Impact of Climate Change on Livestock Disease Occurrences

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Serge Morand

Abstract

The first objective of this chapter is to review how climate change and climate variability may affect livestock diseases' occurrences while emphasizing how little the knowledge on the links between livestock diseases and climate change is. The review of the literature shows that most of the investigated diseases are zoonotic ones with few specific to livestock and, moreover, these diseases appeared to be dramatically affected by climate variability rather than by ongoing climate change. A second objective of this chapter is to introduce some new modelling tools that can help predict diseases' occurrences in space and in time in relation to climate variability and change, namely, environmental niche modelling, epidemiological modelling using R₀ map and teleconnection modelling. A working example on cattle trypanosomiasis in China is given to illustrate teleconnection modelling by using data from the World Organization for Animal Health (OIE). The conclusion of this chapter stresses three points: the need to consider the entangled linkages between ecosystems, society and health of animals and humans; the need of elaborated scenarios of livestock diseases linked to climate change and variability, which necessitates to develop and improve the recording of livestock diseases; and the need to incorporate climate-mediated physiological responses into the programs that manage breeding genetic diversity.

Keywords

Climate variability • El Niño Southern Oscillation • Environmental niche modelling • Zoonotic diseases • Teleconnection epidemiology 114 S. Morand

8.1 Introduction

Numerous studies have investigated the links between infectious diseases and climate factors such as temperature or rainfall (Baylis and Morse 2012). Many reviews have stressed that any significant change in climate will impact infectious diseases as the routes of infectious transmission will be affected (Altizer et al. 2013) although the evidence other than modelling studies is still scarce (de la Rocque et al. 2008; Morand and Guégan 2008; Lafferty 2009). Moreover, several studies pointed out the importance of climate variability on the epidemics of infectious diseases (Anyamba et al. 2012; Morand et al. 2013).

Baylis and Morse (2012) reviewed the literature on this subject and pointed out that the effects of climate change were mostly focused on health and vector-borne (Wittmann and Baylis 2000; Kovats et al. 2001; Harvell et al. 2002; Hay et al. 2002; Patz and Kovats 2002; Randolph 2004; Reiter et al. 2004; Zell 2004; Rogers and Randolph 2006; Semenza and Menne 2009), whereas the effects on animal diseases and particularly livestock had received far less attention (Cook 1992; Harvell et al. 2002; de la Rocque et al. 2008; Gale et al. 2008, 2009; McIntyre et al. 2010; Guis et al. 2011). Moreover, most of these studies concern zoonotic diseases, while few have specifically focused on livestock diseases (Guis et al. 2011).

The first objective of this chapter is to emphasize why climate change and climate variability may affect livestock diseases' occurrences, although this brief review shows how little is the knowledge on the links between livestock diseases and climate change. A second objective is to briefly introduce the new modelling tools that can help predict diseases' occurrences in space and in time in relation to climate variability and change.

8.2 Why Climate Change Should Affect Disease Occurrences

Obviously, the attribution of disease occurrences to climate change needs to be confirmed with changes in both disease and climate at the same time and in the same place (Rogers and Randolph 2003). Although statistical congruence between pathogens and climatic shifts has been repeatedly reported (Paz et al. 2007; Pascual et al. 2008, 2009), these many reviews hide the fact that there are still few evidences of the impact of climate change on infectious disease incidence (Lafferty 2009). The reason lies probably in the difficulty to attribute any change in disease occurrence to climate change only rather than to other drivers (in combination or not with climate change). Some authors have emphasized that most climate drivers are unknown for the majority of infectious diseases (Harvell et al. 2007), which renders any quantification difficult, and others have underlined that causal links between climate drivers and disease are not simple (Martens 2002) as many of the climate-linked factors will interact with each other (Gale et al. 2009).

