Epidemiological alert
Chikungunya

10 February 2026

Between late 2025 and early 2026, there has been a sustained increase in cases of chikungunya in countries and territories in the Americas Region, as well as a resumption of autochthonous transmission in areas that had not reported circulation of the virus for several years. Although the observed dynamics may correspond to expected epidemiological patterns in contexts where the vector is present, the reappearance of cases in certain territories reinforces the need for sensitive surveillance and a timely response. In this context, the Pan American Health Organization/World Health Organization (PAHO/WHO) urges Member States to intensify epidemiological and laboratory surveillance, ensure early detection and appropriate clinical management of cases, and consolidate integrated vector control actions in order to limit transmission and reduce associated morbidity and mortality.

Chikungunya globally

Globally, between 1 January 2025, and 10 December 2025, 502,264 cases of chikungunya were reported, including 208,335 confirmed cases and 186 deaths across 41 countries and territories. By World Health Organization (WHO) Region, cases have been reported in the African Region with 2,211 cases, including 111 confirmed; the Eastern Mediterranean Region with 1,596 cases, including 67 confirmed; the European Region with 56,986 confirmed cases, including 43 deaths; the Americas Region with 291,451 cases, including 110,039 confirmed and 141 deaths, the South-East Asia Region with 115,985 cases, including 34,035 confirmed and two deaths, and the Western Pacific Region with 34,035 confirmed cases and two deaths *(1)*.

Genomic analysis has identified three main genotypes of the chikungunya virus (CHIKV) circulating globally: the West African genotype, the East, Central, and South African (ECSA) genotype, and the Asian genotype. Within the ECSA genotype, the genetically divergent Indian Ocean lineage (IOL) emerged, characterized by the E1-A226V mutation, which has been associated with increased transmissibility of CHIKV by the *Aedes albopictus* vector *(2)*.

Chikungunya in the Americas Region

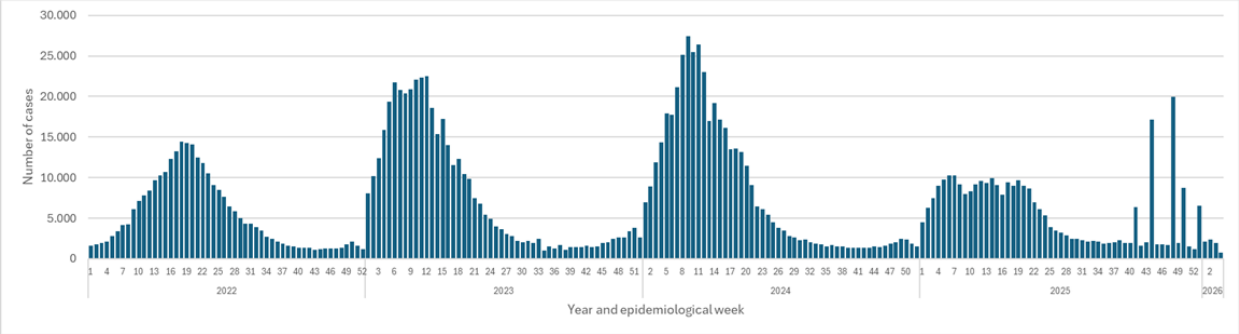
In 2025, between the epidemiological week (EW) 1 and EW 53, 18 countries and one territory in the Americas Region reported 313,132 cases to Pan American Health Organization's (PAHO) Health Information Platform for the Americas (PLISA), of which 113,926 were confirmed, including 170 deaths for chikungunya (**Figure 1**) *(3)*.

Suggested citation: Pan American Health Organization/World Health Organization. Epidemiological Alert: Chikungunya, 10 February 2026. Washington, D.C.: PAHO/WHO; 2026.

Since late 2025 (EW 49) and early 2026 (EW 4), there has been a sustained increase in chikungunya cases in countries and territories in the Americas Region, as well as the resumption of autochthonous transmission in areas that had not reported circulation of the virus for several years. During this period, significant circulation was documented in the central-western and southeastern regions of Brazil, southern Bolivia, and the reappearance of cases in the Guiana Shield area (**Figure 2**) *(3-18)*.

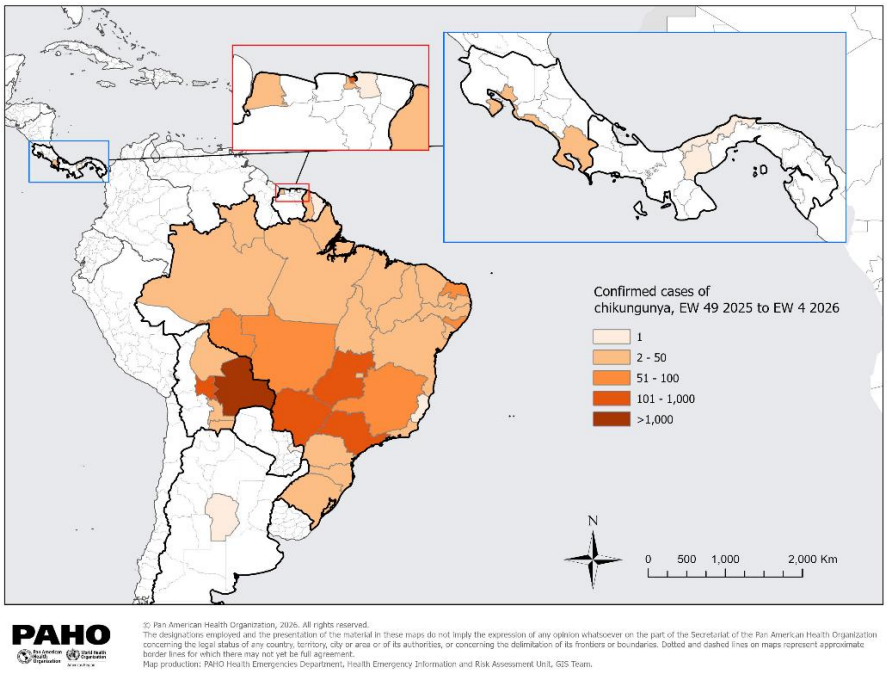
In 2026, as of EW 4, 7,150 cases of chikungunya were reported to PLISA, of which 2,351 were confirmed, including one death *(3)*.

