REGION 2 SOUTH COMMUNICABLE DISEASE SURVEILLANCE SUMMARY
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INTERNATIONAL DISEASE OUTBREAK SUMMARIES – WHO DISEASE OUTBREAK NEWS

Oropouche virus disease - Region of the Americas – 5 December 2024

Situation at a glance

Since the last Disease Outbreak News on this event was published on 23 August 2024, three additional countries and one territory (Ecuador, Guyana, Panama and Cayman Island) have reported confirmed Oropouche virus disease in the Region of the Americas in 2024. In addition, imported Oropouche cases have been reported from Canada, the United States of America and countries of the European Region. As of 25 November 2024, a total of 11 634 confirmed Oropouche cases, including two deaths, have been reported in the Region of the Americas, across ten countries and one territory: Bolivia (Plurinational State of), Brazil, Canada, Cayman Islands, Colombia, Cuba, Ecuador, Guyana, Panama, Peru and the United States of America. Based on available information, WHO assesses the overall public health risk posed by this virus to be high at the regional level and low at the global level. As the arbovirus season is starting in the region, WHO urges countries at risk to strengthen epidemiological and entomological surveillance and to reinforce preventive measures in the population. This is crucial due to the geographical expansion of the virus and the possible new vectors and transmission routes, including vertical transmission, that could affect both the general population and vulnerable groups, such as pregnant women, their fetuses, and newborns.

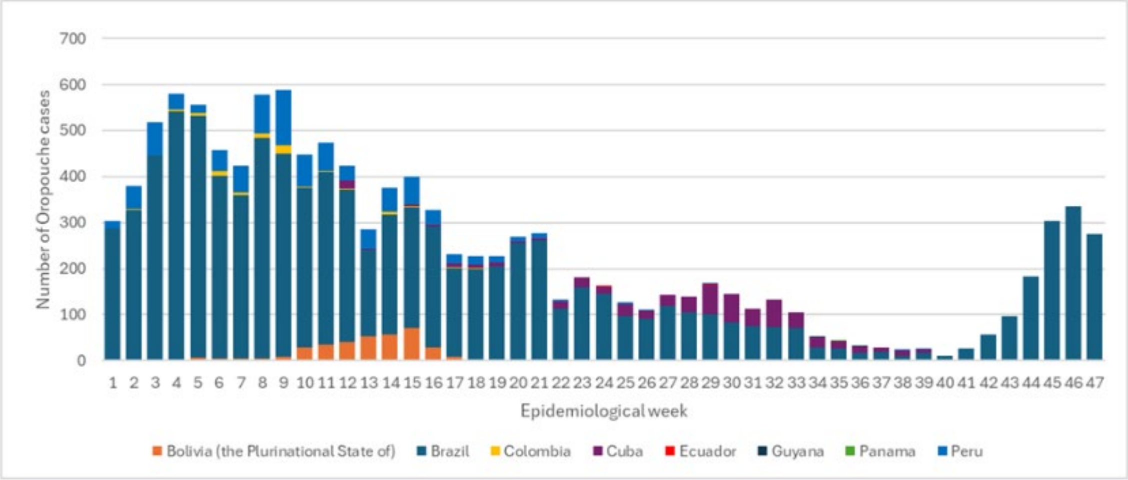
Description of the situation

Since the last Disease Outbreak News on this event was published on 23 August 2024, three additional countries and one territory (Ecuador, Guyana, and Panama) have reported confirmed Oropouche virus disease in the Region of the Americas. In addition, imported Oropouche cases were reported from the Cayman Islands, Canada, the United States of America and a few countries in the European Region.

Between 1 January and 25 November 2024, 11 634 confirmed Oropouche cases, including two deaths, have been reported in the Region of the Americas: Bolivia (Plurinational State of) (356 cases), Brazil (9563 cases, including two deaths), Canada (two imported cases), Cayman Island (one imported case), Colombia (74 cases), Cuba (603 cases), Ecuador (two cases), Guyana (two cases), Panama (one case), Peru (936 cases), and the United States of America (94 imported cases). Additionally, imported Oropouche cases have been reported in countries in the European Region (30 cases) (1).

Cases and consequences of vertical transmission of Oropouche virus infection have been reported in Brazil and Cuba. Brazil has confirmed three cases of vertical transmission (two cases of fetal death and one case of congenital anomaly) and reported that under investigation are 15 fetal deaths, five spontaneous miscarriages, and three cases of congenital anomalies.[1] Additionally, in September, Cuba confirmed a case of congenital anomaly with two further cases under investigation.

Figure 1. Number of confirmed Oropouche cases in 2024 by country and epidemiological week of symptom onset Region of the Americas*



***Source: Adapted and reproduced by PAHO/WHO from the data reported by the respective countries.**

The following is a summary of the situation in the countries that have reported confirmed Oropouche cases in the Americas as of 25 November 2024.

The Plurinational State of Bolivia: Between 1 January and 5 October 2024, there were 356 Oropouche cases confirmed by reverse transcription polymerase chain reaction (RT-PCR) testing. Transmission has been reported in three departments: La Paz with 75.3% of cases (268 cases), followed by Beni with 21.3% of cases (76 cases), and Pando with 3.4% of cases (12 cases). Cases have been reported in 16 municipalities that are considered endemic for this disease, with the highest proportion of cases reported in the municipalities of Irupana, La Paz, with 33% of cases; followed by La Asunta, La Paz, with 13% of cases; Chulumani, La Paz, and Guayaramerín, Beni, with 12% each.

Half of the cases are female (179 cases) and the age group with the highest number of cases is the 30-39 years age group accounting for 20% of cases (70 cases). No deaths have been recorded that could be associated with OROV infection. In addition, between 23 March and 13 April 2024, ten cases of coinfection of Oropouche and dengue were reported in patients in three municipalities of the department of La Paz, all of whom tested positive for dengue by RT-PCR with DENV-1 (two cases) and DENV-2 (eight cases) serotyping (2).

Brazil: Between 1 January and 25 November 2024, 9563 Oropouche cases were confirmed by RT-PCR. Most cases have been reported in municipalities in the northern states; however, to date, cases have been reported in 22 of the country's 27 states. The Amazon region, an area considered endemic for Oropouche, accounts for 70% of the cases reported in the country, with seven states reporting cases: Amazonas (3231 cases), Rondônia (1711 cases), Acre (273 cases), Roraima (277 cases), Pará (157 cases), Amapá (128 cases), and Tocantins (eight cases) (3). Additionally, autochthonous transmission has been documented in 15 non-Amazonian states, some of which had not previously reported cases: Bahia (889 cases), Espírito Santo (1763 cases), Ceará (249 cases), Minas Gerais (194 cases), Santa Catarina (178 cases), Pernambuco (144 cases), Rio de Janeiro (116 cases), Alagoas (116 cases), Sergipe (34 cases), Maranhão (33 cases), Piauí (30 cases), Mato Grosso (18 cases), São Paulo (eight cases), Paraíba (five cases) and Mato Grosso do Sul (one case)(3, 4).

Over half of the cases (52%; 4995) are male and the age group with the highest number of cases is 20-29 years, with 21% of cases (1963 cases) (3).

Brazil’s IHR National Focal Point (NFP) reported two fatal cases of OROV infection detected retrospectively in the state of Bahia1 and six cases are under investigation: one in the state of Parana, with probable source of infection in the state of Santa Catarina, two in Espírito Santo, one in Acre, one in Alagoas, and one in Mato Grosso (4).[2] Additionally, on 12 August 2024, Brazil reported a case of encephalitis associated with OROV. The case is a male resident of the state of

Piauí (3).[3] As of 16 November 2024, three cases of vertical transmission have been confirmed:[4] two cases of fetal death: one in Pernambuco and one in Ceará; and one case of congenital anomaly in Acre. As for cases under investigation in the country, 15 cases of fetal death in Pernambuco (15 cases), three cases of congenital anomaly in Acre (two cases) and Bahia (one case), and five spontaneous miscarriages in Pernambuco have been identified (3-5).

Colombia: Between 1 January and 5 October 2024, 74 confirmed Oropouche cases have been reported in three departments of the country: Amazonas (70 cases), Caqueta (one case), and Meta (one case); additionally, two cases were identified in travellers from Tabatinga, Brazil. The cases were identified through a retrospective laboratory case-finding strategy implemented in 2024 by the National Institute of Health of Colombia based on dengue surveillance (38 cases) and through investigation of febrile syndrome cases (36 cases). Over half of the cases (51.4%; 38) were female and the age group with the highest number of cases was 10-19 years, with 36.5% of the cases (27 cases). No deaths have been recorded that could be associated with OROV infection.

Six cases of coinfection with dengue were reported in the department of Amazonas, four in the municipality of Leticia (two with DENV-1 and two with DENV-2), and one in the municipality of Puerto Nariño (DENV-3), and in the department of Meta, one in the municipality of Guamal (DENV-4). Regarding the surveillance of cases of vertical transmission and its consequences, up to 3 October 2024, two cases of Oropouche have been identified in pregnant women, both from Leticia, aged 18 years (onset of symptoms at 29 weeks of gestation) and 22 years (onset of symptoms at 34 weeks of gestation), respectively. Both evolved favorably and their children were born without complications. To date, none of the infants show evidence of congenital anomalies, neurological syndromes or neurodevelopmental disorders.[5]

Cuba: Between 27 May and 25 November 2024, a total of 603 confirmed cases were reported. Cases continue to be identified through surveillance for non-specific febrile syndrome, with cases recorded in 109 municipalities in the 15 provinces of the country. The provinces of Havana (174 cases), Santiago de Cuba (75 cases), Pinar del Rio (47 cases), and Cienfuegos (39 cases) accounted for 55% of confirmed cases.[6]

More than half of the cases were female (55%, 331) and the highest proportion of cases was recorded in the 19-54 age group (53%, 320). On 19 September 2024, Cuba reported three cases of Guillain-Barré syndrome (GBS) associated with OROV. The three cases, two females and one male aged 51, 53, and 64 years respectively, presented with onset of symptoms in June. The cases are residents of the province of Santiago de Cuba, in the municipalities of San Luis (one case) and Santiago de Cuba (two cases). Serum, cerebrospinal fluid (CSF) and urine samples were collected and tested positive with RT-PCR for OROV.

Seven cases of Oropouche were identified in pregnant women, two of whom delivered live babies without any congenital anomalies being detected. On the other hand, three cases of congenital anomalies of the central nervous system with suspected infectious aetiology have been identified through the national antenatal referral service, of which one has undergone virological testing with a positive result for OROV in fetal heart blood; the other two cases are under investigation.

Ecuador: As of 5 October 2024, two laboratory-confirmed cases of Oropouche virus disease were reported, which were detected during a retrospective analysis of dengue-negative samples by the National Institute of Public Health Research (INSPI per its acronym in Spanish). The first case occurred in a 62-year-old from Bolivar province who developed symptoms on 11 June. The second case occurred in a 36-year-old from Los Rios province who developed symptoms on 17 July. Both patients have no history of recent travel. None of the cases required hospitalization and have fully recovered.

Guyana: Between 8-14 September 2024, two laboratory-confirmed cases of Oropouche virus disease were reported, being the first detection of this disease in the country. The first case was a 47-year-old who presented with symptoms on 21 August 2024. The case sought medical attention on 24 August 2024. Blood samples were collected, and RT-PCR test performed on 3 September was positive for OROV. The second case reported from a 42-year-old who presented with symptoms on 2 September 2024. The case sought medical attention on 3 September 2024. Blood samples was collected, and RT-PCR tests performed on 7 September was positive for OROV. Both cases had resided in the same geographical area in the Mahaica-Berbice region, for at least 14 days prior to symptom onset and neither has reported history of travel.

Panama: On 15 November 2024, the Panama IHR National Focal Point reported the first confirmed case of Oropouche virus diseases in 2024. The case was confirmed by the Gorgas Commemorative Institute of Health studies (ICGES, per its acronym in Spanish) laboratory in Panama. The case age is between 30 and 35 years from Province of Coclé with a recent travel history within the country. The case reported onset symptoms on 27 August 2024, and was diagnosed with suspected dengue. The case didn't require hospitalization and recovered at home. This case was detected through the laboratory surveillance strategy, which involved testing a sample from a patient with dengue-like symptoms who initially tested negative for DENV. On 15 November, the case was confirmed for OROV by RT-PCR. Although recovered, the case is currently under investigation, as the exact site of exposure and transmission has not yet been determined.

Peru: Between 1 January and 5 October 2024, 936 confirmed Oropouche cases have been reported in eight departments of the country. The departments are Loreto (466 cases), Madre de Dios (312 cases), Ucayali (138 cases), Huanuco (15 cases), Junin (two cases), Tumbes (one case), San Martin (one case), and Puno (one case). Over half of the cases (51%; 476) were male, and the age group with the highest number of cases was 30-39 years, with 37% of the cases (348 cases). There were no deaths and no reports of possible vertical transmission reported from the country.

Imported cases in non-endemic countries and territories

Canada: As of 21 September 2024, Canada confirmed two Oropouche cases with a history of travel to Cuba.

Cayman Islands: On 16 September 2024, the Caribbean Public Health Agency (CARPHA) confirmed an imported case of Oropouche virus in an adult woman from the Cayman Islands who had travelled to Cuba. The patient developed symptoms, including fever and muscle pain, on 10 August after returning. The initial test for Oropouche virus in the Cayman Islands on 12 August was positive and confirmed at the CARPHA reference laboratory from a convalescent sample collected on 15 August.

United States of America: As of 8 October 2024, 94 imported cases of Oropouche virus disease were identified in the states of Florida (90 cases), California (one case), Colorado (one case), Kentucky (one case), and New York (one case). The median age of the cases was 51 years (ranging from 6 to 94 years) and 48% were female. A total of three cases were hospitalized. Two of the cases presented with neuroinvasive disease, no deaths were reported, and all cases had a history of travel to Cuba.

Additionally, between 2 June and 20 July 2024, 30 imported cases of Oropouche have been identified in three countries of the WHO European Region: Germany (three cases), Spain (21 cases), and Italy (six cases); 20 of these cases had a history of travel to Cuba and one to Brazil, these cases are of the first cases registered in this region.

Undiagnosed disease - Democratic Republic of the Congo – 8 December 2024

Situation at a glance

Between 24 October and 5 December 2024, Panzi health zone in Kwango Province of Democratic Republic of the Congo recorded 406 cases of an undiagnosed disease with symptoms of fever, headache, cough, runny nose and body ache. All severe cases were reported to be severely malnourished. Among the cases, 31 deaths have been registered. The majority of cases reported are among children, particularly those under five years of age. The area is rural and remote, with access further hindered by the ongoing rainy season. Reaching it from Kinshasa by road takes an estimated 48 hours. These challenges, coupled with limited diagnostics in the region, have delayed the identification of the underlying cause. Rapid response teams have been deployed to identify the cause of the outbreak and strengthen the response. The teams are collecting samples for laboratory testing, providing a more detailed clinical characterization of the detected cases, investigating the transmission dynamics, and actively searching for additional cases, both within health facilities and at the community level. The teams are also aiding with the treatment of patients, risk communication and community engagement. Given the clinical presentation and symptoms reported, and a number of associated deaths, acute pneumonia, influenza, COVID-19, measles and malaria are being considered as potential causal factors with malnutrition as a contributing factor. Malaria is a common disease in this area, and it may be causing or contributing to the cases. Laboratory tests are underway to determine the exact cause. At this stage, it is also possible that more than one disease is contributing to the cases and deaths.

Description of the situation

On 29 November 2024, the Ministry of Public Health of the Democratic Republic of the Congo reported to WHO an alert regarding increased deaths from an undiagnosed cause in Panzi health zone.

Between 24 October and as of 5 December 2024, Panzi health zone in Kwango Province has recorded 406 cases of an undiagnosed disease with symptoms of fever, headache, cough, runny nose and body ache and 31 deaths (Case Fatality Ratio or CFR of 7.6%). The reported cases had a peak in epidemiological week 45 (week ending 9 November 2024). The outbreak is still ongoing. According to a press briefing by the Ministry of Health on 5 December, there have been several additional deaths outside of health facilities (community deaths). These deaths still need to be investigated, characterized (age, gender etc) and verified.

Cases have been reported from nine out of 30 health areas in Panzi health zone: Kahumbulu, Kambandambi, Kanzangi, Kasanji, Kiama, Mbanza Kipungu, Makitapanzi, Mwini ngulu, and Tsakala Panzi. The majority of cases (95.8%) are reported from Tsakala Panzi (169), Makitapanzi (142) and Kanzangi (78) health areas.

