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REVIEW ARTICLE



The issue of climate change and the spread of tropical diseases in Europe and Italy: vector biology, disease transmission, genome-based monitoring and public health implications

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ABSTRACT

Background: Climate change significantly influences the distribution and severity of tropical diseases. Rising temperatures, changing precipitation patterns, and extreme weather events are transforming the habitats of vectors like mosquitoes and ticks, promoting their proliferation and geographic spread. These changes have facilitated the resurgence of diseases such as malaria, dengue, and chikungunya fever in previously unaffected areas, including parts of Europe and Italy.

Objective and methods: This review aims to explore the relationship between climate change and the spread of vector-borne and tropical parasitic diseases across Europe, with a particular focus on Italy. Recent studies are analyzed to identify emerging trends in disease transmission influenced by shifting climates. Genome-based monitoring and predictive models incorporating climatic and ecological data are highlighted as methods to enhance disease surveillance and preparedness.

Results: The analysis reveals a clear link between climate change and altered disease patterns. The proliferation of vectors into new territories is associated with increased incidence of diseases. Genome-based tools demonstrate their utility in tracking the evolution of pathogens, particularly regarding changes in virulence, drug resistance, and adaptability to new climates. Predictive models have proven effective in anticipating outbreaks and supporting timely public health interventions.

Conclusions: To mitigate the risks posed by climate-induced changes in disease dynamics, continuous monitoring and international collaboration are essential. Strengthening health systems’ resilience through mitigation and adaptation strategies is crucial for preventing future epidemics. These insights contribute to the development of sustainable long-term policies for managing tropical diseases in the context of climate change, ensuring timely responses to public health emergencies.

KEYWORDS

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Introduction

For millennia, societies have been profoundly influenced by epidemics and pandemics, like Influenza, Ebola, SARS-CoV-2 and Mpox, and such trends appear an ongoing impact in an era of global change [1–4]. The rapid pace of ecosystemic variation driven by the climate crisis adds further layers of complexity to the emergence, re-emergence and spread of older and newer infectious agents [5–7]. Indeed, changes in ecological dynamics affect not only diseases known for epidemic potential, but also those considered stable, endemic or nearing eradication [8–10]. Vector-borne infectious diseases (VBDs), including both arthropod-borne viruses (arboviruses), e.g. dengue, chikungunya, West Nile and Zika, and tropical parasitic agents, e.g. *Plasmodium* spp. and *Leishmania* spp., have long been recognized as significant public health concerns [10–12]. However, recent decades have witnessed a notable shift in the epidemiology of these diseases, largely attributed to the effects of climate change [10]. For the first time in history, on 3 December 2023, at the '28th United Nations Climate Change Conference' (COP28), world leaders defined climatic changes as the global public health threat of the twenty-first century, since it impacts all aspects of human society [13]. Hence, the evaluation of the intricate relationship between climate variations and tropical diseases epidemiology is now essential for anticipating and mitigating the potential health risks [13,14]. The recent emergence of VBDs autochthonous cases in Europe [15,16], historically associated with tropical and subtropical regions, underscores the threatening change in the epidemiological landscape and the need for enhanced surveillance and control measures [10,17]. In this context, genome-based monitoring represents an emerging and crucial tool for tracking the spread of pathogens and their vectors. By leveraging DNA sequencing technologies, it is possible to monitor genetic changes that affect pathogen virulence, drug resistance and adaptability to new climates. This approach, combined with predictive models integrating climatic and ecological data, could enhance public health preparedness, enabling timely interventions and improved outbreak prevention strategies. Italy, situated at the crossroads of Europe and the Mediterranean area, might serve as a focal point for monitoring and responding to the changing epidemiology of tropical diseases. The Italian ecological landscapes and significant influx of travellers and migrants contribute to its vulnerability to imported and autochthonous cases of tropical infections [18–23].

However, the literature data on the effects of warming and climate change, as well as the projections of the effects on future perspectives are still considerably uncertain [10]. In this review article, we aim to explore the current state of knowledge regarding the influence of climate change on the dynamics of primary VBDs (dengue, Zika, chikungunya and West Nile diseases) and tropical parasitic infections (helminthic and protozoan) in Europe, with a specific focus on Italy. In addition, we discussed how genome-based monitoring, combined with predictive models that integrate climatic and ecological data, provides a valuable resource for anticipating shifts in disease dynamics and strengthening public health preparedness.

Past and future: European epidemiological trends of tropical infectious diseases and association with different climatic variables

Infectious diseases such as dengue and chikungunya were largely confined to tropical and subtropical regions. However, the past few decades have seen an increase in both the incidence and geographic spread of these diseases in Europe [16]. The ecological, biological and geographical networks within which disease vectors operate are highly sensitive to environmental shifts [17,24,25]. Rising temperatures, altered precipitation patterns and changes in ecological dynamics have created favorable conditions for their spread, including in geographic areas previously considered non-endemic [17,24,25] (Figure 1). The West Nile virus (WNV), primarily transmitted by *Culex* mosquitoes, has also exhibited an expanding distribution across Europe in recent years [26–29]. Climate-driven changes in vector ecology and migratory bird patterns have contributed to the increasing risk of WNV transmission in regions previously unaffected by the disease [29,30], such as Spain [31] and Italy [22,32,33]. The potential risks for Zika virus (ZIKV) transmission in European countries by *Aedes* mosquitoes have raised concerns about changing climatic conditions and increasing global travel [18,23,34,35]. Similarly, dengue (DENV) and chikungunya (CHIKV) viruses, transmitted by the same *Aedes* vectors, have demonstrated a propensity for expansion beyond their traditional tropical habitats [19,20,23,36,37]. Furthermore, tropical parasitic infections, including malaria, leishmaniasis and other illnesses, such as fungal diseases, continue to pose challenges for public health in Europe, due to climatic factors influencing the spatial distribution of vectors and reservoir hosts [38–41].

