

# **Health Climate Change impacts report card technical paper**

## **7. Potential impact of climate change on emerging infections in the UK**

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**Key Messages**

An emerging infection is defined as a disease that has newly appeared in a population or that has been known for some time but is rapidly increasing in incidence.

Several vector-borne diseases have emerged in Europe in recent years. These include vivax malaria, West Nile fever, dengue fever, Chikungunya fever, leishmaniosis, Lyme disease and tick-borne encephalitis. The vectors of these diseases are mosquitoes, sand flies and ticks. [H].

The emergence of some of these diseases is linked to increase in transport of people and goods, and land use change. The role of warming is unclear. [M].

Climate factors affect diseases caused by pathogens that spend a part of their lifecycle outside of the human host in a cold-blooded vector (such as a mosquito or tick). [H]

Climate affects three major aspects of disease occurrence: (i) where disease occurs; (ii) when disease occurs within the year, and (iii) the incidence of disease. (H)

The most important vector-borne disease currently established in the UK is Lyme disease [also called Lyme borreliosis], which is transmitted by ticks. It is present throughout the UK, including Scotland.

The UK has endemic mosquito species capable of transmitting malaria and probably other pathogens. [H]

Higher temperatures will increase the suitability of the UK's climate for invasive species (disease vectors from outside the UK), and increase the risk that they may spread disease. [H]

The UK already harbours mosquito species believed to be able to transmit West Nile virus. Higher temperatures will increase their ability to spread West Nile, should the virus be introduced. [H]

The risk of transmission of dengue and Chikungunya viruses is contingent on the risk of invasion by [exotic] mosquito vectors. This remains low in the near term. [M]

The threat of malaria transmission will remain low. [H]

The incidence of Lyme disease will continue increasing, and climate change will enable it to spread to higher altitude. [M]

Actions to reduce the future impact of emerging vector-borne diseases include insect control activity at points of entry of vehicles and certain goods, wider surveillance for mosquitoes and sand flies, research into the threat posed by native species, increased awareness of the medical profession of the threat posed by specific diseases, regular risk assessments, and increased preparedness for the occurrence of a disease emergency. [M]

## Introduction and Scope

Infections are defined as 'emerging' if they "have newly appeared in a population or have existed previously but are rapidly increasing in incidence or geographic range" (Morens et al., 2004). Notable emerging diseases of humans in recent decades include acquired immune deficiency syndrome (AIDS), variant Creutzfeldt-Jakob disease (vCJD), multidrug resistant tuberculosis, severe acute respiratory syndrome (SARS), Middle East respiratory syndrome coronavirus (MERS-CoV), *E. coli* O157, avian influenza, West Nile fever and Ebola. About three quarters of human emerging infections are classified as zoonotic (have a vertebrate animal origin) (Taylor et al., 2001).

There is widespread scientific agreement that anthropogenic activities are contributing to the warming of the world's climate at an unprecedented rate, with concomitant changes in precipitation, flooding, winds and the frequency of extreme events. Innumerable studies have demonstrated links between infectious diseases and climate, and it is highly likely that significant changes in climate will impact on at least some of them. Climate change is just one of several factors that lead to disease emergence. Some of these other factors may themselves be affected by climate change and, therefore, the effects of climate change on disease emergence may be direct (climate change leads to emergence) or indirect (climate change affects another factor which, in turn, leads to emergence).

This technical paper summarises the state of scientific evidence regarding current and future impacts of anthropogenic climate change on the emergence of infectious diseases with potential to impact significantly on the UK human population. Initially it considers a broad range of possible emerging infections but, later, it narrows the focus to vector-borne diseases.

## Evidence of current sensitivity to climate factors (temperature, rainfall, extreme events)

A common feature of human diseases affected by climate is that the pathogen spends a significant period of time outside of the human host, subject to environmental influence. This suggests that the most climate-sensitive diseases are those spread by arthropod vectors, in food, in water, in aerosol, in fomites, and those which have a free-living environmental stage. Examples of such diseases are, respectively, malaria (spread by anopheline mosquitoes), salmonellosis, cholera, legionnaires disease, *Clostridium difficile* and anthrax.

By contrast, most diseases transmitted directly between humans (for example, human childhood viruses, sexually transmitted diseases, tuberculosis caused by *Mycobacterium tuberculosis*) have few or no reported associations with climate. Exceptions are the human respiratory viruses, such as those that cause colds and seasonal flu in humans; these viruses are spread by aerosol between individuals in close contact but are nevertheless sensitive to the effects of ambient humidity and possibly temperature, and have strong seasonal cycles.