In Panzi health zone, children aged 0-14 years represent 64.3% of all reported cases, with the age groups 0-59 months, 5-9 years, and 10-14 years accounting for 53%, 7.4%, and 3.9% of cases, respectively. Females constitute 59.9% of the total cases. Among the deaths, 71% are below the age of 15, with 54.8% of the total in children under the age of five years. All severe cases were reported to be malnourished. There are 145 cases aged 15 and above, of which nine died (CFR: 6.2%). Deaths have primarily occurred in the village communities.

The area experienced deterioration in food insecurity in recent months, has low vaccination coverage and very limited access to diagnostics and quality case management. There is a lack of supplies and transportation means and shortage of health staff in the area. Malaria control measures are very limited.

The clinical presentation of patients includes symptoms such as fever (96.5%), cough (87.9%), fatigue (60.9%) and a running nose (57.8%). The main symptoms associated with death include difficulty in breathing, anaemia, and signs of acute malnutrition. Based on the current context of the affected area and the broad presentation of symptoms, a number of suspected diseases need to be ruled out through further investigations and laboratory testing. These include but are not limited to measles, influenza, acute pneumonia (respiratory tract infection), hemolytic uremic syndrome from E. coli, COVID-19, and malaria.

Marburg virus disease – Rwanda – 20 December 2024

Situation at a glance

On 20 December 2024, after two consecutive incubation periods (total of 42 days) since the second negative PCR test was conducted on 7 November for the last confirmed Marburg case, and without a new confirmed case reported, the Ministry of Health of Rwanda declared the end of the Marburg virus disease (MVD) outbreak, as per the WHO recommendations. The outbreak had been declared on 27 September 2024. As of 19 December 2024, 66 confirmed cases,15 deaths with a case fatality ratio (CFR) of 23%, and 51 recovered cases have been reported. The last confirmed case was reported on 30 October 2024. WHO through its country office and development partners provided technical and financial support to the government to contain this outbreak. The risk of re-emergence of MVD still remains even after the official declaration of the end of the outbreak, linked to viral persistence in body fluids (mostly semen) of recovered patients and the animal reservoir in the country. WHO encourages maintaining early case detection and care capacities in addition to sustaining the ability to quickly respond, also underscoring the importance of the recovered patient program, psychosocial support, and continued risk communication and community engagement.

Description of the situation
Since the last Disease Outbreak News on this event was published on 13 November 2024, no new confirmed cases of Marburg virus disease (MVD) have been reported in Rwanda. As of 19 December 2024, 66 confirmed cases, including 15 deaths (CFR 23%), and 51 recovered cases have been reported. Among the confirmed cases, 68% are males, and 46% are adults between 30 and 39 years of age. Health workers from two health facilities in Kigali account for almost 78% of all confirmed cases. Most cases are reported from the three districts of Kigali city, namely Gasabo, Kicukiro and Nyarugenge.

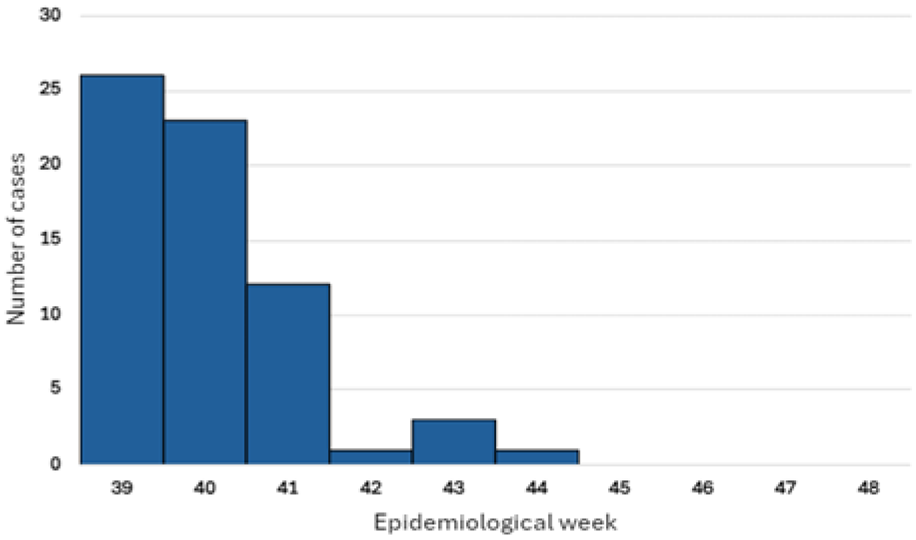
The highest number of confirmed cases (61) were reported in the first three epidemiological weeks (week 39-41, from 23 September to 13 October) of the outbreak. This was followed by a sharp decline, with three or less cases reported between epidemiological week 42 (14 to 20 October) and 44 (28 October to 3 November). The last confirmed case was reported on 30 October and the last death on 14 October 2024.

As of 6 December 2024, 7874 Marburg virus tests had been conducted at the Rwanda Biomedical Center.

On 8 November 2024, the recommended 42-day countdown to declare the end of the outbreak commenced, following two consecutive PCR negative tests from the last confirmed MVD case on 7 November. The 42-day countdown period is twice the maximum incubation period for Marburg virus infections, since the last potential exposure to the last reported case. The last confirmed case was reported on 30 October and the last death on 14 October 2024.

On 20 December 2024, after completion of two consecutive incubation periods (total of 42 days) without a new confirmed case being reported, the Ministry of Health of Rwanda declared the end of the outbreak.

Figure 2. Marburg virus disease cases by week of reporting in Rwanda, as of 19 December 2024, (n=66)



[Acute respiratory infections complicated by malaria (previously undiagnosed disease) - Democratic Republic of the Congo – 27 December 2024]

Situation at a glance
This is an update to the Disease Outbreak News on Undiagnosed disease in the Democratic Republic of the Congo published on 8 December 2024 (now named acute respiratory infections complicated by malaria). It includes updated epidemiological investigation information and preliminary laboratory results. On 29 November, an alert was raised by local health zone authorities of Panzi health zone in Kwango province after an increase in deaths, particularly among

children under five years of age, following febrile illness. Enhanced epidemiological surveillance was rapidly implemented, which in the absence of a clear diagnosis was based on the detection of syndromic cases of febrile illnesses with cough, body weakness, with one of a number of other symptoms compatible with acute respiratory and febrile illnesses. This resulted in a rapid increase in the number of cases meeting the definition, with a total of 891 cases reported as of 16 December. However, the weekly number of reported deaths (48 deaths reported over the period) has remained relatively stable. As of 16 December, laboratory results from a total of 430 samples indicated positive results for malaria, common respiratory viruses (Influenza A (H1N1, pdm09), rhinoviruses, SARS-COV-2, Human coronaviruses, parainfluenza viruses, and Human Adenovirus). While further laboratory tests are ongoing, together these findings suggest that a combination of common and seasonal viral respiratory infections and falciparum malaria, compounded by acute malnutrition led to an increase in severe infections and deaths, disproportionally affecting children under five years of age. Multidisciplinary rapid response teams have been deployed to investigate the event and strengthen the response. Efforts are ongoing to address the health needs in Panzi health zone. Enhanced surveillance in the community and within health facilities continues. The teams have also been providing support for diagnosis, the treatment of patients as well as with risk communication and community engagement. This event highlights the severe burden from common infectious diseases (acute respiratory infections and malaria) in a context of vulnerable populations facing food insecurity. It emphasizes the need to strengthen access to health care and address underlying causes of vulnerability, particularly malnutrition, given the worsening food insecurity.

Description of the situation

Since the last Disease Outbreak News on this event was published on 8 December 2024, 485 additional suspected cases and 17 additional deaths have been reported from Panzi health zone in Kwango Province, Democratic Republic of the Congo, across 25 out of the 30 health areas in Panzi. These cases were identified as a result of enhanced surveillance put in place following the report of deaths in the context of febrile illness with acute respiratory symptoms and anaemia, first reported on 29 November. While the number of reported cases was not deemed particularly unusual in a context of high burden of pneumonia, malaria and acute respiratory infections, particularly at the start of the rainy season, it is the increase in the number of deaths that triggered the alert on 29 November.

In the absence of diagnosis, a broad surveillance case definition was used, with the resulting case numbers reflecting the detection of any febrile illness occurring in Panzi and thus representing a range of diseases and clinical syndromes. The case definition includes: *any person living in the Panzi health zone from September 2024 to date, presenting with fever, cough, body weakness, runny nose, with or without one of the following symptoms and signs: chills, headache, difficulty breathing, malnutrition, body aches*. This was done to better understand the epidemiology and characteristics of deaths and to collect a range of clinical samples for laboratory testing.

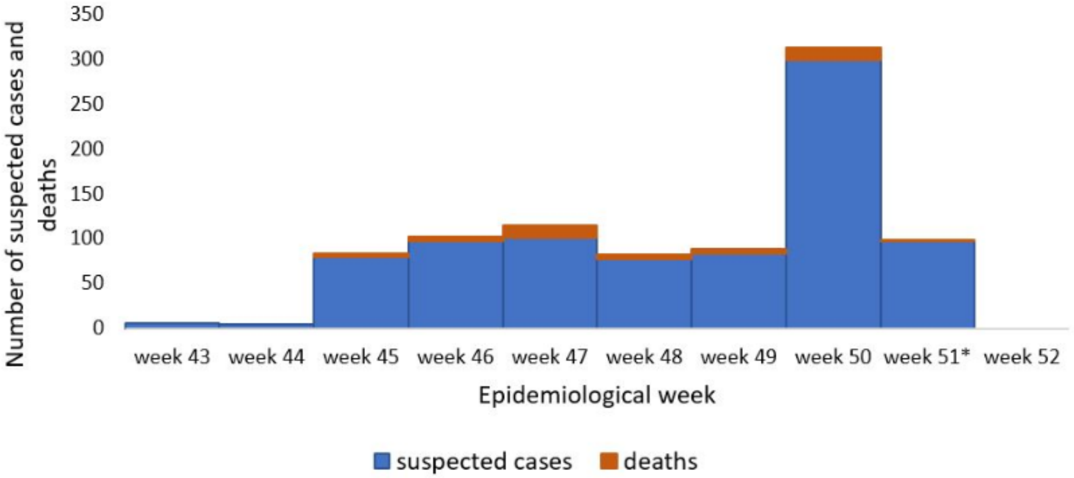
Between 24 October and 16 December 2024, 48 deaths and a total of 891 cases across 25/30 health areas of Panzi health zone met the case definition. Children under five years of age are disproportionally affected, representing 47% of all cases and 54% of all deaths, while they represent around 18% of the population, likely reflecting the vulnerability of young children to severe disease and death in this context. The main symptoms associated with death include difficulty in breathing, anaemia, and signs of acute malnutrition.

A total of 430 samples including blood samples, oropharyngeal and nasopharyngeal swabs, urine and breastmilk samples were collected from suspected cases in Panzi health zone and transported to the laboratory at the INRB. Out of 88 rapid diagnostics tests for malaria performed in the field, 55 (62%) samples tested positive. In addition, out of 26 samples analyzed by PCR BioFire Global Fever Panel test (which tests 18 different pathogens including some of the viral hemorrhagic fevers), 17 (65%) samples tested positive for Plasmodium falciparum. In addition, a total of 89 samples were tested at INRB Respiratory Disease Surveillance Laboratory. Of the 89 samples, 64 samples were positive for common respiratory viruses including Influenza A (H1N1, pdm09) (n=25), rhinoviruses (n=18), SARS-COV-2 (n=15), Human coronaviruses (n=3), parainfluenza viruses (n=2), and Human adenovirus (n=1).

Other laboratory tests on the collected samples, including virological and bacterial analysis, are still ongoing. The ongoing investigations and preliminary laboratory findings suggest that a combination of common viral respiratory infections and falciparum malaria, compounded by acute malnutrition led to an increase in severe infections and deaths.

Enhanced surveillance will continue, alongside response activities. The number of weekly reported suspected cases has remained steady with the exception of an increase in epidemiological week 50 (week ending 15 December 2024, Figure 3). While this may partly reflect an increase in transmission of respiratory viruses and malaria with the rainy season, it is driven by an increase in surveillance and case finding following the deployment of the rapid response teams. Notably, the increase in cases is not matched with a comparable increase in deaths.

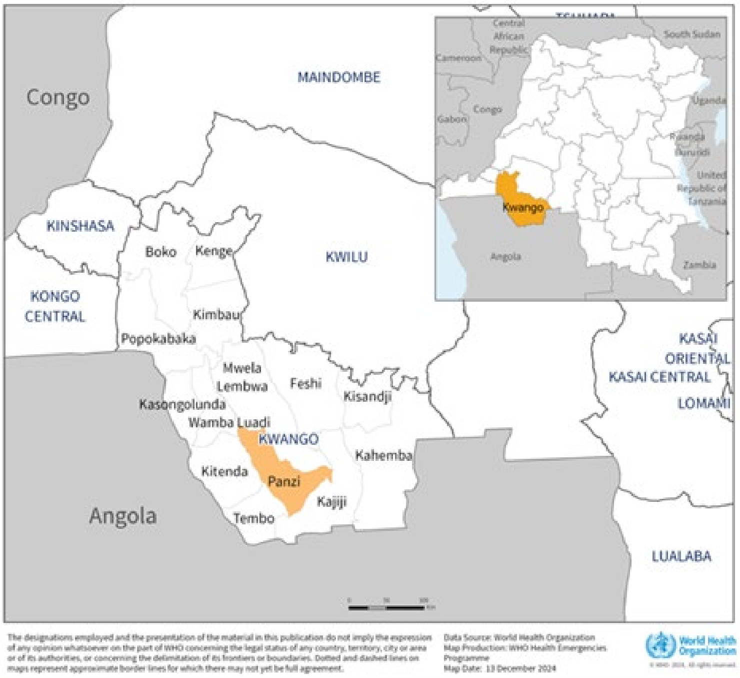
Figure 3. Weekly epidemiological curve showing suspected cases and deaths reported between 24 October to 16 December 2024, Panzi health zone in Kwango Province, Democratic Republic of the Congo



* Data for the epidemiological week 51 is not complete at the time of publication.

There are proportionally more cases reported among females (58%, 514/889), particularly among adults (66% female, 173/262). While data is lacking to better understand this difference, it may stem from contact patterns of respiratory virus transmission within households, particularly a close interaction between mothers and children during acute respiratory illnesses.

Figure 4. Geographic description of the affected health zone in Kwango Province, Democratic Republic of the Congo



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Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme
Map Date: 13 December 2024

The affected area experienced deterioration in food security in recent months, with increasing levels of acute malnutrition. Between July and December 2024, which coincides with a drop in acute malnutrition, Kwango province was in Integrated Food Security Phase Classification (IPC) Acute Malnutrition (AMN) Phase 3 (Serious). Between January and June 2025, an increase in cases of malnutrition is projected in the province with a significant deterioration in the nutritional situation expected, moving to IPC AMN Phase 4 (Critical). Between July 2024 and June 2025, nearly 4.5 million children aged 6 to 59 months in the DRC are facing or expected to face acute malnutrition, including approximately 1.4 million cases of severe acute malnutrition and 3.1 million cases of moderate acute malnutrition. It is also estimated that 3.7 million pregnant and breastfeeding women are facing or expected to face acute malnutrition over the same period.[1]

Severe acute malnutrition is a life-threatening condition that requires medical treatment. In addition, disease and malnutrition combine to worsen each other. The area has low routine vaccination coverage. There is also very limited access to diagnostics and quality case management, and a lack of supplies and transportation, shortage of health staff in the area, as well as financial and geographical barriers to access to health care. Increasing malaria trends are expected with the start of the rainy season, however, malaria control measures in the area are very limited. Together, these factors may increase the severity of malaria, and common respiratory infections.

Overall, this event highlights the severe burden from common infectious diseases (acute respiratory infections and malaria) in a context of vulnerable populations facing food insecurity and emphasizes the need to strengthen access and quality of health care.

