CLIMATE CHANGE AND VECTOR-BORNE VIRAL DISEASES

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1.1 INTRODUCTION

There is an increasing threat of infectious disease due to globalization and climate change. It is now widely accepted in the scientific community that the Earth’s climate system is changing, which has brought great public health challenges around the world. The impact of climate change on the transmission of infectious diseases, particularly on vector-borne diseases (VVD), has been examined in both developing and developed countries (Lafferty, 2009; Weaver and Reisen, 2010). In particular, emerging and reemerging VVD are expected to increase due to climate change and variability (Zell et al., 2008). For the first time, in the last decades, several VVD, such as West Nile virus infection, chikungunya virus infection, and viral hemorrhagic fevers, have been spreading geographically and recorded in areas outside their original ranges. However, the lack of knowledge and effective, safe vaccines and diagnosis for some VVD makes it challenging to prevent and reduce the burden of disease associated with the changing environment.

This chapter aims to present a synthetic view of the health impact of climate change and variability on VVD in order to assist evidence-based decision and policy making for disease prevention and control. We have divided this chapter into three parts. The first part will discuss the epidemiological background of VVD, including the scope; the temporal–spatial distribution around the world; a summary of the factors that affect their transmission, including the causal relationship between climatic factors and VVD; and its prevention and control. The second part will focus on the association between climatic variables and some emerging VVD, such as dengue fever (DF), Rift Valley fever (RVF), viral encephalitis, yellow fever (YF), and others. Implications and recommendations are provided in the third part of this chapter to inform decision and policy making for a range of stakeholders, for example, public health practitioners, doctors, and other health service providers at medical clinics, governments, researcher centers, and local communities.

1.2 EPIDEMIOLOGY OF VVD

1.2.1 What are VVD?

Vector-borne viral diseases are virus infections transmitted via vectors. To clarify the scope of the discussion in this chapter, we adopted epidemiological and biological definitions of vector and virus to select eligible VVD for discussion. Vectors are organisms that transmit infections from one host to another (Last, 2001). Vectors of human disease are typically arthropods (e.g., species of mosquitoes and ticks) that are able to transmit pathogens. A virus is a small infectious agent, consisting of nucleic acid in a protein coat, that can replicate only inside the living cells of organisms with a wide diversity of shapes and sizes (Koonin et al., 2006). There are more than 500 “vector-borne viruses” and about 100 of them are of veterinary and/or human importance, which can cause major epidemics (Moormann, 2012). Some selected emerging VVD have been listed in Table 1.1. Some other important infectious diseases that are sensitive to climate variations, for example, malaria (not viral) and hemorrhagic fever with renal syndrome (not vector borne), are not included in our discussion.
1.2 EPIDEMIOLOGY OF VVD

1.2.2 Temporal–spatial distribution of VVD around the world

Most VVD are restricted to the tropics and are often seen in temperate regions only as imported diseases, because of the required living environment for certain arthropod vectors like the *Anopheles* or *Aedes* mosquitoes. The majority of the mortality and morbidity burden of VVD occurs in Africa, South America, South Asia, and the Pacific Islands (WHO, 2004). However, geographical expanding of VVD has been reported around the world recently. This includes the emergence of West Nile virus in the Americas and Japanese encephalitis (JE) in Australasia, the spread of dengue, and the reemergence of YF virus in South America (Mackenzie and Williams, 2009; Mackenzie et al., 2004).

Due to the development of effective public health preventions and control measures targeted for VVD during the last century, many VVD, particularly mosquito-borne diseases, were controlled in many areas. However, over the last 20 years, some VVD, such as DF and West Nile virus infections, have reemerged in some areas, for example, Asia and the Americas (DeCarlo et al., 2011; Phillips, 2008; Rezza, 2012). Potential invasion of non-zoonotic VVD (only affect animals, not human beings) is of concern. For example, the world has recently witnessed the emergence and spread of a tick-borne VVD, that is, the outbreak of bluetongue, which currently affects sheep, goats, and cattle (Institute of Medicine of the National Academies, 2008).

1.2.3 Factors that affect the transmission

The epidemiology of VVD is influenced by the probability of contact between the vectors, the human population, and, for many viruses, the amplifying hosts, whether birds (most arboviral encephalitis), monkeys (YF virus), or rodents (hemorrhagic fever), which serve as reservoirs for the viruses. Like other infectious diseases, the transmission of VVD is influenced by social, economic, and environmental factors (Figure 1.1).

