Infectious Diseases Threats in a Changing Climates

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Abstract

Background

Factors related to human activity, such as international travel, globalisation, trade, urbanisation and the disruption of ecosystems and biodiversity, have a significant impact on the epidemiology of infectious diseases. Climate change is an additional factor which often amplifies this impact. It is estimated that climate change has exacerbated over half of all infectious diseases worldwide, contributing to 60–80% of emerging infectious diseases.

Objective:

The aim of this narrative review is to provide a concise overview of infectious disease threats linked to climate change, with a focus on Europe.

Methods:

A literature search was conducted in PubMed using the keywords 'climate change', 'infectious diseases' and 'Europe', with results limited to publications from the last 5 years. Additional information was obtained from the websites of the European Centre for Disease Prevention and Control, the European Commission, the European Food Safety Authority, the World Health Organization, the US Centers of Disease Control and Prevention, and Google Scholar.

Results:

The eco-epidemiology of existing and emerging infectious diseases in Europe is impacted by global warming, changing rainfall patterns and extreme weather events resulting from climate change, either directly or indirectly. This article reviews the risk of a new pandemic and of waterborne, foodborne, vectorborne diseases.

Conclusion:

The eco-epidemiology of infectious diseases is complex and influenced by various factors, including climate change. A coordinated, multisectoral approach is required from a One Health perspective to ensure proactive preparedness.

Introduction

Climate change includes rising global temperatures, shifting precipitation patterns, an increased number and intensity of heat waves, as well as more frequent extreme weather events, such as floods, droughts, wildfires and storms. Climate change will continue at least through this century and probably far beyond (1). Since the 1980's Europe has been warming twice as fast as the global average, making it the fastest warming continent on earth (2).

Climate change is a major additional factor that modifies and usually amplifies the influence of other human-activity-related factors on the eco-epidemiology of infectious diseases. These factors include international travel, globalisation, trade exchange, deforestation, land use, close interaction with livestock, population growth, urbanisation and migration. Together with biodiversity loss, climate change, is an important driver of the spread, emergence and persistence of infectious diseases (3, 4). It is estimated that 58% of all infectious diseases reported to have impacted humanity worldwide have been exacerbated by climate change, particularly waterborne and vector-borne diseases (5). Furthermore, it is estimated that 60–80% of newly emerging diseases are of zoonotic origin (6).

The two most important climate factors influencing the emergence of infectious diseases are temperature and precipitation (7). It is estimated that the mean annual temperature in Europe may increase by between 2 and 7°C by 2100. Annual mean precipitation is projected to increase in the north and decrease in the south. Northern and Central Europe are likely to experience more frequent and intense extreme precipitation events (8). Southern Europe is projected to experience more frequent and prolonged droughts, higher risk of wildfires, and increased pressure on water resources.

Although climate change is not the only factor, it is assumed that it can have a direct and indirect influence on the epidemiology of infectious diseases (5, 7-10). Direct influences include extreme weather events, such as outbreaks following water contamination after heavy rainfall or flooding, foodborne infections due to food spoilage during heatwaves, the geographic expansion of pathogens and vectors, increased pathogen replication and transmission. Indirect influences include population displacement or migration due to water and food insecurity, or conflicts. Increased indoor activity and overcrowding also facilitate the spread of airborne or diarrhoeal diseases.

Nevertheless, the most significant global threat is the potential emergence of a new pandemic, which may be influenced by climate change.

Methods

A literature search was conducted in PubMed using the keywords ‘climate change’, ‘infectious diseases’ and ‘Europe’, with results limited to publications from the last 5 years. Additional information was obtained from the websites of the European Centre for Disease Prevention and Control, the US Centres of Disease Control and Prevention the European Commission, the European Food Safety Authority, the World Health Organization, and Google Scholar. Following an initial selection, 364 records were retained, and 90 after the final selection.

Pandemic threat

While any pathogen X could initiate a new pandemic, the WHO believes that a respiratory influenza virus is the most likely candidate (11, 12). The genome of the influenza virus, which consists of eight separate RNA segments, is susceptible not only to mutations during replication but also to segment exchange during co-infection with two different virus strains, potentially creating a new virus. If this new virus can transmit between humans, it has the potential to cause a pandemic. Airborne respiratory pathogens have a significant advantage in terms of speed and extent of transmission. Respiratory manoeuvres like coughing or sneezing can spread thousands of infectious respiratory particles (IRPs). Depending on their size and environmental conditions these IRPs can remain suspended for a long time and can be carried by air currents (13). They can infect many individuals without direct contact with the primary source. The risk of transmission is particularly high in crowded or poorly ventilated spaces. Moreover, in a globalised world, everyone is only a plane ride away from each other (14).

Pandemics often start with pathogen transmission from animals to humans. The highly pathogenic type A H5N1 avian influenza virus is currently a source of great concern.