A systematic review of disease-climate associations lends weight to these assertions. Scrutiny of research papers on 157 high-impact human and animal pathogens of Europe found that 66% have at least one climate driver (i.e. a climate variable that affects the occurrence of disease). Transmission routes of climate sensitive diseases, in decreasing order of importance, were vectors, food/water,

environment, fomite and aerosol. Least important were direct contact and sexual transmission. The most frequent climate drivers were rainfall, moisture and temperature; less frequent, but still important, were particulate matter (dust), extreme weather events, wind and large-scale oscillations (such as El Niño Southern Oscillation [ENSO]) (McIntyre et al., 2016).

Similarly, a weighted risk analysis following systematic review identified 26 (49%) out of 53 reportable infectious diseases of humans in Europe to be directly or indirectly linked to climate (Lindgren et al., 2012).

Therefore, systematic reviews suggest that as many as a half to two-thirds of human diseases in Europe may be affected directly or indirectly by climate. In reality, the proportion may be even greater, as new datasets become available. For example, outbreak occurrences of 11 out of 13 (85%) human diseases in Europe, recorded on the Gideon database, are statistically associated with the cycles of the North Atlantic Oscillation, a large-scale climate phenomenon (similar to ENSO) which affects the climate of Europe (Morand S et al., 2013). Diseases associated with the NAO were air-, water- or food-borne, or spread by rodents or vectors.

Climate affects three major aspects of disease occurrence: (i) where disease occurs; (ii) when disease occurs within the year, and (iii) the incidence of disease. In some cases, mostly macroparasite infections such as those caused by helminths, climate can also affect the severity of clinical disease in infected individuals. The second and third aspects apply to most climate-sensitive diseases. However, the first aspect applies most strongly to vector-borne diseases. Although there are many exceptions, the majority of non-vector-borne diseases either occur worldwide, or have the potential to occur worldwide. By contrast, vector-borne diseases tend to be geographically restricted, and very few occur worldwide. This is a reflection of the strong influence of climate on the spatial and temporal distributions of arthropod vectors. If there are exceptions to this rule, the vectors are likely to be lice or fleas, with lives so intimately associated with humans or animals that they are relatively protected from climate's influences.

A consequence of climate geographically-limiting the distributions of vector-borne diseases is that such infections are particularly likely to spread to new areas with climate change. Many climate-sensitive diseases that are not vector-borne may be similarly affected (especially water-borne diseases) while others will most likely respond to climate change by alteration to their seasonal cycles or the frequency or scale of disease outbreaks in regions that are already affected.

Extreme weather events are an important factor in the spread of water-borne diseases. A systematic review (Cann et al., 2013) of water-borne disease outbreaks following extreme weather events found that more than half were preceded by heavy rainfall and flooding. These events increase run-off from fields and contaminate rivers, coastal waters and wells, and can overwhelm water-treatment plants. At the other extreme, drought can lead to the concentration of water-borne pathogens in rivers and water bodies, increasing exposure risk. The most common pathogens causing water-borne disease were found to be vibrios (especially *Vibrio cholerae*, the cause of cholera) and *Leptospira* spp., the cause of leptospirosis. Other notable water-borne pathogens causing outbreaks after extreme weather events were *Campylobacter*, *E. coli* and *Cryptosporidium*. Water-borne pathogens may also be affected by temperature: higher water temperatures may lead to faster growth rates of disease-causing pathogens, and increased use of bathing waters by the public. In

Scotland average levels of non-viral gastrointestinal infections were found to increase as temperature and relative humidity increased (Eze et al., 2014).

Climate change is one of several forces (“drivers”) that may lead to the emergence of infectious diseases. Other important drivers are man-made changes to the environment through, for example, deforestation and urbanization; developments in agriculture and the food industry; changes in the way people live, behave, eat, travel and trade; changes in medicine, public health and the use of antimicrobials; and the occurrence of “shocks” such as war, population migrations and famine (Jones et al., 2008). An analysis of more than 300 human disease outbreaks over more than 60 years concluded that climate and weather were only infrequently causes of outbreaks of human disease (3%). However, some other drivers, such as changes to land use and agriculture (11%), are themselves affected by climate change. Therefore, climate change’s indirect effects on disease emergence (via effects on other drivers) may be as important as its direct effects. Of the outbreaks attributed to climate and weather, 30% were vector-borne diseases whereas 60% were gastrointestinal disease from seafood (Jones et al., 2008).

