World Health Organization

GLOBAL CHIKUNGUNYA EPIDEMIOLOGY UPDATE

JUNE 2025

Executive summary

Chikungunya virus (CHIKV) is a mosquito-borne virus primarily transmitted by *Aedes* mosquitoes. It causes acute illness characterized by fever, rash, and debilitating joint pain, with some patients experiencing long-term joint pain and disabilities. While the overall fatality rate is low, severe disease can occur, especially in vulnerable populations such as infants, the elderly, and those with pre-existing conditions.

The aim of this update is to provide a comprehensive overview of reported data on chikungunya virus globally. This update is based on data submitted by Member States' Ministries of Health to the World Health Organization (WHO) through various surveillance systems, as well as partner organizations that regularly review global CHIKV epidemiological data to identify areas at risk for CHIKV transmission. These data are summarized and contextualized in this first WHO epidemiologic update for chikungunya which will be updated periodically.

As of December 2024, 119 countries and territories have reported local transmission. High attack rates can lead to temporary interruption of transmission in small populations, but larger populations remain at risk due to ongoing susceptibility. Surveillance and diagnostic limitations hinder accurate global tracking, and underreporting is common. The potential for re-emergence remains high in previously affected areas.

Background

Chikungunya virus (CHIKV) is an enveloped, positive-sense, single-stranded RNA virus in the *Togaviridae* family, *Alphavirus* genus (*1*). CHIKV is transmitted primarily by *Aedes aegypti* mosquitoes; however, *Aedes albopictus* mosquitoes also transmit CHIKV, with particular importance in CHIKVs with specific genetic mutations that enhance transmission in this species (*2,3*). After an incubation period of 4-8 days following the bite of an infected mosquito, infection with CHIKV causes symptomatic illness in most infected people that is characterized in the acute phase by fever, joint pain, and rash. Joint pain and dysfunction may persist for months to years following infection. While overall case fatality rates associated with chikungunya virus infection are low, the disease can be severe and sometimes fatal, particularly in young infants, the elderly, and patients with certain underlying medical conditions, where cardiovascular, central nervous system, and dysfunction of other organs has been documented (*4*). In large outbreaks, although the proportion of severe disease cases remains low, the numbers of patients requiring higher levels of care including neonatal and adult intensive care can exceed the capacity of the health care system to provide the necessary medical management (*5*). CHIKV infections can be diagnosed by direct methods, including virus isolation and RNA detection through nucleic acid amplification testing, or through indirect methods measuring IgM antibody response to recent infection.

Serological cross-reactivity has been documented between CHIKV and related alphaviruses including Mayaro, O'nyong Nyong, and Ross River viruses; thus, in areas where related viruses circulate, cross-neutralization testing may be needed to identify the specific infecting virus if direct viral detection cannot be achieved.(*6*)

CHIKV was first identified in the United Republic of Tanzania in 1952 after which the virus was isolated sporadically and caused occasional outbreaks in Africa and Asia (*7*). The first recorded urban outbreaks occurred in Thailand in 1958, and then in several locations in India in the 1970s (*8,9*). The epidemiology of CHIKV transmission changed markedly in 2004, with accelerated geographic expansion following an outbreak in Kenya which soon spread to Indian Ocean Islands causing large outbreaks, including in urban settings. In December 2013, CHIKV was first detected in the Region of the Americas (Caribbean) and resulted in widespread circulation throughout what was an immunologically naïve population at the time (*10*).

Chikungunya population attack rates are typically high and because of this transmission may be interrupted in smaller island settings where a high proportion of the population is infected and subsequently immune. However, transmission often continues over time in larger populations where sufficient numbers of immunologically susceptible individuals continue to acquire infection and propagate further spread.

Genomic analysis of isolates collected over time and across transmission settings has greatly improved the understanding of CHIKV, which is assumed to have originated in Africa around 500 years ago. The CHIKV African lineage subsequently diverged into three genotypes namely, the West African, the East-Central-South African (ECSA), and the Asian genotypes(*11*). Within the ECSA lineage, an Indian Ocean sub-lineage (IOL) emerged and now appears sufficiently genetically divergent to be considered an independent fourth lineage. Globally, the ECSA and Asian genotypes currently predominate. Differences in the epidemic potential and pathogenicity of these viral lineages, as well as cross-protective immunity across lineages, remains poorly understood (*12*).