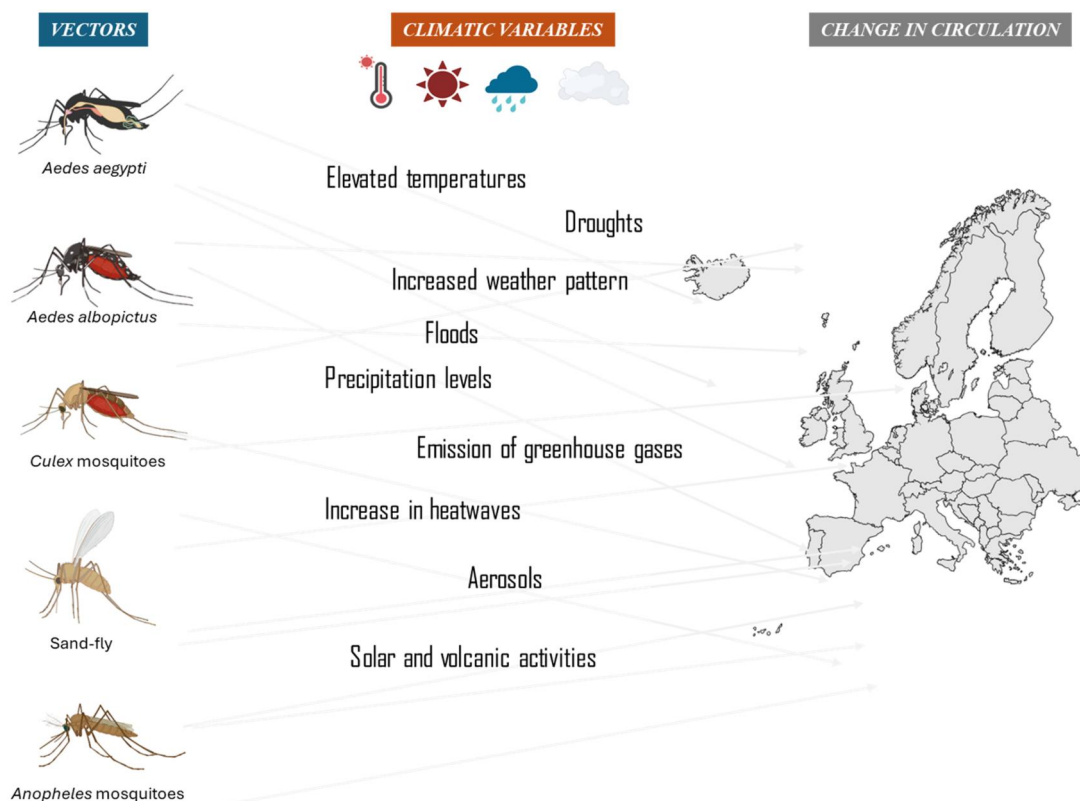


Figure 1. Graphical representation of the impact of climate changes on the vectors circulation in European countries.

The most recent European Environment Agency (EEA) report on ‘European Climate Risk Assessment’ (EUCRA), highlighted the persistent and concerning trend of rising temperatures [16]. In 2023, Europe encountered its second-warmest year on record, resulting in a notable increase in heat waves. These elevated temperatures exacerbated the occurrence and severity of extreme weather phenomena such as droughts, floods and wild-fires. Notably, precipitation levels in 2023 overcame the average by 7%, heightening the risk of floods across various regions of Europe. Additionally, the average sea surface temperature across Europe reached unprecedented levels, further emphasizing the profound impacts of climate change on both the environment and human population [16]. European activities, e.g. factories and other industrial sectors, primarily through the emission of greenhouse gases, have unequivocally caused global warming. It has been reported that from the 1850–1900 to the 2010–2019 years ranges, the total human-caused global surface temperature increases likely ranging from 0.8°C to 1.3°C, with a best estimate of 1.07°C. Mixed greenhouse gases contributed to a warming of 1.0–2.0°C, while other human factors, mainly aerosols, were able to provide a cooling effect of 0.0–0.8°C. Also, natural factors such as solar and volcanic activities and internal variability contributed with minor changes of

$\pm 0.1^\circ\text{C}$ and $\pm 0.2^\circ\text{C}$, respectively [42]. Warmer climates have facilitated the northward migration of *Aedes* mosquitoes, the primary vectors for DENV, ZIKV and CHIKV, leading to several outbreaks in southern Europe [19,20,23,31,36,37]. Southern Europe is now warm enough for mosquitoes to transmit diseases such as dengue, which were once restricted to tropical climates [43]. Klepac et al. [10], recently, conducted an extensive review examining the implications of climate change on malaria and 12 neglected tropical diseases (NTDs), spanning from January 2010 to October 2023. Despite projections indicating the persistence of these trends, with anticipated further warming and increased weather pattern variability across Europe, the overall impact of climate change on the global burden of these tropical diseases remains ambiguous [10]. The studies regarding the inclusion criteria exhibited significant heterogeneity, making comparisons challenging. However, a discernible consequence of climate change, notably affecting VBDs transmission such as malaria, is the escalating frequency of extreme weather events, including severe flooding and cyclones [44]. Predictive models with expanded geographic and temporal scopes foresee a substantial expansion in the future range of relevant *Aedes* vector species [29,30,45], aligning with existing observed trends [46]. Ten years ago, in 2013, the *A. albopictus* mosquito was established in 8 EU/EEA

countries, with 114 regions being affected. Now in 2023, the *Aedes* mosquito is established in 13 countries and 337 European regions [39].

