

Impact of Climate Change on Infectious Diseases

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Abstract

Global climate change is a common phenomenon today. It is mainly caused by increasing greenhouse gas emissions. It has been proven that global climate change affect the emergence and spread of infectious diseases. This applies to both climate change as a whole, as well as individual factors such as temperature, rainfall, humidity, etc. These changes may directly impact the pathogen, and indirectly the vectors of these pathogens. They can also affect the resistance of humans and animals. The association between the emergence of infectious disease outbreaks and global climate change was also shown. This problem should be taken seriously when considering the development of effective prevention programs.

Keywords: climate change, pathogens, vectors, infectious diseases

Introduction

The global climate system has been stable for centuries due to heterogeneous interactions between the atmosphere, oceans, ice core, biosphere, and solar energy [1]. Currently, a phenomenon of gradual global warming caused by increasing greenhouse gas emissions has been observed. During the 20th century, the global surface temperature increased by approximately 0.3-0.6°C [2], which proves the anthropogenic origin of these changes [3]. Global warming and extreme weather events can have a significant impact on the hydrological cycle (heavy rain, flooding, severe storms, heat waves, droughts, shortages of fresh water), and is considered to be a major threat to the biosphere (deforestation, desertification, reduction in the area of coral reefs) [4].

Climate is an important factor affecting human health, exerting an influence on the incidence of infectious diseases, as well as time and intensity of the epidemic emergence [1]. Long-term warming trends encourage geographic expansion of dangerous threats such as malaria [1], while extreme weather events affect the outbreaks [5]. Global warming and instability of the climate play an increasingly

important role in stimulating the global emergence, resurgence and transmission of infectious diseases [6].

Since 1975 the World Health Organization has reported the occurrence of more than 30 new diseases, including AIDS, Ebola, Lyme disease, legionellosis, enterohemorrhagic colitis, and new hantavirus diseases [7]. The resurgence of old diseases such as malaria, tuberculosis, and cholera also has been reported [7]. Declining social conditions and suspension of public health programs has caused more intense disease transmissions from human to human (e.g. tuberculosis, diphtheria). Transmission of infections involving two or more species (mosquitoes, ticks, deer, birds, rodents, and humans) reflects changes in social (suburban sprawl), ecological, and climatic conditions [1].

Climate change is inherently linked to globalization, which is caused by a reduction of many barriers in international relations, so that the globe becomes a space where the boundaries between people, countries, and regions are fading [8, 9]. According to Scholte [8], global relations are formed by social interaction and relationships that exceed the geographical territories. Globalization is driven and enforced by many factors: economic processes, technological development, political influence, cultural and value systems, and natural and social environmental factors. These various factors, being a part of the globalization

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process, directly and indirectly affect health on many different levels [10]. Progressive climate change, a decrease of stratospheric ozone layer, pandemics, and the loss of biodiversity constitute major problems worldwide.

Climate and Pathogens

The most important environmental factors affecting the pathogens are temperature, humidity, and CO₂ level. It was found that the fungi causing plant diseases show better growth at moderate temperature ranges. In temperate climates characterized by seasonally low average temperatures, longer periods of temperatures suitable for pathogen growth may occur due to climate warming. The earlier onset of higher temperatures may lead to greater risks of fungal infections with a tendency to cause epidemic outbreaks and increased usage of fungicides [11].

Humidity can affect the microorganisms in different ways. Some of them tend to be more invasive for the hosts in increased humidity, while others develop better in lower humidity. More frequent and abundant rainfalls, with increasing temperature and higher concentrations of water vapor, will cause favorable conditions for the development of infectious diseases [11].

Increasing CO₂ concentrations may affect the development of pathogens in several ways. It was shown that microbial growth can be stimulated by higher CO₂ concentrations, contributing to more intensive fungal spore production. However, increasing CO₂ levels also can cause physiological changes in the host organism, which may increase its resistance to pathogens [12, 13].