Global overview

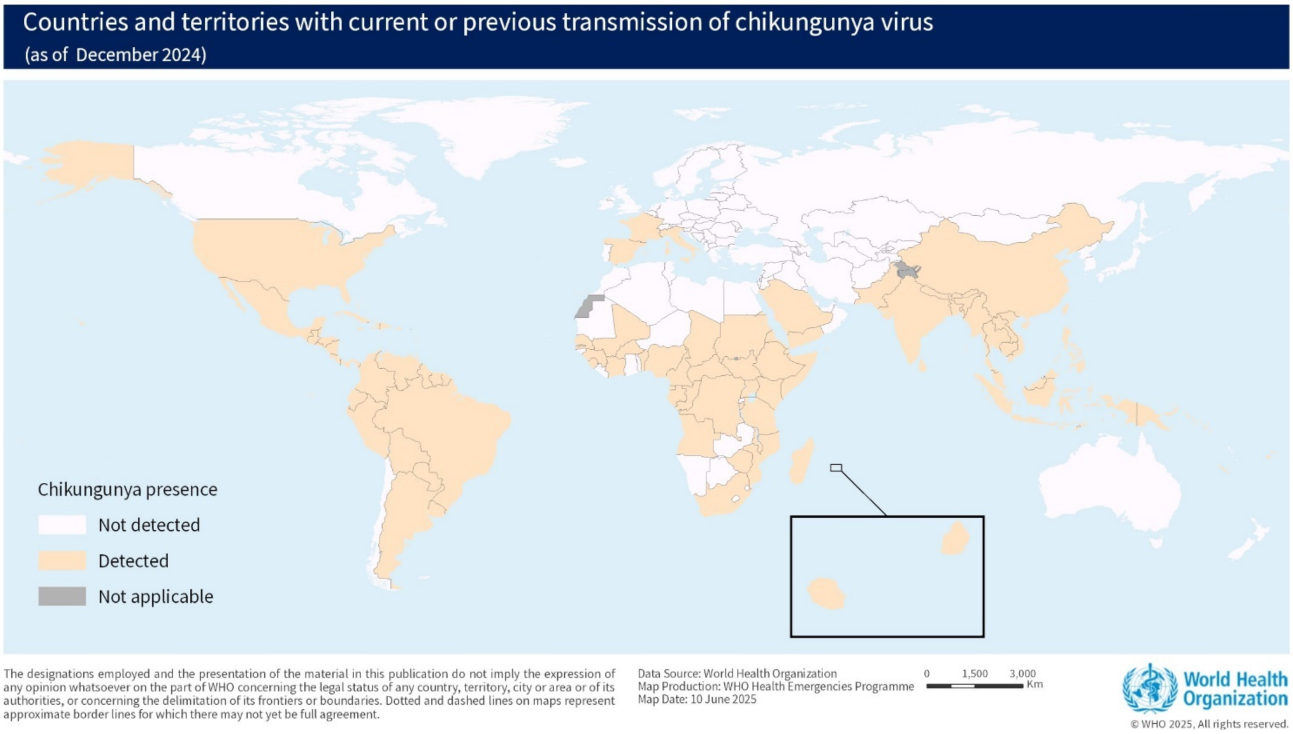
As of December 2024, a total of 119 countries and territories have had documented evidence of autochthonous mosquito-borne transmission of CHIKV (Figure 1), distributed across all six WHO Regions. Reviews of global chikungunya epidemiology have been published, including a review of reported chikungunya outbreaks and seroprevalence data prior to 2020 (*13*). However, accurate and timely global chikungunya epidemiologic data are limited as many countries lack or have limited capacity for routine surveillance, case detection, access to diagnostic tests, and reporting of CHIKV disease cases. Lack of reporting of CHIKV cases, therefore, cannot necessarily be equated with evidence that transmission is not occurring.

Globally, 27 countries and territories in six WHO regions have evidence of established and competent *Aedes aegypti* vector populations but have not yet documented autochthonous CHIKV transmission.[1] In addition, other countries have established populations of *Aedes albopictus*, which are competent to transmit CHIKV, particularly lineages with the IOL mutation increasing transmission efficiency. The presence of either of these vector populations poses an ongoing risk for CHIKV introduction and spread to previously unaffected countries or subnational areas. It is also possible that CHIKV transmission occurs, or has occurred, in some of these countries without being detected or reported. All areas with prior reports of CHIKV transmission have the potential for re-emergence or re-introduction, especially in large countries and territories where pockets of non-immune individuals remain susceptible.

WHO and partner public health agencies, including the European Centre for Disease Control and Prevention and the United States Centers for Disease Control and Prevention[1], regularly review global CHIKV epidemiological data to identify areas at risk for CHIKV transmission. These data are summarized and contextualized in this first WHO epidemiologic update for chikungunya.

The following sections summarize the background of CHIKV transmission in each of the WHO regions in previous decades and highlight countries where chikungunya outbreaks were documented and where autochthonous transmission was first recognized within the past five years (2020-2024).

Figure 1. Global map of countries with current or previous transmission of chikungunya virus



Regional overview

African Region

Overview

Although CHIKV virological identification and chikungunya clinical features and outbreaks were first described in Africa, understanding of more recent epidemiology of the disease in the Region is incomplete. Resource and capacity limitations in many countries hamper surveillance and quantification of CHIKV burden of disease, as well as understanding of the virus-specific immune

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[1] Meetings preceded January 2025

status of the populations where *Aedes* mosquitoes are established. After the initial identification of CHIKV in the Republic of Tanzania, autochthonous transmission was confirmed in several countries in the African Region through virus isolation and immunologic testing in the latter half of the 20th century (*11*). Limited chikungunya outbreaks and sporadic cases were recorded periodically over that time, often associated with spillover from reservoir hosts by mosquitoes incidentally feeding on humans in areas of sylvatic circulation. Serosurveys were also conducted but often lacked laboratory testing to exclude serological responses to infection with O'nyong-Nyong virus, a related alphavirus.

