, Democratic Republic of Congo (DRC), were affected^[38]. CHIKV isolates originated from the ECSA gene, which is more common in Central Africans than in East-South Africans. The isolate of the virus was obtained more than 20 years earlier, which gave room for the hypothesis of a dogged and unknown viral spread^[38], later proven true via CHIKV virological diagnosis among unconfirmed yellow fever patients in the DRC between 2003 and 2012^[39].

Table 2
Chikungunya outbreak by African Region ^[36,37].

Region/country	Area	Year of outbreak	Viral lineage
Cameroon	West (Yaounde)	2006	ECSA
Democratic Republic of Congo	North-west (Kinshasha)	1999–2000	ECSA
Gabon	North-west (Libreville and surroundings)	2006–2007	ECSA
La Reunion	La Reunion	2005–06	ECSA
Madagascar	East (Toamasina)	2006	NR
Mayotte	Mayotte	2005–2006	NR
Senegal	South-east (Kedougou)	2009	West African
Sudan	East (Kassala)	2005	NR
Kenya	—	2004	—

ECSA, East/Central and South African; NR, not reported.

The years 2002 and 2006 demonstrated a few reports of CHIKV infection being documented in Equatorial Guinea^[40] in addition to the period of increased yellow fever incidence in Sudan in 2005^[41]. The massive epidemic that struck Kenya's coastal area in 2004 sickened over 13 500 people. This had a major impact on public health post-transmission to countries like Seychelles, La Réunion, Comoros and Mauritius Island of the Indian Ocean, including the City of Mombasa in 2005–2006^[42].

After 2005, Chikungunya (or dengue) virus outbreaks occurred in several African nations. These outbreaks were primarily caused by *Aedes albopictus* (Asian tiger mosquito or Forest Mosquito), which by 2006 and 2007 had taken over as the primary vector for the dissemination of Chikungunya in Gabon and Cameroon^[43].

At least 20 000 individuals were affected in Libreville during said serious incident in the Gabonese Republic in 2007^[43]. The spread continued till 2010 when it reached the southern deep forest region, affecting villages throughout. In the Republic of Congo (RC), Brazzaville, there was a great outbreak that affected over 8000 people^[19]. CHIKV was reported to cause fever in 8.3% of victims during an eighteen-month prospective study conducted in Kenya on pyrexial children^[8,44]. There have been serious cases of CHIKV (with an ~80% attack rate in Mandera) in Kenya, including the Somalia border, where the first reported case indicated a growth in the capacity of their laboratory. In the years 2017–2018, there was another incidence in Kenya, with Mombasa County having 453 individuals affected^[8,22], said cases were confirmed in the laboratory^[22]. In August 2018, over 13 000 doubtful cases were found in Sudan in a great epidemic that occurred in August 2018^[8,22].

A very great epidemic occurred that caused over 10,500 doubtful cases in RC and an exceeding 1000 cases in the DRC in November 2018. This was due to said experiences in Kinshasa and Brazzaville, the capitals of the DRC and RC, and a newly recorded epidemic that caused over 40 500 doubtful victims and 300 confirmed cases in Ethiopia in 2019 and 2022, respectively. Meanwhile, Kenya recorded 83 cases in 2022^[8,22,45] (Table 1), and following the outbreak of CHIKV infection globally, Europe, Asia and Australia and the Pacific reported no cases of CHIKV in 2022 apart from Paraguay with cases recorded cases of CHIKV and dengue as of 1 December 2022^[37].

However, as of 9 March 2023 more than 110 000 cases of CHIKV and 43 deaths were recorded and the majority of cases and deaths were from Paraguay with 82 240 cases and 43 deaths and 30 386 cases were recorded in Brazil, 655 cases in Argentina, Thailand had 259 cases and Bolivia documented 300 cases while Africa have not reported cases of CHIKV as of 9 March 2023^[13] (Table 1).

Aetiology of Chikungunya

Chikungunya is a word originating from the Tanzanian Makonde language meaning to “bend up”. This describes the bending posture of the patient that is affected by the severity of the disease^[1,8,22,46]. Since the virus outbreak, CHIKV has been identified in ~40 countries, including Africa, Asia, Europe and most recently, America^[33]. The virus is a member of the *Togoviridae* family and the genus *Alphavirus*. There are 30 species of the arthropod-borne *alphavirus*, otherwise known as *arbovirus*, in the genus, which descend from arthropod-borne viruses that share seven distinct antigenic complexes^[47].

