

REVIEW ARTICLE

The effect of climate change on the occurrence and prevalence of livestock diseases in Great Britain: a review

P. Gale, T. Drew, L.P. Phipps, G. David and M. Wooldridge

Veterinary Laboratories Agency, Weybridge, New Haw, Addlestone, Surrey, UK

Keywords

animal health, climate change, livestock, risk assessment, vectors.

Correspondence

Paul Gale, Veterinary Laboratories Agency, Weybridge, New Haw, Addlestone, Surrey KT15 3NB, UK.

E-mail: p.gale@vla.defra.gsi.gov.uk

2008/0691: received 23 April 2008, revised 11 July 2008 and accepted 10 August 2008

doi:10.1111/j.1365-2672.2008.04036.x

Summary

There is strong evidence to suggest that climate change has, and will continue to affect the occurrence, distribution and prevalence of livestock diseases in Great Britain (GB). This paper reviews how climate change could affect livestock diseases in GB. Factors influenced by climate change and that could affect livestock diseases include the molecular biology of the pathogen itself; vectors (if any); farming practice and land use; zoological and environmental factors; and the establishment of new microenvironments and microclimates. The interaction of these factors is an important consideration in forecasting how livestock diseases may be affected. Risk assessments should focus on looking for combinations of factors that may be directly affected by climate change, or that may be indirectly affected through changes in human activity, such as land use (e.g. deforestation), transport and movement of animals, intensity of livestock farming and habitat change. A risk assessment framework is proposed, based on modules that accommodate these factors. This framework could be used to screen for the emergence of unexpected disease events.

Introduction

The recent emergence of BTV in livestock in Great Britain (GB) (Landeg 2007) highlights the need to understand the potential effects of climate change on the occurrence, distribution and prevalence of livestock diseases. BTV is an orbivirus that is transmitted by *Culicoides* midges (Mellor *et al.* 2000; Mehlhorn *et al.* 2007; Meiswinkel *et al.* 2007). Other exotic arboviruses that infect livestock and are probably transmitted by the same midge species as BTV (Mellor *et al.* 2000) include EHDV, Akabane virus and bovine ephemeral fever virus. Incursions of these viruses have been reported recently in Israel (Yadin *et al.* 2008) and they could also spread to the European continent as the climate changes. There is already evidence that climate change is affecting endemic diseases in GB too. For example, liver fluke is expanding in range in GB (Scottish Agricultural College 2004; Pritchard *et al.* 2005) because of warmer, wetter conditions that favour its mud snail intermediate host. National Farmers' Union (2005)

has summarized the key climate concerns for farmers and growers in GB as carbon dioxide levels, temperature (including its effect on growing season), water availability (including relative humidity and soil moisture), cloud cover, wind, weather extremes and sea level rise. Climate change is forecast to affect average annual temperature and precipitation in GB (Hulme *et al.* 2002) as well as to increase the frequency of extreme weather events including torrential rains, very strong winds, heat waves and droughts. Flooding could increase the prevalence of endemic pathogens that are transmitted by the faecal–oral route, and even that of botulism and anthrax (Baylis and Githeko 2006). Here, the factors through which climate change could affect livestock diseases are reviewed as a basis for developing a qualitative risk assessment framework. A case study is presented for liver fluke and the implications of the effect of climate change on livestock diseases are considered.

The abbreviations used for the viral diseases considered here are listed in Table 1.

Table 1 List of abbreviations used for viruses and viral diseases

| Virus/disease | Abbreviation |
|--|--------------|
| African horse sickness (virus) | AHS(V) |
| African swine fever (virus) | ASF(V) |
| Alkhurma haemorrhagic fever (virus) | AHF(V) |
| Avian influenza (virus) | AI(V) |
| Bluetongue (virus)(serotype 8) | BT(V)(8) |
| Chikungunya virus | CHIKV |
| Crimean-Congo haemorrhagic fever (virus) | CCHF(V) |
| Epizootic haemorrhagic disease (virus) | EHD(V) |
| Greek goat encephalitis (virus) | GGE(V) |
| Louping ill (virus) | LI(V) |
| Malignant catarrhal fever | MCF |
| Maedi-visna virus | MVV |
| Ovine herpes virus | OHV |
| Rift Valley fever (virus) | RVF(V) |
| Spanish sheep encephalitis (virus) | SSE(V) |
| Tick-borne encephalitis (virus) | TBE(V) |
| Turkish sheep encephalitis (virus) | TSE(V) |
| Venezuelan equine encephalitis (virus) | VEEV |
| West Nile virus | WNV |

Assessing the implications of climate change on livestock diseases in GB

Livestock diseases in warmer regions of the world as an indication of what might happen in GB

The United Kingdom Climate Impacts Programme Scientific Report (Hulme *et al.* 2002) presents forecasts of GB's climate in the 21st Century for the 2020s, 2050s and 2080s. The emergence of disease is a broad term, which covers not only evolution of new microbes, but also expansion in geographic range, increase in incidence, change in pathways or pathology and infection in new host species or populations (Olival and Daszak 2005). Some indication of which animal diseases may emerge in GB with climate change could be gained from considering those livestock diseases that are emerging or are established in other parts of the world (e.g. southern France or Spain) that have a climate similar to that forecast for GB in the future.

Examples that illustrate this approach include the emergence of BTV8 in northern Europe in 2006 (Meiswinkel *et al.* 2007) and its detection in England in September 2007 (Landeg 2007), despite the fact that its emergence in northern Europe was not preceded by incursions in southern Europe – its origin has been linked to sub-Saharan Africa (Meiswinkel *et al.* 2007). Equine piroplasmiasis, which is a tick-borne disease of horses caused by two intraerythrocytic protozoans (*Theileria equi* and *Babesia caballi*), provides another example of a disease that occurs near GB. A survey of 424

horses in southern France showed seroprevalence of 64.4% for *T. equi* and 19.7% for *B. caballi* (Leblond *et al.* 2005).