A marked increase in the scale and rapidity of transmission was first observed during an outbreak in Kenya in 2004, which spread to Indian Ocean islands; the largest outbreak occurred on La Reunion from 2005-2006, with an estimated 244,000 infections (*14*). The intensity of the outbreak prompted research which identified viral mutations, notably the A226V point mutation, that enabled more efficient transmission by *Aedes albopictus* mosquitoes and was of particular importance in islands where the species was the dominant mosquito vector, or *Aedes aegypti* was not known to be established. To date, autochthonous CHIKV transmission has been documented in 32 countries in the region. In most outbreaks where genomic sequencing data were published, ECSA was the circulating CHIKV genotype and the West African genotype (**Table**) (*13,15,16*).

In December 2018, an outbreak of chikungunya occurred in six sub-counties of Mombasa County of Kenya, where no prior laboratory confirmed chikungunya cases had been reported (*17*). In Cameroon, sporadic outbreaks have occurred since 2006, and recently, researchers conducting a retrospective study of specimens collected from 2016 to 2019 identified an ECSA subclade that they termed the "Central African clade", which demonstrated the A226V mutation (*18*). In the Republic of Congo in 2019, a large chikungunya outbreak with >11 000 cases involved at least eight of the twelve health departments (44 out of 52 health districts) and genomic sequencing during the investigation confirmed an A226V substitution in the ECSA lineage CHIKV (*19,20*) and that the virus was closely related to a CHIKV previously isolated in Central Africa.(*21*) With the additional finding of predominantly *Aedes albopictus* mosquitoes in the outbreak area, investigators concluded there was likely a recent vector-host switch from a CHIKV strain previously circulating in *Aedes aegypti,* to the related CHIKV with the A226V mutation which was primarily transmitted by *Aedes albopictus*. In some countries, there is evidence suggesting a stable endemic pattern of CHIKV transmission (*22*); however, in other countries cases have not been reported for several decades (South Africa, for example, last recorded autochthonous transmission in the late 1970s).

In the period 2020-2024, though not reporting outbreaks, sporadic cases were reported in some countries in the African Region. In 2021 CHIKV infection was confirmed by RT-PCR in one out of 1,060 serum specimens collected from febrile patients in Lambaréné, Gabon, from a 6-year-old male from Sindara (*23*). The viral genome sequence was consistent with the ECSA lineage, in the same group as earlier isolates from Gabon (2007) and Cameroon (2018), which both demonstrated the E1- A226V mutation.

Countries with chikungunya outbreaks and countries with first recognition of autochthonous transmission in the African Region, 2020-2024

Chad, 2020

A chikungunya outbreak that was first detected in July 2020 resulted in more than 38,000 cases in the eastern part of the country (*24*). Testing by reverse transcription polymerase chain reaction (RT-PCR) confirmed CHIKV infection in a subset of samples at both local and reference laboratories; sequencing was performed on two samples at the reference laboratory and confirmed the virus was of the ECSA lineage but without the E1-A226V mutation.(*25*)

Kenya, 2022

Chikungunya cases were reported from mid-February 2022 in Wajir County, with subsequent identification of additional cases during an epidemiological investigation. By December 2022, a cumulative total of 291 cases, 5 of which were laboratory-confirmed, and one death were reported (*26*).

Ethiopia 2022

Following first reported chikungunya outbreak in Ethiopia in 2016, the country reported outbreaks in both 2019 and 2022. From July 2019 to February 2020, 54 908 chikungunya cases were reported (29 confirmed) 51,957 of which occurred in Dire Dawa Administrative City, and cases were also reported from Araf (N=2,782) and Somali (N=169) regions.(*20,27*) Chikungunya outbreak activity was again detected in 2022 in Somali region, with 311 suspected cases reported (three confirmed) as of March 2022 (*28*).

Burkina Faso, 2023

The first documented outbreak of CHIKV in Burkina Faso occurred in 2023; initial cases were detected during multiplex RT-PCR testing of specimens collected from patients with suspected dengue fever during a concurrent dengue outbreak. In total, 311 confirmed cases were reported(*29*). Prior to 2023, evidence of chikungunya transmission in Burkina Faso was limited to viral isolation from a mosquito pool in 1984 and demonstration of seroprevalence, and acute serological response to infection in two separate studies (*29–31*).

The Gambia, 2023

The first autochthonous chikungunya case was confirmed in the Gambia in a patient with illness onset in August 2023; a blood specimen yielded detectable RNA by RT-PCR testing at the National and Regional reference laboratories (*32,33*). The patient lived in the Central River Region and during field investigations, additional specimens were collected from household members but tested negative. Indoor Residual Spraying was already underway in the region for malaria control. As part of active surveillance efforts, chikungunya case definitions were distributed to all healthcare facilities in the country, but no further cases were reported.

