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Review

Beyond Viral Pathogenesis: Climate Change, Zoonotic Spillover, and the Evolving Epidemiology of Viral Hemorrhagic Fevers

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Abstract

Viral hemorrhagic fevers (VHFs) represent a major global health threat because they can cause severe systemic illness, hemorrhage, multiorgan dysfunction, and death. Ebola virus, Marburg virus, Lassa virus, and Crimean–Congo hemorrhagic fever virus contribute substantially to the global burden of these diseases. These pathogens employ diverse transmission routes, including vector-borne transmission, zoonotic spillover, and direct exposure to infected bodily fluids. Climate change, land use alterations, urbanization, population growth, and increased human–animal interactions may reshape pathogen ecology and create new opportunities for viral emergence and transmission. International travel and interconnected human populations further complicate outbreak containment. This review examines the pathophysiological mechanisms, epidemiological patterns, and major outbreaks associated with VHFs, with particular emphasis on how environmental change, ecological disruption, and infectious disease dynamics interact. We also evaluate the roles of global health organizations in strengthening disease surveillance, coordinating outbreak responses, and promoting international preparedness. Furthermore, we discuss the importance of integrated surveillance systems, cross-sectoral collaboration, and climate-informed public health strategies in reducing the risks associated with emerging and recurring VHF outbreaks. By integrating virological, ecological, epidemiological, and public health perspectives, this review highlights critical knowledge gaps and identifies priorities for improving early detection, outbreak preparedness, and coordinated responses to future VHF threats.

Keywords: viral hemorrhagic fevers; climate change; zoonotic spillover; emerging infectious diseases; One Health; disease surveillance; outbreak preparedness; global health

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1. Introduction

Hemorrhagic fever viruses are encapsulated single-stranded ribonucleic acid (RNA) viruses that cause viral hemorrhagic fever. Viral hemorrhagic fevers are defined by a spectrum of syndromes, including fever ranging from moderate to severe, coagulation, bleeding, and in severe cases, organ failure and/or death [1]. Transmission occurs through infected vectors (mosquitoes, ticks), airborne droplets, or direct contact with contaminated body fluids (blood, sweat, feces) [2]. There are four main viruses responsible for causing hemorrhagic fever in humans, Ebola virus, Marburg virus, Lassa virus, and Crimean–Congo hemorrhagic fever virus (CCHFV) [3,4]. The management of viral hemorrhagic fever includes antiviral therapy and supportive care with the suitable treatment required to be administered based on the phase of the disease; during incubation (post-exposure active/passive immunization and antivirals are the most effective), pre-coagulopathy (nucleoside analogues such as ribavirin are used), and coagulopathy (immune-modulating agents, platelet activation inhibitors, and macrophage migration inhibitors) [1]. The last few decades have experienced several outbreaks of viral hemorrhagic fevers, including Ebola, Marburg, Lassa fever, and Crimean–Congo hemorrhagic fever, raising threats to the global health sector with high transmission, morbidity, and mortality rates. Such outbreaks destabilize societies and healthcare infrastructures [5]. The progression from a rare event to a global epidemic is dependent on how easily the disease spreads in non-immune hosts, the density of the population, the role of vectors (natural or man-made) in crossing boundaries, and the ability to spread [6]. Additionally, urbanization, increasing global populations, increased human activity, ageing demographics, and movement of animals and their byproducts, supported by human actions and global travel, are driving environmental changes (Figure 1). These shifts alter the distribution of wild hosts and vectors, as well as agricultural patterns, enabling pathogen transmission between wild and domestic animals [7]. As a result, there is a rise and spread of new and recurring viruses, which pose a major health threat [1]. Climate events, such as rapid changes and extreme temperatures, changes in rainfall patterns and floods, and periods of drought, may influence infectious agents, vectors, hosts, and the propagation of diseases. Climate change can indirectly impact the spread of diseases by altering how humans interact with pathogens, vectors, or hosts. It can affect the transmission of diseases carried by insects such as, mosquitoes and ticks by changing climate patterns and their subsequent effects [8]. Additionally, effects of climate shifts can be noted at different levels, from, flora and surroundings that gradually adapt to altered circumstances, to terrestrial animals that adjust to the new weather patterns and habitats, and to microbial communities that adjust according to changed conditions. The ecosystem is impacted by climate change [9]. As a result, climate change significantly impacts on the occurrence of infectious disease outbreaks, such as cholera, malaria, infectious diarrhea, and Dengue fever. Ticks, responsible for the spread of the Piroplasmorida virus, are an example that can expand in response to warmer weather. Similarly, tick-borne encephalitis became common in the mid-1980s due to increased temperatures in Scandinavia [10]. As a result, vector and reservoir groups spread to new regions, settling at higher elevations or infecting people during new seasons, such as winter, when illnesses were once rare. Changes in climate, soil, biodiversity, and land use have created more favorable conditions for the vectors of infectious diseases, such as ticks and mosquitoes, which in turn increases the spread of diseases [11]. Rising rainfall and droughts both create more breeding opportunities for vectors. More rainfall provides natural breeding sites, whilst drought leads people to store rainwater in containers, which can serve as breeding sites. It is important to adhere to the Paris Climate Agreement's objective of keeping global warming below 1.5 °C over pre-industrial levels to minimize the spread of diseases transmitted by vectors and other climate-related threats [11]. Accordingly, this review aims to synthesize

current evidence on major viral hemorrhagic fever agents and examine how climate change and anthropogenic ecological disturbances influence vector and reservoir distributions, zoonotic spillover, and disease transmission. It further evaluates the contribution of surveillance systems, early-warning approaches, international collaboration, and public health interventions to outbreak prevention and mitigation, while identifying existing knowledge gaps and priorities for future research.

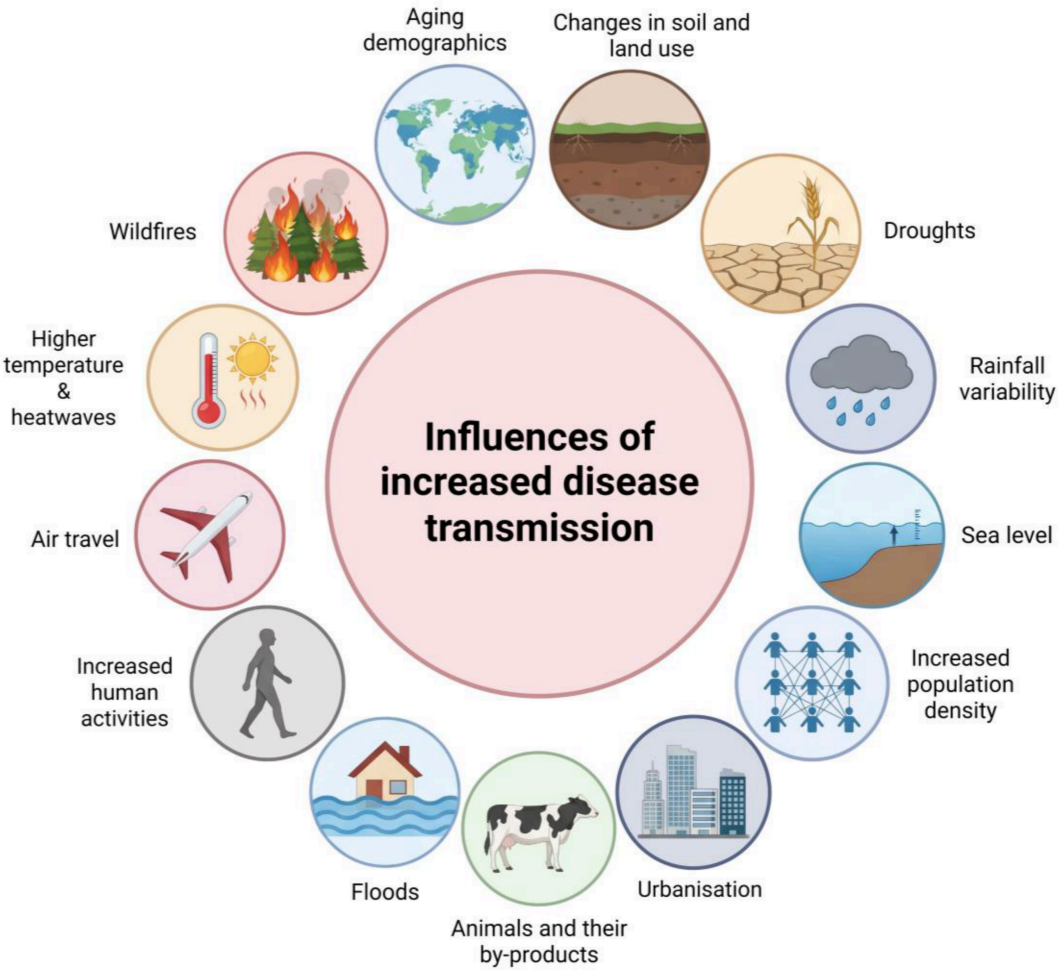


Figure 1. Influences of increased disease transmission.