It is well established that climate is an important determinant of the spatial and temporal distribution of vectors and viruses (Bezirtzoglou et al., 2011; Slenning, 2010). The interplay of climate, vector, and host significantly influences the transmission of VVD (Sellers, 1980). Climate conditions affect the transmission of VVD mainly in three ways: altering the distribution of vector species and their reproductive cycles; influencing the reproduction of the virus within the vector organism, known as the external incubation period (EIP); and affecting human behaviors and activity that may increase the chance of contact with infected vectors (Zhang et al., 2008).

### Table 1.1 Summary of Selected Emerging VVD and Their Vectors

<table>
<thead>
<tr>
<th>Disease</th>
<th>Type of Virus</th>
<th>Vector</th>
<th>Main Reservoir</th>
</tr>
</thead>
<tbody>
<tr>
<td>DF</td>
<td><em>Flaviviridae</em></td>
<td><em>Aedes</em> mosquitoes</td>
<td>None (humans are the only hosts)</td>
</tr>
<tr>
<td>YF</td>
<td><em>Flaviviridae</em></td>
<td><em>Ae. aegypti</em> and others, Haemagogus</td>
<td>Monkeys</td>
</tr>
<tr>
<td>JE/West Nile fever</td>
<td><em>Flaviviridae</em></td>
<td><em>Aedes</em> sp., Culex sp.</td>
<td>Birds, pigs</td>
</tr>
<tr>
<td>Chikungunya fever</td>
<td><em>Togaviridae</em></td>
<td><em>Aedes</em> mosquitoes</td>
<td>Monkeys</td>
</tr>
<tr>
<td>Ross River fever</td>
<td><em>Togaviridae</em></td>
<td><em>Aedes</em> and other mosquitoes</td>
<td>Kangaroos, wallabies</td>
</tr>
<tr>
<td>RVF</td>
<td><em>Bunyaviridae</em></td>
<td><em>Aedes</em> sp., Culex sp.</td>
<td>Sheep, cattle</td>
</tr>
<tr>
<td>OHF</td>
<td><em>Flaviviridae</em></td>
<td>Ticks (<em>Dermacentor</em>)</td>
<td>Field mouse</td>
</tr>
<tr>
<td>CCHF</td>
<td><em>Bunyaviridae</em></td>
<td>Ticks (<em>Hyalomma</em>)</td>
<td>Birds, crows, cows, ostriches</td>
</tr>
</tbody>
</table>

*Source:* Modified from WHO (2012a, b).
Some emerging and reemerging VVD have been selected for discussion in this chapter with a focus on their epidemiology and the association with climatic variability and climate change. These are DF, YF, several types of viral encephalitis, Ross River fever, Barmah Forest virus (BFV) disease, chikungunya fever, RVF, Omsk hemorrhagic fever (OHF), and Crimean–Congo hemorrhagic fever (CCHF). Findings from both historical data analyses and projective modelings indicate an increasing number of cases and expanding epidemic areas with projected climate change scenarios.

### 1.3.1 Dengue fever

Dengue is the most common arboviral infection in the world (Rezza, 2012). The disease, caused by the four dengue virus serotypes, ranges from asymptomatic infection, undifferentiated fever, and DF to severe dengue hemorrhagic fever (DHF) with or without shock. Symptoms may include fever, chills, and joint pain. It can be diagnosed by laboratory testing for virus isolation, viral antigen detection, or specific antibodies (serology). During the last 25 years, there have been increasing reports of dengue infection with unusual manifestations (Pancharoen et al., 2002). Great efforts are being made to understand the pathogenesis of this disease in order to develop a safe and effective dengue vaccine.

Dengue is transmitted by several species of mosquitoes within the genus *Aedes*, principally *Aedes aegypti*. *Ae. aegypti* has adapted well to urban environmental conditions...
such as poor housing, overcrowding, and inadequate sanitation, indicating the persistence of this species in regions with lower socioeconomic status, due to the close association between *Ae. aegypti*, humans, and the environment (Jansen and Beebe, 2010). The resilient vector may be a reason for the observed reemerging of dengue around the world (Bangs et al., 2007; Phillips, 2008; Rezza, 2012). Figure 1.2 shows the reemerging of dengue in the Americas following a successful hemispheric eradication campaign during the 1950s and 1960s (CDC).