However, a difficulty with this approach is that not all factors will change at the same rate as climate changes. As the average temperatures increase across GB, some factors may change faster than others in effect, resulting in mistiming. An example of mistiming because of climate change is the loss of synchrony between nesting and peak food abundance in migratory birds (Both *et al.* 2006). Differential movements of wildlife species' traits (e.g. the range and abundance of species, timing of migration and morphology) in response to the rapid rate of temperature rise together with habitat destructions could result in a disruption of the connectedness among many species in current ecosystems, leading to a reformulation of wildlife species communities (Root *et al.* 2003). Differential rates of change could create novel, or at least different, micro-environments and ecological and agricultural combinations with certain imbalances and provide new opportunities for livestock diseases to emerge in GB compared to in southern Europe at present. Therefore, forecasting which livestock diseases will emerge in GB as a result of climate change is not as simple as looking at current livestock diseases in southern Europe alone. The arrival of exotic diseases in GB from distant parts of the world is not new (Gould *et al.* 2006). To forecast the 'unexpected', all potential routes for disease to enter GB need to be considered in risk assessments. Similarly, the introduction, establishment and rapid spread of WNV in the Americas (Diaz *et al.* 2008) show that there is a risk of livestock diseases from distant parts of the world emerging in Europe. With modern international travel and globalized trade, any risk assessment has to look beyond those diseases currently in Europe. For example, exotic pathogens such as the VEEV and the rickettsia *Ehrlichia ruminantium* need further consideration.

A risk framework approach

The objective is to develop a risk-based framework to screen for any unexpected organism that might have a higher likelihood of emerging in GB as a result of climate change and to identify endemic pathogens and vectors that might be affected by climate change. Central to the risk assessment is the identification of those factors through which climate change could affect livestock diseases. These factors include the molecular biology of the pathogen, the vectors, farming practice and land use, zoological and environmental factors together with the establishment of new microhabitats.

Factors through which climate change could affect livestock diseases

Molecular biology of the pathogen itself

The ability of a microbial pathogen to mutate and hence respond to opportunities arising from change is a key factor in considering the potential impact of climate change. For example, genetic studies (Brault *et al.* 2004) of VEEV in Mexico implicated a single amino acid substitution in the envelope glycoprotein in the adaptation of the virus to an efficient epizootic vector, namely the mosquito *Ochlerotatus taeniorhynchus*. This vector became the most abundant species of mosquito feeding on mammals after deforestation eliminated the habitats of *Culex taeniopus*, which had been the principal mosquito vector. This example illustrates the ability of RNA viruses to respond rapidly to changes in vector populations such as those that could arise as a result of climate change. Another example is a single mutation in CHIKV that promotes infection in the mosquito *Aedes albopictus* over the recognized vector, *Ae. aegypti* (Tsetsarkin *et al.* 2007). This mutation increases the potential for CHIKV to extend its range into Europe and the Americas, where *Ae. albopictus* has established over the past 20 years (Medlock *et al.* 2006). In 2007, transmission of CHIKV was reported for the first time outside the tropics with the occurrence of cases in southern Europe (Enserink 2007).

RNA viruses have a high evolutionary rate ('genetic drift') because there is no proof-reading, and those with segmented genomes are also able to reassort ('genetic shift'). For example, reassortment of the RNA segments in lineages of CCHFV has been reported (Hewson *et al.* 2004). Other examples of segmented RNA viruses include RVFV, AIV, BTV and AHSV. The degree of conservation of the host receptor used by the pathogen is also important, and although not directly affected by climate change would reduce the species barrier, and hence facilitate spillover into new species such as livestock through encroachment into wildlife habitats, for example.

Randolph and Rogers (2006) have argued that because they must remain infective in two host species (i.e. an invertebrate vector and the vertebrate host), the rate of evolution of vector-borne microbes may be more constrained than that of directly transmitted microbes. However, although the UK appears not to be currently at risk of invasion by WNV (Randolph and Rogers 2006), mutations may easily change the nature of the various biotic and abiotic factors that limit the geographical spread of a virus.

Vectors

Many livestock diseases are transmitted by invertebrate vectors. Thus liver flukes are transmitted through lym-

naeid snails, and a range of arboviruses, many of which have RNA genomes, are transmitted by arthropods including biting midges, ticks and mosquitoes. Livestock viruses transmitted by *Culicoides* biting midges include BTV, AHSV, Akabane virus and EHDV and are not zoonotic. However, many mosquito-transmitted livestock viruses including WNV, RVFV and the equine encephalitis group of alphaviruses (e.g. VEEV) are zoonotic. Tick-borne livestock viruses listed by the World Organisation for Animal Health (Office International des Epizooties 2006) include ASFV and CCHFV. LIV is included in the TBEV complex (Gould *et al.* 2006) and is transmitted by *Ixodes* spp. ticks causing disease in domestic animals and grouse in GB. Related tick-borne flaviviruses of the TBEV group including SSEV, GGEV and TSEV can cause fatal encephalomyelitis in livestock exposed to infected ticks (Gould *et al.* 2006; Randolph and Rogers 2006). *Amblyomma* ticks are vectors for *Eh. ruminantium*, which causes cowdriosis (Uilenberg 1996).

Climate change may affect not only the geographical range and abundance of vectors, but also the interaction between a pathogen and a vector (e.g. such that the pathogen may be transmitted by new vectors). The emergence of BTV in Europe since 1998 has been facilitated by both mechanisms.

Change in vector range with climate change

There are several examples of recent changes in vector range that are related to changes in climatic variables, and that are accompanied by disease. The incursions of BTV into southern Europe reflect the northwards expansion of the traditional vector, *Culicoides imicola* (Purse *et al.* 2005), which has also supported excursions of AHSV from endemic areas (sub-Saharan Africa) into Portugal and Spain (Mellor and Hamblin 2004). Argasid (soft) ticks survive well in very dry, desert conditions and *Ornithodoros sonrai* has expanded its range, and that of tick-borne borreliosis, into areas of sub-Saharan Africa as the 750-mm isohyet (Trape *et al.* 1996) has moved in association with the drought. *O. sonrai* serves as the primary vector for ASFV in Senegal (Vial *et al.* 2007) and its expansion in range could be accompanied by persistence of ASF. The soft tick *O. savignyi*, which transmits AHFV, is well-established through countries in the Persian Gulf region (Charrel *et al.* 2007). AHFV was discovered in 1995 and there is little information on its geographic distribution in relation to the wide range of *O. savignyi*, which could potentially expand with climate change. Argasid ticks have a higher critical temperature (which controls water permeability) than ixodid (hard) ticks and thus have a greater ability to resist desiccation (Davis 1974), which may facilitate their expansion in range with climate change. Although it is unlikely that those

Ornithodoros ticks which serve as vectors for ASF and AHF could establish in GB through climate change, other Argasid ticks are present on bats (*Argas vespertilionis*) and pigeons (*Argas reflexus*) in GB although only one species of *Ornithodoros* tick occurs in north west Europe. This is *O. maritimus*, which is found on seabirds around GB (Martyn 1988).