Trends of acute respiratory infection, including human metapneumovirus, in the Northern Hemisphere – 7 January 2025

Situation at a glance

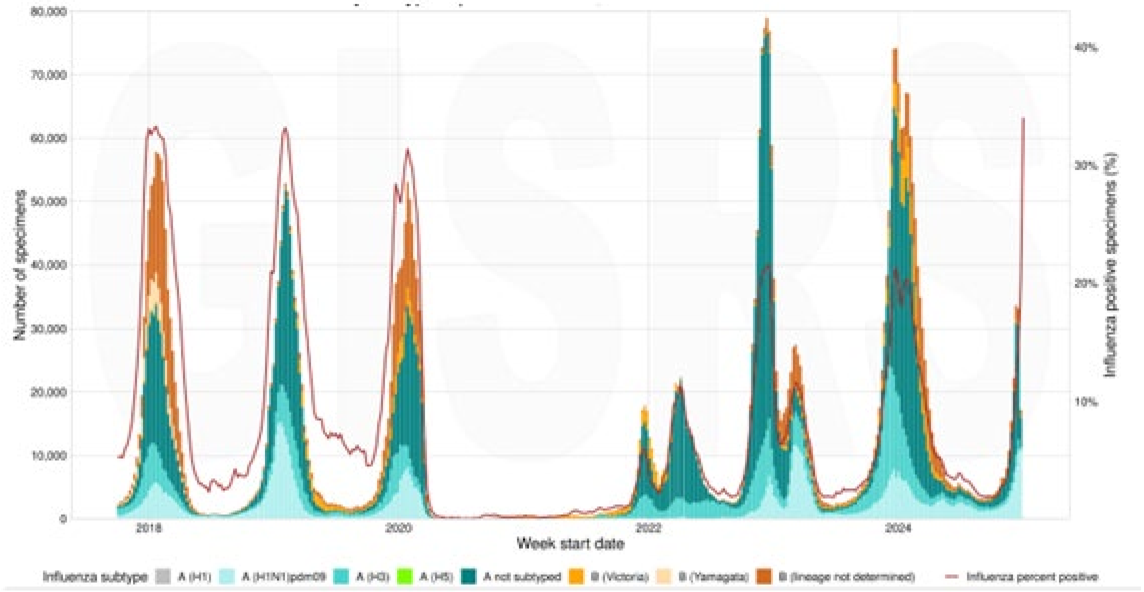
In many countries of the Northern Hemisphere, trends in acute respiratory infections increase at this time of year. These increases are typically caused by seasonal epidemics of respiratory pathogens such as seasonal influenza, respiratory syncytial virus (RSV), and other common respiratory viruses, including human metapneumovirus (hMPV), as well as mycoplasma pneumoniae. Many countries conduct routine surveillance for acute respiratory infections and common respiratory pathogens. Currently, in some countries in the temperate Northern hemisphere, influenza-like illness (ILI) and/or acute respiratory infection (ARI) rates have increased in recent weeks and are above baseline levels, following usual seasonal trends. Seasonal influenza activity is elevated in many countries in the Northern hemisphere. Where surveillance data is available, trends in RSV detections currently vary by region with decreases reported in most regions except in North America. Recently, there has been interest in hMPV cases in China including suggestions of hospitals being overwhelmed. hMPV is a common respiratory virus found to circulate in many countries in winter through to spring, although not all countries routinely test and publish data on trends in hMPV . While some cases can be hospitalized with bronchitis or pneumonia, most people infected with hMPV have mild upper respiratory symptoms similar to the common cold and recover after a few days. Based on data published by China, covering the period up to 29 December 2024, acute respiratory infections have increased during recent weeks and detections of seasonal influenza, rhinovirus, RSV, and hMPV, particularly in northern provinces of China have also increased. The observed increase in respiratory pathogen detections is within the range expected for this time of year during the Northern hemisphere winter. In China, influenza is the most commonly detected respiratory pathogen currently affecting people with acute respiratory infections. WHO is in contact with Chinese health officials and has not received any reports of unusual outbreak patterns. Chinese authorities report that the health care system is not overwhelmed and there have been no emergency declarations or responses triggered. WHO continues to monitor respiratory illnesses at global, regional and country levels through collaborative surveillance systems, and provides updates as needed.

Description of the situation

In many countries of the Northern Hemisphere, trends in acute respiratory infections increase at this time of year. These increases are typically caused by seasonal epidemics of respiratory pathogens such as seasonal influenza, RSV, and other common respiratory viruses, including hMPV, as well as mycoplasma pneumoniae. The co-circulation of multiple respiratory pathogens during the winter season can sometimes cause an increased burden on health care systems treating sick persons.

Currently, in some countries in the temperate Northern hemisphere, influenza-like illness (ILI) and/or acute respiratory infection (ARI) rates have increased in recent weeks and are above baseline levels, following usual seasonal trends. Influenza activity is elevated in many countries in Europe, Central America and the Caribbean, Western Africa, Middle Africa, and many countries across Asia, with the predominant seasonal influenza type and subtype varying by location, typical for this time of year, except during most of 2020 and 2021, when there was little influenza activity during the COVID-19 pandemic (Figure 1). SARS-CoV-2 activity as detected in sentinel surveillance and reported to Global Influenza Surveillance and Response System (GISRS), along with wastewater monitoring from the reporting countries, is currently low in countries in the Northern hemisphere following prolonged high level activity during summer months in the Northern hemisphere. Where surveillance data is available, trends in RSV activity are variable by region with downward trends observed in most subregions of the Americas, except in North America where RSV activity has increased, and decreases have been observed in the European region in recent weeks. Some countries conduct routine surveillance and report trends for other commonly circulating respiratory pathogens, such as hMPV, and report such information on a routine basis. Some countries in the Northern hemisphere have reported increased trends, varying by virus, in recent weeks, typical for this time of year.

Figure 5. Virus detections by subtype reported to FluNet, 01 October 2017 to 30 December 2024 from countries in the Northern hemisphere, as of 07 January 2025



Source: (https://worldhealthorg.shinyapps.io/flunetchart/).

There has been international interest in a potential increase of respiratory virus transmission in China, particularly hMPV, including suggestions of hospitals being overwhelmed. China has an established sentinel surveillance system for ILI and severe acute respiratory infections (SARI), including hMPV, and conducts routine virological surveillance for common respiratory pathogens with detailed reports published weekly on the China Center for Disease Control and Prevention (CDC) website.[1] Surveillance and laboratory data for hMPV is not available routinely from all countries.

According to the most recent surveillance data on acute respiratory infections shared by the China CDC with data up to 29 December 2024, there has been an upward trend of common acute respiratory infections, including those due to seasonal influenza viruses, RSV and hMPV – as expected for this time of year during the Northern Hemisphere winter. Influenza is currently the most reported cause of respiratory disease, with the highest positivity rate among all monitored pathogens for all age groups except children aged 5-14 years for whom mycoplasma pneumoniae had the highest positivity rate. SARS-CoV-2 activity remains low however with an increase in reported severe COVID-19 cases. The predominant circulating SARS-CoV-2 variant in the country is XDV and its sublineages accounting for 59.1%

detection among sequenced samples. ILI activity in China's northern and southern provinces have been increasing since late 2024, following the previous year's trends. Current ILI activity in the southern provinces remains below that of the previous two years, while current ILI activity in the northern provinces is similar to levels seen at this time in the previous two years.

China's reported levels of acute respiratory infections, including hMPV, are within the expected range for the winter season with no unusual outbreak patterns reported. Chinese authorities confirmed that the health care system is not overwhelmed, hospital utilization is currently lower than this time last year, and there have been no emergency declarations or responses triggered. Since the expected seasonal increase was observed, health messages have been provided to the public on how to prevent the spread of respiratory infections and reduce the impact of these diseases.

Outbreak of suspected Marburg Virus Disease - United Republic of Tanzania – 14 January 2025

Description of the situation

An addendum was added to this Disease Outbreak News on 21 January 2025 to include the declaration of the outbreak by national authorities of the United Republic of Tanzania.

Introduction

On 13 January 2025, WHO informed its Member States and IHR State Parties of an outbreak of suspected Marburg Virus Disease (MVD) in the Kagera region of the United Republic of Tanzania using our secure web-based platform—the Event Information Site (EIS). Under the International Health Regulations, the EIS is used to issue rapid alerts to Member States of acute and rapidly developing public health risks and events with possible international implications.

Summary of the situation

On 10 January 2025, WHO received reliable reports from in-country sources regarding suspected cases of MVD in the Kagera region of the United Republic of Tanzania. Six people were reported to have been affected, five of whom had died. The cases presented with similar symptoms of headache, high fever, back pain, diarrhoea, haematemesis (vomiting with blood), malaise (body weakness) and, at a later stage of disease, external haemorrhage (bleeding from orifices).

As of 11 January 2025, nine suspected cases were reported including eight deaths (case fatality ratio (CFR) of 89%) across two districts – Biharamulo and Muleba. Samples from two patients have been collected and tested by the National Public Health Laboratory. Results are pending official confirmation. Contacts, including healthcare workers, are reported to have been identified and under follow-up in both districts.
The Bukoba district in Kagera region experienced its first MVD outbreak in March 2023, and zoonotic reservoirs, such as fruit bats, remain endemic to the area. The outbreak in March 2023 lasted for nearly two months with nine cases including six deaths.

Addendum to DON on suspected MVD outbreak in the United Republic of Tanzania published on 14 January 2025

On 20 January 2025, the President of the United Republic of Tanzania officially declared an outbreak of Marburg Virus Disease (MVD) following the detection of one confirmed case from Biharamulo district, Kagera region, located in the northwestern part of the country. The case was confirmed positive at the Kabaile mobile laboratory in the Kagera region and the National Reference Laboratory in Dar es Salaam. In addition, 25 suspected cases tested negative for MVD. Additional epidemiological information on the cases including the health status is not currently available. Epidemiological investigations are ongoing related to additional probable and suspected cases reported previously and a field mission, comprising of experts from the Ministry of Health, WHO and partners is being deployed.

WHO is supporting Tanzanian health authorities to enhance key outbreak control measures including disease surveillance, testing, treatment, infection prevention and control, case management, and increasing risk communication and public awareness among communities to prevent further virus spread.

Chapare haemorrhagic fever- the Plurinational State of Bolivia – 20 January 2025

Situation at a glance

On 7 January 2025, the International Health Regulations National Focal Point for the Plurinational State of Bolivia notified WHO of a laboratory-confirmed case of Chapare virus infection in an adult male from La Paz Department. Chapare haemorrhagic fever is an acute viral illness caused by Chapare virus. The virus was first identified in 2003 in Bolivia and has been associated with five documented outbreaks to date, all occurring within the country. These outbreaks have primarily affected rural areas in the La Paz Department, with the most recent case. There is no significant risk of international spread of the disease, as person-to-person transmission of the Chapare virus is possible but remains rare in the general population. As of 13 January 2025, no secondary cases have been reported, and all contacts remain without symptoms. Public health measures, such as disinfection and rodent control, have been implemented.

Description of the situation

On 7 January 2025, the International Health Regulations (IHR) National Focal Point (NFP) for the Plurinational State of Bolivia notified the World Health Organization (WHO) of one laboratory-confirmed human infection with Chapare virus (CHAPV) from one of the municipalities of La Paz Department. The patient is an adult male farmer in the age group of 50-60 years.

The patient developed symptoms including fever, headache, muscle pain, joint pain, and bleeding gums on 19 December 2024 and sought medical attention on 24 December. On 30 December, he was transferred to the local Health Center of the municipality due to worsening symptoms, where he died the same day. Blood samples were collected on 30 December before his death and sent to the National Center of Tropical Diseases (CENETROP), which confirmed CHAPV detection through real-time polymerase chain reaction (RT-PCR specific for CHAPV) testing on 2 January 2025.
An epidemiological investigation revealed significant risk factors for zoonotic disease transmission, including severe rodent infestation in and around the patient's home. Environmental conditions such as wooden and corrugated metal housing, dirt floors, and peri-domestic coconut plantings created a conducive environment for rodent activity. The patient's occupation as a farmer likely involved exposure to rodent burrows, further increasing the risk of infection.

Blood samples were collected from two close contacts of the case, which were negative. As of 13 January 2025, no secondary cases have been reported, and all identified contacts remain asymptomatic. Public health measures, including disinfection and rodent control, have been implemented, and investigations are ongoing. This is the fifth documented outbreak of Chapare haemorrhagic fever (CHHF) in Bolivia and globally since the virus was first identified in 2003.

2022-2024 Mpox Outbreak – Global Trends

This report provides an overview of the mpox[1] epidemiological situation in Africa, on a weekly basis (as of 05 January 2025), as well as the global epidemiological situation on a monthly basis (as of November 2024).

Data in this report are based on global surveillance data collected from 01 January 2022, initiated due to the unprecedented human-to-human spread of monkeypox virus (MPXV) globally occurring in the same year.
On 14 August 2024, under the International Health Regulations (2005), the WHO Director General declared that the increase in mpox cases in the Democratic Republic of the Congo and its expansion to neighboring countries constitutes a Public Health Emergency of International Concern (PHEIC). This spread presents a public health risk to other Member States and requires a coordinated international response.

Based on currently available information, the spread of mpox cases in the Democratic Republic of the Congo is attributed to two main outbreaks - spread of MPXV clade Ia in Equateur and other previously affected provinces of the country, and the spread of clade Ib MPXV in the provinces of North and South Kivu, as well as several clade Ib cases detecrted in Kinshasa. Current sequencing in the country is limited and clade distribution might be broader than what is currently known.

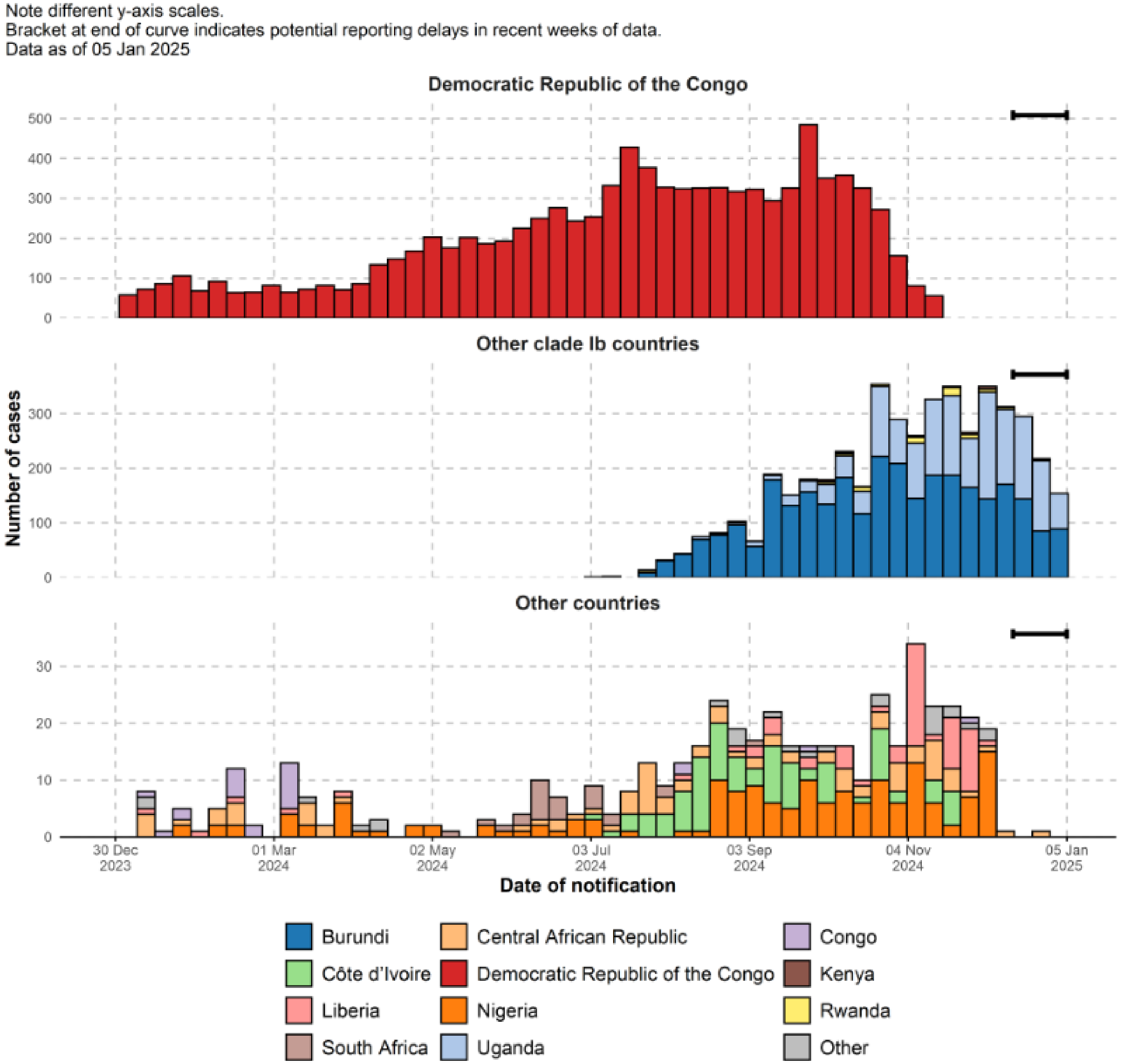
WHO conducted the latest global mpox rapid risk assessment in November 2024. Based on the available information, the risk is assessed as follows:

- **Clade Ib MPXV**: Predominantly affecting non-endemic areas for mpox in the Democratic Republic of the Congo and neighboring countries — **High**
- **Clade Ia MPXV**: Primarily affecting endemic areas for mpox within the Democratic Republic of the Congo — **High**
- **Clade II MPXV**: Observed in Nigeria and other endemic countries in West and Central Africa — **Moderate**
- **Clade IIb MPXV**: Associated with the global mpox epidemic — **Moderate**

Please note that regardless of geographic area, epidemiological context, biological sex, gender identity or sexual behaviour, individual-level risk is largely dependent on individual factors such as exposure risk and immune status.
This report mainly focuses on laboratory confirmed case and deaths[2] as defined by WHO's working case definition published in the Surveillance, case investigation and contact tracing for monkeypox interim guidance. In Africa, laboratory confirmed and suspected cases are both shown where possible. Note that countries[3] may use their own case definitions separate from those outlined in the above document.