At the end of the 1990s, an H5N1 epidemic broke out in poultry in Asia, likely introduced by migrating wild birds. The virus was capable of crossing species and infecting humans who were in close contact with sick poultry, causing severe illness with a high mortality rate. However, human-to-human transmission was rare. Since the end of the 2000s, the virus has spread to other continents. Next, it expanded its host range, likely due to adaptive mutations in viral proteins that facilitate infection of terrestrial and marine carnivorous mammals. These animals become infected by ingesting infected birds or through exposure to a contaminated environment (15-17). Mammal-to-mammal transmission was observed in 2022 among farmed minks in Spain. A second larger fur farm outbreak (71 farms) occurred in 2023 in Finland that affected mink, arctic foxes and raccoon dogs. The same year, large numbers of sea lion carcasses washed up on beaches along the coasts of Peru and Chile when the H5N1 avian influenza virus outbreak in marine mammals surged (18). The first confirmed detection of H5N1 avian influenza in U.S. dairy cattle was announced in 2024 (19, 20). As of 28 July 2025, the infection has been detected in 1,063 herds across 17 states. It is believed that the cows became infected via feed contaminated with faeces from migrating wild birds. Disease symptoms in cattle are usually mild. Bovine-to-bovine spread occurs within herds. There is also evidence that the virus can spread from dairy cattle premises to nearby poultry facilities. In November 2024, the H5N1 virus was detected in two pigs on a farm where poultry and livestock were mixed, representing the first time the virus had been found in US swine. Between March 2024 and October 2025, the United States reported 70 human infections with highly pathogenic avian influenza H5N1, including two children (21). Of these, 41 were linked to exposure to infected dairy cattle, 24 to commercial poultry, 2 to backyard poultry, and 3 to unidentified sources of exposure. While symptoms were generally comparable to classic flu symptoms, serious illness has occurred and one infected person with underlying health conditions has died. So far, no cases of human-to-human transmission have been observed in the U.S..

The ability of the H5N1 virus to spread across species demonstrates both its remarkable adaptability and the serious threat it poses as a potential source of the next pandemic, underscoring the urgent need for a One Health (an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems) approach. Climate change may amplify this risk by altering the migration patterns and behaviours of wild birds, disrupting ecosystems, and bringing humans and animals into closer contact — conditions that facilitate viral adaptation and interspecies transmission. In addition, rising temperatures and humidity fluctuations can influence human behaviour, indoor crowding, and the environmental persistence of IRPs, further shaping the dynamics of disease spread.

Waterborne infections

Heavy rainfall and flooding

Pluvial and fluvial floods are the most common types of natural disaster in Europe (22), and these are expected to become more frequent across all European regions (23). In 2024, Europe experienced its most extensive flooding since 2013. Beyond the immediate risk of injury or drowning, exposure to hazardous chemicals, infrastructure loss, and long-term psychological and economic consequences, floods also increase the risk of infectious diseases. Flooding is associated with waterborne, rodent-borne and vector-borne diseases, which typically occur sequentially over time. Floodwater-borne infections typically occur acutely (0–7 days), rodent-borne infections in the mid-term (1–4 weeks), and vector-borne infections in the longer term (4 weeks to several months) (24). The greatest risk to children is posed by floodwater-borne gastrointestinal infections and vector-borne infections.

Extreme rainfall on 14 and 15 July 2021 caused flooding in Belgium, Luxembourg and Germany. The worst-hit areas were western Germany and eastern Wallonia in Belgium, particularly the provinces of Liège and Luxembourg. 31,563 households were flooded in 209 municipalities, affecting more than 100,000 people, and there were 37 deaths and 6 missing persons (25, 26).

The Walloon health officer conducted a retrospective analysis of the impact of flooding on a number of targeted notifiable diseases. Covid-19 (the pandemic was still happening), legionellosis, leptospirosis and Shiga toxin-producing *Escherichia coli* (STEC). Although underreporting occurred due to an overwhelming workload and communication difficulties for practitioners, as well as limited access to primary care for the population, an increase in reports of all these diseases was observed in the weeks following the flood.

A cluster of 10 STEC cases was identified. 6 children (range 2 – 17 years) developed a haemolytic uremic syndrome (27). Surveillance questionnaires linked the infection to contaminated tap water.

Floodwater-borne infections result from the contamination of water supplies with animal or human excreta carried in soil washed away by flooding and/or from malfunction or destruction of sewage systems.

In general, flooding increases the risk of gastrointestinal infections, including bacterial infections caused by *Campylobacter* spp., *Escherichia coli* (including Shiga toxin-producing *E. coli*), *Salmonella* enterica serotypes, and Shigella spp.; viral infections caused by norovirus, rotavirus, and hepatitis A virus; and parasitic infections caused by *Cryptosporidium* spp. and *Giardia lamblia* (25). Children are particularly vulnerable to severe disease progression and complications arising from gastrointestinal infections. Contaminated water can also lead to contamination of food. Malfunction or destruction of distribution lines, as well as cooling and cooking systems, can contribute pathogen transmission via food. In addition, population displacement and overcrowding in temporary shelters increase the risk of infection transmission.

A lack of garbage collection and management increases the rodent population, thereby raising the risk of leptospirosis. Rodents shed *Leptospira* in their urine, and flooding prevents it from being absorbed into the soil or evaporating. *Leptospira* can then persists in the water or mud (25). Humans may become infected through contact with contaminated water or mud via mucous membranes or damaged skin, or by drinking contaminated water or inhaling small droplet nuclei. Warm and humid conditions also promote the *Leptospira* survival (28).

Stagnant water left behind after flooding promotes mosquito breeding, potentially increasing the risk of mosquito-borne diseases. This risk also depends on the presence of pathogens in human and non-human reservoirs, as well as the competence of mosquito vectors (i.e., their ability to harbour and transmit a pathogen). For example, West Nile virus (WNV) is transmitted by Culex species mosquitos, whereas dengue and chikungunya are transmitted by Aedes species. Heavy rainfall and floods in Europe have already been associated with WNV outbreaks (Czech Republic) and chikungunya cases (France) (29, 30). As the geographical range of the tiger mosquito (Aedes albopictus) in Europe steadily expands, along with cases of imported and locally transmitted dengue and chikungunya, flooding may further promote the expansion and risk of these diseases.