There are, therefore, strong arguments to expect climate change to impact on human disease outbreaks, especially those transmitted by vectors or in food/water, but in practice there are relatively few examples. In recent years, however, Europe has seen an upsurge in vector-borne diseases, as well as the spread of vectors.

The main vectors threatening or affecting the health of people in Europe are mosquitoes, sandflies and ticks. Mosquitoes spread malaria and a number of viruses (“arthropod-borne viruses” or arboviruses). Malaria, caused by *Plasmodium vivax* and spread by the bites of *Anopheles* mosquitoes, used to be endemic in the UK but there has been no person-to-person transmission (via mosquitoes) of the disease in this country for over 60 years (Kuhn et al., 2003); instead, all recorded cases were either infected overseas or, in a small number of instances, were infected in the UK by a mosquito originating from overseas. The reason for the disappearance of malaria from the UK is believed to be changes to the environment (drainage of marshes) and farming ((Kuhn et al., 2003). Similar changes have occurred in mainland Europe such that there are now no areas endemic for malaria in Europe. However, in 2011 an outbreak of *P. vivax* malaria was recorded among non-travellers in a region of Greece, after nearly 40 years of only sporadic cases in the country (Danis et al., 2011), warning other European countries that there remains a risk of disease transmission while potential vectors are present.

West Nile fever, caused by West Nile virus (WNV) and spread by *Culex* mosquitoes, is endemic in a number of southern and eastern European countries. There is evidence that it is spreading to new regions and the incidence of human cases is increasing (EFSA/ECDC, 2014). In the UK there have been reports of the transmission of virus among birds but these have not been confirmed. However, one of the most important vectors of WNV in Europe, *Culex modestus* has recently been rediscovered across a large area of southern England, after no reports in the UK for more than sixty years (Medlock and Vaux, 2012).

As with vivax malaria, indigenous UK mosquito species may present a risk for the transmission of arboviruses. Indeed, native species may be more able to transmit pathogens at the UK’s relatively low temperatures than an invasive species that prefers warmer climates. For a mosquito to act as a vector, it needs to live longer than the time required for a pathogen to develop and mature within it, and UK native

species may be more able to survive (and hence live longer) at the UK's relatively cool temperatures than exotic species. There is a good example from the field of animal disease: bluetongue, a midge-borne viral disease of ruminants, is endemic to Africa but is also transmitted in Mediterranean countries by an invasive, African midge species. It was not foreseen that indigenous midges could transmit bluetongue in climates as cool as southern Scandinavia. In 2006-2009, tens of thousands of farms across northern Europe, including the UK, were affected by this disease (Mellor et al., 2008), transmitted by indigenous midge species. In this regard, it is noteworthy that a UK native mosquito species, *Ochleratatus detritus*, which feeds readily on humans, is now known to be a good vector of a virus closely related to WNV, and it may also be competent for WNV itself (Mackenzie-Impoinvil et al., 2015).

Invasive mosquitoes also present a risk of the introduction of new diseases. There was an outbreak of Chikungunya fever in north Italy in 2007 (Angelini et al., 2007); and both Chikungunya fever (Grandadam et al., 2011) and dengue fever (La Ruche et al., 2010) were reported in southern France in 2010. Dengue fever was also reported from Croatia in 2010 (Gjenero-Margan et al., 2011) and France in 2013 (Marchand E, 2013). In all cases, the vector is believed to be the Asian tiger mosquito, *Aedes albopictus*, which is one of the world's most invasive species, having spread from Asia to both North America and Europe. It was first detected in Europe (Albania) in 1979, and is now found in most southern European countries. It has also been reported in Belgium and the Netherlands, but not yet in the UK. A more important dengue vector, *Ae. aegypti*, was once widespread in Europe but disappeared in the Mediterranean region in the mid-20<sup>th</sup> century. However, it has regained a foothold in Europe, being reported from Madeira (an autonomous region of Portugal) in 2004-05. Despite extensive vector control efforts, the mosquito has thrived; and in 2012 there were more than two thousand dengue cases reported from the island. This represents the first sustained transmission of dengue in Europe since the 1920s (Sousa et al., 2012).

Sandflies are vectors of cutaneous (CL), and visceral (VL) leishmaniasis caused by *Leishmania* parasites. Both are endemic in people and dogs in southern Europe. There is a low incidence of disease in people (about 700 cases per year in southern Europe) but a much higher incidence in dogs (about 5,000 cases per year in France alone) (Dujardin et al., 2008). Sandflies have not been detected in the UK; however, they have been found in central and northern France and southern Germany (Ready, 2010). The proximity of known vectors to the UK, and the passport-controlled movement of potentially infected dogs into the UK (Shaw et al., 2009), raises the possibility of the eventual introduction of leishmaniasis.