Figure 1. Distribution of chikungunya cases by year and epidemiological week in the Americas Region, 2022-2026.



Source: Adapted from Pan American Health Organization. PLISA Health Information Platform for the Americas, Chikungunya Indicators Portal. Washington, D.C.: PAHO/WHO; 2026 [Cited 5 February 2026]. Available from: https://www.paho.org/es/arbo-portal/chikunguna-datos-analisis/chikunguna-analisis-por-pais *(3)*.

Figure 2. Geographic distribution of chikungunya confirmed cases in the Americas Region, between EW 49 of 2025 and EW 4 of 2026.



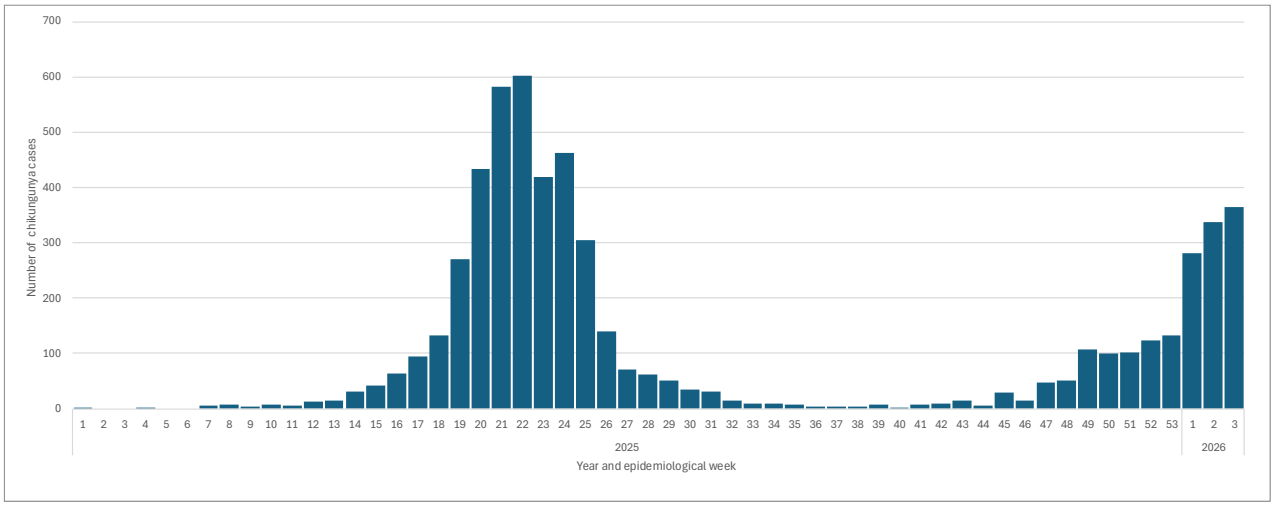
Source: Adapted from data provided by the respective countries and reproduced by PAHO/WHO *(4-18)*.

Below is a brief summary, in alphabetical order, of the epidemiological situation of chikungunya in select countries in the Americas Region that have reported cases between late 2025 and early 2026:

In **Bolivia,** between EW 1 and EW 53 of 2025, a total of 4,696 confirmed cases of chikungunya were reported, including four deaths. In 2026 (as of EW 3), 984 cases of chikungunya were confirmed, with no deaths reported *(4)*.

During 2025, an increase was observed from EW 12, with the highest number of cases reaching in EW 22. This increase was mainly associated with the outbreak in the department of Santa Cruz. A second increase, although less pronounced than the previous one, was recorded since EW 41 of 2025, a trend that has continued into the first weeks of 2026 (**Figure 3**) *(4)*. In Bolivia, the circulation of the ECSA genotype of CHIKV has been documented during 2025; however, the E1-A226V mutation has not been identified *(4, 5)*.

Figure 3. Distribution of confirmed chikungunya cases by EW of symptom onset. Bolivia, 2025–2026 (as of EW 3 of 2026).



Source: Adapted from data provided by the Bolivia International Health Regulations (IHR) National Focal Point (NFP). Communication received on 3 February 2026, by email. La Paz; 2025. Unpublished *(4)*.

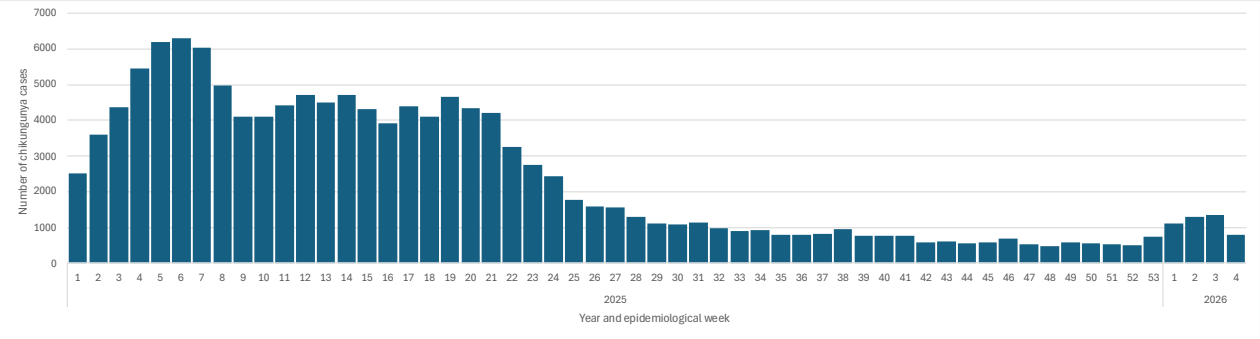
In **Brazil**, between EW 1 and EW 53 of 2025, 129,123 probable cases of chikungunya were reported, including 121 deaths, of which 107,975 were confirmed. So far in 2026 (as of EW 4), 4,544 probable cases have been reported, of which 1,535 cases were confirmed, with no deaths reported (**Figure 4**) *(6)*.