Flooding can also increase the risk of *legionellosis*. Floodwaters may disperse Legionella bacteria from their natural habitat, depositing them in soil or sediment. Humans can become infected through aerosols generated when cleaning these areas, for example with high-pressure jet cleaners. Damage to water supply infrastructure may further elevate the risk of infection.

Risks related to the increase in global temperature

Pathogens can contaminate freshwater bodies - lakes, ponds, rivers, streams, canals or artificial reservoirs - through direct release of sewage or wastewater, or via excreta from livestock or wild animals washed in by rain. Pathogens may also infiltrate groundwater through soil fertilised with organic fertilisers or via seepage from contaminated surface water. In Europe, 60–70% of soils are degraded, and 62% of freshwater bodies are in poor ecological condition (2). Apart from industrial pollution, the main pressures on surface and groundwater come from the use of fertilisers and pesticides in agriculture. Furthermore, nitrogen and phosphorus fertilisers stimulate bacterial growth and replication. Climate change can increase pressure on farmers to use more fertilizers and pesticides. Rising global temperatures also promote the development of bacteria such as *Salmonella* and *E. coli*, *Leptospira*, *Legionella* and toxin-producing cyanobacteria, as well as the survival of protozoa such as *Cryptosporidium* oocysts. A major concern is the evidence linking climate change to the development and spread of antimicrobial resistance (31-34).

Freshwater bodies are commonly used for recreational activities such as swimming, boating, and fishing. During longer and warmer summers, recreational freshwater activities are likely to increase, along with the bacterial load in contaminated water, thereby raising the risk of waterborne infections. Drinking water can be extracted from either groundwater or surface water. The main challenges in ensuring the safety of public drinking water systems are water purification, disinfection, storage, and distribution. Biofilms often form in old, corroded metal or rough-walled concrete pipelines. These consist of various bacteria and fungi, including *Pseudomonas aeruginosa*, non-tuberculous *Mycobacteria*, *Legionella* and *Aspergillus fumigatus*, even in chlorinated drinking water. Higher temperatures, especially in summer, increase biofilm formation and microorganism concentrations (35-37). Biofilms and *Legionella* are often associated with infections linked to public drinking water (38). Infections from private drinking water supplies, such as wells or springs, are typically caused by enteric pathogens — bacteria, viruses, or protozoa — present in contaminated groundwater or surface water.

Due to climate change and the resulting increase in sea surface temperatures, the risk of vibriosis in coastal waters is rising, particularly during warm periods.

An eleven-year-old boy is on holiday at a holiday park near the Oosterschelde estuary. As it is a hot summer, he goes swimming and plays in the water every day. One day, he steps on a sharp shell and gets a small cut on his ankle. However, this didn't stop him from continuing to play in the water. The next morning, his ankle was red, swollen and painful, and he had a fever of 39°C. Fortunately, the doctor who examined him was aware of the presence of *Vibrio* spp. in the waters of the Oosterschelde and recognised a potential *Vibrio* wound infection with cellulitis. Given the potential severity of *Vibrio* infections, she decided to hospitalise him. A blood sample and a swab of the wound were taken for culture and he was started on intravenous antibiotics (ceftriaxone plus ciprofloxacin). Three days later, the wound culture tested positive for *Vibrio alginolyticus*, which is known to cause milder disease. He was discharged on a course of oral ciprofloxacin.

Vibrio spp. are naturally found in brackish coastal waters where saltwater and freshwater mix. They are traditionally detected during the summer in the Baltic Sea, where the lower salinity favours their growth. Such conditions are becoming increasingly common in other parts of Europe due to climate change. *Vibrio* spp. have been found in other regions, including the North Sea, and their range is expected to expand to additional coastal areas (39). These are non-cholera *Vibrio* spp., such as *V. vulnificus*, *V. parahaemolyticus* and *V. alginolyticus*. *V. vulnificus* can cause septicaemia, severe wound infections and diarrhoea; *V. parahaemolyticus* can cause diarrhoeal disease following the consumption of seafood; and *V. alginolyticus* can cause wound infections and otitis externa. A 2012 study by the National Reference Centre in Belgium (Centre

Hospitalier Universitaire de Liège) also demonstrated the presence of *Vibrio* in recreational waters, particularly in the northern part of the country (40).

Foodborne infections

Contamination of food with pathogenic microorganisms can occur at any point along the food chain. At the production stage, pathogens may originate from animal faeces, contaminated soil or water. At the processing stage, improper handling or cross-contamination can introduce pathogens. At the distribution stage, poor temperature control can augment pathogen replication. At the retail stage, poor hygiene practices and cross-contamination further increase the risk. Finally, during food preparation, undercooking and improper hygiene can contribute to the presence of pathogenic microorganisms.

Many of the pathogens that cause foodborne infections are transmitted from animals to humans. In Europe, in 2023, the five most frequently reported zoonoses were all foodborne: campylobacteriosis, salmonellosis, yersiniosis, listeriosis, as well as infections caused by Shiga toxin producing *E.coli* (STEC) (41). For these five bacteria combined, 247574 cases of foodborne infections were reported in 2023, representing a 12.5% increase compared to 2022 (220089 cases) and a 22.3% increase compared to 2021 (202446 cases). Foodborne infections can lead to outbreaks of severe diarrhoea, with children being particularly vulnerable. We could not find any figures on the number of children with foodborne infections in Europe. According to the WHO, 30% of foodborne infection-related deaths occur in children worldwide (42).

