World Health Organization

ZIKA EPIDEMIOLOGY UPDATE

MAY 2026

Global overview

Ten years after being declared a Public Health Emergency of International Concern, Zika continues to be reported from countries in several WHO regions, albeit at much lower incidence rates. There is now evidence of current or previous autochthonous Zika virus (ZIKV) transmission in 97 countries and territories globally. However, Zika surveillance remains limited and asymptomatic or mildly symptomatic ZIKV infections are typically missed. Vigilance and preparedness thus remain important, particularly in areas with conditions suitable for transmission and where the immunologically susceptible proportion of resident populations is increasing. This update follows previous iterations, focusing on documentation of transmission published in 2024 and 2025, to inform public health authorities, epidemiologists, clinicians, travel medicine providers and other stakeholders engaged in Zika-related work.

As of 31 December 2025, there was evidence of current or previous autochthonous mosquito-borne transmission of Zika virus (ZIKV) in **97** countries and territories, distributed across all six WHO Regions. WHO and partner agencies have previously published global Zika epidemiology updates covering the period up to December 2023 (*1*–*3*). Through ongoing review of literature and official government reports published after 2023, **four** additional countries with evidence of autochthonous, mosquito-borne transmission were identified: Madagascar, Pakistan, Seychelles, and Yemen. In the WHO African Region, ZIKV transmission in the Seychelles in 2024 was identified through laboratory confirmation of infection in returning travellers and through subsequent testing of locally collected specimens by the Seychelles Ministry of Health (*4*–*6*). In Madagascar, five ZIKV infections were confirmed by RT-PCR testing of specimens collected from patients with suspected arboviral disease in late 2025. In the WHO Eastern Mediterranean region, where ZIKV circulation had not been documented previously, autochthonous transmission was identified in Pakistan through detection of Zika genomic sequences during retrospective testing of specimens collected during a dengue outbreak in 2021-2022, and in Yemen through RT-PCR testing of specimens from patients with undifferentiated febrile illness in 2025 (*7*,*8*).

In the Region of the Americas, where incidence of ZIKV infection peaked in 2016 and declined substantially thereafter, transmission continues to be reported in some countries and it remains the WHO Region with the highest number of reported ZIKV disease cases annually, with 44 490 suspected cases (2117, or <5% confirmed) in 2024 and 27 187 suspected cases (1841, or <7%, laboratory confirmed) in 2025 (*9*). In the South-East Asia region India reported a cumulative total of 151 Zika cases from three states (Gujarat, Karnataka, and Maharashtra states) over the course of 2024; Thailand reported 423 cases in 2024 and 236 cases in 2025; and Bangladesh reported 10 autochthonous cases detected around Dhaka in 2024 (*10*). In the African Region, among countries with prior evidence of ZIKV circulation, sporadic cases were detected in Senegal in 2024 and 2025, and ZIKV infections were confirmed by molecular testing in Kenya (Lamu Island) and Burkina Faso. Additionally, ZIKV infections were diagnosed in travellers returning from the Seychelles that suggested autochthonous transmission, which was subsequently confirmed by the Ministry of Health (MoH) through retrospective testing of locally collected patient specimens and in Madagascar, five ZIKV infections were confirmed by RT-PCR testing of specimens collected from patients with suspected arboviral disease (*4–6*). In the Western Pacific Region, only descriptions of sporadic ZIKV disease cases have been reported in 2024-2025 (*11*). In the European Region, cases in travellers returning from endemic areas increased in 2024 compared with recent years, however, no autochthonous cases have been detected since the first and only three-case cluster following autochthonous ZIKV transmission was reported in France in 2019 (*12*).

Globally, **55** countries and territories in six WHO regions have established and competent *Aedes aegypti* vector populations, but no evidence of autochthonous ZIKV transmission to date. In addition, other countries have established populations of *Aedes albopictus* mosquitoes, which are competent to transmit ZIKV but to a lesser extent than *Aedes aegypti* and are thus less likely to propagate and sustain large-scale ZIKV outbreaks (*13*). The presence of either of these vector populations poses an ongoing risk for ZIKV spread to additional countries. It is also possible that ZIKV transmission occurs, or has occurred, in some of these countries without being detected or reported. All areas with prior reports of ZIKV transmission have the potential for re-emergence or re-introduction, although population immunity to ZIKV, and to the closely related dengue virus (DENV) serotypes 1-4, might reduce the likelihood and extent of re-emergence or re-introduction (*14*,*15*).