The association between climatic variables and DF has been documented worldwide, indicating a positive relationship between notified cases and increasing temperature (Banu et al., 2011; Johansson et al., 2009; Patz et al., 1998; Russell et al., 2009; Vezzani and Carbajo, 2008). Climate change, in particular a warming climate, along with globalization and international traveling, may broaden the transmission range for *Ae. aegypti*. Accordingly, a slight increase in temperatures could result in epidemics of dengue in the world. But the vector population may develop independently from rainfall (Pontes et al., 2000), which could be due to the characteristics of the vector, *Ae. aegypti*, in the urban environment. Using logistic regression analysis, Hales et al. (2002) found that the annual vapor pressure (humidity) was the most important indicator of DF outbreak globally. This study was the only one to point out the very important effect of vapor pressure on dengue transmission, which indicated that the incidence of DF for the people living in humid areas could be 30% higher than people living in areas with less humidity (odds ratio 1.3). Recently, a series of papers studying the association between climatic factors and dengue have been published, which suggest a nonstationary influence (not with a single trend or a stable pattern) of climatic situation on dengue epidemics in Thailand (Nagao et al., 2012).

Projective modelings also provide evidence of potential expanding of DF to nonendemic areas. Globally, it is suggested that climate change could increase the number of people living in areas of higher dengue risk, from 1.5 billion in 1990 to about 50–60% of the global population by 2085 (Hales et al., 2002). It is estimated that there might be a dengue threat for southern parts of Australia where there have been no previous outbreaks, which may lead to 1.6 million people living in northern Australia at risk of dengue infection by 2050, due to the southwest expanding of suitable conditions for the transmission (Russell et al., 2005) (Figure 1.3).
Figure 1.3. Areas at risk of dengue transmission. Source: Image from WHO. For color detail, please see color plate section.
1.3 ASSOCIATION BETWEEN CLIMATIC VARIABLES AND EMERGING VVD

1.3.2 Yellow fever

Yellow fever is a viral disease transmitted by infected mosquitoes from, principally, *Aedes* and *Haemagogus* mosquito species. Yellow fever varies in severity with some mild symptoms as fever, headache, chills, and back pain. Severe patients may have yellow coloring of the skin and kidney and liver function failure (Bell, 2007). Although safe and effective vaccination is available, there are an estimated 200,000 cases of YF, causing 30,000 deaths worldwide each year. When epidemics occur in unvaccinated populations, case-fatality rates may exceed 50% (WHO, 2011). The true number of cases is estimated to be 10–250 times what is now being reported due to underreporting.

Yellow fever is endemic in tropical and subtropical regions in African and Central/South American countries. The World Health Organization (WHO) has highlighted a greater risk of international spread of YF than in previous years (WHO, 2011). Historically, YF was once common in the United States but is no longer present mainly due to quarantine and mosquito control and improvements in living standards. However, the virus has the potential to spread to Asia and the Pacific, and the United States and Europe could expect a dramatic increase in imported YF cases for the same reasons as those applying to DF (Gubler et al., 2001). The tremendous growth in international travel as well as increasing temperature and rainfall will increase the risk of importation of YF in the United States (Monath and Cetron, 2002). The invasive YF mosquito species in Europe raised the concern of the potential risk of YF (Scholte et al., 2010). Although the disease has never been reported in Asia, the region is at risk due to the presence of the conditions required for transmission.

The number of YF cases has increased over the past two decades due to declining population immunity to infection, deforestation, urbanization, population movements, and climate change. Climate change will likely further exacerbate inequality in global health due to the potential to exacerbate endemic YF in developing countries, for example, India, where there is poor environmental sanitation, malnutrition, and a shortage of drinking water (Bush et al., 2011). Increasing temperature and rainfall were associated with the outbreak of YF in Brazil in 2000 (Vasconcelos et al., 2001). Concern regarding the reemergence of YF has risen in Brazil because of the large susceptible human population; high prevalence of vectors and primary hosts (monkeys); favorable climate conditions, especially increased rainfall; emergence of a new genetic lineage; and circulation of people and/or monkeys infected with the virus (Vasconcelos, 2010).