The common sheep tick, *Ixodes ricinus*, is the most abundant tick species in north-west Europe, and is confined to humid environments because of its relatively permeable cuticle (Hillyard 1996). It requires microclimates provided by vegetation cover with at least 80% humidity for survival, in addition to an abundance of hosts, including small and large mammals (Pietzsch *et al.* 2005). Its distribution from historical records has been mapped in GB (Pietzsch *et al.* 2005). The brown dog tick, *Rhipicephalus sanguineus*, is the vector for *Eh. canis* and *Babesia canis* in dogs and also for human rickettsioses including Rocky Mountain spotted fever (*Rickettsia rickettsii*) and Boutonneuse fever (*Ri. conorii*). Dogs transported from the south of France, Spain and Italy have introduced this tick into northern Europe (Hillyard 1996). Infestations of this hard tick have been reported within and outside GB quarantine kennels (Bates 2008), with a case of its establishing in a well-heated house in London reported more than 20 years ago (Fox and Sykes 1985). *Rhipicephalus* species require temperatures above 18°C to complete their life cycle and milder winters could facilitate their establishment in GB. Climate-related change was attributed as the major factor in the marked shift in the distribution of *I. ricinus* to higher altitudes (by up to 500 m) in the Krkonose National Park in the Czech Republic, where two human cases of TBE have occurred at altitudes higher than any previously reported (Daniel *et al.* 2004; Danielova *et al.* 2006).

Olwoch *et al.* (2003) used climatic data to forecast tick distributions over sub-Saharan Africa. They acknowledged that they were not suggesting a climate envelope approach alone is adequate to forecast the fine-scale distribution of tick species across sub-Saharan Africa. They noted that tick distribution and abundance are more likely to be affected by factors other than climate such as host abundance, host resistance to ticks, acaricide use and grazing management. Olwoch *et al.* (2003) suggested that employing climate variables as the main limiting factors for tick distributions remains the best option available, arguing that the other factors mentioned interact with climatic variables so that it is not possible to separate the effects of these interrelated factors.

Change in vector abundance with climate change

Rainfall can alter the abundance and type of aquatic habitats available to the mosquito for oviposition (Shaman

and Day 2005). The abundance of midges and mosquitoes may be increased through the generation of vector breeding sites by periods of drought followed by heavy rainfall. Heavy rainfall and flooding can trigger epidemics of mosquito-borne disease in areas where the climate is usually too dry to maintain an abundant mosquito population (Ahern and Kovats 2006). In Africa, epizootics of AHS and RVF are associated with the combination of drought followed by heavy rainfall brought by the warm phase of the El Niño Southern Oscillation (Baylis and Githeko 2006).

Change in vector/pathogen interaction

Vector competence may be affected by temperature. For example, BTV is transmitted most efficiently by *C. imicola* at temperatures of 28–30°C, much less efficiently at lower temperatures, and not at all below 10°C (Gloster *et al.* 2007). Midges of the *C. obsoletus* complex (Mehlhorn *et al.* 2007), which are indigenous to the north Palaearctic, have served as vectors for BTV8 outbreaks in north-western Europe since 2006. The higher temperatures recently experienced in northern Europe have increased the competence of the indigenous species of midge which, for the first time, have served as vectors for BTV. Similarly, the competence of *Culicoides* midges for transmitting AHSV increases with temperature (Mellor and Hamblin 2004). In contrast, infection of Western equine encephalitis virus in the mosquito vector, *Cu. tarsalis*, is suppressed at higher temperatures (Reeves *et al.* 1994). For many arboviruses, the extrinsic incubation period, which is the time between when an uninfected vector feeds on a viraemic host and is able to infect a susceptible host, is shorter at higher temperatures. This reflects a higher rate of virogenesis, which compensates for the shorter lifespan of the vector at higher temperatures.

Effect of temperature and other climatic variables on vector activity

The feeding rate of many arthropod vectors increases at higher temperatures, thus increasing exposure of livestock to pathogens, and hence the spread of disease. The main effect of climate change on mean temperature is through warmer night-time temperatures (Beniston and Diaz 2004). This is important for many insect vectors that fly and feed at night. In the heat wave of summer 2003, night-time temperatures did not cool off to any great extent in Switzerland (Beniston and Diaz 2004), compounding the effects of heat stress on both humans and livestock. The very high minimum temperatures distinguished the 2003 heat wave from those that occurred in 1947 and 1976. In this respect, the 2003 event was a 'climatic surprise' and Beniston and Diaz (2004)

forecast that similar events are likely to occur with increasing frequency in the latter part of the 21st century. Rainfall may affect mosquito abundance by increasing mosquito flight activity and thus accelerating the reproductive cycle, which requires mating, host-seeking, and blood-feeding flights (Shaman and Day 2005).

Impact of climate on the persistence and survival of pathogen in the vector population

The longer a pathogen can maintain infection in a vector population, the longer it will persist. Pathogens move from one vector individual to another through mechanisms such as sexual transmission and transovarial transmission. For example, transovarial transmission of ASFV occurs in *O. moubata* ticks (Rennie *et al.* 2001), although not in *O. erraticus* (cited in Basto *et al.* 2006). Of particular importance is the impact of climate change on tick-to-tick (nonviraemic) transmission of flaviviruses (e.g. LIV) in the TBEV group (Randolph *et al.* 2000; Rogers and Randolph 2006). Norman *et al.* (2004) have modelled the role of nonviraemic transmission on the persistence and dynamics of LIV in red grouse and mountain hares. They concluded that if the level of nonviraemic transmission is high enough, the virus can persist in the absence of the viraemic host. Nonviraemic transmission requires synchrony between the timing of feeding larval and nymphal stages and is susceptible to climatic conditions.

Vector-borne pathogens also exploit the longevity and multistage life cycles of the arthropods. Mechanisms include transtadial transmission, diapause and survival of desiccation. The transmission of ASFV through *O. erraticus* ticks in southern Iberia may have contributed to the persistence of this disease (APHIS 2001) after its introduction, probably through imported meat products. ASFV DNA is detectable in *O. erraticus* ticks 63 weeks following an outbreak (Basto *et al.* 2006). In 2000, ticks were still positive for ASFV in sites of previous outbreaks in the early 1990s (APHIS 2001). Milder winters enable over-wintering of viruses in latently infected vectors, such as is postulated for AHSV in latently infected *Culicoides* midges that can now survive the milder winters in southern Europe (Mellor and Hamblin 2004).