Zika virus infection in older children and adults is typically asymptomatic or causes mild disease, but can result in rare but severe outcomes, including Guillain-Barré syndrome, transverse myelitis, and other systemic and neurologic sequelae (*16*). Infection during pregnancy can cause severe adverse outcomes that include increased risk of preterm birth, foetal death and stillbirth, and congenital malformations collectively characterized in their most severe form as congenital Zika syndrome (CZS) (*17*,*18*). CZS includes microcephaly and other abnormal cranial morphologies, abnormal brain development, limb contractures, eye abnormalities, brain calcifications, and other neurologic clinical features. The provision of long-term supportive care for children with CZS, as well as for their families, remains a substantial demand on healthcare systems and community-based programs.

The widespread expansion of genomic sequencing capacity for sequencing of ZIKV isolates and gene fragments has aided the assessment of trends in endemic transmission and patterns of global spread; however, as with diagnostic testing, findings should be interpreted carefully in light of epidemiological context and quality assurance of the methods and reagents used. Through earlier phylogenetic analysis ZIKV has been characterised into two major lineages namely the African and Asian lineages (*19*). ZIKV African lineage was isolated sporadically in non-human and human specimens since 1947 (*20*). Asian lineage viruses were first isolated in Malaysia in 1951 and later in the Pacific Islands from 2007 onwards, with some activity in other Western Pacific and Southeast Asia countries documented since that time. The 2015-16 epidemic in the Americas was caused by a strain of the Asian lineage commonly referred to as the American strain. Presence of the ZIKV Asian lineage has been documented in the African Region and was implicated in outbreaks in Angola and Cabo Verde which included microcephaly cases; more recently, Asian lineage ZIKV was identified from Lamu Island, Kenya in specimens collected from acutely febrile patients in 2024 (*21–23*).

The differences in the epidemic potential and pathogenicity of these viral lineages and strains remain poorly understood. Although an earlier report postulated the association of a specific viral mutation of the Asian lineage with the observation of teratogenic effects of ZIKV infection following the outbreaks in French Polynesia and the Americas in 2015-2016, this hypothesis was challenged by the documentation of a case of microcephaly in Thailand after congenital infection with Asia lineage-Asian strain ZIKV without the mutation, and subsequent reports of foetal microcephaly following maternal travel to Thailand during pregnancy and evidence of recent Zika virus infection (*24–26*). In contrast, to date, adverse pregnancy outcomes and cases of CZS caused by ZIKV African lineage viruses have not been recognized and it is not known whether this is because they do not occur, or because of limitations of detection and surveillance. Studies of the African lineage *in-vitro* and in animal models suggest the potential for increased pathogenesis in pregnancy compared with the Asian lineage, suggesting a propensity to cause foetal loss rather than birth defects (*19*). The epidemiological and clinical impact of introduction of novel ZIKV lineages and strains into areas where others have previously circulated is currently not known.

Accurate and up-to-date epidemiologic data on ZIKV are limited in many countries due to insufficient or absent systems and procedures for routine surveillance, detection and reporting of ZIKV disease cases (*27*). The majority of ZIKV infections are asymptomatic, and when disease occurs, symptoms are generally mild and non-specific and therefore may not be recognized or reported. In the absence of routine laboratory confirmation of ZIKV infections, as is typical in low-resourced settings, recognition of ZIKV circulation is often based on clinical case reports, traveller cases, and research studies. Even in settings with laboratory capacity, case detection and surveillance are challenging due to limited availability of diagnostic tests and difficulties with interpretation of serologic test results because of known cross-reactivity of ZIKV with related circulating flaviviruses, most notably DENV.

Lack of detection or reporting of ZIKV transmission, therefore, cannot necessarily be equated with evidence that transmission is not occurring, particularly in areas with low levels of transmission. In addition, transmission may have continued or resumed and not been detected in areas where vector surveillance and control efforts have been impaired, particularly over the course of the COVID-19 pandemic and recent reductions in public health funding. Decisions to guide family planning or travel to countries with a history of ZIKV transmission, particularly for pregnant women, women who may become pregnant, and their male partners, should be based on an assessment of information provided by country public health departments and consultation with the individual's healthcare provider (*28*).

WHO remains committed to strengthening public health systems for early detection and response to emergence, re-emergence, and global spread of ZIKV infection and its complications, including monitoring for CZS and Guillain-Barré syndrome. 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 ZIKV transmission, as well as to other *Aedes*-borne arboviruses and other emerging and re-emerging threats to public health.

- Read "Prevention of sexual transmission of Zika virus"
- Read "Information for travellers visiting Zika affected countries"
- Map of countries with current or previous Zika transmission
- List of countries with Zika and vectors

The following sections provide Zika epidemiology updates by WHO region, highlighting recent ZIKV circulation and new evidence of current or previous autochthonous transmission contained in reports and publications from 2024 and 2025.

