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Workpackage 7.4:- Impact of environmental effects on the risk of the occurrence of epizootic diseases in Europe: Identification and prioritisation.

Hazard Identification

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Executive Summary

Workpackage 7.4 aims to identify and prioritise the impact of environmental effects on the risk of the occurrence of epizootic diseases in Europe. In particular, it is focusing on the risk of new, emerging and re-emerging vector-borne viruses entering and becoming established in the EU due to the effect of climate change. Many epizootic viruses are transmitted by arthropod vectors including midges, mosquitoes, ticks and sand flies. Climate change will impact not only on the distribution and abundance of arthropod vectors but also on the interaction between the virus and its vector.

Projections have been made for the climate of Europe up to the year 2100. It is predicted that in addition to higher temperatures, Europe will be drier, although with more extreme weather events including flooding, and drought. At the kick-off meeting in February 2007, it was agreed to find information about dividing Europe up into regions on the basis of climate change predictions. This would provide a basis for qualifying the potential impact of climate change on vectors for livestock disease viruses in the different regions of Europe. Indeed, it is essential that any risk assessment incorporates the impact of climate change at a regional level, if not on a smaller scale, for example, at the level of the micro-environment. However, unfortunately, it is currently not possible to divide Europe up into future climatic regions because of the uncertainty in the predictive models. Recently, the European Environment Agency have assessed the vulnerability of Europe to climate change on a regional basis. Those regions could form a basis for risk assessment.

Through a network of scientists from Europe and China, a hazard identification has been developed that aims to identify potential new and emerging epizootic viruses (and their vectors) that could enter the EU due to climate change. The hazard identification has being structured according to a framework that was developed specifically for this task and aids the information gathered on climate change and also for vector/virus combinations. This ensures that the information collected is equivalent and that qualitative conclusions can be drawn on the risks to the EU. The framework considers the following factors:-

1. Identification of epizootic viruses that could be spread by vectors in EU;
2. Impact of climate change in Europe on the vector population;

3. Possible routes of infected vector introduction into Europe which may act synergistically with climate change;
4. Identification of climatic factors that affect susceptibility of a vector to replication of the virus, or to maintaining infection in the vector; and
5. Host reservoir and immune status of host.

The above factors are considered for each vector type considered here, i.e. *Culicoides* biting midges; mosquitoes; ticks and sand flies. For each vector a number of new, emerging and re-emerging vector-borne viruses are considered.

The general conclusions are that the distribution and abundance of vectors for livestock disease viruses will change not only in Europe, but also in locations bordering Europe. In particular, an extension of the northerly ranges of certain vector species is anticipated, although establishment of vectors from distant tropical parts of the world (e.g. through international trade and travel) may also occur. An example, here, is the tropical mosquito, *Aedes albopictus*, which has established in temperate regions after the introduction of eggs through the world trade in car tyres. The abundance of many vector species is likely to increase through climate changes although other factors may impact too. The rate of transmission of virus will increase as both the rate of virogenesis within the vector and the proportion of vectors able to transmit virus increase with temperature. Furthermore, warmer winters offer the potential for latently-infected vectors to survive the winter, giving a mechanism for overwintering of livestock diseases during incursions. In this respect sandflies may play a role in transmission and overwintering of vesicular stomatis virus and Rift Valley fever.

It has been established that the minimum temperature is sometimes a factor in disease outbreaks (e.g. West Nile fiver in Israel), and higher night time temperatures (due to climate change) will enable higher feeding rates of flying vectors on livestock. In addition, with higher temperatures, vector species presently indigenous to northern Europe may become better able to support replication and transmission of livestock disease viruses (e.g. midges of the *Culicoides obsoletus* complex in the case of the current incursion of Blue tongue virus in northern Europe). This is known as the baton effect. This may also apply to viruses (e.g. Akabane virus and bovine ephemeral fever virus) currently endemic in countries bordering Europe.

The impact of extreme weather events on vector abundance within Europe is a further consideration. It is well documented that the combination of drought followed by heavy rainfall serves to increase vector breeding sites and is a risk factor for outbreaks of Rift Valley fever and African horse sickness. Increased windiness may serve to disperse flying vectors such as midges and even mosquitoes further aiding the colonisation of new habitats, and regions within Europe. Although ticks cannot fly, there are several potential routes of entry of new tick species into Europe, include travel, international trade and importation of animals and migration of wild animals.

Currently, there are some data available on the distribution and abundance of vectors within the EU. However, more data need to be collated to allow the impact of climate change on vector-borne livestock diseases to be better prioritised. This includes assessing the creation of suitable habitats and micro-environments. In addition from this work, it has been concluded that quantitative data on the distribution and abundance of vectors within the EU are not available. Due to this, it is a complex task to predict the influence of climate on vectors and therefore we recommend that appropriate data be collected.

A comparison of the outbreaks of BTV in Mongolia and Europe was initiated because both areas have the same latitude. Farming practice, latitude of BTV outbreaks, temperature and theories for over-wintering mechanisms were to have been considered. While some information has been obtained for BTV outbreaks in China, which is at lower latitude than much of Europe, few data are available for Mongolia. It is recommended that a more detailed comparison of latitudes, temperatures and times of year for BTV outbreaks in Mongolia with those for northern Europe should be made as this would shed further light on the possible impacts from climate change on the emergence of this livestock disease.

It is hoped that these conclusions will be used by risk managers to increase awareness of the impacts that climate change may have on livestock diseases viruses and so help them manage these risks.

Acknowledgements

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1. Introduction

The introduction and spread of epizootic disease to the EU livestock population has large veterinary and economic consequences and possibly impact on human health policy. There are many ways in which epizootic disease can enter livestock production, including international trade in livestock, food products and companion animals (through the PETS travel scheme); exposure to faeces from wild animals (particularly wild birds) and transmission via vectors (e.g. bluetongue virus is transmitted by several species of *Culicoides*) which are susceptible to global warming. Workpackage 7.4 focuses on the new and emerging viruses and, in particular, considers the effect that climate change may have on the risk of the introduction, establishment and spread of new and emerging viruses within the EU.

Climate change is a phenomenon that is affecting not only EU, but worldwide and there is strong evidence that warming is attributable to human activities, in particular to the emission of greenhouse gases (IPCC 2001a). The Earth's climate has warmed rapidly since the beginning of the 20th century, by about 0.7ºC (CRU 2003) and these changes have been unusual in both the magnitude and the rate of temperature change. The warming exceeds by far all natural climate variations of the last 1000 years (IPCC 2001a). Chapter 2 focuses on climate change in Europe and, in particular, the likely changes to air temperature, precipitation, wind speed and sea temperatures. The information gathered here has been used by the authors of the report to produce the Hazard Identification.

Climate change will have many direct and indirect consequences. In particular, it will effect arthropod vectors (species and abundance) and other types of wildlife. It may also have an impact on agriculture (including livestock production) in the EU. Consequently the challenges of preventing and controlling animal and zoonotic disease are likely to change and it is important that risk managers at both the national and EU level have identified the risks and have contingency plans in place. In Workpackage 7.4 we focus on the impact of climate change on vector borne disease and, in particular, those that are carried by midges, mosquitoes, ticks and sand flies.

A hazard identification has been developed that aims to identify potential new and emerging epizootic viruses (and their vectors) that could enter the EU due to climate change (Chapter 3). The hazard identification has being structured according to a framework that was

developed specifically for this task and aids the information gathered on climate change and also for vector/virus combinations. This ensures that the information collected is equivalent and that qualitative conclusions can be drawn on the risks to the EU. In this approach, we consider factors such as (i) Identification of epizootic viruses that could be spread by vectors in EU; (ii) Impact of climate change in Europe on the vector population; (iii) Possible routes of infected vector introduction into Europe which may act synergistically with climate change; (iv) Identification of climatic factors that affect susceptibility of a vector to replication of the virus, or to maintaining infection in the vector and (v) Host reservoir and immune status of host. The above factors are considered for each vector type, i.e. *Culicoides* biting midges (Section 3.1); mosquitoes (Section 3.2); ticks (Section 3.3) and sand flies (Section 3.4).

This report will only consider sand flies and not biting flies. Biting flies are distributed throughout the world and, in addition to nuisance biting, some are responsible for the transmission of diseases in humans and livestock in many countries. The biting flies of greatest significance are the horse flies or March flies (Family Tabanidae), the stable flies (Family Muscidae) and the black flies (Family Simuliidae), as well as the biting midges (Family Ceratopogonidae) and the mosquitoes (Family Culicidae), which are dealt with elsewhere. Adult flies of veterinary importance may feed on blood, sweat, skin secretions, tears, saliva, urine or faeces of the domestic animals to which they are attracted. They may do this either by puncturing the skin directly, in which case they are known as biting flies, or by scavenging at the surface of the skin, wounds or body orifices, in which case they may be classified as non-biting or nuisance flies. Biting flies may act as biological vectors for a range of pathogenic diseases and both biting and non-biting flies may also be mechanical vectors of disease. Mechanical transmission may be exacerbated by the fact that some fly species inflict extremely painful bites and, therefore, are frequently disturbed by the host while blood-feeding. As a result, the flies are forced to move from host to host over a short period, thereby increasing their potential for mechanical disease transmission. Because feeding is often interrupted, there are numerous opportunities for the mechanical transmission of a number of human and livestock diseases, such as anthrax, tularemia, animal trypanosomes, and recently bartonellosis (Chung *et al.*, 2004). Since some hundred species of biting flies exist, with different biology, it is unlikely to cover exhaustively this section in the report and more efforts will be made to discuss flies which are strictly biological

vectors and therefore more deeply implicated in the transmission and/or maintenance of the disease agents into the animal population.

Due to the recent outbreak of Bluetongue virus (BTV) in Northern Europe (Netherlands, Belgium, Luxemburg, Western Germany and in parts of North Eastern France) in 2006, a comparison of BTV in Europe and China has been carried out. This is particularly relevant in relation to climate change because Inner Mongolia and Europe have the same latitude and hence insight may be gained by comparing BTV incursions, farming practices and climate for these two regions. Details of this comparison are given in Chapter 4.

From the Hazard Identification and also the comparative study, conclusions can be drawn on the risk of introduction, establishment and spread of epizootic viruses that are spread via *Culicoides* biting midges, mosquitoes, ticks and sand flies. Such conclusions are provided in Chapter 5. It is hoped that these conclusions will be used by risk managers to increase awareness of the impacts that climate change may have on animal health and to help them manage these risks.

2. Climate change in Europe

Since the beginning of the 20th century, the Earth's climate has warmed rapidly by about 0.7ºC (CRU, 2003). These changes are unusual in both the magnitude and the rate of temperature change. The warming exceeds by far all natural climate variations of the last 1000 years. There is strong evidence that warming is attributable to human activities, in particular to the emission of greenhouse gases (IPCC, 2001a).

Such changes in our climate may directly or indirectly impact on the risks to animal health within the EU. In particular, as noted by the National Farmers Union (NFU) (NFU, 2005) in the UK, climatic changes such as carbon dioxide levels, temperature (including growing season), water availability (including relative humidity and soil moisture), cloud cover, wind, weather extremes and sea level rise are a concern to agriculture (including livestock production).

Extreme weather events could be potentially more damaging than steady long-term average changes in climate, especially if the switch from a benign to destructive climate results in unpredictable weather. Extreme weather events will have an impact on farming management and practice with respect to livestock. For example, heat stress in livestock, flooding, shortage of water and poor grass supply will impact not only on housing, but also on the movement and transport of livestock. Predictions for the UK climate in the 21st century are presented in the UKCIP02 Scientific Report (Hulme *et al.*, 2002). UKCIP expects more erratic weather patterns including:-

- torrential rains
- very strong winds
- short periods of exceptionally high or low temperatures
- droughts.

Table 1: UKCIP02 climate scenarios for 2080s – emissions scenarios. Data taken from Hulme *et al.* (2002)

SRES Emissions Scenario	UKCIP02 climate change scenario	Global temperature increase (ºC)	Atmospheric CO_2 concentration (ppm)
A1F1	High emissions	3.9	810
A2	Medium-high emissions	3.3	715
B2	Medium-low	2.3	562

	emissions		
B1	Low emissions	2.0	525

Climate change is expected to increase the frequency of extreme events. For Europe as a whole, results of high resolution climate modelling (Christensen & Christensen, 2002) have indicated that episodes of severe flooding may become more frequent, despite a general trend towards drier summer conditions.

In this chapter we review the available literature on climate scenarios for Europe and, in particular, we consider the changes to air temperature, precipitation, wind speed and sea temperatures. Sources of information on climate change include PRUDENCE; European Environment Agency (EEA) (2004); Hadley Centre HadCM3 model, and IPCC.

In the EU project PRUDENCE[1], the high-resolution (50 km grid) regional climate model HIRHAM4 created by the Danish Meteorological Institute has been applied to two of the emission scenarios, A2 and B2, drawn up by the Intergovernmental Panel on Climate Change (IPCC). The scenarios and ensembles include a common period a (1961-1990), A2 and B2 (both 2070-2100). Three 30-year time slice experiments were carried out for periods representing roughly the present (1961-1990) and two future scenarios (2071-2100), respectively. The large-scale controlling conditions originated from transient climate-change simulations using the coupled ocean-atmosphere global climate model (OAGCM) with 300 km grids. Those models are referenced in Christensen & Christensen, 2002.

2.1 Air Temperature

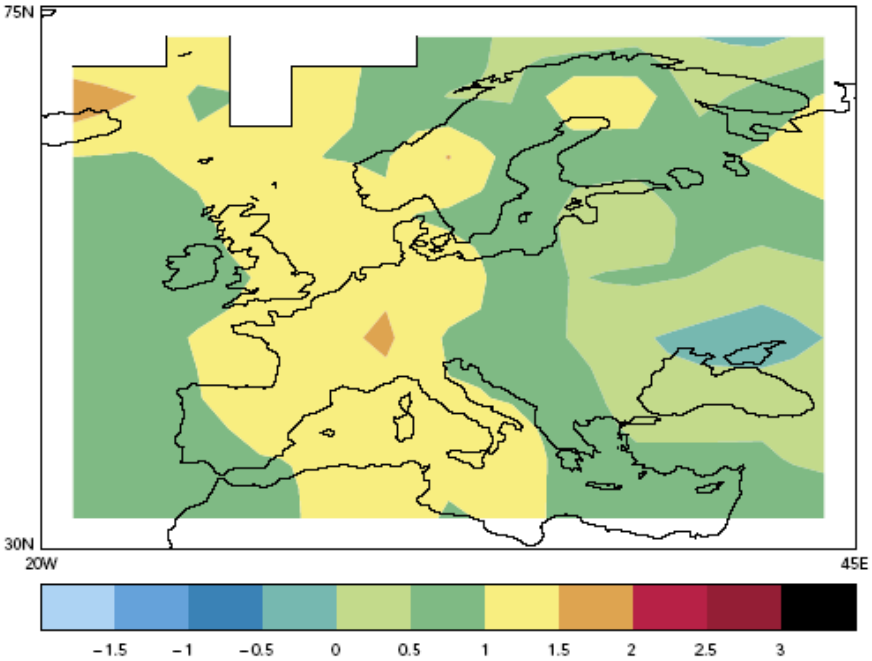
2.1.1 From 1900 - 2000

The temperature increase in Europe over the last 100 years is about 0.95 °C (CRU, 2003; Jones & Moberg, 2003), which is higher than the global average. The warmest year in Europe was 2000; the next

[1] **Prediction of Regional scenarios and Uncertainties for Defining EuropeaN Climate change risks and Effects – PRUDENCE.** PRUDENCE was a project funded by the European Commission under its fifth framework programme. It had 21 participating institutions from a total of 9 European countries. For further information, see PRUDENCE: http://prudence.dmi.dk/

seven warmest years occurred in the last 14 years. There is a wide variation in increasing temperatures across the continent (Figure 1).

The warming has been greatest in northwest Russia and the Iberian Peninsula (Parry, 2000; Klein Tank *et al.*, 2002). In line with the global trend, temperatures are increasing in winter more than in summer (+ 1.1 °C in winter, + 0.7 °C in summer), resulting in milder winters and a decreased seasonal variation (Jones & Moberg, 2003).



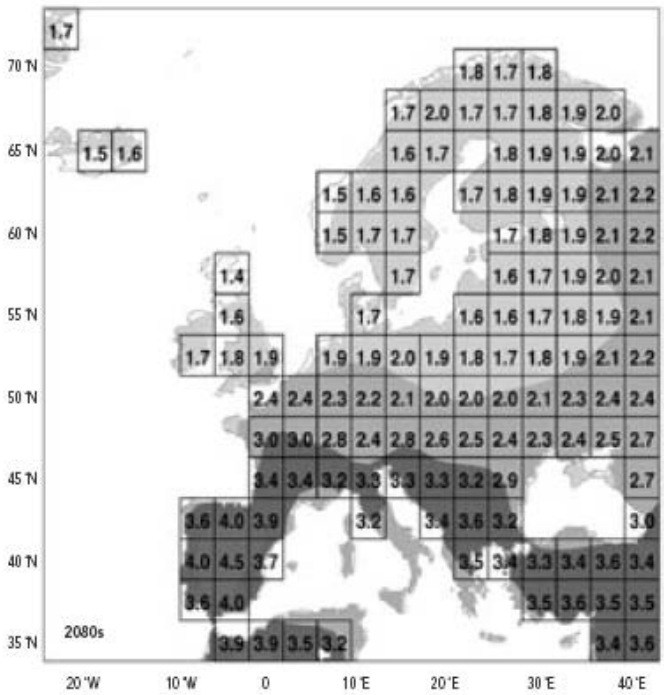
Note: Temperature deviation, relative to average temperature from 1961–1990 (°C).
Source: CRU, 2003; Jones and Moberg, 2003.

Figure 1: Annual temperature deviation in Europe from 1961-1990. Taken from EEA (2004)

2.1.2 Projected to 2100

The projected temperature increase between 1990 and 2100 is likely to be in the range of 1.4–5.8 °C for the global mean (IPCC, 2001a) and 2–6.3 °C for Europe (Parry, 2000). This is shown in Figure 2. This range results from potential different pathways of technological, demographic and economic development (leading to different

emissions), and is due to uncertainties related to the climate system's response to changing concentrations of greenhouse gases. Another plot of Europe for the 2080s is shown in Figure 3. Within Europe, the warming is estimated to be greatest over southern countries (Spain, Italy, Greece) and the northeast (e.g. western Russia) and less along the Atlantic coastline. In southern Europe, especially, this may have severe consequences such as increasing drought stress, more frequent forest fires, increasing heat stress and risks for human health. The European trend that winters will warm more rapidly than summers will continue (with the exception of southern Europe). Winter temperatures are predicted to increase as the century progresses, with slightly lower increases in the UK (Figure 4).