Photoperiodic egg diapause in *Ae. albopictus* allows this tropical mosquito to over-winter and establish in temperate climates. Females lay their eggs in water, which has transiently collected in man-made containers including flower vases and discarded car tyres. The eggs of *Ae. albopictus* are resistant to desiccation. The international trade in used car tyres provides a potential mechanism for the eggs of this mosquito to be moved around the world and imported into GB (Medlock *et al.* 2006).

Farming practice and land use

Several examples from outside GB show how changes in livestock farming practice affect the emergence of epizootic and zoonotic diseases. Thus pigs in Malaysia were exposed to Nipah virus in fruit bats through being housed in deforested areas used to grow palm oil trees (Hsu *et al.* 2004; Olival and Daszak 2005). In West Africa, the emergence of CCHF in humans was due to movement of livestock nearer to cities to obtain animal feed during drought (Nabeth *et al.* 2004).

The effect of climate change on farming practice and land use in GB is uncertain, and the effects on livestock and dairy production are likely to be extremely complex and variable (National Farmers' Union 2005). Climate change could affect the nature and intensity of livestock farming in GB through drought, climate variability (which could reduce grass supply and hence increase reliance on supplementary feed), the requirement for shade and housing to protect against heat stress, new types of animal feed supplement, industry competition and response to extreme weather events such as heat waves and flooding. It is unlikely to become hot enough in GB to require dairy cattle always to be housed during the day in summer and only to graze at night (Department for Environment, Food and Rural Affairs 2000). For the purpose of risk assessment, the main considerations are the effect of climate change on the intensity of farming and the movement of livestock. More intensive farming, requiring housing to meet food and water shortages and to provide protection from heat stress, could increase the frequency and duration of direct animal-to-animal contacts and hence increase the risk of transmission of diseases. An increase in extensive farming, for example because of a longer grass-growing season (National Farmers' Union 2005), may reduce the frequency of such contacts, but may increase the opportunities for contact between livestock and wildlife. Flooding is likely to confine livestock to smaller areas, and may promote mixing of breeds and species (e.g. mixing sheep and cattle grazing pastures). Increased transport and movement of livestock within GB to areas with better grasslands or to avoid drought and flooding may also increase between-farm livestock contacts and the risk of exposure of susceptible animals and herds to infection and infestation (Baylis and Githeko 2006).

Adaptation to climate change may lead to a shifting of cattle farming from traditional livestock farming areas within GB to make way for biofuel production. The encroachment of livestock farming on new habitats through such changes in land use may increase contact between livestock and wildlife. Climate change may also decrease the quality of grasslands, resulting in livestock

eating more soil, with greater exposure to soil pathogens such as *Bacillus anthracis*. It is possible that GB livestock farmers will introduce breeds of livestock better able to withstand different climatic conditions. Some breeds of sheep are much more susceptible to certain livestock diseases e.g. BTV (Darpel *et al.* 2007) and MVV (Berriatua *et al.* 2003) than are others and their introduction by GB farmers would alter the susceptibility of GB herds to disease.

Zoological factors

Vertebrate reservoir hosts, including both livestock and wildlife, play an important role in the replication, maintenance and dissemination of many arboviruses and other vector-borne pathogens such as *Babesia* species and *Ehrlichia* species. Examples are birds for WNV (Buckley *et al.* 2003), rodents (spiny rats) for VEEV (Carrara *et al.* 2007), zebras and donkeys for AHSV (Mellor and Hamblin 2004), roe deer for certain *Babesia* species (Bonnet *et al.* 2007), and wildebeest, hares and tortoises for *Eh. ruminantium*. Hares have been shown to play a role as reservoir hosts for CCHFV in Bulgaria and countries of the former Soviet Union, as well as in southern Africa (Nalca and Whitehouse 2007). It is unlikely that BTV persists in cattle or sheep as an over-wintering mechanism for the virus in the absence of *Culicoides* midges (Lunt *et al.* 2006), although transplacental transmission has recently been demonstrated.

Host immunity is an important factor as illustrated by WNV. WNV arrived in the United States (US) in 1999 and has seriously affected certain North American wild bird populations (LaDeau *et al.* 2007), although wild bird deaths do not appear to be a feature of WNV epidemiology in Europe (Buckley *et al.* 2003). This is attributed to the herd immunity built up in the Old World where the disease has been endemic for many years, whereas the virus appears to be more virulent in the immunologically naïve wild bird populations of the New World (Rogers and Sanderson 2006). Transmission of VEEV depends on the constant generation of immunologically naïve rodents and other reservoir hosts may be required to maintain enzootic VEEV transmission when spiny rat populations are low (Carrara *et al.* 2005). The geographical origin of cotton rats is an important determinant of their reservoir potential and of the outcome of VEEV infection (Carrara *et al.* 2007).

Wild mammals such as deer and rodents are wildlife hosts in GB for the tick *I. ricinus* (Pietzsch *et al.* 2005), which serves as a vector for pathogens such as the TBEV group of viruses including LIV. Migrating birds may carry infected ticks from one country to another, although the percentage of TBEV-infected ticks on migrant birds in Sweden was very low (Waldenström *et al.* 2007). There

are eight records of *Hyalomma marginatum*, the tick vector for CCHFV, on newly arrived migrant warblers in GB (Marty 1988). All records of *H. marginatum* in GB refer to larvae and nymphs with adult ticks not having been detected so far (Hillyard 1996). Changes in the habitats and ecology of vertebrate reservoirs through climate change and human factors such as deforestation may affect the transmission of pathogens from wildlife to livestock and humans. The climate change effects on the interactions of wildlife, pathogen and livestock are complex, but can usefully be considered as the effects on abundance, behaviour and movement.