The first outbreak of CHIKV was isolated, and the epidemic was reported in Tangankiya province, now Tanzania, from 1952 to 1953. The patient had incapacitating arthralgia, high fever and rash^[1,46,48]. Infected *Aedes* mosquito bites, particularly those of *Aedes aegypti* and *Aedes albopictus*, are the primary vectors for the transmission of this disease of high mortality to humans^[49]. The virus is transmitted via an infected mosquito as it feeds on a viraemic human who has the virus circulating in its blood, which starts the cycle. The virus may then spread to a new, unaware victim when the mosquito feeds, a brief period of internal virus replication ensuing. When a mosquito bites an individual who possesses an active virus in their blood, the infection begins to spread. Infection of the mosquito that then consumes a blood meal from the infected host can start a new cycle of transmission^[46].

The virus reproduces inside the mosquito's mid-gut, where following dissemination to the Auxillary tissues like salivary glands ensue. Compared to other mosquito-borne viruses, CHIKV can infect a new naive host more quickly. Laboratory tests demonstrate that CHIKV may be observed in saliva as soon as 2–3 days after subsequent blood meal^[50]. This illustrates that it can take less than a week for the full transmission cycle to occur from a human to a mosquito and back again. Once infected, it is believed that the mosquito can continue to spread viruses for the remainder of its life^[47]. The virus then replicates in the skin and fibroblasts where dissemination through the blood to the lymphoid tissue, brain, liver and joints occurs^[23,24,48]. Although CHIKV infection is linked to a low mortality rate, the primary syndrome of acute CHIKV infection is a high fever (39–40 °C) which may persist for seven days in two phases^[51]. Post-pyrexia, sequelae such as “Post Chikungunya Chronic Polyarthralgia (pCHIKV-CPA)” may occur. This poses a profound negative impact on the quality of life of infected individuals, causing crippling arthralgia lasting several months to years^[52]. Other signs and symptoms include asthenia, arthritis, conjunctivitis, myalgia, gestational distress and pruritic or maculopapular rash (Table 3).

Table 3
Current CHIKV outbreak in Africa.

Countries	Date	Total cases	Confirmed cases	Note
Democratic Republic of Congo	2019	6149	—	The outbreak is still ongoing and has spread to eight of the twelve health departments of the country.
Sudan	2011, 2020	—	—	
Gabon	2015	13 978	—	Seven states (Kassala, Red Sea, Al Gadaref, River Nile, Northern State, South Darfur and Khartoum) have been affected by the outbreak.
Senegal	2010	—	—	The outbreak was declared in South-east (Franceville and surroundings)
Republic of Congo	2010, 2015	10	—	The outbreak was declared in the region of kedougou.
Sierra Leone	2011	—	—	South (Brazzaville)
Kenya	2019–2020	—	—	West (Diosso)
Ethiopia	2012–2013	—	—	The outbreak was declared in the region of South (Bo)
	2016	1792	—	The outbreak was confined to the Mandera East sub-county
	2018	453	—	The outbreak has spread to three sub-counties (Changamwe, Jomvu, Kissauni, Likoni, Mvita and Nyal) of Mombasa and one of Kilifi: with the majority of suspected cases reported from Mvita and Likoni in Mombasa.
	2022	83	5	
	2019	—	—	The outbreak was declared in East (Dire Dawa)
	2022	311	3	

CHIKV, Chikungunya virus.

Recent medical advances in Chikungunya diagnosis

However, because Chikungunya's clinical symptoms are arthralgia, myalgia, headache, vomiting, backache and diffuse maculopapular rashes^[53], like that of Dengue and Zika viruses, it is challenging to diagnose Chikungunya only from its clinical manifestations. For that reason, laboratory tests are needed for diagnosis. These include serology testing, CHIKV isolation and applying reverse transcription–polymerase chain reaction (RT-PCR) for detecting viral RNA^[54]. Diagnosis mainly concerns the time of specimen collection, as CHIKV replicates rapidly, reaching high RNA titres. Viruses are usually detected by real-time RT-PCR during the first seven days of infection, post-clinical symptom presentation^[54]. However, although rapid diagnostic kits are available, their sensitivity rarely correlates with that of RT-PCR. That is because such kits detect host-derived anti-CHIKV immunoglobulin M antibodies. In addition, the detection of immunoglobulin M antibodies is usually less sensitive than antigen detection^[55].