Rising global temperature, along with more frequent heat waves and heavy rainfall linked to climate change, threaten food security. Higher global temperatures can stimulate the replication and/or survival rates of bacteria in the environment and in food (e.g. *Salmonella*, *E. coli* and *Campylobacter*), and can also accelerate toxin production by toxin-producing bacteria (e.g. *Staphylococcus aureus* or STEC) (43, 44). A warmer climate may additionally expand the geographic range of certain pathogens, such as *Vibrio* spp. in seafood.

Prolonged hot summers or heatwaves can lead to water shortages. When water is scarce, untreated wastewater may be used for irrigation, contaminating crops (43, 45). Such wastewater often contains high levels of enteric bacteria and protozoa, including *Giardia lamblia* and *Cryptosporidium*, as well as viruses such as hepatitis A virus, norovirus and rotavirus. Extended periods of high temperatures or heatwaves can also place considerable strain on the cold chain. Overall, prolonged heat and heatwaves driven by climate change represent a significant risk factor for foodborne infections.

The consequences of heavy rainfall have already been discussed.

Models predict that foodborne infections and outbreaks will increase in Europe - particularly in the central and southern regions – driven by higher temperatures and more frequent extreme weather events (43, 44).

Arthropod vector-borne infections

The recent emergence of 'tropical' vector-borne diseases in Europe is a captivating phenomenon. The vectors - *Aedes albopictus* (the tiger mosquito) and, to a lesser extent, *Aedes aegypti* – along with the pathogens they harbour - dengue, chikungunya and Zika viruses – have been introduced to the continent through human travel and global trade. Climate change has created increasingly favourable conditions for the establishment and spread of arthropod vectors, like mosquitoes, ticks and sandflies, by altering the habitat and life cycle. This has facilitated their geographical expansion towards higher latitudes and altitudes (46, 47).

Rising temperatures accelerate vector development and reproduction, increase population density, biting rates, and human contact, and shorten the intrinsic incubation period of pathogens, all factors that elevate the risk of human disease (28, 46, 48). However, temperature increases also have limitations. Optimal conditions for the development of pathogens and vectors are relatively narrow; for example, *Ae. albopictus* transmits dengue and chikungunya most efficiently at daily average temperatures of 24–26 °C, though transmission can occur between 12–30 °C (49). As a result, the future spread of vector-borne diseases may differ from the current situation and predictions (10, 50).

Table 1 provides an overview of current arthropod-borne diseases in Europe (51).

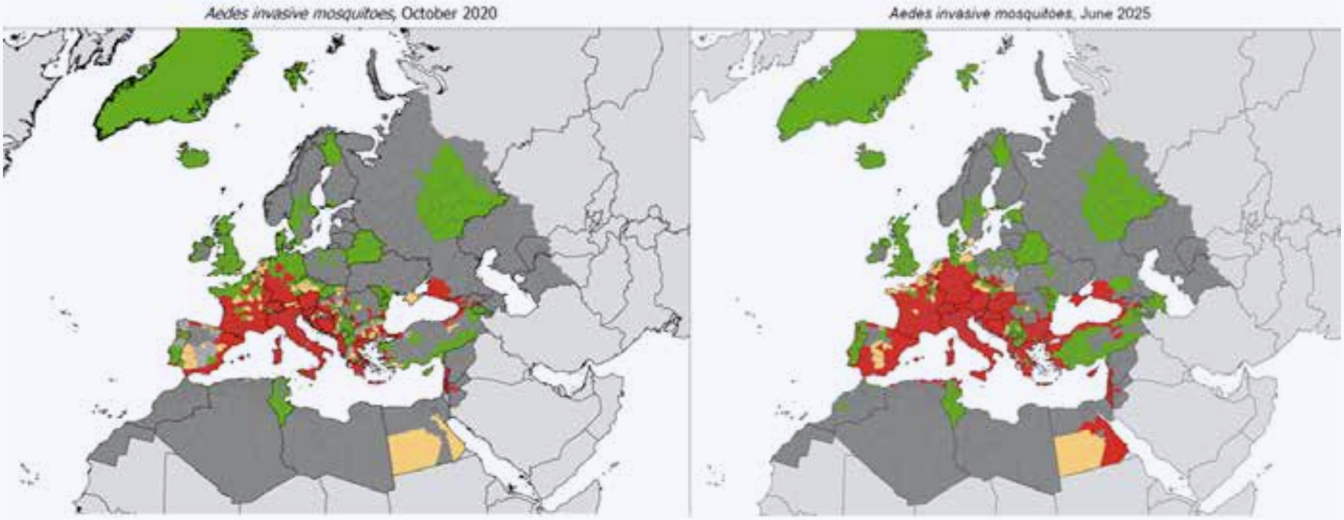
The European Centre for Disease Prevention and Control (ECDC) defines an invasive vector species as 'introduced' when it has been detected without evidence of established populations, and as 'established' when there is evidence of reproduction and overwintering. *Aedes* mosquitoes are now established and introduced in a large part of Europe (Figure 1) (52). Northern Europe is relatively spared but climatic projections suggest that *Ae. albopictus* will expand in the coming decade. These mosquitoes are both diurnal and nocturnal, adapted to urban and inhouse environments. Vertical transmission of the dengue virus - and probably the chikungunya and Zika viruses - from infected

TABLE 1: Overview of the most current arthropod-borne diseases in Europe.