African Region

Overview

There is evidence of ZIKV presence, either currently or in previous years, in 18 countries in the African Region. Microcephaly has only been described in the offspring of women in Africa followed detection (importation/emergence) of the Asian lineage ZIKV, first in Cabo Verde in 2015–2016 and subsequently in Angola in 2016–2017, in association with the heightened transmission in the Americas (*21*,*22*,*29*).

Information on the current incidence and trends of ZIKV transmission in the African Region remains limited because of paucity of testing and reporting of all arboviral diseases, including Zika. In countries with previously reported ZIKV circulation, sporadic cases were detected in Senegal in 2024 and 2025, and molecular evidence of infection in humans was described for the first time in Burkina Faso and in Kenya's Lamu Island. Confirmation of ZIKV infection in travellers described in publications and public health reports in 2024-2025 has revealed ZIKV autochthonous transmission in the Seychelles, where ZIKV circulation was not previously documented (*4*,*5*).

The identification and sequencing of Asian lineage ZIKV in Kenya's Lamu Island and in specimens from travellers to the Seychelles in 2024 mark the first indications of the circulation of this lineage in the western Indian Ocean over at least several months in that year (*4*,*5*,*23*). The Indian Ocean islands subregion concurrently grappled with increased chikungunya virus (another *Aedes*-borne arbovirus) transmission in 2024-2025, although the chikungunya transmission was predominantly driven by *Aedes albopictus* mosquitoes (*30*).

Kenya

ZIKV infections were confirmed in patients residing in Lamu Island, Kenya, who presented with acute febrile illness between August-September 2024 and were enrolled in a prospective febrile illness surveillance study (*23*). Arboviral sequencing identified a ZIKV homologous to an Asian lineage genome isolated from specimens collected during the 2018 Zika outbreak in Rajasthan, India (*23*).

Senegal

Two RT-PCR-confirmed Zika cases were reported in 2024 in Sédhiou and Sokone districts, respectively; limited additional case details were available [unpublished data provided by the WHO Regional Office for Africa].

Burkina Faso

Although serological studies have shown seroprevalence to Zika and the virus was previously identified in mosquito specimens in Burkina Faso, laboratory confirmation of acute infection in humans was not previously reported in the country (*31*,*32*). In April 2025, the Ministry of Health (MoH) reported confirmation of ZIKV infection by RT-PCR testing in a blood specimen collected from a 6-year-old girl from the Central Plateau region with dengue-like illness that started in late 2024 and no recent travel history (*33*). The patient recovered fully and no further cases were reported following an active case search in the community.

Seychelles

Zika virus infections were confirmed in two travellers in 2024, one returning to Italy and diagnosed in April 2024, and the other returning to France and diagnosed in August 2024, as described in peer reviewed literature (*4*,*5*). In addition, the UK Health Security Agency reported an imported Zika case in a traveller who had visited the Seychelles between January-June 2024 (*34*). Autochthonous ZIKV transmission was subsequently confirmed by the MoH through retrospective testing of locally collected patient specimens (*6*).

Madagascar

Seroprevalence studies have yielded variable results suggesting possible circulation of ZIKV in Madagascar, however, ZIKV infections in the country have not previously been confirmed (*35*,*36*). The MoH is expanding entomological and human surveillance to improve arbovirus preparedness and response (*37*). ZIKV infection was confirmed by RT-PCR testing in five blood specimens collected from patients in the Toamasina region of Madagascar with suspected arboviral disease in late 2025; no confirmed ZIKV infections have been reported in 2026 to date [WHO Regional Office for Africa]. Zika infections were also reported in two travellers returning to European countries from Madagascar in 2024-2025 [unpublished data provided by the European Centre for Disease Prevention and Control (ECDC)].

Region of the Americas

Overview

The WHO Regional Office for the Americas (AMRO)/Pan American Health Organization (PAHO) maintains data on reported cases of ZIKV disease (*9*). Data from ongoing surveillance are reported by countries and territories directly to PAHO/WHO or collected from epidemiological bulletins posted on Ministry of Health websites (*33*). Regional Zika data are updated weekly in the PAHO Health Information Platform, PLISA (*38*). It should be noted that there is variability in reporting practices by country or territory; some countries, such as Mexico, report only laboratory-confirmed cases, while others also report suspected and probable cases. Therefore, data from different countries and territories in the Americas are not directly comparable.