1. ***On of 28 November 2022, WHO recommended using the name mpox as a new name for monkeypox. The words were used synonymously for one year as the term monkeypox was phased out. The virus causing mpox is named monkeypox virus (MPXV).***
2. ***For the WHO European region, both confirmed and probable cases are included within confirmed case counts and detailed case data.***
3. ***Throughout this document, any use of the word country should be considered shorthand for a country, area, or territory***

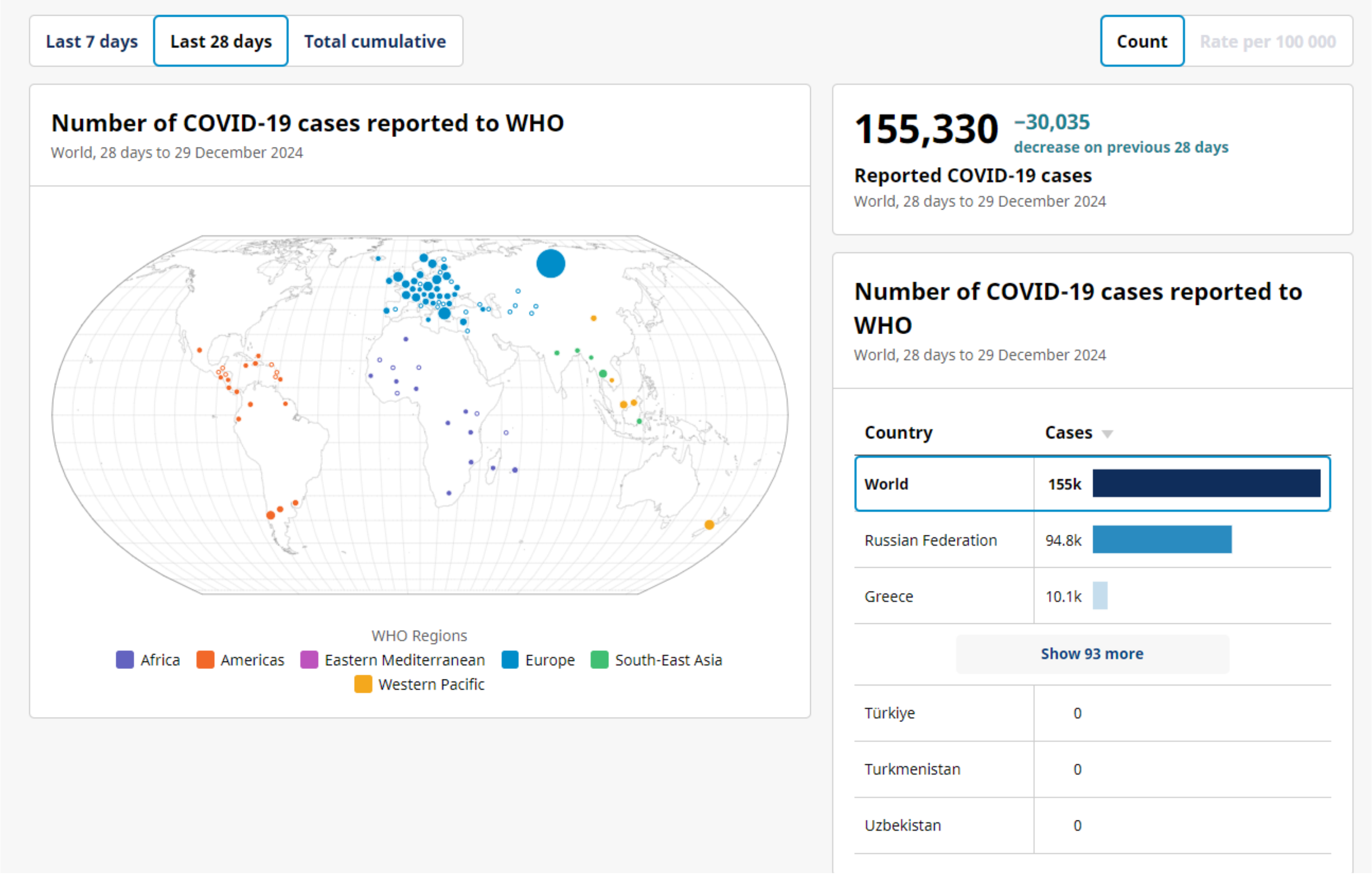
Figure 6a-6c. Data as updated weekly; from 01 January 2024 to 05 January 2025. Note that data shown here includes **laboratory confirmed cases only.** The most recent weeks presented in the epidemic curves should be interpreted with caution, as there are delays associated with reporting. In the Democratic Republic of the Congo, confirmed and suspected cases reported at the national level are not updated as of the 17th November 2024. Efforts are ongoing to update this data.



Note different y-axis scales.
Bracket at end of curve indicates potential reporting delays in recent weeks of data.
Data as of 05 Jan 2025

Source: WHO

WHO COVID-19 DASHBOARD – Updated as of 29 December 2024



Number of COVID-19 cases reported to WHO

World, 28 days to 29 December 2024

155,330 −30,035 decrease on previous 28 days

Reported COVID-19 cases

World, 28 days to 29 December 2024

Number of COVID-19 cases reported to WHO

World, 28 days to 29 December 2024

Country	Cases
World	155k
Russian Federation	94.8k
Greece	10.1k
Türkiye	0
Turkmenistan	0
Uzbekistan	0

NATIONAL COMMUNICABLE DISEASE ACTIVITY

First H5 Bird Flu Death Reported in United States – January 6, 2025

January 6, 2025 -- CDC is saddened by Louisiana's report that a person previously hospitalized with severe avian influenza A(H5N1) illness ("H5N1 bird flu") has passed away. While tragic, a death from H5N1 bird flu in the United States is not unexpected because of the known potential for infection with these viruses to cause severe illness and death. As of January 6, 2025, there have been 66 confirmed human cases of H5N1 bird flu in the United States since 2024 and 67 since 2022. This is the first person in the United States who has died as a result of an H5 infection. Outside the United States, more than 950 cases of H5N1 bird flu have been reported to the World Health Organization; about half of those have resulted in death.

CDC has carefully studied the available information about the person who died in Louisiana and continues to assess that the risk to the general public remains low. Most importantly, no person-to-person transmission spread has been identified. As with the case in Louisiana, most H5 bird flu infections are related to animal-to-human exposures. Additionally, there are no concerning virologic changes actively spreading in wild birds, poultry, or cows that would raise the risk to human health. (CDC reported previously on its analysis of the viruses isolated from the patient in Louisiana.) However, people with job-related or recreational exposures to infected birds or other animals are at greater risk of infection. For these and others, CDC has developed prevention resources about how to protect yourself.

CDC is continually:

- Supporting critical epidemiologic investigations with state and local partners to assess the public health impact of each H5 case.
- Working closely with state and local partners to conduct active surveillance for H5 cases.

- Monitoring for changes that might suggest H5 viruses are becoming better adapted to mammals and therefore might spread more easily from animals-to-humans or human-to-human or cause more severe disease.
- Monitoring for any viral changes that could make these viruses less responsive to flu antiviral medications or the available candidate vaccine viruses.

Additional information about H5 bird flu is available on the CDC website.

Salmonella Outbreak Linked to Cucumbers – updated January 8, 2025

This investigation is considered closed as of January 8, 2025.

Fast Facts

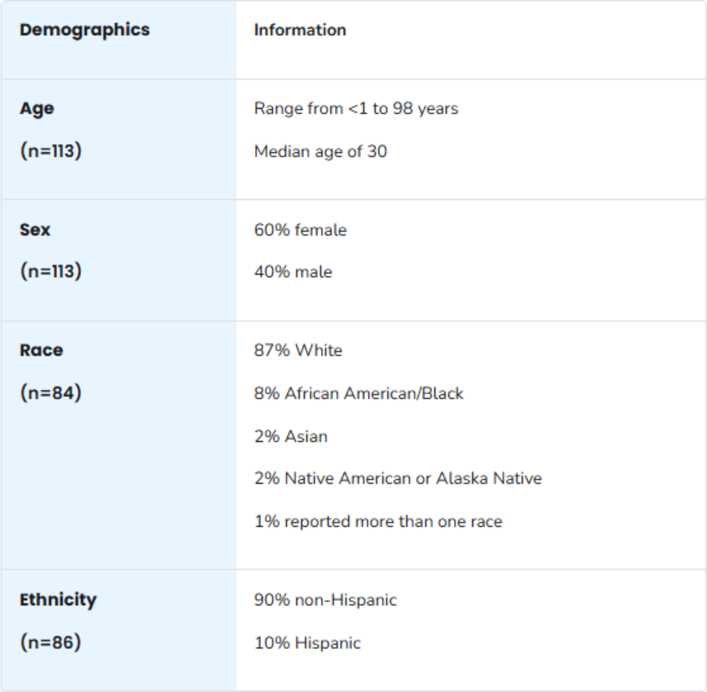
- **Cases**: 113
- **Hospitalizations**: 28
- **Deaths**: 0
- **States**: 23

CDC, public health and regulatory officials in several states, and the U.S. Food and Drug Administration (FDA), collected different types of data to investigate a multistate outbreak of *Salmonella* Typhimurium infections**.** Epidemiologic and traceback data showed that cucumbers grown by Agrotato, S.A. de C.V. in Sonora, Mexico, were contaminated with *Salmonella* and made people sick.

Epidemiologic Data

A total of 113 people infected with the outbreak strain of *Salmonella* were reported from 23 states. Illnesses started on dates ranging from October 12, 2024, to December 7, 2024. Of the 99 people for whom information was available, 28 were hospitalized. No deaths were reported. The true number of sick people in this outbreak was likely much higher than the number reported, and the outbreak may not have been limited to the states with known illnesses. This is because many people recover without medical care and are not tested for *Salmonella*.

Public health officials collected many different types of information from sick people, including their age, race, ethnicity, other demographics, and the foods they ate in the week before they got sick. This information provided clues to help investigators identify the source of the outbreak.



Demographics	Information
Age **(n=113)**	Range from <1 to 98 years Median age of 30
Sex **(n=113)**	60% female 40% male
Race **(n=84)**	87% White 8% African American/Black 2% Asian 2% Native American or Alaska Native 1% reported more than one race
Ethnicity **(n=86)**	90% non-Hispanic 10% Hispanic

Table 1. The table has information about sick people in this outbreak ("n" is the number of people with information available for each demographic).

State and local public health officials interviewed people about the foods they ate in the week before they got sick. Of the 69 people interviewed, 56 (81%) reported eating or likely eating cucumbers. This percentage was significantly higher than the 50% of respondents who reported eating cucumbers in the FoodNet Population Survey—a survey that helps estimate how often people eat various foods linked to diarrheal illness. This difference suggests that people in this outbreak got sick from eating cucumbers.

CDC and states identified seven illness sub-clusters at three assisted living facilities, three school districts, and one restaurant. An illness sub-cluster is a group of unrelated sick people who all ate at the same location or event, such as a restaurant, long-term care facility, or school. Investigating sub-clusters can help identify a food item eaten by all the sick people that could be the source of the outbreak. Cucumbers were served at all seven sub-cluster locations.

Laboratory and Traceback Data

Public health investigators used the PulseNet system to identify illnesses that may have been part of this outbreak. CDC PulseNet manages a national database of DNA fingerprints of bacteria that cause foodborne illnesses. DNA fingerprinting is performed on bacteria using a method called whole genome sequencing (WGS). WGS showed that bacteria from sick people's samples were closely related genetically. This suggests that people in this outbreak got sick from the same food.

WGS analysis of 109 people's samples did not predict resistance to any antibiotics. More information is available at the National Antimicrobial Resistance Monitoring System (NARMS) site.
People reported eating cucumbers at different restaurants and sub-cluster locations or buying cucumbers from multiple stores. FDA's traceback investigation identified Agrotato, S.A. de C.V. in Sonora, Mexico as a common grower of cucumbers.

Public Health Actions

Many companies recalled cucumbers or foods made with them. The products are no longer available for sale.

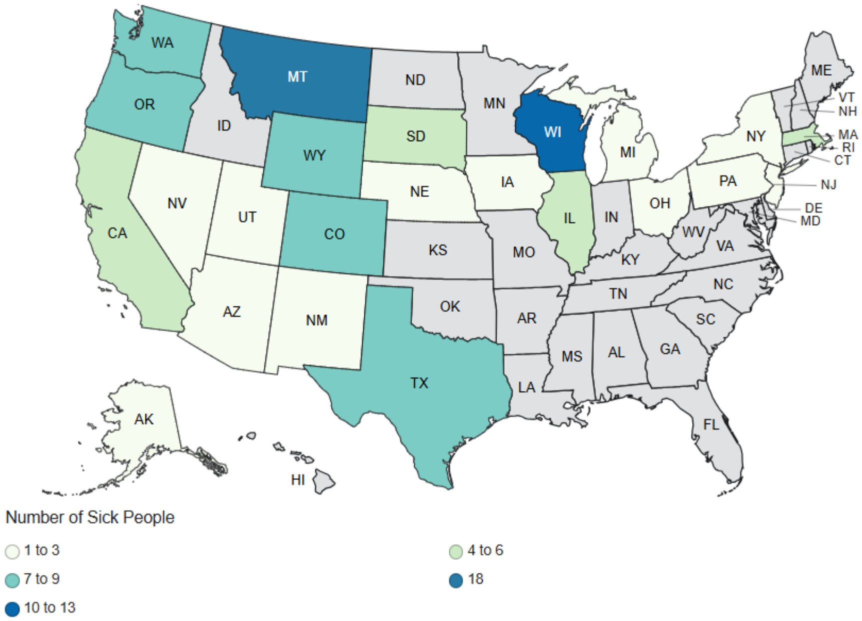


Figure 7. The map shows where the ill people due to the Salmonella-associated cucumber products were found in the USA. Out of the total 113 cases, 69 were interviewed and 81% of them reported eating cucumbers. This number is likely an underestimate of those sickened by this product because some people recover from illness without ever getting tested or reported.

Listeria Outbreak Linked to Ready-to-Eat Meat and Poultry Products – Updated December 5, 2024

CDC, public health and regulatory officials in several states, and the U.S. Department of Agriculture's Food Safety and Inspection Service (USDA-FSIS) are collecting different types of data to investigate a multistate outbreak of *Listeria monocytogenes* infections**.** Epidemiologic and laboratory data show that ready-to-eat meat and poultry products distributed by Yu Shang Food Inc are contaminated with *Listeria* and are making people sick.

Epidemiologic Data

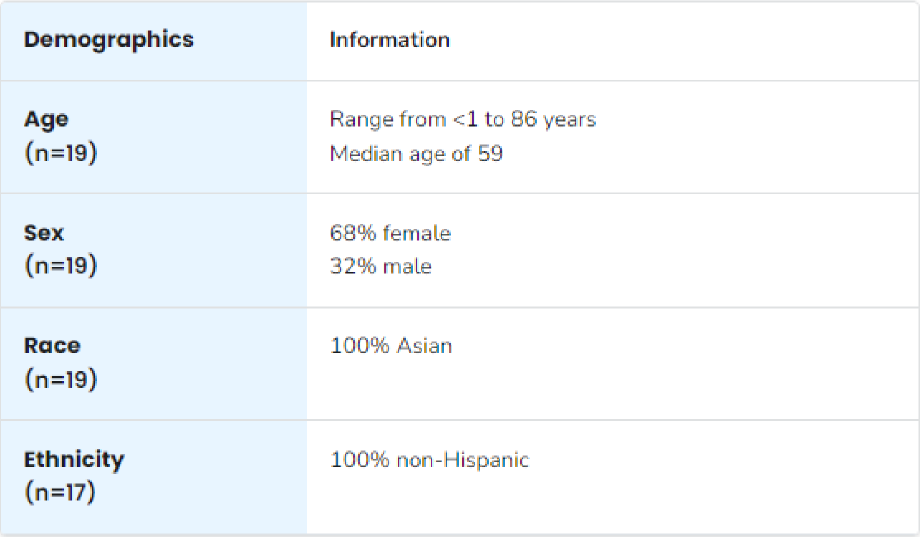
Since the last update on November 22, 2024, eight new illnesses were reported from five states. These sick people were identified after food and environmental sampling found a second strain of *Listeria*. As of December 5, 2024, 19 people from eight states have been infected with the outbreak strains of *Listeria.*

Sick people's samples were collected from October 24, 2021, to October 28, 2024.