2. Understanding Hemorrhagic Fevers

2.1. Definition and Classification of Hemorrhagic Fevers

Hemorrhagic fever is primarily caused by viruses (Lassa fever virus, Crimean–Congo hemorrhagic fever virus, Marburg virus, Dengue virus, Yellow fever virus, Ebola virus). These infectious agents cause symptoms of fever and hemorrhagic symptoms (bleeding), and in some instances can be life-threatening [12]. Hemorrhagic fever viruses are spread via infected mosquito bites (*Aedes* mosquitoes; Dengue and Yellow fever), rodents, especially saliva, urine, droppings (Lassa fever virus and Crimean–Congo hemorrhagic fever virus), contaminants in food, water or surfaces, or through direct contact with infected bodily fluids such as saliva, sweat and blood (Ebola, Marburg, Lassa fever) [12]. The World Health Organization states that viral hemorrhagic fever can be transmitted through various viruses. It is described as a severe sickness that can occasionally be accompanied by bleeding. Typically, this term has been employed to describe ailments initiated by the *Arenaviridae* family, which includes Lassa fever, Lujo, Guanarito, Machupo, Junin, Sabia,

and Chapare viruses; *Bunyaviridae*, which provides for Crimean–Congo hemorrhagic fever, Rift Valley fever, and Hantaan hemorrhagic fevers; *Filoviridae*, which includes Ebola and Marburg hemorrhagic fevers; and *Flaviviridae*, which includes Dengue, Yellow fever, Omsk hemorrhagic fever, Kyasanur Forest disease, and Alkhurma viruses [13]. These might be categorized based on how they pass along, like infection vectors, airborne droplets, direct contact with infected material, etc., or by the family of viruses they belong to. There are four primary families of hemorrhagic fever viruses: *Arenaviridae*, *Bunyaviridae*, *Filoviridae*, and *Flaviviridae* [2,14] (Table 1).

Table 1. Categorization of hemorrhagic fever based on family and mode of transmission.

Family	Virus	Mode of Transmission	Reference
Arenaviridae	Lassa virus/Lassa fever	The primary host is the rodent species *Mastomys nataliensis*	[14,15]
	Sabia virus/Brazilian hemorrhagic fever	The host is suspected to be a rodent species via aerosol exposure to an infected person	[14,16]
	Machupo virus/Bolivian hemorrhagic fever	Via exposure of secretions of untamed native rodents in Bolivia	[14,17]
Nairoviridae	Crimean–Congo hemorrhagic virus/Crimean–Congo hemorrhagic fever	Transmission of disease to humans is via bites of contaminated ticks (primarily species of the genus Hyalomma) and contact with blood or tissue of infected animals	[14,18]
Bunyaviridae	Rift Valley fever virus/Rift Valley fever	Mosquito bites	[14,19]
Hantaviridae	Hantaan virus/Hemorrhagic fever with renal syndrome	Transmitted by rodents (*Apodemus agrarius*), to humans, via respiratory pathway during dry seasons	[14,20]
Filoviridae	Bundibugyo ebolavirus/Ebola virus disease	Fruit bats are believed to be regular carriers of infection through direct contact with body secretions, such as blood from infected humans or animals	[14,21]
	Marburg virus (MARV)/Marburg hemorrhagic fever	The *Rousettus aegyptiacus* species of fruit bat is the natural source of the infection. The infection is likely transmitted to humans and NHPs through secretions (saliva) and excretions (feces, urine) of bats or fruits contaminated with MARV. Sexual intercourse may also be a means of transmitting MVD, as the antigens of MARV have been detected in the semen of infected males. Direct contact with blood and other body fluids (e.g., feces, urine, tears, breast milk) can also facilitate human-to-human transmission	[14,22]
Flaviviridae	Dengue virus/Dengue fever	Transmission via peri-domestic mosquitoes to humans, including *Aedes albopictus* and *Aedes aegypti*	[14,23,24]
	Yellow fever virus/Yellow fever	The *Aedes aegypti* mosquito is a highly effective vector for transmission of Yellow fever virus	[14,25]

2.2. Key Viruses Involved in Hemorrhagic Fevers

2.2.1. Ebola Virus

Ebola virus belongs to the *Filoviridae* family, which is distinguished by a thread-like (filamentous) shape, its negative-stranded RNA composition, lipid-envelopment to facilitate entry into the cell, having a nucleocapsid structure, a matrix protein such as VP40, and its 50 nm diameter [26]. The ebolavirus genus comprises five different species, each characterized by a distinct virus and each responsible for different outbreaks. These include (i) Ebola virus (also known as Zaire ebolavirus), (ii) Reston ebolavirus, (iii) Bundibugyo ebolavirus, (iv) Sudan ebolavirus, and (v) Taï Forest ebolavirus (also known as Cote d'Ivoire Ebola virus) [27]. Ebola virus primarily infects immune cells, particularly monocyte-derived macrophages, and dendritic cells, which help the virus spread throughout the body. It also infects endothelial cells, causing damage to blood vessels and leading to hemorrhaging. The virus then spreads to vital organs, including the kidneys, liver, and spleen, causing widespread damage and potential organ failure, which can result in death in severe cases. However, in some instances, the body's innate and adaptive immune systems can control the virus, limit its spread, and improve the chances of survival [28]. The yearly dry season, occurring from December to May, is identified as a reproductive period for fruit bats, which serve as a reservoir for ebolavirus, possessing a significant capacity for replication, increasing risk of spread. Ebola predominantly occurs around 10° of the equator, where climatic conditions and other variables facilitate the virus's transmission, as was noted in the 2014–2016 Ebola outbreak, which led to over 11,325 deaths [29]. As there are no approved anti-virals or vaccines against Ebola viruses, the most effective method to mitigate outbreaks is to regulate the disease's dissemination, including early detection, isolation of infected individuals, quarantine, contact infection control measures, travel restrictions and medical treatment support [30]. More recently, a major outbreak of Bundibugyo virus disease was reported in the Democratic Republic of the Congo in 2026, highlighting the continuing potential for filovirus emergence and cross-border spread [31]. According to the World Health Organization (WHO), the outbreak had resulted in 9704 confirmed cases and 4687 deaths in the DRC as of 20 October 2026, with imported cases also reported in Kenya and Nigeria [32]. This event reinforces the importance of rapid laboratory confirmation, epidemiological surveillance, contact tracing, infection prevention and control, and coordinated regional preparedness. Unlike the Ebola virus disease caused by Ebola virus (formerly Zaire ebolavirus), for which a licensed vaccine and specific therapeutics are available, no licensed vaccine or specific approved treatment is currently available for Bundibugyo virus disease; clinical management therefore relies on supportive care and outbreak-control measures [33].

2.2.2. Marburg Virus

Marburg virus (MARV), together with Ravn virus, is associated with Marburg virus disease and belongs to the family Filoviridae, genus Orthomarburgvirus [34]. These enveloped, predominantly filamentous viruses contain non-segmented, negative-sense single-stranded RNA genomes [35]. The Egyptian rousette fruit bat (*Rousettus aegyptiacus*) is recognized as the natural reservoir of Marburg virus [36]. Human index cases have been associated with prolonged exposure in caves or mines inhabited by bat colonies, where contact with infected bats or contaminated environments may permit spillover [37]. Once introduced into human populations, transmission occurs through the direct contact of broken skin or mucous membranes with infected blood, secretions, organs, or other body fluids, and through contaminated materials [38]. Healthcare-associated transmission has occurred when adequate infection-prevention measures were not maintained [39].

The incubation period ranges from 2 to 21 days. Clinical onset is typically abrupt, with fever, severe headache, malaise, and myalgia, followed by gastrointestinal manifestations such as diarrhoea, abdominal pain, nausea, and vomiting [40]. In severe disease, hemorrhagic manifestations, shock, and multiorgan dysfunction may develop. Reported case-fatality ratios have varied considerably between outbreaks and settings. Early supportive care, including rehydration and management of complications, remains important, alongside surveillance, laboratory confirmation, contact tracing, and infection prevention [39,40].

The ecological distribution of the reservoir bat and human activities that bring people into caves, mines, or bat-inhabited environments are important components of spillover risk [37]. Land use change and the disturbance of natural habitats may alter human–bat contact, although the contribution of individual climatic variables to Marburg virus emergence is less clearly established than the role of direct exposure and subsequent person-to-person transmission [41]. Risk assessment should therefore consider bat distribution, occupational and recreational exposure, habitat disturbance, and local outbreak history rather than assuming a uniform climate-driven pattern [37]. This distinction is relevant to the broader One Health perspective of the present review, in which ecological disruption may modify opportunities for zoonotic contact, but does not, by itself, establish that an outbreak will occur [42].