Note: Temperature change (°C). Relative to average temperature in the period 1961–1990. Intermediate ACACIA scenario in a broad range of possible future emissions.
Source: IPCC, 2001b; Parry *et al.*, 2000.

Figure 2: Projected temperature changes in Europe up to 2080. Taken from EAA (2004).

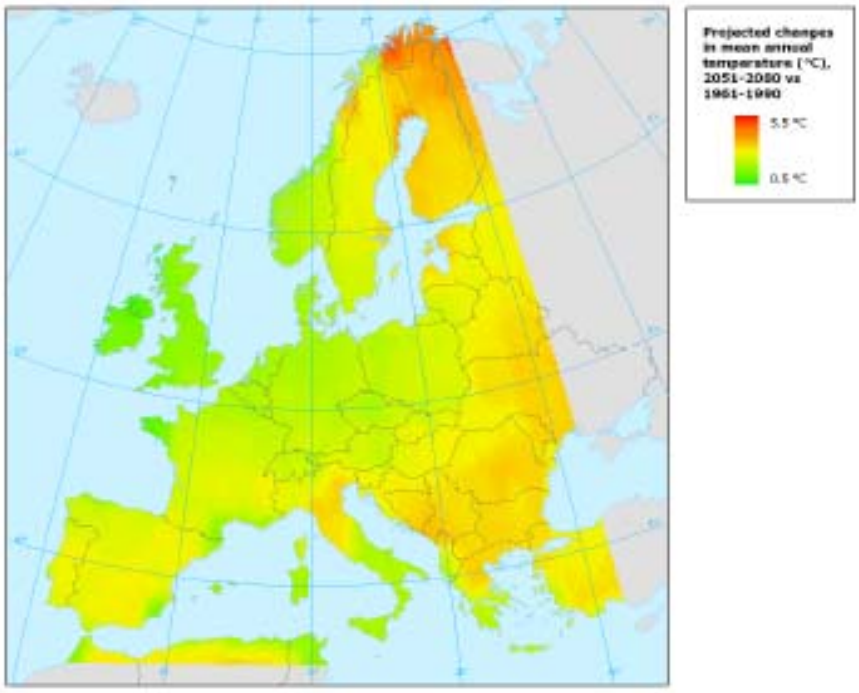


Figure 3: Predicted changes in mean annual temperature for Europe in 2080. Temperature is projected to increase in Northern, Eastern and Southern Europe. Data source: Hadley Centre HadCM3 model, B2 scenario, taken from Kristensen (2006).

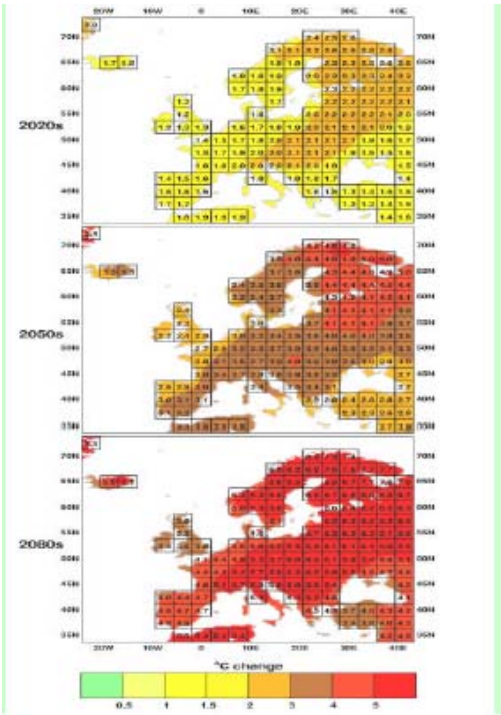


Figure 4: Predicted winter temperatures in Europe for the 2020s, 2050s and 2080s (Parry 2005).

2.1.3 Warmer night-time temperatures

The effect of climate change on mean temperature is noticeable due to warmer night-time temperatures. This is important for many insect vectors which fly at night, and also for survival through the winter; thus badgers are able to forage earthworms through the winter. In the heat wave of summer 2003, night-time temperatures did not cool off to any great extent in Switzerland (Beniston & Diaz, 2004). This compounds the effects of heat stress on both humans and livestock. According to certain statistics, the 2003 summer has not broken all records in terms of extremes (Beniston & Stephenson, 2004). A distinguishing feature, however, of the summer 2003 heat wave (compared to the 1947 or 1976 heat waves) is the very high minimum temperatures. Indeed, the fact that night-time temperatures did not cool off at the time when daily temperatures were extreme was one contributing factor to the excess mortality related to the heat wave. In this respect the 2003 event was a

"climatic surprise", and according to Beniston & Diaz, 2004 is likely to occur with increasing frequency in the latter part of the 21st century.

2.1.4 More summer days exceeding 30°C and year-to-year variability

For Basel in Switzerland, Bensiton & Diaz, 2004 predict that the total number of days during which the 30°C threshold is exceeded is projected to increase almost five-fold in the future, as it did during the 2003 heat wave, from about 8 days currently in an average summer to over 40 days in the future. As a result of the higher variability that the regional model projects for the future, absolute annual maximum temperatures may reach 48°C, i.e., about 6–8°C more than the temperature records that were observed in Switzerland in 2003.

The summer of 2003, however, is not particularly unusual if compared with simulations of the future climate towards the end of the century, as a result of man-made greenhouse gas emissions. As part of the Prudence project, Schär *et al.*, 2004 show that not only are average temperatures expected to be higher (Figure 5), but also in many places a significant increase in year-to-year variability during the summer seasons is predicted. Observations show that the temperature has increased over the previous 150 years, but an increase in variability has not yet been detected. The anticipated increase in variability might make the adaptation to warmer climatic conditions even more challenging than previously expected.

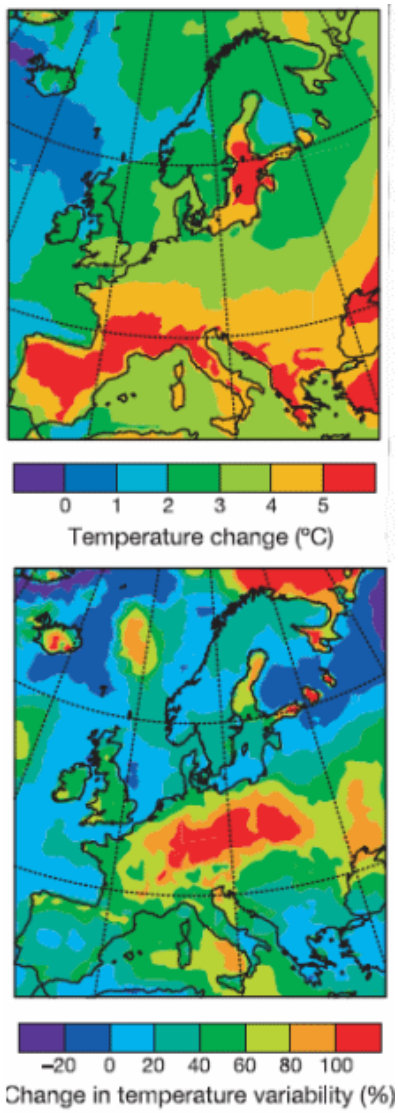


Figure 5: Simulated change in average summer temperature (upper panel) and in inter-annual variability (lower panel) from the period 1961-1990 to the period 2071-2100 (Schar *et al.*, 2004).

2.1.5 Frequency of hot summers

The probability of one in ten summers being hot is set to increase between 2020 and 2080 (Figure 6). Greatest increases are in southern, northern and western Europe.

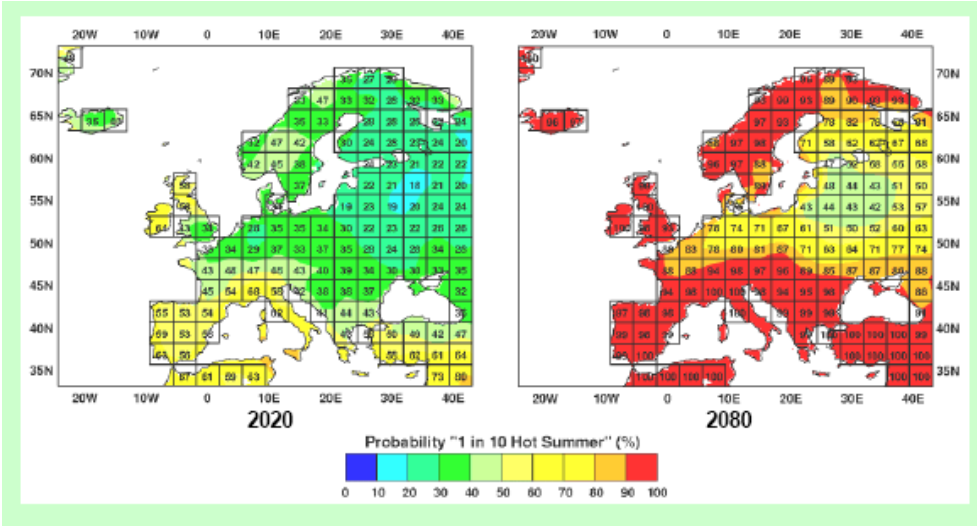


Figure 6: Changing frequency of hot summers (Parry 2005)

2.1.6 Predicted changes in length of hot and cold spells

Figure 7 shows the example of the change in hot spells between 1961-1990 and 2070-2099, in terms of the average for each period from the DMI model. The future extension of hot spells by up to 70 days over Africa, Iberia, and parts of Italy, Turkey, and Greece threatens the huge tourist industry in those countries. The picture for agriculture in terms of length of cold spells is much more reassuring. Winters in Turkey, particularly, are indicated to become much warmer with a future reduction in the length of cold spells by up to 60 days.

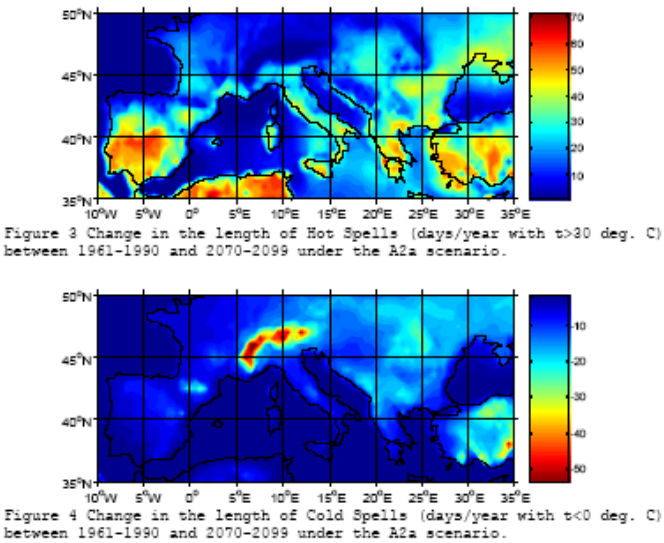


Figure 7: Predicted changes in lengths of hot and cold spells between 1961-1990 and 2070 and 2099. (Taken from PRUDENCE final report; Christensen, 2005).

2.2 Precipitation

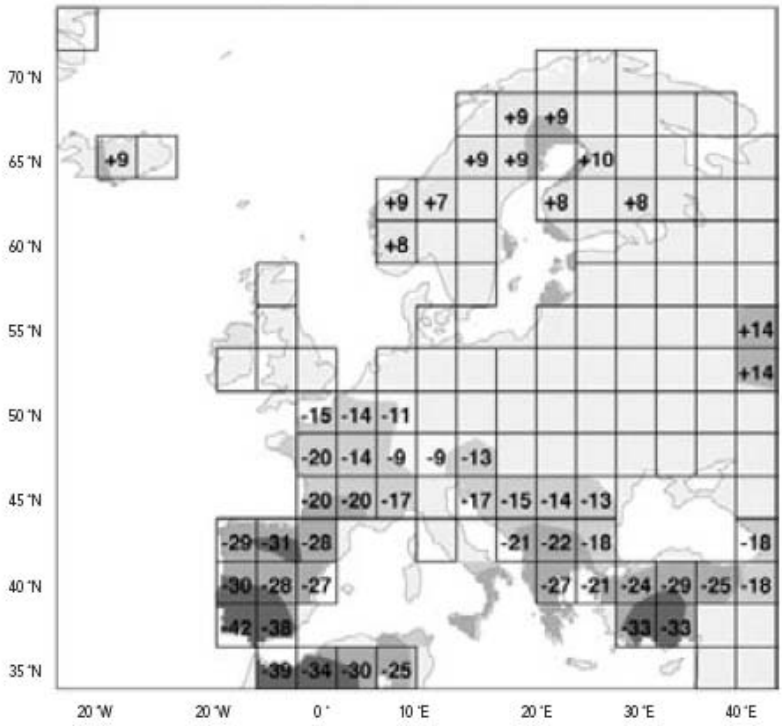
2.2.1 Annual precipitation

According to the EEA (EEA, 2004) annual precipitation trends in Europe for the period 1900–2000 show a contrasting picture between northern Europe (10–40 % wetter) and southern Europe (up to 20 % drier). Changes have been greatest in winter in most parts of Europe. Projections show a 1–2 % increase per decade in annual precipitation in northern Europe and up to 1 % per decade decrease in southern Europe (in summer, decreases of 5 % per decade may occur). The reduction in southern Europe is expected to have severe effects, e.g. more frequent droughts, with considerable impacts on agriculture and water resources.

Uncertainties are high in projected (regional) precipitation change, resulting in a considerable range of projections, although scientific confidence in the ability of climate models to estimate future precipitation has gradually increased. Global average (land and ocean) precipitation is projected to increase by 2–7 % between 1990

and 2100 (IPCC, 2001a). The range is due to uncertainties within the climate models and differences in emission scenarios. Projections for Europe show more annual precipitation for northern Europe (an increase of 1–2 % per decade) and decreasing trends across southern Europe (maximum – 1 % per decade). In winter, most of Europe is likely to become wetter (1–4 % per decade) with some exceptions, notably in the Balkans and Turkey. Despite this increase, the amount of snow is projected to decline due to rising temperatures. In summer, northern Europe might become wetter (up to 2 % per decade), whereas southern Europe may become up to 5 % drier per decade (Figure 8) (Parry, 2000; IPCCb). A plot of predicted changes in rainfall for the 2080s is presented in Figure 9. Predicted summer precipitations for 2020s, 2050s and 2080s are presented in Figure 10. The predicted fall in precipitation in Southern Europe as the century progresses is apparent, with increases in Northern Europe. These same conclusions were also identified by Räisänen *et al*., 2004, as part of the PRUDENCE project. Räisänen *et al*. investigated four different realizations of future climate change and, in particular, two different emission scenarios and two different driving global models were used (Figure 11). The magnitude of the simulated climate changes differs between the experiments but all four experiments agreed with the conclusions above, i.e. increased precipitation in northern Europe, especially during winter, and decreased precipitation in southern Europe during summer.

In some regions there are considerable differences between the experiments. A prominent example concerns the changes in wintertime precipitation in Norway. Depending on choice of the driving global model, precipitation is either increased or decreased. The simulations show the profound impact on the regional modelling results from the driving global model.



Note: Summer precipitation change (%). Relative to average precipitation in the period 1961–1990. Intermediate ACACIA scenario in a broad range of possible future emissions.
Source: IPCC, 2001b; Parry *et al.*, 2000.

Figure 8: Projected change in summer precipitation in Europe up to 2080. Taken from EEA (2004).

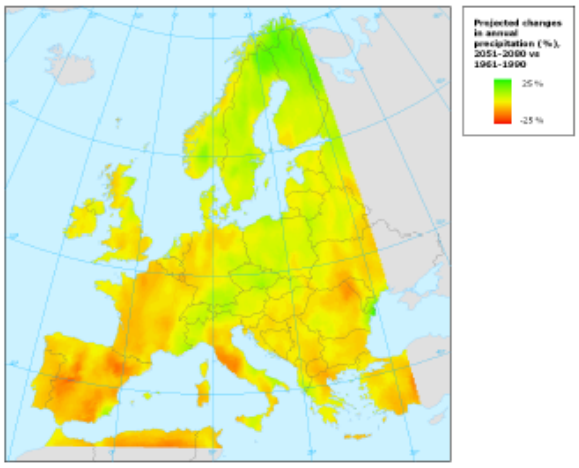


Figure 9: Predicted precipitation changes for Europe in 2080. Data source: Hadley Centre HadCM3 model, B2 scenario, taken from Kristensen (2006).

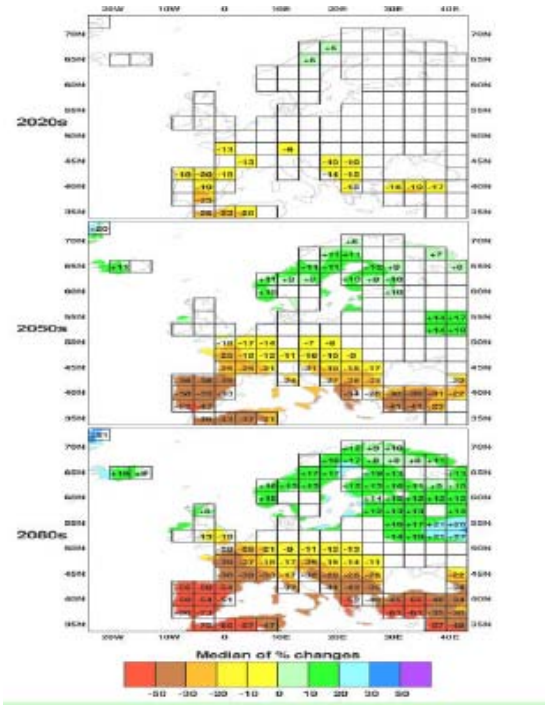


Figure 10: Predicted summer precipitation in 2020s, 2050s and 2080s (only significant changes shown). Taken from presentation by Parry (2005).

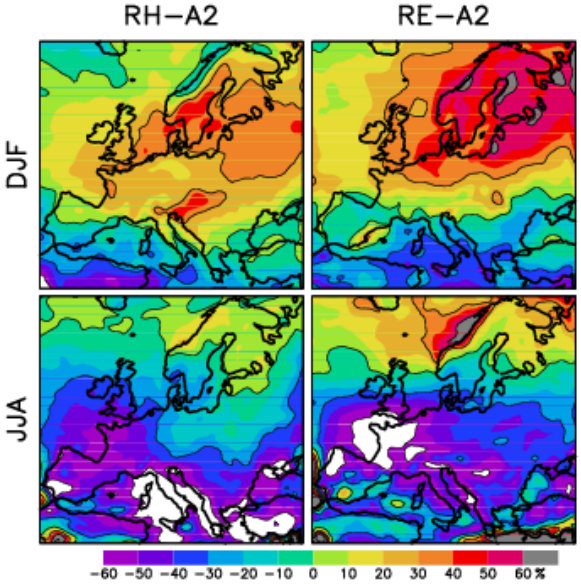


Figure 11: Simulated changes in winter (DJF) and summer (JJA) precipitation from the period 1961-1990 to 2071-2100. Results from the Rossby Centre regional climate model are shown. To the left boundary conditions from the Hadley Centre and to the right boundary conditions from the Max-Planck Institute for Meteorology are used. Taken from PRUDENCE final report; Christensen, 2005.