Although the number of probable and confirmed cases reported in the first four weeks of 2026 is significantly lower than that reported in the same period in 2025 (15,929 cases), it is important to note that the virus remained active during the last four weeks of 2025 (EW 49) and the first weeks of 2026 (EW 4). During this period, 26 federal units reported cases, with 71.5% of the total cases (probable and confirmed) concentrated in five states: Minas Gerais (n= 1,515 probable cases, 81 laboratory-confirmed), Mato Grosso do Sul (n= 1,326 probable cases, 388 laboratory-confirmed), Goiás (n= 1,318 probable cases, 377 laboratory-confirmed), São Paulo (n= 784 probable cases, 143 laboratory-confirmed), and Mato Grosso (n= 364 probable cases, 84 laboratory-confirmed, including one death) *(6)*. All 7,413 probable

and confirmed cases reported during this period were classified as autochthonous. Of the laboratory-confirmed cases, 959 were among females. The highest proportion of cases was recorded in the 30-39 age group (n= 261 cases), followed by the 40-49 age group (n= 237 cases) *(6)*.

Likewise, 405 cases requiring hospitalization and 14 cases in newborns were reported[1] . In Brazil, the circulation of the ECSA genotype without the presence of the E1-A226V mutation has been documented *(6)*.

Figure 4. Distribution of probable and confirmed chikungunya cases by week of symptom onset. Brazil, 2025–2026 (as of EW 4 of 2026).



Source: Adapted from data provided by the Brazil IHR NFP communication received on 5 February 2026, by email. Brasilia; 2026. Unpublished *(6)*.

In **Cuba**, since the outbreak began in July 2025 and as of EW 53, 51,217 suspected cases of chikungunya were reported, including 46 deaths and 1,959 laboratory-confirmed cases. Cases have been identified in 13 of the 15 provinces: Artemisa, Camagüey, Ciego de Ávila, Cienfuegos, Granma, Guantánamo, Holguín, Havana, Matanzas, Pinar del Río, Sancti Spíritus, Santiago de Cuba, and Villa Clara *(1, 3)*. At the time of publication of this alert, no information on cases reported in 2026 has been received.

In **French Guiana** between EW 4 and EW 5 of 2026, five cases of chikungunya were confirmed by laboratory testing, of which four were classified as autochthonous and one as imported. The autochthonous cases were reported in Saint-Laurent-du-Maroni (n= 3 cases) and Kourou (n= 1 case), while the imported case corresponds to a resident of Cayenne with a history of travel to Suriname. Sequencing of the first autochthonous cases showed high genetic similarity among themselves and a close relationship with recent sequences from Cuba and Brazil *(7, 8)*.

In **Guyana**, a total of six suspected cases of chikungunya were reported in 2025, all of which were confirmed by laboratory tests. The cases were recorded between EW 42 and EW 48 in region 4 and were classified as autochthonous, as there was no history of travel prior to the onset of symptoms *(9)*. These cases were recorded after nine years without any reported autochthonous cases. So far in 2026, no new cases have been reported.

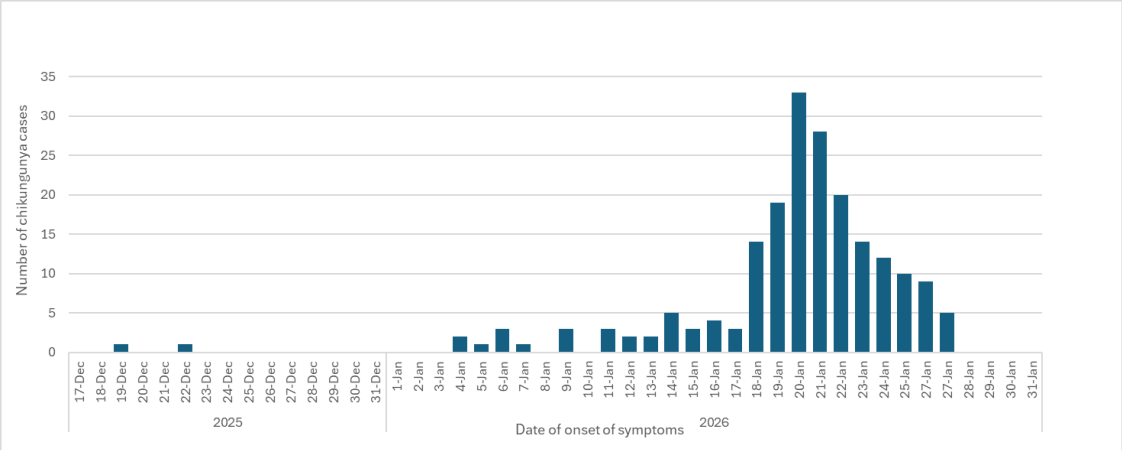
[1]During the first 7 days of life.

In **Panama,** between EW 1 and EW 53 of 2025, 336 cases of chikungunya were reported, of which 41 were confirmed, with no associated deaths recorded during this period. The confirmed cases are in the process of genotyping *(10)*. So far in 2026, no cases have been reported *(10)*.

In **Paraguay,** 51 confirmed cases of chikungunya were reported between EW 1 and EW 53 of 2025. One additional confirmed case was reported between EW 1 and EW 4 of 2026. No deaths were reported during this period *(11)*. This situation represents a marked decrease compared with the outbreak that occurred between 2022 and 2023, when 2,248 and 83,522 confirmed cases were reported respectively, including 297 deaths associated with chikungunya in 2023 *(11)*. Between April and July 2025, circulation of the ECSA genotype of the chikungunya virus was documented in Paraguay, with no detection of the E1-A226V mutation *(11)*.