2.2.3. Lassa Virus

Lassa virus (LASV) is an enveloped, bisegmented, ambisense RNA virus in the family Arenaviridae and genus Mammarenavirus. It causes Lassa fever, an endemic zoonotic disease in several West African countries, including Nigeria, Sierra Leone, Liberia, Guinea, Benin, and Ghana [43]. The multimammate rat, particularly *Mastomys natalensis*, is the principal reservoir host. Infected rodents generally remain asymptomatic and shed virus in urine and feces, allowing the contamination of household surfaces, stored food, and nearby environments [44]. Human infection occurs mainly through contact with contaminated food or household materials, or direct exposure to infected rodents [45]. Person-to-person transmission can also occur through contact with infected blood or other body fluids, particularly in healthcare settings where infection-prevention practices are inadequate. Available studies do not support routine airborne transmission between humans [45,46].

The incubation period is generally 2–21 days, and infection ranges from asymptomatic or mild illness to severe multisystem disease [45]. Symptomatic cases may begin gradually with fever, weakness, headache, and malaise, followed by sore throat, myalgia, chest pain, and gastrointestinal symptoms [47]. Severe disease may involve facial swelling, bleeding, hypotension, and shock, with the liver, spleen, and kidneys among the affected organs. Sensorineural hearing loss is a recognized complication in some survivors [45,48]. Although the overall case-fatality rate across infections is relatively low, mortality is higher among hospitalized patients with severe disease [49]. Early recognition, supportive care, safe laboratory diagnosis, and infection prevention in healthcare facilities are important for patient management and outbreak control [45].

The ecology of Lassa fever is closely linked to the distribution and behavior of its rodent reservoir. *Mastomys* rodents occupy houses, food-storage locations, fields, and disturbed landscapes, bringing infected animals into contact with people [50]. Food availability, housing, sanitation, agricultural practices, and land use change may modify exposure opportunities [51]. More broadly, climate variability, urbanization, and deforestation can influence rodent populations and rodent–human interactions. However, their effects on Lassa virus transmission are context-dependent and should not be interpreted as a direct or uniform climate-driven causal relationship [50]. This ecological complexity supports

integrated surveillance combining human case detection with rodent monitoring, environmental assessment, community hygiene, and safe food storage [52].

2.2.4. Crimean–Congo Hemorrhagic Fever Virus

Crimean–Congo hemorrhagic fever virus (CCHFV) is an enveloped virus with a tripartite, negative-sense RNA genome belonging to the family Nairoviridae and genus Orthonairovirus [52,53]. It is maintained in a tick–vertebrate host cycle, with ticks of the genus *Hyalomma* recognized as the principal vectors [53]. Wild and domestic mammals, including cattle, sheep, and goats, can become infected; viremia in these animals supports continued transmission when uninfected ticks feed on them [54]. Livestock generally show no obvious clinical disease, meaning that infected animals may enter markets or slaughter facilities without being recognized as infected [53,54]. Human infection occurs primarily through bites of infected ticks or contact with blood and tissues of viremic animals, particularly during animal handling, slaughter, and veterinary or agricultural work [54]. Person-to-person transmission may follow direct exposure to the blood or body fluids of infected patients, including in healthcare settings with inadequate infection-prevention measures [55].

CCHFV occurs across parts of Africa, the Middle East, and Asia, with its distribution influenced by the geographical range of competent tick vectors and vertebrate hosts [56]. The incubation period varies according to the route of exposure [57]. Illness commonly begins with sudden fever, headache, myalgia, dizziness, and gastrointestinal symptoms; severe cases may progress to hemorrhagic manifestations, coagulopathy, shock, and multiorgan dysfunction [54]. Disease severity and reported case-fatality vary between outbreaks and settings. Because infection in livestock is often unapparent, animal and tick surveillance can help identify areas where human exposure may occur [54,55].

Environmental and anthropogenic conditions can influence CCHFV risk by modifying tick abundance, seasonal activity, host distribution, and human contact with livestock or tick-infested habitats [58]. Temperature and precipitation may affect tick development and activity, while land use change, livestock movement, farming practices, and animal trade can alter contact at the human–animal interface [59,60]. These relationships vary across regions; climatic suitability alone does not establish that transmission will occur [61]. Risk assessment therefore requires the combined interpretation of entomological, veterinary, climatic, and human epidemiological data. Protective clothing, tick checks, appropriate livestock management, occupational precautions, and infection prevention in healthcare facilities remain important [62,63].

2.2.5. Hantaviruses and Hemorrhagic Fever with Renal Syndrome

Hantaviruses are enveloped viruses with a tripartite, negative-sense RNA genome belonging to the family Hantaviridae, order Bunyavirales [64]. They are maintained through host-specific associations with small mammals, particularly rodents, which may remain persistently infected without apparent illness and shed virus in urine, feces, and saliva [65]. Human infection usually follows the inhalation of aerosols generated from contaminated excreta or direct contact with infected rodents or contaminated materials [66]. Farming, forestry, cleaning poorly ventilated buildings, and occupying rodent-infested dwellings can increase exposure. Hantaan virus is an important cause of hemorrhagic fever with renal syndrome (HFRS) in Asia; Seoul, Dobrava–Belgrade, and Puumala viruses are associated with HFRS in other regions [67].

The clinical presentation varies with the infecting Hantavirus. HFRS, reported mainly in Europe and Asia, affects the vascular system and kidneys and may involve fever, hypotension, thrombocytopenia, increased vascular permeability, hemorrhagic manifestations,

and acute kidney injury [68]. Severity ranges from relatively mild illness to renal failure and shock. In contrast, several hantaviruses circulating in the Americas cause hantavirus cardiopulmonary syndrome (HCPS), characterized by pulmonary edema and respiratory compromise rather than the renal-predominant presentation of HFRS [68,69]. This distinction is important when interpreting the term hemorrhagic fever across Hantavirus infections. Person-to-person transmission is not a recognized feature of HFRS-causing Hantaviruses in Europe and Asia; limited transmission has been documented for Andes virus in the Americas [70].

Rodent population dynamics and human exposure patterns are central to Hantavirus epidemiology. Changes in vegetation, food availability, land use, agriculture, housing, and waste management can influence rodent abundance or opportunities for contact with contaminated environments [71]. Climate variability may also affect rodent distribution and seasonal patterns, although effects differ by host species, virus, and region [72]. The suggested review of rodent-borne viruses highlights the combined influence of environmental and anthropogenic pressures, including urbanization and deforestation, on rodent-associated zoonotic risks [72,73]. Surveillance should therefore integrate human case detection with information on rodent hosts, environmental conditions, and high-exposure occupations [71]. Reducing rodent access to homes, safe cleaning of contaminated spaces, and community awareness are important preventive measures; treatment is primarily supportive [74].

2.2.6. Dengue Virus

Dengue virus belongs to the *Flaviviridae* family and is part of the Flavivirus genus. Other viruses in this genus include the Yellow fever virus, the Zika virus, and the West Nile virus. Dengue virus has several key features: positive-stranded RNA; spherical and smooth shape; a diameter of 50 nm; enveloped, with surface glycoproteins (E and prM) that facilitate entry to host cells. There are four distinct serotypes, DENV-1, -2, -3, and -4. Dengue virus primarily infects immune cells, including dendritic cells, macrophages, monocytes, and lymphocytes [75]. Transmission to humans is via bites from infected mosquitoes with an incubation period of 4–10 days (*Aedes aegypti* and *Aedes albopictus*) and is not transmitted between humans [76]. Climate change is believed to have had an impact on the spread of Dengue virus outbreaks due to the direct effect on the density of the *Aedes aegypti* populations, which changes seasonally depending on rainfall and temperatures. In general, warmer temperatures increase the life-cycle of mosquitoes (they thrive at 25–30 °C, and accelerate above 30 °C), and increased rainfall provides more stagnant water areas, increasing mosquito breeding sites, and floods can result in the spread of mosquitoes to new geographic areas [77,78]. Understanding how climate change affects the spread of Dengue is crucial for public and global health. It is essential to take action to reduce the disease's transmission, including efforts in education and raising public awareness [79]. There are no antivirals for the Dengue virus; hence, the prevention of mosquito bites, use of insect repellents, and eliminating breeding sites are imperative. In the past, Dengvaxia (CYD-TDV) was used in specific settings with specific eligibility recommendations, especially in areas where there was a need for evidence of prior dengue infection. The manufacturer, however, subsequently discontinued its marketing, and its marketing authorization in the European Union was withdrawn in October 2025. It should therefore be described as a previously available vaccine rather than a routinely available current prevention option [80].