2.2.2 Flooding

Serious flooding occurred in Central Europe during the summer of 2002 with much media attention given to Prague and Dresden. More flooding in Europe in the 21st century is expected to take place as a consequence of global warming. Christensen & Christensen, 2003 quantified the likely changes related to summer time precipitation amounts and intensity due to global warming at a European scale. concluding that towards the end of the 21st Century:

- The total summer time precipitation amounts will be substantially reduced over major parts of Southern and central Europe.
- Intensive rain events - like those leading to the flooding in the Moldau, Donau, Elbe and Rhône in 2002 - will become more frequent and even more. intensive

Christensen & Christensen, 2002 investigated the relationship between climate change and heavy precipitation episodes lasting for 1-5 days for July to September. Figure 12 (upper) shows the relative

change in mean precipitation between now and the 2080s. Figure 12 (lower) shows the relative change in the mean five-day precipitation for July-September that exceeds the 99th percentiles. It is concluded that CO_2-induced warming can lead to a shift towards heavier intensive summertime precipitation over large parts of Europe. This finding may be explained by the fact that the atmosphere will contain more water in a warmer climate, which will provide further potential for latent-heat release during the build-up of low-pressure systems, thereby possibly both intensifying the systems and making more water available for precipitation.

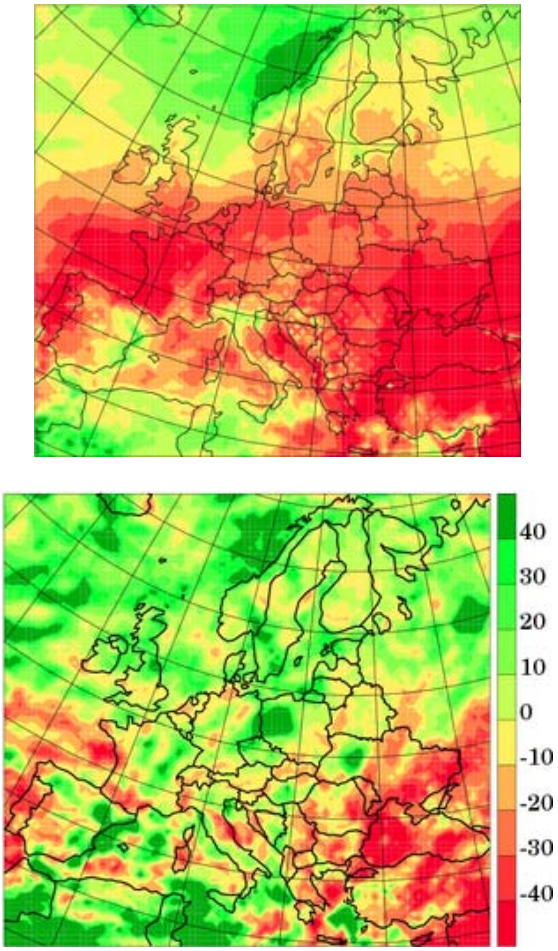


Figure 12: Top panel: Change in seasonal average precipitation in July-August-September from 1961-1990 to 2071-2100 in per cent. Bottom panel: Change in the exceedance of the 99th percentile, i.e., the change in the five-day precipitation on the 1% of the days during this season and

period where it rains the most. Taken from Christensen & Christensen, 2003.

2.2.3 Predictions of annual river discharge

Changes in annual river discharge are projected to vary significantly across Europe, related to regional/local changes in precipitation and temperature. By 2070, river discharge is expected to decrease by up to 50 % in southern and southeastern Europe, and to increase by up to 50 % or more in most parts of northern and northeastern Europe (Figure 13). As a result, stress on water resources may continue to grow significantly in southern Europe.

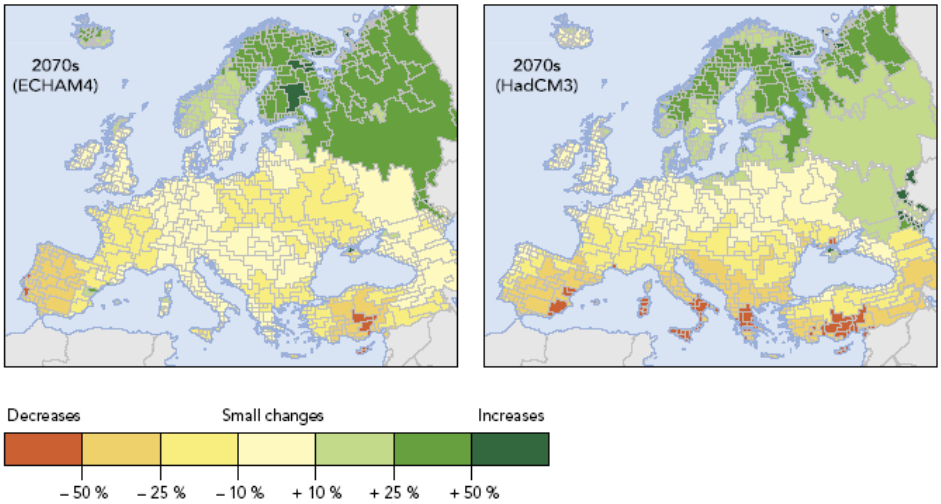


Figure 13: Predicted changes in annual river discharge in European river basins for the 2070s compared to 2000. Source EEA , 2004.

2.3 Windspeed

Changes between the 20th (1961-90) and the 21st (2071-2100) centuries, in extreme wind speed indicators have been investigated over Europe on the basis of climate simulations from five different GCM-RCM model chains. Based on percentile rather than on absolute thresholds, the developed wind speed indices allow a consistent analysis over Europe and better avoid for model discrepancies. Relative changes in both intensity and frequency indices of extreme winds have been studied and the related uncertainties assessed for the halfwinter months. Significant positive changes are obtained over

at least 20% and 10% of the European study area (15°W-43°E; 35°-72°N), respectively. Higher changes are obtained for the only December, January and February (DJF) winter months (Figure 14).

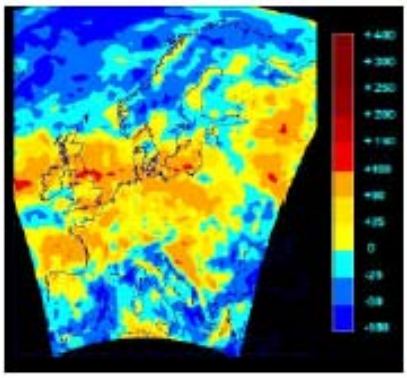


Figure 14: HadAM3H-RCAO model chain: Change (%) in the number of days above 1961-90DJF 99th percentile of the daily maximum wind speed between the 20th (1961-90) and 21st(2071-2100) centuries, based on A2 scenario. Taken from PRUDENCE final report; Christensen, 2005.

2.4 Sea temperatures

2.4.1 Atlantic Sea Surface Temperature (SST) and the Atlantic Multidecadal Oscillation (AMO)

According to Beniston & Diaz, 2004, it is well known that surface temperatures in the North Atlantic Ocean exhibit considerable decadal scale variability and has a fundamental influence in modulating the climate of Europe. The record of summer temperature in Basel region (Figure 15) exhibits considerable interannual and decadal-scale variability (Beniston & Diaz, 2004). It has also been shown that Atlantic sea surface temperature (SST) changes modulate the climate of western Europe through remote air–sea interactions, known as teleconnections. A key mode of variability of Atlantic SST is known as the Atlantic multidecadal oscillation (AMO). Figure 16 illustrates the changes in this mode of SST North Atlantic SST variability. Beniston & Diaz, 2004 noted that the low-frequency variations in SST mimic to a considerable extent the variability in summer temperatures in Basel. Climate changes associated with the increasing greenhouse-gas loading of the atmosphere will act in concert with the changes in North Atlantic SST, and either exacerbate or diminish its impact on European climate in the future. The temperature changes that are

illustrated in Figure 15 exhibit considerable decadal variance. It should be kept in mind that in a

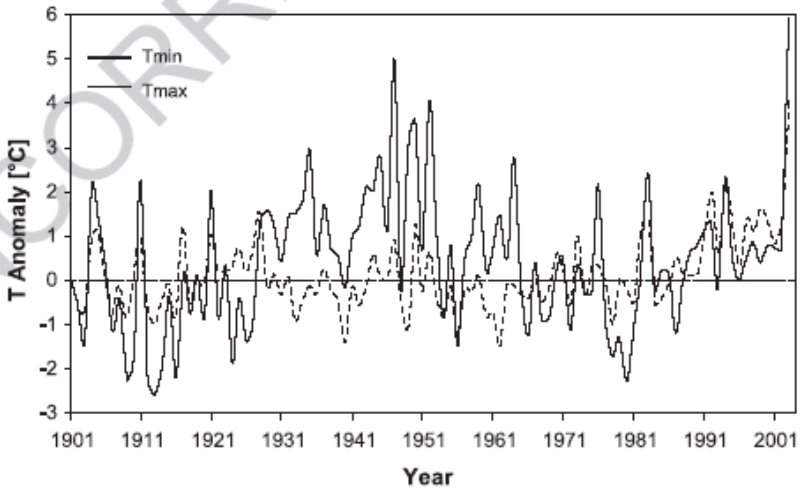


Figure 15: Departures of summer minimum and maximum temperatures from the 1961-1990 means at Basel (1901-2003). Taken from Beniston & Diaz, 2004.

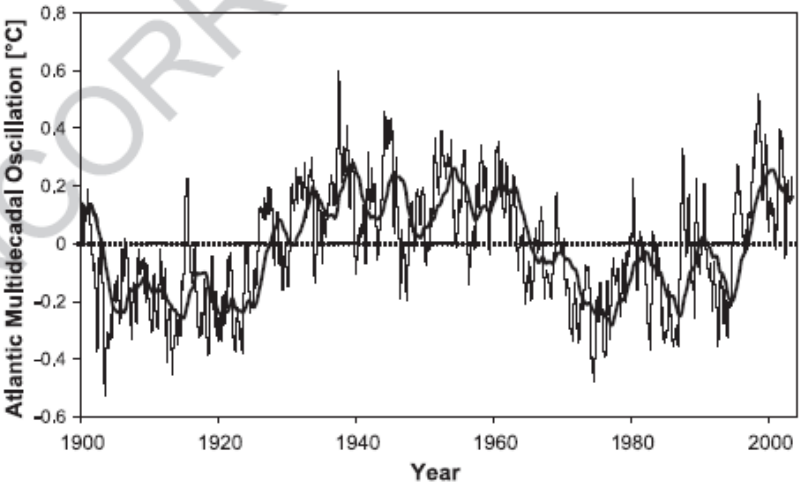


Figure 16: Time series of de-trended North Atlantic monthly sea surface temperature (SST) anomalies. Taken from Beniston & Diaz, 2004.

future warmer world, these decadal fluctuations, which are intrinsic characteristics of the climate system, may add considerably to the seasonal distributions of daily temperature values, such that even in the first half of the present century, hot summers in Europe could become much hotter than in the past, faster than is projected by some of the global climate models.

2.4.2 The North Atlantic Oscillation and ice in the Baltic Sea

The severity of the preceding winter and approaching spring can be quantified using the North Atlantic Oscillation (NAO) index; positive values indicate mild winters. In northern Europe, the NAO-index correlates with ice cover and timing of ice break-up of the Baltic Sea (Lehikoinen *et al.*, 2006).

2.5 Conclusions

A summary of the climate projections for Europe in the future (2071-2100) is set out in Table 2 together with an outline of the changes that occurred in the 20th century. This is taken from EEA (2004) but is also consistent with the results from other studies or projects.

Table 2: Summary of projections for Europe's climate. Taken from EEA, 2004.

	From 1900 to 2000	**Projected to 2100**
Global and European air temperatures	Europe has warmed more than the global average, with a 0.95 °C increase since 1900. Temperatures in winter have increased more than in summer. The warming has been greatest in northwest Russia and the Iberian Peninsula	From 1990 to 2100, the global average temperature is projected to increase by 1.4–5.8 °C and 2.0–6.3 °C for Europe (without policy measures). The 'sustainable' EU target of limiting global temperature increase to no more than 2.0 °C above pre-industrial levels is likely to be exceeded around 2050
European precipitation	Annual precipitation trends in Europe for the period 1900–2000 show a contrasting picture between northern Europe	Projections for Europe show a 1–2 % increase per decade in annual precipitation in northern Europe and an up to 1 %

	(10–40 % wetter) and southern Europe (up to 20 % drier). Changes have been greatest in winter in most parts of Europe.	per decade decrease in southern Europe (in summer, decreases of 5 % per decade may occur). The reduction in southern Europe is expected to have severe effects, e.g. more frequent droughts, with considerable impacts on agriculture and water resources.
Temperature and precipitation extremes	In the past 100 years the number of cold and frost days has decreased in most parts of Europe, whereas the number of days with temperatures above 25°C (summer days) and of heatwaves has increased. The frequency of very wet days significantly decreased in recent decades in many places in southern Europe, but increased in mid and northern Europe	Cold winters are projected to disappear almost entirely by 2080 and hot summers are projected to become much more frequent. It is likely that, by 2080, droughts as well as intense precipitation events will become more frequent

The European Environment Agency (EEA 2005) have assessed the vulnerability of Europe to climate change on a regional basis. They identify **South-Eastern Europe, the Mediterranean** and **central Europe** as most vulnerable to climate change, while Northern and some western regions of Europe may experience benefits. Vulnerability issues include ecosystems and biodiversity, agriculture and fisheries, forestry, tourism, and water resources. This could form the basis of breaking Europe up in to regions for livestock disease risk assessment.

3. Hazard Identification

A hazard identification has been developed that aims to identify potential new and emerging epizootic viruses (and their vectors) that could enter the EU due to climate change. The hazard identification has being structured according to a framework that was developed specifically for this task and aids the information gathered on climate change and also for vector/virus combinations. This ensures that the information collected is equivalent and that qualitative conclusions can be drawn on the risks to the EU. In this approach, we consider factors such as (i) Identification of epizootic viruses that could be spread by vectors in EU; (ii) Impact of climate change in Europe on the vector population; (iii) Possible routes of infected vector introduction into Europe which may act synergistically with climate change; (iv) Identification of climatic factors that affect susceptibility of a vector to replication of the virus, or to maintaining infection in the vector and (v) Host reservoir and immune status of host. The above factors are considered for each vector type, i.e. *Culicoides* biting midges (Section 3.1); mosquitoes (Section 3.2); ticks (Section 3.3) and sand flies (Section 3.4).

3.1 Culicoides *biting midges*

3.1.1 Introduction

Culicoides biting midges are among the most abundant of haematophagous insects, and occur throughout most of the inhabited world, with the exception of Iceland, the Hawaiian islands and New Zealand. Across this broad range they transmit a great number of assorted pathogens of human, and domestic and wild animals, but it is as vectors of arboviruses, and particularly arboviruses of domestic livestock, that they achieve their prime importance. To date, more than 50 such viruses have been isolated from *Culicoides* spp. and some of these cause diseases of such international significance that they have been designated Office International des Epizooties (OIE) Important Notifiable Disease status. *Culicoides,* therefore, are world players in the epidemiology of many important arboviral diseases. In this context this section deals with those aspects of midge biology facilitating disease transmission, describes the factors controlling insect-virus interactions at the individual insect and population level, and illustrates the far-reaching effects that certain components of climate have upon the midges and, hence, transmission potential.

3.1.2 Identification of epizootic viruses that could be spread by biting midges in the EU.

There are as series of potential or proven epizootic pathogens that are transmitted by biting midges and that occur close to the borders of Europe or have previously occurred in Europe or are present in Europe now. These include bluetongue virus (BTV), African horse sickness virus (AHSV), equine encephalosis virus (EEV), epizootic haemorrhagic disease virus (EHDV), which are all Orbiviruses, Akabane virus (AKAV), which is a Bunyavirus and bovine ephemeral fever virus (BEFV) which is a Rhabdovirus. BEFV has previously occurred in Turkey and Israel. AKAV has also been reported from Turkey (in the 1980s) and Israel (2002 and 2003), EEV has been recorded during 2001 in parts of west and north Africa, and the Middle East, while EHDV has been reported from Morocco, Algeria and Israel in 2006. AHSV has previously occurred in parts of Europe, i.e. Spain in 1966, and 1987-90, and Portugal in 1988. It has also occurred in North Africa (1965-66 and 1988-91) and the Middle East (generally during the 1960s, but in Yemen it is probably enzootic). In the past BTV has occurred, sporadically, in SW Europe (Spain and Portugal 1955-60) and certain Greek islands (1979-80) but since 1998 a widespread epizootic has affected 17 countries across southern Europe and the Mediterranean Basin, and during 2006 northern France, Belgium, Holland, Luxembourg and Germany were also involved. Of the above viruses BTV and AHSV pose the most severe threat because they both cause OIE Important notifiable diseases.

In relation to the other *Culicoides*-transmitted viruses listed above, these have been associated with a range of *Culicoides* species including those that have been shown to transmit AHSV and BTV (Mellor *et al.*, 2000; Mellor, 1990). One might therefore expect that these viruses might also extend their distributions northwards into Europe under the influence of climate-change in a similar way to BTV and AHSV. However, all arboviruses require a number of day degrees or hour degrees (physiological heat) to be accumulated that is specific for each species of arbovirus, before vector transmission can be achieved. As yet there are no data on these requirements for BEFV, AKA and EEV so at present it is not possible to predict the level of range expansion that climate-change will have on these viruses. This information is urgently required to facilitate such predictions.

3.1.3 Impact of climate change in Europe on the biting midge populations.

Climate change brings changes in temperature, saturation deficit (SD) and precipitation and, an increase in extreme weather events (EWE). All of these will impact upon biting midge populations, and hence upon their ability to transmit or vector pathogens.

Temperature

Increases in temperature will, perforce, increase the metabolic rate of midges, as they are poikilothermic. This will increase the rate of blood feeding and hence the number of eggs produced which will potentially increase population sizes and abundances. In addition, if temperature increases this is likely to extend the range of many biting midge species, especially in a northerly direction in the northern hemisphere, as it is temperature that most constrains the distributions of many midge species. It is also the case that if temperatures were to increase more in the night time than the day time and during the winter rather than the summer this would be particularly beneficial to biting midges as, by and large, they are active during the night not during the day and because sub-tropical species have difficulty overwintering - and of course most climate-change scenarios predict precisely these patterns of temperature change. The downside of temperature increases are that midges will be pushed through their life cycle more quickly and therefore daily survival rates are likely to decrease.