In **Suriname,** no autochthonous cases had been reported since 2016; however, in EW 51 of 2025, the first autochthonous case of chikungunya was reported. Between EW 51 of 2025 and EW 4 of 2026, a total of 712 suspected cases of chikungunya were reported, of which 327 were laboratory confirmed, including one death (**Figure 5**). According to the available information (n=150 cases), confirmed cases were reported in four of Suriname's ten districts: Paramaribo (n= 127 cases, including one death), Commewijne (n= 1 case), Nickerie (n= 15 cases), and Wanica (n= 7 cases). Age information was available for 585 cases, ranging between 11 months and 85 years of age. Children aged 0–14 years accounted for the largest proportion of cases (28%; n= 163 cases), closely followed by adults aged 30–49 years (28%; n= 162 cases). Sex was reported in 585 cases, of which 52% (n= 305 cases) were female; notably, females accounted for 71% of cases in the 30-49 age group. Hospitalization information was available for 55 cases, of which 12 (7.7%) required hospitalization *(12)*. One death is being investigated, involving a 72-year-old male with underlying comorbidities who died on 26 January 2026. Samples from the 2026 cases are currently undergoing genotyping analysis; results are pending *(12)*.

Figure 5. Distribution of confirmed cases of chikungunya by date of symptom onset. Suriname, between EW 51 of 2025 and EW 4 of 2026.



Source: Adapted from data provided by the Suriname IHR NFP. Communication received on 4 February 2026, by email. Paramaribo; 2026. Unpublished *(12)*.

Guidance for national authorities

Given the increase in the number of chikungunya cases in some countries, both within and outside the Region, and considering the risk of the chikungunya virus spreading to new areas with susceptible populations, PAHO/WHO urges Member States to take the necessary measures to prevent and respond promptly to possible outbreaks.

In this regard, it is recommended to strengthen epidemiological and entomological surveillance, ensure timely diagnosis and appropriate clinical management of cases of chikungunya and other arboviruses, and intensify vector prevention and control actions. Likewise, health care services should be prepared to ensure that patients have access to comprehensive and adequate care.

PAHO/WHO reminds Member States that the guidance issued in the Epidemiological Alert of February 13, 2023, on the increase in chikungunya in the Americas Region, remains in effect and is available from: https://www.paho.org/en/documents/epidemiological-alert-chikungunya-increase-region-americas *(13)*.

Adequacy of health care services

Given the risk of increased incidence of chikungunya in some areas of the Region, PAHO/WHO advises Member States to adapt their health services to ensure a timely response at all levels of care in the event of outbreaks *(13)*. This includes:

- Organizing clinical triage, patient flow, follow-up, patient hospitalization, and the patient referral and counter-referral system in each institution and level of care.
- Adapting health services and the care network to respond to outbreaks or epidemics.
- Strengthening patient care networks for the diagnosis, management, and follow-up of patients with suspected chikungunya (including comprehensive follow-up of patients in the chronic phase).

Integrated Surveillance

PAHO/WHO encourages maintaining and strengthening epidemiological surveillance at the national level and sharing reports of chikungunya, Oropouche, dengue, and Zika cases with the Organization to facilitate regional characterization and analysis.

Given that cases of these diseases (chikungunya, dengue, Oropouche, and Zika) can occur in the same territory but are transmitted by vectors with different habits and characteristics, it is important to intensify efforts to analyze their spatial distribution. This will enable a faster and more targeted response in the most affected areas. Information on critical transmission points for dengue, Zika, chikungunya, and Oropouche should be used to guide intensive vector control actions *(13, 14)*.

Entomological surveillance should not only identify the main vector species involved in transmission, such as *Aedes aegypti* and *Aedes albopictus* for chikungunya, dengue, and

Zika *(13)*, and the main vector *Culicoides paraensis* for Oropouche *(14)*, but also measure their density in risk areas and evaluate the impact of the control measures implemented. As these are vectors with different ecosystems (*Aedes aegypti* versus *Culicoides*), transmission dynamics regularly occur in different areas.

Laboratory confirmation

The initial diagnosis of the chikungunya virus (CHIKV) infection is clinical, and adequate suspicion can guide the confirmation protocol. However, laboratory results should always be analyzed in conjunction with epidemiological information and context for surveillance purposes and not as a basis for clinical decision-making *(15)*.

Clinical suspicion of CHIKV infection can be confirmed in the laboratory using virological techniques, mainly molecular detection by PCR. The ideal sample for detection is serum collected during the acute phase of infection, preferably within the first 5 days after symptom onset. However, because CHIKV often presents with more prolonged viremia, a sample taken up to day 8 from symptom onset may be useful for molecular confirmation *(15)*.

There are different algorithms for the molecular detection of CHIKV, depending on the epidemiological and clinical context. Thus, when there is clinical suspicion compatible with CHIKV infection, it is suggested to start with a specific PCR, where a positive result confirms the infection. if the result is negative, detection of other arboviruses can be continued sequentially, mainly dengue virus (DENV) and Zika virus (ZIKV), or other pathogens considered in the differential diagnosis (**Figure 6**) *(15)*.

On the other hand, when the clinical suspicion is unclear and the nonspecific symptoms may be consistent with other arboviruses (or even other pathogens), or in the context of syndromic surveillance, a multiplex amplification protocol that allows the simultaneous detection of at least three of the most likely endemic arboviruses (DENV, CHIKV, and ZIKV) may be more efficient (**Figure 7**) *(15)*.