Figure 1 provides a schematic representation of the key climate changes that have contributed to the altered epidemiology of tropical diseases and related vector circulation in Europe and Italy.

Pathogens, vectors and hosts

Viruses

Dengue virus

Dengue is a mosquito-borne infectious disease that spans over two centuries, marking its evolution from a tropical illness to an 'emerging' public health challenge. The World Health Organization (WHO), as of 30 April 2024, reported 3.4 million confirmed cases, over 16,000 severe cases, and over 3000 deaths globally [47]. Its etiological agent, DENV, is a single-stranded positive-sense RNA virus, a member of the *Orthoflavivirus* genus, belonging to the *Flaviviridae* family. DENV is primarily transmitted to humans by the females of *Aedes* mosquito species [48]. The *A. aegypti* is considered the main mosquito vector, but *A. albopictus* (called 'tiger mosquito'), although less competent, is also capable of transmitting the infectious agent [49]. DENV has four distinct serotypes: DENV-1, DENV-2, DENV-3 and DENV-4 [50]. Most dengue cases are asymptomatic or present as mild febrile illness. However, some cases progress to severe form characterized by symptoms such as severe bleeding, significant organ impairment and even shock [47]. DENV was first identified in the late eighteenth century; however, dengue fever became more widely recognized in the 1950s during outbreaks in Southeast Asia [51]. Since then, dengue fever is endemic in over 100 countries across Africa, the Americas, South and Southeast Asia, and the Western Pacific region [52]. Before 2010, Europe was considered 'free for dengue', even if had reported sporadic cases due to travelers infected outside of mainland EU/EEA. Since 2010 to the present, when the environmental conditions became favorable for the establishment of competent vectors, viraemic travel-related cases have generated a local transmission of the virus, as demonstrated by the autochthonous DENV transmission events ranging from France, Croatia, Spain and Italy [53]. In 2023, Italy reported 82 local-acquired DENV transmission cases, followed by France and Spain with 43 and 3 cases, respectively [54]. In Italy, there has been one reported death, while no additional fatalities have been reported in other European countries [54].

Over the past decade, *A. albopictus* has extended its range northward and westward in Europe. Furthermore, *A. aegypti* has already become established in Cyprus and Madeira, Portugal. Although the cold winters in most of Europe prevented year-round transmission, climatic changes, including higher temperatures and milder winters, could enhance the region's suitability for DENV transmission [55]. The continuous climatic changes might further expand the geographical range of competent vectors, improving conditions for virus transmission. Additionally, alterations in humidity and precipitation, such as increased rainfall leading to floods and stagnant water pools, could create more favorable conditions for vector populations, thereby enhancing the potential for DENV transmission [55–57]. In 2024, no autochthonous cases in European countries have yet been indicated [54], although the risk is high given the incoming summer season and the possible start of mosquito vector circulation. However, the limited availability of diagnostic tests in many European Member States, particularly outside the European Union, and the large number of asymptomatic or mild cases could underestimate the notification of DENV infection (Table 1).

Zika virus

The ZIKV is a positive-sense, single-stranded RNA virus belonging to the *Flaviviridae* family, closely related to other *Flaviviruses* such as DENV, yellow fever and WNV. The ZIKV is primarily transmitted by *Aedes* mosquitoes (*A. aegypti* and *A. albopictus*), posing a significant public health concern, due to its association with severe congenital and neurological disorders [58,59]. The ZIKV was first isolated in Uganda in 1947 by researchers from the Rockefeller Foundation, who were studying yellow fever, from a febrile sentinel rhesus monkey held in a cage on a platform in the canopy of the Zika Forest [60]. The first human infection was recorded in Nigeria in 1968 [61]. From 1968 to 2007, human infections were reported only in Central Africa and Southeast Asia. The first outbreak occurred in 2007 in Yap Island (Micronesia), with 185 suspected cases reported [62]. Between 2013 and 2014, outbreaks were reported on several Pacific islands, including French Polynesia, Easter Island, the Cook Islands and New Caledonia [63]. On 2 March 2015, Brazilian health authorities reported the emergence of a febrile illness with a rash in the northern of the country. From February to April 2015, nearly 7000 cases of suspected ZIKV disease were reported, later identified as caused by the ZIKV [64,65]. The increased spread of ZIKV infection, its potential link to microcephaly in newborns

Table 1. A summary of the pathogens, hosts, impact of climatic changes, their historical circulation in Europe, and the epidemiological scenario as of 2024.