Disease	Vector	Pathogen	Main host reservoir	Reported cases in EU/EEA in 2023 [x]
Dengue virus disease	*Aedes* spp. mosquito	*Orthoflavivirus (4 serotypes)*	Humans	5510
Chikungunya	*Aedes* spp. mosquito	*Alphavirus*	Humans	337
West Nile virus disease	*Culex* spp. mosquito	*Flavivirus*	Birds	742
Zika virus disease	*Aedes* spp. mosquito	*Flavivirus*	Humans	80
Malaria	*Anopheles* spp. mosquito	*Plasmodium spp.*	Humans	7245
Tick borne encephalitis	*Ixodes* spp. ticks	*Flavivirus*	Small rodents	3578
Lyme neuroborreliosis	*Ixodes* spp. ticks	*Borrelia spp.*	Small rodents	1497
Lyme disease (non-neurological)	*Ixodes* spp. ticks	*Borrelia spp.*	Small rodents	No registration
Leishmaniasis	*Phlebotomus* spp. sandflies	*Leishmania spp.*	Dogs and rodents	No registration

x European Centre for Disease Prevention and Control. Surveillance Atlas of Infectious Diseases. 2023 (EU/EEA = European Union and European Economic Area)

FIGURE 1: Expansion of the Aedes mosquitoes in Europe over five years, from October 2020 to June 2025. Red = established, yellow = introduced, green = absent. Source: ECDC invasive mosquito maps, available from https://www.ecdc.europa.eu/en/disease-vectors/surveillance-and-disease-data/invasive-mosquito-maps.



female mosquitoes to their offspring has been documented (53). Once infected, these mosquitoes remain infectious and are capable of transmitting the virus to multiple individuals. Additionally, European species can survive winter by hibernating as eggs in diapause (54).

Mosquito-borne diseases

> A seven-year-old girl was admitted to Cesena Hospital (Emilia-Romagna, Italy) at the end of summer 2007 with a persistent high fever (40°C) for three days. She reported severe pain, particularly in her lower limbs, which prevented her from walking or sleeping. Clinical examination revealed a rash on her face, but no other specific abnormalities. A week earlier, her grandfather had experienced a high fever, joint pain, epigastric pain and vomiting, all of which resolved spontaneously within a few days. One month before, at the end of June, an imported case of chikungunya had been reported in a traveller returning from Kerala, India (55). The first locally acquired case was reported at the beginning of August. Ultimately, 330 locally acquired cases of chikungunya were notified to public health authorities, including 12 in children and adolescents up to 19 years of age, with the girl being one of them (56). PCR testing of her blood confirmed the presence of the virus.

This first large outbreak of autochthonous chikungunya warned us of the potential for invasive vectors and pathogens to become established in temperate climates when conditions are favourable.

Most chikungunya cases in Europe also involve travellers infected abroad. However, local outbreaks are increasing: Italy reported 330 and 270 cases in 2007 and 2017; and in 2025, France and Italy recorded 700 and 353 indigenous cases, respectively (57). Climatic conditions likely contributed: experienced wetter-than-average conditions in March 2025 and a hotter, longer summer, creating favourable conditions for mosquitoes (58). While direct attribution to climate change is uncertain, the transmission of chikungunya by *Aedes albopictus* has increased by 46.3% since the mid-20th century (59).

Chikungunya typically causes a sudden high fever, vomiting, muscle pain, a maculopapular rash and often severe joint pain. However, compared to adults, joint involvement is less frequent in children. Instead, neurological manifestations such as headaches, altered sensorium and irritability are more common. Prolonged, debilitating inflammatory arthritis, a common complication in adults, is less common in children (60).

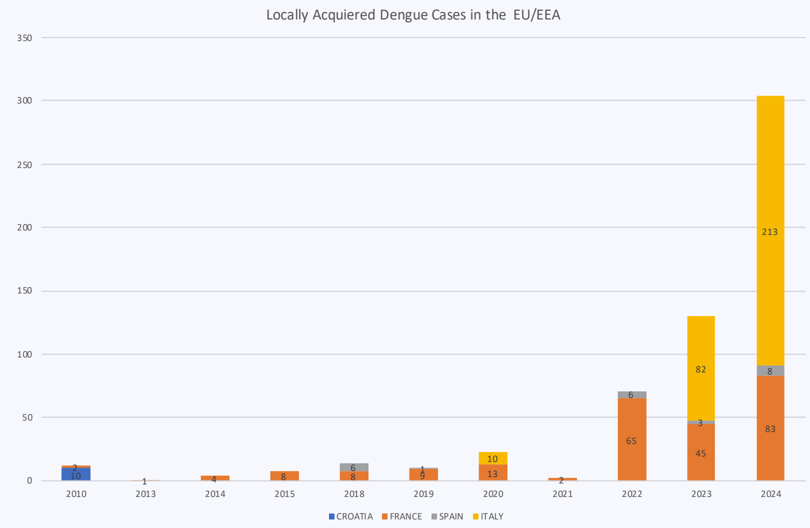
Dengue is the fastest-spreading mosquito-borne disease worldwide (4). Climate suitability for dengue transmission, measured by the basic reproduction number (R_0), has increased significantly for both *Ae. albopictus* and *Ae. Aegypti*, by 46.3% and 10.7% respectively, between 1951–1960 and 2016–2023 (59). The risk of dengue rose by approximately 13% for each 1°C increase in temperature (28). A study has estimated that, by the end of the century, half of the world's population could be at risk of contracting dengue fever (61).

Most dengue virus infections are asymptomatic. If symptoms are present, dengue typically presents with a sudden high fever, severe headache, retro-orbital pain, muscle and joint pain, nausea, vomiting, rash and haemorrhagic manifestations. In severe cases, it can progress to dengue haemorrhagic fever, which is characterised by plasma leakage and may progress to dengue shock syndrome. Importantly, infection with one serotype provides no lasting immunity against the others (there are 4 serotypes). Reinfection with a different serotype is possible and often results in more severe illness, making secondary infections a major public health concern.