2.2.7. Yellow Fever Virus

The Yellow fever virus is also a mosquito-borne virus that belongs to the Flaviviridae family and the Flavivirus genus. It is a spherical, encased, enveloped, positive-sense, single-stranded RNA virus of 40–50 nm in diameter [81]. Upon infection, the Protein E

on the surface of the Yellow fever virus interacts with host cells for its internalization and replication, and the incubation period is usually 3–6 days before symptoms appear [82]. Mosquitoes act as vectors for the transmission of the Yellow fever virus, including *Aedes aegypti* in Africa (urban areas) and *Haemagogus* species or *Sabethes* species (*Sabethes albirivus*) in South America (forest areas). The virus survives in the environment by propagating among non-human primates, which serve as major reservoirs. Climate change can impact the transmission of the Yellow fever virus through increased temperatures and changes in rainfall patterns [83,84]. In this regard, the population maxima occur during the rainy summer, marked by increased temperatures and rainfall [85].

2.3. Pathophysiology and Clinical Manifestations

Viral hemorrhagic fevers are distinguished by irregular vascular modulation and injury. Although they exhibit similar clinical signs, the cell and organ tropism, as well as the molecular pathways driving their pathogenesis, differ based on the causal agent [1]. Hemorrhagic fever viruses circulate through encounters with or ingestion of contaminated substances from livestock reservoirs or mosquito carriers [1]. Although human-to-human transmission is less common, direct contact with infected blood can also transmit the virus. The incubation period ranges from 2 to 35 days, commencing with a prodromal phase generally lasting less than 7 days [1]. This phase is succeeded by heightened viral replication, resulting in an overstimulation of pro-inflammatory cytokines, which induces endothelial activation, augmented vascular permeability, vasodilation, subsequent lower blood pressure, multiorgan dysfunction, and mortality [1] (Figure 2).

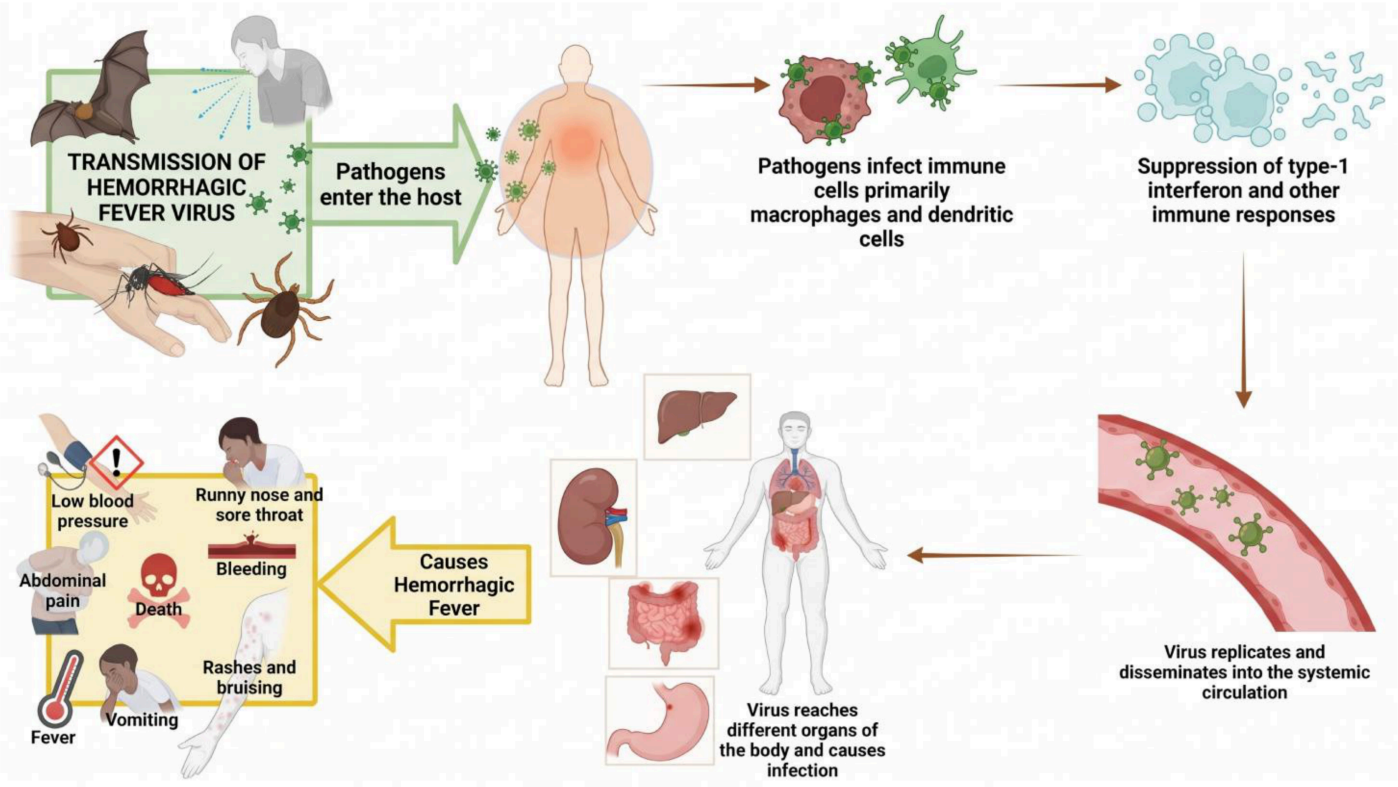


Figure 2. Pathophysiology of hemorrhagic fevers.

3. Historical Context of Hemorrhagic Fever Outbreaks

3.1. Major Outbreaks and Their Impact on Public Health

3.1.1. Dengue Hemorrhagic Fever

Over time, Dengue epidemics have occurred in several regions across the globe, with Thailand and the Philippines reporting cases in the early 1900s, but it was not formally recognized that the *Aedes* mosquito vector was connected to transmission until the 1920s [86]. Dengue virus was identified in the 1950s as the cause of Dengue fever, especially during significant outbreaks in the Philippines (1953–1954) and Thailand (1958–1959). Other notable outbreaks include Cuba 1981, Sri Lanka 2004–2005, Asia (India, Indonesia, Malaysia, Vietnam) 2010–present and Brazil 2015–2016, and in 2019–2020 there were global cases with over 5 million cases reported [86]. Whilst the overall incidence of Dengue infections is generally underreported, the WHO predicts 390 million Dengue cases annually with increasing frequency and scale in Southeast Asia, the Western Pacific, the Americas, Africa, and the Mediterranean [86]. Factors like human movement, global travel, urbanization, climate change and poor mosquito control significantly contribute to the growing worldwide burden of Dengue, making it a rising public and global threat [87]. In Dengue-endemic regions, children and adolescents show a disproportionately higher burden of the disease, while in developed areas where Dengue is not endemic, adults tend to be more susceptible to infection [88]. Symptoms of Dengue range from high fever, joint and muscle pain, nausea, fatigue, mild bleeding to severe Dengue with excessive bleeding, organ failure or shock. As no specific antiviral treatment is currently available for dengue, clinical management primarily relies on supportive care. Dengvaxia was previously recommended only for eligible individuals with evidence of prior dengue infection because the vaccination of seronegative individuals was associated with an increased risk of severe dengue. However, the manufacturer subsequently discontinued its marketing, and the vaccine should be discussed as a historical prevention option rather than a routinely available current intervention [80,89]. Over the last few decades, extensive studies have enhanced our understanding of Dengue's epidemiology, including disease burden and distribution, indicators of risk, and management and preventative measures [90].