Impact of climate change on the abundance of vertebrate hosts and reservoirs

Increased precipitation may enhance food resources for small mammals (Parmenter *et al.* 1999). In New Mexico, wetter than average winter spring periods have led to an increased abundance of rodents that, in turn, led to an increase in human cases of plague (Parmenter *et al.* 1999). In the southwestern US, the abundance of the deer mouse, a reservoir for Sin Nombre hantavirus, has increased with increased rainfall during recent years (Kruse *et al.* 2004). Root *et al.* (2007) reported a doubling of badger numbers in Wytham Woods (Oxfordshire, UK) between 1987 and 2001 and an increase in numbers in southern Finland. They suggested that this may be because of the increase in the availability of earthworms as a result of milder, damper microclimatic conditions and the absence of winter frosts, enabling badgers to feed throughout the winter. In GB, there is some evidence that the common rat increased in abundance between 1996 and 2002, although large annual population fluctuations may obscure trends (Battersby 2005). Similarly, roe deer and muntjac are increasing in abundance in GB (Battersby 2005). This may be related to climate change (for example milder winters), although other factors such as the creation of more deer-friendly habitats through recent changes in land use are also important. Farming practice also affects wildlife abundance. For example, changes in farming practice in GB have resulted in a considerable decline in the abundance of the house mouse (Battersby 2005).

Some livestock viruses such as AIV and WNV are bird-borne. Changes in habitat and food supply as a result of climate change may lead to the extinction of some wild bird species. In northern Europe, mistiming of breeding with maximal food abundance is responsible for population declines in long distance, insectivorous migrants such as the pied flycatcher (Both *et al.* 2006) and in species resident in GB such as the great tit (Visser *et al.* 1998). An increase in caterpillar abundance and hence tree damage is forecast (Root *et al.* 2007). The decline in predation

because of a loss of insectivorous bird species may increase the abundance of some invertebrate vectors resulting in an increase in some vector-borne diseases.

Impact of climate change on the behaviour and interaction of wildlife

Climate change will affect wildlife habitats and food sources, which could result in changes in wildlife behaviour and feeding patterns in response to the new conditions. For example, the Daubenton's bat, 2% of which are sero-positive for European bat lyssavirus (Fooks *et al.* 2006) is increasing in abundance across GB (Battersby 2005) and feeds on insects over water. The effect of climate change (e.g. hot, dry summers interspersed with periods of extreme flooding) on the behaviour of this bat is not known.

Competition between wildlife species within an ecosystem often limits the abundance and/or distribution of one or more species. For example, global decline in amphibian populations is already occurring as a result of habitat loss, infection by a chytridiomycete fungus and climate change, with some species now extinct in Latin America (Lips *et al.* 2005). Tadpoles compete with and suppress mosquito larvae in the same water body and there may be a resulting increase in mosquito abundance and hence mosquito-borne disease if numbers of tadpoles decline (Mokany and Shine 2002, 2003). Many wildlife species are social, with the individuals forming groups. Infectious contact rates will be greater within social groups than between them (Riordan *et al.* 2007), particularly where individuals aggregate in shared roosts, colonies and dens. Climate change may affect the social structure of such wildlife groups, creating new opportunities for social flux and hence interaction with livestock.

Impact of climate change on the movement and distribution of wildlife

Climate change could promote biological invasion of nonindigenous species with their associated pathogens and parasites. Reptiles serve as reservoirs of certain pathogens (e.g. *Salmonella* species) that infect livestock and humans (Chomel *et al.* 2007). Climate change could enable certain reptile species to survive in GB. Reptiles could enter and establish in GB inadvertently via trade (e.g. in shipping containers) or through escape of legally imported pets. Reptiles imported through GB airports carry a number of tick species. Pietzsch *et al.* (2006) reported three species of *Amblyomma* tick on imported reptiles at London's Heathrow airport.

Climate change will affect animal migration and distribution. In the long term, could wild bird movements be reduced by climate change? This would depend on the availability of food and the day length for finding food in

the breeding grounds during winter. Climate change could also result in wild bird breeding ranges shifting northwards from Mediterranean regions into GB, as occurred with the little egret in the mid 1990s and more recently with the cattle egret. Little egrets, in particular, are vulnerable to long periods of cold (Voisin 1991) that may be diminishing as a result of climate change.

The serotine bat is currently restricted to southern England (Battersby 2005) and climate change might facilitate a northwards expansion of its range. Warming trends in Fenno-Scandinavia have allowed badgers to extend their distribution 100 km northwards in Finland since the mid 1940s and badgers now occur as far north as the Arctic Circle (Root *et al.* 2007).

Environmental factors

Environmental conditions such as temperature, humidity and sunlight affect the survival of those pathogens that are able to survive outside the host in the environment. These include *B. anthracis*, *Cryptosporidium*, *Giardia*, *Escherichia coli* O157, salmonellas and campylobacters. Viruses, (oo)cysts and bacteria survive better in soil in cooler, winter conditions than in warmer, summer conditions (Tierney *et al.* 1977; Olson *et al.* 1999). *Campylobacter* species have a number of survival mechanisms enabling adaptation to stress conditions in the environment. These are reviewed by Murphy *et al.* (2006) and they include heat stress, cold stress, aerobic stress, ultraviolet stress, and survival of desiccation. *Campylobacter* species are very sensitive to desiccation and will survive only on wet surfaces.

The transmission of many diarrhoeal diseases in humans is associated with seasonal rains and flooding (Ahern and Kovats 2006). Time series analyses by Pascual *et al.* (2000) showed that outbreaks of cholera in Bangladesh reflect the El Niño Southern Oscillation (and also previous disease levels and host immunity). Koelle *et al.* (2005) showed that once the interplay of climate forcing and disease dynamics is taken into account, there is clear evidence for a role of climate variability in the transmission of cholera. From a risk assessment perspective, flooding has three effects for faecal–oral pathogens. First, flooding causes animal wastes to breach lagoon walls and spill across fields and into surface waters, directly increasing the environmental load of faecal pathogens, and providing a transfer mechanism both within and between farms to contaminate pasture and other areas where livestock have access (Schmidt 2000; Tyrrel and Quinton 2003). Second, puddles may have a protective factor in the survival of some bacterial pathogens. Third, dispersion of pathogens is increased, thus increasing the group risk depending on the dose–response (Gale 2005).