Saturation deficit (humidity

Midges are small insects and so are perennially at risk of desiccation, therefore any increase in SD, which is a measure of the drying power of air, is likely to decrease survival rate while a decrease in SD will have the reverse effect.

Precipitation

Midges, in common with virtually all other blood feeding insects require an aquatic or semi aquatic breeding site for their developmental stages. Increases in precipitation will be likely to increase the number of such breeding sites, the size of such breeding sites and their persistence, all with positive effects upon midge population sizes - and the reverse will also be the case.

Extreme weather events

Climate-change is predicted to bring an increase in EWE, which for the purposes of this paper is interpreted to mean that there is likely

to be an increase in "windiness". Biting midges have been shown to travel passively on winds as aerial plankton over distances of scores or hundreds of kilometres. An increase in EWE is therefore likely to lead to more such aerial movements with a consequent increase in the likelihood of colonization of new habitats - and hence extensions in midge distributions.

3.1.4 Possible routes of infected midge introduction into Europe which may act synergistically with climate-change

Clearly infected midges could be transported into Europe by human intervention (i.e. by aeroplane or other conveyance), with imported animals or with other imported product or foodstuff from an infected area. However, data do not exist to assess the likelihood of such movements as biting midges have not been specifically looked for when such routes have been and have not been recorded, though many other species of insect have, including blood feeding species such as mosquitoes.

The other most obvious route of incursion of infected midges is via their movement on winds from infected source areas. This sort of incursion is extremely difficult to prove with certainty but the incursions of AHSV from Morocco into southern Spain in 1966, and in the reverse direction in 1989, in the absence of movement of equids, were circumstantially attributed to infected midges conveyed on the wind. Similarly, the movement of BTV from Sardinia into the Spanish Balearic islands, a distance of some 200 km, during 2000 was attributed to airborne midges, and winds from Sardinia were identified that fitted in with the first occurrence of disease on Minorca (see Alba *et al*., 2004). In 2004 the Met Office's NAME model was used to identify a plume of wind from the source area of BTV-4 infection in north-central Morocco into southern Spain, where the first incursion of BTV-4 was identified in a sentinel herd of cattle at a location situated in the centre of the plume. In addition, Sellers and his co-authors have produced a series of papers implicating the movement of infected midges on the wind over distances of up to 700 km as the cause of introduction of BTV, AHSV, EHDV and AKAV into locations remote from the source and in the absence of movement of animals (Sellers & Maarouf, 1991; Sellers & Pedgeley, 1985; Sellers *et al*.,1978; Sellers *et al.*, 1977).

3.1.5 Identification of factors (climatic or other) that affect susceptibility of a midge to replication of the virus, or to maintaining infection in the midge

Vector Species of Culicoides – barriers
The ability of vector species of *Culicoides* to become infected with BTV and AHSV, and presumably other arboviruses, and to transmit these viruses is determined by a number of barriers which act to prevent or constrain virus dissemination through the body of the insect (Mellor *et al.*, 2000; Mellor, 1990). The occurrence of these barriers is under genetic control, but in addition, their efficacy is also influenced by temperature so that the higher the temperature the less effective they are.

Vector species of Culicoides - effects of temperature
AHSV and BTV infection rates, and rates of virogenesis within vector *Culicoides* have been shown to be temperature dependent (Mullens *et al.*, 1995; Wellby *et al.*, 1996). At elevated temperatures, infection rates were higher, rates of virogenesis were faster, and transmission occurred earlier. However, individual midges survived for a relatively shorter period of time. As temperature was reduced, infection and virogenesis rates fell, the time to earliest transmission was extended, but midge survival rates were enhanced. The optimal temperature for BTV transmission was identified as 27-30°C, as within this temperature range maximum numbers of *Culicoides* survived long enough to transmit at least once and viral polymerase activity (i.e. viral replication rate) was also maximal (Purse *et al.*, 2005). No published data exist in relation to the temperature requirements of AKA, BEFV and EHDV.

With both BTV and AHSV replication was not detected in midges maintained at or below15^{o}C, transmission was never recorded at these temperatures, and the apparent infection rate rapidly fell to zero. However, when midges that had been maintained for extended periods at such temperatures were transferred to temperatures within the virus permissive range (more than 20°C) ''latent'' virus replicated to high titres. Other work with AHSV has shown that under variable temperature regimes chosen to simulate nocturnal-diurnal variations, the infection rates and rates of virogenesis in vector midges were proportional to the time spent at permissive temperatures, and the total time spent at these temperatures was a major factor controlling transmission potential (Mellor *et al.*, 1999). On the basis of these and

related studies, an overwintering mechanism for AHSV in temperate areas has been suggested (Mellor, 1998).

''Non-Vector'' Species of Culicoides - effects of temperature

The Palaearctic midge *C. nubeculosus* has an oral susceptibility rate for AHSV of less than 1% when reared at 25°C, and when the adults are fed upon virus at a standard titre. Unlike *C. variipennis* (= *C. sonorensis*) this rate of oral susceptibility cannot be enhanced by selective breeding from susceptible parents (Mellor *et al.*, 1998). However, if the rearing temperature is raised to 30° - 35°C, the oral susceptibility rate increases to more than 10% and virus replicates to levels indicating transmission is possible. Similar results have also been obtained when using *C. nubeculosus* and BTV (Wittmann 2000). Because selective breeding had no effect upon the *C. nubeculosus* oral susceptibility rate, in this instance, oral susceptibility is clearly not a genetically controlled, heritable trait. Instead, it may be that the increase in developmental temperature not only gives rise to smaller adults but to adults with an increased incidence of the so-called ''leaky gut'' phenomenon (Boorman, 1960). A similar increase in infection rates in small adults, brought about by poor larval nutrition and crowding, has been described by Tabachnick (Tabachnick, 1996) when working with BTV and *C. sonorensis*, though the underlying mechanism was not speculated upon. In female *C. nubeculosus* with a ''leaky gut,'' virus may be able to pass directly from the ingested blood meal in the gut lumen into the haemocoel without first infecting and replicating in the gut cells. Once in the haemocoel it is well documented that most arboviruses will replicate and then may be transmitted, even by normally non-vector insects. Such a sequence of events may be envisaged as a hybrid mechanism whereby infection is initiated by a mechanical event (i.e. passage of virus from the lumen of the mid-gut through the gut wall and into the haemocoel, without replication in the gut cells) but transmission is the result of a series of subsequent biological events (i.e. virus infection of the salivary gland cells, replication in these cells, and release of progeny virus particles into the salivary ducts). This work with *C. nubeculosus* suggests that under the appropriate environmental conditions (i.e. increasing temperature) species of *Culicoides*, not normally considered vectors, may be able to transmit AHSV, BTV and possibly other viruses. Indeed, the isolations of AHSV 4 from mixed pools of *C. obsoletus* and *C. pulicaris* in Spain during 1988 (Mellor *et al.*, 1990), two *Culicoides* species complexes that are not considered AHSV vectors may be an example of the leaky gut phenomenon in operation, potentiated by the warm conditions prevailing at the time. Similarly, the isolations of BTV from *C.*

pulicaris and *C. obsoletus* complex midges in Italy in 2002, species which had not previously been considered vectors, may be due to the same phenomenon.

Conclusions

Increasing temperature, due to climate-change, is likely to enhance BTV and AHSV-transmission potential by increasing the abundance of vectors, increasing the distribution of vectors, increasing the proportion of a vector population able to transmit and by recruiting new vector species of *Culicoides*, through the mechanisms described above. Similar changes might also be expected for the other *Culicoides*-borne viruses but as yet detailed data do not exist to confirm this

3.1.6 Host reservoir and immune status of host

African horse sickness virus

AHSV is infectious for all species of equid, though horses as an indicator species are the most severely affected clinically, and in naïve populations over 90% of infected animals may die. Mules and donkeys are affected much less severely and zebra can be regarded as the natural reservoir host, rarely if ever exhibiting clinical disease. The virus replicates in parts of the haemopoetic and, in the blood, tends to be cell associated which protects it from the effects of humeral antibody. This can lead to extended viraemia, especially in zebra where virus has been detected for up to 40 days post infection. In horses viraemia has not been shown to persist beyond 18 days. Dogs are occasionally infected with AHSV and can die from the infection but these animals are thought to acquire the infection only by consuming virus contaminated meat and to have a very transient low level viraemia insufficient to infect vector midges. They are therefore not considered to be important in the epidemiology of AHS. Once an equid has recovered from an infection with an AHSV serotype it develops an enduring resistance to re-infection with the homologous serotype, but remains susceptible to infection with any of the heterologous 8 serotypes.

Bluetongue virus

BTV is infectious for all species of ruminant, though severe disease is usually seen only in certain breeds of sheep (the fine wool and mutton breeds) and certain species of deer (e.g. white-tailed deer).

Cattle are only occasionally affected clinically by BTV but are the most important domestic reservoir of infection, possibly because they are most attractive to vector midges and because they tend to have a longer viraemia than other domestic ruminants. Maximum viraemia detected in sheep is 54 days while in cattle, occasionally, it may extend beyond 60 days. In both species it is usually of a much lesser duration (i.e. < 30 days). Duration of viraemia in deer and antelope (possibly the natural reservoir host) is uncertain. A ruminant which has been infected with a BTV serotype and has recovered from the infection develops a life-long solid immunity to re-infection with that serotype however it remains susceptible to infection with any of the remaining 23 serotypes.

3.1.7 Impact of climate-change on the risk of incursion of exotic viruses into Europe

African horse sickness and bluetongue viruses are transmitted between their respective vertebrate hosts by the same species of *Culicoides* biting midge. As it is the biting midges that are affected by climate-change the viruses may therefore be considered together. In essence the risk of incursion of these viruses into Europe is increased because:

- Warmer temperatures mean that they are more likely to become enzootic in locations closer to Europe (e.g. North Africa and western Turkey), thus providing a more immediate threat.
- In concert with warmer temperatures the increased windiness due to climate-change means that infected midges from these nearby infected regions will have enhanced likelihood of being blown into Europe and then surviving long enough to initiate an infection. Also, the increasing temperatures mean that more of the year will be suitable for midge survival and transport, so such incursions will be possible over an increasing proportion of the year.

3.1.8 Impact of climate-change in the EU on risk of establishment of exotic viruses in Europe

For all of the reasons stated in sections 3.1.5 and 3.1.7 climate-change is likely to enhance the likelihood of BTV and AHSV

establishing in Europe. It is already the case that the traditional southerly vector of these viruses (*C. imicola*) has extended its range northwards by >700 kms so that it now occupies the whole northern side of the Mediterranean Basin. In this position its range overlaps with the distributions of novel Palearctic vector species of *Culicoides* which had not previously been significantly involved with virus transmission.

For the first time Palearctic species of *Culicoides* (*C. obsoletus* complex and *C. pulicaris* complex) have become significantly involved in the transmission of BTV and during the current BTV incursions have precipitated the movement of this virus further north than ever before (c.f. the Baton effect).

It is also the case that in temperate regions, until recently, BT has been known as a disease of late summer and autumn as its occurrence is controlled by the seasonal presence of vector midges which peaked during these times. However, during the current BTV incursions into Europe, cases of disease have occurred throughout a greater proportion of the year (June to December). The occurrence of adult vector insects also seems to have extended throughout more of the year so that in many locations, even in northerly areas of Europe such as the UK, Belgium and northern France, midges can be collected throughout the year including the winter period.

3.1.9 What is the consequence of exotic viruses becoming established in the EU

AHSV

As AHSV can be expected to cause a mortality rate of between 80-95% in naïve horse populations the establishment of this virus in Europe would be catastrophic to both the leisure and horse-race industry. The existing vaccines, which are manufactured in South Africa, are live attenuated preparations of uncertain efficacy which are not licensed for use in Europe. In addition to the direct effects of the virus on equids, international movement of all equids would be most severely constrained, so trade and movement of animals to and from international horse events would not easily be possible.

BTV

The current incursions of BTV in Europe since 1998 have been a major disaster to the ruminant industries of the affected countries. Not only have there been the direct costs from animal mortality and

morbidity to contend with but trade between infected and free countries has been significantly disrupted. Also, movement of animals between infected and free zones in infected countries or on the infected premises have been curtailed. This has meant significant difficulties in maintaining internal as well as external markets, and in supporting stock that have been forced to stay on the farms of origin for many months when grazing may have run out. In relation to control, live attenuated vaccines manufactured in South Africa are all that has been available for most of the outbreak periods. These vaccines are not licensed for use in Europe, though veterinary authorities can elect to use them in an emergency situation. However, recent research has shown that the live vaccines can cause a significant viraemia in vaccinated stock, that vector insects can ingest, replicate and transmit such viruses and that the vaccine viruses themselves may cause significant pathology in some breeds of sheep. Furthermore, the occurrence of reassortants between vaccine viruses and wild strains of virus has now been confirmed in the field - the long term consequences of this are as yet uncertain. Other methods of control (animal movement restrictions, vector control, husbandry modifications) have been insufficient to prevent the spread of BT in Europe. How best to control/eliminate this virus from the affected areas is at present uncertain and the possibility that it may now be able to overwinter in northern Europe because of climate-change is causing great anxiety in the affected and neighbouring countries.

3.1.10 Conclusions

Climate-change will increase temperature, affect saturation deficit and precipitation and, will also bring an increase in extreme weather events. In relation to *Culicoides* biting midge-transmitted viruses for the reasons set out above this is likely to have the following effects: The predicted temperature rises may cause:

- An extension in the northerly range of some vectors (e.g. *C. imicola*) ***- so transmission will occur more extensively***
- An increased abundance of vectors ***- so transmission occurs more easily***
- A longer vector season leading to a longer virus season ***- so transmission will occur for more of the year***
- An increase in the proportion of vectors able to transmit ***- so transmission will occur more frequently***

- The extension of ability to transmit to additional *Culicoides* spp. & individuals ***- so transmission will occur more widely***
- The faster development of the virus in the vector ***- so transmission will occur more quickly***

The increase in extreme weather events e.g. windiness may cause:

- Enhanced dispersion of vectors aiding colonization of new habitats ***- so vector distributions will quickly track the opportunities presented by climate-change***
- Extensions in the range of the viruses if the dispersing vectors are infected***- so traditional virus distributions may extend dramatically***

All this is likely to mean more *Culicoides*-borne viruses over a wider area for a longer time - which, in the case of BTV, is already happening

3.2 Mosquitoes

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3.2.1 Introduction

Mosquitoes are insects that belong to the family Culicidae in the order Diptera. They are found throughout the whole world except in places that are permanently frozen. There are about 3500 species, of which nearly three-quarters are native to the humid tropics and subtropics. The largest populations of individual species occur in the Arctic tundra, where colossal numbers emerge in a single brood each summer from snowmelt pools that overlie the permafrost (Reiter, 2001; Jupp, 2004). There is a large number of mosquito species in Europe that belong to the subfamilies Anophelinae (*Anopheles* spp.) and Culicinae with representatives of the genera *Culex*, *Aedes* and *Culiseta* (Maier *et al*., 2003; see Table 2).

Mosquitoes transmit a large number of epizootic and epidemic viruses, i.e. representatives of the virus families *Togaviridae* (different alphaviruses, i.e. Sindbis virus, Semliki forest virus, Chikungunya virus and equine encephalomyelitis viruses, Wesselsbron virus), *Flaviviridae* (e.g. yellow fever virus, dengue virus, West nile virus, Japanese encephalitis virus) and *Bunyaviridae*

(e.g. Tahyna virus, Rift Valley Fever virus). Some of these viruses are listed by the Office International des Epizooties (OIE) as notifiable diseases (OIE, 2007). The causative agents of diseases notifiable to the OIE are those affecting multiple species (Rift Valley fever virus, RVFV; West nile virus, WNV; Japanese encephalitis virus, JEV) or horses alone (Eastern, Western and Venezuelan equine encephalomyelitis viruses; EEEV, WEEV, VEEV). Alphaviruses, like the three different equine encephalomyelitis viruses, are also listed by the Centers of Disease Control and Prevention as Category B bioterrorism agents (CDC).

Another important example of a mosquito-transmitted disease is malaria, where extensive studies on the history of the disease and its potential correlation to changes in climate and human life during the past were carried out (Reiter, 2001).

3.2.2 Identification of epizootic viruses that could be spread by mosquitoes in the EU

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The unexpected emergence of WNV during the summer of 1999 in New York city and its rapid spread throughout the US and its "arrival" in Argentina in 2006 underlines the ability of long-distance introduction of mosquito-borne viruses. The epizootic viruses mentioned above may have the potential for introduction to Europe, although the likelihood for this event might differ drastically from virus to virus.

West Nile virus

WNV is widely distributed in Africa, the Middle East, and southern Europe. Birds are involved in the transmission cycle as amplifying hosts. The first epidemics of encephalitis were reported in Israel in the 1950s and then in France in 1962-1963, affecting both humans and horses. More recently, West nile fever has become a major public health and veterinarian concern. During the previous 10 years, several human outbreaks have been reported in the Mediterranean basin (Algeria 1994, Tunisia 1997) and southern Europe (Romania 1996, Russia 1999) with fatal cases of encephalitis. Epizootics in horses have also been described in Morocco (1996), Italy (1998), France, and Israel (2000). WNV has been recovered from 11 genera of mosquitoes in Africa and America. In Israel, Egypt and Algeria the virus was isolated mostly from *Culex* mosquitoes. In Europe the virus was isolated from mosquitoes of four genera. Members of the *Culex*

genus are thought to be the most efficient for virus spreading. There is field evidence of natural vertical transmission in *Culex* in Kenya and persistence of the virus in overwintering mosquitoes in North America. In addition, ticks may also play a substiantial role in the geographical distribution and maintenance of WNV. Circulation of WNV in Europe was assumed from serological surveys, particularly in biotopes of migratory birds (Zeller & Schuffenecker, 2004). Approximately 40% of equine WNV cases results in the death of the horse (CDC, 2007). Figure 17 shows the occurrence of West-Nile fever worldwide in 2005 – 2007 based on OIE data.