1.3.3 Viral encephalitis: Japanese encephalitis, Murray Valley encephalitis, and West Nile encephalitis

Like dengue virus, JE virus (endemic throughout Asia and the Pacific), Murray Valley encephalitis virus (mainly in northern Australia), and West Nile virus (spread in Africa, Europe, the Middle East, west and central Asia, Oceania, and, most recently, North America) are of the family *Flaviviridae* (Endy and Nisalak, 2002). Encephalitis (inflammation of the brain) is the most severe neurological symptom of these virus infections, although many may be asymptomatic. The viral encephalitis diseases are transmitted by mosquitoes, but the infected mosquito species vary according to geographical area, for examples, *Culex pipiens* in East United States and *Culex tritaeniorhynchus* in Asia. Birds are the main reservoir of these viruses. In recent years, these diseases have extended beyond their traditionally recognized boundaries. For example, outbreaks of JE occurred in the Torres Strait and north Queensland (Australia) in 1995 and 1998, and West
Nile virus epidemics recently occurred in America and Europe (Monaco et al., 2011; Reisen et al., 2008; van den Hurk et al., 2010).

The threats posed by the importation of exotic arboviruses, the introduction of exotic mosquitoes and reservoirs, and the potential geographic expansion of key local vectors are of great concern to public health. Climate change and anthropogenic influences provide additional uncertainty regarding the future health burden of viral encephalitis. Studies on JE indicate that increasing rainfall and temperature may bring more cases and high humidity may reduce the health burden in India (Murty et al., 2010). In China, it is suggested that the transmission of JE in both rural and urban areas may be affected by temperatures, rainfall, humidity, and air pressure with a threshold temperature of 21.0–25.2 °C and a lagged effect of 1–2 months (Bi et al., 2003, 2007). Incorporating variables for mosquito density, seasonal factors, and density of pigs (which are reservoir for the virus) can be of assistance in forecasting JE epidemics in Taiwan (Hsu et al., 2008).

There are very limited studies on the impact of climate variation on Murray Valley encephalitis virus in Australia, necessitating the need for analysis to prevent future potential risks relevant to climate change. Retrospective analysis of the epidemics of Murray Valley encephalitis in southern Australia during 1951 and 1974 indicated that mosquito longevity, extrinsic incubation period, and duration of the feeding cycle were the most important variables predisposing rapid amplification (Kay et al., 1987). Evidence also suggests that an early warning system for Murray Valley encephalitis could be effective when considering patterns of the Southern Oscillation, a synthetic indicator of climate change (Nicholls, 1986).

The relationship between climate variables and West Nile infection is not well understood. However, recent outbreaks with severe cases of West Nile encephalitis in America and European countries have led to more studies in this field. In New York, specific favorable weather conditions, for example, wet winter, warm and wet spring conditions, and dry summer, are associated with the increased local prevalence of West Nile virus among Culex mosquitoes (Shaman et al., 2011). Studies in other U.S. states have suggested that temperature and low precipitation alone are strong predictors of Culex vector population growth and more effective early warning systems can be achieved by including climate variables (Deichmeister and Telang, 2011; Liu et al., 2009; Ruiz et al., 2010). In 2009, an expansion of West Nile virus into the Canadian province of British Columbia was detected, and analysis shows that the establishment and amplification of West Nile virus in this region was likely facilitated by above-average nightly temperatures and a rapid accumulation of hot days in late summer (Roth et al., 2010). Expert opinions are consistent that climate change is predicted to increase the risk of incursion of vectors for West Nile virus infections in Canada (Gale et al., 2010). Analysis of the reemerging of West Nile infection in Russia in 2007 revealed the climate conditions favorable for the epidemic in mild winters and hot summers (Platonov et al., 2008). In addition, great concern of the potential risk of West Nile encephalitis for other countries has risen due to the changing climate and environment that are conducive to the vectors and reservoirs (van den Hurk et al., 2010).