Analysis of cerebrospinal fluid composition is also used to aid the detection of CHIKV presence in the central nervous system. This cerebrospinal fluid composition analysis examines how CHIKV alters specific central nervous system components. Examples of these factors are marginally elevated protein, mildly lowered glucose, pleocytosis and mildly elevated lactate levels. These changes help aid the diagnosis of CHIKV. The outcomes of this method, though, might be the same for many virus types. Hence, the clinical findings and immunological analyses should be combined with this information to make a clear diagnosis^[56].

The most recent diagnostic technique is the application of rapid diagnostic immuno-chromatography (IC) testing kits. These IC testing kits use anti-CHIKV monoclonal antibodies derived from mice^[53]. The rate of disease detection via IC testing kits is 6 days post-fever onset since the testing kits detect viral envelop protein, which usually reduces after 4–5 days post-infection. Furthermore, the IC testing kit detection rates are the best method of diagnosis when compared to other diagnostic techniques^[53] since the majority of patients typically contact a doctor to examine the condition causing their symptoms early.

Current efforts to mitigate Chikungunya in Africa

Chikungunya is often self-limiting, with a resolution of symptoms spontaneous and full recovery observed. However, currently, no targeted antiviral medication or treatment to mitigate symptomatic Chikungunya is in circulation^[12]. Conservative management of affected individuals comprises immunological boosting through vitamin administration, hydration and rest^[12]. The second main goal is to treat arthralgia by lowering the temperature with non-steroidal anti-inflammatory medicines like Ibuprofen. Additionally, any infected individual works as an incubating agent as illness begins, and patient isolation while avoiding additional mosquito bites help to interrupt the cycle of CHIKV transmission^[57]. Taking further precautions against contracting the virus includes purifying water to kill larvae and decreasing the mosquito's natural and artificial habitat by spraying pesticides on surfaces and containers^[46]. It is also essential to protect against the *Aedes aegypti* mosquito bite by applying repellents and using insecticide-treated mosquito nets^[46]. There has not been a CHIKV vaccine created as of yet. However, several vaccines have advanced to late phases of clinical testing and, in terms of both safety and immunogenicity, are suitable to prevent the emergence of the disease^[58].

The challenges and obstacles in fighting Chikungunya in Africa

Due to several outbreaks, interest in CHIKV has surged recently. In 2019, an outbreak was declared in Congo where 6149 cases had been reported and eight of the country's twelve health departments had been affected by this outbreak. Also in 2018, 13 978 cases have been documented in Sudan, in which seven states have been affected, and Kenya has reported around 453 cases^[12]. Due to climate change and greater travel, many diseases have unexpectedly spread, especially throughout tropical and subtropical regions but even to temperate zones^[59].

A possible method of disease prevention is the creation of vaccinations or specialised antiviral medication therapy regimens to fight against and eradicate the CHIKV^[12]. It is crucial for the

creation of efficient vaccinations since, in most cases, the virus was brought back by travellers from impacted areas^[59].

Many challenges and obstacles were faced to eradicate CHIKV. Unfortunately, vaccines and antivirals were not available until now. Symptom-relieving medications are the mainstay of treatment, such as analgesics and antipyretics^[12]. The inability to quickly deploy clinical trials during outbreaks, unpredictable disease epidemiology and regulatory processes are impeding the development of desperately needed vaccinations^[59].

The effective use of resources is aided by surveillance, but if misused, it could compromise an individual's privacy. Quarantine effectively slows the spread of disease despite sacrificing human rights and liberty. Restrictions on travel are burdensome. Despite screening initiatives, they will not have much of an impact on CHIKV's spread; infected people will still spread the virus even if they appear healthy during the initial 4–10 days of the viral incubation period^[57].

Along with unprecedented population growth in developing countries, drug-resistant infections, unregulated urbanisation in tropical regions where vector-borne diseases are most common, and insecticide-resistant vectors are all factors contributing to the globalisation of diseases caused by arboviruses.

Ecosystems are altered by human activities in the environment, such as population pressure and agriculture. Additionally, in underdeveloped nations, anarchic urbanisation is frequently accompanied by social behaviours that favour the growth of vectors. For example, abandoned auto tires in residential areas that gather rainwater are perfect mosquito breeding grounds that help spread the virus^[58].