The ZIKV outbreak in the Americas peaked during the first half of 2016 and declined from 2017, when 56 904 cases (21 796 confirmed) were reported, with subsequent fluctuations between 22 978 and 40 528 suspected cases annually until 2023. In 2024, a total of 44 490 suspected cases (2 117 confirmed) and in 2025 a total of 27 187 suspected cases (1 841 confirmed) were reported in the Region (*9*). The majority of cases over the two years were reported by Brazil (95%) followed by Argentina (2%) and Bolivia (2%); however, the latter two countries did not report any confirmed cases. In 2024-2025, ZIKV confirmed cases were only reported by Brazil, Mexico, the United States of America (all imported cases), and Guatemala. The data from the Region indicate that ZIKV transmission persists at low levels in several countries, with observed heterogeneity between and within countries and a paucity of laboratory confirmation. While some countries have maintained strong surveillance programs that indicate that transmission may have been interrupted, surveillance and reporting are not uniform or consistent across the region and in some cases may not be sufficiently sensitive to detect low levels of transmission. Ongoing vigilance remains key to ensure early detection of potential re-emergence or re-introduction of ZIKV transmission, particularly as the proportion of immunologically naïve population grows.

Eastern Mediterranean Region

Overview

Prior to 2024, there was no documented evidence of autochthonous ZIKV transmission in any WHO Eastern Mediterranean Region countries. However, because of the documented presence of *Aedes aegypti* populations in several countries in the region, the WHO Regional Office for the Eastern Mediterranean Region developed ZIKV preparedness plans and developed a framework for monitoring and evaluation of their implementation (*39*,*40*)

Pakistan

During retrospective testing of specimens collected in 2021 from suspected dengue cases in Karachi, Pakistan, ZIKV RNA was detected in two specimens by metagenomic sequencing and one of those had evidence of coinfection with DENV (*7*). The study authors reported that the ZIKV sequences identified were more closely related to those circulating in South America than those circulating in neighbouring countries in South Asia. This represents the first recognized autochthonous Zika virus transmission in the Eastern Mediterranean Region. In 2022, samples were collected from a cohort of 13 patients with antibodies to ZIKV; one of those had detectable ZIKV RNA on real time quantitative RT-PCR testing and three patients had serological results suggestive of recent ZIKV infection. The Pakistan MoH is planning to conduct additional testing and to scale up surveillance testing to further explore these findings.

Yemen

During surveillance of acute undifferentiated febrile illness by the Malaria Control Program of the Yemen MoH in collaboration with the United States Naval Medical Research Unit EURAFCENT, screening of 186 patient specimens collected in late May/early June 2025 for ZIKV infection by RT-PCR identified ZIKV RNA in the specimens of 8 patients (*8*). Three of the specimens also had evidence of dengue RNA (two dengue serotype 4, and one dengue serotype 3), with the cases occurring concurrent with a recognized dengue outbreak. The Yemen MoH is planning to expand current dengue surveillance to include testing for ZIKV infections.

European Region

Although numerous cases of travel associated ZIKV infections were reported in European travellers from 2015-2018, no autochthonous cases were documented. In 2019, however, autochthonous, mosquito-borne transmission of ZIKV was identified in the Var department in South-eastern France (*12*). To maintain vigilance about areas at risk for introduction and autochthonous transmission of ZIKV and other mosquito-borne arboviruses, the distribution of mosquito vectors in the European Union is regularly updated and as of 2025, autochthonous cases of Zika and a subset of other arboviral diseases are mandatorily reportable in real time.

South-East Asia Region

Overview

ZIKV has been circulating since at least the 1960s in several countries of the South-East Asia Region. The region as a whole remains at risk for ZIKV transmission because of the presence of competent vectors, often in high densities. Zika cases have been confirmed in Bangladesh, India, the Maldives and Thailand in the period from 2024-2025. In addition, the Institute of Public Health reported the first confirmed Zika case in Timor Leste in 2024 during differential diagnostic testing in the context of a chikungunya outbreak; however, additional clinical and travel history are not available [unpublished data provided by the Timor Leste MoH] (*41*).

Bangladesh

ZIKV was first detected retrospectively in a sample that was collected from a suspected dengue case in 2014. In 2023, ZIKV infection was confirmed in five patients living in close geographic proximity as part of a diagnostic evaluation study conducted at the time of a dengue outbreak in Dhaka (*42*). During September–December 2024, 10 confirmed Zika cases were detected across a wider area in and around Dhaka and in patients with no history of international travel, suggesting autochthonous transmission (*43*). Systematic screening for Zika virus infections, in addition to dengue and chikungunya, continued into the subsequent year and provisional data from 2025 indicated that fewer than 10 confirmed Zika virus disease cases were identified in Bangladesh during June–November 2025 (IEDCR, unpublished data, November 2025) (*43*).