- Of 19 people with information available, 17 (89%) have been hospitalized**.**
- Seven illnesses are related to pregnancy.
- One person who was pregnant was sick and recovered.
- Two unrelated infants were also sick and recovered.
- In California, a mother and her twins were sick and both infants died. *Listeria* was found in a sample from the mother and from one of the twin infants, but it could not be found in a sample from the other infant. Because of this, only the mother and one twin are included as confirmed cases in this outbreak.
- In Tennessee, a mother and her infant were sick and her infant died.

The true number of sick people in this outbreak is likely higher than the number reported, and the outbreak may not be limited to the states with known illnesses. This is because some people recover without medical care and are not tested for *Listeria*. In addition, recent illnesses may not yet be reported as it usually takes 3 to 4 weeks to determine if a sick person is part of an outbreak.

Public health officials collect many different types of information from sick people, including their age, race, ethnicity, other demographics, and the foods they ate in the month before they got sick. This information provides clues to help investigators identify the source of the outbreak.



Demographics	Information
Age (n=19)	Range from <1 to 86 years Median age of 59
Sex (n=19)	68% female 32% male
Race (n=19)	100% Asian
Ethnicity (n=17)	100% non-Hispanic

Table 2. This table has information about people identified as ill from *Listeria monocytogenes* linked to this particular company's distributed food products.

State and local public health officials are interviewing people about the foods they ate in the month before they got sick. People reported buying their foods from multiple stores. Among the 14 people interviewed, 11 people shopped in person and online at markets where Yu Shang food products are sold. Among the 13 people asked about precooked chicken products, eight (62%) people reported eating precooked chicken products, and three people (38%) specifically reported eating Yu Shang brand ready-to-eat chicken products.

Laboratory Data

Public health investigators are using the PulseNet system to identify illnesses that may be part of this outbreak. CDC PulseNet manages a national database of DNA fingerprints of bacteria that cause foodborne illnesses. DNA fingerprinting is performed on bacteria using a method called whole genome sequencing (WGS). WGS showed that bacteria from sick people's samples are closely related genetically. This suggests that people in this outbreak got sick from the same food. On October 21, 2024, FSIS conducted routine testing and follow-up activities of finished product by Yu Shang Food, Inc. Testing confirmed that the product was contaminated with *Listeria.* WGS showed that the *Listeria* in the pork snout product is closely related to bacteria from sick people. This means that people likely got sick from eating foods produced by Yu Shang Food, Inc.

In response to the investigation, FSIS collected additional samples of product produced at Yu Shang Foods, Inc. and from the production environment. The *Listeria* found in those samples was related by WGS to the bacteria from eight other sick people in the PulseNet database and is different from the strain found in the pork snout sample and the 11 illnesses already included in the outbreak. These illnesses were combined into one investigation.

Public Health Actions

On November 9, 2024, Yu Shang Food, Inc recalled ready-to-eat meat and poultry products. On November 21, 2024, Yu Shang Food, Inc expanded their recall. CDC is advising people not to eat, sell, or serve recalled products.

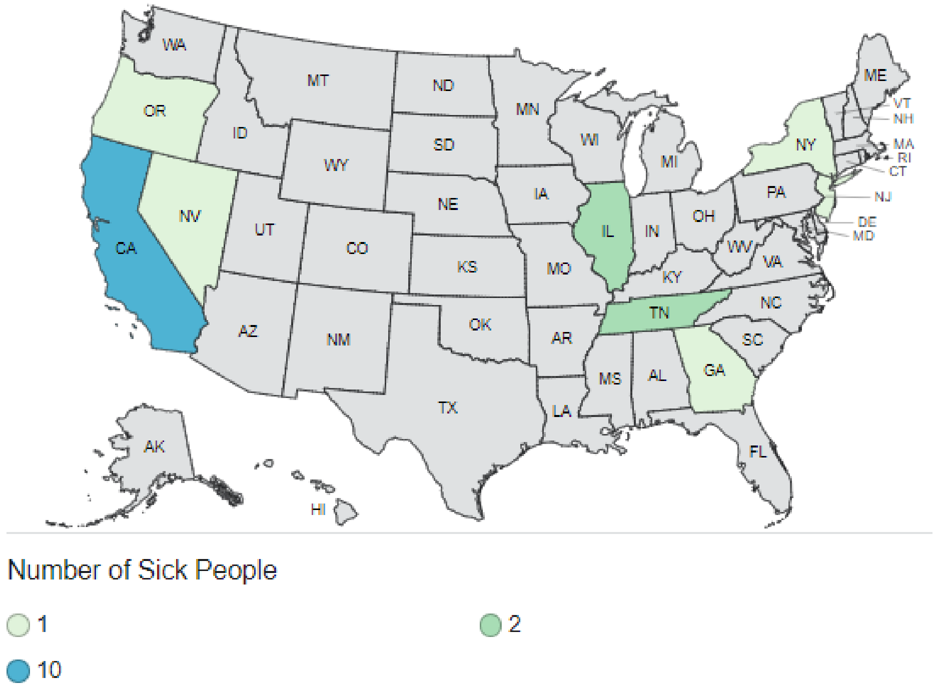


Figure 8. This map shows where the 19 people in this *Listeria* outbreak lived (n=19), the majority who presently were identified in California but also live in other states like Illinois, Tennessee, and New York. This outbreak may not have been limited to the states with known illnesses, and the true number of sick people is likely higher than the number reported. This is because some people recover without medical care and are not tested for *Listeria*.

E. coli O121 Outbreak Associated with Organic Carrots – Updated December 18, 2024

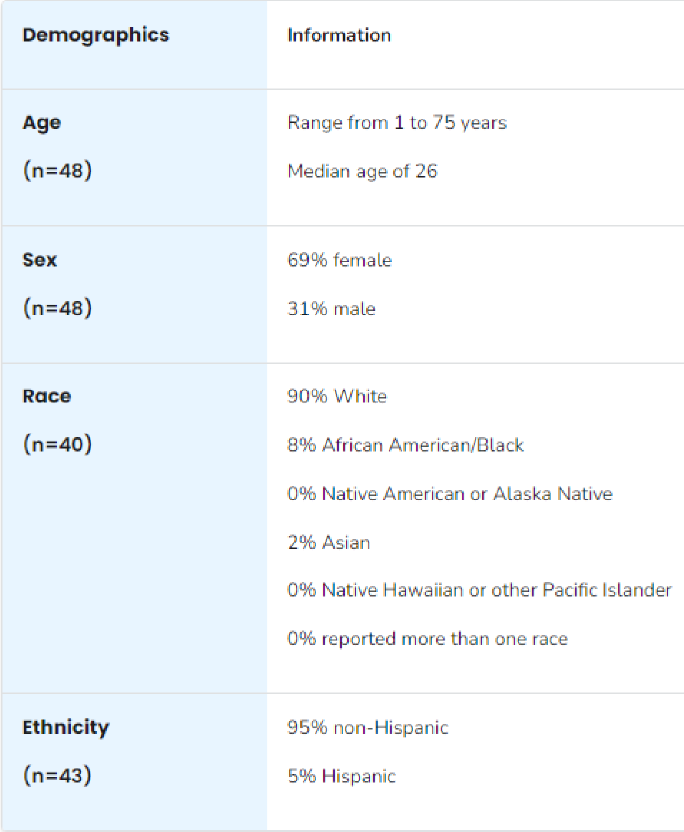
CDC, public health and regulatory officials in several states, and the U.S. Food and Drug Administration (FDA) collected different types of data to investigate a multistate outbreak of *E. coli* O121 infections**.**
Epidemiologic and traceback data showed that organic carrots supplied by Grimmway Farms were likely contaminated with *E. coli* and made people sick.

Epidemiologic data

A total of 48 people infected with the outbreak strain of *E. coli* were reported from 19 states. Illnesses started on dates ranging from September 6, 2024, to November 10, 2024. Of 47 people with information available, 20 were hospitalized and one developed hemolytic uremic syndrome, a serious condition that can cause kidney failure. One death was reported from California.

The true number of sick people in this outbreak was likely much higher than the number reported, and the outbreak may not have been limited to the states with known illnesses. This is because many people recover without medical care and are not tested for *E. coli*.

Public health officials collect many different types of information from sick people, including their age, race, ethnicity, other demographics, and the foods they ate in the week before they got sick. This information provides clues to help investigators identify the source of the outbreak.



Demographics	Information
Age (n=48)	Range from 1 to 75 years Median age of 26
Sex (n=48)	69% female 31% male
Race (n=40)	90% White 8% African American/Black 0% Native American or Alaska Native 2% Asian 0% Native Hawaiian or other Pacific Islander 0% reported more than one race
Ethnicity (n=43)	95% non-Hispanic 5% Hispanic

Table 3. The table has information about sick people in this outbreak ("n" is the number of people with information available for each demographic).

State and local public health officials interviewed people about the foods they ate in the week before they got sick. Of the 37 people interviewed, 33 (89%) reported eating carrots. This percentage was significantly higher than the 63% of respondents who reported eating carrots in the FoodNet Population Survey—a survey that helps estimate how often people eat various foods linked to diarrheal illness. This difference suggests that people in this outbreak got sick from eating carrots.

Laboratory and traceback information

Public health investigators used the PulseNet system to identify illnesses that may be part of this outbreak. CDC PulseNet manages a national database of DNA fingerprints of bacteria that cause foodborne illnesses. DNA fingerprinting is performed on bacteria using a method called whole genome sequencing (WGS).

WGS showed that bacteria from sick people's samples were closely related genetically. This suggests that people in this outbreak got sick from the same food. WGS analysis of bacteria from 45 people's samples did not predict resistance to any antibiotics. More information is available at the National Antimicrobial Resistance Monitoring System (NARMS) site.

These findings do not affect treatment guidance since antibiotics are not recommended for patients with Shiga toxin-producing *E. coli* (STEC) infections.

People reported buying different brands of carrots from multiple stores. FDA's traceback of some of these purchases identified Grimmway Farms as the common supplier of organic whole and baby carrots in this outbreak. FDA conducted inspections at Grimmway Farms and collected environmental samples. Two environmental samples collected outside were positive for STEC. Although both strains of *E. coli* detected in the samples are capable of causing human illness, neither match the strain of *E. coli* causing illnesses in this outbreak. The strain of *E. coli* causing illnesses in this outbreak was not found in environmental samples; however, epidemiologic and traceback evidence shows that recalled carrots were the likely source of illnesses in this outbreak.

Public health actions

This outbreak is over. These products are no longer in stores and are past shelf life. However, they may be in your refrigerator or freezer. Check your freezer for any recalled products and throw them away or return them to where you bought them. Always take steps to protect yourself from getting sick from *E. coli*.

On November 16, 2024, Grimmway Farms initiated a voluntary recall of these carrots and contacted their distributors. On November 21, 2024, the recall expanded to include additional bag sizes for organic whole carrots. Additional recalls were conducted by companies that used or repackaged carrots that may have come from Grimmway Farms.

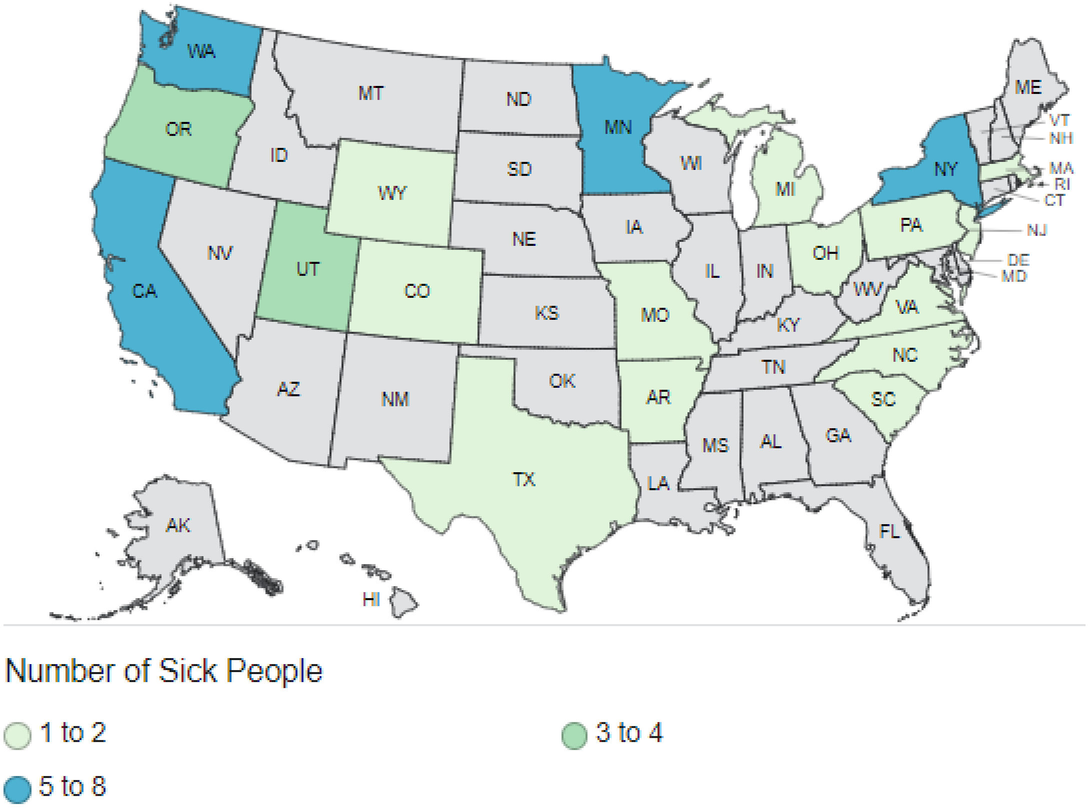


Figure 9. This map shows where the 48 people in this *E. coli* outbreak lived. (n=48, MI=1). This outbreak may not be limited to the states with known illnesses, and the true number of sick people is likely much higher than the number reported. This is because many people recover without medical care and are not tested for *E. coli*.

Measles Activity in 2024 in USA

As of December 19, 2024, a total of 284 measles cases were reported by 32 jurisdictions: Arizona, California, District of Columbia, Florida, Georgia, Idaho, Illinois, Indiana, Louisiana, Maryland, Massachusetts, Michigan, Minnesota, Missouri, New Hampshire, New Jersey, New Mexico, New York City, New York State, North Carolina, Ohio, Oklahoma, Oregon, Pennsylvania, South Carolina, South Dakota, Tennessee, Vermont, Virginia, Washington, Wisconsin, and West Virginia.

There have been 16 outbreaks (defined as 3 or more related cases) reported in 2024, and 70% of cases (198 of 284) are outbreak-associated. For comparison, 4 outbreaks were reported during 2023 and 49% of cases (29 of 59) were outbreak-associated.