Global climate change may also affect the microbial evolution and their stress response, as well as the emergence of new germs. Over a long period of time, many bacteria have developed mechanisms allowing them to survive and even grow in the unfavorable stress conditions. Stress responses are determined genetically and, in many cases, the initial exposure to sublethal doses of stressors affect adaptation of bacterial cells to unfavorable conditions. This has been well proven in the case of *E. coli* O157: H7, which is able to survive in acidic conditions at pH 2, after its previous exposure to pH 5. Organisms acquiring higher tolerance after the initial exposure to sublethal doses of the agent often become more resistant to other types of stress [14], and therefore climate-induced changes in intrinsic factors may induce stress responses, making the bacteria more resistant. It is thought that gene transfers between related and unrelated bacterial species may be facilitated, because many species occur in large and diverse communities in which a horizontal gene transfer can take place, often through bacteriophages. For example, non-toxigenic *V. cholerae* strains may acquire the genes encoding cholera toxin from bacteriophage naturally occurring in the environment [15]. The processes of infection with bacteriophages, as well as induction of prophages, may be susceptible to environmental factors (temperature, sunlight, and pH) [16], which means that environmental changes can have a significant impact on pathogen growth and virulence.

Most *V. cholerae* strains isolated from the environment have lost genes necessary for cholera toxin (CT) production, but can acquire them back from the environment, which leads to the emergence of new toxigenic clones of this bacterium. Gene transfer also contributes to the emergence of antibiotic resistance, which may also be linked to environmental conditions. The organisms with a very short life cycle respond to environmental changes rapidly so, for example, bacteria whose life cycle is measured in minutes can respond to changes over months or years. The best known example is the emergence of MRSA (methicillin-resistant *Staphylococcus aureus*), which was first discovered in 1961, whereas methicillin was discovered in 1959. Organisms with longer lifecycles (plants and animals) adapt more slowly to the newly formed conditions [13]. It was shown that climate and environmental changes affect the pathogens, making them able to survive in soil and water, and therefore contributing to the infection sources of drinking water. Genomic changes in *E. coli* O157: H7 have influenced the development of tolerance to a more acidic environment, so bacteria can easily overcome the gastric barrier of humans and animals, and hence contaminate drinking water systems and agricultural fields [17]. Climate change may also affect the emergence of the agents causing infectious diseases. For example, food-borne pathogens (*Salmonella*, *Campylobacter*, rotavirus, *Vibrio cholerae*) may reemerge in the population by increasing their frequency of occurrence and enlargement of their geographical coverage [15].

Climate and Vectors

In recent years an increase in human exposure to vector-borne diseases has been observed [10]. Due to increases in global temperature, tropical insects can expand their territories to further (northern or southern) latitudes, and find living conditions at higher altitudes that affect the transmission of local viral pathogens [4, 18].

During the past 50 years patterns of the emergence of arbovirus diseases have changed significantly. Climate is the major factor contributing to i.a. the geographical and temporal distribution of arthropods, their life cycle, their spread to vertebrates and the evolution of arboviruses. Under the influence of rising temperatures and rainfalls, as well as changes in natural cycles that stabilize the climate, arboviruses may emerge on entirely new territories [19].

In 1999 there was an epidemic of West Nile fever (WNF) in southern Russia (over 500 cases in the Volgograd Province). In 2000-04 WNF incidence decreased to zero, whereby the next epidemic occurred in 2007 (64 cases). Historical climate data analysis for the Volgograd from 1900 until today showed that the years 1999 and 2007 were among the warmest, due to very mild winters [20]. WN virus was recently introduced into North America, where it was first detected in 1999 in New York. Phylogenetic studies have shown the presence of two main lineages of WN strains, among which are strains from the lineage I, present in Africa, India, and Australia, were found to be responsible for epidemics in Europe and the Mediterranean basin, while

the strains from lineage II were previously detected only in sub-Saharan Africa [21]. In 2000 in Israel, the increased number of WNF cases was predominantly caused by extreme temperatures rather than high air humidity [21]. The potential occurrence of WNF in the UK is nowadays greatly considered due to the presence of mosquito species such as: *Culex pipiens*, *Culiseta annulata*, and *Aedes cinereus*. [23]. Global warming may lead to changes in distribution patterns of West Nile virus vectors (e.g. *Cx. tarsalis*) toward higher altitudes, as observed in Colorado [24].