1.3.4 Ross River fever and Barmah Forest fever

Ross River fever, caused by infection with Ross River virus (RRV), is the most common mosquito-borne disease in Australia. There have been more than 41 000 notified cases during the last decade with the most serious situation occurring in 1996. The RRV causes a flu-like illness with joint pains, rash, and fever in approximately 30% of infected people 3–11 days after being infected. The vertebrate reservoir hosts of RRV could include
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Marsupials, placental mammals and birds, kangaroos, horses, and rats. There are over 40 species of mosquito vectors, with *Aedes vigilax*, *Aedes camptorhynchus* (saltmarsh along coastline), and *Culex annulirostris* (inland) being the most important (McMichael et al., 2003). Peak incidence of the disease is through the summer and autumn months, when the mosquito vectors are most abundant. Most affected people are middle aged and there seems to be no gender difference.

Barmah Forest virus and RRV demonstrate many similarities in disease symptoms and seasonal distribution (Flexman et al., 1998). They are both characterized by arthralgia, arthritis, and myalgia, often accompanied by fever and rash. Arthritis is more common and more prominent in RRV infection, and rash is more common and florid with BFV infection. These symptoms may continue for at least 6 months in up to 50% of patients with RRV, but in only about 10% of patients with BFV. Both diseases can be confirmed by serological tests. However, BFV infection has not yet been as intensively studied as RRV (Jacups et al., 2008a, b).

Studies suggest that climate variables, for example, temperature, rainfall, level of river flow, and sea level, are related to the transmission of Ross River fever, but associations vary in different regions due to different vector species and ecological situations (Bi et al., 2009; Tong et al., 2002, 2005, 2008). It has been suggested that climate variability might be a contributor to the spatial change of the disease in Queensland, Australia, over the period from 1985 to 1996 (Tong et al., 2001). The response of RRV to climate variability between coastline and inland regions is also different (Tong and Hu, 2002). A recent study in Queensland confirmed the various associations, depending on different environmental conditions (Gatton et al., 2005). Kelly-Hope et al. found that the environmental risks of RRV outbreaks varied among different regions throughout Australia and that the Southern Oscillation Index (SOI) could be a predictor only for the southeast temperate region (Kelly-Hope et al., 2004). Projections of RRV epidemics from regional weather data were conducted in different areas in Australia, demonstrating high accuracy of early warning models that combined data on local patterns of climate change and mosquitoes (Woodruff et al., 2002). In Western Australia, predicted climatic changes, especially rising sea level and greater rainfall and flooding, might significantly increase RRV activity (Lindsay et al., 1996). In Darwin, a model that included rainfall, minimum temperature, and three mosquito species was proven to have the best accuracy of disease prediction that could explain 63.5% model fit (Jacups et al., 2008a, b).

Projected various ecological scenarios could result in the transmission of RRV infection being different across Australia. Recent outbreaks of RRV in the state of Victoria suggest an increasing risk in southern Australia due to increasing global temperatures. Therefore, it would be useful to generate a complete map of the vulnerability of RRV infection by systematic ecological studies across the whole of Australia, noting the relationship between environmental factors and RRV, which will lead to a better understanding of RRV transmission and control strategies.

1.3.5 Chikungunya fever

Similar to RRV and BFV, chikungunya virus is an alphavirus, first identified in an outbreak in southern Tanzania in 1952. Characterized by sudden onset of fever and severe joint pain, symptoms are very similar to those of dengue but, unlike dengue, there is no hemorrhagic or shock syndrome form (Kamath et al., 2006). There is currently no specific treatment and no vaccine available for this disease. Both *Ae. aegypti* and *Aedes albopictus* mosquitoes have been implicated in large outbreaks of chikungunya. Whereas *Ae. aegypti* is confined
within the tropics and subtropics, *Ae. albopictus* spreads in temperature areas. *Ae. albopictus* is generally considered to have a low vectorial capacity because of its lack of host specificity. Nevertheless, *Ae. albopictus* is abundant in rural and urban areas due to the diversity of the habitats (Delatte et al., 2008).

Chikungunya fever cases once occurred only in Africa, Asia, and the Indian subcontinent. However, there has recently been emergence of chikungunya globally, with thousands of people affected in Singapore, Malaysia, Thailand, and the Republic of the Congo (Kelvin, 2011; Pulmanausahakul et al., 2011). The major outbreak in 2005 in India resulted in a large number of imported cases in 2006 in Europe, and local transmission was first identified in Italy in 2007 (WHO, 2008).