Globally, children are the age group most affected by dengue. The younger the child, the more serious the disease. Children are at greater risk of developing symptoms, haemorrhagic dengue fever with plasma leakage and shock. Dengue has a higher mortality rate in children (62-64).

Dengue is not currently endemic in Europe ; most cases are travel-related, with 9603 cases reported in the EU/EEA (European Union / European Economic Area) in 2024, representing all four dengue virus serotypes (51, 65, 66). Where *Aedes* mosquitoes are established, viraemic travellers can trigger local transmission, leading to sporadic cases or outbreaks. Over the past 15 years, the majority of locally acquired cases have been reported in France, Italy and Spain. As Figure 2 illustrates, the number of cases has steadily increased, suggesting that sporadic local outbreaks may be evolving into a substantial and growing arboviral threat.

FIGURE 2: Number of locally acquired dengue cases in Europe.



As of today, the majority of cases of Zika virus disease in Europe are travel-related. Only three autochthonous, vector-borne cases have been reported in France, all in 2019 (67). A modelling study, assuming competence of the European *Ae. albopictus* population for transmitting the Zika virus, identified potential areas for autochthonous transmission, including Italy, southern France, the southern and eastern coasts of Spain, the western regions of the Balkans, and southern and northern Greece (68). However, it is now believed that European *Ae. albopictus* mosquitoes are relatively less competent at transmitting the Zika virus (67). But things might change.

About 25% of people infected with the Zika virus experience clinical symptoms, which include low-grade fever, conjunctivitis, maculopapular rash and arthralgia of the small joints. The virus has neurotropic properties and has been associated with Guillain-Barré syndrome, myelitis and meningoencephalitis. The virus is notorious for causing microcephaly and developmental disorders in babies following intrauterine infection. The course in children infected postnatally is similar to that in adults.

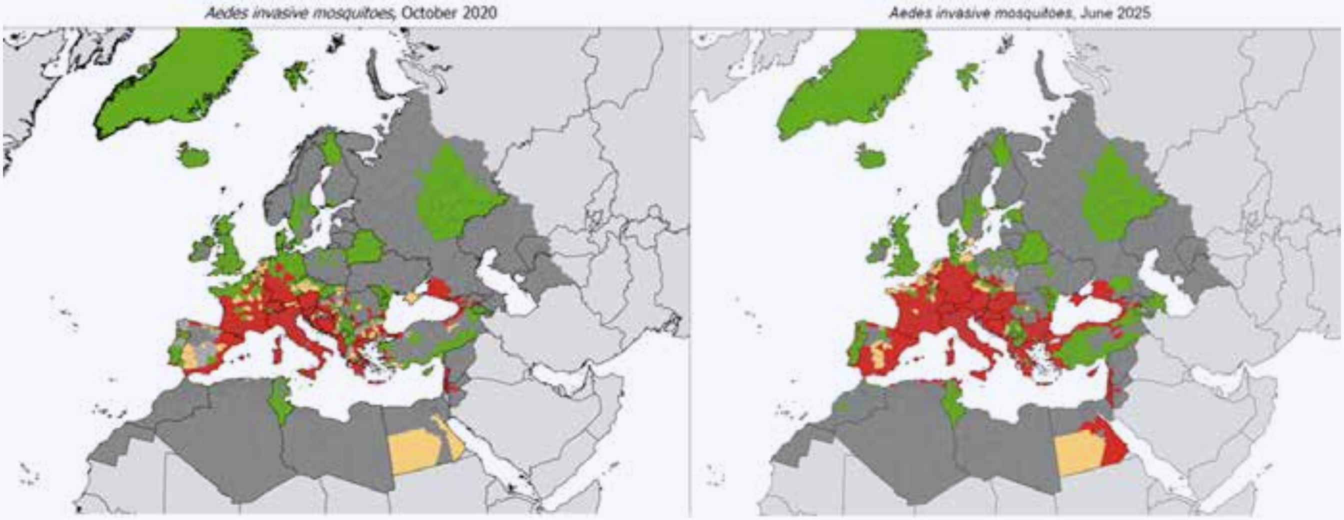
West Nile virus (WNV) is the most widely distributed arbovirus globally. The virus is transmitted by *Culex* spp., a mosquito species native to Europe. Birds are the primary hosts. but humans and other mammals, particularly horses, can be infected by a mosquito bite. In humans, infection is asymptomatic in approximately 80% of cases. Symptomatic infections may present as West Nile fever, a febrile illness, or as West Nile neuroinvasive disease, which affects the central nervous system and can present as meningitis, encephalitis or acute flaccid paralysis. Meningitis is more frequent in children than in adults (69). The circulation of WNV in Europe has detected since the 1950s. In 2025, Belgium reported three WNV outbreaks in wild birds to the EU Animal Diseases Information System (ADIS) for the first time ever (70). Notably, infected birds are often identified before human cases, highlighting their role as sentinels for virus circulation (10).

Rising temperatures and altered rainfall patterns are facilitating the northward expansion of mosquito vectors, as illustrated for the *Culex pipiens* group in Figure 3. At the same time, migratory birds are shifting their wintering and breeding grounds further north and adjusting their migration routes, aiding the virus's geographical spread. Higher temperatures also promote WNV genetic diversification and adaptation, enhancing transmission potential (71). As a result, the virus's basic reproduction number (R) increased by 4.3% in the 2014–2023 period compared with 1951–1960 (59).

According to US Centers for Disease Control and Prevention (CDC) data, WNV is less commonly reported in children than in adults (5%) (72). However, given the many prolonged outdoor activities that children engage in during the summer months, they are also at risk of infection. As infection often presents asymptomatically and WNV may not be systematically considered in cases of "viral meningitis" during the summer months, the true incidence may be underestimated.