In addition to affecting mobility and overall health, and after generating explosive epidemics on a global level after decades of regionally confined outbreaks, tremendous suffering and significant economic costs, as well as financial strain in impacted regions, were established^[59].

Future recommendations

Because Chikungunya is a vector-borne virus, a variety of vaccines (i.e. virus-like particles^[59,60], chimeric, sub-unit^[60] and DNA vaccines^[61,62]) are currently being tested. No vaccine has been approved^[22,61,63]. Some antivirals and other compounds were studied as well, with no progress^[58]. Given the potential for chronic symptoms, ongoing research is necessary^[46]. Current management includes supportive treatment such as anti-inflammatories, antipyretics and analgesics^[19,64]. Basic prevention consists of avoiding water reservoirs and containers (which are known to attract the mosquito vector), insect repellent, mosquito nets and conservative clothing^[47]. However, the virus is still spreading despite these precautions. A massive global effort and funding are needed to avoid future outbreaks (Fig. 2). To start, each country, especially those where CHIKV is endemic, must employ an appropriate risk-assessment unit. Said responsibilities include (1) surveillance of areas known to have the vector, (2) detecting vector-attracting habitats and (3) reporting back to the appropriate units^[66]. Furthermore, more clinical research is needed to better understand the virus's transmission, pathogenicity and strain diversity to impede epidemics^[65]. Additional investments involve affordable, easily available diagnostic tests (i.e. serology, virology) that help increase the level of reporting^[65]. Since some African countries suffer economically, not all cases may be discovered. Not to

mention that other vector-borne diseases (i.e., Dengue virus) are

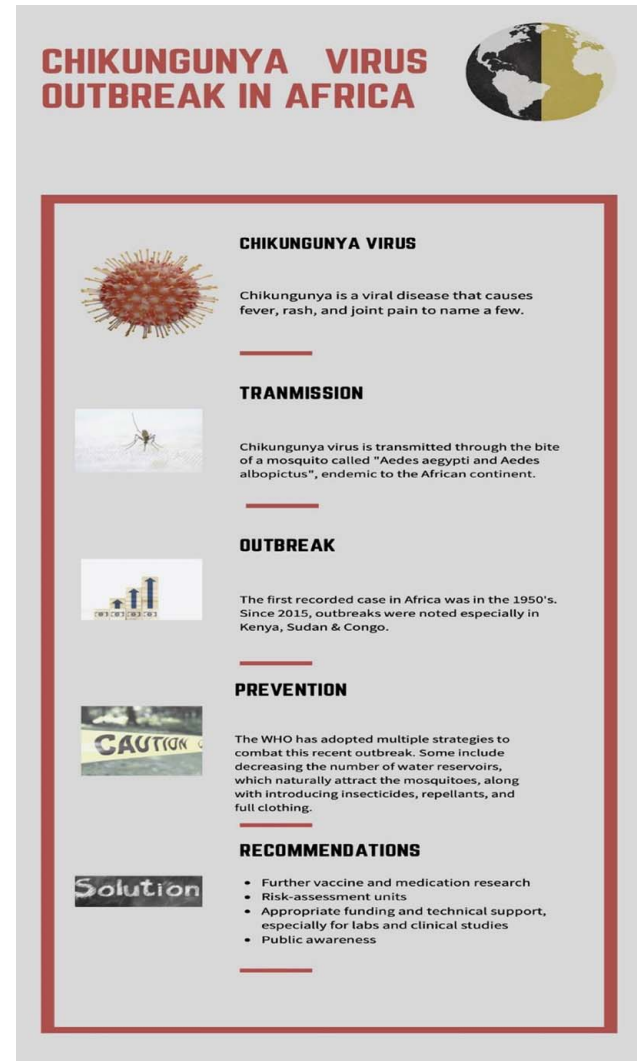


Figure 2. Poster highlighting CHIKV outbreak in Africa^[46,63–65]. CHIKV, Chikungunya virus.

present similarly^[22]. Extra care is necessitated to increase lab capacity and capability, in addition to any required technical support. This might be accomplished by boosting financing under the control of international organisations that are actively researching strategies to halt the spread of CHIKV^[46]. Lastly, and of especially equal importance, is public awareness concerning the vector, the virus, the mechanism of transmission, symptoms, habitat and preventative measures.