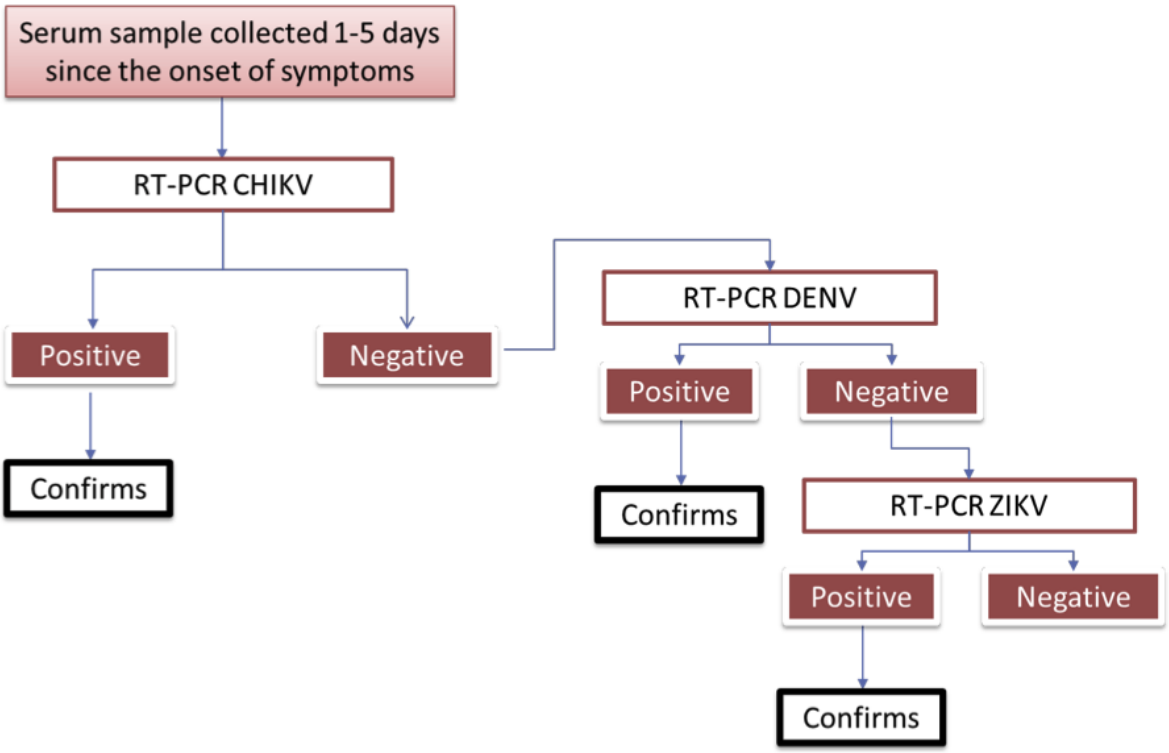
In fatal cases, tissue samples, mainly from the liver and spleen, are recommended for molecular detection. These samples are also useful for histopathological analysis to support the diagnosis and better characterize the case *(15)*.

Serological confirmation of CHIKV infection is only possible when paired samples collected at least one week apart (acute phase and convalescent phase) are processed. Seroconversion (IgM negative in the initial sample and positive in the second sample, by ELISA or neutralization) or at least a 4-fold increase in antibody titer (using a quantitative methodology) can confirm the diagnosis. However, it is important to note that serological tests are susceptible to cross-reactions, especially with other alphaviruses including Mayaro. Furthermore, a positive result in a single sample is not considered confirmatory, since in addition to the possibility of cross-reaction, IgM may remain detectable for several months or even years after infection, and therefore detection may reflect past infection *(15)*.

In cases with neurological manifestations (e.g., meningoencephalitis), molecular and serological detection can be performed on cerebrospinal fluid (CSF) samples. However, this sample should only be taken for clinical reasons and not for the specific purpose of identifying the etiological agent. While a positive result on a molecular test of CSF confirms infection, a negative result does not rule it out *(15)*.

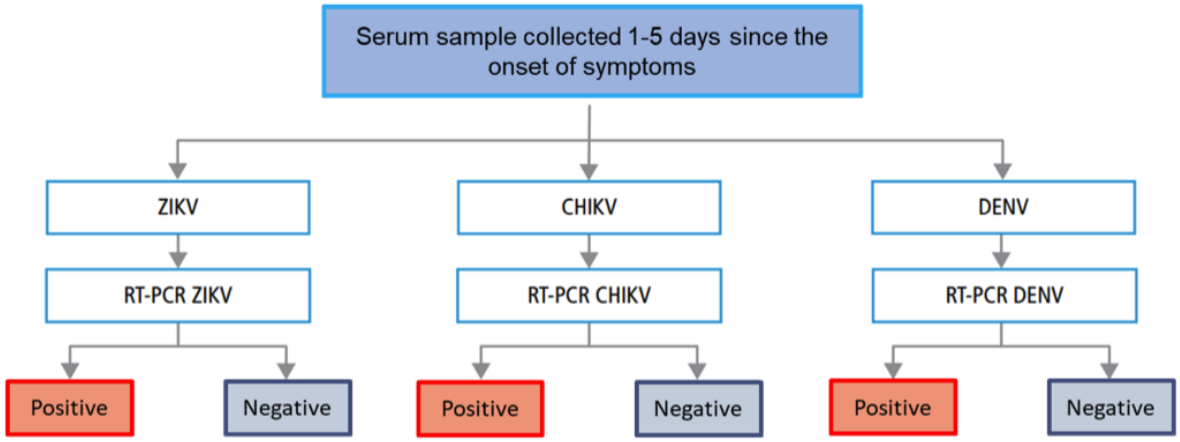
Finally, given the initial clinical similarity between chikungunya and measles, and considering the risk that the latter poses to the Region, it is recommended that measles be included as a differential diagnosis *(16)*.

Figure 6. Sequential algorithm for virological testing in suspected cases of chikungunya



Source: Pan American Health Organization. Recommendations for Laboratory Detection and Diagnosis of Arbovirus Infections in the Americas Region. Washington, D.C.: PAHO; 2022. Available from: https://iris.paho.org/items/810bf92c-a06a-44e6-8561-5b2a97f3e670 *(15)*.

Figure 7. Multiplex algorithm for virological testing in suspected cases of chikungunya



Source: Pan American Health Organization. Recommendations for Laboratory Detection and Diagnosis of Arbovirus Infections in the Americas Region. Washington, D.C.: PAHO; 2022. Available from: https://iris.paho.org/items/810bf92c-a06a-44e6-8561-5b2a97f3e670 *(15)*.