In addition to the result of viral genetic mutations leading to the adaptation of new vector hosts and insecticide resistance, the rapid global spread may also be attributed to climate change. The relationship between climate change and reemerging of chikungunya has been reviewed in India, indicating potential risk of increased disease burden associated with changed patterns of temperature and rainfall (Dhiman et al., 2010). Using geographic information system (GIS) techniques, the investigation of the 2008/2009 incidence of chikungunya suggested that the direction of the outbreaks moved from south to north with a median speed of 7.5 km per week and the number of cases increased after 6 weeks of increasing cumulative rainfall with variation of average daily temperatures (23.7–30.7 °C) (Ditsuwan et al., 2011). Climate change that shortens the extrinsic incubation period was also considered as one of the drivers for an outbreak in Italy in 2007, the first large outbreak documented in a temperate climate country (Bezirtzoglou et al., 2011; Poletti et al., 2011). Hence, there is an increasing risk of tropical VVD in temperate climate countries, as a consequence of globalization and a changing climate.

### 1.3.6 Rift Valley fever

Rift Valley fever is caused by Rift Valley virus affecting humans and a wide range of animals. Infected patients usually suffer from only a mild illness with fever, headache, myalgia, and liver abnormalities. Outbreaks of RVF have occurred across Africa. Since the outbreak in Kenya/Tanzania in 1997–1998 when the Rift Valley virus claimed over 400 deaths, outbreaks in 2000 in Yemen and Saudi Arabia, 2007 in Kenya/Tanzania/Somalia, and 2008 in Sudan/Madagascar and South Africa have caused nearly 1000 deaths (WHO, 2010). The outbreak in 2000 marked the first reported occurrence of the disease outside the African continent and raised concerns that it could extend to other parts of Asia and Europe (Gale et al., 2010). With *Aedes* and *Culex* mosquitoes as major vectors, RVF virus has the potential to infect a wide range of vectors, for example, ticks and flies, unlike the majority of arboviruses that tend to be adapted to a narrow range of vectors (Pepin et al., 2010). Different species of vectors can play different roles in sustaining the transmission of the virus.

Although research on the association between climate change and RVF is limited, it is likely that the geography of RVF and the vectors will be altered by climate change and extreme weather events that will create the necessary conditions for RVF to expand its geographical range northward and cross the Mediterranean and Arabian seas (Martin et al., 2008). Consistent findings indicate that increasing rainfall, especially heavy rainfall events, is closely related to the outbreaks of RVF in Africa, Saudi Arabia, and Yemen (Andriamandimby et al., 2010; Hightower et al., 2012). A study in Senegal using remote-sensing techniques that simply relied upon rainfall distribution provided a new approach to enhance early warning systems for RVF based on both natural and anthropogenic climatic
1.3 ASSOCIATION BETWEEN CLIMATIC VARIABLES AND EMERGING VVD

and environmental changes (Tourre et al., 2009). These findings will assist the development of forecasting models and early warning systems for RVF using climate forecasting data so as to better predict and respond to RVF outbreaks in Africa and other regions.

1.3.7 Omsk hemorrhagic fever and Crimean–Congo hemorrhagic fever

Omsk hemorrhagic fever (OHF) and Crimean–Congo hemorrhagic fever (CCHF) are tick-borne viral diseases. Omsk hemorrhagic fever virus is a member of the family Bunyaviridae, while CCHF virus is of the family Flaviviridae (Bajpai and Nadkar, 2011; Ruzek et al., 2010). They have symptoms of viral hemorrhagic fever but CCHF has a shorter incubation period (1–3 days) after tick bite than OHF (3–7 days). Specific symptoms for viral hemorrhagic fever vary, but initial signs often include marked fever, fatigue, dizziness, muscle aches, loss of strength, and exhaustion. Severe cases often show symptoms of bleeding under the skin, in internal organs, or from body orifices, for example, the mouth, eyes, or ears.