Malaria is one of the five leading causes of death in children worldwide (73). Malaria is strongly influenced by climate change,

FIGURE 3: Expansion of *Culex pipiens* group mosquitoes in Europe between 2020 and 2023. Red = present, green = absent. Source: ECDC. Native mosquitoes maps, available from: https://www.ecdc.europa.eu/en/disease-vectors/surveillance-and-disease-data/native-mosquito-maps.



which affects mosquito vector distribution and expands suitable transmission zones. Since the mid-20th century, an additional 17.1% of global land has become suitable for *Plasmodium falciparum* transmission and 21.8% for *Plasmodium vivax* (28, 59).

Malaria was once endemic in Europe. Native *Anopheles* mosquitos can still transmit malaria, and although most current cases are travel-related, a few locally acquired 'airport malaria' cases have occurred (74, 75). If conditions become favourable, malaria could re-establish local transmission cycles, but it remains impossible to predict whether it will become endemic again in Europe.

Tick-borne diseases

Climate change - particularly in terms of temperature, rainfall and humidity - affects the geographic distribution and behaviour of ticks. Shifts and expansions to higher latitudes (northwards) and altitudes have already been reported (76, 77). Shorter winters and longer springs and autumns further extend the period of tick activity (3, 78). Rising temperature and humidity also increase tick biting rates and enhance oviposition and larval survival (46). Tick abundance is additionally influenced by host availability, which is shaped by land use and land-use changes, including human outdoor activity, agricultural and livestock practices, and deforestation.

> In May 2024, a six-year-old girl presented with a six-day history of fever, diarrhoea and myalgia. Initial clinical and blood tests revealed mild thrombocytopenia, leukopenia and elevated creatine kinase levels. No clear cause of the fever was identified. The fever subsided after three to four days.
>
> Four days later, the fever recurred and she had arthralgia. She was admitted to hospital. Blood tests were normal, but meningeal signs developed on day 4, with cerebrospinal fluid (CSF) analysis showing leukocytosis. Intravenous cefotaxime was initiated. After seven days, tick-borne encephalitis virus (TBEV) IgM was detected in her CSF. Her symptoms resolved and she was discharged with no residual effects. A follow-up brain MRI scan showed no abnormalities. This is the first reported case of locally acquired TBEV infection in a child in Belgium (79). Three autochthonous adult cases had been described in 2021 (80).

Ticks transmit a broad range of pathogens, including viruses, bacteria and parasites. *Ixodes ricinus* is the most widespread tick in Europe (Figure 4) and the primary vector for *Borellia burgdorferi* sensu lato, which causes Lyme disease and neuroborreliosis, as well as for tick-borne encephalitis virus (TEBV), a *Flavivirus* (76). Tick-borne encephalitis is characterised by a biphasic fever. During the first phase, symptoms such as fever, tiredness, arthralgia, myalgia, headache and gastrointestinal symptoms predominate. Following an afebrile period of approximately seven days, the fever recurs with neurological manifestations. Nevertheless, two-thirds of infected individuals are not symptomatic, and some exhibit only the initial phase..

The second most common tick in Europe is *Dermacentor reticularis*, a vector for various pathogens including *Coxiella burnetti* (Q-fever) and *Ricktesia* spp. (tick-borne lymphadenopathy) (81). The ECDC also monitors *Hyalomma marginatum*, a vector for the Crimean-Congo haemorrhagic fever (CCHF) virus, a *Bunyavirus*. This thick is widely distributed across North Africa and Asia and is present in southern and eastern Europe. CCHF virus considered an emerging pathogen in Europe (82).

Sandfly-borne diseases

Different sandfly species can transmit *Leishmania* spp. parasites. *Leishmania* is an obligate intracellular parasite that infects macrophages. The species present in Europe belong to the so-called 'Old World' group. *L. major*, *L. tropica* and *L. aethiopica* cause cutaneous leishmaniasis, which is the mildest form and presents as painless nodules or ulcerative lesions. *L. aethiopica* can also cause mucocutaneous disease, characterised by destructive lesions of mucous membranes and cartilage in the nose, mouth, and pharynx. The most severe form, visceral leishmaniasis, is caused in Europe by the parasite *L. donovani infantum* and manifests with intermittent fever, anaemia, hepatosplenomegaly, and weight loss (83). Because of its non-specific systemic symptoms and cytopenias, visceral leishmaniasis is often initially mistaken for haematological malignancy.

The main reservoir of *Leishmania* in Europe is domestic dogs, although a range of other animals - including rodents, horses, birds and reptiles - can also harbour the parasite (28). The continued spread of *Leishmania* across European countries has been facilitated in part by the frequent and largely uncontrolled movement of infected pet dogs, but human migration from endemic regions may also contribute to the parasite's spread (8). Children and young adults appear to be at the greatest risk of infection.

Leishmaniasis is endemic in southern Europe (84). In Europe most *Phlebotomus* sandfly species are distributed in around the Mediterranean basin, although *P. perniciosus* is also found in parts of France and Germany (see VectorNet phlebotomine sandfly maps (85)). Sandflies are thermophilic, thriving in environments where average temperatures consistently exceed 15°C (83). As a result, global warming is expected to influence their distribution, potentially making more northern regions increasingly suitable for their establishment. In recent years, sporadic locally acquired cases of leishmaniasis have been reported in central European countries, including Germany, Austria, and England.