Conclusion

Chikungunya is caused by CHIKV, a mosquito-borne virus known to cause fever, myalgia, arthralgia and headaches. Rarely, manifestations include chronic neurological or cardiovascular sequelae. The vector, mosquitoes belonging to *Aedes* spp. (*Aedes aegypti* and *Aedes albopictus*), is endemic on the African continent. The first instance was identified in Tanzania in 1952, and since then, it has spread to several African nations as well as the Indian subcontinent and South Asia. The most recent outbreak

was in Kenya and Ethiopia and is currently ongoing. Despite the current high number of instances, likely, there are still more cases than are being reported due to the poor economic situation in many African nations, the absence of competent, accessible and affordable laboratory tests, as well as the lack of technical equipment. The need for additional funding and investment is made clear by this, both for better detection and to fund additional research on transmission, strains and vaccines. Other than conservative measuring, there is yet no vaccine or treatment that is effective.

Ethical approval

Ethics approval was not required for this review.

Consent

Informed consent was not required for this review.

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Author contribution

Conceptualization of ideas: all authors. Critical reviews with comments: all authors. Final Draft: all authors approved the final manuscript.

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References

- [1] Ross RW. The Newala epidemic. III. The virus: isolation, pathogenic properties and relationship to the epidemic. *J Hyg (Lond)* 1956;54: 177–91.
- [2] Pialoux G, Gauzere B-A, Jaureguiberry S, *et al.* Chikungunya, an epidemic arbovirolosis. *Lancet Infect Dis* 2007;7:319–27.
- [3] Zuckerman AJ, Banatvala JE, Pattison JR, *et al.* Principle and practice of Clinical Virology, 5th ed.. J Wiley & Sons, Ltd; 2005.
- [4] Aubry M, Teissier A, Roche C, *et al.* Chikungunya outbreak, French Polynesia, 2014. *Emerg Infect Dis* 2015;21:724–6.
- [5] Nhan TX, Musso D. The burden of Chikungunya in the Pacific. *Clin Microbiol Infect* 2015;21:e47–8.
- [6] Leparac-Goffart I, Nougairède A, Cassadou S, *et al.* Chikungunya in the Americas. *Lancet* 2014;383:514.
- [7] Venturi G, De Luca M, Fortuna C, *et al.* Detection of a Chikungunya outbreak in Central Italy, August to September 2017. *Eur Surveill* 2017;22:39.
- [8] Bettis AA, L’Azou Jackson M, Yoon I-K, *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.
- [9] Pastula DM, Hancock WT, Bel M, *et al.* Chikungunya virus disease outbreak in Yap State, Federated States of Micronesia. *PLoS Negl Trop Dis* 2017;11:e0005410.
- [10] Aubry M, Teissier A, Huart M, *et al.* Seroprevalence of dengue and Chikungunya virus antibodies, French Polynesia, 2014–2015. *Emerg Infect Dis* 2018;24:558–61.
- [11] Vairo F, Haider N, Kock R, *et al.* Chikungunya: epidemiology, pathogenesis, clinical features, management, and prevention. *Infect Dis Clin North Am* 2019;33:1003–25.