Ticks spread a variety of disease agents. A major concern in Europe is the spread and emergence of tick-borne encephalitis (TBE) virus (Stefanoff et al., 2012). There are thousands of cases of human disease each year, the incidence is increasing, and the endemic region is growing. Possible causes of this emergence are socioeconomic (especially post-Soviet Union), environmental and climatic changes, as well as increased awareness (Stefanoff et al., 2012). While TBE has occurred in many European countries including Scandinavian countries (indicating that the UK climate should not be a barrier to disease), and the primary European vector (*Ixodes ricinus*, the sheep tick) is found throughout the British Isles, TBE itself has not been reported in the UK. However, a bacterial spirochaete disease, called Lyme borreliosis and also spread by *I. ricinus*, is emerging in the UK. Lyme disease is the

most common vector-borne disease in temperate climates, with an estimated 85,000 human cases per year in Europe; some two to three thousand cases occur per year in the UK. Tick-borne disease threats also include Crimean Congo Haemorrhagic Fever (CCHF). This viral disease is spread largely by *Hyalomma* ticks, is endemic in parts of Eastern and south-eastern Europe; and it appears to be emerging (Maltezos et al., 2010). *Hyalomma* ticks are not endemic to the UK although they may arrive on migrant birds (Jameson et al., 2012); and CCHF may arrive in infected travellers. The first laboratory confirmed fatal case of CCHF in the UK (in a traveller returning from Afghanistan) was reported in 2012 (Atkinson et al., 2012).

### **Review of studies that have estimated the current burden attributable to observed climate change (1970-2013)**

The World Health Organization (WHO) has undertaken the most comprehensive assessment of the current burden of disease attributable to climate change (Campbell-Lendrum et al., 2003). The WHO used models to estimate the additional disease burden (in terms of numbers of deaths, and years of life lost to death and disability (DALYS)) per year in the year 2000 compared to a baseline period of 1961 – 1990. It finds that climate change has led to an additional 74,000 deaths and nearly two and a half million DALYS, from diarrhoea (caused by food-and water-borne disease) and malaria. The main burden falls in the developing world. Specific estimates for the UK are not provided but the assessment finds that the climate-change-attributable burden in Western Europe, from both causes (diarrhoea and malaria), is less than its minimum sensitivity of 500 deaths or 500 DALYS. A more detailed analysis of one cause of gastrointestinal disease, salmonellosis, concluded that a 1°C increase in temperature equates to about 12% more reported disease in England and Wales (Kovats et al., 2004). As The Central England mean temperature has increased by approximately 1°C since the 1961-1990 baseline ([http://www.ukcip.org.uk/wordpress/wp-content/PDFs/UKCP09\\_Trends.pdf](http://www.ukcip.org.uk/wordpress/wp-content/PDFs/UKCP09_Trends.pdf)), this equates to about 1,600 cases annually in recent years attributable to increased temperature since the baseline period.

These should be considered to be conservative estimates of the climate-change attributable burden of disease in Western Europe (Patz et al., 2005). One reason is that the only vector-borne disease quantitatively assessed is malaria caused by *Plasmodium falciparum*. It does not attempt to estimate the burden of other insect-borne or tick-borne diseases, two of which (Lyme disease and tick-borne encephalitis) are prevalent in Western Europe, with Lyme disease present in the UK. A second reason is that the incidence of diarrhoeal disease is likely to be significantly under-reported to UK authorities.

As described earlier, since 2000 several mosquito-borne diseases have emerged or re-emerged in Western and Eastern Europe: *P. vivax* malaria, dengue, Chikungunya and West Nile. None have occurred in the UK and so the UK disease burden is zero.

There is little evidence for a role of climate change in the emergence of malaria, dengue and Chikungunya. The origin of the malaria outbreak in Greece is likely to be migrant workers introducing *P. vivax* into an agricultural region where potential vectors were present (Danis et al., 2011). The emergence of dengue and Chikungunya are associated with the establishment of populations of the Asian tiger mosquito, *Aedes albopictus*, in southern France and northern Italy, and *Ae. aegypti* in Madeira; together with mutation of Chikungunya virus that facilitated infection of

*Ae. albopictus*. The mosquitoes became infected after feeding on returning travellers carrying infections obtained overseas. There is no suggestion that the spread of the *Aedes* mosquitoes is associated with climate change.