WNF epidemics in poultry farms, as well as human infections, were observed in Hungary after 2004 [25]. Since cross-protection is limited between Flaviviruses, the risk of clinical symptoms should be taken into account in relation to climate changes [26]. The temperature rise is an important factor, because the viruses can replicate in mosquito cells only at temperatures above 20°C [27]. Thus, the risk of viral infections will increase with the rising temperature of the environment.

Dengue virus in Australia is currently limited to Queensland, where it occurs in ticks from *Aedes aegypti* species. It is predicted that the transmission of Dengue virus to the Mediterranean countries will be possible due to global climate change [28, 29].

Climate change may also affect the incidence of infectious diseases in Arctic regions. Higher ambient temperatures in the Arctic may cause an increased incidence of food-borne infection. The increase in average temperature can also affect the incidence of animal infectious diseases, spreading to humans (zoonoses) by altering the range of animal hosts and insect vectors [30]. It has been suggested that immunosuppressed patients might be the source of exotic viral infections [31].

Through the surveillance of vector-borne diseases in Germany, the accurate detection of spatial and temporal changes of indigenous and imported infection (Hantavirus infection, Chikungunya fever – most recently appearing in Europe, and Dengue fever) is possible. From 2001 to 2007, 3005 symptomatic hantavirus infections, 85 cases of chikungunya fever, and 1,048 cases of dengue fever (2002-07) were reported. The geographic source of hantavirus infection was reported in 95.5% of all cases (compared with 98.4% of dengue virus and 100% of chikungunya virus). In 2007 there was a significant increase in cases of hantavirus disease, mainly in endemic areas. In 2006, imported cases of chikungunya fever came primarily from several islands of the Indian Ocean, while the majority of reported cases in 2007 was imported from India.

The reported number of Dengue fever cases in the world has increased since 2004, wherein the largest percentage of cases of this disease were reported in Thailand (17-43% in single years), followed by India, Brazil, and Indonesia [32].

Epidemics of Nephropathia epidemica (NE), caused by Puumala bunyavirus, were preceded by an abundant seed production by trees (supposedly caused by specific weather conditions) and related maximum abundance of bank vole (*Myodes glareolus*), which is a known reservoir of this virus.

It was found that high temperatures in summer and autumn are associated with a high incidence of NE. Future climate change projections predict warmer temperatures in Europe, therefore bunyavirus Puumala infections in humans may constitute a high risk [33]. This family of rodent-borne hantaviruses, can also be considered as a potential biological weapon [34].

Bluetongue disease (BT) occurs in ruminants and is caused by bluetongue virus (BTV), which is transmitted by insects of the genus *Culicoides*. Historically, BT outbreaks in Europe were rare and short-term [35]. However, during the last 10 years BT has been noted in southern Europe and from 2006 it began to be observed in northern Europe. There is a lot of evidence showing the association between this phenomena and climate change [36]. For example, it was found that a range of *C. imicola* has spread to some areas due to climate change in Europe, increasing the number of *C. imicola*. The occurrence of multiple bluetongue virus strains, transmitted by mosquitoes in southern Europe since the late 1990s, indicates the impact of climate change on vector-borne diseases. Subsequent spread of the disease also depends on changes in biotic interactions of the vector and host in newly affected areas. Virus transmission by Palearctic vectors contributes to the presence of the disease in the cold and wet areas of northern and southern Europe [37].

Potential vectors of bluetongue virus are present in natural and livestock-farm habitats in the Netherlands. Under favorable climatic conditions after virus introduction, BTV could spread among animals (cattle, sheep, and goats), depending on the nature of the viral serotype [38].