- [12] Vairo F, Aimè Coussoud-Mavoungou MP, Ntoumi F, *et al.* On Behalf Of The Pandora-Id-Net Consortium Chikungunya Outbreak Group Taskforce. Chikungunya Outbreak in the Republic of the Congo, 2019-Epidemiological, Virological and Entomological Findings of a South-North Multidisciplinary Taskforce Investigation. *Viruses* 2020;12:1020.
- [13] European Centre for Disease Prevention and Control. Chikungunya worldwide overview and situation report 2023. <https://www.ecdc.europa.eu/en/chikungunya-monthly>
- [14] Selhorst P, Makiala-Mandanda S, De Smet B, *et al.* Molecular characterization of Chikungunya virus during the 2019 outbreak in the Democratic Republic of the Congo. *Emerg Microbes Infect* 2020;9:1–25.
- [15] Bower H, el Karsany M, Adam AAAH, *et al.* “Kankasha” in Kassala: A prospective observational cohort study of the clinical characteristics, epidemiology, genetic origin, and chronic impact of the 2018 epidemic of Chikungunya virus infection in Kassala, Sudan. *PLoS Negl Trop Dis* 2021;15:e0009387.
- [16] PAHO/WHO. Epidemiological Alert Increase in cases and deaths from chikungunya in the Region of the Americas (2023) <https://www3.paho.org/data/index.php/en/mnu-topics/chikv-en/550-chikv-weekly-en.html>
- [17] National Center for Vector Borne Diseases Control (NCVBDC). Chikungunya situation in India 2017–2022. <https://ncvbdc.mohfw.gov.in/index4.php?lang=1&level=0&linkid=486&lid=3765>
- [18] Adam A, Jassoy C. Epidemiology and laboratory diagnostics of dengue, yellow fever, zika, and Chikungunya virus infections in Africa. *Pathogens* 2021;10:1324.
- [19] Moyon N, Thiberville S-D, Pastorino B, *et al.* First reported Chikungunya fever outbreak in the Republic of Congo, 2011. *PLoS ONE* 2014; 9: e115938.
- [20] Schilte C, Staikowsky F, Couderc T, *et al.* Chikungunya virus-associated long-term arthralgia: a 36-month prospective longitudinal study. *PLoS Negl Trop Dis* 2013;7:e2137.
- [21] Goupil BA, Mores CN. A review of Chikungunya virus-induced arthralgia: clinical manifestations, therapeutics, and pathogenesis. *Open Rheumatol J* 2016;10:129–40.
- [22] Russo G, Subissi L, Rezza G. Chikungunya fever in Africa: a systematic review. *Pathog Glob Health* 2020;114:136–44.
- [23] Tritsch SR, Encinales L, Pacheco N, *et al.* Chronic joint pain 3 years after Chikungunya virus infection largely characterized by relapsing-remitting symptoms. *J Rheumatol* 2020;47:1267–4.
- [24] Nyamwaya DK, Otiende M, Omuoyo DO, *et al.* Endemic Chikungunya fever in Kenyan children: a prospective cohort study. *BMC Infect Dis* 2021;21:186.
- [25] Althouse BM, Guerbois M, Cummings DAT, *et al.* Role of monkeys in the sylvatic cycle of Chikungunya virus in Senegal. *Nat Commun* 2018;9:1046.
- [26] Eastwood G, Sang RC, Guerbois M, *et al.* Enzootic circulation of Chikungunya virus in East Africa: serological evidence in non-human Kenyan primates. *Am J Trop Med Hyg* 2017;97:1399–404.
- [27] Weaver SC, Lecuit M. Chikungunya virus and the global spread of a mosquito-borne disease. *N Engl J Med* 2015;372:1231–9.
- [28] Wahid B, Ali A, Rafique S, *et al.* Global expansion of Chikungunya virus: mapping the 64-year history. *Int J Infect Dis* 2017;58:69–76.
- [29] Voss JE, Vaney MC, Duquerroy S, *et al.* Glycoprotein organization of Chikungunya virus particles revealed by X-ray crystallography. *Nature* 2010;468:709–12.