Omsk hemorrhagic fever has only been notified in Russia so far. Since the first description of OHF in the 1940s in Siberia, the clinical course, pathology, and epidemiology of the disease, as well as the ecology of the virus, vectors, and natural hosts (rodents), have been studied extensively, although English studies are scarce (Ruzek et al., 2010). Given the lack of a specific treatment or vaccine against OHF virus, elimination of wild rodents is a basic approach to reduce the disease burden. The morbidity from OHF has two seasonal peaks (autumn and winter, being the hunting seasons of muskrats) that correlate with activity of muskrats. There were outbreaks of OHF in the early 1990s after remarkably decreased incidence in 1970s and severe and fatal cases in 1998. As a family of tick-borne flaviviral disease, the transmission of OHF virus, like other vector-borne agents, is affected by a range of factors, including changes in climate and ecology. Climate conditions that favor the activities of muskrats and OHF ticks have not been studied. The reemergence of OHF in Russia is, nevertheless, an example of a human disease that emerged owing to human-mediated disturbance of an ecological function. Therefore, further research is necessary for a better understanding of the climatic factors that may contribute to the reemergence of OHF in Russia and other regions.

Crimean–Congo hemorrhagic fever is a severe disease in humans, with a high mortality rate. Treatment can be with antiviral agents such as ribavirin. However, review of ribavirin for patients with CCHF found that data are inadequate to support its efficacy in CCHF (Ascioglu et al., 2011). Crimean–Congo hemorrhagic fever is now endemic in many countries in Africa, Asia, and Europe and continues to emerge. The geographical distribution of the CCHF virus is widespread around the world (Leblebicioglu, 2010). Since the first disease was described in the Crimea in 1944 and later in 1956 in the Congo, the disease incidence has dropped significantly due to increasing living standards. However, reports of sporadic cases and outbreaks have recently increased significantly since 2000. In Turkey, the annual number of reported CCHF cases increased dramatically from 17 in 2002 to 1315 cases in 2008 and 1318 in 2009 (Yilmaz et al., 2009). In 2010/2011, outbreaks with severe and fatal cases were reported in Pakistan and India.

There is a strong need to better understand the underlying reasons of the reemergence of CCHF in different regions. Potential reasons for the emergence or reemergence of CCHF include climate changes, which may have a significant impact on the reproduction rate of the vector (Hyalomma ticks), as well as anthropogenic factors (Maltezou and Papa, 2010). A possible picture of the interaction among the potential factors for the emergence of
CCHF may include climate and other environmental change, migratory birds, increase in tick density, livestock movement, and increase in host animals (Leblebicioglu, 2010). Nevertheless, the association between climate change and CCHF, the virus, and its reservoir is not clear at all. Tick-borne disease has already been labeled as a “clear and present danger in Europe,” and the probability of CCHF extending to other countries around the Mediterranean basin suggests that veterinarian and human surveillance should be enhanced (Chinkar et al., 2010; Heyman et al., 2010).

1.4 Invasion of Nonzoonotic VVD to Humans

There are some nonzoonotic VVD, such as bluetongue, currently only affecting animals (e.g., sheep, goats, cattle) but not human beings. Recent emergence of bluetongue, an arthropod-borne viral disease of both domestic and wild ruminants in Europe, has raised concerns for the increasing risk to livestock and potential threats to humans. Bluetongue is widely distributed in Australia, the United States, Africa, the Middle East, Asia, and Europe, and the virulence of different strains of the virus varies considerably across countries (Maclachlan, 2011). However, disease invasion, that is, the emergence of a pathogen into a new host species, may happen in the future because of increased contact between humans and wildlife and potential unexpected impacts of a changing environment/climate on genetic mutations of the serotypes of these viruses (Daszak et al., 2001). Reasons for the spread are complex and the role changes in climate patterns and landscapes play is unclear, although increasing temperature and other meteorological variables may extend existing spatial and vector transmission models (Maclachlan, 2010). Surveillance for the vectors and vulnerable animals should be strengthened to ensure closer monitoring and better prediction of these diseases. This may avoid any unexpected transmission to humans within a changing world (Tabachnick, 2010).

1.5 Implications and Recommendations for Prevention and Control

Despite a century of success in prevention and control efforts, infectious diseases remain a major challenge to public health around the world. Effective detection and control of VVD requires an integrated system that can provide effective early warning of an epidemic activity (Britch et al., 2008). It should also be built on a comprehensive surveillance system including diagnosis for VVD. In recent years, landscape epidemiology has used satellite remote sensing and GIS to develop predictive modelings that allow for incorporation with spatial and temporal climatic patterns that may influence the intensity of a vector-borne disease and predict risk conditions associated with future potential epidemics (Pinzon et al., 2005).