Genomic characterization and surveillance

Understanding CHIKV genotypes [Asian, East/Central/South African (ECSA), and West African] is essential for anticipating transmission dynamics, guiding public health interventions, and monitoring viral evolution *(17)*. These genotypes and their sublineages differ in their geographic spread, epidemic potential, and adaptation to mosquito vectors such as *Aedes aegypti* and *Aedes albopictus*.

Genomic surveillance plays a critical role in identifying circulating strains by detecting key mutations such as A226V. This amino acid substitution in the E1 envelope glycoprotein (alanine to valine at position 226) is recognized for enhancing viral replication in *Aedes albopictus*, a mosquito species widely distributed in temperate and subtropical regions *(18)*. The A226V mutation was crucial in previous explosive outbreaks driven by the Indian Ocean lineage (IOL), a sublineage of the ECSA genotype, particularly on the island of Réunion (2005-2006), in India (2006-2007), and in Thailand (2019). This mutation was again characterized in outbreaks in Réunion, Mayotte, Mauritius, and mainland France (2025) in an ECSA sublineage distinct from IOL *(19, 20)*.

The IOL lineage continues to circulate in South and Southeast Asia and the Middle East, often associated with the A226V mutation, and has displaced the Asian genotype in some settings due to its greater epidemic potential. The ECSA genotype, considered ancestral to both the IOL and Asian genotypes, remains endemic in many parts of sub-Saharan Africa and has also been identified in the Americas, particularly since 2014. Notably, ECSA strains have caused indigenous transmission in Argentina, Brazil, Paraguay, Bolivia, and parts of the Caribbean *(17, 21)*. These introductions were independent of the Asian genotype that initially drove the 2014-2015 outbreaks in the Americas. Although some ECSA strains in the region have acquired

mutations of epidemiological importance, the A226V mutation has not been documented in any strain detected in the Americas. The co-circulation of ECSA and Asian genotypes in the Americas has raised concerns about increased viral adaptability and possible recombination or genotype changes in the future.

The Asian genotype, initially responsible for large-scale epidemics in the Americas between 2014 and 2020, continues to circulate at lower levels, but is generally less adapted to *Ae. albopictus* and lacks the A226V mutation.

Case management

CHIKV disease can cause a wide range of clinical manifestations, although it is mainly characterized by the onset of fever associated with arthritis or arthralgia. Joint pain is often severe and incapacitating. Other common manifestations include headache, muscle pain, rash, and pruritus.

The duration of symptoms varies from a few days to several months, thus determining the different phases of the disease: acute, post-acute, and chronic, each with specific care requirements. The acute phase lasts up to 2 weeks, the post-acute phase lasts from the third week to the third month, and the chronic phase begins after the fourth month and can last for years *(22)*. In most patients in the chronic phase, a significant deterioration in quality of life is observed during the first few years after chikungunya infection.

Consequently, it is recommended that the clinical capacities of health personnel at all levels and for all phases of the disease be strengthened.

- Implement continuing education programs for health professionals on the suspected diagnosis and clinical management of chikungunya cases, as well as other arboviruses prevalent in the Region, particularly dengue and Zika.
- Strengthen competencies at different levels of care for the prevention and treatment of sequelae of the chronic phase of chikungunya.
- Adapt the "Guidelines for the Clinical Diagnosis and Treatment of Dengue, Chikungunya, and Zika" *(22)* to the national and subnational levels.
- Offer training workshops for public and private health personnel on the organization of health services, including outbreak response.

Likewise, pregnant women, children under 1 year of age, older adults, and people with comorbidities (hypertension, chronic renal failure, diabetes, obesity, heart disease, among others) should be advised to go immediately to the nearest health facility at the first suspicion of chikungunya infection, given the increased risk of severe manifestations or complications from this disease. In addition, all newborns of mothers with suspected or confirmed chikungunya in the 15 days prior to delivery should be hospitalized due to the risk of vertical transmission.

It is important to note that chikungunya disease can be fatal during the acute phase, mainly in this group of patients (pregnant women, children under 1 year of age, older adults, and people with comorbidities). Severe manifestations include shock, meningoencephalitis, and Guillain-Barré syndrome *(23, 24, 25)*. CHIKV infection can decompensate the underlying

disease in people with comorbidities, thus increasing the risk of severity and death in this population group *(23)*.

Community Participation

Every effort should be made to enlist community support in the prevention of dengue, chikungunya, Oropouche, and Zika.

Simple information, education, and communication (IEC) materials can be disseminated through various media, including social media.

Household members should be encouraged to eliminate mosquito breeding sites, both indoors and outdoors.

Highly productive mosquito breeding sites, such as water storage containers (drums, elevated tanks, clay pots, etc.), should be targeted for vector breeding prevention measures. Other breeding sites, such as roof gutters and other water retention containers, should also be cleaned regularly.

Local teams often know how to make this information more effective, and in many cases national campaigns and messages are not as effective as local initiatives.

Entomological surveillance, prevention, and vector control

PAHO/WHO urges Member States to make effective use of available resources to prevent and/or control vector infestation in affected areas and in health services *(26)*. This will be achieved through the implementation of integrated vector control strategies in emergencies, which include the following processes:

- Selection of control methods based on knowledge of vector biology, disease transmission, morbidity, and PAHO/WHO recommendations.
- Use of multiple interventions, often in combination and synergistically, with adequate coverage.
- Collaboration between the health sector and public and private sectors involved in environmental management whose work has an impact on vector reduction.
- Integration of individuals, families, and other key partners (education, finance, tourism, water and sanitation, and others) into prevention and control activities.
- Strengthening of the legal framework to enable an integrated and intersectoral approach.

Aedes prevention and control measures

Given the high infestation by *Aedes aegypti* and the presence of *Aedes albopictus* in the Region, it is recommended that prevention and control measures be aimed at reducing vector density and have the acceptance and collaboration of the local population.