Mali, 2023

In September 2023, health authorities reported two suspect cases of chikungunya, one of which was confirmed as CHIKV infection (*32*). Subsequently, four additional suspect cases were identified in Bamako and Kayes health districts.

Senegal, 2023-2024

In August 2023, initial cases of chikungunya were reported from the Kedougou region of Senegal and subsequent expansion of the outbreak to involve six regions (*34*). By December 2023, over 280 cases were confirmed, with the Kedougou and Tambacounda regions accounting for the highest number of cases overall. The CHIKV genome was sequenced and identified as an emerging West African lineage virus, which is typically transmitted by *Aedes aegypti.* Sequencing also highlighted possible under-detection of cases using molecular assays validated only for ECSA lineage viruses (*35,36*). In 2024, a total of nine chikungunya cases were reported in Senegal (*37*).

Côte d'Ivoire, 2023-2024

Chikungunya virus was detected in mosquitoes in Côte d'Ivoire in 1981 and 1993, and cases were identified in travellers returning from Côte d'Ivoire from 1997 to 2022 (*38,39*). In 2023-2024, CHIKV infections were confirmed in 12 French travelers returning from Côte d'Ivoire, with some reporting illness while in country and others upon their return to metropolitan France (*39,40*). Infection was confirmed by RT-PCR testing in nine patients and by serology in three; specimens from seven patients were sequenced and found to be consistent with the West African lineage virus but distinct from the viruses previously isolated in the country.

Mauritius, 2025

Since March 2025, and as of 1 April, a total of 23 confirmed cases of chikungunya were reported, including 17 autochthonous cases and six cases imported from La Réunion (*41*).

Region of the Americas

Overview

Transmission of CHIKV was first detected in the Americas on the French side of the Caribbean island of Saint Martin in December of 2013 (*42*). This was followed by rapid epidemic spread of CHIKV across most of the countries in the region, with cases peaking during 2014-2015 with about 1.8 million suspect chikungunya cases reported. Since the time of CHIKV regional introduction, the Pan American Health Organization/WHO Regional Office for the Americas (PAHO) has collected data on reported cases either transmitted to PAHO by countries and territories directly, or PAHO extracts the data from publicly posted epidemiological data posted on Ministry of Health websites. The data are collated and made publicly available through the Health Information Platform for the Americas/ Plataforma de Información en Salud para las Américas (PLISA) (*43*). PAHO continues to work with member states and territories to systematize and strengthen arbovirus surveillance and reporting by increasing access to diagnostic assays, training clinicians, and providing virtual collaboration spaces shared by countries or territories and the PAHO regional surveillance support team (*44*).

Annual case totals declined to less than 186 000 per year from 2018 to 2021, followed by successive annual increases to a peak of 411 548 in 2023 (*45–47*). Chikungunya cases are reported annually from around 15 countries, and a marked increase in reported cases occurred in late 2022 and early 2023 in at least five countries in the region, mirroring increased dengue incidence trends over the same period (*48*). In 2023 a cumulative total of 411 548 chikungunya cases, including 515 deaths were reported to PAHO with earlier peaks in transmission within countries and territories, rapid expansion and distribution of cases in Paraguay in previously unaffected areas, and reemergence of local transmission in Argentina (*47,49*). In 2024, 427 622 chikungunya cases were reported, exceeding the record total from the previous year, but with a reduction in the number of deaths to 213.

Outbreaks in the Region of the Americas 2020-2024

Brazil, 2020-2024

Brazil typically reports the highest number of CHIKV cases in the Region annually and both the Asian and ECSA lineages have circulated in the country (*50*). From 2018-2023, Brazil reported between 87 687 (68 962 confirmed) and 266 297 (154 659 confirmed) cases annually and until the end of 2022, it was the only country in the Americas that reported any chikungunya fatalities, ranging from 12-218 per year and with case fatality rates from <0.04% to 0.08%, largely attributable to the high case numbers. In 2024 a total of 422 615 chikungunya cases were reported, 227 619 of which were confirmed, for a cumulative incidence of 199 per 100 000 population.

Uruguay, 2023

In 2023 Uruguay reported the first documented autochthonous chikungunya cases with 85 confirmed cases reported for the year. *Aedes aegypti* mosquitoes are present in the country but *Aedes*-borne arbovirus infections have been rare, with only limited dengue and no prior Zika cases (*51*).

Paraguay, 2022-2024

From late 2022, Paraguay reported increasing numbers of CHIKV disease cases compared with previous years, with rapid escalation over the first quarter of 2023 totaling 140 905 cases (cumulative incidence 1,865 per 100,000 population) and 297 deaths by the end of that year (*46*). Sequencing demonstrated that ECSA was the circulating genotype, which was first identified in the country in 2018 and did not contain the E1-A226V mutation (*52*). Transmission continued into 2024 but at much lower levels with a cumulative total of 3 134 cases and no deaths during the year.