Vectors of West Nile virus have long been present in Europe, yet the disease appears to be emerging (Paz and Semenza, 2013). West Nile virus' mosquito vectors are very sensitive to changes in temperature, in terms of abundance and activity (Morin and Comrie, 2013), and increasing temperature is considered to be one of the drivers of its emergence in Europe (Pradier et al., 2012). While the UK has not experienced West Nile, in recent years a known WNV vector, *Culex modestus*, has become re-established in southern England (Medlock and Vaux, 2012). While its establishment cannot be linked to climate change, it is interesting to note that it was last detected in the 1940s on England's south coast; the 1940s was the warmest recorded period in England (Central England time series) until the present period (Parker et al., 1992).

Two tick-borne diseases have emerged in Europe in recent decades, tick-borne encephalitis (TBE) and Lyme disease, both transmitted mostly by *Ixodes ricinus*. TBE has increased in incidence and spread to higher elevation and new regions of Europe; its emergence is linked to changes to habitats, the density of wildlife and socioeconomics; there is also greater awareness. Climate change may have played a role (Stefanoff et al., 2012; Lukan et al., 2010), but this is contested (Randolph, 2004; Sumilo et al., 2007) and other drivers of disease emergence, such as change in human behaviour, shown to be important (Sumilo et al., 2007). TBE does not occur in the UK, perhaps because *I. ricinus* in the UK transmit a closely related virus (Louping ill virus) that causes disease in sheep and only rarely affects people. Lyme disease has also increased in incidence and spread to new regions, possibly because of climate-change influences on the tick vector. Increased *I. ricinus* density and its spread to higher latitude in Sweden have been linked to milder winters (Lindgren et al., 2000).

Most consideration has been given here to vector-borne diseases. It is important to note that many non-vector-borne diseases have emerged in recent years, some of which have affected or threaten the UK. Public Health England lists 38 human pathogens that have emerged (globally) from 1980 to the present ([http://www.hpa.org.uk/webc/HPAwebFile/HPAweb\\_C/1204100434554](http://www.hpa.org.uk/webc/HPAwebFile/HPAweb_C/1204100434554)). Three are transmitted by ticks and one by mosquitoes; no others are vector-borne. The emergence of 25 of these 38 pathogens is included in a study of drivers of emergence (Jones et al., 2008). None of the 25 emergence events are attributed to climate. Instead, the most common drivers are changes in human susceptibility to infection (as a consequence of human immunodeficiency virus, HIV) and changes in land use and agriculture. In other words, the majority of emerging diseases are not vector-borne, and their emergence is not linked to climate change.

#### **Review of studies that have estimated future health impacts (two time periods 2010-2050 and 2050-2100)**

The World Health Organization has attempted to quantify the additional amount of human disease that might arise as a consequence of climate change (McMichael et al., 2004). Inevitably, there is significant uncertainty in such estimates. There are three major sources of uncertainty: (i) how climate, and hence climate change,



quantitatively affects the incidence of a disease; (ii) by how much climate will have changed at future time points (which in turn has multiple sources of uncertainty, such as the climate model to be used, and the scenario of CO<sub>2</sub> emissions to follow); and (iii) the effect of other disease drivers that may change on similar or faster time scales than climate.

WHO (McMichael et al., 2004) considered the effects of temperature increase by 2030 on diarrhoeal disease and malaria caused by *P. falciparum*. While WHO predicts an increase in the risk of diarrhoeal disease in developing countries by 2030, it predicts that there will be no change in risk in developed countries. There is some uncertainty around this estimate, however, such that the risk might increase or decrease by about 5%. For malaria caused by *P. falciparum*, WHO projects an increase in risk in areas bordering the endemic zone, and an increase in mortality and morbidity within the endemic zone. However, it does not predict any change in the risk of malaria caused by *P. falciparum* in developed countries.

A recent and more extensive assessment by WHO (Hales et al., 2014) for the years 2030 and 2050, found increases of 20 - 86,000 deaths globally from diarrhoeal disease of children attributable to climate change, under a range of socioeconomic growth scenarios. However, the number in Western Europe was very small (1 or 2). Equally, climate change was projected to lead to no deaths in Western Europe from *P. falciparum* malaria or dengue.