Two examples concerning human health and wildlife health may illustrate the difficulty of finding a simple causal link between disease spread and climate change. The first one concerns malaria, which has decreased consistently in the tropics over the last 100 years, but for which temperature or rainfall observed changes do not seem to explain alone this reduction (Gething et al. 2010). Indeed, change in drivers other than climate seems to have played far more dominant roles in reducing malaria occurrence than the role climate change may have played in increasing it. If in the highlands of Eastern Africa rates of malaria had increased, yet again regional climate change is just one explanation, along with changes in patterns of land use, population movements, increased urban poverty, a decline in the use of pesticides for mosquito control, agricultural practices such as irrigation, public health programmes (e.g. monitoring and treatment), the rise of resistance to antimalarial drugs by the parasite or changes in the socio-economic status

of the population (Hales and Woodward 2003; Martens 2002; McMichael and Woodruff 2005). In such cases, the relative importance of climate change versus that of other drivers is difficult to determine and is case dependent (Cohen 2000; McMichael 2004; Patz 2002; Semenza and Menne 2009; Sutherst 2004).

The second well-studied case concerns the extinction of endemic anurans in Costa Rica linked to the emergence of pathogenic chytrid fungi. The emergence of the fungi was hypothesized to be due to global warming (Pounds et al. 2006), but the potential link between global warming and amphibian extinction was challenged by Lips et al. (2008). Although statistical reinvestigations of the data confirmed the positive multi-decade correlation between extinctions and mean tropical air temperature in the previous year, the direct causal link between climate change and the fungi emergence seems to be very weak. Indeed, Rohr et al. (2008) found numerous other variables, such as regional banana and beer production, as better predictors of these extinctions than climate factors. Finally the authors concluded by "Although climate change is likely to play an important role in worldwide amphibian declines, more convincing evidence is needed of a causal link."

Climate change is mostly hypothesized to influence the geographic distribution of pathogens and/or vectors (Rosenthal 2009). A documented case of climate change-related geographic distribution concerns the protist *Perkinsus marinus* parasitizing oyster. The northward movement of the parasite along the Atlantic coast of North America was associated with increasing surface waters (Cook et al. 1998; Harvell et al. 2009).

Concerning livestock and poultry diseases, few studies have been done. Bluetongue disease, vector-borne viral disease of ruminants, was confined to southern Europe along the Mediterranean. The increasingly warm weather since 1998 has favoured midges that carry the virus to move towards northern Europe (Purse et al. 2005).

The effects of climate factors on the transmission and outbreaks of several animal infectious diseases are summarized in Table 8.1. Most diseases concern viruses and few bacteria and parasites (protist or helminths), and half of them involve vectors: African horse sickness, Rift Valley fever, bluetongue, Japanese encephalitis, trypanosomiasis, trichinosis and fasciolosis.

Some of these diseases are affected by humidity and cold or hot weather. However, most of them seem to be dramatically affected by climate variability (see below). Moreover, several of these diseases are zoonotic—avian influenza, Rift Valley fever, Japanese encephalitis, anthrax, trichinosis and fasciolosis—while relatively few are restricted to livestock and poultries: foot-andmouth disease, peste des petits ruminants, rinderpest, Newcastle disease, African horse sickness, bluetongue, animal trypanosomiasis, haemonchosis and other strongyloidiasis.

8.3 Why Climate Variability Matters

Outbreaks of several infectious diseases, mostly vector-borne ones, have been linked to the occurrence of ENSO (El Niño Southern Oscillation) (Baylis et al. 1999; Kovats 2000; Gagnon et al. 2001, 2002; Anyamba et al. 2002) or to the NAO (Hubálek 2005; Morand et al. 2013). The outbreaks of vector-borne diseases are the consequences of the increase in the vector population size in response to heavy rainfalls associated with ENSO (Baylis et al. 1999; Anyamba et al. 2002, 2012).