Argentina, 2023-2024

In 2023 Argentina reported the first autochthonous CHIKV transmission since 2016 and the first documented local transmission in Buenos Aires province (*47,53*) Cases subsequently increased in 2023 in other provinces throughout the season to a total of 1 746 confirmed cases. In 2024, the cumulative number of reported cases decreased to 768 (*46*).

Eastern Mediterranean Region

Chikungunya transmission in the Region was suggested by findings of serological surveys and Pakistan in 1983, and the first human case documented in in Lahore during a dengue outbreak in 2011. The first recognized outbreak in the Region occurred in Yemen in 2010-2011; CHIKV infection was confirmed by RT-PCR testing in 55 patient samples and by the end of the outbreak >15,000 suspected cases were reported, including 104 deaths (*54*). Sequencing of the viral RNA from isolates showed a high degree of similarity with the Indian Ocean sublineage. Chikungunya outbreaks have since been reported in Djibouti, Pakistan, Saudi Arabia, Somalia and Sudan, and intercurrent sporadic cases in Saudi Arabia and Sudan (*55*). The outbreak in Pakistan in 2016-2017 involved over 8000 cases and affected multiple provinces. A large outbreak occurred in the eastern states of Sudan in 2018-2019, with 48,763 cases reported by the end of the outbreak (*56*). In 2019, a chikungunya outbreak occurred in Djibouti with CHIKV infection confirmed by RT-PCR in 57 members of the French Defense Community stationed in Djibouti City (*57*).

Serosurveys in other countries in the Eastern Mediterranean Region have yielded seropositive results suggesting transmission; however, confirmatory evidence of acute infection has been lacking. Imported chikungunya cases have been reported in Oman (*55*) which is common in travellers to outbreak affected areas within the Region. It is likely that the true burden of chikungunya in the Eastern Mediterranean Region is under-reported due to limited national capacities for detection and confirmation, which can result in missed or delayed case identification.

Outbreaks in the Eastern Mediterranean Region, 2020–2024

Sudan 2022

After its largest outbreak in the eastern states in 2018, only sporadic cases were reported in Sudan until the occurrence of a small outbreak of chikungunya occurred in the White Nile State from October to December 2022, coinciding with an outbreak of dengue (*58*). Of 773 suspected arboviral disease cases, 49 were confirmed with CHIKV infection.

Pakistan 2024

In 2024, increased transmission of chikungunya was reported in Karachi starting in May and continuing throughout the year, with a cumulative total of 5,726 suspected cases reported as of mid-December (*59–61*) The last large outbreak in the country had occurred in 2016 with approximated 30,000 suspected cases and 4000 confirmed by RT-PCR (*62*).

European Region

Since 2007, autochthonous, mosquito-borne transmission of CHIKV has been reported in mainland Europe on six occasions since 2007, all occurring in Italy and France (*63*). The largest of these outbreaks occurred in Italy in 2007 with 334 suspected and probable case, of which 204 were confirmed with CHIKV infection by RT-PCR (*64,65*). Transmission has been driven by *Aedes albopictus* mosquitoes that are established in the southern and central parts of mainland EU and are expanding in their geographic distribution (*66*). To maintain vigilance about areas at risk for introduction and autochthonous transmission of CHIKV and other mosquito-borne arboviruses, the distribution of mosquito vectors in the European region is regularly updated *(58)*.

In July 2024, a single autochthonous case of chikungunya was reported in Paris, with potential exposure in Paris or Gennevilliers in a person with no history of travel to an area with CHIKV transmission (*67*).

Outbreaks in the Indian Ocean French territories, 2020–2024

In the Indian Ocean French territories, chikungunya previously circulated on the islands of La Reunion and Mayotte, with widespread outbreaks in 2005-2006(*14,68*).

La Réunion, 2024-2025

In August 2024, France reported that 118 cases of autochthonous chikungunya from the island of La Réunion from September to December, across five active clusters on the west and south of the island (*69*). This was the first detected autochthonous CHIKV transmission on the island since it was last documented in 2014. Transmission continued into 2025, and as of 16 March 2025 over 13000 cases have been reported since the outbreak began (*70*).

Mayotte, 2025

In March 2025, following two reports of an imported chikungunya cases from La Réunion, the Mayotte Regional Health Agency confirmed the first autochthonous chikungunya case on the island (*71*).

South-East Asia Region

CHIKV has been circulating since at least the 1960s in the South-East Asia Region and all countries with established *Aedes* mosquito vectors have reported autochthonous mosquito-borne transmission. Outbreaks have been reported from Bangladesh, Bhutan, India, Indonesia, Maldives, Myanmar, Nepal, Sri Lanka and Thailand.(*72–75*) CHIKV strains isolated in India during an outbreak in 2006, as well as in other countries in the Region experiencing subsequent outbreaks, were closely related to Indian Ocean sublineage strains isolated the same year from La Réunion; however, all three of the IOL, Asian and ECSA lineages are have been circulating in South Asia in recent decades (*76*). The region remains at risk for CHIKV transmission because of the presence of competent vectors, often in high densities. Chikungunya transmission in Nepal was first identified in 2013, with frequent occurrence in subsequent years, including suspected transmission during a dengue outbreak in 2022 (*75*).