Prevention and control measures to be implemented by national authorities should include the following:

- Strengthen environmental management actions, mainly the elimination of vector breeding sites in homes and common areas (parks, schools, health facilities, cemeteries, etc.).
- Reorganize solid waste collection services to support actions to eliminate breeding sites in areas of highest transmission and, if necessary, plan intensive actions in specific areas where regular garbage collection has been interrupted.
- Implement measures to control breeding sites through the use of physical, biological, and/or chemical methods that actively involve individuals, families, and the community *(27)*.
- Define areas of high transmission risk (risk stratification) *(16)* and prioritize those where there are concentrations of people (schools, terminals, hospitals, health centers, etc.). In these facilities, the presence of mosquitoes should be eliminated within a radius of at least 400 meters. Special attention should be paid to health facilities, which should be free of the vector and its breeding sites so that they do not become sources of virus transmission.
- In areas where active transmission is detected, it is recommended to implement measures aimed at eliminating infected adult mosquitoes (mainly through the use of insecticides) in order to stop and interrupt transmission. This action is urgent and is only effective when carried out by properly trained personnel under internationally accepted technical guidelines and when performed concurrently with the other proposed actions. The main action to interrupt transmission when it occurs intensively is the elimination of infected adult mosquitoes (active transmission) through indoor fumigation, using individual equipment, combined with the destruction and/or control of vector breeding sites inside homes.
- An effective method of adult control that can be used, considering the operational capabilities available, is indoor residual spraying, which should be applied selectively to the resting places of *Aedes aegypti,* taking care not to contaminate containers used to store drinking water or water used for cooking. This intervention in treated areas is effective for up to four months and can be used in shelters, homes, health services, schools, and other locations. For more information, consult the Manual for applying indoor residual spraying in urban areas for the control of *Aedes aegypti (28)* and the document Control of *Aedes aegypti* in the context of simultaneous transmission of COVID-19 *(29)*.
- Choose the appropriate insecticide to be used (following PAHO/WHO recommendations), its formulation, and be aware of the susceptibility of mosquito populations to that insecticide *(30)*.
- Ensure the proper functioning and calibration of fumigation equipment and its maintenance, and ensure insecticide reserves.
- Intensify supervision (quality control) of operators' field work, both during focal treatment and adulticide treatment (fumigation), ensuring compliance with personal protection measures.

Personal protection measures

Patients infected with the chikungunya, dengue, Oropouche, or Zika virus are the reservoir of infection for other people both in their homes and in the community. It is necessary to inform patients, their families, and the affected community about the risk of transmission and ways to prevent infection by reducing the vector population and contact between the vector and people. It is important to reinforce these measures in the case of pregnant women, given the risk of vertical transmission of chikungunya, Oropouche, and Zika *(31, 32)*.

To minimize vector-patient contact, the following is recommended:

- Protecting homes with fine mesh screens on doors and windows[2] .
- Wearing clothing that covers the legs and arms, especially in homes where someone is ill with Oropouche, Zika, or another arbovirus.
- Use repellents containing DEET, IR3535, or icaridin, which can be applied to exposed skin or clothing, and use them strictly in accordance with the product label instructions.
- Use mosquito nets, impregnated or not with insecticides, for those who sleep during the day (e.g., pregnant women, babies, sick or bedridden people, the elderly).
- During outbreaks, outdoor activities should be avoided during the period of greatest vector activity (at dawn and dusk).
- For people at higher risk of being bitten by culicoides, such as forestry and agricultural workers, etc., it is recommended to wear clothing that covers exposed parts of the body, as well as to use the repellents mentioned above.

[2] It is recommended that the mesh holes be smaller than 1.0 mm, as the average size of the female *Culicoides paraensis*, considered to be the main vector involved in OROV transmission, is 1 to 1.5 mm.

References

1. World Health Organization. WHO Rapid Risk Assessment – Chikungunya virus disease, Global v.1. Geneva: WHO; 2025. Available from: https://www.who.int/publications/m/item/who-rapid-risk-assessment---chikungunya-virus--global-v.1
2. World Health Organization. Chikungunya epidemiology update - June 2025. Geneva: WHO; 2025. Available from: https://www.who.int/publications/m/item/chikungunya-epidemiology-update-june-2025.
3. Pan American Health Organization. PLISA Health Information Platform for the Americas, Chikungunya Indicators Portal. Washington, D.C.: PAHO/WHO; 2026 [Cited 5 February 2026]. Available from: https://www.paho.org/en/arbo-portal/chikungunya-data-and-analysis/chikungunya-analysis-country.
4. Bolivia International Health Regulations National Focal Point (IHR NFP). Email information dated 3 February 2026. La Paz; 2026. Unpublished.
5. Ministerio de Salud y Deportes de Bolivia. Programa Nacional de Vigilancia de Enfermedades Endémicas y Epidémicas – Unidad de Vigilancia Epidemiológica y Salud Ambiental – Dirección General de Epidemiologia. La Paz; 2026. Unpublished.
6. Brazil International Health Regulations National Focal Point (IHR NFP). Email communication dated 5 February 2026. Brasilia; 2026. Unpublished.
7. France International Health Regulations National Focal Point (IHR NFP). Email information dated 5 February 2026. Paris; 2026. Unpublished.
8. Sante Publique France. Bulletin bi-mensuel de surveillance épidémiologique. Région Guyane. Semaines 04 et 05 (du 19 janvier au 1er février 2026). Saint-Maurice; 2026. Available from: https://www.santepubliquefrance.fr/regions/guyane/documents/bulletin-regional/2026/surveillance-sanitaire-en-guyane.-bulletin-du-5-fevrier-2026.
9. Guyana International Health Regulations National Focal Point (IHR NFP). Email information dated 4 February 2026. Georgetown; 2026. Unpublished.
10. Panama International Health Regulations National Focal Point (IHR NFP). Email information dated 30 January 2026. Panama City; 2026. Unpublished.
11. Paraguay International Health Regulations National Focal Point (IHR NFP). Email information dated 1 and 9 February 2026. Asunción; 2026. Unpublished.
12. Suriname International Health Regulations National Focal Point (IHR NFP). Email information dated 3 February 2026. Paramaribo; 2026. Unpublished.
13. Pan American Health Organization/World Health Organization. Epidemiological Alert: Increase in Chikungunya in the Region of the Americas. 13 February 2023. Washington, D.C.: PAHO/WHO; 2023. Available from: https://www.paho.org/en/documents/epidemiological-alert-chikungunya-increase-region-americas.