3.1.2. Crimean–Congo Hemorrhagic Fever

Crimean–Congo hemorrhagic fever was first identified in the Crimean Peninsula (now Ukraine) during an outbreak in 1944. Over a decade later, in 1956, in Congo (now Democratic Republic of Congo), a similar outbreak was noted, hence the term 'Crimean–Congo' [91]. In the 1960s, the Hyalomma tick was identified as the primary carrier of Crimean–Congo hemorrhagic fever virus and is now known for its broad geographic distribution, making it one of the most prevalent tick-borne illnesses among humans [91]. The vector is commonly found in Africa, Southern and Eastern Europe, India, the Middle East, and Asia. One hundred fifty-eight incidents of nosocomial infections were identified in 20 countries between 1958 and 2016 in the review conducted in 2019. The reported mortality rate was 32.4% [91], and almost every episode was symptomatic. Globally, the prevalence is projected to be around 10,000–15,000 cases yearly, with a gradual and consistent increase. Fetal and neonatal mortality (58%) is linked to spontaneous abortion or mortality of the mother [92]. Notable outbreaks occurred in 1970–1980 (Africa, Asia, Middle East, Eastern Europe), and nosocomial outbreaks in 1980–1990 (especially in Pakistan and Turkey), with sporadic outbreaks in the last 20 years in Turkey, Kenya, Afghanistan, Pakistan, Iran and Uzbekistan [93]. The growth and relocation of tick habitats to higher altitudes can be influenced by various factors, such as the accessibility of optimal animal hosts, raised summer evapotranspiration, reduced precipitation and increased temperatures during the winter [93]. Patients may exhibit symptoms of deteriorating hemorrhagic diathesis as

the disease progresses, including petechiae, bleeding from the mucous membranes and conjunctiva, hematuria, vomiting of blood, and melena. Circulatory shock and dispersed intravascular coagulation are potential complications [93]. Crimean–Congo hemorrhagic fever virus is commonly found in livestock such as sheep, goats and cattle, and the spread is of a zoonotic nature; however, the virus can spread between individuals or contact with virally infected blood or tissues, and can cause nosocomial outbreaks in healthcare facilities, especially when hygiene and sanitation standards are inadequate [94]. Vaccines are not available; however, the ribavirin antiviral may provide some benefit if used early in the infection phase. The increase in people's movement and livestock, the spread of ticks, and the effects of climate change have raised concerns of ongoing outbreaks and potential spread to new regions, including the Americas and western–central Europe.

3.1.3. Yellow Hemorrhagic Fever

Yellow fever, also known as Yellow hemorrhagic fever, has been referred to in ancient civilizations, including Africa and indigenous Americas, but it was not until the late 1800s that it was identified and linked to *Aedes aegypti* mosquitoes [95]. In the era of 1600–1800, Yellow hemorrhagic fever spread rapidly due to European colonization, especially in the Caribbean and central and south America (New Orleans in the USA, Cuba, Havana), which affected trade and colonization. Approximately 200,000 global cases are recorded annually, with an exceptionally high mortality rate [95]. The development of a vaccine and large-scale vector control programs in affected regions has led to decreased global health priority [96]. However, Yellow fever continues to pose a public health danger, with the potential for regional geographic spread [97]. Following an incubation time frame of 3 to 6 days, about 70–90% of infected persons continue to be asymptomatic or exhibit flu-like symptoms without further consequences. Those who remain will experience a severe illness that may result in hemorrhagic fever and death. The previous case fatality rate for patients entering the toxic phase has ranged from 20 to 50%. In preceding epidemics, the case fatality rate among diagnosed patients ranged from 13.5 to 35% [98].

3.2. Lessons Learned from Epidemics

Modern human activities, including urbanization, deforestation, and agriculture, increase our interactions with wildlife and the diseases they carry [99]. Practices like poultry farming, the animal trade, and forest clearing bring people closer to species that may harbor new pathogens, such as bats, cattle, and poultry, which are likely to contain novel viruses. Climate change further exacerbates this issue where infectious diseases can spread rapidly [99]. To control such diseases, it is essential that public and private health facilities adhere to strict infection prevention protocols to avoid nosocomial infections, particularly when treating fever patients. In endemic areas, effective surveillance is key to the early detection of viral hemorrhagic fevers, and accurate laboratory diagnoses during the acute phase can help improve patient care and reduce mortality [99]. In addition to regulating genetically modified mosquitoes, effective vector control measures (mosquito bite prevention, removing stagnant waters) and promoting hygiene in urban areas are necessary to manage mosquito populations. In areas with large non-vaccinated populations, these efforts are crucial to prevent the re-emergence of diseases that can cause significant mortality. Strengthening surveillance, replenishing health supplies, and preparing healthcare systems for emerging diseases is vital, especially for vulnerable populations (i.e., pregnant women and children [100–103]).

3.3. The Role of Global Health Organizations

The rapid emergence of diseases allows for repurposing resources, including personnel, funding, and expert knowledge. Worldwide, public health agencies at the national and international levels work under the auspices of the WHO to control emerging infectious diseases due of the urgency with which they affect people [104]. The government of India made significant attempts to improve the National Center for Disease Control and Prevention, which monitors and responds to infectious diseases that are prone to epidemics. As such, the Indian government's Ministry of Health and Family Welfare and the World Bank launched the Integrated Disease Surveillance Program [105]. In the decade 2017–2026, the WHO implemented its worldwide plan to eradicate Yellow fever outbreaks, known as EYE (Eliminating Yellow Fever Epidemics) [95]. As part of this plan, the development of facilities and production of Yellow fever vaccines are increasing, aiming for almost two billion doses in order to protect and reduce spread [97]. In addition, zero fatalities from Dengue fever cases by 2030 is the goal of the WHO's Global Strategy for Dengue Prevention and Control 2021–2030. To raise awareness and mobilize global resources to combat Dengue, the forum urged the WHO and the United Nations (UN) to declare a World Dengue Day, which is observed on June 15 annually [106]. Within this plan, there are education and community engagement plans seeking to reduce mosquito breeding sites and the use of insecticides [107], strengthening integrated surveillance, the expansion of vaccination programs and their efficacy in different regions, improving infrastructure and health systems, as well as funding and collaborations in research and innovation. All these measures are aimed at eliminating Dengue as a public health threat in endemic areas.

4. Climate Change and Its Impact on Infectious Diseases

4.1. Overview of Climate Change Effects on Overall Health

Numerous health issues are susceptible to climatic variations. Various variables influence the prevalence of climate-sensitive infectious illnesses, including Dengue fever and Ebola. Environmental variables, including land utilization and climate-related influences on ecosystems, might alter the availability of appropriate vector environments, resulting in regional expansion or a reduction in linked illnesses [108]. The aggregation of pathogenic diseases exacerbated by climate risks constitutes 58% of the infections documented to have affected humans globally [109]. Both precipitation and temperature frequently serve as significant environmental determinants of infectious illness, encompassing illnesses transmitted through water such as cholera, vector-borne diseases like parasitic helminths and malaria, fungal diseases linked to global amphibian declines, and marine diseases impacting corals, sea stars, fisheries, and aquaculture operations [110]. Climate change affects the patterns of vector-borne, food-borne, water-borne, rodent-borne, and air-borne infectious illnesses. Further, research has projected that climate change may exacerbate antibiotic resistance [111]. Evidence indicates that non-mitigated prospective climate change would likely affect the duration of the spread season and the geographical spread of a substantial number of infectious illnesses. The direct effects of climate change on habitats and subsequent ecosystem alterations, along with escalating human-induced pressures on the natural environment, significantly compromise biodiversity, influencing the origin and spread of infectious illnesses [112].

4.2. Mechanisms Linking Climate Change to Disease Transmission

Long-term rainfall, temperature variations, wind, humidity and moisture, define the impact of climate change. Temperature is a critical component in the survival of living organisms, irrespective of the ecology. As a result, a given living thing requires a complex spectrum of temperatures to survive on earth [113]. Extreme temperatures accelerate the

growth and reproduction of infections transferred by vectors, external incubation time, or the environment [114]. Warming at higher elevations enabled vectors and diseases to endure the winter, exacerbating many viruses like Dengue. Warming, drought, heatwaves, forest fires, storms, floods, and shifts in land cover have all been linked to diseases becoming more prevalent [109]. High precipitation can facilitate the spread of viral hemorrhagic fevers by drawing pathogens from pastures and fields, overwhelming water treatment and conveyance systems, and contaminating drinking water. The resulting contamination can increase the risk of human exposure to infectious agents. Residual water from downpours is an ideal habitat for larvae and pupae for mosquitoes, and water-storage activities amid a drought can enhance water availability, which provides mosquito breeding grounds, vectors for several hemorrhagic fever viruses such as Dengue and Yellow fever, and increasing the risk of mosquito–human contact and viral transmission [115].

4.3. Climate Change and Dengue Hemorrhagic Fever, an Example

Two *Aedes* mosquitoes predominantly transmit Dengue: *Aedes aegypti* and *Aedes albopictus*. *Aedes aegypti*, regarded as the principal vector, is prevalent in numerous tropical and subtropical regions globally and is well-suited to urban settings, whilst *Aedes albopictus* has an expanded distribution into temperate zones and is predominantly located in rural and peri-urban areas [116]. As mentioned above, climatic variables, including moisture, temperature and rainfall, significantly influence the Dengue epidemiological triangle, which comprises the virus, vector, and host (Table 2). The Intergovernmental Panel on Climate Change projected that by 2080, 1.5–3.5 billion individuals globally will be susceptible to Dengue fever outbreaks as a result of climate change [117]. Dengue, passed on by various mosquito genera inhabiting distinct ecological niches, is affected by rainfall, which either facilitates new mosquito breeding areas or leads to their elimination during intense rainfall events. In addition, the onset of the rainy seasons elevates air humidity and promotes a surge in mosquito breeding habitats [118]. Temperature influences the mosquito's development from egg to larva to mature adult and its expansion within the life cycle. The biting behaviors of mosquitoes and their reproduction, both of which contribute to how often the female mosquito feeds on human hosts, are influenced by temperature; hence, rising temperatures elevate disease spread rates [119]. According to the mechanistic modeling informed by the thermal biology of the mosquitoes, the temperatures at which the transmission is optimal differ among mosquito vectors. For instance, one review study estimated optimum temperatures for transmission at about 28.1 °C for Aedes aegypti and 26.4 °C for *Aedes albopictus* [120]. According to another study using mechanistic modeling, the optimal temperatures for transmission have been estimated to be approximately 29.1 °C for *Aedes aegypti*, while maintaining that the optimum for *Aedes albopictus* is 26.4 °C. The above optimum temperatures are not universal and are model specific [121].