Outbreaks in the South-East Asia Region, 2020–2024

Thailand 2020

Chikungunya is endemic in Thailand and sporadic outbreaks are reported. In 2018-2020, Thailand experienced a large outbreak of more than 27,000 chikungunya cases, with cases reported in 60 provinces through the country (*77*). Although the earliest documented chikungunya outbreaks in Thailand were caused by the Asian lineage CHIKV, more recent epidemics since 2008 were caused by ECSA lineage CHIKV. Similarly, the CHIKV sequenced in the 2018-2020 outbreak was of the ECSA lineage but was clustered with a CHIKV circulating in South Asia and bearing mutations that enhanced fitness in *Aedes aegypti* (*78*).

India 2020-2024

India has historically reported numerous CHIKV outbreaks since the 1960s. The MoH website includes data on suspected and confirmed chikungunya cases; from 2018 to 2020 annual cumulative case totals ranged from 43,424 to 81,914 cases and the proportion of those that were laboratory confirmed ranged from 15-17% (*79*). From 2021 to 2023, there were over 115,000 suspected cases each year, 4-10% of which were laboratory confirmed (*80,81*) As of 31 December 2024, the MoH has publicly reported 192,343 suspect chikungunya cases on their surveillance web page, of which 12,587 (7%) were laboratory-confirmed.

Indonesia 2023-2024

Chikungunya is considered to be endemic in Indonesia, with sporadic outbreaks being reported. In 2022 there were 2,974 cases reported and a case series was published including confirmed chikungunya in four travellers returning to their home countries from Bali (*82*). In 2023 Indonesia reported 6,049 chikungunya cases, representing an important increase compared to previous year; data on chikungunya cases came from 29 provinces, compared to only five provinces in 2022 (*83*). Indonesia reported a total of 571 chikungunya cases in 7 provinces in 2024 (reference pending at https://kemkes.go.id/id/category-download/profil-kesehatan if available before posting).

Timor Leste 2024

In early 2024 the MoH reported an outbreak of chikungunya in the country that had last reported transmission two decades earlier, although probable or confirmed cases in travellers with infection acquired in the country had been reported in the intervening years (*84,85*). A total of 195 cases of chikungunya were diagnosed using investigational RT-PCR tests on specimens from patients with clinically compatible febrile arthralgia. Testing was limited by reagent availability precluding assessment of trends in chikungunya incidence over time.

Maldives 2024

In 2024, there was a sharp increase in cases noted in April compared to the first three months of the year, reaching a cumulative total of 389 cases by the end of April (*86*). This country had last experienced a chikungunya outbreak in 2019, when 1,736 cases were reported (*87*).

Bangladesh 2024

Chikungunya first emerged in Bangladesh in 2008, with significant outbreaks recorded in subsequent years(*72*). Following the last major outbreak in 2017 with over 2 million suspected cases, chikungunya outbreak activity concurrent with dengue and Zika virus transmission was noted in 2024, with PCR confirmation of infection in 55 patients from September to November in one study, and 67 cases reported by the Bangladesh Institute of Epidemiology, Disease Control and Research for the year (*88,89*).

Sri Lanka 2024-2025

After a large chikungunya outbreak in 2006, Sri Lanka has recorded intermittent cases and outbreaks. Between November 2024 and March 2025, increased transmission was noted with 151 chikungunya cases reported from health care centres serving as sentinel sites in Colombo, Gampaha and Kandy Sri Lanka (*90*).

Western Pacific Region

Although serosurveys suggested presence of CHIKV immunity in Malaysia in 1958, CHIKV was first confirmed in the Region in Singapore in 1960 and Cambodia in 1961 (*74,91*).

Clusters of infection had been reported in various countries since the 1960s but larger epidemics were uncommon before 2000. In the Western Pacific Region, large chikungunya outbreaks have been reported in the Philippines and Cambodia (*92*,*93*). Chikungunya outbreaks also occurred in Malaysia in 1998-1999 and 2006, followed by low level transmission with <100 cases reported from 2019 onwards; in 2024, as of September, a total of 72 cases were reported by the MoH (*94*,*95*).