Baylis et al. (1999) investigated the links between African horse sickness (AHS), one of the most lethal infectious horse disease (with mortality rates up to 95%), in South Africa where major epizootics of this viral disease occurred every 10–15 years. They found a strong association between the timing of epizootics of this disease and the warm (El Niño) phase of the El Niño Southern Oscillation (ENSO) and proposed that this association is mediated by the combination of rainfall and drought brought to South Africa by ENSO.

Here, we show with a working example (Fig. 8.1) how climate variability can affect the incidence of cattle trypanosomiasis in China. For this, we used the data on trypanosomiasis occur116 S. Morand

Table 8.1 Effects of climate factors on the transmission and outbreaks of several animal infectious diseases

	*			D-6
Disease	Agents/transmission	Zoonouc	Climate factors	Kererences
Foot-and-mouth disease (FMD)	Virus, direct	No	Wind-borne spread is favoured by the humid, cold weather in temperate regions	Donaldson (1972)
Peste des petits ruminants (PPR)	Virus, direct	No	Outbreaks associated with the onset of the rainy season or dry cold periods	Wosu et al. (1992)
Rinderpest	Virus, direct	No	Virus survives best at low or high relative humidity	Anderson et al. (1996)
Newcastle disease (ND)	Virus, direct	No	Wet and cold period favours survival and spread of the virus	Band-Bo et al. (2013)
Avian influenza (AIV)	Virus, direct	Yes	Wet and cold period favours survival and spread of the virus	Brown et al. (2007)
African horse sickness (AHS)	Virus, transmitted by Culicoides biting midges	No	Outbreaks associated with the combination of drought and heavy rainfall during the El Niño Southern Oscillation (ENSO)	Baylis et al. (1999)
Rift Valley fever (RVF)	Virus, transmitted by Aedes and Culex mosquitoes	Yes	Epizootics associated with periods of heavy rainfall and flooding or with the combination of heavy rainfall following drought associated with ENSO	Davies et al. (1985), Linthicum et al. (1987, 1999), Anyamba et al. (2002), and Martin et al. (2008)
Bluetongue	Virus, transmitted by Culicoides biting midges	No	Temperature	Guis et al. (2011)
Japanese encephalitis	Virus, transmitted by Culex mosquitoes	Yes	Temperature, precipitation	Hsu et al. (2008)
Anthrax	Bacillus anthracis, direct (soil)	Yes	Outbreaks with alternating heavy rainfall and drought and high temperatures	Parker et al. (2002)
Animal trypanosomiasis	Protist, transmitted by tsetse flies	No	Tsetse flies vectors sensitive to climate	Rogers and Packer (1993)
Haemonchosis and other strongyloidiases	Nematode, direct (soil)	No	Nematode larvae can survive for months under warmth and moderate humidity conditions	Baylis and Morse (2012) and Fox et al. (2012)
Trichinosis	Nematode, food-borne (reservoirs)	Yes	Warmer temperatures and longer summers increase the number of amplification cycles for parasites and lead to longer summer hunting seasons in Arctic regions	Greer et al. (2008)
Fasciolosis	Trematode, transmitted by aquatic snails	Yes	Areas subject to periodic flooding that favour intermediate snail host	Hall (1988)

Completed from Baylis and Morse (2012)

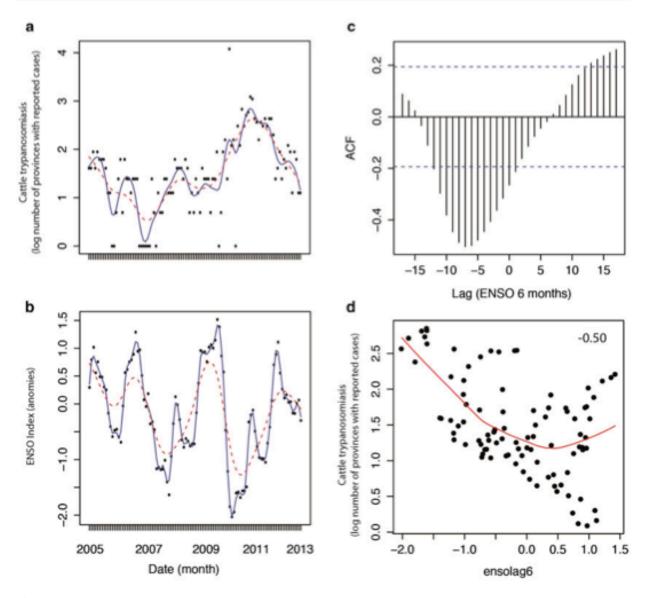


Fig. 8.1 Climate disease teleconnection: a working example using cattle trypanosomiasis in China