Table 2. Dengue hemorrhagic fever cases in different countries influenced by climate changes.

Area, Country	Impact of Climatic Change on the Transmission of Dengue Hemorrhagic Fever	Reference
Lahore, Pakistan	A 34.2% model accuracy in predicting that Dengue cases would increase in response to increased rainfall. It was noted that Dengue fever increased with the rise in the mean monthly temperature. In addition, a positive correlation of 44.6% was observed between Dengue cases and climate factors, as indicated by multiple regression.	[122]

Table 2. *Cont.*

Area, Country	Impact of Climatic Change on the Transmission of Dengue Hemorrhagic Fever	Reference
Dhaka, Bangladesh	Dengue incidence was lower than observed during "normal" temperatures (26 °C) when annual average temperatures ranged from 26.1–26.6 °C. During the monsoon season, an increase in *Aedes* mosquito abundance was correlated with an increase in temperature, relative humidity, and rainfall, leading to a subsequent increase in Dengue incidence. The regression model demonstrated that climate factors were responsible for ~72% of the variability in the Berteau Index, a tool that is employed to forecast the transmission of Dengue fever by quantifying the number of containers containing mosquito larvae or pupae per 100 inspected dwellings.	[123]
Africa	The study determined that temperature is the most significant climatic variable in the incidence of Dengue fever in eastern Africa and western Africa. This variable collectively determined 70.8% of the prospective distribution of *Aedes aegypti*. It was suggested that the current and future climate conditions of countries with an annual rainfall of 500 mm and a temperature between 25 and 30 °C were highly to moderately suitable for infectious *Aedes aegypti*. It also noted the potential for the development and survival of *Aedes aegypti* to be facilitated by the anticipated gradual increase in temperature and precipitation in the continent due to global warming, thereby increasing the successful propagation of Dengue fever in the future.	[124]
Bangkok, Thailand	The transmissibility of Dengue in Bangkok was positively correlated with rainfall and humidity. In the model, a 1% increase in rainfall resulted in a 3.3% increase in the monthly incidence rate of Dengue, while a 1% increase in humidity resulted in a 0.7% increase in Dengue cases. Nevertheless, a 1.6% decrease in Dengue cases was observed for every 1% increase in temperature.	[125]
India	The suitability of *Aedes aegypti* was more significantly influenced by temperature-related factors, whereas *Aedes albopictus* was considerably influenced by precipitation-related factors in eastern and western coastlines, northeastern states, and in the lower Himalayas.	[126]

5. Ecological Factors Influencing Hemorrhagic Fevers

5.1. Vector Ecology and Climate Interactions

Vector ecology, significantly influenced by climate change, plays a crucial role in transmitting hemorrhagic fevers like Dengue, Yellow fever, and Crimean–Congo hemorrhagic fever. Climatic factors such as temperature, humidity, and rainfall affect the survival, reproduction, and spread of disease vectors like mosquitoes and ticks. For instance, warmer temperatures accelerate the life cycle of *Aedes aegypti*, the primary Dengue vector, enabling faster reproduction and transmission [77]. One primary study in the Honduras showed the direct relationship between El Niño events and warmer and wetter conditions with the emerging Dengue hemorrhagic fever cases. Thus, climate variability plays a role in disease outbreaks [127]. Similar findings were observed in Southeast Asia, where environmental fluctuations like higher temperatures and rainfall directly lead to Dengue outbreaks. Increased rainfall allows more breeding sites, while higher temperatures bring about greater survival and biting rates [128]. Climate's influence on tick-borne diseases, like Crimean–Congo hemorrhagic fever, by altering temperature and precipitation patterns, expands disease transmission risks, as well as their spread into some previously unaffected regions [129]. The climatic change in temperate zones results in other species becoming extinct, and conditions are given for the presence of disease vectors in the changed zones [93]. Outbreak prediction models from climate data and vector-borne disease ecology offer an early warning system (EWS) for community preventive measures and interventions [130].

It is important for such models to be tailored to specific localities to protect against variability in climatic and vector behaviors [131].

5.2. Environmental Changes and Disease Outbreaks

Alterations to the natural environment are critical to a pandemic's swift propagation [132]. Extreme pollution, climate change, periodic natural catastrophes, diminished habitats, and loss of biodiversity are just a few of the growing environmental challenges. Due to these changes, the world's environment is different, and animals' habits and behaviors have changed. This includes viruses and other biological pathogens, which impact the spread and development of infectious illnesses [133] (Table 3).

Table 3. Environmental changes have impacted major illness epidemics, such as Ebola, Dengue, Crimean–Congo hemorrhagic fever, Yellow, and Lassa.

Disease	Role of Environmental Changes in the Outbreak	Reference
Dengue	Environmental factors, i.e., light intensity, ventilation, drainage and building distance impact the density of *Aedes* larvae.	[134,135]
	Many water receptacles, such as tree axils, rotting leaves, and paddy fields, can serve as aquatic mosquito homes.	
Crimean–Congo hemorrhagic fever	Distribution of ticks may influence disease emergence.	[136,137]
	Changes in environmental conditions, i.e., increased humidity and favorable temperature (28 °C and above) encourage tick reproduction and proliferation.	
Yellow fever	*Aedes aegypti* immatures are more prevalent in artificial and vast water containers.	[120]
	Density of mosquitoes increases because of suitable habitats for mosquito breeding provided by vegetation.	
	The lifecycle of mosquitoes is influenced by humidity, which is regulated by a combination of temperature and rainfall, a potential source of virus transmission.	
Lassa fever	Can extend its spread and crossover into human communities due to seasonal changes, urbanization, inadequate sanitation, deforestation, and voluntary or involuntary migration.	[138]

5.3. Geographic Distribution and Risk Assessment

It is important to identify the specific hemorrhagic fever virus when assessing potential risks as their distribution varies. Understanding how these viruses spread and infect humans is essential, especially considering the emergence of new infectious diseases, which pose significant concern worldwide [139]. The geographic regions where viruses are most prevalent should also be considered. For example, *Aedes albopictus* is widely distributed in the United States, as was first identified in the 1980s, likely as a result of international trade [140], and it is abundant in tropical and subtropical cities due to their rapid expansion. It is now said that *Aedes albopictus* are widely distributed in Eastern Europe and are expected to spread farther throughout the rest of Europe and non-colonized regions of China [116]. For instance, *Aedes albopictus* are not known to be native in the United Kingdom (Western Europe); however, in recent years they have been detected, raising the potential for disease transmission if they become more prevalent and/or if conditions change. By considering the unique characteristics of a region, hemorrhagic fever virus risk maps offer local risk assessments. These geographical representations can identify virus-prone locations by evaluating data at a finer scale, such as urban areas or suburbs. This data is vital for local healthcare to reduce the strain on resources, implement targeted treatments, and allocate

resources effectively [141]. Further, animals can be host-reservoirs for several hemorrhagic fever viruses, for example, wild animals, rodents, livestock can be a source of infection of Crimean–Congo hemorrhagic fever virus to humans [53]. Indeed, animals have been found infected with Crimean–Congo hemorrhagic fever throughout several continents, including Asia, Eastern Europe, the Middle East, and most of Africa [142]. Anthropogenic pressures may also influence geographic patterns of viral hemorrhagic fever risk [143]. Deforestation, agricultural expansion, livestock intensification, and urbanization can alter wildlife habitats and increase contact between people, domestic animals and wildlife reservoirs [144]. Exposure may also occur through wildlife capture, trade and consumption, while industrialization, population growth, pollution and poor waste management can change local ecological conditions [145]. These activities are discussed by Tazerji et al. as broad drivers of zoonotic emergence and re-emergence, including for viral pathogens such as Ebola virus and Hantaviruses. These factors need to be assessed alongside local reservoir, vector, land use and epidemiological data, as the effects can vary by pathogen and setting [146]. To effectively combat ticks, it is necessary to conduct local risk assessments in locations where viruses are prevalent, such as Crimean–Congo hemorrhagic fever virus. Consequently, to regulate and prevent Crimean–Congo hemorrhagic fever, multidisciplinary and local and regional teams must work together to determine gaps and coordinate their efforts, including improvements in health infrastructure [147]. Another risk assessment to consider is international trade, as this can significantly contribute to the spread of hemorrhagic fever viruses to non-endemic areas. Finally, where vaccines are available, vaccination campaigns and education are important to the control of disease, in addition to vector control efforts. Reducing the risk of infection involves a comprehensive approach, including avoiding exposure to mosquitoes, being cautious around animals and their products, and steering clear of contaminated bodily fluids, tissues, and potential aerosolized vectors [141].