Pathogen	Host	Vector	Climatic change	Past circulation	Current epidemiological scenario
Dengue virus (DENV)	Humans	<i>Aedes</i> mosquitoes (<i>A. aegypti</i> , <i>A. albopictus</i>)	Higher temperatures and milder winters could enhance DENV transmission by improving conditions for mosquito vectors. Increased rainfall and stagnant water pools can also favor vector populations, enhancing transmission potential.	Sporadic cases in Europe before 2010; local transmission noted post-2010.	As of early 2024, no autochthonous cases reported in Europe, though the risk remains high due to favorable climatic conditions and diagnostic test availability and asymptomatic cases might underestimate infection rates. No new autochthonous cases in Europe in 2024, but the presence of <i>Aedes</i> mosquitoes poses a risk for potential outbreaks.
Zika virus (ZIKV)	Humans	<i>Aedes</i> mosquitoes (<i>A. aegypti</i> , <i>A. albopictus</i>)	Higher temperatures and changes in precipitation may create favorable conditions for vector populations, increasing the risk of ZIKV transmission.	No autochthonous cases reported in Europe before 2019; isolated local transmission in 2019 in France.	No autochthonous cases reported in Europe in 2024. Climatic changes increase the potential for future outbreaks. As of January 2024, 728 human cases reported in Europe, with 709 locally acquired. The highest number of cases since peak years of 2018 and 2022. Local transmission noted from May to November, with most cases between July and September.
Chikungunya virus (CHIKV)	Humans	<i>Aedes</i> mosquitoes (<i>A. aegypti</i> , <i>A. albopictus</i>)	Higher temperatures, humidity and precipitation intensity favor <i>Aedes albopictus</i> , increasing the risk of CHIKV transmission.	Local transmission first reported in Italy in 2007, followed by cases in France and Italy in subsequent years.	No autochthonous cases reported in Europe in 2024. Climatic changes increase the potential for future outbreaks. As of January 2024, 728 human cases reported in Europe, with 709 locally acquired. The highest number of cases since peak years of 2018 and 2022. Local transmission noted from May to November, with most cases between July and September.
West Nile virus (WNV)	Birds, humans (incidental hosts)	<i>Culex</i> mosquitoes	Higher temperatures facilitate mosquito breeding and virus incubation, enhancing WNV spread. Increased rainfall can create more breeding sites, and proximity to migratory bird routes also influences virus distribution.	Circulated in Europe since the 1950s. Significant outbreak in Romania in 1996. Annual outbreaks in Mediterranean and central Europe since then.	As of January 2024, 728 human cases reported in Europe, with 709 locally acquired. The highest number of cases since peak years of 2018 and 2022. Local transmission noted from May to November, with most cases between July and September.
Helminths (e.g. <i>Ancylostoma</i> , <i>Necator</i> , <i>Ascaris</i> , <i>Trichuris</i> and <i>Schistosoma</i>)	Humans	Snails (<i>Schistosoma</i> spp.), various animals (intermediate hosts)	Warmer, moist conditions could facilitate the spread of hookworm infections, especially in areas with poor sanitation. Changes in water management and increased temperatures can support the expansion of snail habitats, potentially leading to the spread of schistosomiasis in southern Europe. The soil-transmitted helminths could see increased prevalence in regions experiencing warmer and wetter conditions, which favor the survival and development of their eggs in the soil.	The initial identification of helminths in Europe dates back to ancient times, with historical records indicating their presence and impact on human health.	Climate change may affect the viability and spread of these parasites; potential increase in regions with warming climates and altered rainfall patterns.
Protozoa (e.g. <i>Leishmania</i> spp., <i>Plasmodium</i> spp.)	Humans, animals (reservoir hosts)	Sand-fly (<i>Leishmania</i> spp.), <i>Anopheles</i> mosquitoes (<i>Plasmodium</i> spp.)	Climate change drives disease incidence of leishmaniasis by affecting vector distribution and survival. Higher temperatures and rainfall can increase sandfly populations, expanding the geographical range of <i>Leishmania</i> spp. Climate change affects the life cycle of <i>Plasmodium</i> spp. vectors (<i>Anopheles</i> mosquitoes). The optimal temperature range for parasite development is 20–30 °C. Increasing temperatures and rainfall could extend mosquito distribution and transmission season.	<i>Leishmania</i> : Endemic in Mediterranean area; Malaria: historical presence in southern Europe	Potential northward expansion of vector species and increased transmission risk; climate and environmental changes may enhance vector habitats and parasite prevalence.

when contracted during pregnancy, and other neurological disorders led the WHO's International Health Regulations Emergency Committee to declare a Public Health Emergency of International Concern on 1 February 2016 to 18 November 2016 [66]. Following the 2015–2016 epidemic, ZIKV transmission has remained at lower levels. In European countries, from 2015 to 2018, no ZIKV autochthonous cases were reported. Beginning July 2019, the WHO reports that 87 countries have documented cases of autochthonous ZIKV transmission, including Denmark, Finland, Germany, Italy, the Netherlands, Portugal, the United Kingdom, Spain and Sweden and 61 countries and territories have confirmed the presence of competent vectors (*A. aegypti*) despite the absence of documented transmission cases [67]. However, in the same year, a ZIKV autochthonous case was identified in south-eastern France, corroborating the vector role of the Asian tiger mosquito *A. albopictus* in this European area [34]. Following the initial cluster, no further autochthonous European cases were reported [67]. While sporadic cases of ZIKV infection are reported in Europe, typically by travelers returning from endemic regions, the risk of autochthonous transmission remains relatively low compared to endemic tropical and subtropical areas. However, the presence of *A. albopictus* in Europe, as reported above for DENV, highlights the potential for local outbreaks if the virus were introduced into areas where the mosquito is established (Table 1).