Climate and Immunity

Each climate type is characterized by seasonal variability, which affects the function of human and animal immune systems. Most energy is consumed by the organism in winter. Non-tropical animals have developed physiological and behavioral mechanisms of adaptation to winter conditions. Seasonal reproduction is a major adaptation to climate change in small animals. Seasonal cycles of infectious diseases and deaths among many populations of mammals and birds have been found. Challenging winter conditions such as low average temperatures and decreased food availability may directly cause death from hypothermia, starvation, or shock. In some cases, survival in demanding winter conditions causes great physiological stress, defined as an adaptive process manifested by increased blood levels of glucocorticoids. Stress associated with energetically unfavorable conditions may also indirectly contribute to the emergence of diseases and death through inhibition of immune functions. Presumably, the increasing blood concentration of adrenocortical steroids in response to winter stressors inhibits immune function and accelerates the catabolic mechanisms. Although many data suggest that immune function and disease processes are enhanced during the winter, the reverse situation also has been observed. Inhibition of immune function occurs in some populations, especially during harsh winters with

short days. In small mammals, exposure to short days inhibits reproduction and simultaneously reduces plasma levels of prolactin and steroid hormones. It also changes the pattern of melatonin secretion. These hormones affect the immune function and influence the development of opportunistic diseases. Additionally, it appears that the secretion of prolactin and melatonin mediates the effects of photoperiod on immune function [39].

Effects of Climate on Outbreaks of Selected Endemic Diseases

The transmission of vector- and rodent-borne diseases, including malaria, Dengue fever, Ross River virus infection, and hemorrhagic fever with renal syndrome has recently been investigated [40-43]. The possibility of transmission of selected diseases to some tropical regions around Northern Australia cannot be excluded [44]. Their spread may be affected by climate change. For example a correlation between the increase in temperature, rainfalls and humidity, and the incidence of disease caused by Ross River virus (RRV) has been observed [44].

Malaria is one of the major diseases in the world, causing the deaths of 742,000 children under 5 years of age every year [45]. The disease is transmitted by mosquitoes, which breed in both fresh and brackish water. Despite attempts to control this disease, from 300 to 660 million clinical cases are reported each year and this number may still increase [45]. Out of the four species causing malaria in humans, *Plasmodium falciparum* is the most dangerous and widespread in the tropics. *P. vivax*, which is widespread in the tropics, is of slightly less significance. The problem of malaria is particularly worrying because of the rapid spread of antibiotic-resistant strains of the parasite and the possibility of untreatable forms of the disease [46].

P. vivax is better adapted to the British climate than *P. falciparum*. It requires lower temperatures (approximately 1-2°C) to develop in mosquitoes and also functions better at lower temperatures. *P. vivax* parasites, in contrast to *P. falciparum*, isolated from the liver of infected people, were able to infect new generations of mosquitoes in the spring. Although the parasites develop in mosquitoes at a temperature below 15°C, a convenient time for potential transmission in the UK occurs between June and August [46].

The risk of *vivax* malaria in the UK is modeled for *An. atroparvus*. Maps of malaria prevalence in recent years (average from 1961-90), including future climate scenarios, showed the number of months in which *vivax* malaria could persist each year in different parts of the country. For example, it could persist the longest in the southeastern area of the country (2 and 3 months), was present for 1 month in the middle areas, while in the northern parts it did not appear at all. These maps show the approximate risk, based on the influence of temperature changes on changes in the transmission process, but do not include changes in rainfall intensity, humidity, and availability of mosquito breeding sites.

Currently, the risk of malaria transmission correlates very well with previous records on the distribution of malaria in the UK [47]. All climate change scenarios show that the risk of transmission will increase in Southern England, spreading to the north, to Scotland [46]. Currently, in the southern part of the UK, only in a few months of the year, there are atmospheric conditions conducive to the transmission of *P. vivax* through local mosquitoes. As the climate warms up, the transmission conditions will become more favorable [46].

Both temperature and rate of rainfalls affect the level of malaria transmission [48]. Higher temperatures increase the rate of mosquito development, females feeding and maturation of the malaria parasites inside their bodies, but may also reduce the possibility of survival of adult mosquitoes. Rainwater provides mosquito breeding conditions and a humid environment conducive to their survival [46].

The current distribution of *falciparum* malaria is recorded with high accuracy (78%) when four climatic factors are taken into account: maximum and minimum temperature, precipitation, and water vapor pressure. According to the climate change scenario, the most significant threat to UK citizens traveling abroad is the gradual spread of malaria in the northern parts of the potential malarious areas, through Mexico until the southern states of the USA. These changes are predicted to begin in the 2050s [46].