Small CHIKV outbreaks have been reported in China, specifically in Guangdong, Zhejiang and Yunnan Provinces where *Aedes albopictus*, but not *Aedes aegypti*, were present (*96–98*). In 2017 a small autochthonous cluster of three cases was identified with sequencing consistent with the IOL lineage of the ECSA genotype and suspected importation from Bangladesh. In Lao People's Democratic Republic, an outbreak of chikungunya occurred in 2012-2013 and since that time imported and sporadic autochthonous chikungunya cases have been documented, with genomic identification of the presence of different CHIKV lineages, representing geographically disparate sources of introduction (*99*). A cross-sectional serosurvey conducted in 2015 in four provinces in central and south Viet Nam found evidence of prior CHIKV exposure in 13% of participants overall; however, the age-stratified seroprevalence suggested that the last transmission of CHIKV ended around 30 years earlier (*100*). A 2017 study of mosquitoes in areas of Viet Nam that bordered on Cambodia detected CHIKV in two *Aedes aegypti* mosquitoes and a study of cord blood plasma samples from neonates in central Vietnam in 2017-2018 identified CHIKV infections by RT-PCR and by IgM with confirmatory neutralizing antibody testing (*101,102*). Data on recent transmission in Viet Nam appear to be lacking, despite transmission of CHIKV in neighbouring Cambodia (*103*).

Among the Pacific Island countries, the first recorded CHIKV transmission occurred in New Caledonia in 2011 (*104*). Large chikungunya outbreaks have occurred since then, including in Papua-New Guinea, French Polynesia, the Federated States of Micronesia, Fiji, New Caledonia, American Samoa, Samoa, Tokelau, Tonga, Cook Islands, Kiribati, Marshall Islands, Nauru and Tuvalu (*91,105,106*).

In general, information on the incidence and trends of CHIKV transmission in the Region remains limited since surveillance is focused on dengue-like illness surveillance, given the significant historical and current burden of DENV disease in the region.

Outbreaks in the Western Pacific Region 2020-2024

Cambodia 2020-2021

In 2020-2021, a large CHIKV outbreak occurred in Cambodia that affected multiple provinces; the last outbreak prior to that occurred in 2012 (*92,107*). In an ongoing cross-sectional study of undifferentiated febrile illness cases, chikungunya virus infections were confirmed in 331 of 1194 blood samples tested. The sites with the highest proportions of laboratory-confirmed infections were in the urban areas in Kandal province (adjacent to Phnom Penh) and in the predominantly rural Kratie province, bordering Viet Nam.

Malaysia 2020-2021

Since 2019, eleven years after the previous chikungunya outbreak, an increase in chikungunya cases was reported; over 2000 cases were reported mainly in the states bordering Thailand in 2020, and expansion across the Peninsular Malaysia in 2021 (*108*). Smaller case numbers continue to be reported annually and as of October 2024, the Malaysia MoH had reported 80 chikungunya cases for the year (*109*).

Philippines 2023

In 2023, the Philippines Ministry of Health reported an outbreak of chikungunya in Paracelis Mountain Province with nine barangays affected (*110*). Overall, the country recorded a threefold increase in annual chikungunya case numbers from <600 cases in 2022 to 2,889 cases as of 2 December 2023, with the highest numbers reported from the Cordillera Administrative region (*111*).

Summary

Chikungunya is a clinically and epidemiologically important arbovirus, with widespread distribution globally and intercurrent outbreaks in many countries in recent years. The public health impact of chikungunya outbreaks is associated with both the high incidence of symptomatic illness including disabling arthritis and arthralgia (which may be prolonged for months to years in some patients), and the strain on health services. Although the proportion of cases that develop severe disease is typically <0.1%, the scale of outbreaks and the need for specialized in-patient care for patients with organ dysfunction, such as infected neonates, can place substantial strain on hospitals in low-resourced settings(*5*).

Factors associated with increased CHIKV transmission include:

- vector expansion associated with climate change and periodic extreme events is expanding the range of *Aedes* mosquitoes, increasing the geographic range with transmission potential;
- unplanned urbanization and poor water management contribute to vector reproduction and persistent transmission cycles;
- political instability and conflict in countries at risk, such as Yemen, Sudan, and Somalia face exacerbated public health challenges include disruption of healthcare infrastructure hampering case detection and outbreak response;
- increased travel to and from endemic regions introducing cases into areas with vectors may not be captured in national surveillance reports, particularly in low-resource countries.

Countries vary in their capacity to detect and report chikungunya and other vector-borne diseases, and outbreaks are often reported retrospectively, meaning real-time epidemiological data necessary for public health response is lacking. Improved surveillance and epidemiologic investigations are needed to better ascertain the incidence of CHIKV infection and to target risk communication and vector surveillance and control strategies. Transmission is probably occurring in countries where laboratory testing for CHIKV infections is not performed, and cases are thus not reported. In addition, because surveillance systems frequently focus on dengue rather than other *Aedes*-borne arboviruses that may be circulating, cases are clinically misdiagnosed and misreported as dengue. Although many countries have acquired the capacity to perform RT-PCR testing in recent years, the availability of reagents for chikungunya testing is limited and costs may be prohibitive. Serology is generally cheaper and more accessible but, in some regions, serological tests can cross-react with other alphaviruses and produce false positives test results.