6. Socioeconomic Factors and Vulnerability

6.1. Impact of Socioeconomic Status on Disease Susceptibility

The socio-economic characteristics of a specific area might be crucial for the continued persistence of a disease following the establishment of local dissemination. Individuals residing in areas with higher socioeconomic status can mitigate mosquito exposure and limit virus spread through grassroots initiatives (e.g., private measures) or governmental actions like regional pest management [148]. Nevertheless, it is crucial to acknowledge that elements linked to elevated financial standing may also increase human exposure to mosquitoes, such as householders with vegetable gardens, potted plants and water bodies, or convenient access to places of recreation conducive to mosquito breeding [149]. The deterioration of public health infrastructure necessary for illness prevention and management, and extraordinary population expansion, particularly in rapidly expanding urban areas, has contributed to their conveyance and geographic spread [144]. The expansion of towns and cities, or urbanization, may provide new breeding sites for mosquitoes due to the rise in human waste, inadequate sanitation, and substandard housing, all of which can influence the dispersion of vectors of mosquitoes [150]. Accelerated worldwide mobility facilitated by contemporary transportation systems establishes a vast metropolitan network that enhances the likelihood of vector and viral transmission to new regions. The global expansion of the virus leads to its genetic diversification, complicating efforts to manage its spread [151].

6.2. Health Infrastructure and Response Capacities

Exposure to timely, superior medical care from robust healthcare systems is crucial for the worldwide potential to avoid, spot, and react to illnesses that can become pandemics [152]. Viral hemorrhagic fevers such as Ebola, Lassa fever, Marburg, and Crimean–

Congo hemorrhagic fever have exceptionally high mortality rates, hence it is crucial to diagnose these infections quickly and provide treatment as soon as possible [152]. This requires easy access to healthcare facilities and competent personnel, appropriate medical supplies, high-quality lab testing to determine the agents responsible, and the proper application of infection prevention and control strategies to avoid secondary transmission [152]. Public health systems in low-resource nations require a long-term plan for managing and building capacity, even though a lot has been done to address health challenges in the last few decades. To address new public health concerns as they arise, preparedness for catastrophes is an ongoing process [153]. Community involvement, infection prevention and control, case management, laboratory testing, contact tracing, and improved monitoring have all been priorities in the fight against the epidemic [154]. National authorities receive logistical and technical help from the WHO and its partners. A significant part of this response comes from healthcare professionals, who may shed light on the tactics used, the difficulties encountered, and the community's reaction to these actions [155]. Insights gained from their stories shed light on how governmental decisions, infrastructure problems, and socio-cultural variables influence disease management [156]. Accordingly, all four fields, human, animal, environmental, and wildlife, were represented in a 2017 One Health Zoonotic Disease Prioritisation Workshop. Using a multi-sectoral, One Health approach, the workshop sought to prioritize endemic and growing zoonotic diseases that pose a significant public health risk [157]. There are a variety of resources that nations may employ to enhance their One Health capabilities [158,159]. The Sustainable Development Goals and health security cannot be attained without high-quality emergency services, and those making choices in settings with limited resources must recognize this in order to enhance the delivery of critical care services. The development of personnel strategy, dependable medicine and equipment supply chains, and the provision of fundamental hospital facilities, should all be part of these amenities [160].

6.3. Disparities in Global Health Outcomes

Disparities in global health outcomes caused by hemorrhagic fever viruses arise from socioeconomic, geographic, and healthcare factors. Low- and middle-income countries are hit hardest by hemorrhagic fevers like Dengue, Ebola, and Lassa fever since they have little access to healthcare, have poor sanitation conditions, and are not provided with adequate vector control programs [118,128]. Diseases in sub-Saharan Africa, Southeast Asia, and Latin America influence the health systems in those places [161]. One of the main difficulties that can be found in those areas is the insufficient surveillance of and response to diseases, which in turn reduces the capacity to predict and prevent outbreaks [121,162]. Additionally, people in those places usually live at a close distance to carriers and reservoirs, which increases the likelihood of infection [163]. For example, the lack of basic amenities in urbanizing areas can lead to the buildup of standing water, where mosquitoes could multiply in large numbers and transmit diseases, like Dengue [164]. The consequences of climate change further worsen these inequalities. Places already fragile because of poor healthcare infrastructure tend to be the most affected by climate change, specifically the rise in temperatures and the increase in rainfall, which in turn create a favorable environment for vectors [165,166]. To deal with these differences, the countries of the world should work together, health systems should be developed, and research into and development of new vaccines and treatments should be invested in [167,168].

7. Surveillance and Response Strategies

7.1. Importance of Surveillance Systems

Premature contagion identification and other related public health risk identification uses methods for surveillance, including Event Based Surveillance. This objective is reached via a systematic strategy to identify signals that could reflect occurrences of public health relevance [169]. Included in the Crimean–Congo hemorrhagic fever surveillance plans ought to be serological investigations across both domestic and exotic animal populations, as well as surveys of distribution and virus prevalence among tick species [170,171]. By tracking the frequency of viruses in individuals, animals, or tick vectors, setting up Crimean–Congo hemorrhagic fever surveillance programs might help ascertain possible amounts of risk to people living in endemic locations, and help pinpoint where disease control actions could be most beneficial [171]. A portion of the change in the healthcare sector is technological endeavors, including the implementation of online monitoring systems, global positioning systems (GPSs), telephone-based tracking systems, the building of isolation departments and high-dependency units (HDUs), the supply of more accommodation, and the recruiting of healthcare workers [172].

7.2. Early Warning Systems for Outbreak Prediction

The main objective of a system for early detection is to gather data that may be used to make quick decisions that can initiate initiatives to intervene in disease and lessen its impact on a particular community. Several methods have been employed to enhance the public health monitoring system by utilizing EWS's capacity to be an efficient instrument for risk reduction [173]. Accurate outbreak forecasts would enable public health authorities to prepare in advance. Standard operating procedures (SOPs) are necessary for early warning systems (EWSs) to reliably detect, through alarm signals, an elevated danger of an epidemic in terms of both time and geography, allowing for an early reaction [174]. In areas prone to natural catastrophes, developing EWSs in tandem with better response capabilities at the state, federal, and regional levels is especially important. Verification, decision-making processes, investigation, and engagement are necessary for early warning indicators of a pandemic [175]. If these early warning signs are used, there may be time and money savings in zoonosis control and readiness for public health emergencies [176].

7.3. Global Collaboration and Data Sharing

Collaboration on the advancement and implementation of molecular approaches for the identification and demographic evaluation of communities of invasive species and emerging infectious diseases (EIDs), tracking in field investigations (which involves the assessment of the indirect consequences of attacks on health), and interactive observing (and enhanced surveillance) for EIDs and intrusive species at stages of entry are some of the fields in which complementary tasks may boost productivity [104]. The World Bank has collaborated with the WHO to establish a two-pronged Pandemic Emergency Financing Facility (PEF). The main structure is pandemic assurance, which has been active since July 2017 and provides coverage for economically disadvantaged client countries (i.e., those eligible to borrow from the International Development Association) [177]. The insurance can be paid out in the event of epidemics of six viruses that the World Bank has identified as the most likely to cause a pandemic. These viruses include Crimean–Congo hemorrhagic fever, filovirus (e.g., Ebola, Marburg), Rift Valley fever, and Lassa fever [178]. Various types of studies, such as epidemiological studies, mathematical modeling, environmental monitoring, life-sciences work (e.g., microbial genomics), and cultural anthropological research, yield evidence that could be used to inform mitigation, identification, and response activities [179]. The communication of these and other data to public health decision-makers

plainly and concisely is crucial for converting research investments into public health practice [180]. A substantial quantity of disease information is gathered and assessed to detect prospective epidemics, identify the underlying factors and prospective transboundary dangers, and implement adjusted prevention strategies. A prompt warning system has been adopted to execute preventive measures punctually [105].