Figure 17: West-Nile fever worldwide in 2005 – 2007 based on OIE data

Japanese encephalitis virus

A disease resembling Japanese encephalitis was recognized in horses and humans as early as 1871. Japanese encephalitis virus (JEV) is widely distributed in Asia, including Japan, China, Taiwan, Korea, Philippines, far eastern former Soviet Union, all of South-East Asia and India. About 50,000 cases and 10,000 deaths are recognized annually throughout Asia, but the disease is greatly underreported. In tropical areas, there is an endemic pattern of infection, with

occurrence of sporadic cases throughout the year. In temperate zones and in northern part of the tropical zone, outbreaks have a marked seasonal incidence during the rainy season. Precipitation and temperature are important determinants of vector density and rate of transmission. Birds and pigs are effective viremic amplifying hosts. Cattle are frequently infected, but have low viremias and do not perpetuate virus transmission. Main epidemic vectors are Culex species. Vertical transmission has been demonstrated for Culex and Aedes (Burke & Monath, 2001).

The last reported outbreaks in the OIE database (handistatus) were in 2004 in Japan and Korea, but in previous years several outbreaks occurred in other Asian countries and Australia reported serological evidence in some regions (**http://www.oie.int/hs2/report.asp**).

Equine encephalomyelitis viruses (EEEV, WEEV, VEEV)

The Eastern, Western and Venezuelan equine encephalomyelitis viruses (EEEV, WEEV, VEEV) are mosquito-borne viruses distributed in different parts of the Americas.

EEEV causes localized outbreaks of equine, pheasant and human encephalitis in the summer. It is enzootic in certain parts of North and South America. In North America, the primary enzootic cycle is maintained in shaded swamps where the vector is the ornithophilic mosquito *Cs. melanura*. The enzootoic vectors in the Caribbean is probably *Cx. taeniopus* and in South and Central America *Culex* (*Melanoconion*) spp. Birds are the primary reservoir host and many species are susceptible to infection, but often remain asymptomatic despite prolonged viremia. In North America different birds are amplifying species, whereas in Central and South America rodents, bats and marsupials may represent additional reservoirs. The overwintering mechanism in temperate areas is not known, perhaps remaining in resident birds or reintroduction annually by migratory birds or wind-borne infected mosquitoes coming from subtropical areas. There is no convinincing evidence for overwintering in mosquitoes so far, although experimental transovarial transmission by *Cq. perturbans* was demonstrated. The case fatality rate in humans is about 30-40%. EEEV is an important cause of disease in horses, pheasants, emus and turkeys in North America and reported to cause encephalitis in dogs and pigs as well. The case fatality rate in horses is 80-90%, with most survivors being left with neurologic sequelae.

WEEV is widely distributed in certain parts of the US, Canada and in South America. WEEV is maintained in an endemic cycle involving domestic and passerine birds and *Cx. tarsalis*. In addition, WEEV has been occasionally isolated from *Ae. melanimon* and *Ae. dorsalis*. In some areas mammals are involved in feeding of the mosquitoes. Epidemics due to WEEV resulted in case fatality rates of 10% for humans, 20-40% for horses and 10% for emus. WEEV outbreaks correlated with increases in the population densities of *Cx. tarsalis*. The epizootic vector in South America is *Ae. albifasciatus*.

Enzootic VEE complex viruses are involved in perennially active transmission cycles in subtropical and tropical areas of the Americas. In endemic areas, mosquito isolates are made primarily from *Culex* (*Melanocion*) spp. mosquitoes. These mosquitoes feed on a wide variety of rodents, birds and other vertebrates. The incidence in clinically ill humans is generally less than 5% and the case fatality rate less than 1%. VEEV epizootic/epidemics have occured at approximately 10- to 20-year intervals in cattle-ranching areas of Venezuela, Colombia, Peru and Ecuador, when heavy rainfall lead to increased populations of the epizootic vectors *Ae. taeniorhynchus* and *Ps. confinnis*. Epizootic and enzootic strains were thought to be maintained in separate transmission cycles. During outbreaks virus has been isolated from several species of mosquitoes. During epizootics horses are an important amplifying species and availability of susceptible equines provides a means for virus spread. Infection of horses with enzootic strains results in asymptomatic or mild courses. Disease induced by epizootic strains is characterized by fever, depression and diarrhoea leading to death after 6-8 days after infection (Griffin, 2001).

OIE reports on outbreaks of equine encephalitis are lacking since 2004. But in 2004 outbreaks were reported in several countries in North, Central, and South-America (http://www.oie.int/hs2/report.asp).

Rift valley fever virus

The ecology and epidemiology of Rift valley fever (RVF) is complex and poorly understood. The geographic distribution of RVF covers much of Africa, from Senegal to Madagascar and from Egypt to South Africa, with most epizootics in livestock being reported in East and Southern Africa. Beginning in autumn 2000, the presence of RVF in the Arabian peninsula was confirmed for the first time, with large epizootics in Saudi Arabia and Yemen. Mosquitoes have long been

known to play an important role in RVF epizootics frequently occurring at times of unusually high precipitation. The floodwater *Aedes* species of the subgenera *Aedimorphus* and *Neomelaniconion* are likely the principal vectors. Epidemiological investigations suggested that flooding of damboes at times of unusually heavy rainfall triggers a population explosion in floodwater *Aedes* mosquitoes. In *Ae. mcintoshi* a transovarial transmission was demonstrated in an endemic area during an interepidemic period. Viremic livestock act as amplifying host, transmitting the virus to other floodwater *Aedes* species as well as to other mosquito species. Such an infection cycle can result in a relatively synchronous eruption of RVF activity with associated abortion storms in livestock. Lethality rates of greater than 90% can be seen in animals less than 1 or 2 weeks of age. Transmission to humans can result in less than 1% in a severe disease. For instance about 200,000 human cases with 600 lethal outcomes were estimated for an RVF outbreak in Egypt in 1977/78 (Nichol, 2001). Figure 18 shows the occurrence of Rift-valley fever worldwide in 2005 – 2007.

Figure 18: Occurrence of Rift-valley fever worldwide in 2005 – 2007 based on OIE data

Wesselsbron disease (WSL)

Wesselsbron disease (WSL) is an acute arthropod-borne flavivirus infection of sheep, cattle, and goats. WSL has been isolated from several *Aedes* spp., *Culex univattatus* and *Mansonia uniformis*. The

virus causes relatively high mortalities in new-born lambs and kids, subclinical infection in adult animals. However, when infecting adults the virus can cause abortion and congenital malformations of the central nervous system of foetuses. In humans it can cause a non-fatal influenza like illness (Swanepoel & Coetzer, 2004).

WSL is not listed by the OIE, so there are no OIE data on outbreaks, although WSL is an important disease of sheep in Southern Africa, there are no report diseases caused by WSL elsewhere in Africa, or outside Africa. The virus has, however, sporadically been isolated in outside Southern Africa.

The reservoirs of mosquito-borne viruses and coincidental "dead-end" hosts from where the virus cannot be transmitted are provided in Table 3.

Table 3: Reservoirs of mosquito-borne viruses and coincidental "dead-end" hosts from where the virus cannot be transmitted

Virus	Vectors	Reservoir hosts	Dead-end hosts
West nile virus	*Culex* spp. : *Culex pipiens*, *Culex tarsalis* Bridge vector: *Aedes albopictus*	Birds	Humans Horses Other mammals
Japanese encephalitis virus	*Culex* spp.: *Culex tritaeniorhynchus* group, *Culex* spp.	Birds Secondary amplifica-tion host: pigs	Humans
Eastern equine encephalomyelitis virus (EEEV)	*Culiseta melanura*, *Culex* (*Melano-conion*) spp.	Passerine birds	Humans
Western equine encephalomyelitis virus (WEEV)	*Culex tarsalis*, *Culex quinquefasciatus*	Birds	Humans
Venezuelan equine encephalomyelitis virus (VEEV)	*Culex* (*Melano-conion*) spp.	Rodents Secondary amplifica-tion host: horses	Humans
Rift valley fever virus	*Aedes* species (*Ae. vexans*, *Ae. ochraceus*, *Ae. dalzieli*, *Ae. cumminsii*, *Ae. circumluteolus*, *Ae. mcintoshi*)	Amplifying host : livestock animals	Humans

3.2.3 Impact of climate change in Europe on mosquito populations

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Surveillance for mosquito's in countries not affected by mosquito-borne diseases is almost absent. So it is difficult to measure changes in mosquito distribution in Europe due to climatic change. Some information on mosquitoes detected in Europe is shown in Table 4. Changes observed in other parts of the world might not be an adequate predictor for the changes in Europe, because in other parts of the world there has also been a huge change in human distribution and land-use during the period climate changes have occurred. E.g. the availability of open water in slum areas in large cities in Africa and Asia has probably increased the possibility of mosquito survival irrespective of the change in temperature.

The different genera of mosquitoes have very different life styles which are influenced differently by environment and climate changes. For species that hibernate at the larval stage the -1°C January isotherm is decisive for their distribution (Maier *et al*., 2003). The influences of climate changes on the pathogens transmitted by *Culex* or *Aedes* vectors may differ. For *Culex* spp. small pools of stagnant water are important for hatching of the eggs, because they do not withstand drying. This is in contrast to the eggs of the *Aedes* spp. whose eggs are resistant to desiccation. However eggs of *Aedes* spp. hatch when they are inundated often occurring with the next river flooding. For both vector genera abundance of water, often after rainfall is essential for their life cycle (Reiter, 2001; Jupp, 2004).

One should realise that the conditions in Europe for mosquitoes transmitting malaria have been more favourable in the past, but irrigation of wetlands and thereby reducing the habitat for the species together with the treatment of humans has been efficient to combat malaria in Europe. This indicates that human intervention; capable of reducing, but possibly also increasing the habitat of *Anopheles* spp. had a very big influence on the densities of the vector of malaria. This indicates that even though climate had significant influence on malaria (Hulden & Heliovaara, 2005), the role of human interventions which influence the micro-climate and thereby the habitat could have a more relevant consequence.

Climatic factors influence arboviruses not only indirectly via the vector but also directly in their ability to replicate.

Table 4: List of mosquitoes detected in Europe (taken from Maier et al., 2003, and Italian distribution data between brackets)

Subfamily	Species	Vector competence
Anophelinae	*An. beklemishevi*	
	Anopheles (Anopheles) algeriensis (**N, S, Si, Sa**)	
	Anopheles (Anopheles) atroparvus (**N, S**)	WNV (possibly)
	Anopheles (Anopheles) claviger (**N, S, Si, Sa**)	
	Anopheles (Anopheles) hyrcanus (**N, S, Si, Sa**)	
	Anopheles (Anopheles) labranchiae (**S, Si, Sa**)	
	Anopheles (Anopheles) maculipennis (**N, S, Si**)	
	Anopheles (Anopheles) marteri (**N?, S, Si, Sa**)	
	Anopheles (Anopheles) melanoon (**N, S, Sa**)	
	Anopheles (Anopheles) messeae (**N, S**)	
	Anopheles (Anopheles) petragnani (**N, S, Si, Sa**)	
	Anopheles (Anopheles) plumbeus (**N, S, Si, Sa**)	
	Anopheles (Anopheles) sacharovi (**N, S, Sa**) [**M**]	
	Anopheles (Anopheles) subalpinus (**N, S**) (*****)	
	An. italicus	
	Anopheles (Cellia) hispaniola (**S, Si, Sa**)	
	Anopheles (Cellia) sergentii (**Si**) [**M**]	
	Anopheles (Cellia) superpictus (**N, S, Si**)	
	An. plumbeus	
	An. claviger-Komplex	
Culicinae	*Culex Europeanus*	WNV (possibly)
	Culex (Barraudius) modestus (**N, S, Si, Sa**)	WNV (possibly)
	Culex (Culex) brumpti (**Sa**)	
	Culex (Culex) laticinctus (**S, Si, Sa**)	
	Culex (Culex) mimeticus (**N, S, Si, Sa**)	
	Culex (Culex) pipiens (**N, S, Si, Sa**) (*****)	WNV (moderate) WEEV (very low) JEV
	Culex (Culex) theileri (**N, S, Si, Sa**)	
	Culex (Culex) torrentium (**N**)	
	Culex (Culex) univittatus (**S, Si**)	
	Culex (Maillotia) hortensis (**N, S, Si, Sa**)	
	Culex (Neoculex) impudicus (**S, Si, Sa**)	

	Culex (Neoculex) martinii (**N**, **S**, **Si**, **Sa**)	
	Culex (Neoculex) territans (**N**, **S**)	
	Aedes (Aedimorphus) vexans (**N**, **S**, **Si**, **Sa**)	RVFV, WNV (low, bridge vector)
	Aedes (Finlaya) echinus (**S**, **Si**, **Sa**)	
	Aedes (Finlaya) geniculatus (**N**, **S**, **Si**, **Sa**)	
	Ae. cinereus	
	Aedes (Aedes) cinereus (**N**)	WNV (possibly)
	Aedes (Ochlerotatus) annulipes (**N**)	
	Aedes (Ochlerotatus) berlandi (**N**, **S**, **Si**, **Sa**)	
	Aedes (Ochlerotatus) cantans (**N**)	WNV (possibly)
	Aedes (Ochlerotatus) caspius (**N**, **S**, **Si**, **Sa**)	WNV (possibly)
	Aedes (Ochlerotatus) cataphylla (**N**, **S**)	
	Aedes (Ochlerotatus) communis (**N**, **S**)	
	Aedes (Ochlerotatus) detritus (**N**, **S**, **Si**, **Sa**)	
	Aedes (Ochlerotatus) dorsalis (**N?**)	
	Aedes (Ochlerotatus) mariae (**N**, **S**, **Si**, **Sa**)	
	Aedes (Ochlerotatus) pulchritarsis (**N**, **S**, **Si**, **Sa**)	
	Aedes (Ochlerotatus) pullatus (**N**, **S**)	
	Aedes (Ochlerotatus) punctor (**N**, **S**)	WNV (possibly)
	Aedes (Ochlerotatus) rusticus (**N**, **S**, **Si**, **Sa**)	
	Aedes (Ochlerotatus) surcoufi (**N**, **S**)	
	Aedes (Ochlerotatus) sticticus (**N**, **S**)	
	Aedes (Ochlerotatus) zammitii (**N**, **S**, **Si**)	
	Aedes (Rusticoidus) refiki (**N**, **S**, **Si**)	
	Aedes (Stegomyia) aegypti (**N**, **S**, **Si**, **Sa**) (*****)	WNV (moderate, bridge vector)
	Aedes (Stegomyia) albopictus (**N**, **S**, **Sa**) (*****)	WNV (high, bridge vector)
	Aedes (Stegomyia) vittatus (**S**, **Si?**, **Sa**)	
	Mansonia richiardii	
	Culiseta annulata	
	Culiseta (Allotheobaldia) longiareolata (**N**, **S**, **Si**, **Sa**)	
	Culiseta (Culicella) fumipennis (**N**, **S**, **Si**, **Sa**)	

	Culiseta (Culicella) litorea (**S**, **Si**, **Sa**)	
	Culiseta (Culicella) morsitans (**N**, **S**, **Si**, **Sa**)	
	Culiseta (Culiseta) annulata (**N**, **S**, **Si**, **Sa**)	
	Culiseta (Culiseta) subochrea (**N**, **S**, **Si**, **Sa**)	
	Coquillettidia (Coquillettidia) buxtoni (**N**, **S**, **Si**, **Sa**)	
	Coquillettidia (Coquillettidia) richiardii (**N**, **S**, **Si**, **Sa**)	WNV (possibly)
	Orthopodomyia pulcripalpis (**N**, **S**, **Si**, **Sa**)	
	Uranotaenia (Pseudoficalbia) unguiculata (**N**, **S**, **Si**, **Sa**)	

WNV, West nile virus; RVFV, Rift valley fever virus; WEEV, Western equine encephalomyelitis virus
N = North-Italy, **S** = South-Italy, **Si** = Sicily, **Sa** = Sardinia

Temperature conditions e.g. affect the multiplication of the virus in the mosquito vector, low temperatures slowing down viral replication and lowering vector competence. However, the most important influence of climatic factors will be on the geographical distribution and prevalence of the viral hosts, both mosquito and vertebrate. In the case of mosquitoes, high rainfall and temperatures can lead to higher population densities of the species belonging to all genera, particularly *Aedes* (Jupp, 2004). Natural factors that cause climatic variability include fluctuations of the sun´s radiant energy, alterations in the transparency of the atmosphere (due to sand, volcanic dust, and other air-borne particles), and cyclic changes of the earth´s rotation on its axis and its orbit around the sun. In addition, the circulations of the atmosphere and the oceans, which are major components of the climate system, are subject to internal variations on time scales ranging from weeks to millenia. It is the complex interaction of all these variables that generates the continually changing patterns of climate. As a result, the yearly averages of climatic elements, such as temperature, humidity, rainfall, wind and airborne particles, differ from one another (Reiter, 2001).

Climate change scenarios for the forthcoming 50 year period suggested an increase of the daily mean temperature and changes in precipitation. The influence of these postulated global changes may result in different changes on the local geographical level and especially the microclimate in different habitats. Thus e.g. for Germany different patterns of climate change in the next 50 years have been postulated for the North-Eastern and South and South-Western parts of Germany. Whereas the Southern part is postulated

to get more precipitation and a daily temperature increase of about 1.8 °C, the North-Eastern part may show a different pattern (lower increase of the mean temperature, reduced level of precipitation). (Personal communication Prof. Gerstengarbe, Potsdam Climate Research Institute, at the Jena symposium, March 2007).

Although statistic and dynamic models on climate changes and potential influences on the distribution of certain arbovirus vectors have been developed, it is difficult to assess whether these models will be applicable in other areas than where they were developed and changes to the micro-climate, often due to human intervention, might have a much larger influence. Therefore it is difficult at the moment to predict if the risk of introduction and maintenance of the vector is increasing or decreasing. Longitudinal monitoring programs on microclimate change, habitat changes and vector distribution and competence for mosquito-borne viruses are urgently needed to prove the validity of the models and their potential consequences on human and animal health issues.

3.2.4 Possible routes of introduction of mosquito-borne viral infections of livestock into Europe which may act synergistically with climate-change

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The means of introduction of WNV to the US is still under investigation. But based on the available information there are a couple of potential routes for introduction of mosquito-borne viruses to Europe. The introduction via insects or mosquitoes (eggs, larvae, adults) in containers on ships or airplanes is a sustainable assumption. Another possibility is the legal/illegal introduction of infected birds. The introduction by humans is very unlikely due to the low viral load and the short duration of viremia in humans (Zeller & Schuffenegger, 2004). As shown in Table 2 several competent mosquito species are present in Europe, so an important route of introduction will also be the trade of infected livestock from areas close to regions where the disease is present but currently thought to be free of the disease.