Personal protection measures against arthropod vector- borne diseases

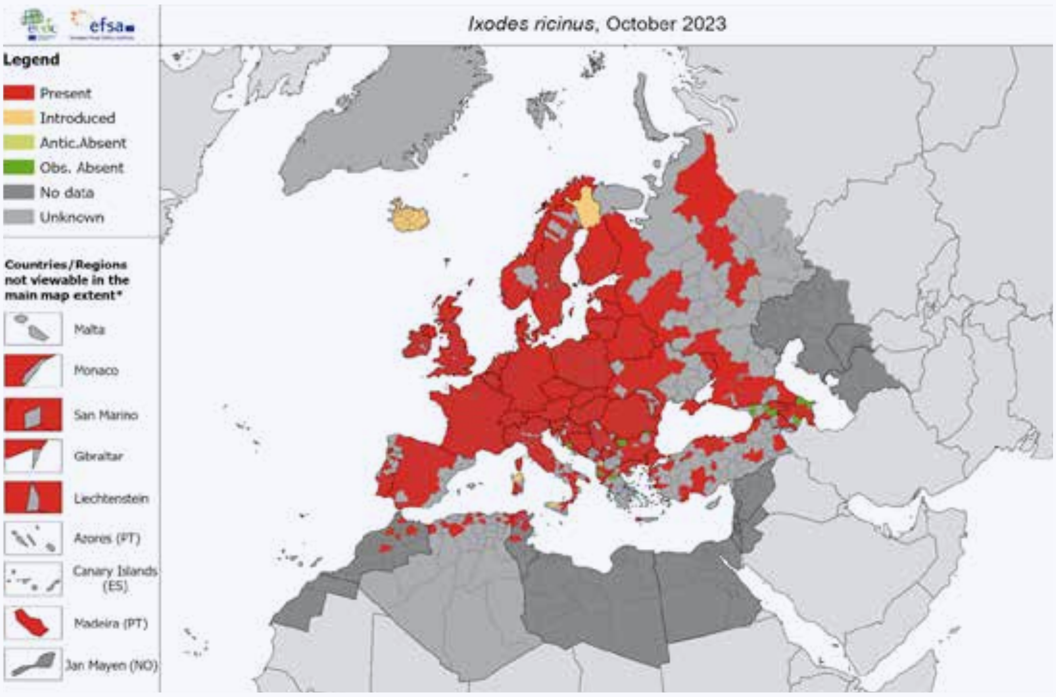
Personal protection against arthropod vectors generally includes wearing clothing that minimises exposed skin, applying insect repellents outdoor, and, when appropriate, using insecticides and impregnated bed nets indoors. Reducing mosquito breeding sites in residential areas is also essential measurement in vector control; this involves eliminating standing water in items such as buckets, uncovered rain barrels, plant saucers, and clogged gutters.

Vaccines are recognized as a critical tool for climate adaptation strategies. Immunisation protects against several climate-sensitive infectious diseases, strengthens health system resilience and serves as an important enabler of climate adaptation, particularly for vulnerable communities (86). Currently, licensed vaccines exist for several climate-sensitive diseases, including tick-borne encephalitis (TBE), dengue, chikungunya. TBE vaccine is an inactivated virus, whereas the dengue and chikungunya vaccines are live attenuated virus vaccines. Each vaccine has specific indications (for example, dengue vaccination is recommended only for children aged six years and older with confirmed previous dengue infection) which are out of the scope of this article but guidance on vaccine indications can be consulted on the website of the Institute of Tropical Medicine in Antwerp (www.wanda.be) or in the Superior Health Council Vaccination Reports (87).

Conclusion

The eco-epidemiology of infectious diseases is increasingly influenced by changes in human behaviour, including urbanisation, travel, land use changes, biodiversity loss and climate change.

FIGURE 4: Distribution of *Ixodes ricinus* in Europe. Source: ECDC. Tick maps, available from: https://www.ecdc.europa.eu/en/disease-vectors/surveillance-and-disease-data/tick-maps.



These changes together increase the risk of diseases caused by both indigenous and introduced pathogens, the emergence of antimicrobial resistance, and potential pandemic outbreaks. While infectious disease threats linked to these changes affect everyone, children—especially the youngest—are the most vulnerable, not only because of their heightened biological susceptibility but also because they will be exposed to the evolving consequences of a changing climate for many more years.

A concerted One Health approach is imperative to address this serious threat. The WHO defines One Health as an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems. In July 2021, the WHO established the One Health Initiative to coordinate the adoption of the One Health approach in national, regional, and international health policies (88). The EU and Belgium are collaborating on this initiative. The one health approach includes, for example, implementing interdisciplinary collaboration and data sharing, enhancing surveillance of diseases, vectors and pathogens and incorporating climate data. It also implies the need for shared research agendas on the impact of biodiversity loss on health. Policies should be implemented to control and prevent vector-borne diseases, for example through vector control strategies and vaccine development and administration. At the level of paediatricians, climate change issues should be integrated into medical education and training. Paediatricians could educate parents and children about the health risks associated with climate change issues. When working with vulnerable families, climate change should be integrated into practice by asking about housing and food storage issues, and the availability of safe water and by providing anticipatory guidance (89, 90).

Let us hope that we can help make the world a safer place for children.

Statements

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Artificial intelligence (AI): Le Chat – Mistral AI was used to formulate suggestions (with source references) for detailed questions that arose during the writing process. DeepLwrite was used when there was doubt about English syntax or word choice. ChatGPT was used to improve language.

Due to the large number of references and the limited page count of the printed journal, the editors have decided to publish the references only in the online version. This is available via the journal's website https://belgjpaediatrics.com. The article can also be found on Google Scholar (https://scholar.google.com/).

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