Establishment of new microclimates and micro-environments

Microclimates are particularly important for creating suitable habitats for vectors including arthropods and snails. Danielova *et al.* (2006) noted that a particular (and common) habitat at altitudes above 1000 m in the Krkonose Mountains (Czech Republic) is formed by a solitary tree (or small groups of trees) in grassy land, with branches reaching the ground. These 'canopy trees' provide a specific favourable microclimate throughout the year for *I. ricinus* ticks and also provide shelter for the ticks' vertebrate hosts. Such micro-environments could include new plant species, greenhouses, pig sties (which provide habitats for certain ticks), or water-collecting containers for *Aedes* mosquito larvae. A recent study of breeding sites in Belgium for midge species of the *C. obsoletus/scotius* complex (a major vector for BTV8) identified mainly anthropic environments (e.g. maize silage) close to farms (Zimmer *et al.* 2008). Microclimates may change the micro-environment, altering the survival properties of environmental stages of pathogens such as enteric viruses and protozoal cysts transmitted by the faecal-oral route. By altering the vegetation, climate change may affect the soil porosity and structure and thus the retention of pathogens within the soil (Sobsey *et al.* 1980).

Interaction of factors

Many of those factors through which climate change affects livestock diseases will interact with each other in ways that, as yet, may not be fully understood. Changes in farming practice and land use because of climate change may occur concurrently with anthropogenic changes such as deforestation, economic change and social change, including the demand for more free-range and 'organic' produce. During periods of drought, the risk of escalation of a low level conflict increases (Giles 2007). Military action although not likely in GB, could increase the prevalence and distribution of livestock diseases in other parts of the world, which in turn would increase the risk of release into GB. Farming of exotic livestock species such as camelids, alpacas and ostriches may increase in GB, and these species may serve as reservoirs or vector hosts for certain livestock diseases. Changes in farming practice in response to climate change, together with the effect of climate change on habitats, will affect the distribution and abundance of wildlife and these changes will affect both the vector species that can be supported and the availability of reservoir hosts of livestock pathogens. Contact between humans, livestock and wildlife may increase, thus creating opportunities for the emergence of new livestock diseases. Local anthropogenic changes may also have an

important effect on the vectors. For example, in the Camargue region of France, the abundance of *Cu. modestus*, which is the main mosquito vector for WNV, has been affected by expansion of rice cultivation, pesticide use and pest-management strategies (Poncon *et al.* 2007). Change in crop type and hence pesticide use because of adaptation to climate change could affect vectors and host reservoirs, as indeed could growth of small copses to provide a local supply of wood for fuel. Extreme weather events such as flooding in GB can prevent distribution of treated water to households, thus increasing the tendency to store water in containers, which if left stagnant, could provide breeding sites for mosquitoes.

The increase in incidence of TBE in humans in the Baltic States from 1992 to 1993 (Sumilo *et al.* 2006) provides an indication of the complexity of the effects of climate change on disease. Land cover (i.e. the type of habitat with regard to suitability of the tick vector) and precise seasonal patterns of climatic indices (namely the land surface temperature and the normalized difference vegetation index which indicates moisture availability) explained 55% of the observed spatial variation in TBE incidence across the Baltic States. However, the study recommended the investigation of other factors such as the abundance of tick hosts, human behaviour in relation to exposure to ticks and public health services (e.g. regional differences in vaccination rate) to fully explain the spatial variation observed. Temporal analysis of climatic variables indicated a very specific change in the spring temperature conditions since 1993 that could have enhanced tick-to-tick (nonviraemic) transmission of TBEV. Other causes might explain the increased incidence of a tick-borne disease in persisting foci, despite a reduction in the number of foci because of climate change. Such factors include socio-political changes (including the fall of communism in Poland and the Baltic States) and increases in deer abundance (Rogers and Randolph 2006).

The risk of infection with vector-borne diseases in livestock depends on the abundance of infected vectors and the rate of contact of livestock animals with those infected vectors. For human tick-borne diseases, the abundance of infected ticks and the rate of contact of humans with those infected ticks can change independently (Randolph 2006). Indeed, climatic variables could affect both independently, and in different ways. According to Rogers and Randolph (2006), there is often a multitude of causes for changes in vector-borne diseases and in a number of cases, these causes are clearly not climatological. They add that it is important to adopt a landscape-epidemiological approach in which the 'landscape' includes not just the physical environment and its changing climate but also the economic and sociological environments as well. For example, changing land-use

and livestock practices in Europe were more responsible for diminishing the geographical extent of malaria in Europe than were any concurrent climatological changes.

Some vector–pathogen effects are directly related to temperature and Gloster *et al.* (2007) recently developed a qualitative risk assessment, which uses information on wind, temperature and rainfall, to assess the risk of introduction to GB of wind-borne BTV-infected midges. Elfadil *et al.* (2006) studied the environmental and animal risk factors associated with RVF in south-west Saudi Arabia. Positive associations were found between RVF and the following factors: a dense mosquito population, high rainfall and the presence of lakes and/or ponds. Linthicum *et al.* (1999) showed that accurate forecasts of RVF outbreaks can be made up to 5 months in advance of their occurrence in East Africa, based on the normalized difference vegetation index and sea surface temperature anomalies. RVF in East Africa is a specific example of a well-studied disease that is endemic in that area. The objective of the work here was more to screen for the emergence of the unexpected in GB against a background of change. The scenarios could be complicated. However, elucidating the combinations of factors and events that interact may facilitate forecasting the unexpected. An

example for the unexpected is the sudden introduction and rapid spread of WNV in the Americas. Although the timing of such an event may be difficult to forecast, importation of an exotic infected bird or indeed an infected mosquito via an airport has been identified as a risk factor for WNV (see Rogers and Sanderson 2006). Other factors such as the existence of both an immunologically naïve bird population (Buckley *et al.* 2003) and a high density of competent mosquitoes are also important (Glaser 2004). There is also evidence from the WNV outbreak in Israel in 2000 that the magnitude of the minimum temperature during prolonged heat waves is the key climatic variable (Paz 2006). The 1999 outbreak in New York was preceded by a 3-month drought and a 2-week heat wave (cited in Rogers and Sanderson 2006).

Development of a risk framework to screen for the emergence of the unexpected in GB

A prototype risk framework based on six modules is set out in Table 2, together with the main factors. Module 1 reflects the release assessment of the risk analysis framework of Office International des Epizooties (2004) and identifies the routes of transmission to and/or within GB.