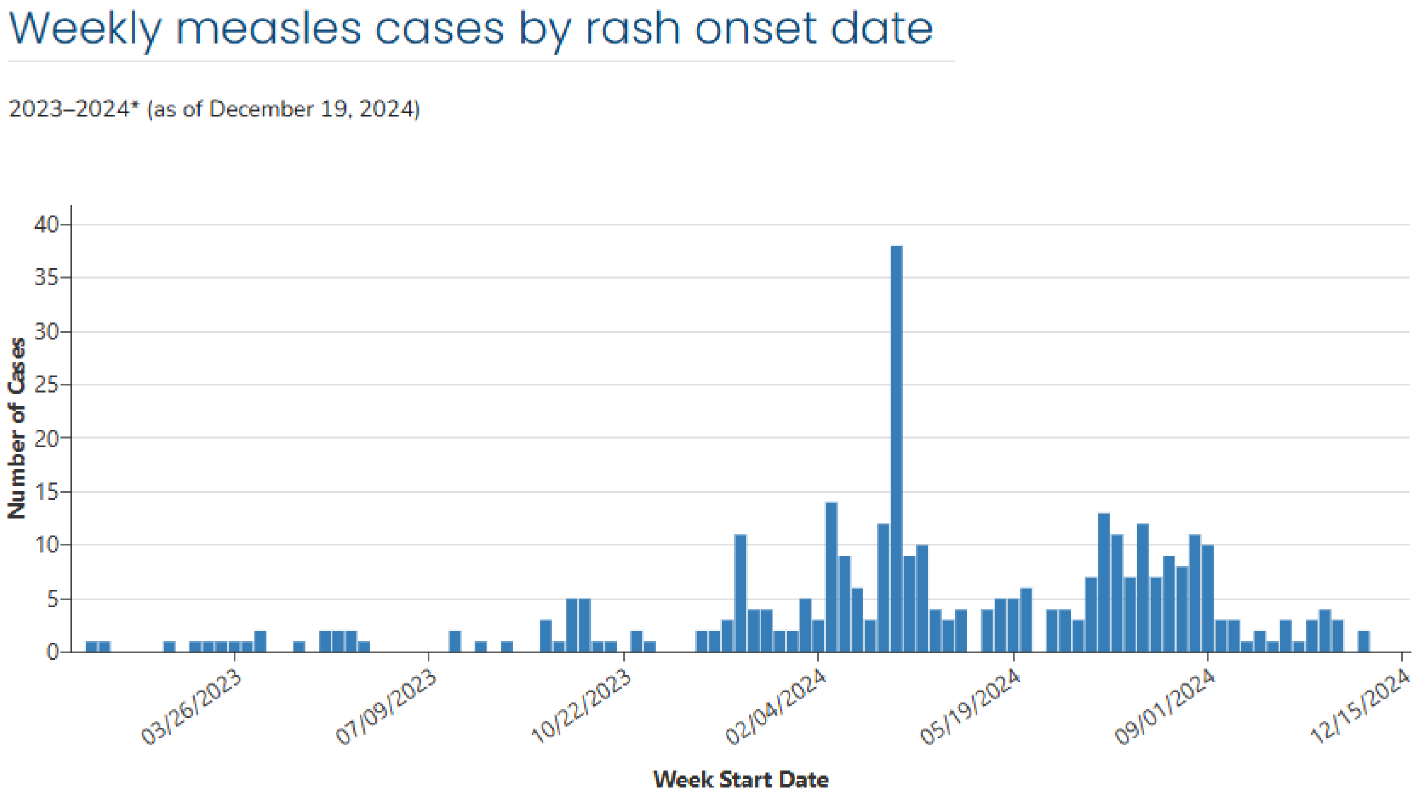
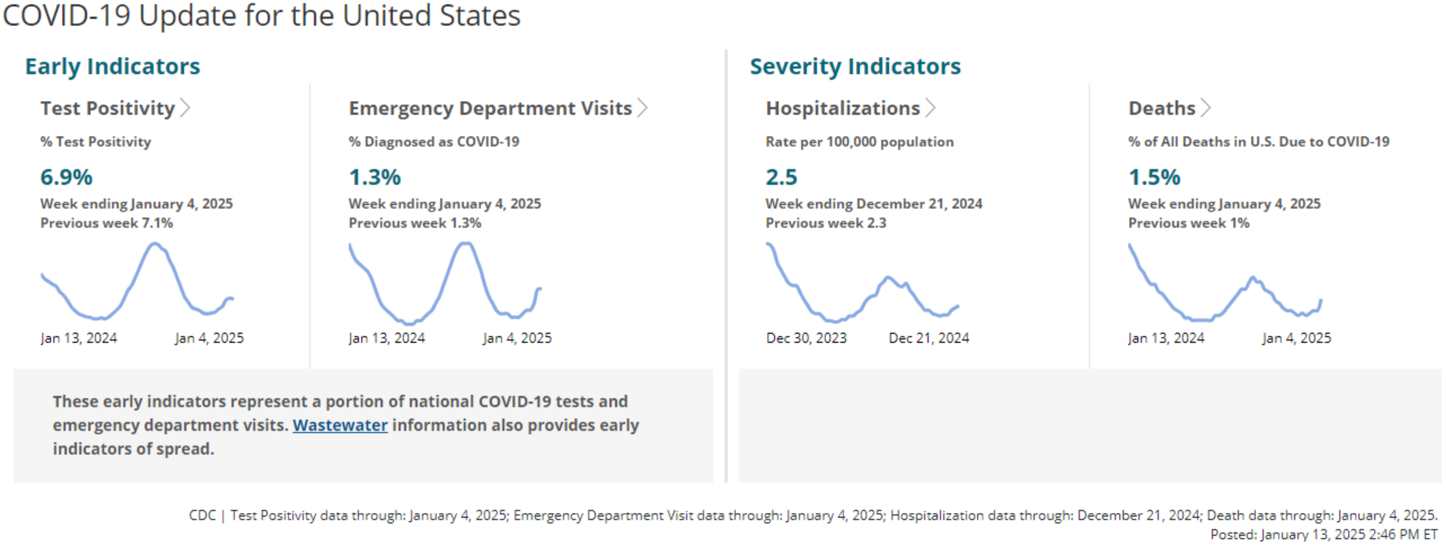


Figure 10. Measles cases reported weekly in the USA from 2023 up until December 19, 2024.

NATIONAL COVID-19 ACTIVITY – January 13, 2025 Updated


COVID-19 Update for the United States

Early Indicators

Test Positivity
% Test Positivity
6.9%
Week ending January 4, 2025
Previous week 7.1%

Emergency Department Visits
% Diagnosed as COVID-19
1.3%
Week ending January 4, 2025
Previous week 1.3%

These early indicators represent a portion of national COVID-19 tests and emergency department visits. Wastewater information also provides early indicators of spread.

Severity Indicators

Hospitalizations
Rate per 100,000 population
2.5
Week ending December 21, 2024
Previous week 2.3

Deaths
% of All Deaths in U.S. Due to COVID-19
1.5%
Week ending January 4, 2025
Previous week 1%

CDC | Test Positivity data through: January 4, 2025; Emergency Department Visit data through: January 4, 2025; Hospitalization data through: December 21, 2024; Death data through: January 4, 2025.
Posted: January 13, 2025 2:46 PM ET

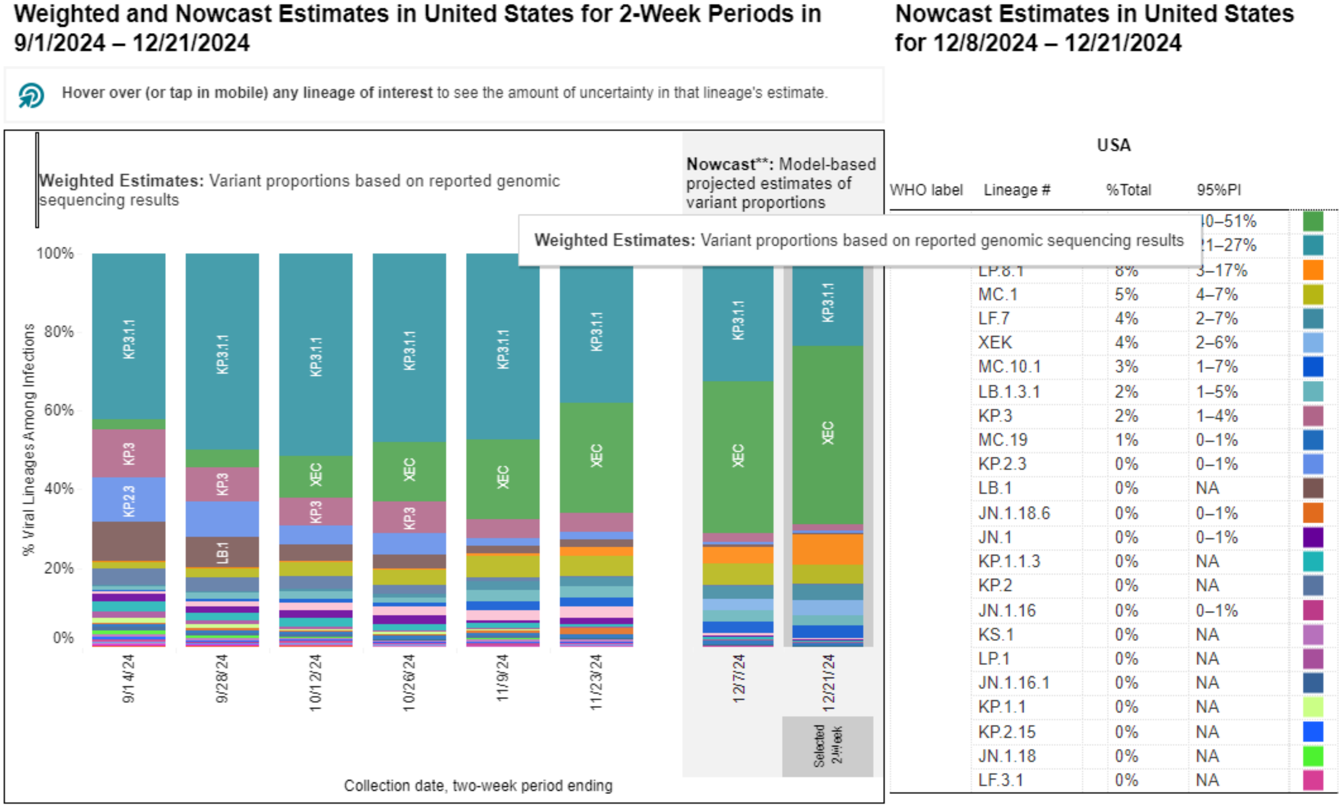
The Figure 11a on the following page are describe the US Variant of Concern activity from September 1 – December 21, 2024

Bar Charts:

The bar charts present point estimates of weighted proportions of the most common SARS-CoV-2 lineages grouped into selected 2-week intervals at the national-level or selected U.S. Department of Health & Human Services (HHS) region.

Table:

The table presents point estimates and associated 95% confidence intervals for the weighted proportions of the most common SARS-CoV-2 lineages per selected 2-week interval at the national-level or selected HHS region.



Weighted and Nowcast Estimates in United States for 2-Week Periods in 9/1/2024 – 12/21/2024

Nowcast Estimates in United States for 12/8/2024 – 12/21/2024

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in that lineage's estimate.

Weighted Estimates: Variant proportions based on reported genomic sequencing results

Nowcast**: Model-based projected estimates of variant proportions

Weighted Estimates: Variant proportions based on reported genomic sequencing results

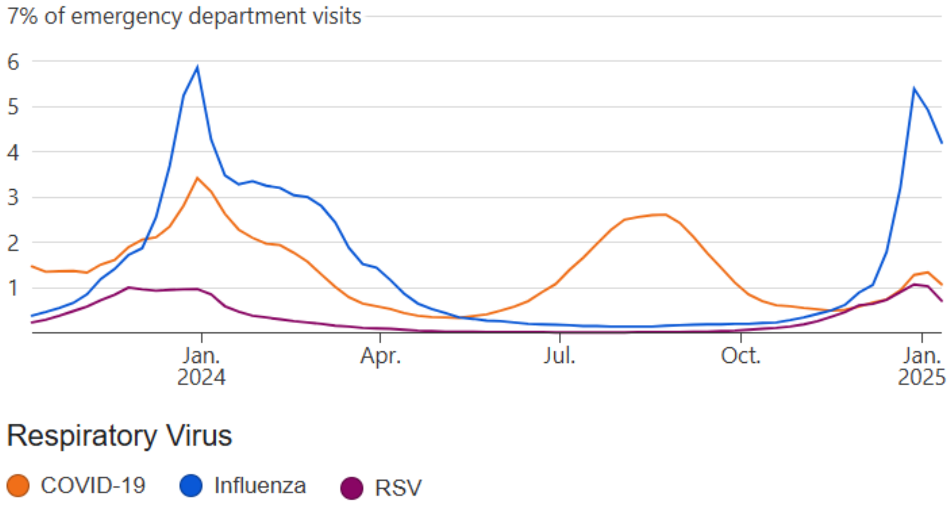
USA

WHO label	Lineage #	%Total	95%PI	
			0–51%	🟩
			1–27%	🟦
	LP.8.1	8%	3–17%	🟧
	MC.1	5%	4–7%	🟨
	LF.7	4%	2–7%	🟦
	XEK	4%	2–6%	🟦
	MC.10.1	3%	1–7%	🟦
	LB.1.3.1	2%	1–5%	🟦
	KP.3	2%	1–4%	🟪
	MC.19	1%	0–1%	🟦
	KP.2.3	0%	0–1%	🟦
	LB.1	0%	NA	🟫
	JN.1.18.6	0%	0–1%	🟧
	JN.1	0%	0–1%	🟪
	KP.1.1.3	0%	NA	🟦
	KP.2	0%	NA	🟦
	JN.1.16	0%	0–1%	🟪
	KS.1	0%	NA	🟪
	LP.1	0%	NA	🟪
	JN.1.16.1	0%	NA	🟦
	KP.1.1	0%	NA	🟩
	KP.2.15	0%	NA	🟦
	JN.1.18	0%	NA	🟩
	LF.3.1	0%	NA	🟪

** These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates
# Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one 2-week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all 2-week periods displayed. While all lineages are tracke by CDC, those named lineages not enumerated in this graphic are aggregated with their parent lineages, based on Pango lineage definitions, described in more detail here: https://web.archive.org/web/20240116214031/https://www.pango.network/the-pango-nomenclature-system/statement-of-nomenclature-rules.

Figures 11a. Bar Chart, and Table to Describe Variant of Concern Activity in USA for Past Three Months.

Respiratory Activity in US – Updated January 15, 2025



Data last updated on January 15, 2025 and presented through January 11, 2025. View this dataset on data.cdc.gov.

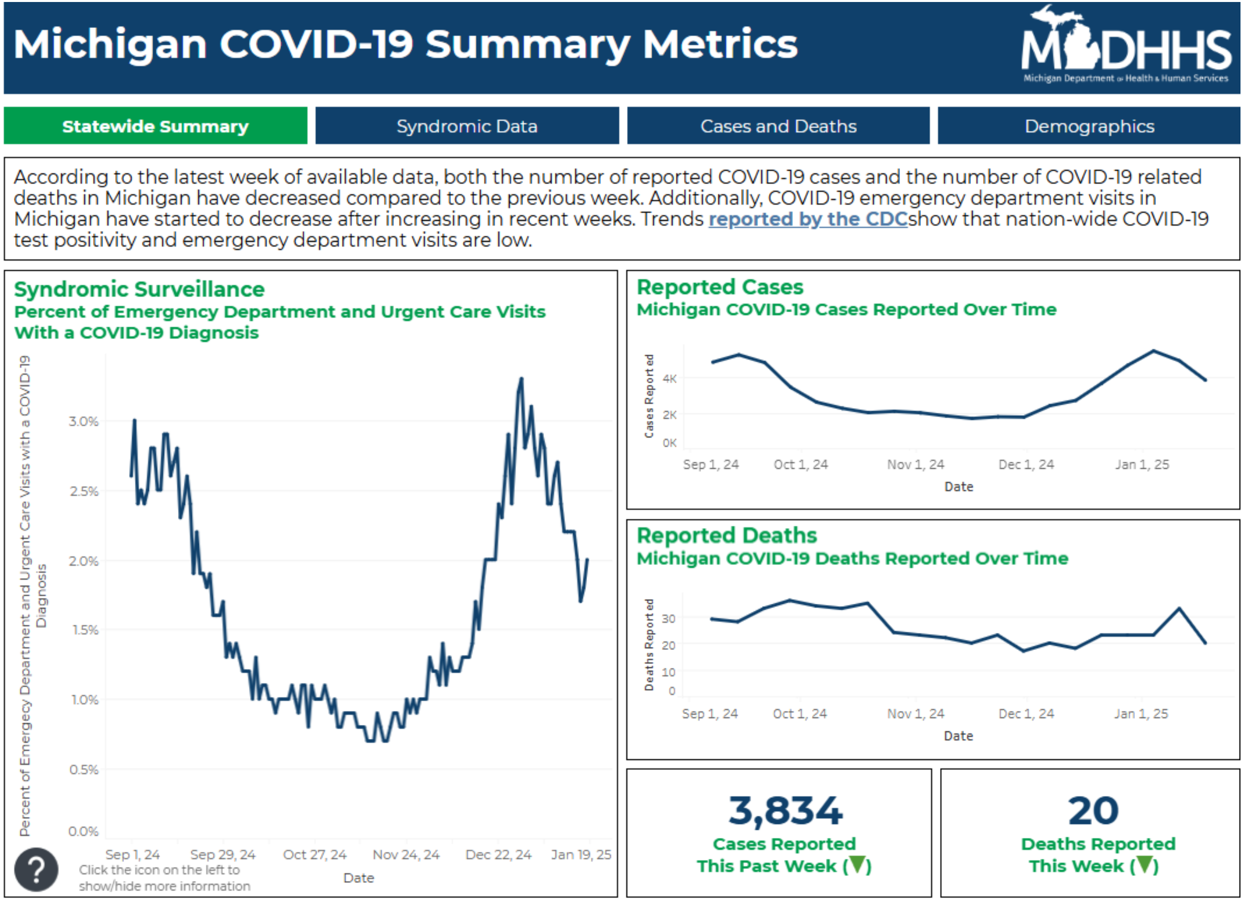
Figure 12. This graph combines the activity of respiratory viruses of Novel Coronavirus COVID-19 (COVID-19), Influenza (flu), and Respiratory Syncytial Virus (RSV) documented in Emergency Department and other Healthcare Systems syndromic surveillance systems across the United States up to January 11, 2025 (7% Combined,1.1% COVID, 4.2% Flu, 0.7% RSV).