Leishmaniasis is another important disease transmitted by the mosquito *Phlebotomus papatasi*. Results of investigations show that the distribution of *Phlebotomus papatasi* in Southwestern Asia is dependent on temperature and relative humidity [49]. Similarly, the range of areas of Chagas' disease occurrence may be increased under the influence of anthropogenically induced climate change [50].

Tick-borne diseases are another important group from the viewpoint of climate change. Lyme disease is considered the most important [51, 52], as it is the most commonly occurring vector-borne disease in the temperate zone of the northern hemisphere. There have been roughly 85,000 cases (based on available national data) every year in Europe. In the United States, from 15,000 to 20,000 cases are registered each year and the disease is endemic in 15 states [53].

Lyme disease (Lyme borreliosis – LB) is transmitted to humans by ticks of the genus *Ixodes*; in Europe mainly by *Ixodes ricinus* and to a lesser extent by *I. persulcatus* [51].

There is a broad contemporary knowledge about the effects of various climatic factors on vectors abundance and disease transmission [46, 49]. Climate determines the latitude and altitude borders of tick distribution. Daily climate conditions during several seasons (as ticks can live for more than 3 years) affect directly and indirectly the density of the tick population. *B. burgdorferi* is not usually sensitive to ambient climate conditions, with the exception of high temperatures, but human exposure to the pathogen (tick bite) can be determined by weather conditions [51].

In recent decades, ticks have spread in Europe, occupying greater latitudes (observed in Sweden) and altitudes (in the Czech Republic), where they exist in high density [54, 55]. Tick distribution and the changes in density of

their population were associated with climate change, which is among the main factors affecting the border of tick occurrence. Lindgren [56] showed that the observed distribution of ticks in the northern areas was associated with winter season, during which extremely low temperatures (below -12°C) are observed. Further south, the combination of mild winters (only a few days with minimum temperature below -7°C) and longer spring and autumn seasons (with more days having minimum temperatures of 5 to 8°C) had an impact on the increased density of ticks. The incidence of LB and other tick-borne diseases in Europe also increased during the same periods. Taking into account the existing knowledge from various fields, it is possible to create a theoretical prediction of future changes in frequency of infections in Europe. Based on the results, it seems probable that future climate change in Europe will facilitate the spread of LB at higher geographical latitudes and altitudes (mountain areas), contributing to the emergence of extended and more intensive periods of LB transmission in certain areas. The risk of LB infection will decrease in areas of recurrent drought and floods [51].

TBE (tick-borne encephalitis) is as important as LB tick-borne disease. Currently, TBE occurrence is observed mainly in some disease foci in central Europe, in the Baltic region, and the area of the entire Russian Federation [57]. Therefore, there is a real risk of infection for tourists traveling to these countries. The virus circulation depends on the specific model of tick seasonal activity [58], which occurs only in certain parts of the ticks' geographical range, where the seasonal temperature profile is typically continental (as opposed to oceanic climate characterized by high summer temperatures followed by rapid cooling in the autumn) [59]. In dry regions and other areas in which tick survival is difficult, maintenance of the TBE virus will be limited.

The predicted increase in temperature and reduction of humidity in the summer seem to gradually stimulate the distribution of TBE virus in the greater latitude and altitude in the 2020s, 2050s, and 2080s. However, high-altitude regions are not conducive to TBE virus survival. In the 2020s France, Switzerland, Slovenia, Hungary, and a great part of Austria will be free of TBE virus and the range of the virus occurrence (though not necessarily its vector) will diminish to inland regions of the Baltic states. In the 21st century, TBE will be present in areas currently free from contamination, in particular the mountains of the Polish-Slovak border and northwestern Scandinavia. Central Europe will become virtually free of TBE. This is consistent with the conclusion that rising temperatures increase the northern limit of *I. ricinus* in Sweden [56]. The final occurrence of TBE in the 2080s will be limited to a small part of Scandinavia, including new foci in Southern Finland. It is predicted that the area of TBE virus prevalence will be significantly reduced, although a few areas presently free from the pathogen may be infected – particularly the mountainous regions of the Czech Republic and Slovakia, parts of Scandinavia, and north and west of the present coastal endemic regions [51].