Chikungunya virus

Chikungunya, a viral illness transmitted by mosquitoes *A. aegypti* and *A. albopictus*, is caused by the CHIKV, an enveloped virus with a single-stranded positive-sense RNA genome belonging to the *Alphavirus* genus of the *Togaviridae* family [68,69]. The term 'chikungunya' indicates 'to become contorted', due to symptoms of CHIKV infection characterized by abrupt onset fever and severe joint pain [68]. Globally, the disease affects more than 1 million people every year. Initially identified in the United Republic of Tanzania in 1952, subsequently CHIKV emerged in various African and Asian countries. Urban outbreaks were first documented in Thailand in 1967 and India in the 1970s [70]. Since 2004, CHIKV outbreaks have increased due to virus adaptation, facilitating transmission by *A. albopictus* mosquitoes [71]. Afterward, the CHIKV cases have been identified in over 110 countries across Asia, Africa, Europe and the Americas [72]. In Europe, a total of 3671 cases were reported, of which >90% were travellers-imported cases [73]. For the first time, local transmission was reported

in 2007 in North-Eastern Italy [74,75]. Subsequently, chikungunya autochthonous cases were reported in 2010 in France (two cases) [76]. In 2014, 11 local transmissions were diagnosed in France [77], and in 2017, also in France and Italy [78,79]. Overall, Italy reported 489 autochthonous CHIKV cases, of which 282 were laboratory-confirmed. Among these confirmed cases, 206 were reported by the Lazio region, with epidemic clusters identified in Anzio, Rome and Latina, and 74 cases were reported by the Calabria region, with an outbreak in Guardavalle Marina. Only 6% of the patients required hospitalization. The initial infections were confirmed on 6 September 2017 and 7 September 2017, in three patients who developed febrile symptoms with arthralgia during their stay in Anzio. It is estimated that local transmission began in June 2017 or earlier [19,79,80]. No autochthonous cases of CHIKV have been reported in Europe in 2024 [73]. Climatic changes in Europa, including higher mean temperatures, humidity and precipitation intensity, lead to a favorable climatic suitability for *A. albopictus*, with higher risks for CHIKV infections in most parts of Europe [81,82] (Table 1).

West Nile virus

The WNV is a notable and widespread emerging mosquito-borne pathogen in Europe [28,29], with a single-stranded positive RNA genome, belonging to the genus *Orthoflavivirus* of the family *Flaviviridae*. The virus is primarily maintained in a bird–mosquito transmission cycle, predominantly involving *Culex* mosquito species, with the *C. pipiens* complex being the most prevalent and competent vector in Europe [83,84]. Mosquitoes become infected by feeding on infected birds and, following an incubation period that depends on ambient temperature and ranges from 2 to 14 days, become capable of transmitting the virus to other hosts through subsequent blood meals [85]. In this transmission cycle, mammals, including humans, serve as incidental dead-end hosts, unable to further transmit the virus to mosquitoes [86]. Human and animal infections with WNV are often asymptomatic, only approximately 25% of infected individuals develop symptoms such as fever and headache, and less than 1% experience severe neurological complications, potentially leading to death [87]. Since 1950s, WNV was circulated in Europe [88], with a significant outbreak occurring in Romania in 1996, involving 393 human cases [89]. The virus exhibits high genetic diversity, with eight phylogenetic lineages identified [90], but only lineage 1 (WNV-1) and lineage 2 (WNV-2) are primarily associated with disease in humans [91]. Phylogenetic studies have

identified six WNV lineages in Europe, with WNV-2 being the most prevalent, accounting for 82% of the sequences and detected in at least 15 European countries [92]. Annual WNV outbreaks have been reported each summer in the Mediterranean and central Europe areas since its emergence on this continent. The first significant human outbreak was recorded in the Camargue region of southern France during 1962–1963 [93]. A major epidemic followed in Romania in 1996, where around 400 cases were identified [94]. Subsequently, WNV cases and outbreaks have been reported across southern, eastern and western European nations. Before the lineage 2 strain was detected in Hungary in 2004 [95], Europe primarily experienced sporadic cases and occasional outbreaks of WNV linked to WNV-1 [96]. From 2008 onwards, the WNV-2 lineage has spread throughout central Europe and the eastern Mediterranean, leading to significant outbreaks in countries like Greece, Hungary and Serbia. Another WNV-2 lineage appeared in southern Russia in 2007 and spread to Romania and Italy by 2010 [97–99]. In 2018, WNV circulation both in Italy and several other European countries began earlier than usual, resulting in a higher-than-expected number of human cases. There was also significant evidence of increased virus circulation among mosquitoes and birds, which are the primary reservoirs of WNV [94]. According to ECDC report [100], the number of autochthonous WNV infections reported in 2018 (2083 cases) exceeded the total number of cases reported over the previous seven years combined (1832 cases). Compared to 2017, there was a 7.2-fold increase in reported cases. The largest increases relative to the previous season were observed in Bulgaria (15-fold increase), France (13.5-fold increase) and Italy (10.9-fold increase). A total of 180 deaths associated with WNV infection were reported in 2018 [100]. However, the case fatality rate among symptomatic human infections did not exceed the rates observed in the preceding two years [100]. Temperature is a key environmental factor influencing WNV activity in Europe, impacting mosquito breeding and the extrinsic incubation period of the virus [101]. It has been reported that the higher-than-average summer temperatures are crucial for the virus's spread to new regions [101]. In particular, Tran et al. [102] have been stated that July temperature anomalies, adequate water surfaces in June, the presence of wetlands, proximity to migratory bird routes, and prior WNV presence are all associated with the emergence of new cases. It is most probable that local WNV circulation in Europe depends on weather conditions; however, the impact of long-term climate change on human infections remains

unquantified [10]. Environmental changes, such as land use alterations, also influence the spread of WNV. In particular, the irrigated croplands and fragmented forests are associated with increased WNV outbreaks, while the presence of standing lakes facilitates mosquito and bird population interactions [29].