Several other workers have developed models of climate change's future impacts on malaria. A recent study has examined the projections of five different malaria impact models, each driven by five different global climate models, which in turn were run for four different emission scenarios (Caminade et al., 2014). This is the most comprehensive study yet of the impact of climate change on malaria, and allows for similarities in projections from different models and scenarios to be identified, and for uncertainties to be quantified. The four emission scenarios (RCP2.6, RCP4.5, RCP6.0 and RCP8.5) project similar temperature changes by 2030 (approximately +1.5°C) and range from +1.5°C (RCP2.6) to +5°C (RCP8.5) by 2100. The probability of sustained malaria transmission occurring in the UK in the current century is small, even under the most extreme emission scenario (RCP8.5). One of five malaria impact models (the MIASMA model), under the three most extreme emission scenarios, consistently predicts that the climate of southern England will become suitable for sustained malaria transmission (> 1 month) by 2080. Under one climate model, with all four emission scenarios, it even predicts some suitability by the 2030s. One other malaria impact model (the LMM) predicts some suitability of the UK climate by 2080, under the most extreme emission scenario, but for two climate models only. The remaining three malaria impact models do not predict any suitability of the UK climate with any climate model under any emission scenario. For all combinations of emission scenario and climate model therefore, more than half of malaria models predict no suitability of the UK climate, even by the 2080s and, across all of the models and scenarios, there is significant uncertainty in projected outcome.

However, it is important to note that all five malaria models were developed and parameterized for malaria caused by *P. falciparum*, while it was malaria from by *P. vivax* that was previously endemic in the UK and which has recently reoccurred in Europe. *Plasmodium vivax* transmission by European mosquito vectors requires lower temperature thresholds than *P. falciparum* and, therefore, all five malaria

models underestimate the risk of malaria in Europe. By contrast, under a medium-high scenario of climate change, a model parameterized for *P. vivax* predicts that the southern half of Great Britain will be climatically-suitable for *P. vivax* malaria transmission by 2030 for 2 months of the year, and parts of the southeast of England for 4 months per year (Lindsay et al., 2010); while by 2080 regions as far north as southern Scotland will be climatically-suitable for 2 months of the year, and the southern half of Great Britain for 4 months per year (Lindsay and Thomas, 2001).

All authors agree, however, that the risk of malaria transmission is determined by many factors other than climate; and while climate change may increase the suitability of the UK climate for transmission, other factors (such as drainage of marshes and changes in land use, which have reduced mosquito populations) make the probability of it occurring very small, even under future climates.

The main threat to the UK from dengue and Chikungunya viruses is tied to the risk of invasion of the UK by *Aedes aegypti*, which is widespread globally, including Madeira in Europe (Almeida et al., 2007), and *Ae. albopictus*, which is now found in many European countries. The European Center for Disease Prevention and Control has modeled the suitability of the current European climate for both vectors and dengue transmission (Rogers and Hay, 2012). Much of Europe, including many parts of the UK, is found to be suitable for *Ae. albopictus*, with a probability of suitability of 0.5 to 1; however, hardly any areas of Europe, and none in the UK, are found to be suitable for *Ae. aegypti*. The UK is found to have a climate somewhat similar to those of other parts of the world where dengue is present, although less so than parts of southern Europe.

Other workers report similar findings for *Ae. albopictus* for the current period (Caminade et al., 2012). Three climate-suitability models for the occurrence or activity of this species were developed using observed climate data (EOBS) for the recent past, and modeled climate data for 2030-2050. Modelled climate data come from ten European regional climate models (RCMs), all driven by the A1B emission scenario. The three models indicate that large parts of the UK are suitable for *Ae. albopictus* within the 1990-2009 time period. Under future climate scenarios the UK is predicted to become more climatically suitable for the vector. Importantly, for two of the three vector models, there is agreement from eight or more of ten RCMs that the south of England will be suitable for *Ae. albopictus* by 2030-2050.

Transmission of an arbovirus requires that environmental conditions are suitable for both virus and vector, and it is possible for a known vector to be present, but for it to be too cold for viral transmission. The major limit here is the time required for virus development in the vector, which increases exponentially with decreasing temperature; thus, at cool temperatures vector species may not live long enough for virus development. As described above, models suggest that parts of the UK are currently climatically suitable for at least one dengue and Chikungunya virus vector (*Ae. albopictus*). However, studies of the climatic needs of Chikungunya virus (based on conditions at past outbreaks) indicate a threshold minimum temperature of 20-22°C. Combining this threshold with the climatic needs of the vector, the UK is found to be climatically unsuitable for Chikungunya transmission at the present time (Fischer et al., 2013). Future suitability is examined using a single RCM driven by two emission scenarios (A1B and B). Under both emission scenarios the UK remains unsuitable for Chikungunya in 2011-2040. Under the A1B scenario, the extreme southeast of England becomes 'rather unsuitable' (the second lowest of five risk

classes) by 2041-2070 while a much larger area of southern England is 'rather unsuitable' by 2071-2100. Under the B1 scenario, England remains unsuitable in 2041-2070, but a small area of southern England becomes 'rather unsuitable' by 2071-2100.