Preparedness and response to outbreaks in most settings relies on vector surveillance and control, and personal protective measures to prevent infected mosquito bites. Considering that the level of vector control remains suboptimal albeit with variations across regions, there is need to unlock efficiencies by strengthening integrated entomological surveillance and vector control across diseases. Particular attention should be paid to populations at risk for severe disease, for example, during the 2023 chikungunya outbreak in Paraguay, health authorities observed that neonates and young infants could develop severe disease not only when infected intrapartum from viremic mothers, but also through early post-partum mosquito-borne transmission and thus should also be protected from mosquito bites (*5*). It is important to include measures for appropriate clinical detection and management as well as preparing health services for surges in case counts. To date, one live attenuated chikungunya vaccine has received approvals for use from several international regulatory agencies and other vaccine candidates are in various stages of development and evaluation (*112*). However, the vaccine is not widely available and has not been assessed for deployment in emergencies.

WHO remains committed to strengthening public health systems for early detection and response to emergence, re-emergence, and global spread of CHIKV and other *Aedes*-borne arbovirus infections, including monitoring for complications of CHIKV infection such as severe disease which is more common in patients with underlying morbidities and among those at the extremes of age i.e., neonates and elderly people.

In 2022, WHO launched the Global Arbovirus Initiative to address arboviral threats through an integrated and coordinated approach, convening both governmental and non-governmental multisectoral partners (health, urban administration, environment) and building on existing disease-specific programmes to strengthen national integrated arbovirus preparedness and response (*113*). In addition, the Global Strategic Preparedness, Readiness and Response Plan (SPRP) to tackle dengue and other *Aedes*-borne arboviruses aims to reduce the burden of disease, suffering and death from dengue and other *Aedes*-borne arboviral diseases such as Zika and chikungunya, by fostering a global coordinated response (*114*). Aligned with the principles laid out in the Initiative and SPRP, WHO continues to work with regional and national health authorities to enhance health system capacity to detect, report, and respond to the continued threat of CHIKV transmission, as well as to other *Aedes*-borne arboviruses and other emerging and re-emerging threats to public health.

Additional information can be accessed on the WHO website:

- Chikungunya information for travelers
- See map Countries and territories with current or prior CHIKV transmission
- See list Countries and territories with current or prior CHIKV transmission

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Countries and territories with current or previous chikungunya virus transmission by WHO regional office

WHO Regional Office	Country / territory	Total
AFRO	Angola; Benin; Burkina Faso; Burundi; Cameroon; Central African Republic; Chad; Comoros; Congo; Côte d'Ivoire; Democratic Republic of the Congo; Equatorial Guinea; Eritrea; Ethiopia; Gabon; Guinea; Gambia; Kenya; Madagascar; Malawi; Mali; Mauritius; Mayotte; Mozambique; Nigeria; Réunion; Senegal; Seychelles; Sierra Leone; South Africa; Uganda; United Republic of Tanzania; Zimbabwe	**33**
AMRO/PAHO	Anguilla; Antigua and Barbuda; Argentina; Aruba; Bahamas; Barbados; Belize; Bolivia (Plurinational State of); Brazil; British Virgin Islands; Cayman Islands; Colombia; Costa Rica; Cuba; Curaçao; Dominica; Dominican Republic; Ecuador; El Salvador; French Guiana; Grenada; Guadeloupe; Guatemala; Guyana; Haiti; Honduras; Jamaica; Martinique; Mexico; Montserrat; Nicaragua; Panama; Paraguay; Peru; Puerto Rico; Saint Barthélemy; Saint Kitts and Nevis; Saint Lucia; Saint Martin; Saint Vincent and the Grenadines; Sint Maarten; Suriname; Trinidad and Tobago; Turks and Caicos Islands; United States of America; United States Virgin Islands; Uruguay; Venezuela (Bolivarian Republic of)	**48**
EMRO	Djibouti; Pakistan; Saudi Arabia; Somalia; Sudan; Yemen	**6**
SEARO	Bangladesh; Bhutan; India; Indonesia; Maldives; Myanmar; Nepal; Sri Lanka; Thailand; Timor-Leste	**10**
WPRO	American Samoa; Cambodia; China; Cook Islands; Fiji; French Polynesia; Kiribati; Lao People's Democratic Republic; Malaysia; Marshall Islands; Micronesia (Federated States of); New	**20**

	Caledonia; Papua New Guinea; Philippines; Samoa; Singapore; Solomon Islands; Tokelau; Tonga; Viet Nam	
EURO	France; Italy	**2**
Total		**119**

Countries and territories with established *Aedes aegypti* mosquito vectors, but no known cases of chikungunya virus transmission, by WHO regional office

WHO Regional Office	**Country / territory**	**Total**
AFRO	Botswana; Ghana; Liberia; Mauritania; Namibia; Niger; Rwanda; Sao Tome and Principe; South Sudan; Zambia	**10**
AMRO/PAHO		**0**
EMRO	Afghanistan; Egypt; Oman	**3**
EURO	Cyprus; Georgia; Região Autónoma da Madeira – Portugal; Russian Federation; Turkey	**5**
SEARO		**0**
WPRO	Australia; Brunei Darussalam; Christmas Island; Guam; Nauru; Niue; Northern Mariana Islands (Commonwealth of the); Tuvalu; Wallis and Futuna	**9**
		27