MICHIGAN COMMUNICABLE DISEASE ACTIVITY

New Releases from MDHHS – Full Index Available at: https://www.michigan.gov/mdhhs/0,5885,7-339-73970_71692_71696---Y,00.html

New Releases from MDARD – Full Index Available at: https://www.michigan.gov/mdard/about/media/pressreleases

Michigan Respiratory Virus Activity



Michigan COVID-19 Summary Metrics

Statewide Summary | Syndromic Data | Cases and Deaths | Demographics

According to the latest week of available data, both the number of reported COVID-19 cases and the number of COVID-19 related deaths in Michigan have decreased compared to the previous week. Additionally, COVID-19 emergency department visits in Michigan have started to decrease after increasing in recent weeks. Trends **reported by the CDC**show that nation-wide COVID-19 test positivity and emergency department visits are low.

Syndromic Surveillance
Percent of Emergency Department and Urgent Care Visits With a COVID-19 Diagnosis

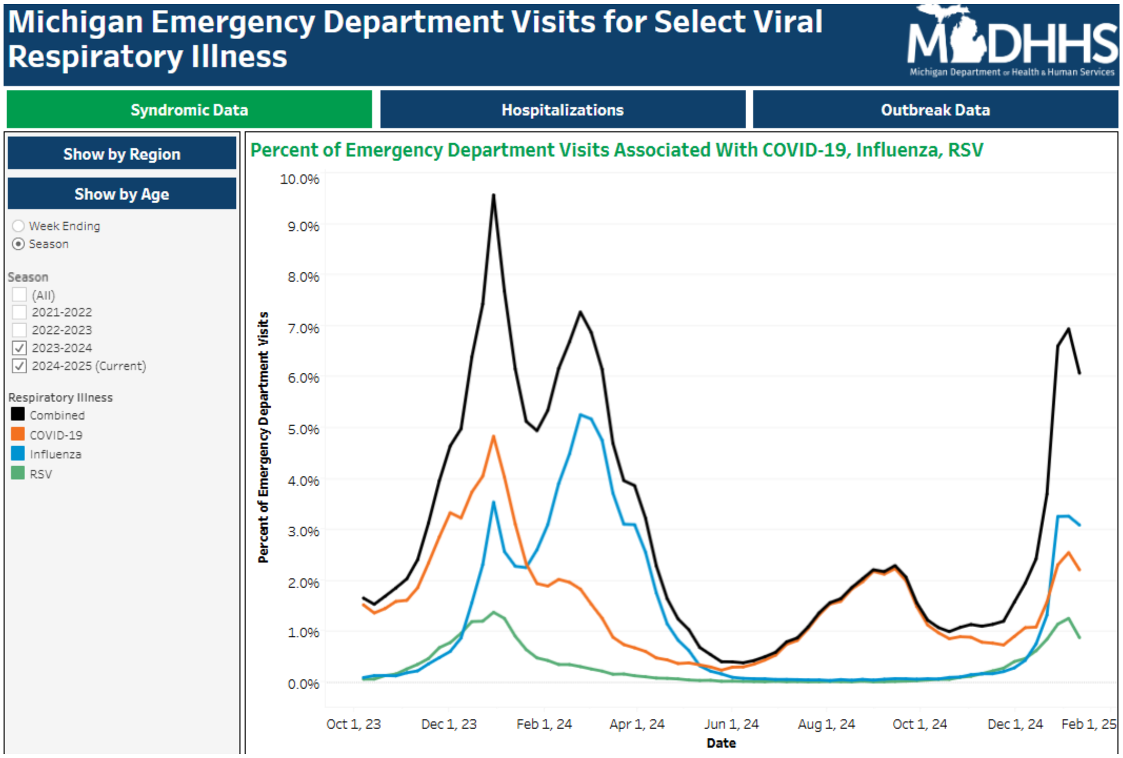
Reported Cases
Michigan COVID-19 Cases Reported Over Time

Reported Deaths
Michigan COVID-19 Deaths Reported Over Time

3,834
Cases Reported This Past Week (▼)

20
Deaths Reported This Week (▼)

Figure 13. MDHHS Coronavirus 2019 Data Dashboard for COVID-19 Activity up to January 18, 2025



○ Week Ending
● Season

Season
☐ (All)
☐ 2021-2022
☐ 2022-2023
☑ 2023-2024
☑ 2024-2025 (Current)

Respiratory Illness
■ Combined
■ COVID-19
■ Influenza
■ RSV

Figure 14. This graph shows the percentage of Michigan Emergency Department (ED) visits that were classified as one of three viral infections: COVID-19, Influenza (Flu), and Respiratory Syncytial Virus (RSV) as of January 16, 2025. The overall percentage of ED visits diagnosed as respiratory were 6.1%, with COVID-19 at 2.2%, Flu at 3.1%, and RSV at 0.9%

Michigan COVID-19 Activity

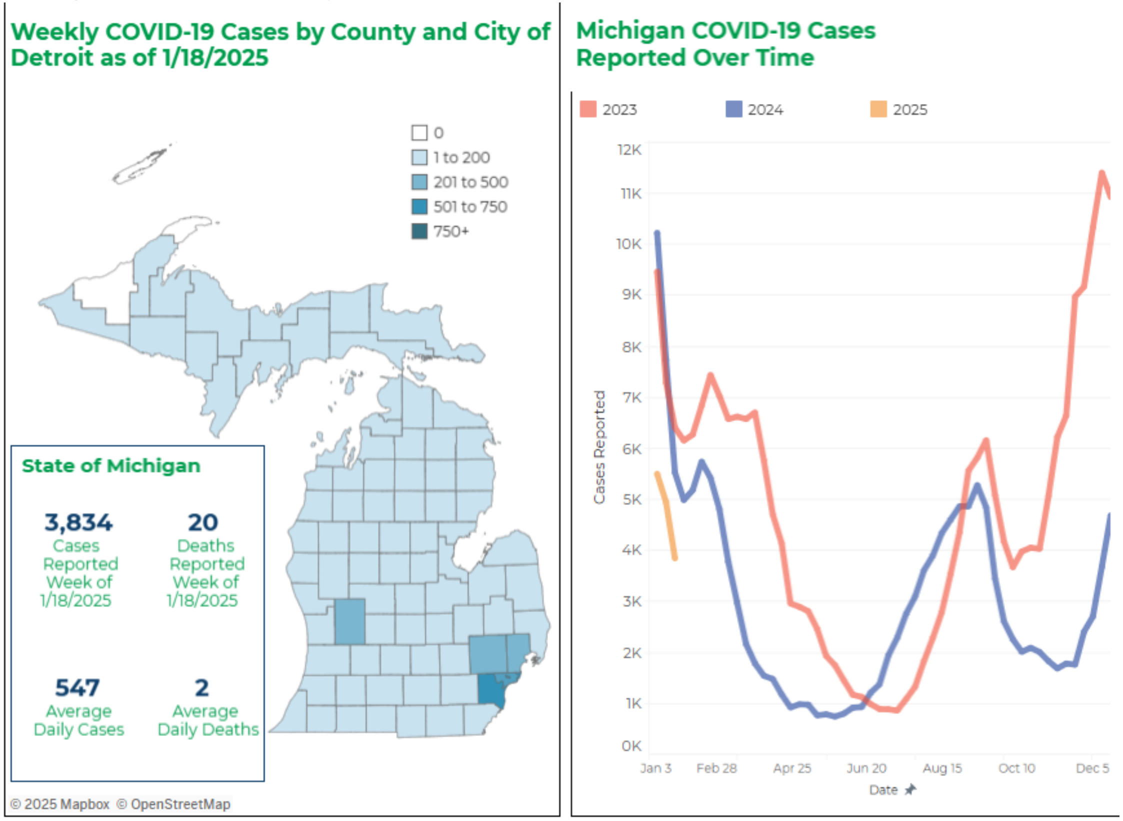
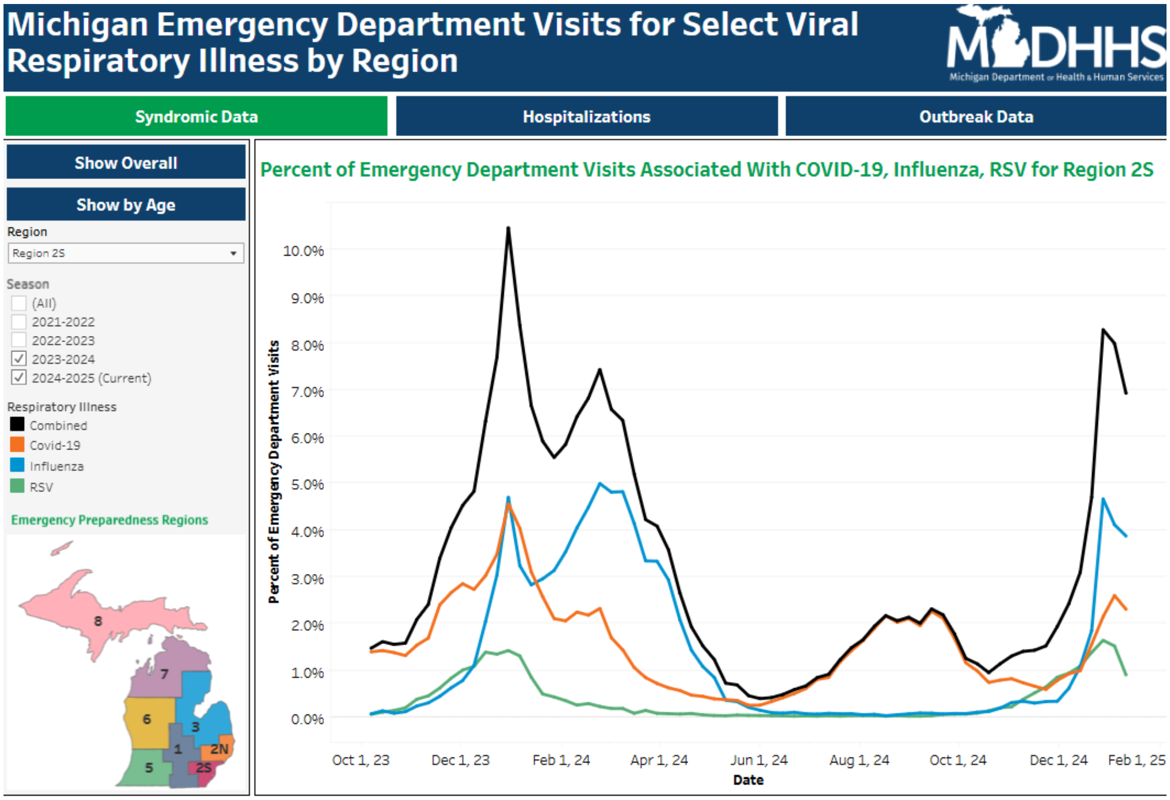


Figure 15. Cases of Confirmed and Probable COVID-19 by County or Local Health Jurisdiction in Michigan as January 18, 2025 (data from MDSS).



Region
Region 2S

Season
☐ (All)
☐ 2021-2022
☐ 2022-2023
☑ 2023-2024
☑ 2024-2025 (Current)

Figure 16. This graph shows the Region 2 South (City of Detroit; Monroe, Washtenaw and Wayne Counties) ED visits related to respiratory viruses – COVID-19, Influenza and Respiratory Syncytial Virus infections from October 2023 up until January 18, 2025. (6.9% Combined – 2.3% COVID-19, 3.9% Flu, 0.9% RSV)

Region 2 South Communicable Disease Activity

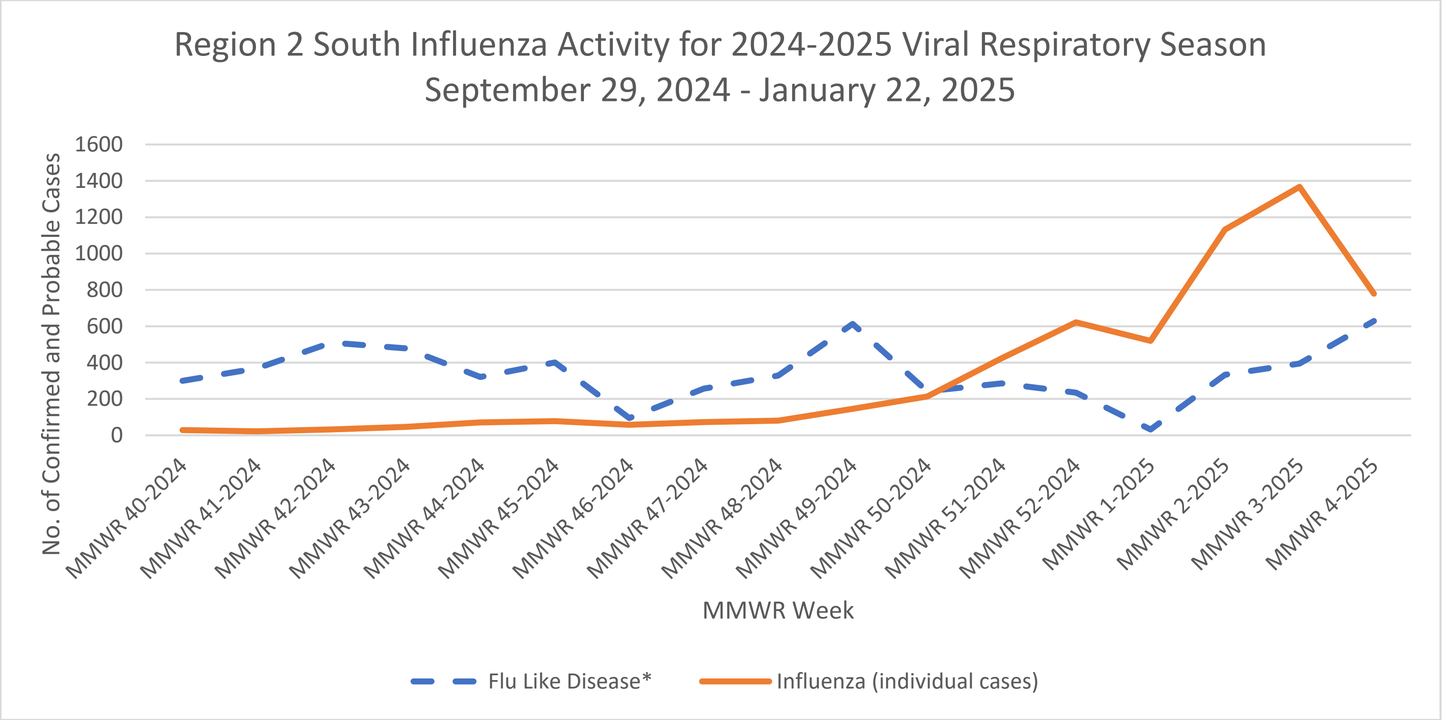


Figure 16. This graph shows Influenza-like Disease as well as confirmed and probable influenza cases reported in Region 2 South residents for 2024-2025 Viral Respiratory Season. After some early activity in September and October, overall

respiratory activity is increasing slowly. The peak of confirmed and probable influenza activity appears to have happened in the early weeks of January 2025 but activity will continue to be monitored.