India

Over the course of 2024 a total of 151 Zika cases were reported from three states (*44*). Most cases (N=140) were reported from Maharashtra State, including 125 cases from Pune district, 11 from Ahmednagar district, and one case from each of Kolhapur, Sangli and Solapur districts and Mumbai suburban area. Additionally, Karnataka state reported ten cases in 2024, with seven reported from Bengaluru urban district and three from Shivamogga district. Gujarat state reported one Zika case in Gandhinagar Corporation in 2024.

Maldives

From 2016 to 2025, a total of 10 Zika cases were reported, with no cases detected between 2019 and 2022; however, two cases were observed in 2024 and 2025, with test positivity increasing from 0.26% in 2024 to 1.04% in 2025 [unpublished data provided by the Maldives MoH]. Zika infections were also reported in travellers returning to European countries from the Maldives (*45*) [unpublished data provided by the ECDC].

Thailand

The Thailand Ministry of Public Health reported 423 Zika cases in 2024 and 245 Zika cases in 2025 (*10*). This was preceded by a year of increased transmission in 2023, when over 700 cases were reported. A recent review of data on outbreaks in Thailand and cases detected in travellers showed widespread transmission in several regions and continued risk of exposure annually, particularly from May-October (*46*). Over the same time period, ZIKV infections with pregnancy complications continued to be reported in travellers returning from Thailand (*25*,*26*,*47*).

Western Pacific Region

Overview

In the Western Pacific Region, ZIKV transmission has been documented previously in some countries and areas although the availability and sensitivity of surveillance systems vary across the region (*3*). Between 2024 and 2025, Zika detections remained low and sporadic, with most notifications identified as travel-related cases reported by countries outside the exposure location. During this period, Australia, China Macao SAR, France, Japan, Republic of Korea, New Zealand, the United Kingdom, and the United States reported imported Zika cases linked to travel to Fiji, Indonesia, Lao People's Democratic Republic, Malaysia, the Philippines (*48*). However, Zika confirmed cases were not officially reported by these source countries during 2024–2025. In addition, Kiribati has now been included as a country with evidence of prior autochthonous transmission based further review of the data presented in a previous WHO Zika epidemiology update (*2*,*49*).

Singapore

As of epidemiological week 53, 28 December 2025 to 3 January 2026, Singapore recorded 13 laboratory-confirmed Zika cases in 2024 and 16 cases in 2025, according to the Weekly Infectious Disease Bulletin of the Communicable Diseases Agency, Singapore (*50*). Reported Zika cases remained sporadic, and no active clusters were identified during this period. Public health authorities intensified integrated vector control activities, including targeted elimination of mosquito breeding sites and strengthened entomological and environmental surveillance, such as the deployment of Gravitraps and wastewater-based monitoring.

Tonga

Preliminary findings from a serological study conducted in 2024 provided evidence of Zika virus seroprevalence (*51*). However, laboratory confirmation of acute human infection had not been reported in the country since 2016.

Conclusions

Ten years after the declaration of the Public Health Emergency of International concern, Zika remains a public health challenge as a disease for which there are no approved antiviral treatments or vaccines available. Infections are largely asymptomatic, but complications can occur if there is infection during pregnancy, and neurological illness can occur in some children and adults. ZIKV continues to circulate across multiple regions where infection, disease, and sequelae are likely underrecognized, and there is a growing proportion of people without immunity to ZIKV infection living in areas with competent *Aedes* mosquito vectors, who will be vulnerable to infection if ZIKV is introduced or reintroduced locally. In addition to residents of areas with ZIKV transmission, travellers to such areas and their sexual partners, particularly pregnant women, are also at risk of adverse outcomes. Continued vigilance, strengthened surveillance, and enhanced preparedness for introduction or reemergence of Zika should therefore be prioritized.

Recommended country actions

Member states are encouraged to strengthen epidemiological surveillance through support for monitoring and testing practices and implementation of clear case definitions and epidemiologically appropriate laboratory testing algorithms. Surveillance efforts for ZIKV could focus in particular on potentially high-yield patient populations such as patients with fever and rash, neonates with birth defects including microcephaly, and pregnant women with defined adverse pregnancy outcomes.

Clinicians should be equipped through continuing education programs in clinical diagnosis and management. Vector surveillance and control activities should be strengthened in accordance with integrated vector management principles and health authorities should engage communities using validated risk communication tools to enable symptom recognition and protective measures against ZIKV infection. Research and development of improved diagnostics and medical countermeasures are ongoing priorities to ensure better diagnosis and early detection of ZIKV transmission

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