14. Pan American Health Organization/World Health Organization. Epidemiological Update on Oropouche in the Region of the Americas, 13 August 2025. Washington, D.C.: PAHO/WHO; 2025. Available from: https://www.paho.org/en/documents/epidemiological-update-oropouche-region-americas-13-august-2025.

15. Pan American Health Organization. Recommendations for the detection and laboratory diagnosis of arbovirus infections in the Region of the Americas. Washington, D.C.: PAHO; 2022. Available from: https://iris.paho.org/items/810bf92c-a06a-44e6-8561-5b2a97f3e670 .

16. Pan American Health Organization. Case definitions, clinical classification, and disease phases Dengue, Chikungunya, and Zika. Washington, D.C.: PAHO; 2023. Available from: https://www.paho.org/en/documents/case-definitions-clinical-classification-and-disease-phases-dengue-chikungunya-and-zika.

17. Barreto M, Cardoso C, dos Santos F, dos Santos J, Alto B, Honório N et al. Spatial–temporal distribution of chikungunya virus in Brazil: a review on the circulating viral genotypes and Aedes (Stegomyia) albopictus as a potential vector. Frontiers in Public Health. Volume 12 – 2024. Available from: https://doi.org/10.3389/fpubh.2024.1496021.

18. Tsetsarkin K, Vanlandingham D, McGee C, Higgs S. A single mutation in chikungunya virus affects vector specificity and epidemic potential. PLoS Pathog. 2007 Dec;3(12):e201. Available from: https://pubmed.ncbi.nlm.nih.gov/18069894/

19. Frumence E, Piorkowski G, Traversier N, Amaral R, Vincent M, Mercier A, et al. Genomic insights into the re-emergence of chikungunya virus on Réunion Island, France, 2024 to 2025. Euro Surveill. 2025; 30(22): pii=2500344. Available from: https://doi.org/10.2807/1560-7917.ES.2025.30.22.2500344.

20. Ramuth M, Tegally H, Ubheeram A, Ramphal Y, Iyaloo D, Singh L, et al**.** Reemergence of chikungunya in Mauritius driven by a novel lineage with pandemic potential. [Preprint]. *Research Square*. 2025. doi:10.21203/rs.3.rs-8288410/v1. Available from: https://doi.org/10.21203/rs.3.rs-8288410/v1.

21. Giovanetti M, Vazquez C, Lima M, Castro E, Rojas A, de la Fuente A, et al. Rapid epidemic expansion of chikungunya virus-ECSA lineage in Paraguay. medRxiv [Preprint]. 2023 Apr 17:2023.04.16.23288635. doi: 10.1101/2023.04.16.23288635. Update in: Emerg Infect Dis. 2023 Sep;29(9):1859-1863. Available from: https://pmc.ncbi.nlm.nih.gov/articles/PMC10153315/.

22. Pan American Health Organization. Guidelines for the Clinical Diagnosis and Treatment of Dengue, Chikungunya, and Zika. Washington, D.C.: PAHO; 2022. Available from: https://iris.paho.org/items/f63304c2-4d16-48c3-acc5-6187f60ccee6.

23. Benítez I, Torales M, Peralta K, Dominguez C, Grau L, Sequera G, et al. Clinical and epidemiological characterization of the Chikungunya epidemic in Paraguay. ANALES [Internet]. 22 August 2023 [Cited 25 August 2025];56(2):18-26. Available from: https://revistascientificas.una.py/index.php/RP/article/view/3669.

24. Torales M, Beeson A, Grau L, et al. *mNotes from the Field:* Chikungunya Outbreak — Paraguay, 2022–2023. MMWR Morb Mortal Wkly Rep 2023;72:636–638. Available from: http://dx.doi.org/10.15585/mmwr.mm7223a5

25. Aguilar G, Estigarriba-Sanabria G, Ríos-González C, Torales J, Morel Z, Aguero M, et al. Characteristics of acute chikungunya virus infection in children: an epidemiological study in the Department of Caaguazú, Paraguay. *Revista De Salud Pública Del Paraguay*, *14*(1), 10–14. Available from: https://doi.org/10.18004/rspp.2024.abr.02.

26. Pan American Health Organization. Métodos de vigilancia entomológica y control de los principales vectores en las Américas. Washington, D.C.: PAHO; 2021 Available from: https://iris.paho.org/handle/10665.2/55241.

27. Pan American Health Organization. Technical document for the implementation of interventions based on generic operational scenarios for the control of Aedes aegypti. Washington, D.C.: PAHO; 2019. Available from: https://iris.paho.org/items/2d2f23af-1bfe-4c29-8dc4-6f0a1418214a.

28. Pan American Health Organization. Manual for Indoor Residual Spraying in Urban Areas for Aedes aegypti Control. Washington, D.C.: PAHO; 2019. Available from: https://iris.paho.org/items/c65c2ddd-859f-4766-9feb-e0e72eb1ef16 .

29. Pan American Health Organization. Control of *Aedes aegypti* in the scenario of simultaneous transmission of COVID-19. Washington, D.C.: PAHO; 2020. Available from : https://www.paho.org/en/documents/control-aedes-aegypti-scenario-simultaneous-transmission-covid-19.

30. Pan American Health Organization. Procedimientos para evaluar la susceptibilidad a los insecticidas de los principales mosquitos vectores de las Américas. Washington, D.C.: PAHO; 2023. Available from: https://iris.paho.org/handle/10665.2/57424

31. Pan American Health Organization. Criaderos de *Culicoides paraensis* y opciones para combatirlos mediante el ordenamiento del medio. Washington, D.C.: OPS/OMS; 1987. Available from: https://iris.paho.org/handle/10665.2/17928.

32. World Health Organization. Vector control. Methods for use by individuals and communities. Geneva: WHO; 1997. Available from: https://www.who.int/publications/i/item/9241544945.