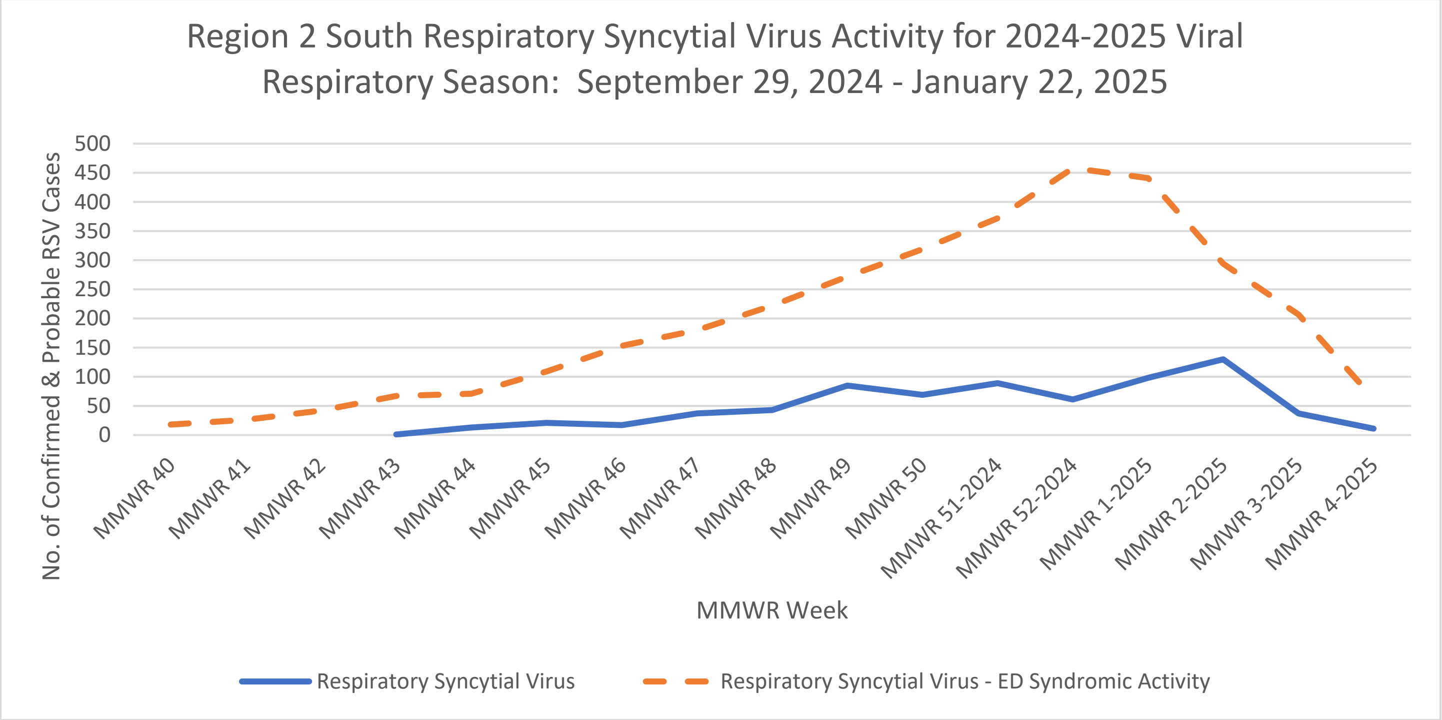


Figure 17. This graph shows the confirmed and probable Respiratory Syncytial Virus (RSV) cases reported in MDSS along side of those Emergency Department (ED) visits classified as a RSV – related visits for the 2024-2025 Viral Respiratory Season in Region 2 South jurisdictions. As can be seen, there appears to have been a peak in ED-related visits back in the end of December 2024 with corresponding peak in cases reported in early January 2025. Activity continues to be monitored.

Vaccine Preventable Disease Activity

Disease	Jan-24	Feb-24	Mar-24	Apr-24	May-24	Jun-24	Jul-24	Aug-24	Sep-24	Oct-24	Nov-24	Dec-24	Jan-25
Chickenpox (Varicella)	5	2	0	2	3	3	3	1	4	4	6	2	1
Diphtheria	0	0	0	0	0	0	0	0	0	0	0	0	0
H. influenzae Disease - Inv.	7	4	9	8	3	2	5	2	4	5	11	6	4
Measles	0	2	2	0	0	0	1	0	0	0	0	0	0
Mumps	1	0	0	0	0	0	1	0	0	0	0	0	0
Pertussis	5	7	5	5	19	31	26	51	61	69	69	69	23
Polio	0	0	0	0	0	0	0	0	0	0	0	0	0
Rubella	0	0	1	1	0	0	0	0	0	0	0	0	0
Shingles	17	19	29	31	16	31	40	20	42	23	25	20	9
Tetanus	0	0	0	0	0	0	0	0	0	0	0	0	0
VZ Infection, Unspecified	25	27	25	27	30	17	25	18	21	5	11	7	3
Subtotal	60	61	71	74	71	84	101	92	132	106	122	104	40

Table 5. This table shows the confirmed and probable cases of vaccine preventable disease reported in MDSS January 1, 2024 – January 22, 2025 for Region 2 South. Both chickenpox and pertussis activity has persisted throughout the years,

which is expected. There has been a smaller increase in activity in the region for Chickenpox, Shingles, and VZ infection unspecified but they are still be reported in MDSS throughout the year.

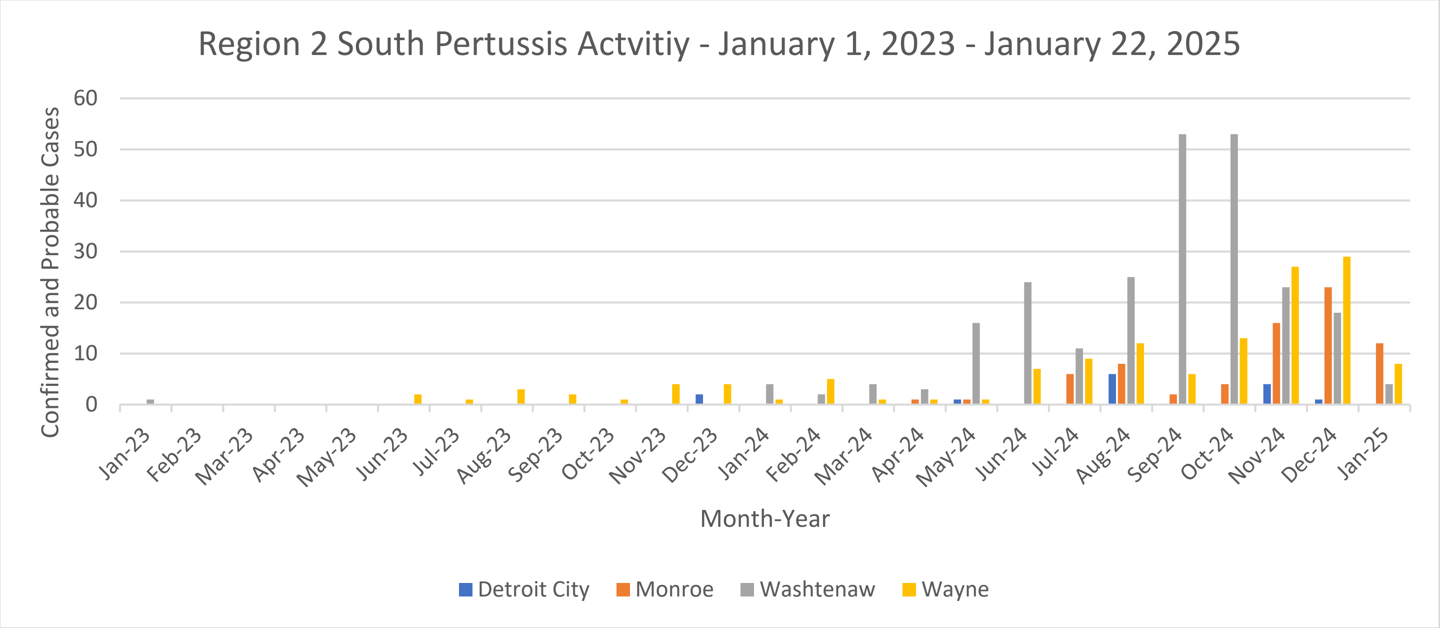


Figure 18. This graph shows the pertussis activity in Region 2 South. June through December 2023 showed sporadic activity in Wayne County residents. Starting January 2024, more cases started showing up in all jurisdictions with a rise initially in Washtenaw County in March 2024. Since July 2024 onwards all four jurisdictions in Region 2 South have been increasing in activity, especially Washtenaw County.

Foodborne Illness Disease Activity

Disease	Jan-24	Feb-24	Mar-24	Apr-24	May-24	Jun-24	Jul-24	Aug-24	Sep-24	Oct-24	Nov-24	Dec-24	Jan-25
Amebiasis	0	0	0	0	0	0	0	0	0	0	0	0	0
Botulism - Foodborne	0	0	0	1	0	0	0	0	0	0	0	0	0
Campylobacter	25	20	24	24	23	43	42	38	50	23	21	29	5
Cryptosporidiosis	4	3	2	2	2	6	13	11	6	13	4	0	1
Giardiasis	6	8	9	4	5	12	12	9	11	9	2	6	1
Listeriosis	2	1	0	0	1	0	0	1	0	0	1	0	0
Norovirus	7	5	15	6	4	1	1	2	7	2	16	51	2
Paratyphoid Fever	0	0	0	0	0	0	0	0	0	0	0	0	0
Salmonellosis	14	7	15	15	24	20	22	21	22	17	18	17	7
Shiga toxin-producing *Escherichia coli* -- (STEC)	3	5	4	6	8	6	12	5	10	7	5	6	3
Shigellosis	9	6	11	4	8	3	6	15	11	6	2	3	2
Typhoid Fever	0	1	0	0	0	0	0	0	2	0	0	0	0
Yersinia enteritis	3	10	3	4	5	4	3	5	7	5	2	7	1

Table 6. This table highlights the foodborne disease reported into MDSS for January 1, 2024 – January 22, 2025 in Region 2 South. Campylobacter and shigellosis activity is steady throughout the year. Salmonellosis cases are also reported every month with increases in June through October likely due to multi-state outbreaks. Giardiasis and

cryptosporidiosis activity also starts to rise in warmer months due to exposure to outdoor environment including lakes and outdoor activities.

Zoonotic Activity in Michigan and Region 2 South

The Arbovirus Surveillance Summary is available on the Emerging Diseases website (https://www.michigan.gov/emergingdiseases/)

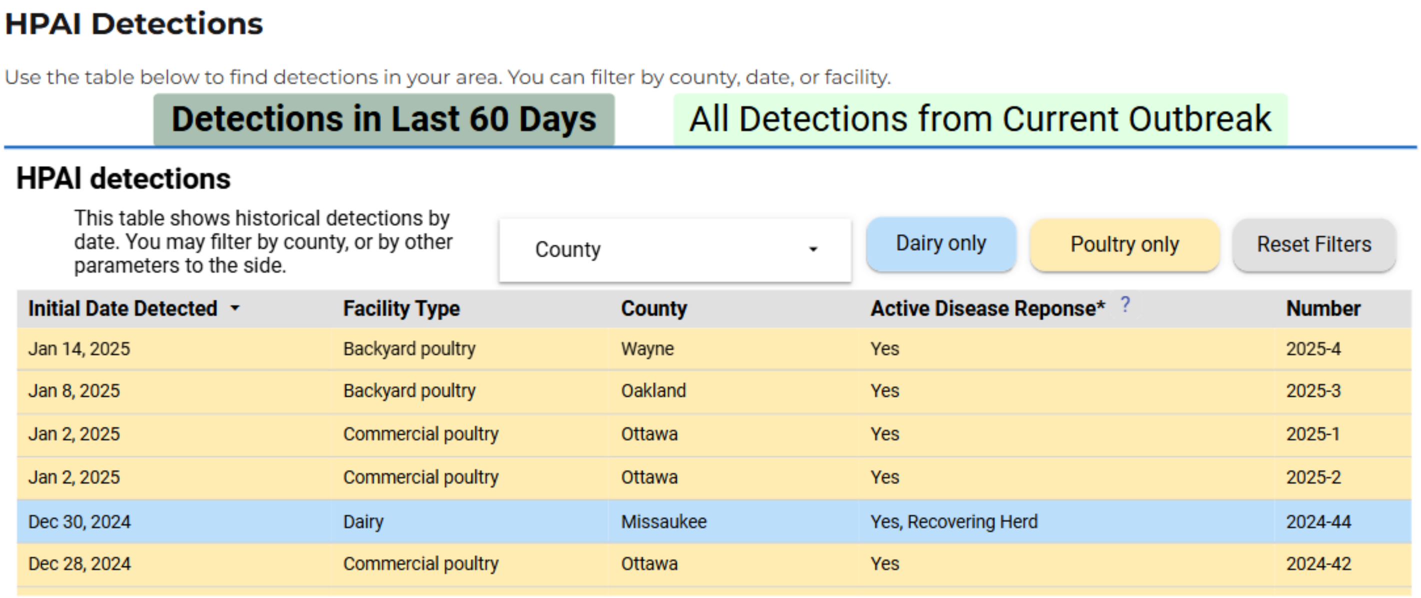
So far in 2024 (as of December 6, 2024):

- Thirty-one residents of Berrien, Calhoun, Delta, City of Detroit, Eaton, Genesee (3), Ingham, Jackson (3), Kent, Lapeer, Lenawee, Livingston, Macomb(6), Midland, Monroe, Oakland (4), St. Clair and Wayne (2) counties have been sickened by West Nile virus (WNV).
- Five residents from Alpena, Eaton, Houghton, Livingston and Wayne counties have tested positive for Jamestown Canyon Virus (JCV).
- Thirteen horses from Allegan, Cass, Clare, Kalamazoo, Lapeer, Menominee, Osceola (2), St. Joseph, Tuscola, Van Buren (2) and Wexford counties and five birds from Antrim, Marquette, Newaygo, Otsego, and Roscommon counties have tested positive for Eastern equine encephalitis virus (EEEV).
- Eight horses from Eaton (2), Kalamazoo, Kent, St. Joseph, Tuscola, Van Buren and Washtenaw counties and 106 birds from Alger, Allegan, Alpena, Antrim (3), Bay (6), Branch (3), Calhoun, Cass (2), Cheboygan, Chippewa, City of Detroit, Crawford, Delta (3), Eaton (4), Emmet, Genesee, Grand Traverse (5), Gratiot, Ingham, Iosco, Iron (2), Isabella, Jackson (3), Kalamazoo (3), Kalkaska (2), Kent (2), Lenawee, Livingston (2), Luce (3), Macomb (2), Manistee, Marquette (2), Mason, Menominee (4), Monroe, Montmorency, Muskegon (2), Oakland (9), Ogemaw, Ontonagon, Otsego (2), Ottawa, Roscommon (3), Saginaw (8), St. Clair, Tuscola, Van Buren, Washtenaw (4), Wayne and Wexford counties have tested positive for WNV.
- Three mosquito pools from Arenac, Cass and Kent counties have tested positive for EEEV.
- 150 mosquito pools from Arenac (2), Bay (79), Calhoun, Huron, Iosco, Jackson, Kent (27), Macomb (4), Oakland, Ottawa (2), Saginaw (12), St. Clair (12), Washtenaw (6) and Wayne counties have tested positive for WNV.
- Fourteen mosquito pools from Bay (3), Berrien (2), Calhoun, Dickinson, Kent and Saginaw (6) counties have tested positive for JCV
- Rabies Update - For 2024, there have been a total of **48 positive rabies** specimens**.**
    - Wayne County – 3 bats
    - Washtenaw County – 4 bats

Current Status in Michigan's Domestic Animals

As detections of highly pathogenic avian influenza continue to be discovered throughout Michigan, it remains vital for every producer to take steps to protect their animals.

Cases of the disease continue to be found in Michigan’s wildlife and domestic animals. In March 2024, the virus was also detected in Michigan dairy cattle. Regardless of the species, biosecurity remains the best tool to combat HPAI. MDARD continues to diligently work with local, state, and federal partners to quickly respond to reports of HPAI, mitigate the spread of the disease, and provide additional outreach to producers, industry, and other key stakeholders. Stay up to date with the latest information by signing up to receive notifications on HPAI in Michigan.



HPAI Detections

Use the table below to find detections in your area. You can filter by county, date, or facility.

HPAI detections

This table shows historical detections by date. You may filter by county, or by other parameters to the side.

Initial Date Detected	Facility Type	County	Active Disease Reponse* ?	Number
Jan 14, 2025	Backyard poultry	Wayne	Yes	2025-4
Jan 8, 2025	Backyard poultry	Oakland	Yes	2025-3
Jan 2, 2025	Commercial poultry	Ottawa	Yes	2025-1
Jan 2, 2025	Commercial poultry	Ottawa	Yes	2025-2
Dec 30, 2024	Dairy	Missaukee	Yes, Recovering Herd	2024-44
Dec 28, 2024	Commercial poultry	Ottawa	Yes	2024-42

Figure 19. This graphic shows the areas where Highly Pathogenic Avian Influenza (HPAI) was detected by county in the State of Michigan for the past 60 days as of January 22, 2025. As can be seen, not only the western side of Michigan but presently the Southeastern part of Michigan including Region 2 South jurisdictions have also been affected by HPAI.