- [30] Rezza G, Weaver SC. Chikungunya as a paradigm for emerging viral diseases: evaluating disease impact and hurdles to vaccine development. *PLoS Negl Trop Dis* 2019;13:e0006919.
- [31] Gouglas D, Thanh Le T, Henderson K, *et al.* Estimating the cost of vaccine development against epidemic infectious diseases: a cost minimisation study. *Lancet Glob Health* 2018;6:e1386–96.
- [32] Halstead SB. Reappearance of Chikungunya, formerly called dengue, in the Americas. *Emerg Infect Dis* 2015;21:557–61.
- [33] Pan American Health Organization [PAHO/WHO]. Chikungunya [Internet]. 2022 Jul 6. <underline><https://www.paho.org/en/topics/chikungunya></underline>.</p>
</p>
<div data-bbox="60 198 479 221" data-label="Text">
<p>[34] Petersen LR, Powers AM. Chikungunya: epidemiology. *F1000Res* 2016;5:82.</p>
</div>
<div data-bbox="60 221 479 244" data-label="Text">
<p>[35] Powers AM, Logue CH. Changing patterns of Chikungunya virus: re-emergence of a zoonotic arbovirus. *J Gen Virol* 2007;88(Pt 9):2363–77.</p>
</div>
<div data-bbox="60 244 479 277" data-label="Text">
<p>[36] Waggoner J, Brichard J, Mutuku F, *et al.* Malaria and Chikungunya detected using molecular diagnostics among Febrile Kenyan Children. *Open Forum Infect Dis* 2017;4:ofx110.</p>
</div>
<div data-bbox="60 277 479 311" data-label="Text">
<p>[37] Sadiq Safi ur Rehman, Eneh Stanley C, Nazir Abubakar, *et al.* Tackling Chikungunya and dengue crisis in Paraguay amidst COVID-19: an epidemiological alert—a correspondence. *Int J Surg* 2023;109:624–5.</p>
</div>
<div data-bbox="60 311 479 345" data-label="Text">
<p>[38] Pastorino B, Muyembe-Tamfum JJ, Bessaud M, *et al.* Epidemic resurgence of Chikungunya virus in democratic Republic of the Congo: identification of a new central African strain. *J Med Virol* 2004;74:277–82.</p>
</div>
<div data-bbox="60 345 479 390" data-label="Text">
<p>[39] Makiiala-Mandanda S, Ahuka-Mundeké S, Abbate JL, *et al.* Identification of dengue and Chikungunya cases among suspected cases of yellow fever in the Democratic Republic of the Congo. *Vector Borne Zoonotic Dis* (Larchmont, NY) 2018;18:364–70.</p>
</div>
<div data-bbox="60 390 479 413" data-label="Text">
<p>[40] Collao X, Negrodo AI, Cano J, *et al.* Different lineages of Chikungunya virus in Equatorial Guinea in 2002 and 2006. *Am J Trop Med Hyg* 2010;82:505–7.</p>
</div>
<div data-bbox="60 413 479 447" data-label="Text">
<p>[41] Gould LH, Osman MS, Farnon EC, *et al.* An outbreak of yellow fever with concurrent Chikungunya virus transmission in South Kordofan, Sudan, 2005. *Trans R Soc Trop Med Hyg* 2008;102:1247–54.</p>
</div>
<div data-bbox="60 447 479 481" data-label="Text">
<p>[42] World Health Organization [WHO]. Chikungunya in La Réunion (France), Mayotte, Maurice, Seychelles and India. 2006 https://www.who.int/emergencies/disease-outbreak-news/item/2006_03_17-en</p>
</div>
<div data-bbox="60 481 479 515" data-label="Text">
<p>[43] Leroy EM, Nkoghe D, Ollomo B, *et al.* Concurrent Chikungunya and dengue virus infections during simultaneous outbreaks, Gabon, 2007. *Emerg Infect Dis* 2009;15:591–3.</p>
</div>
<div data-bbox="60 515 479 549" data-label="Text">
<p>[44] Zavala-Colon M A, Gonzalez-Sanchez J. History and geographic distribution of Chikungunya virus. In: Engohang-Ndong J, editor. *Chikungunya Virus - A Growing Global Public Health Threat*. IntechOpen; 2022.</p>
</div>
<div data-bbox="60 549 479 561" data-label="Text">
<p>[45] European Centre for disease prevention and control, June 2022.</p>
</div>
<div data-bbox="60 561 479 583" data-label="Text">
<p>[46] World Health Organization [WHO]<https://www.who.int/news-room/fact-sheets/detail/chikungunya></p>
</div>
<div data-bbox="60 583 479 605" data-label="Text">
<p>[47] Caglioti C, Lalle E, Castilletti C, *et al.* Chikungunya virus infection: an overview. *N Microbiol* 2013;36:211–27.</p>
</div>
<div data-bbox="60 605 479 639" data-label="Text">
<p>[48] Lumsden WH. An epidemic of virus disease in Southern Province, Tanganyika Territory, in 1952-53. II. General description and epidemiology. *Trans R Soc Trop Med Hyg* 1955;49:33–57.</p>
</div>
<div data-bbox="498 71 914 105" data-label="Text">
<p>[49] Centers for Disease Control and Prevention [CDC]. Transmission [Internet]. 2022 Jul 6. Available from: <https://www.cdc.gov/chikungunya/transmission/index.html></p>