As of 4 January 2024, a total of 728 human cases of WNV infection were reported. Of these, 709 were locally acquired, with the distribution as follows: Italy (336 cases), Greece (162), Romania (103), France (43), Hungary (29), Spain (19), Germany (6), Croatia (6) and Cyprus (5) [103]. Fatalities were recorded in Italy (29 deaths), Greece (23), Romania (12) and Spain (3). This season witnessed the highest number of locally acquired cases since the peak years of 2018 (1549 cases) and 2022 (1116 cases). The earliest onset of the disease among locally acquired cases was noted on 30 May 2023, in Italy, with the latest onset recorded on 5 November 2023, also in Italy. The majority of cases (96%) occurred between July and September [103] (Table 1).

Parasites

Helminths

Ancylostoma and *Necator* larvae found on land surfaces in Africa may remain viable up to a temperature of 40 °C [104–106]. Eggs of *Ascaris lumbricoides* and *Trichuris trichiura* may develop to larva stage at 38 °C [105,107]. Such higher temperatures may increase the motility of infective hookworm larvae [105,107,108] and stimulate a quicker development (3–10 days versus 10–30 days and 28–84 days for *T. trichiura* and *A. lumbricoides* eggs, respectively) and longer lifespans are associated to adult hookworms. *Schistosoma* belongs to the trematode helminths family and requires snails to complete its biological cycle. Therefore, increasing high temperatures in some regions of Africa, e.g. coastal East Africa, might reduce *Biomphalaria* spp. life, and this fact impairs the biological cycle of *S. mansoni* and its transmission [109]. Global warming might favor the expansion of *Oncomelania* snails involved into *S. japonicum* spread over new Asian territories [109]. Intermediate hosts may exhibit higher mortality because cercarial production is increased at elevated temperatures [109,110], and such higher temperatures may reduce cercarial survival [109]. The above-reported features will induce a 13–19% reduction in the transmission area of *S. mansoni* infection in Africa by 2080 [111]. Climate change in East African regions may reflect on the biological cycle of

parasites, and this fact has had no impact on disease burden [112]. Also, a substantial enhancement in the incidence of *S. stercoralis* infection has been reported with heavy changes in climate and environment [112]. Such changes, including deforestation and silting of local rivers, have caused periodic flooding with deposition on a layer of sandy loam, which could increase soil humidity; such geological changes, in addition to low quality of sanitation facilities and standards of personal hygiene, caused an increase of *S. stercoralis* diffusion. The recent flooding in some European regions, including North Italy, where *S. stercoralis* infections were previously quite rare, associated with general temperature increase and tropicalization of weather would increase the incidence of *S. stercoralis* diffusion [113]. Regarding the effects of climate changes on *Echinococcus* infection, several authors reported a significant direct correlation between increased precipitations and enhanced temperature with the life length and vitality of *Echinococcus* eggs spread in the environment [114,115]. Also, in some countries (China), the increase in forestation and pastoral areas, associated with the increase in precipitation, relative humidity and warmth, has been correlated with an increase in *Echinococcus* infections [116,117]. Finally, the most important species of *Echinococcus* (*E. multilocularis*, *E. granulosus*) behave differently regarding the change of precipitation and warmth. Indeed, *E. granulosus* eggs are much more resistant to environmental and climate changes; on the contrary, *E. multilocularis* eggs can survive only one day at 25 °C and 27% relative humidity. Therefore, *E. granulosus* would take advantage of the recent climate changes compared with other *Echinococcus* species, and such successful behavior might account for an evolutionary advantage of this species in terms of world spreading and infection prevalence [116] (Table 1).

Protozoa

Climate changes, such as increasing temperature and rainfall, drive protozoan disease incidence and prevalence worldwide by affecting the spatial distribution of parasites and their vectors and host species. Climate change can potentially make habitable regions of our planet previously uninhabitable by parasitic organisms. Protozoan diseases, including malaria and leishmaniasis, are sensitive to climate changes that can alter the life cycle of parasites, characterized by different vectors and reservoirs [118]. Several studies were performed to predict the future climatic suitability patterns and prevalence of *Leishmania* infection and its vectors due to climate change [119]. Parameters such as the mean monthly temperature or rainfall influence the