A similar exercise found that no parts of the UK become suitable for dengue virus development (in *Aedes aegypti*) under either A1B or B1 scenarios by 2071-2100 (Thomas et al., 2011). There is no equivalent work on the modeling of dengue in *Ae. albopictus*, which is the more likely vector to enter the UK in the near future.

While there is consensus that climate affects the transmission of tick-borne Lyme borreliosis, and some agreement that the northward spread of the vector in Sweden is attributable to recent warming, there are no published models projecting its future incidence in Europe under scenarios of climate change. Models for other temperate regions predict that climate change will allow northern expansion of the range of the tick vectors (Ogden et al., 2006). Lyme and its vectors are already found throughout the UK and, therefore, increasing climate suitability may be limited to increase in altitude (Gilbert, 2010) and change in incidence. However, there is widespread agreement that non-climate drivers play a dominant role in the epidemiology of Lyme disease (Rizzoli et al., 2011) and future trends in agriculture, land use, wild animal populations and tourism will play as large or a larger role in determining future patterns of the disease (Lindgren and Jaenson, 2006).

### **Potential for impacts to be avoided by adaptation measures**

Adaptation to the risk presented by emerging infections requires three major actions: (i) improved surveillance of disease and, where appropriate, vectors, so that sporadic cases and outbreaks, or the heightened risk of these, can be detected early; (ii) risk assessment of the likelihood of cases or outbreaks of an emerging disease, regularly updated as new data become available; and (iii) increased preparedness for such events. In the UK, advice on these activities is currently provided to government by the UK Zoonoses, Animal Diseases and Infections Group (UK-ZADI) and the Joint Human-Animal Infections and Risk Surveillance group (HAIRS).

The northward spread of *Aedes albopictus*, a vector of dengue and Chikungunya, indicates the need for active surveillance for invasive mosquitoes. There is strong evidence that some of the spread of *Ae. albopictus* in Europe is associated with transport in vehicles as, for example, it has been trapped in motorway service areas in mainland Europe. The extensive movement of cars and goods vehicles into the UK from mainland Europe, via Eurotunnel or on boats, should be considered a likely route of entry of this mosquito. Insecticidal treatment of vehicles entering the UK, especially if travelling at night, could help to reduce this risk. 'Disinsection', as described by the International Health Regulations of the WHO ([http://www.who.int/ipcs/assessment/aircraft\\_disinsection\\_review/en/](http://www.who.int/ipcs/assessment/aircraft_disinsection_review/en/)) is already used to kill insects in airplanes arriving in certain countries. *Aedes albopictus* has also entered many countries in used vehicle tyres or in 'lucky bamboo', a houseplant imported from China. Increased mosquito surveillance at ports of entry of such products is recommended.

A known vector of West Nile virus, *Culex modestus*, has already been detected in the UK and is widespread. Surveillance within the areas of presence can be used to

identify areas of particular risk of virus transmission; and surveillance outside such areas can be used to monitor its further spread. In addition to invasive species, indigenous mosquito species may be competent vectors for certain pathogens. The UK harbours vectors of malaria (principally *Anopheles atroparvus*), and a mosquito that breeds in salt marshes was recently shown to be a competent vector of Japanese encephalitis virus (Mackenzie-Impoinvil et al., 2015).

There is also a threat of invasion by sand fly vectors of leishmaniosis. Sandflies can be caught in the same traps as mosquitoes and, therefore, a single surveillance system could be developed for both types of vector.

Lyme disease is present and increasing in incidence in the UK. Key measures of adaptation are to increase awareness of the public, in terms of recognizing symptoms and taking tick-avoidance measures; and improving national level surveillance. For surveillance purposes, it has been recommended to base the clinical definition of Lyme disease on the skin rash that occurs in about 90% of cases, rather than on the rare Lyme neuroborreliosis that needs laboratory confirmation (Lindgren et al., 2012). The ability to forecast the risk of exposure to tick vectors or Lyme, based on geographic and climatic information, will help the public to take suitable precautions when risk is high.