</div>
<div data-bbox="498 105 914 139" data-label="Text">
<p>[50] Dubrulle M, Mousson L, Moutailler S, *et al.* Chikungunya virus and Aedes mosquitoes: saliva is infectious as soon as two days after oral infection. *PLoS One* 2009;4:e5895.</p>
</div>
<div data-bbox="498 139 914 162" data-label="Text">
<p>[51] Ng KW, Chow A, Win MK, *et al.* Clinical features and epidemiology of Chikungunya infection in Singapore. *Singapore Med J* 2009;50:785–90.</p>
</div>
<div data-bbox="498 162 914 207" data-label="Text">
<p>[52] Consuegra-Rodríguez MP, Hidalgo-Zambrano DM, Vásquez-Serna H, *et al.* Post-Chikungunya chronic inflammatory rheumatism: follow-up of cases after 1 year of infection in Tolima, Colombia. *Travel Med Infect Dis* 2018;21:62–8.</p>
</div>
<div data-bbox="498 207 914 241" data-label="Text">
<p>[53] Jain J, Okabayashi T, Kaur N, *et al.* Evaluation of an immunochromatography rapid diagnosis kit for detection of chikungunya virus antigen in India, a dengue-endemic country. *Virol J* 2018;15:84.</p>
</div>
<div data-bbox="498 241 914 275" data-label="Text">
<p>[54] Johnson BW, Russell BJ, Goodman CH. Laboratory diagnosis of chikungunya virus infections and commercial sources for diagnostic assays. *J Infect Dis* 2016;214(suppl 5):S471–4.</p>
</div>
<div data-bbox="498 275 914 309" data-label="Text">
<p>[55] Mello CDS, Cabral-Castro MJ, Faria LCS, *et al.* Use of cerebrospinal fluid for the diagnosis of neuroinvasive dengue, zika, and Chikungunya: a 19-year systematic review. *Rev Soc Bras Med Trop* 2021;54:e0891 2020.</p>
</div>
<div data-bbox="498 309 914 343" data-label="Text">
<p>[56] Rianthavorn P, Wuttirattanakowit N, Prianantathavorn K, *et al.* Evaluation of a rapid assay for detection of IgM antibodies to Chikungunya. *Southeast Asian J Trop Med Public Health* 2010;41:92–6.</p>
</div>
<div data-bbox="498 343 914 377" data-label="Text">
<p>[57] Harvard University Chikungunya Virus on the Move Special edition on infectious disease 2014 <https://sitn.hms.harvard.edu/flash/special-edition-on-infectious-disease/2014/chikungunya-virus-on-the-move/></p>
</div>
<div data-bbox="498 377 914 400" data-label="Text">
<p>[58] Devaux CA. Emerging and re-emerging viruses: a global challenge illustrated by Chikungunya virus outbreaks. *World J Virol* 2012;1:11–22.</p>
</div>
<div data-bbox="498 400 914 434" data-label="Text">
<p>[59] Schrauf Sabrina, Tschisnarov Roland, Tauber Erich, *et al.* Current efforts in the development of vaccines for the prevention of zika and Chikungunya virus infections. *Front Immunol* 2020;11:592.</p>
</div>
<div data-bbox="498 434 914 479" data-label="Text">
<p>[60] Oqbazgi Merhawi. “Treatment and prevention of Chikungunya fever: current status and prospective” in chikungunya virus: a growing global public health threat. Jean Engohang-Ndong. London: IntechOpen; 2021.</p>
</div>
<div data-bbox="498 479 914 502" data-label="Text">
<p>[61] Powers Ann M. Vaccine and Therapeutic options to control Chikungunya virus.. *Clin Microbiol Rev* 2017;31:e00104–16.</p>
</div>
<div data-bbox="498 502 914 536" data-label="Text">
<p>[62] Akahata W, Yang ZY, Andersen H, *et al.* A virus-like particle vaccine for epidemic chikungunya virus protects nonhuman primates against infection. *Nat Med* 2010;16:334–8.</p>
</div>
<div data-bbox="498 536 914 570" data-label="Text">
<p>[63] Metz SW, Geertsema C, Martina BE, *et al.* Functional processing and secretion of chikungunya virus E1 and E2 glycoproteins in insect cells. *Virol J* 2011;8:353.</p>
</div>
<div data-bbox="498 570 914 593" data-label="Text">
<p>[64] Ferraro B, Morrow MP, Hutnick NA, *et al.* Clinical applications of DNA vaccines: current progress. *Clin Infect Dis* 2011;53:296–302.</p>
</div>
<div data-bbox="498 593 914 616" data-label="Text">
<p>[65] World Health Organization [WHO]. Chikungunya – Kenya. 2016 <https://www.afro.who.int/news/chikungunya-kenya></p>
</div>
<div data-bbox="498 616 914 639" data-label="Text">
<p>[66] Sallberg M, Frelin L, Ahlen G, *et al.* Electroporation for therapeutic DNA vaccination in patients. *Med Microbiol Immunol* 2015;204:131–5.</p>
</div>
</div>
<div data-bbox="469 925 506 940" data-label="Page-Footer">3552</div>