onset of leishmaniasis [120]. Humidity levels highly influence the survival and reproduction of sandflies: vectors are more likely to multiply in wetter environments, increasing the risk of disease transmission. Using generalized additive models, Saadene et al. examined the relationships and interactions between climatic variables (temperature, average humidity, wind speed, rainfall, normalized difference vegetation index (NDVI)) to predict the emergence in Algeria [121]. Concerning Europe, Koch et al. [122] applied an ensemble forecasting niche modeling approach based on temperature and precipitation variables to estimate future changes in climatic suitability for 10 vector-competent sandfly species. Although vectors are mainly distributed in the Mediterranean area, models have predicted a future northward expansion in areas with suitable climatic conditions for most species of *Phlebotomus*, such as *P. papatasi*, *P. neglectus*, *P. alexandri*, *P. tobbi* and *P. perfiliewi*. Only two species, *P. ariasi* and *P. mascittii*, were predicted to have a declining distribution range in the future. A higher number of competent vector species is expected in Central Europe. An important factor often overlooked in the modeling of ecological niches is biotic interaction (e.g. interspecific competition): a more significant number of species in a particular area can lead to greater competition between them. For example, although *P. perniciosus* adapts more quickly to climate change, the highly specialized *P. ariasi* seems to compete with *P. perniciosus*, especially in colder regions [122]. In addition to climate change, human actions on the landscape co-occur with population growth, altering habitat availability for hosts and vectors [123]. According to Waitz et al. any environmental change that alters the structure of the landscape inhabited by vectors and hosts can positively or negatively affect diseases in humans [124]. In settled regions, the presence of domestic (dogs) and wild animals provides a source of food for the vectors, thus facilitating adaptation to new environments. The involvement of mammal species such as dogs in the spread of leishmaniasis in urban areas is well established. However, other species (such as horses and bats) could represent potential reservoirs [123]. Climate also plays a vital role in the control and outbreak of malaria. It is known as a climate-dependent disease because environmental and climatic conditions affect the life cycle and proliferation of *Plasmodium* spp. and their related vector, *Anopheles* mosquito. Environmental factors such as fluctuations in temperature, rainfall and humidity of both air and soil are important stimuli for the activity of *Anopheles*. *Plasmodium falciparum* is mainly present in areas with temperatures above 16 °C: a temperature below this threshold contributes to malaria control [125]. It is reported that the

temperature ranges from 20 to 30 °C, which is optimal for the development of the *Plasmodium* spp. [126]. Malaria is less common in mountainous regions where the climate is colder. However, due to global warming, these areas have also become favorable environments for mosquitoes to spread, resulting in the presence of *Plasmodium* spp. among mountainous birds. To prevent a wide spread of the disease, global warming must be contained [125]. Increasing nighttime temperatures and the decrease in the diurnal temperature range are some of the markers of climate change [127]. Using a stochastic transmission model, Beloconi et al. showed that in malaria-endemic western Kenyan lowlands, variations in climatic factors played a crucial role in determining malaria incidence over the period 2008–2019 [128]. Increased rainfall extends the mosquito distribution area and prolongs the duration of the transmission season [129]. Rainfall directly influences the malaria vector because it alters the number, quality and location of breeding sites for oviposition (egg laying) [127]. Adequate humidity is essential for the survival of mosquitoes, as the insects are susceptible to desiccation. The optimal relative humidity range is around 60–80% [127]. While, according to some models, climate is the only factor influencing the distribution of infectious diseases such as malaria, Grobusch and Grobusch emphasize that both climatic effects and immunity in host populations should be included in the models. Climate change will mainly affect the spread of infectious diseases; therefore, in the next decade, it will be crucial to implement adequate mitigation and adaptation strategies for these changes [130].

Table 1 summarizes the key concepts discussed in this review, providing a clear overview of the relationships between climate change, VBDs, and the current epidemiological scenario in Europe and Italy. Literature data on parasitic diseases and their relationship with climate change, as well as European and Italian epidemiological data on these pathogens, remain limited compared to those available for viruses. Nonetheless, presenting this information is essential to provide a more comprehensive perspective on the broader implications of climate change for parasitic diseases

Genome-based monitoring, predictions and a new awareness

Genome-based monitoring represents a significant innovation in the fight against tropical diseases, especially in the context of climate change. With rising global temperatures and shifts in climate patterns, many

tropical diseases are expanding their range into non-traditional areas, including temperate and even northern regions. This phenomenon necessitates new tools and strategies for disease control and prevention, and genomic monitoring is proving to be crucial in this regard. Genome-based monitoring uses DNA sequencing technologies to track the spread of pathogens and disease vectors with unprecedented precision. This approach allows for the rapid identification of genetic mutations that can affect the virulence, drug resistance and transmissibility of pathogens [131]. For instance, genomic analysis of the ZIKV and DENV has helped to better understand their spread and adaptation to new climatic environments, aiding in the development of more effective containment measures [132].

A significant case on the usefulness of the genome-based monitoring is given by malaria, considering that rising temperatures and changes in precipitation are expanding the habitats of vectors mosquitoes. Genomic monitoring of mosquito populations and the *Plasmodium* parasites that cause the disease enables the detection of genetic changes that may indicate the emergence of drug-resistant strains [133]. This type of monitoring allows for timely interventions to prevent outbreaks and develop new drugs or vaccines. A further example is represented by dengue and yellow fever. Indeed, thanks to the sequencing of the genomes of *Aedes* mosquitoes, it has been possible to reveal crucial information about their resistance to insecticides and their ability to adapt to new climates. Additionally, genomic monitoring facilitates the surveillance of zoonoses, diseases transmitted from animals to humans, which are also influenced by climate change. Changes in animal migration patterns and the loss of natural habitats can increase contact between wildlife and human populations, facilitating pathogen transmission. Technologies such as Next-Generation Sequencing (NGS) [134] enable the rapid mapping of the genomes of emerging pathogens, providing critical data to understand their origin, transmission pathways and potential public health threats.

Another challenge exacerbated by climate change and the movement of tropical diseases into new geographic areas is represented by antimicrobial resistance. Genomic monitoring can identify resistance genes in pathogens, enabling more targeted treatment strategies [135]. For instance, through environmental metagenomics, it is possible to analyze DNA extracted from the environment (such as water or soil) to monitor the presence of resistance genes in ecosystems, providing early warnings about the spread of antimicrobial resistance.