rence by Chinese province from the OIE (World Organization for Animal Health) information database, where the reporting cases started from January 2005 to June 2013. The data on ENSO was extracted from NOAA (National Oceanic and Atmospheric Administration). A lag correlation analysis performed on the detrending data negative correlation trypanosomiasis incidence and ENSO with a 6-month lag (Box 8.1). This result suggests that high negative anomalies of ENSO, corresponding to the La Niña event and characterized by a wet and cool season in China, seem to induce cattle trypanosomiasis outbreaks. However, we are to be aware that the validity of this analysis is

Box 8.1 Climate disease teleconnection: a working example using cattle trypanosomiasis in China

Data on trypanosomiasis occurrence by Chinese province were obtained from OIE (World Organization for Animal Health) information database (http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home). The reporting cases started from January 2005 to June 2013.

Data on ENSO was extracted from NOAA (National Oceanic and Atmospheric

(continued)

Box 8.1 (continued)

Administration) (http://www.esrl.noaa. gov/psd/data/climateindices/list/#mei).

Among several potential indices, Multivariate ENSO Index (MEI) was used (Wolter and Timlin 1998).

Cubic smoothing spline was used as a detrending method for long-term series using the function smooth.spline in the R 2.10 statistical freeware package (http://www.R-project.org). This was done for try-panosomiasis incidence (Fig. 8.1a) and for MEI (Fig. 8.1b).

Then a lag correlation analysis was performed using the function cff in the package stats of the R freeware to identify the correlation between ENSO monthly values (MEI) and monthly trypanosiamasis incidence values (using detrended values). The better lag correlation obtained was 6 months between trypanosomiases incidence and MIE (Fig. 8.1c). There was a negative correlation between trypanosomiasis incidence and ENSO with a 6-month lag (Fig. 8.1d).

High negative anomalies of ENSO, corresponding to La Nina event and characterized by a wet and cool season in China, seem to induce cattle trypanosomiasis outbreaks.

crucially depending in the quality of the OIE reporting incidence.

8.4 Prevision of Diseases' Occurrences

Research on climate change has led to the development of elaborated models of future climate change that help at improving policies on mitigation of greenhouse gas emissions and preparing adaptation to the consequences of climate change on human economics and well-being. These climatic models are easily accessible to many other research domains particularly that of animal health science. However, because of the complex links between climate and infectious diseases, the methods and subsequently the results of several climate-based models on infectious diseases spread should be interpreted with caution.

8.4.1 Niche Modelling

Ecological niche modelling is used in biogeography to predict the distributional range of species from existing occurrence data (Anderson et al. 2003). Using appropriate algorithms in a geographic information system (GIS) containing layers of environmental information (such as topography, climate and vegetation), epidemiological and spatial risk stratification can be achieved from data on the location of vectors or pathogens. This approach has been used in the case of Chagas disease and for vectors of leishmaniasis and filovirus infections (Peterson et al. 2002, 2004). Moreover, using scenarios of climate change, it is then possible to project scenarios of pathogen and vector distribution changes.

Niche modelling requires disease occurrence data as a listing of geographical coordinates of localities where the agent/disease of interest is known to exist, raster GIS layers of environmental and/or climate variables and an environmental niche modelling (ENM) algorithm. Environmental data and software tools are now easy to obtain and to manipulate. However, the lack of adequate geo-referenced cases for many animal diseases, particularly in tropical countries, is an obstacle for the development of this approach.