Avian influenza is another disease whose spread may be related to climate change. It is caused by a highly pathogenic strain of H5N1 virus (HPAI). Wild water birds are the natural reservoir of this virus. It has been shown that climate change is affecting the distribution of wild birds. For many species a northward shift in migration has been attributed to climate change [60-62]. The potential impact of climate change on increases in species diversity in northern latitudes is possible. A decrease in the number of species, and induced long-distance migration, have been observed in many cases [60]. The data on the influence of climate change on spring migration show that it occurs earlier than previously, and the impact of climate change on autumn bird migration appears to be species-specific and heterogeneous [62-64]. It has been observed that the changes in the populations of some species of water birds [65] may affect the redistribution of AI viruses in birds of different species and age groups. Extreme climate events may stimulate unusual population distribution. For example in January 2006 a mute swan population migrated to the Caspian Sea region in order to escape from the cold, possibly spreading HPAI H5N1 virus into Western Europe [66].

The breeding and wintering areas of *Anatidae* (ducks, geese, and swans) in the Western Palearctic were studied, showing the wide range of locations for summer breeding and distinct concentration of locations for winter breeding. The areas of winter breeding involved mainly the coastal areas of the North Sea and Westland shores of the Mediterranean, Black, and Caspian seas. Local food availability, weather, hunting patterns, agriculture, and wetland water management affect local bird distribution, even in a short period of time [66].

Climate change predictions estimate a larger increase in average temperatures in the areas near the Arctic than in southern latitudes. Taking this into account and comparing the results of previous studies [67], we can conclude that *Anatidae* breeding habitats coincide with areas where the predicted temperature changes are larger: therefore, the climate change will directly affect the migration cycle of these birds. AI viruses have co-evolved with migratory waterfowls over millions of years and have survived many eras of climatic turbulence [66].

Probably the indirect influence of climate on poultry diseases are even more pronounced, considering that natural and farming landscapes are not fully separated. The increase in the number of birds wintering in the subarctic areas leads to an increase in population density and higher competition for limited feed resources. This may elevate interspecies virus transmission, which could include a greater spectrum of hosts. Also, the method of virus transmission may change, comprising both wild birds and domestic poultry. Rising temperatures may change the terms of AI virus survival and its ecology [68].

Predictions for changes in virus survival in the environment, including changes in host migration models, may affect the epidemiology of AI. Wild bird migration patterns are related to the AI evolution, and climate change exerts an impact on both wild bird behavior and virus survival outside

the host organism, as well as on the seasonal and geographic patterns of the AI cycles in wild birds.

Several authors have indicated the influence of climate change on food-borne diseases [15, 69], water-borne diseases (e.g. cryptosporidiosis) [70], and cholera [71-73]. The impact of global climate change on food safety has been emphasized. For example, an increase in the number of cases of salmonellosis [74], and to a lesser extent campylobacteriosis [75], in high ambient temperatures has been observed. In Australia, an increased rate of notification of salmonellosis has been observed in correlation with decreasing geographical latitude and increasing average yearly temperature [76]. It has also shown that higher temperature and humidity are correlated with the decreasing rate of children's hospitalization due to rotavirus infection. This is interesting, because survival of the virus is favored at lower temperatures and humidity [77]. It is thought that this virus is a significant cause of food-borne diseases [78]. The association of El Niño phenomenon with increasing cases of cholera and diarrheal diseases in Peru and Bangladesh has been demonstrated [76]. In light of this evidence, it appears that changes in both temperature and humidity play a great role in food poisoning transmission. It is probable that global climate change will result in prolonging the period with the largest number of cases of food poisoning and/ or enlargement of their geographical range [15].

The above-mentioned examples illustrate the potential impact of climate change on the occurrence and spread of some infectious diseases that should be taken seriously under consideration in the development of effective prevention programs.

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