Potential routes for introduction of mosquito-borne viruses therefore might be:

- introduction via insects or mosquitoes in containers on ships or airplanes

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- legal/illegal introduction of infected birds or other reservoir hosts, especially when they remain asymptomatic despite prolonged viremia
- migratory birds (or perhaps bats)
- transportation and introduction of infected livestock and pet animals that might play a role in the epidemiology
- wind transportation as aerosol plankton

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3.2.5 Identification of factors (climatic or other) that affect susceptibility of a mosquito to replication of the virus, or to maintaining infection in the mosquito

As indicated above there are many factors that can affect the microclimate of the habitat of possible mosquito vectors. E.g. draining most wetlands in Europe and America has reduced the potential of mosquitoes to transmit malaria. But there is evidence that in the past malaria epidemics were also influenced by the temperature in the preceding summer (Hulden & Heliovaara, 2005). However less is known on vectors responsible for mosquito-borne viral diseases of livestock. In a study on distribution of WNV in Georgia a correlation was found in one year between the minimum temperature in January and the probability to detect WNV-specific antibodies in serum samples collected from wild bird. There was also a consistent, though weak relation with urban/suburban regions (Gibbs *et al.*, 2006), showing again that microclimate is possibly more important than the overall climate.

Temperature

For all mosquitoes, increased temperature is favourable for an increase vector density and thereby increased transmission. But as said before temperature alone is not sufficient.

Rainfall

For both *Culex* and *Aedes* spp. water is necessary but for *Culex* spp. mainly stagnant pools of water at a relative high temperature is necessary, whereas for *Aedes* spp. flooding is necessary.

Vector competence

The vector competence of a given mosquito species and likelihood of transmission is determined by the level of virus replication and transportation to the salivary glands via the haemolymph. However, these limitations seem to be not very stringent as most of the

mosquito-borne viruses can be found in different mosquito species, even of different genera. For instance, WNV was isolated in Europe from mosquitoes of four genera. Therefore it might be assumed that mosquito-borne viruses have a larger host range with strong impact on the epidemiology of mosquito-transmitted diseases.

Vector competition

There is evidence for competition between mosquito species with regard to the habitat, which may influence the epidemiology of mosquito-borne viruses, e.g. competition between Ae. Albopictus and Cx. Pipiens repreenting WNV vectors (Carrieri *et al*., 2003).

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3.2.6 Host reservoir and immune status of host

In Table 1 information is given on the discussed mosquito-borne viruses, and it is shown that these viruses are able to infect a broad range of vertebrate species. For instance, forty-nine species of mosquitoes and ticks and 225 species of birds are susceptible to infection by WNV. WNV has been detected in dead birds of at least 317 species. Although birds, particularly crows and jays, infected with WNV can die or become ill, most infected birds do survive. Other hosts are horses, cattle, llamas, alligators, cats, dogs, wolves and sheep (Weaver & Barrett, 2004; CDC, 2007).

Immunoprohylaxis (vaccination) could be considered as an option in case of an outbreak. For mosquito-borne flaviviruses, like WNV in livestock and humans, and dengue virus in humans heterologous immunisation by other flaviviruses has been thought to induce a partial cross-protective immunity (Zeller & Schufferegger, 2004; Burke & Monath, 2001). For WNV it is known that competent bird reservoirs will sustain an infectious viremia for 1 to 4 days after exposure, after which these hosts develop a life-long immunity (http://www.cdc.gov/ncidod/dvbid/westnile/birds&mam-mals.htm).
In addition, for some of the viruses commercial vaccines are available, i.e. WNV and EEV vaccines for horses, JEV vaccine for swine, RVFV vaccine for veterinary use, however their safety and efficiency might not be sufficient to get a complete and sterile immunity.

3.2.7 Impact of climate-change on the risk of incursion of exotic viruses into Europe

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The scenarios for introduction are based on two alternative assumptions:

- Introduction by a non-mosquito source and spread to a competent vector species population in Europe
- Introduction of an infected mosquito population

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When considering the introduction by a non-mosquito source it is very important to have an exact knowledge on the geographical distribution of mosquito species, and the competent vector species in particular, in Europe. In the European Mosquito Bulletin Jackson, 1999 initiated the generation of a distribution map of all European mosquitoes (Maier *et al*., 2003), these distribution maps are however not finalised yet. In Table 2 we combined the data from Maier et al. with unpublished data from Italy. A large number of mosquito species of the subfamilies Anophelinae and Culicinae are present in Europe which may represent putative vectors (Table 2). Climate change will probably not have an influence on the risk of introduction into Europe of the virus by a non-mosquito vector, but the climate will probably influence the density of the putative vector and its competence for transmitting the virus, and thereby influence the risk of establishment of the virus. The latter will be discussed in the next paragraph.

Climate change might well influence the distribution of mosquitoes on the globe. Higher temperatures combined with sufficient rainfall might not only increase the density of mosquitoes in general but probably will also allow species that that are competent vectors of viral diseases of livestock to move to the North. An increase in distribution of competent vectors will increase the risk of introduction. However as stated before the influence of climate on the mosquitoes is very complex and more quantitative data should be compiled on current vector distributions in Europe and the changes due to climate change.

3.2.8 Impact of climate-change in the EU on risk of establishment of exotic viruses in Europe

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The risk of mosquito-borne viral diseases of livestock becoming established depends on several factors. As indicated in Table 2 the

mosquitoes responsible for transmission of WNV and RVFV virus are already present in Europe. There is also evidence that WNV is or has been present in parts of Europe. It is probable that the expected increase in temperature and the predicted increase in rainfall will cause an increase in vector densities and thereby increase the risk of viral transmission. Not only increase of vector densities of vectors already present, it will probably also increase the competence of the vectors present, but the predicted climate change will probably also introduce other vectors previously not present in Europe. For the vectors not present yet an important factor in establishment will be the possibility of over wintering in Europe, but also annual introduction by e.g. migratory birds is possible.

The risk for establishment might be higher if several vectors can transmit the virus, like ticks in the case of WNV, but also for the viruses transmitted by several mosquito species the risk might be higher if these species overlap spatially and in time.

As indicated before other human interventions might have a larger influence on the increase or decrease of the risk of transmission. E.g. the increase in JEV transmission in South-East Asia is linked to deforestation, agricultural development and irrigation schemes for rice cultivation, leading to high density breeding of *C. tritaeniorhynchus* (Burke & Monath, 2001). Similar human interventions will probably have a huge impact on mosquitoes already present and thereby increase the risk of establishment of exotic viruses in Europe.

It is not likely that extreme weather events like heavy rainfall and flooding that occur only once in a few years will be of great influence on the establishment of a new vector. These extremes might influence the annual differences in density, but for the establishment for a long time it is essential that the temperature will increase not only once during a short period but for a longer time.

Climate will probably also influence the distribution of the reservoir host. For WNV e.g. the routes of migratory birds might change due to climate change. One should, however, remember if due to climate change migratory birds will over winter at a higher latitude, e.g. Spain instead of somewhere in Africa, this might even decrease the risk of introduction of WNV by migratory birds. However in the latter case it is likely that also the vector will have migrated to a higher latitude and thereby compensating this effect.

3.2.9 What is the consequence of (exotic) viruses becoming established in the EU

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All viruses mentioned above are not only pathogenic to animals but are highly pathogenic to humans as well. Therefore the introduction and establishment of these viruses in Europe will have a large impact not only in agriculture but also for human health. Due to the human health risk, the impact on agriculture will probably be huge, where the direct production losses will be low compared to the losses due to loss of markets. Introduction of any of these diseases will therefore have a huge reduction in the benefits from agriculture, due to lower prices.

Of the viruses mentioned above RVFV causes the highest mortality in livestock. In Africa it was noticed that imported European animals were especially susceptible for infection. Perhaps this reflects the fact that the virus is affecting a naive population. If this is true, the introduction and establishment of RVFV in Europe would cause huge direct losses in agriculture. Also the equine encephalitis viruses can cause serious disease in horses, and although cattle, sheep and pigs are mostly though of as economically important, the importance of the horse industry is increasing as more people are riding and especially trade in breeding horses is increasing.

The situation for WNV is different as the virus is already present in certain regions of Europe. The rapid distribution of WNV after its introduction into the US in 1999 suggested that the virus met a completely susceptible naive population. It has been suggested that this might be not the case in Europe where other flaviviruses are present and vaccines are used, e.g. against tick-borne encephalitis virus. Therefore the impact of introduction of WNV on livestock into Europe might be lower. But in that case the impact of several people dying from WNV infection might have a much higher impact, also on the livestock industry.

3.2.10 Conclusions

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It is most likely that the distribution of mosquito-borne viral diseases of livestock will move towards the North; climate change will have an

influence on this increased distribution. But most likely other factors often due to human intervention will have a larger influence on the increased risk of transmission. It is therefore not only essential to monitor the distribution of the viruses and their vectors, but also to increase awareness by the public for rapid reporting of disease.

3.3 Ticks

3.3.1 Introduction

Ticks are arthropods of the order *Acarina*, which constitute the suborder *Ixodida*, including about 900 known species, all obligatory but temporally haematophagous ectoparasites. The order includes two families of ticks; the hard ticks (*Ixodidae*) which possess a chitinised scutum on their dorsal surface and the soft ticks (*Argasidae*) which lack a scutum. Their life cycle is complex and includes eggs, larvae, nymphs and female/male adults. The *Ixodidae* are referred to as being one, two or three host ticks according to their feeding habits. One host ticks spend their entire feeding life cycle (larva, nymph and adult) on a single host. Two host ticks attach as larvae and complete their development to the nymphal stage on the first host, the nymph feeds and then drops off the host to complete metamorphosis to the adult which later seeks a second host to complete the life cycle. Three host ticks require a single blood meal at each stage on three separate hosts, dropping to the ground and completing metamorphosis in the environment between feeds. Most tick species spend far less time feeding on their hosts than spent undergoing transtadial metamorphosis or oviposition and larval development off the host and their survival depends upon adaptation to their environment. In general tick genera are adapted to the climatic conditions under which they have evolved. Tropical or sub tropical hard tick genera such as Hyalomma, Amblyomma and Rhipicephalus sp tend to possess more heavily chitinised exoskeletons to prevent dehydration than tick genera found in cooler climates. Ticks found in more Northerly or Palaearctic climates such as Ixodes ricinus, the vector of LIV and TBEV, may only feed for a total of 14 – 20 days during their entire life cycle of more than 3 years and subsequently require higher levels of humidity in the microclimate of the host than ticks adapted to tropical or sub tropical climates which may complete a generation within one year.

The Argasid life cycle is more complex, some species may have as many as seven nymphal stages with each stage feeding briefly on separate hosts. According to the different species, ticks spend part of their life in the environment and their presence, distribution, development and density depends on climate, together with other important factors such as host availability, host immune status and land use.

3.3.2 Identification of epizootic viruses that could be spread by ticksin EU

Table 5 lists the viruses/diseases that can be transmitted by ticks. Each virus is considered in more detail below.

Table 5: Viruses/diseases that can be transmitted by ticks

Virus / disease	**Tick species**
Crimean-Congo Haemorrhagic Fever (CCHF)	Hyalomma sp (*Rhipicephalus rossicus*, *Dermacentor marginatus*)
African swine fever (ASF)	*Ornithodoros* (soft ticks)
Tick Borne Encephalitis virus complex (TBEVs):	
Central Siberian and Far Eastern TBE (Russian Spring Summer Encephalitis)	*Ixodes persulcatus* *Haemaphysalis concinna*
European TBE (Central European Encephalitis)	*Ixodes ricinus*, *Haemaphysalis punctata*
Omsk Haemorrhagic fever	*Dermacentor reticulatus* *D.marginatus*
Louping ill	*Ixodes ricinus* , (*I.persulcatus* , *Rhipicephalus appendiculatus*, *Haemaphysalis anatolicum)*
Thogoto virus	*Boophilus sp (now placed in the genus Rhipicephalus)* *Amblyomma sp* *Hyalomma sp.* *Rhipicephalus sp.*
Dugbe virus	*Amblyomma variegatum*
Nairobi sheep disease virus	*Amblyomma sp* *Rhipicephalus appendiculatus* *Rhipicephalus pulchellus*

Crimean-Congo haemorrhagic fever virus (CCHV)

Crimean-Congo haemorrhagic fever virus (CCHV) is a Bunyavirus which is widely distributed throughout Africa, the Middle East, Europe and Asia. Severe disease only affects humans, however cattle, sheep and small mammals such as hares (*Lepus sp*) and hedgehogs (*Erinaceus* and *Hemiechinus sp*) may develop mild fever and a short viraemia following infection. The primary vectors are *Hyalomma sp* particularly *H.marginatum marginatum*, *H.m.rufipes* (in Africa) and *H. anatolicum anatolicum* although the virus has been isolated from 31 different tick species.

African swine fever virus (ASFV)

African swine fever virus (ASFV) is the only member of the family Asfaviridae and is naturally transmitted by the wart hog tick *Ornithodoros moubata porcinus*. The virus may be transmitted horizontally between domestic pigs. The disease was probably introduced to Europe via the movement of infected domesticated pigs or pork products from Angola to Portugal in 1957. ASFV replicates and persists in *O. erraticus*, but a viral clearance occurs at later times in both natural and experimental infections (Basto *et al*. 2006). Subsequent eradication programmes have dramatically reduced disease outbreaks in the Iberian peninsula and none have been recorded since 1999. ASFV has been endemic from 1978 to 2005 in Sardinia (Italy). Until 2006, out of Africa the disease is present in Sardinia only, where ASFV has been notified in 2007 both in domestic pigs and wild boar (Pestivirus and Asfivirus National Reference Centre, http://www.pg.izs.it/). However, ASF has recently emerged in Georgia and by mid-June 2007, 52 of 65 districts were suspected to be affected by ASF, more than 30 000 pigs had died and a total of 22 000 pigs have been culled.

Tick Borne Encephalitis virus (TBEV)

Tick Borne Encephalitis virus (TBEV) is a zoonotic flavivirus which naturally circulates primarily between ticks of the *Ixodes ricinus* complex (*I.ricinus* in Western Europe and *I. persulcatus* in Central Siberia and the far East) and small rodents and insectivores. It is endemic in all European countries with the exception of Great Britain, the Benelux countries and the Iberian peninsula. Based onnucleotide sequence homologies, three different subtypes are now recognised; European, Central Siberian and Far Eastern subtypes. Large domestic animals are considered to be amplifying hosts for the tick vectors however, apart from rare cases, infected livestock appear to be

asymptomatic and only produce low viraemia. However TBEV is excreted in the milk and local human outbreaks have been associated with consuming milk or milk products such as cheese.

Omsk haemorragic fever virus (OHFV)

Omsk haemorragic fever virus (OHFV) is a zoonotic flavivirus related to the TBEVs which may be transmitted to humans either by tick bite or by direct handling of infected musk rats. Sporadic cases and outbreaks are seen in western Siberia and more recently in adjoining regions of Russia. The virus naturally circulates between the primary tick vector *Dermacentor reticulatus* and Muskrats (*Ondatra zibethicus*), although the virus has also been isolated from *Dermacentor marginatus* ticks. Transmission of virus in the tick appears to occur by both transtadial and transovarial routes. Although antibodies have been detected in other animal species the infection only appears to be pathogenic in humans.

Louping Ill virus (LIV)

Louping Ill virus (LIV) is also a zoonotic Flavivirus closely related to the TBEV group of viruses transmitted principally by *Ixodes ricinus* ticks which causes an encephalomyelitis in sheep and Red Grouse (*Lagopus lagopus*) in upland areas of the UK. Similar disease associated with *I. ricinus* tick bite has been described in Scandinavia, Greece, Turkey and Bulgaria. In humans, the disease is similar to European TBE, however symptoms are generally milder and no fatalities have been recorded. Cases of louping ill have also been detected in horses and cattle and the mountain hare (*Lepus timidicus scoticus*) has been shown to play a part in transmission of virus via co-feeding infected and uninfected ticks.

Thogoto virus (ThV)

Thogoto virus (ThV) is a tick borne Orthomyxovirus, related to influenza viruses, which causes abortion storms in sheep, cattle and goats in Africa north of the equator and has also been isolated from camels (*Camelus dromedarius*). ThV has also been isolated from southern Europe and the Middle East, these strains appear to be antigenically similar to African strains and it has been suggested that ticks carried on migrating birds may play a role in introducing the virus to these areas (Calisher *et al*., 1987). The virus has been islolated from numerous tick species of the genera *Amblyomma*, *Boophilus*, *Hyalomma* and *Rhipicephalus* in which the virus is

transmitted transtadially. Experimental transmission from co-feeding infected to uninfected tick cohorts on uninfected guinea pigs has also been described.

Nairobi Sheep Disease virus (NSDV)

Nairobi Sheep Disease virus (NSDV) is a Bunyavirus, closely related to CCHVand Dugbe viruses which is transmitted principally by *Rhipicephalus appendiculatus* ticks in East Africa. The ticks *Amblyomma variegatum* and *R. pulchellus* also play a role in transmission in other enzootic areas of Africa. Climatic changes leading to heavy rains appearing in 5 – 15 year cycles favour the extension of the geographical range of *R. appendiculatus* and thus the range of the virus. Severe disease with high fever and diarrhoea may be seen in naïve sheep and goats resulting in mortalities exceeding 90%. A less pathogenic Asian strain of the virus (Gamjam strain) has been described in the Indian subcontinent which is possibly transmitted by *Haemaphysalis intermedia* and occasional isolates have been obtained from *H. wellingtoni* ticks. In cross protection and serological studies, there seem to be no discernible differences between African NSD strains, Dugbe virus and Gamjam virus, however genetic studies comparing these strains have yet to be carried out.

Other potential tick-borne viruses

Venezuelan Equine Encephalitis virus (VEEV) is a zoonotic arbovirus of the family *Togaviridae* naturally transmitted by mosquitoes. Equines and rodents are believed to be the principal amplifying hosts as high viraemias are produced in these species. Other mammals and some bird species are also involved in the circulation of virus. Larval *Amblyomma cajennense* ticks, found in South and Central America and southern states of the USA, have been experimentally infected with VEE. Transtadial transmission from larva to nymph was subsequently demonstrated followed by horizontal transmission of the virus from feeding nymphs to a vertebrate host. The significance of ticks as natural vectors is unknown.

Bluetongue virus (BTV) is an orbivirus naturally transmitted by *Culicoides sp.* Experimental evidence has shown that *Ornithodoros coriaceus* found in Mexico, Peru and Western USA (California, Oregon and Nevada) is capable of transmitting virus to uninfected cattle 42 days after artificial feeding on BTV serotype 13 infected cultures.

Although *Ornithodoros sp* can live for up to 5 years without feeding, the role ticks play in the maintenance of infection in nature is not known (Stott *et al*., 1985).

West Nile virus (WNV) is a zoonotic flavivirus naturally transmitted in enzootic cycles between mosquitoes and wild birds which can cause a very serious encephalomyelitis in humans and horses. WNV has been isolated from a number of Argasid and Ixodid ticks however their role in the epidemiology of WNV is probably minor.