The risk of emerging disease outbreaks in the UK, particularly vector-borne, food-borne and water-borne diseases, is likely to continue to rise as our climate changes. New data will also become available with time, such as updated maps of the occurrence of potentially invasive vectors in continental Europe. The risk presented by such diseases should therefore be regularly re-assessed.

Preparedness for outbreaks of vector-borne diseases requires (i) knowledge of the vectors, so that control measures can be targeted at the right species; (ii) identification of areas of high risk so that prevention or control measures can be targeted; (iii) in such areas, raised awareness of General Practitioners and hospital staff of the possible risks to people who are regularly exposed to vector bites, to allow earlier and higher rates of detection; and (iv) development of policy and approval of legislation to permit vector control programmes (e.g. insecticide spraying). A contingency plan should be developed for the event that *Aedes albopictus* is detected in the UK.

## **Conclusions / Evidence Gaps**

Numerous diseases have emerged in recent years and will continue to do so in the future. Climate is one of several causes of disease emergence. Half or more of infectious diseases are known to be affected by climate, but it appears to be a relatively infrequent cause of human disease emergence. Climate mostly affects diseases caused by pathogens that spend a part of their lifecycle outside of the host, exposed to the environment. The most important routes of transmission of climate sensitive diseases are by arthropod (insect and tick) vectors, in water and in food.

Given the sensitivity of many diseases to climate, it is very likely that at least some will respond to future climate change. Many diseases that are not vector-borne, especially water-borne and food-borne disease, are climate sensitive but there is a relative paucity of published studies on the impacts of climate change upon them. Notable exceptions are the diarrhoeal diseases modelled by WHO (Hales et al., 2014) although their projected impact on Western Europe (and the UK) is very small.

The impact of climate change on infectious respiratory diseases requires further study: such diseases can spread rapidly and cause significant health impact; and they show some climate-sensitivity, with seasonal cycles that are often linked to climate. However, detailed studies of the impacts of climate change on their seasonal cycles, or health impact, has received little attention (Ayres et al., 2009).

This review has focused extensively on vector-borne diseases because they are the most climate-sensitive type of disease. Several vector-borne diseases have emerged in Europe in recent years; these include vivax malaria, West Nile fever, dengue fever, Chikungunya fever, leishmaniosis, Lyme disease and tick-borne encephalitis. The vectors of these diseases are mosquitoes, sand flies and ticks. Some of these vector-borne diseases threaten the UK. The greatest risk is probably presented by West Nile virus, as at least one competent vector species is already present here, and it is now widespread in southern and eastern Europe. Climate change is likely to increase this risk in the future. There is a strong threat of invasion by the Asian tiger mosquito, *Ae. albopictus*, in vehicles returning to the UK from continental Europe; however, if the vector enters and survives in the UK it may be too cold for sustained transmission of dengue or Chikungunya viruses. Increased summer temperatures resulting from climate change will increase the risk of transmission of these viruses in the future, should this invasive vector be present. The UK is, and long has been, climatically suitable for the transmission of malaria caused by *P. vivax*. Climate change will increase the climatic suitability even further, but this is unlikely to lead to any sustained malaria transmission if land use and agricultural practices remain largely as they are today. However, the recreation of extensive wetlands and salt marshes, combined with warmer temperatures, may create a situation where local vivax malaria transmission is possible.

The threat of virus transmission posed by our native species of mosquito should not be under-estimated, as some are known to be vector-competent, and they may survive well enough at the UK's relatively low temperatures to be able to spread disease after becoming become infectious.

The emergence of Lyme disease in the UK is likely to continue in the future. Climate change may contribute to this emergence, but other drivers will probably play a larger role. The risk presented by TBE, which is emerging in many parts of Europe, remains difficult to gauge.

There appear to be no published studies estimating the future disease burden, attributable to climate change, from emerging vector-borne infections in the UK. Instead, published studies have tended to focus on aspects of 'climate suitability'. Interestingly, suitable climate-driven models remain to be developed for the two diseases, West Nile and Lyme disease, whose emergence to date might be linked to climate change. Instead, there have been several climate-driven models developed for the Asian tiger mosquito and the diseases it transmits (dengue and Chikungunya), even though their emergence is not linked to climate change.

Key research gaps are, therefore, (i) assessment of the impact of climate change on diseases that are not vector-borne, including respiratory infections; (ii) evaluation of the vector potential of UK native species; (iii) development of climate driven models for the risk of West Nile and Lyme disease in the UK; (iv) evaluation of the threat posed by TBE to the UK and (v) incorporation of environmental and agricultural variables into models of the risk of vivax malaria in the UK.

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