The importance of genomic monitoring extends to the management of healthcare resources and emergency response planning. The ability to track and predict disease spread in real-time through genomic data can guide decisions on vaccinations, drug distribution and the implementation of quarantine measures. In an increasingly interconnected world subject to climate change, these capabilities are essential for protecting global health. International collaboration is essential for the success of genomic monitoring. Sharing genomic data among countries and scientific institutions allows for the tracking of global pathogen spread and the coordination of responses [136]. Initiatives like the Global Virome Project (<https://www.globalviromeproject.org>) aim to map and characterize as many viruses as possible in wildlife, to predict and prevent future pandemics.

The integration of genome-based monitoring with predictive analytics is paving the way for a new era of disease prediction and prevention [137] crucial in the context of climate change. Predictive models that incorporate genomic data, climate variables and ecological factors can forecast the emergence and spread of tropical diseases with remarkable accuracy. These models help identify regions at the highest risk for disease outbreaks, enabling preemptive measures to protect vulnerable populations.

Moreover, the awareness generated by these predictive models is fostering a proactive approach to public health. Governments, health organizations and communities are becoming more cognizant of the links between climate change and disease dynamics. This heightened awareness is leading to more robust health infrastructure, improved disease surveillance systems and better preparedness plans. The public is also becoming more informed about preventive measures and the importance of environmental sustainability in curbing the spread of diseases. Additionally, the integration of genomic data with other forms of big data, such as mobile phone tracking and satellite imagery, is enhancing our ability to monitor and respond to disease outbreaks in real time. For instance, mobile health applications can provide real-time data on disease symptoms reported by users, while satellite imagery can track environmental changes that may affect vector populations. Combined with genomic data, these technologies offer a comprehensive and dynamic view of disease ecology. The new awareness brought about by these advances is also driving policy changes. Governments are increasingly recognizing the need for interdisciplinary approaches that

integrate public health, environmental science and data analytics. Policies aimed at mitigating climate change, preserving biodiversity and reducing human-wildlife conflict are becoming integral to national and international health strategies.

Furthermore, international collaboration is being strengthened as countries share data and resources to combat the global threat of emerging infectious diseases. Initiatives like the Global Health Security Agenda (GHTSA) and the One Health approach emphasize the interconnectedness of human, animal and environmental health, advocating for collaborative efforts across sectors and borders [138].

In conclusion, the combination of genome-based monitoring and predictive analytics is transforming our ability to foresee and combat tropical diseases in a changing climate. This approach not only enhances our immediate response capabilities but also fosters a broader awareness and preparedness that are essential for long-term global health security. As we move forward, continued innovation and cooperation will be key to protecting public health in an increasingly interconnected and climate-affected world.

Conclusions

In conclusion, climate change is significantly reshaping the landscape of tropical diseases. In Italy rising temperatures, shifts in precipitation patterns, and more frequent extreme weather events are altering the natural habitats of many disease-carrying vectors, such as mosquitoes and ticks, enabling their expansion into previously unaffected regions, including temperate areas of Europe. Italy, given its geographic position at the crossroads of the Mediterranean and its diverse ecological landscapes, is particularly vulnerable to these shifts. This has been evidenced by the recent autochthonous cases of vector-borne diseases like DENV, CHIKV and WNV, which highlight the urgent need for enhanced surveillance and rapid response measures. In this context, genome-based monitoring emerges as a pivotal tool in Italy and Europe for tracking and understanding the genetic evolution of pathogens and their vectors, providing crucial insights into their adaptability to new environments and emerging drug resistance. The integration of genomic data with climate models can facilitate more accurate predictions of disease outbreaks, allowing for preemptive actions that are tailored to the specific ecological conditions of the region. Moreover, this approach is crucial for addressing the rising issue of antimicrobial

resistance by identifying resistance genes in local pathogen populations and monitoring their spread across different environmental reservoirs. To effectively manage the challenges posed by the changing epidemiology of tropical diseases in Europe and Italy, international collaboration and sustained investment in genomic surveillance are essential. Strengthening data-sharing networks between European countries and fostering cooperation with international initiatives like the GHSA can enhance the collective capacity to respond to emerging threats. Additionally, aligning local health policies with global climate goals and incorporating climate-adaptive strategies into national health plans will be critical for building resilient health systems that can adapt to future climate-driven shifts in disease dynamics. In summary, while the impact of climate change on tropical diseases presents significant challenges, it also offers an opportunity for Europe and Italy to lead in developing innovative approaches for disease surveillance and control. With proactive measures, ongoing genomic monitoring, and a commitment to international collaboration, the region can mitigate the risks associated with these diseases and protect public health in an era of global climate change. This has resulted in the resurgence of diseases like malaria, dengue and chikungunya fever in regions that were previously unaffected. Continuous monitoring and international collaboration are essential to effectively tackle these changes. Through sustained and coordinated efforts, we can implement strategies for mitigation and adaptation, bolster the resilience of health systems, and prevent future epidemics. Ongoing monitoring will not only ensure timely responses to health emergencies but also support the creation of long-term policies for the sustainable management of tropical diseases in the context of climate change. Genomic monitoring also addresses the growing issue of antimicrobial resistance by identifying resistance genes in pathogens and analyzing environmental DNA to monitor resistance gene prevalence. This information is vital for developing targeted treatment strategies and guiding public health responses. Only with the ongoing monitoring will be able to provide prompt responses to health emergencies and craft long-term policies for the sustainable management of tropical diseases amidst climate change.

Author contributions

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Ethics statement

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