Again, ecological niche modelling has been widely used for zoonotic diseases such as tularaemia (Nakazawa et al. 2010), caused by Francisella tularensis. Few have investigated specifically livestock disease as the notable and recent exception of the causative agent of the anthrax, Bacillus anthracis (Mullins et al. 2011). As emphasized by the authors, ecological niche modelling of B. anthracis helps at finding the potential associations between spore survival and ecological conditions, including climate factors, and can be used as a tool for disease risk and surveillance strategies.

A last point emphasized by many authors is the lack of extensive data collection needed for tuning and running models (Fox et al. 2012).

8.4.2 Epidemiological Modelling (R₀ Map)

Mathematical models of disease transmission may help to gain insight into the epidemiology of disease and estimate parameters such as the basic reproductive number R₀, which represents the number of new infections that arise, on average, from one infected individual when the entire population is susceptible. Integrating observed high spatial resolution climate data to its calculation has enabled the bluetongue transmission risk to be evaluated for the past period of time and simulation of future climate to drive the model in the future (Guis et al. 2011). The model showed that the increase in temperature over the last two decades explains the recent emergence of bluetongue (especially in the north part of Europe). The model can incorporate future climate scenarios, which leads to predictions of further increases in the risk of bluetongue in Europe up to 2050.

8.4.3 Teleconnection Modelling

Anyamba et al. (2012) recently emphasized that teleconnection maps, which correlate long-term monthly global precipitation data with index of climate variability (such as ENSO anomaly index), may help at identifying regional hotspots of rainfall variability influencing the ecology of vector-borne diseases. They showed that reported outbreaks of Rift Valley fever in Africa occurred after 3-4 months of above-normal rainfall. This rainfall was associated with green-up in vegetation, which favours the mosquito vectors. The authors also stressed that the immune status of livestock is a factor that needs to be considered (although largely unknown) as it may likely play a role in the spatial-temporal patterns of these disease outbreaks.

8.5 Conclusion

"Ecosystem approaches to health" or "ecohealth" considers inextricable linkages between ecosystems, society and health of animals and humans (Rapport et al. 1998, 1999). The ongoing global change concerns not only climate change but also land use changes and biodiversity changes, all of these changes affecting the epidemiological environment of humans and their domestic animals.

The frequency and severity of extremes in climate will increase as such the potential for globalization of vectors and disease. Understanding how the global and regional climate variability may impact the ecological drivers of livestock diseases is critical for planning and improving response, control and mitigation strategies. A better adaptation of livestock to the ongoing climate change depends on better scenario of diseases' occurrences on one hand and on improvement of genetic breed to face new climate regime on the other.

8.5.1 Scenarios of Livestock Diseases Linked to Climate Change

We need to develop and improve both the recording of livestock diseases and the modelling of diseases' occurrences in relation to climate change and climate variability. Indeed, the quality of the model prediction is depending on the quality of the data. Each country member depends on the ability and quality of their veterinary services to fill the OIE information database. Indeed, strong variability can be observed between countries in relation to their economic development.

8.5.2 Adaptation and Managing Breed Genetic Diversity

Host susceptibility to a pathogen can be altered by the environmental modulation of host immunocompetence (Dobson 2009). Host immune capacity affects the severity of the infection, and climate factors are able to modulate immune functions, which impact the virulence of the pathogen in hosts. Hence, several studies have shown that altered immunocompetence may increase disease spread (Dobson 2009; Murdock et al. 2012). Immune-mediated changes in host susceptibility and resistance as well as climaterelated changes in parasite transmission may alter the interaction between hosts and their pathogens. Together with other climate stressphysiological impacts, an impairment of the immunological responses of hosts, and especially livestock, to diseases may favour disease outbreaks. Then preserving the genetic diversity of breed required for maintaining the evolutionary adaptation, the immune system responses to climate change or climate variability, is an imperative.

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