Even as recently as 2006 a new tick-borne flavivirus was discovered in *Rhipicephalus evertsi evertsi* ticks taken from goats and sheep in Ngoye, Senegal and named Ngoye virus (Grard *et al*., 2006). It is not yet known whether the virus is a tick-borne pathogen of livestock and the authors note that there may be a large number of other tick-borne viruses to be discovered.

3.3.3 Impact of climate change in Europe on tick populations

The potential effect of climate change on vector-borne disease should take into account the transmission system as a whole and combine climate data with concurrent measurements of the vectorial capacity and infection rate of vectors, abundance and infection rate of reservoir hosts (if any). However, information on the climate effects on vectors is often collected separately from disease data.

The link between ticks and climate can be *spatial*, with climate affecting distribution, *temporal*, with weather affecting the timing of an outbreak, or relate to the *intensity* of an outbreak.

In general temperature and moisture impose limits on tick distribution (Baylis and Githeko 2006). Cold winter may cause mortality and a slow rate of recovery during following warmer weather; by contrast warmer summer temperatures may contribute to excessive moisture loss. Therefore, climate change resulting in warmer conditions for regions of Europe previously too cold for certain species of tick vectors may allow their establishment and future population increase. Climate change may extend both the length of the transmission season and facilitate spread of tick-borne diseases to higher latitude and altitudes. There is some evidence that the distribution of the tick *Ixodes ricinus* in Sweden has expanded

north between 1980 and 1994, and this is consistent with observed climate changes (Tallcklint & Jacnson 1998).

3.1.4 Possible routes for the introduction of tick vectors into Europe which may act synergistically with climate change.

Animal trade and natural movement/migration.

Both domestic and wild animals are able to carry and spread ticks in the environment. International trade and globalization has increased the chance of animal movement and there is currently no EU legislation or OIE regulatory policies to ensure that infected vectors will not enter Europe (Liebisch *et al*., 2006). A recent case was reported of an imported horse arriving in Germany from Montana, USA (via Amsterdam airport) that was found to be infested with more than 200 engorged *Dermacentor albipictus* ticks on arrival at its final destination. *Dermacentor sp* are known vectors of *Babesia*, *Theileria*, viruses and *Rickettsiae*. The tick is known to occur up to 60 ^{0}N in Canada and it is thought the woods of Northern Europe could also be a suitable habitat. In an outdoor experiment, engorged adult females, collected from the imported horse, laid eggs, which hatched, to larvae within 25 weeks of engorgement (Liebisch *et al*., 2006).

Wildlife

Wild animals can also be responsible of the spread of ticks, since they are less easily controllable and can move depending on their home range and food availability. Carnivores such as foxes and wolves have typically wide home ranges and can cross natural barriers such as rivers or mountains. Red foxes (*Vulpes vulpes*) as an example have been shown to cross the Alps between Italy and Austria. Migratory birds have also been shown to be important in the spread of ticks including larval stages of *Ixodes ricinus* and *Hyalomma marginatum*. Birds can carry soft ticks too. If the viral biology permits transovarial transmission within the tick vector or transmission via co-feeding infected and uninfected ticks, these immature ticks may already be infected when arriving with their host in a new environment, even if the host is not viraemic or not a reservoir of the disease concerned.

Increased range of ticks

Vectors, such as ticks, can conquer new areas both in altitude and latitude according to climate change.

3.1.5 Identification of factors (climatic or other) that affect susceptibility of a tick to replication of the virus, or to maintaining infection in the tick

Viraemia of the hosts

Viraemia has to be long and intense enough to cause infection in the tick (threshold of viraemic transmission). For TBEv for instance wild ruminants play a minor role as a reservoir since they show short viraemia and a long lasting immunity, while small rodents are the main source of virus for ticks.

Transovarial transmission.

If transovarial transmission of virus is possible the tick itself may become the reservoir of the disease since the virus can survive in the environment in the absence of infected hosts. Transovarially-infectable ticks need feed only once for successful transmission.

Co-feeding.

Hard ticks (Ixodidae) tend to attach in close proximity to each other whilst feeding and uninfected ticks are able to acquire infection from infected ticks even if feeding on a non-viraemic host (Jones et al., Randolph et al.). Virus transmission from infected to uninfected ticks occurs through the migratory skin cells of vertebrates (Jones *et al*. 1997).

Increasing Temperatures.

Warmer spring temperatures may accelerate tick development rates and therefore the virus transmission cycle; on the other hand drier summers (i.e. less humidity) may cause higher tick mortality or reduced host-seeking by ticks, especially in southern Europe. Warmer winter temperatures in central and northern Europe may promote higher survival rates of quiescent ticks in the environment. This may lead to larger populations of hungry ticks seeking hosts in the following spring and subsequent higher transmission rates of tick borne pathogens.

3.1.6 Host reservoir and immune status of host

Ticks exhibit a range of characteristics that have made them particularly successful for virus transmission and also agents for cross-species transmission (Hudson *et al.*, 2001). Ticks feed on a wide range of species and once a stage becomes infected with a pathogen each of its life stages in a single generation may remain infective via transtadial transmission. Epidemiology is complicated by transovarial transmission. Reservoir hosts are able to maintain virus transmission in nature; their competence as a reservoir depends on their abundance and the virus threshold for transmission. The virus has usually none or a limited impact on survival and/or fitness of reservoir hosts. Tick hosts which develop low or no detectable viraemia can also have an impact on susceptible hosts which do produce viraemia, either amplifying the tick population leading to virus persistence or diluting the infection and causing it to die out (Norman *et al.*, 1999). Table 6 summarises, for each virus, the host reservoirs, hosts that transmission the virus and also hosts that amplify the tick population.

Table 6:Host reservoirs, virus-transmission hosts and hosts that amplify the tick population for diseases spread by ticks.

Virus / disease	**Reservoirs**	**Virus-transmission hosts**	**Hosts amplifying tick population**
CCHF	Small vertebrates (hare,….)	Many mammals	Large vertebrates
ASF	African wild pigs	Wild and domestic pigs	Wild and domestic pigs
TBEVs complex:			
RSSE	ticks	small rodents (*Apodemus*)	Wild and domestic ruminants
CEE	ticks	small rodents (*Apodemus*)	Wild and domestic ruminants
OHF	ticks	Muskrat (*Ondatra zibethicus*)	Wild and domestic ruminants
Louping ill	sheep	sheep, red grouse	domestic and wild ruminants, horses, pigs, hares

In the case of RSSE and CEE , small rodents species are shorted-lived reservoirs of the virus, whereas ticks maintain the virus within natural foci for many months and even years (Charrel *et al.*, 2004).

Immune status of the hosts directly affects the rate of infection in ticks. In TBEv infection, wild ruminants develop a short lived

viraemia after which they develop immunity and are no longer able to transmit the virus. Animals that survive Louping ill infection develop high levels of antibodies in their blood which provide solid protection for the rest of their lives. In addition such protection is passed on very efficiently in colostrum ensuring that lambs can be solidly protected for the first 6 to 8 weeks of life. Direct transmission of Thogoto virus from infected to uninfected *R. sanguineus* and *Amblyomma variegatum* ticks co feeding on uninfected guinea pigs has been demonstrated, however this was markedly reduced if the guinea pigs were allowed to develop resistance to tick infestation.

3.3.7 Impact of climate change in the EU on risk of incursion of viruses into free-areas of Europe

It is very difficult to predict future changes in tick fauna and hence presence or incursion of tick borne viruses to a particular region. However predictions should be based upon climate as the dominant factor, at the broadest level, and factors such as topography and land cover types as well as biotic interactions and microclimate at the lowest level.

Some models of climate change predict a hotter and drier climate in Southern Europe and a more Mediterranean climate for North Western Europe. Tropical and subtropical tick species may fill this new ecological niche and diseases such as CCHV, or Thogoto virus transmitted by Hyalomma spp. ticks in the hotter and drier Eastern regions of Europe, the Middle East and Africa may appear in more Westerly and Northerly zones of Europe. Tick fauna presently occupying the Mediterranean climatic zones may appear in more Northerly zones or areas of higher latitude.

All the viruses and their tick vectors below are already present in Europe, some confined to small geographically defined areas, like LIV in UK and ASF in Spain, Sardinia and more recently in Georgia. CCHF has been reported in Russia, (Source: IA Regnum News Agency, ProMED mail, 12 May 2007), Bulgaria, Greece, Kosovo and Albania. The natural focus of RSSE is in forested regions of Russia, CEE in central Europe, Sweden, Norway and north-eastern Italy. In Latvia all three subtypes of TBE have been isolated (Bormane *et al*., 2004). However if Southern Europe becomes progressively hotter and drier in future years, the risk of establishment of sub Saharan tick species such as Rhipicephalus appendiculatus and Amblyomma

variegatum, vectors of Nairobi sheep disease virus and Thogoto virus, increases. It is also possible that tick species presently indigenous to southern Europe may become increasingly competent in supporting virus replication and transmission due to increasing temperature levels.

3.3.8 Impact of climate change in the EU on risk of establishment of (exotic) viruses in Europe

The risk of establishment and spread of exotic tick species and their future competence as vectors of tick borne viral diseases in the EU would obviously be affected by the stabilisation of a warmer climate, host availability and the ability of hosts to move between habitats through corridors of suitable vegetation types governed by future land use in these areas. Studies are already being carried out to investigate the ecological niches of the most prominent Mediterranean tick species using two artificial neural networks (ANN) (Estrada-Pena, 2006) involving two different scales of measurement. The first scale is a set of 19 climatic variables as observed at a resolution of 5km in the Mediterranean region to describe the ecological niche of each tick. The first ANN evaluates the records of each tick species in the region and produces a map of climatic suitability and the second ANN evaluates the vegetation using data from satellite imagery at a 1km resolution and produces the final output. It is only by surveillance and the development of robust statistical models that future changes in European tick fauna can be predicted.

3.3.9 What is the consequence of (exotic) viruses becoming established in the EU

The obvious consequence would be the establishment of new vector/exotic pathogen disease cycles in what may indeed be a naïve population of animals. Possible consequences of their establishment in the EU through climate change may also include the ability of exotic viruses to infect and replicate in indigenous European tick vectors either through co-feeding or through feeding on viraemic hosts. The establishment of ASFV in Ornithodoros erraticus ticks in the Iberian peninsular in the 1960s is already a case in point. The effects on international trade in animals and bloodstock would be unpredictable although it can be assumed that some measures will be

taken to prevent spread to further destinations by this route. New foci of disease in naïve animals may mean higher degrees of pathogenesis and more economic loss potentially exacerbated by extreme weather events. It has been shown in Africa that tick control as a solution to the eradication of diseases such as East Coast fever transmitted by Rhipicephalus appendiculatus is difficult and expensive. Dipping programmes need to be carried out regularly with effective acaricidal compounds. As soon as breakdowns in dipping schedules or acaricidal resistance occurs, disease incidence can increase dramatically as does economic losses in what amount to naïve populations of susceptible livestock.

The initiation of surveillance initiatives and vaccination programmes would all add to the overall economic cost.

3.3.10 Conclusions

Climate changes including European average temperature increases of between 2 – 6^0C , increased precipitation in Northern Europe, drought in Southern Europe and an increase in extreme weather events have been predicted to occur in the next 100 years.
It is a central premise of biogeography that climate exerts a dominant control over the natural distribution of species. It is likely that indigenous European tick spp will be affected by this climate change both beneficially in some species and detrimentally in others. It can therefore be expected that the geographical incidence of endemic tick borne virus diseases such as LIV, CCHV and TBEV will change according to climate and subsequent effects on vegetation as an ecological niche for the survival of tick species off the host. Ticks are probably being introduced regularly via annual wild bird migrations and through international trade in animals, these routes would seem the most obvious in the introduction of exotic species.

While some powerful models exist that are able to predict the habitat suitability and abundance of ticks in defined regions, we are still far from predicting the risk of occurrence of tick borne diseases. These diseases are the result of complex transmission patterns and governed by the presence of susceptible animals and reservoir hosts. However, perhaps the most important factor is the presence and dynamics of human activity in the vicinity of tick foci

3.4 Sand flies

3.4.1 Introduction

Phlebotomine sandflies (Diptera: Psychodidae) are the vectors of leishmaniases, and carry and transmit phleboviruses (Tesh, 1988) and certain flaviviruses, orbiviruses and vesiculoviruses (Comer & Tesh, 1991), causing health problems for humans and domestic animals.

The family is constituted by six genera of which only two are of medical importance, namely *Phlebotomus* of the Old World, divided into 12 subgenera, and *Lutzomyia* of the New World, divided into 25 subgenera and species groups (Killick-Kendrick, 1999). Although sand flies are principally found in the warm parts of the world including southern Europe, Asia, Africa, Australia, and Central and South America, their distribution extends northwards to just above latitude 50°N in south west Canada and just below this latitude in northern France and Mongolia. Their southernmost distribution is at about latitude 40°S, but they are absent from New Zealand and the Pacific islands. Their altitudinal distribution is from below sea level (by the Dead Sea) to 3300 meters above sea level in Afghanistan (*P. rupester*). The species present in southern Europe are: *Phlebotomus perniciosus*, *P.perfiliewi*, *P.neglectus*, *P.ariasi*, *P.papatasi*, *P.mascittii*, *P.sergenti*, *Sergentomyia minuta.* Many others are present in the countries facing the Mediterranean basin or in far eastern Europe, a total of 18 Phlebotomus species have been identified from Turkey (Ozer, 2005; Toprak & Ozer, 2007).

3.5.2 Identification of epizootic viruses that could be spread by sandflies in EU

Two viruses have been identified, which can be spread by sandfiles. Further information is given in Table 7.

Table 7: Viruses that can be transmitted by sandflies

Virus / disease	Sandfly species	Other vectors
Vesicular Stomatitis Virus (VSV)	Lutzomyia (*L.trapidoi*, *L.ylephiletrix*, *L.shannoni)*	mosquitoes, blackflies
Rift Valley Fever (RVF)	*Phlebotomus duboscqi*, *P.papatasi* (less efficient in laboratory studies)	mosquitoes, culicoides, blackflies, other biting flies

Vesicular Stomatitis Virus (VSV)

Classical Vesicular Stomatitis (VS) occurs only in North and Central America and the northern part of South America. The disease occurs throughout the year in subtropical and tropical areas of the Americas. The disease occurs sporadically during the warm months in southern and western United States. Epidemics have occurred irregularly at 10 to 15 year intervals. The virus is spread by insect vectors, movement of infected animals and contaminated objects.

Vesicular stomatitis (VS) was described in the United States of America (USA) in 1926 and 1927 as a vesicular disease of horses, and subsequently of cattle and pigs. Vesicles are caused by the VS virus on the tongue, lips, buccal mucosa, teats and in the epithelium of the coronary band of the feet of cattle, horses, pigs, and many other species of domestic and wild animals. Many species of laboratory animals are also susceptible. The disease is limited to the Americas (from southern Mexico to northern South America); however, it was described in France (1915 and 1917) and in South Africa (1886 and1897). Influenza-like signs, normally without vesicles, have been observed in humans who are in contact with animals with VS or who handle infective VS virus. All manipulations involving VS virus, including infective materials from animals, should be undertaken with using proper biosafety procedures. There are two major immunological types of VS virus, New Jersey (NJ) and Indiana (IND). Both viruses are members of the genus *Vesiculovirus*, family Rhabdoviridae and have been extensively studied at the molecular level. Several other closely related rhabdoviruses have been isolated from sick animals over the past decades. These VS viruses are represented by the Salto-Argentina/63 and Alagoas-Brazil/64 strains, which are considered to be subtypes 2 and 3, respectively, of the IND serotype. Strains of the serotype NJ and subtype IND-1 are identified in the endemic areas of the disease: south-eastern USA, Mexico, Central America, Panama, Venezuela, Colombia, Ecuador and Peru. The IND-2 Salto-Argentina/63 strain was isolated from horses in Argentina in 1963. This strain, along with the IND-2 Maipú-Argentina/86 and two other strains isolated in 1966 and 1979 in Brazil, and classified in the same subtype, only affected horses. Cattle living together with the affected horses did not present antibody conversion. The IND-3 subtype, represented by the strain IND-3 Alagoas-Brazil/64, has been identified, sporadically, in Brazil only. Until 1977, strains of the IND-3 subtype were isolated from horses only. However, the IND-3 Espinosa-Brazil/77 was the first strain isolated from cattle. The known IND-3 strains affect cattle to a lesser

degree than horses. This finding confirms the first descriptions, in 1926 and 1927, of the NJ and IND serotypes in horses, and subsequently in cattle and pigs. The mechanism of transmission of VS virus is unclear. The fact that the virus has been isolated from sandflies (Lutzomyia spp.), black flies (Simulium spp.), gnats, mosquitoes, and other insects (during VS outbreaks or in the absence of outbreaks in endemic areas) tends to substantiate the hypothesis that it could be transmitted by insects. Transmission of VSV can occur by direct contact or by insect bites. There are also hypotheses that the VS virus is a plant virus present in pasture and that animals are the end of the epidemiological chain and, in special circumstances, the virus could undergo an adaptation process to infect animals, followed by direct transmission between susceptible animals. In infected animals, VSV is primarily localized to epithelial surfaces on the snout, mouth, tongue, coronary bands, teats, and lymph nodes draining the affected areas. Virus is not found in blood or urine and only rarely in faeces, but saliva, vesicular fluid, and sloughing epithelium can contain large amount of virus. Virus has been found in epithelial samples and oropharyngeal fluids for up to 10 days after initiation of clinical signs. During the 1982 epizootic in western USA, there were a number of cases where there was direct transmission from animal to animal. VSV pathogenesis is dependent on viral strain, host characteristics, route of inoculation, and virus dose. While VS is not diagnosed in livestock every year in the USA (but in sporadic cycles at approximately 10-year intervals), it is considered to be endemic in feral pigs on Ossabaw Island, Georgia. The incidence of disease can vary widely among affected herds. Usually 10-15% of the animals show clinical signs, and the great majority of infections are subclinical. Clinical cases are mainly seen in adult animals. Cattle and horses under 1 year of age are rarely affected. Mortality is close to zero in both species, but in swine can approach 90-100% of individuals in pig herds. That high mortality rates have been observed in pigs affected by the NJ virus rather by the IND virus. Sick animals recover in about 2-3 weeks. Factors affecting clinical signs are not clearly defined. It is hypothesized that environmental factors, such as insect bites, influence the development and severity of disease by modulating the immune response or other host-protective mechanisms. The most common complications of economic importance are mastitis and loss of production in dairy herds. Both NJ and IND-1 serotypes in the 1995, 1997 and 1998 US outbreaks primarily caused clinical disease in horses, although seroconversion was seen in cattle.