Table 2 Modules comprising risk framework for assessing potential impact of climate change on livestock pathogens in GB

| No. | Description | Aims | Main factors |
|-----|--|---|---|
| 1 | Routes to and within GB | To identify all known and theoretical routes to and/or within GB. To assess whether climate change could promote new routes, or increase the risk of release through old routes | Effects on prevalence of diseases in other parts of the world. Routes to/within GB may be affected through changes in vectors, farming practice and land use, and zoological and environmental factors |
| 2 | Molecular biology of the pathogen itself | To establish the potential of the pathogen to evolve in response to novel opportunities from climate change, and to develop resistance to chemical treatments | High mutation rate in RNA viruses, recombination of genomes in segmented viruses. Ability to adapt to new environments and development of resistance to flukicides (in the case of liver flukes) |
| 3 | Host reservoirs | To identify potential and known hosts in GB. To assess the effect of climate change on the range, abundance and diversity of potential vertebrate hosts | Zoological factors together with farming practice and land use. Herd immunity |
| 4 | Vector route | To assess the effect of climate change on the entomological risk (i.e. range, abundance and competence of the vector) and the risk of livestock exposure to infected vectors | Changing microhabitats and zoological factors that affect vector range. Changing environmental factors (e.g. drought followed by heavy rainfall) that may affect vector abundance through breeding sites. Climatic variables that affect vector competence and feeding rate |
| 5 | Degree of animal contact and movement | To assess the effect of climate change on the transmission through direct and indirect contacts with other livestock and wildlife, both between farm and within farm | Changes in farming practice and land use affect the density, movement and mixing of animals. Changes in zoological factors affect wildlife contact with livestock |
| 6 | Environmental routes | To assess the effect of climate change on the transmission through environmental routes (e.g. fomites, water and soil) | Impact of changes in environmental factors and microclimates on survival, dispersion or distribution of environmental stages of the pathogen. Impact of changes in farming practice and land use on exposure of livestock to environmental pathogen stages |

It is important to consider all theoretical routes, however minor and irrespective of whether or not epidemiological studies have demonstrated that they occur. Potential routes include imported livestock, germplasm, animal feeds, meat and meat products, pets, vectors, wild animals and persons. Specific examples of routes of introduction include:

- 3–4% of migrating birds in Sweden in 2001 were infested with ticks (*I. ricinus*); four of 13 260 birds carried ticks infected with TBEV (Waldenström *et al.* 2007);
- Zebras, horses or donkeys infected with AHSV imported into Spain in 1987 (Mellor and Hamblin 2004);
- Imported reptiles with *Amblyomma* ticks (see Pietzsch *et al.* 2006);
- Importation of eggs of the mosquito *Ae. albopictus* in car tyres to GB, although there is no evidence that this happened yet (Medlock *et al.* 2006) and
- *Culicoides* midges infected with BTV virus were blown from areas of northern Europe with BTV (Gloster *et al.* 2007).

In module 2, the ability of the pathogen to respond to change through consideration of its molecular biology is assessed. Modules 3–6 reflect the exposure assessment of the risk assessment framework of Office International des Epizooties (2004) and assess the effect of climate change on the establishment of a reservoir of disease in vertebrate hosts, the exposure of livestock through vectors and environmental routes, and the effects on the degree of animal contacts and movement. Each module requires consideration of the effect of climate change through the factors described above, as set out in Table 2. For example, in module no. 3, the host reservoirs module, consideration should be given to which wildlife species could serve as hosts in GB, what is known about immunity to the pathogen in that host, and how the range and abundance of potential hosts could be affected by climate change.

Liver fluke – a case study

The liver fluke trematode (*Fasciola hepatica*) is transmitted through lymnaeid snails, which thrive in low-lying wet pastures subject to periodic flooding, and in temporary or permanent bodies of water (Baylis and Githeko 2006). Liver fluke is endemic in GB. Increased influx of sheep from endemic areas (Pritchard *et al.* 2005) because of climate-related factors (e.g. flooding, poorer pastures, changing land use) could promote release into new areas of GB (module 1). There is evidence that liver flukes can adapt not only to flukicides but also to new environmental and climatic niches (module 2). Thus, liver flukes and its snail hosts were introduced from Europe into Bolivia (Mas-Coma *et al.* 2001), where they have adapted to the extreme environmental conditions of the high altitude

(3800–4100 m). For module 4, mild winters and high rainfall in summer have enabled its snail intermediate host (*Lymnaea truncatula*) to survive in areas of GB previously considered to be too dry (Scottish Agricultural College 2004; Pritchard *et al.* 2005), although extensive droughts could decrease snail populations. For module 5, more mixing of cattle and sheep through changes in land use and farming intensity with climate change, or in response to flooding, may increase the exposure of cattle to liver fluke. Wetter conditions may also promote survival of the eggs and dispersion of the mobile larvae in the pasture (module 6). It is concluded that climate change could affect the prevalence of liver fluke in GB through factors considered in modules 1, 2, 4, 5 and 6.

Implications of the effect of climate change on livestock diseases

Consideration of the factors identified in the framework in Table 2 leads to some broad conclusions on the effect of climate change on livestock diseases. In general, for endemic livestock pathogens (e.g. anthrax, liver fluke and faecal–oral pathogens), the main effect of climate change may be through increased flooding. In contrast, for exotic livestock diseases, the main effect is through an increase in the range and/or competence of the nonvertebrate vectors, although immunity within vertebrate host reservoirs is also an important consideration.

Vector-borne livestock diseases

An increase in prevalence of some vector-borne diseases in livestock in GB is likely through changes in climate, and in the case of BTV, it has already occurred. Concerning Europe in particular, other livestock viruses including AHSV (Mellor and Hamblin 2004) and EHDV (Yadin *et al.* 2008) are transmitted by *Culicoides* midges. World-wide, the distribution of tick-borne livestock pathogens such as equine babesia, *Eh. ruminantium*, CCHFV and ASFV, and of mosquito-borne viruses such as VEEV, RVFV and WNV, may be affected by changes in climate that lead to changes in the distribution of vectors.

The immunity of the rodent reservoir hosts is a key factor in transmission of VEEV (Carrara *et al.* 2005, 2007), and rodents in GB would be expected to be immunologically naïve. With TBEV, Rogers and Randolph (2006) suggested that the effect of climate change may actually be advantageous, with central Europe being virtually cleared of infection by the 2050s and the infection being confined to a small part of Fenno-Scandinavia by the 2080s. This is due to breaking the temporal synchrony required for tick-to-tick transmission. This raises the question of whether climate change will clear

foci of LIV from GB and of other related flaviviruses such as SSEV, TSEV and GGEV from other parts of Europe.