8. Mitigation and Adaptation Strategies

8.1. Public Health Interventions to Combat Hemorrhagic Fevers

A complete comprehension of the spread of diseases, readiness for disease onset, pathogen and vector identification, and the execution of effective control measures and treatments for prevention is essential [181]. For example, epidemiological information on Dengue hemorrhagic fever cases can assist public health authorities in executing targeted interventions, including public awareness campaigns and mosquito control measures, to mitigate risks [182]. Current control measures predominantly depend on vector control strategies, particularly pesticide application, which have seen modest success [183]. Public health groups should implement systematic mosquito control strategies. Insect bites can be prevented or greatly minimized using insect repellent, applying permethrin lotion to clothing or skin, and utilizing bed nets and window screens. Public health must be scrutinized for potential neurological and immunological consequences in high-risk regions [184].

8.2. Climate Adaptation Strategies for Vulnerable Populations

One of the most crucial adaptation strategies for the climate is to intensify the public health systems and disease surveillance capabilities for the prompt identification of and response to outbreaks of hemorrhagic fevers. Meteorological early warning models, such as climate data and predictive modelling, are necessary to follow vector distribution alterations and identify preparedness measures for outbreak prevention [185]. Furthermore, environmental management issues are key factors in decreasing the vector habitats that cause diseases. For instance, the struggle to maintain mosquito populations by disposing of swamped areas and implementing biological controls such as introducing predatory fish has been successful in limiting Dengue fever [186]. These strategies are specifically crucial in urban areas where rapid population growth and inadequate infrastructure are contributing to vector-caused diseases [145]. Education and community engagement are equally important for adaptation strategies. People living in vulnerable areas should also be educated about the impacts of climate change on the spread of diseases and the measures they can take to reduce their vulnerability. For example, the use of safety gear such as mosquito nets and repellents can lower the exposure of vectors to disease [186]. International cooperation and financial support, which are essential to support low-income areas in adapting with limited resources, will be the requirements. Methods such as drawing from climate funds, i.e., the Green Climate Fund, can also be applied to set up health infrastructure improvement projects in regions sensitive to climate [187].

8.3. Artificial Intelligence for Prevention and Mitigation

Artificial intelligence (AI) and machine learning approaches offer further opportunities to enhance the prediction, surveillance and mitigation of viral hemorrhagic fever outbreaks [188–190]. Predictive models may be useful in identifying geographical areas where environmental conditions favor vector proliferation or increased human–animal contact, and may be used to integrate meteorological observations, satellite derived environmental information, land use patterns and vector distribution and epidemiological surveillance data [176,189,191]. Machine learning algorithms can also help in early warning systems by identifying patterns in historical disease incidence and climate variables [188,191,192],

whereas natural language processing can help detect nascent outbreak signals from epidemiological reports and other surveillance sources [190,193,194]. These approaches could help public health officials to prioritize high-risk locations, plan laboratory and healthcare resources, and implement targeted vector-control and community-protection measures [176,189,192]. However, their reliability depends on the quality, completeness and geographical representativeness of the underlying data [188,189,195]. They may be of limited use, however, due to under-reporting, limited digital infrastructure, algorithmic bias, and difficulties interpreting model outputs, especially in resource-limited settings [190,195,196]. Hence, AI-based systems should be used as decision-support tools alongside traditional epidemiological surveillance, field investigations and expert public health assessment, rather than as a substitute [195,196].

8.4. Role of Policy and Governance in Health Resilience

To be well-prepared, health systems must do more than just monitor for and control epidemics; they must also strengthen the endurance of populations and guarantee the security of health workers and patients amid emergencies [197]. To be certain that each healthcare organization is prepared for the next pandemic, there must be significant governance as well as architectural and monetary modifications on many levels [197]. A thorough multisectoral strategy, comprising strong leadership and management, a suitable strategy and cooperation, the recognition and building of partnerships and networks, and excellent governance, is necessary for national health emergency preparation [197]. To improve community social engagement and interactions, regarding the threat of hemorrhagic fevers, it is important to implement community-based initiatives linked to federal ministries, municipalities, social organizations, and other relevant stakeholders in the fields of medical care, schooling, surroundings, farming, irrigation, customs operations, knowledge dissemination, and media [198]. The purpose of creating a Health System Resilience Checklist ('the checklist') was to ensure that healthcare institutions, organizations providing medical services, and national health authorities could all utilize it. Healthcare system players may use the checklist to quantify the precise capabilities and procedures needed to be resilient in the face of epidemics of infectious diseases and natural disasters, which will help operationalize the idea of health systems' robustness [199].

9. Future Directions and Research Needs

9.1. Gaps in Current Research on Hemorrhagic Fevers

The field of hemorrhagic fevers has improved in recent years; however, researchers have not been able to answer all the research questions. In fact, the long-term effect of climate change on vector activity and disease transmission is one of the main areas that needs further investigation. Although recent studies have shown that temperature and precipitation changes are the short-term causes of these epidemics, additional longitudinal studies are required to establish how sustained temperature and precipitation changes will affect the prevalence of these diseases [200]. Over and above this, the limited knowledge of how climate will change the zoonotic transmission patterns of hemorrhagic fevers like Ebola and Lassa fever is another crucial issue concerning the adaptation of micro-organisms to new climate conditions. Studies on the connections involving the interaction of animal reservoirs, vectors, and human populations in the context of shifting environmental circumstances are immensely important in the forecast and the control of future outbreaks [201].

9.2. Innovations in Vaccine Development and Treatments

Innovative advancements in vaccine development are considered as one of the most effective strategies to manage hemorrhagic fevers. Innovations, such as mRNA-based or

nanoparticle-based vaccines, along with new delivery technologies, play a crucial role in enabling responses to newly emerging pathogens. For example, mRNA-based vaccines and their rapid use in COVID-19 have raised the concept of applying this type of technology to other diseases, including hemorrhagic fevers such as Ebola and Dengue [202]. Moreover, progress in monoclonal antibody treatments, which are non-invasive and thus promise to open new therapeutic options for hemorrhagic fever, is being made. In this case, these treatments were carried out on clinical trials, and so far, they have proven to be successful, especially in the treatment of Ebola virus disease, and they offer hope for other viral hemorrhagic fevers [203].

9.3. The Role of Technology in Disease Monitoring

Technology, particularly using remote sensing, geographic information systems, and machine learning, forms the base upon which vector habitat mapping, disease mapping, outbreak tracking, and environmental change-based future disease spread can be done [204]. One of the latest trends is the widespread use of mobile health technology to collect real-time data in resource-limited areas. Due to the flexibility of frontline healthcare providers reporting instances of viral hemorrhagic fevers through mobile applications, public health authorities can react faster and distribute resources more efficiently during outbreaks [205].

9.4. Limitations of the Review

This review has several limitations that must be taken into account when interpreting its findings. First, the evidence available on viral haemorrhagic fevers is heterogeneous including different viral families, transmission routes, reservoir hosts, geographical settings and epidemiological outcomes [1,4,7,18,91,92]. Thus, results from one pathogen or region may not be directly applicable to other pathogens or regions. Second, most of the evidence for a link between climatic and environmental change and disease emergence is based on observational studies, ecological analyzes and predictive models. Such approaches provide useful insights into potential transmission patterns, but do not always imply direct causal links between environmental change and outbreak occurrence [77,79,110,111]. Third, disease surveillance and diagnostic capacity is still patchy across endemic regions, resulting in possible under-reporting and incomplete epidemiological datasets [15,100–103,152,153]. These limitations can influence the accuracy of geographic risk estimates and climate-based projections [79,115,129,141,174]. Finally, publication bias and differences in study methodology may influence the scope and interpretation of the conclusions, as this review synthesizes available published evidence. Future research should focus on longitudinal surveillance, standardized epidemiological datasets, field-based validation of predictive models, and integrated One Health investigations to enhance the reliability of climate-informed VHF risk assessment [116,138,171,176,181].

10. Conclusions

Climate change drives major changes in the ecology and behavior of vectors responsible for transmitting hemorrhagic fevers. The temperature rise, the increase in rainfall, and the other climatic factors constitute favorable instances for mosquitoes and ticks, which will consequently exacerbate diseases such as Dengue, Yellow fever, and Crimean–Congo hemorrhagic fever. The underprivileged populations in low- and middle-income countries are those affected most by these changes due to inadequate healthcare infrastructures and limited access to preventive systems. Addressing climate change is essential since it is the only way to reduce the threats related to public health that are caused by hemorrhagic fevers. A situation of extreme negligence will likely lead to the further spread of these diseases to more areas and people. Investing in climate adaptation measures, including but not

limited to disease surveillance strengthening, public health infrastructure development, and community sensitization, is an important approach to protect communities. Future studies should address the existing holes in our knowledge of how climate change impacts vector biology and disease transmission. In addition, further resources for research, public health interventions, and international cooperation will help us overcome these climate-driven diseases more effectively.

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