Some efforts to control VVD focus on one aspect of the epiregion, for example, vaccination for certain viruses. Fortunately, effective and safe vaccination is already available or will hopefully be available in the next 5 years for some important VVD, for example, dengue and JE, tick-borne encephalitis, and YF (WHO, 2012a, b). Regardless of this, there has still been an observed increase or expansion of some of those diseases, for example, JE in Australasia. The vertebrate host and/or reservoir may also be the target for control measures. Reduction of vectors, such as control for mosquitoes and flies, has been proven to be a cost-effective public health method to reduce the risk of vector-borne disease.
in some areas (Tomerini et al., 2011). By recognizing the complex role of vector ecology that affects the transmission of vector-borne diseases, the WHO is calling for integrated vector management with cross-sectoral collaboration (WHO, 2012a, b).

It is clear that factors affecting the transmission of VVD, including the vectors, the viruses, and human beings, are influenced by a range of factors including climate variations and changes. Therefore, integrated approaches with considerations of the changing environment should be adopted to allow for climate-based health monitoring systems to respond to the emergence and reemergence of VVD around the world.

Some recommendations have been articulated in the following text:

- **Development of comprehensive surveillance strategies for new vectors and viruses, incorporating the ecoclimatic conditions associated with VVD**
  Given that climate variables, for example, maximum and minimum temperatures, rainfall, humidity, and El Niño events, are drivers for emerging and reemerging VVD, it is expected that early warning systems that include local meteorological variables would be useful in predicting future risks of VVD. In addition, the various types of vectors and complicated transmission routes from the viruses to the infection of human beings and integrated surveillance systems that monitor the activities of the virus inside the major vectors and host animals are key for VVD prevention and control, particularly when the associations between climate change and some VVD are not fully understood.

- **Modeling and risk assessments for future vulnerability**
  With the increasing concern of the projected global climate change and extreme weather events, the key questions for infectious disease prevention and control are “what is the vulnerability map?” for example, “who will be the most affected?” and “where would be the most affected regions?” Suitable time-series statistical methods (e.g., the seasonal autoregressive integrated moving average model) could be used to quantify the relationship between weather variables and the VVD because these models have intrinsic functions that can be used to effectively control for the autocorrelations, seasonal variations, any long-term trend, and lagged effects, to make the results of environmental health risk assessments more valid and reliable (Bi et al., 2001). In addition, the burden of disease attributed to future climate change or variations can be estimated to inform evidence-based decision and policy making.

- **Collective endeavor for the development of laboratory techniques for virus diagnosis and vaccines**
  Accurate and early diagnosis of VVD is the strong basis of an effective disease surveillance system. Due to the huge amount of money needed to develop new effective and safe vaccines and laboratory technologies, governments and other stakeholders need to endeavor to allocate enough research and development funding to fill the gaps in current clinical and epidemiological research. This will help to ensure adequate preparedness for future risks of VVD.

- **Identification of adaptive needs of society in different geographical areas so as to plan public health preparedness**
  Better adaptation to projected climate change and extreme weather events should be taken, with consideration of the local climate and geographic situation. For example, people living in temperate low-lying locations need be warned about possible risks of VVD that may not have been a public health concern previously and informed about adaptation strategies (e.g., using insect repellent and avoiding intensive
contact with certain wild animals) when unusual or extreme weather events are projected. The importance of public health education and health promotion in the community should be fully recognized in order to have better preparedness for public health emergencies.

- **Necessity of international and intersectoral cooperation**

  The spread of infectious diseases today is faster than ever in our “global village.” When we humans are enjoying the increasing freedom of international travel, the viruses, vectors, and host animals also take advantage of this, making VVD prevention and control very challenging. Collaborations are often required beyond the health sector (e.g., environment sector, export/import economic sector, agriculture sector) and across borders of countries. Coordination by global leaders at high levels of government could certainly assist the WHO in preventing occurrences of VVD pandemics.

In summary, recognizing the complexity of the transmission of VVD, climate change may play a role in the emerging and reemerging of VVD around the world. Integrated prevention and control measures of the VVD should consider global climate change and local weather patterns to minimize projected adverse impacts on human health and society.

**REFERENCES**


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