The potential spread of pathogens associated with bird ectoparasites (e.g. ticks) will change according to the effect of climate change on migrating birds. Thus, a decline in abundance of migrants from sub-Saharan Africa (Both *et al.* 2006) would reduce the risk of introduction of infected ticks. This may be an important consideration for the geographic spread of CCHFV for example (Turell 2007), although Randolph and Ergonul (2008) argue against birds introducing CCHFV into Turkey.

Livestock diseases spread by direct contact with livestock and wildlife

It may not be the case that livestock diseases transmitted directly by animal-to-animal contact are less affected by climate change than are those involving an environmental stage or a vector. The prevalence of livestock diseases transmitted by direct contact may change because of changes in the frequency and duration of animal contacts. For example, studies on MMV in Spain have shown that transmission of MMV in sheep is affected by the intensity of rearing with seroprevalences of 77% and 5% in intensive and extensive flocks respectively (Leginagoikoa *et al.* 2006). This could explain why MVV has not been reported in countries with mainly extensively reared sheep such as Australia and New Zealand. MVV does occur in GB and routes include imported sheep for restocking (Otter and Boundy 2005). Changes in the degree of mixing of cattle and sheep will affect the prevalence of diseases such as MCF, which is caused by OHV and spread by direct contact. An increased incidence of MCF in cattle would depend on more sheep-cow contact rather than cow-cow contact (Radostits *et al.* 2000). Scottish Agricultural College Veterinary Services (2007a) reported more cases of MCF in Scotland with the lambing season bringing sheep closer to cows on some farms. Although herpes viruses are affected by stress (Heuschele and Reid 2001), the role of stress in MCF caused by OHV remains unclear. A scenario in which extreme climatic conditions (e.g. heat stress) induced the cell-free OHV in nasal secretions combined with other farming management responses to climate change (e.g. housing of cattle in response to heat stress, or co-mingling of cattle and sheep in response to flood) that increase direct contact could promote the spread of the disease.

The emergence of wildlife diseases caused by RNA viruses (e.g. coronaviruses, paramyxoviruses, rhabdoviruses) in livestock is a possibility in GB if livestock come in greater contact with species such as bats and rodents as a result of the effects of climate change. Such increased contact may be because of increasing encroachment of farming into wildlife habitats, changing wildlife behaviour

or distribution, or increasing wildlife abundance. In this respect, forecasts of the effect of climate change on rodent and bat populations are important.

The effect of climate change on the spread of avian diseases transmitted by migrating birds or trade in poultry is complex. It could be speculated that the risk of release into GB may decrease because of the long-term extinction of some migratory birds through failure to adapt to climate change (Both *et al.* 2006). A reduction in extreme winter conditions in central Europe might reduce the likelihood of wintering wildfowl flying west to GB. This would reduce the probability of release of avian diseases, such as AIV into GB. Warmer climate may decrease the risk of exposure of wild birds to AI through environmental routes (e.g. in lakes) because of reduced persistence of AIV at higher temperatures. Poultry farms in GB adopt biosecurity measures with most poultry being raised indoors, so the intensity of farming is less likely to be affected by climate change than more extensively raised livestock such as cattle and sheep. However, the trend towards 'organic' and free-range poultry production in GB might make some poultry more likely to be affected by climate change and to be exposed to wild birds.

Livestock diseases spread through environmental routes

The prevalence of diseases caused by spore-forming bacteria (e.g. botulism and anthrax) may increase because of wetter conditions after flooding and increased exposure as a result of poorer quality grass and over-grazing. For example, heavy rainfall after drought may stir up *B. anthracis* spores, leading to outbreaks of anthrax (Baylis and Githeko 2006). Botulism outbreaks in wild birds in GB in 1975 occurred in areas of shallow water and the unusually hot summer that year may have provided a suitable temperature for growth of *Clostridium botulinum* (Lloyd *et al.* 1976). Botulism outbreaks in the US are associated with periods of wet weather in agricultural land prone to flooding (Lloyd *et al.* 1976). The prevalence of endemic diseases (e.g. those caused by *E. coli* O157, *Toxoplasma*, *Giardia* and *Salmonella*) transmitted by faecal-oral routes may increase because of flooding and wetter conditions, although environmental survival is typically less in warmer conditions. Pneumonia caused by lungworm infection and scours caused by gastrointestinal parasites increased in cattle in the south-west of GB in 2007 as a result of the very wet summer, which suited the development and spread of helminth larvae on pasture (Scottish Agricultural College Veterinary Services 2007b). Listeriosis is associated with consumption of soil, although there is no evidence of any increase in either encephalitic or reproductive listeriosis over the past 10 years. *B. licheniformis* is a soil-borne organism that can cause abortion through build-up in

silage and there has been a progressive increase in this type of abortion over the past 10 years.

Discussion

The approach here assesses the effect of climate change on livestock diseases by identifying the main factors through which changing climatic conditions affect the biology, transmission and epidemiology of the pathogens and vectors. Dufour *et al.* (2006) addressed issues such as the effect of climate change on the vector, host reservoir, characteristics and epidemiology of the pathogen to evaluate the risk of emergence and development of infectious diseases in France as a result of global warming. They concluded that the probability of the evolution of the epidemiological situation of disease in France was negligible to low for RVFV, low to moderate for AHSV and high for WNV and BTV. These biological approaches can be coupled with methods for eliciting expert opinion that ask experts separately, through questionnaires or workshops, to assess the risks of release and exposure and the potential consequences for GB according to the World Organisation for Animal Health framework for risk assessment (Office International des Epizooties 2004). Such an approach has recently been applied to assess the risks of incursion of five vector-borne epizootic viruses into Europe from other parts of the world (P. Gale, unpublished data). Experts can also be asked to assess risks not only for a top-level 'all routes' overview but also for specific routes for example, vectors, meat products, wildlife, livestock, persons and companion animals. Comparing results from the two approaches provides complementary information and a powerful tool to address the question of the effect of climate change on livestock diseases.

Acknowledgements

This work is part of a project (SD0441) funded by Department for Environment, Food and Rural Affairs (Defra) to investigate the impact of climate change on agricultural pathogens and chemical contaminants. The collaborators are the Central Science Laboratory, the Hadley Centre for Climate Prediction and Research, and the Centre for Environment, Fisheries and Aquaculture Science. We thank the two anonymous referees for their helpful comments.

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