Rift Valley Fever (RVF)
RVF is generally found in regions of eastern and southern Africa where sheep and cattle are raised, but the virus also exists in most countries of sub-Saharan Africa and in Madagascar. In September 2000, a RVF outbreak was reported in Saudi Arabia and subsequently Yemen. These cases represent the first Rift Valley fever cases identified outside Africa. RVF is most commonly associated with mosquito-borne epidemics during years of unusually heavy rainfall.

Many different species of mosquitoes are vectors for the RVF virus. There is, therefore, a potential for epizootics (epidemics amongst animals) and associated human epidemics following the introduction of the virus into a new area where these vectors are present. This has been demonstrated in the past and remains a concern (WHO, 2000). The virus can be transmitted by sandflies too. For a more exhaustive description of the disease see the mosquitoes section.

3.4.3 Impact of climate change in Europe on the sandfly population

The preimaginal stages of sand flies are the egg, four larval stages (instars), and the pupa. Although the natural breeding sites of sand flies are poorly characterized, the larvae are known to be terrestrial, not aquatic, and from observations on colonized flies their principal requirements appear to be moisture, a comparatively cool temperature, and organic matter for food. Precise periods for the development of the stages cannot be given because they are affected by the ambient temperature with low temperatures increasing, and high temperatures shortening, the times. The eggs usually hatch in 7–10 days. Larval development is relatively slow, taking at least 3 weeks before pupation. Adult flies emerge from the pupae after 10 days, with males predominating at the beginning. In temperate regions the whole development (egg-adult) take at least 7-8 weeks and so far one generation or a maximum of two generations of sandflies are possible. Palaearctic species overwinter as diapausing 4th instar larvae whereas in warmer, wetter habitats, diapause is in the egg stage. The activity of sand flies is crepuscular or nocturnal, although a few species will bite during daylight. Diurnal resting places are comparatively cool and humid and include houses; latrines; cellars; stables; caves; fissures in walls, rocks or soil; dense vegetation; tree holes and buttresses; burrows of rodents and other mammals; bird’s nests; and termitaria. Females of most species are predominantly exophagic (biting outdoors) and exophilic (resting outdoors during the maturation of eggs). Ecotopes occupied by

immature phlebotomines are usually organically rich moist soils, such as the rain forest floor (*Lutzomyia intermedia*, *Lu. umbratilis*, *Lu. whitmani* in the Amazon; *Lu. gomezi*, *Lu. panamensis*, *Lu. trapidoi* in Panama), or contaminated soil of animal shelters (*Lu. longipalpis* s.*l.* in South America, *Phlebotomus argentipes* in India; *P. chinensis* in China; *P. ariasi*, *P. perfiliewi*, *P. perniciosus* in Europe). Developmental stages of some species (*P. langeroni* and *P. martini* in Africa; *P. papatasi* in Eurasia; *Lu. longipalpis s.l*. in South America), have been found in a wide range of ecotopes, and many species of sandflies employ rodent burrows as breeding sites, although the importance of this niche is unclear. Larvae of some phlebotomines have been found in what appear to be specialized niches such as *Lu. ovallesi* on buttress roots of trees in Panama; *P. celiae* in termite hills in Kenya; *P. longipes* and *P. pedifer* in caves and among rocks in East Africa. Old World species found as immatures in the earthen floor of human habitations include *P. argentipes*, *P. chinensis*, *P. martini* and *P. papatasi*.

Temperature

- *warmer winter:* increases the rate of survival of overwintering stages and can increases the rate of viruses transmission too
- *warmer spring*: can affect the time of overwintering stages awaking and give rise to more sandfly generation per year, in conclusion prolonging the transmission season.
- *warmer mean annual temperature* in general can increase the range of sandflies diffusion. The current population structure of *P. perniciosus* is consistent with it having suffered a range contraction during the last Ice Age, in the Pleistocene epoch, when its European populations could have survived only in southern Spain and Italy (Aransay *et al*., 2003). The spreading of canine leishmaniosis in northern Italy (Capelli *et al*., 2004), Spain and Greece in the past 10 years is consistent with an increased density of sandfly population, maybe due to climate change, together with other non climatic factors. Recently *P.mascittii* has been reported in Belgium, the first records of Phlebotomine sandflies from this country (Depaquilt *et al.*, 2005).

Precipitation

Precipitation could increase humidity and so offer more breeding sites for larvae. However sandflies do not require acquatic environment and extreme heavy rain or floading could have a negative effect.

3.4.4 Possible routes of infected sandflies introduction into Europe which may act synergistically with climate change.

Wind

The hopping behavior has given rise to the assumption that sanflies do not disperse far from breeding sites. However, one species (*P. ariasi*) has been shown to move further than 2 km although several studies show that the distance varies with species and habitat and that maximum dispersal seldom exceeds one kilometre. Preliminary studies with a wind tunnel suggest that their maximum flight speed is a little less than 1 m/sec (Killick-Kendrick R., 1999). Wind has been shown to transport other insects such as mosquitoes and Culicoides, so this evenience can not be excluded for sandflies too, even if very difficult to demonstrate.

Human intervention

By aeroplane or others. Airport-borne malaria has been already documented or suspected in many cases.

Animals trade.

This route is unlikely to be responsible of sandfly transportation, the blood meal is rather quick and when disturbed, sandflies can finish their meal on an other host. Anyway can not be excluded.

Increasing Temperatures.

It may turn a previous too cold environment (central, northern Europe) in a suitable habitat for sand fly development, so far increasing the geographic range of the vectors

3.4.5 Identification of factors (climatic or other) that affect susceptibility of a sand fly to replication of the virus, or to maintaining infection in the sandfly

Sandfly species

Species differ in the number of blood meals taken during a gonotrophic cycle; some will take more than one blood meal on

different days whereas others feed only once for each batch of eggs. Frequent blood meals increase the contact between vectors and vertebrates and, therefore, the efficiency of transmission of the pathogen. Infected sand flies tend to probe several times when biting; this is another factor which may increase the efficiency of transmission (Killick-Kendrick *et al*., 1977). Furthermore not all the species are vectors or good vectors, depending on san dfly and viruses genetics and parasite-host interaction.

Viraemia of the hosts

Nonviraemic transmission is an important mechanism for the survival of certain arboviruses in nature (Labuda *et al.* 1993). Therefore viraemia of the hosts may be an important consideration. VSV is a localized infection, with no viremia detected in cattle, horses, or swine. Primary replication seems to occur locally in keratinocytes. Virus is readily found at the site of lesions or in the tonsil from which virus is shed in saliva or from local draining lymph nodes. Virus is not found in other tissues, including muscle, brain, liver, spleen, mesenteric lymph nodes, kidneys, and spinal cord. Subclinically infected pigs can shed virus for several days via the saliva and transmit infection to other swine by direct contact.

Transovarial transmission.

Researchers have shown transovarial transmission of VSV in the sand fly and black fly; this may be a way the virus can overwinter

3.4.6 Host reservoir and immune status of host

Table 8 gives details of the reservoirs and host ranges of the viruses (VSV and RVF) that can be transmitted by sandflies.

Table 8: Reservoirs and host ranges of viruses spread by sandflies.

Virus / disease	Reservoirs	Host range
VSV	Cattle, horses, swine	wide host range, most mammals to insects. Cattle, horses, pigs, deer, raccoons, bobcats, and monkeys , humans
RVF	Not known; Amplifying host: livestock animals; According to OIE, mosquitoes (Aedes) are the reservoir host, but rodents may participate in	cattle, buffalo, sheep, goats, camels, some wild antelopes and humans

	the amplification of virus during the epizootic, but not in the endemicity	

The source of a VSV-NJ isolate may determine its virulence in an animal species. When compared to bovine VSVNJ isolates, lower titers of swine VSV-NJ isolates are required to produce experimental disease in swine, the incubation period is shorter, and secondary vesicle formation is more likely to occur (Clarke *et al.,* 1996). However, immune response to VSV in livestock species are poorly understood. Neutralizing antibodies are readily detectable as early as 4 days after clinical infection. In endemic regions, neutralizing antibody titers fluctuate among animals without clinical disease. Furthermore, antibody titers after subclinical infection in livestock do not correlate well with protection. Field evidence suggests that neutralizing antibodies are not protective, even against homologous serotype, and animals can become clinically ill despite the presence of significant titers of neutralizing antibodies. Young animals are less susceptible to clinical disease than adults, but the basis of this resistance is unknown.

3.4.7 Impact of climate change in the EU on risk of incursion of exotic viruses in Europe (i.e. first animal infected)

The impact of climate change in the EU is likely to be less significant for the risk of incursion, respect to animal legal/illegal trade. This is probably true for VSV, present oversea only. RVF is closer to EU and this increases the probability of infected mosquitoes population incursion, maybe via unexpected routes, like the introduction in Europe of *Aedes albopictus* by tires import.

3.4.8 Impact of climate change in the EU on risk of establishment of (exotic) viruses in Europe

Once the viruses have been introduced in a free area, flies can contribute to maintain the infections even if the sand fly is not the principal way of transmission of the diseases. However the recent discovery of transovarial transmission of VSV in the plebotomine insect arise the problem of VSV persistence, long time after the initial

focus/i has been eradicated or controlled. Climate change can increases the density of the vector and therefore the force of transmission or may cause the incursion in a new area by the vector itself. This imply a longer period of surveillance as follow up of a focus, and the introduction of controlling measures against flies in and around the focus.

3.4.9 What is the consequence of (exotic) viruses becoming established in the EU

Both VSV and RVF are exotic diseases for EU and the immediate consequence will be the economic impact for the focus eradication and trade restrictions. The human health is also implicated, especially for RVF. In the hypothesis of an establishment of the diseases, the economic impact will be worsened by animal mortality rates (expected to be high in a naive population) and surveillance programs (including vaccination if necessary). An other not negligible economic impact could be represented by the need of new or improved diagnostic techniques both for veterinary and human laboratories, as well as education programs for health operators.

3.4.10 Conclusions

VSV and RVF are more likely to be introduced in EU by animal trade or by infected mosquitoes (see Section 3.2) rather than by an infected sandfly. However, once a focus occurs great attention has to be placed on the presence of sandflies and other biting flies, since they can be involved in the transmission. More important, they can be the way the virus overwinter and cause new foci even in absence of infected animals.

4. Comparison of Blue Tongue Virus in Europe, Mongolia and China.

4.1 Introduction

Bluetongue disease (BT) was first described in 1876 in South Africa by an anonymous author, later referred as "fever" and "malarial catarrhal fever of sheep" by Hutcheon. In 1906, Theiler suggested that this disease was the result of infection by a virus. The disease caused a number of clinical signs in infected sheep including cyanosis of the tongue which gives rise to the blue colouration from which the disease derived its name. The disease also causes a range of other clinical signs, particularly haemorrhage and oedema, that are induced through damage to the circulatory system.

BTV is a member of the genus Orbivirus in the family Reoviridae. BTV causes a non contagious infectious, insect-borne disease of wild and domestic ruminants, particularly sheep. After its initial description in South Africa in the late 18th century, the disease has been recorded widely throughout much of the world and now affects ruminants on six continents, causing losses in terms of and trade estimated at USD 3,000 million each year. For these reasons BT has been designated by OIE as a serious notifiable disease.

4.2 Latitudes of Mongolia and Europe

Mongolia is located in the northern Asia, between China and Russia. The Inner Mongolia Autonomous Region is in the north of China, ranging from 37'24'' to 53'23'' north latitude. The latitude of Ulaanbaatar, the capital city of Mongolia country is 47º 55' N. The main latitude of Netherlands is 52º 30'North, while southern Spain is 37º 24' N.

4.3 Farming structure in China

Animal husbandry has become one of the pillar industries in rural economy and an important source of raising farmers income. Ruminant industry plays a important role in the relatively poorer areas, e.g, in western China. At the end of 2004, there were 137.818 million heads in stock. There included 101.371 million yellow cattle,

11.08 million dairy cattle, and 22.361 million buffalos. The off-take was 50.189 million. In terms of off-take volume, Henan, Hebei and Shandong from the Central China took up 35.1%, the biggest proportion in China, Liaoning, Jilin and Heilongjiang from the Northeast shared 15.9%, and the two large pastoral regions of Inner Mongolia and Xinjiang shared 8.1% of the national total. Beef production reached 6.759 million tons in 2004, and the carcass rate for commercial cattle was 134.7 kg/head. The beef production had a geographically high degree of concentration. The top three provinces for beef production were Henan, Shandong and Hebei, taking up the biggest share national total in terms of off-take rate as well as output. 23.684 million tons of milk was produced in 2004, including 22.606 million tons of cow milk. Dairy was mainly produced in the north. Inner Mongolia, Heilongjiang and Hebei were the three leading milk farms, yielding 5.021 million tons, 3.781million tons and 2.77 million tons. At the end of 2004, there were 366.391 million sheep in stock. There included 195.509 million goat, 6.7% higher in comparison to 2003, and 170.882 sheep or 8.6% higher. The off-take was 283.43 million, making the rate reach 83.2%. Henan, Inner Mongolia, Shandong, Xinjiang and Hebei are the top five provinces that claimed 58.3% of the national off-take. Mutton production was 3.993 million tons in 2004, accounting for 5.5% of the total animal meat output. Inner Mongolia, Xinjiang, Henan, Shandong, and Hebei were the top five provinces, whose mutton yield exceeded 300,000 tons, taking up 56.0% of the national total. There were 37,727.1 tons of goat wool harvested in 2004 and 373,901.7 tons of sheep wool,

4.4 Serotypes of BTV in Europe and China

Bluetongue virus is the type species of the genus Orbivirus in the family Reoviridae, at present 24 distinct serotypes of the virus are recognized. In Europe BTV 9 was recently detected in four Greek islands in 1998. Since then, there has been the almost simultaneous invasion of BTV 1, BTV2, BTV4, BTV 16 into southern Europe, and the distribution of BTV has expanded more widely than ever before in the continent with at least 12 countries affected over 7 years and outbreaks recorded more than 800 km further north than before. Starting in August 2006, BT was detected for the first time in the Netherlands, Belgium, Germany, northern France and Luxembourg. Serological tests as well as reverse transcript polymerase chain reaction (RT-PCR) proved the occurrence of BTV in sheep and cattle, and the virus was identified as serotype 8. This outbreak was the

furthest north that BTV has ever been recorded anywhere in the world.

In China, BT was first described by Zhang in Shizong county Yunnan province in 1989. Up to 2000, the Yunnan Tropical and Subtropical Animal Virus Laboratory identified Bluetongue virus BTV1, BTV2, BTV3, BTV4, BTV12, BTV15 and BTV16 from the isolates collected from Yunnan, Sichuan, Hubei, Anhui, Shannxi, Xinjiang, Inner Mongolia and, BTV2, BTV4, BTV 9, BTV 15, BTV16, BTV23 were detected from sera collected in these areas. Thus there is evidence of 9 serotypes of BTV in China: BTV1, BTV2, BTV3, BTV4, BTV9, BTV12, BTV15, BTV16 and BTV23. Of these, serotypes 1 and 16 were the dominant ones, and furthermore, these two serotypes were more pathogenic than the others.

4.5 Animals affected by Bluetongue

Bluetongue virus has a very wide host range and probably all species of ruminant are susceptible to infection. In certain breeds of sheep and some species of deer the outcome can be severe and often fatal, while in most other species of ruminants infection is usually inapparent.

In Europe, BT mainly affects sheep but cattle have also been reported to have been showing signs of illness in the current epidemics. In China, epidemiological investigation of 224,000 animals demonstrated that goats, sheep, cattle and buffalo are susceptible to BT. In northern China, the infection rate of goats were higher that cattle, and in some areas, it was higher that that of sheep. Positive cases were also reported in yak and deer. However, there were no reports of infection in camels. There are no suggestions as to why the infection rate is higher in goats than in cattle.

4.6 Distribution and Epidemiology

As a general rule, BTV can be considered as infecting ruminant livestock in all countries lying in the tropics and subtropics. The global distribution of BTV lies approximately between latitude 35°S and 40°N, within these areas the virus has a virtually worldwide distribution, being found in north, central and south America, Africa,

the Middle East, the India subcontinent, China, Southeast Asia and Australia.

4.6.1 Europe

Bluetongue has at times made excursions into Europe. The 1956-1960 epizootic in Spain and Portugal resulted in the death of almost 180,000 sheep and is the most severe outbreak on record. The current BT epidemic due to BTV 9 began during October 1998 on four Greek Islands. The serotype spread northward into a region of Turkey, Bulgaria, Kosovo, Albania, Bosnia and Herzegovina, the FYR of Macedonia, Serbia and Montenegro and Croatia and westward into mainland Greece, Italy, Sicily, Sardinia and Corsica. A further three serotypes, BTV 1, BTV 2 and BTV 16 entered Greece and spread westwards. In 2000, BTV 2 occurred in Sardinia, Sicily, mainland Italy, Corsica, and the Balearic Islands. In 2004, BTV 4 occurred in southwestern Spain and southern Portugal. BTV incidence has increased most markedly in areas where temperature increase are greatest, such as eastern Europe. Central Europe was considered to be safe from an incursion of BTV, since *Culicoides imicola* the major BTV vector is absent and the temperatures are generally considered to be too cold for BTV to establish. However, in August 2006, infected cattle and sheep were diagnosed in the Netherlands, Belgium, North France, Luxembourg and Germany. By December 2006, BTV had spread to include more than 2000 farms.

4.6.2 China & Mongolia

Since the first description of the disease in Yunnan in 1989, BTV and evidence of disease has been reported in several provinces in south China, including Hubei province in 1983, Anhui province in 1985, Sichuan province in 1988, and Guangdong, Guanxi and Jiangxi provinces between 1988 and 1991. In 1992, BTV was first reported in Shanxi province in north China and later positive serological cases were described in Xinjiang in 1986, Inner Mongolia in 1986, Gansu province in 1990, and Liaoning province, Hebai province, Tainjing and Jilin provinces in 1998. In China, the disease occurred in the period June to October in southern China and August to October northern China. Most cases of outbreak or sick animals were reported between latitude 35-37°N. In Northern China, and in Inner Mongolia and Shanxi province, disease occurred from August to October.

In Bayanzhuoer, Inner Mongolia, a serological survey of sera from 549 goats was done with agar diffusion test, the results suggested that 298 of them were positive and the infection rate was reported to be 53.2%. Later, between 1986-1989, another investigation was carried out in this region of China which lies between latitudes 40°13'N and 42 28'N. Agar diffusion tests on 2799 sera from sheep, goats and camels indicated that 650 animals were positive (23.22%). 523 goats out of 903 were positive giving an infection rate of 57.9%. Of 1684 sheep, 127 were positive and infection rate was 7.54%. No positive case was found in sera from cattle and camels. None of the serologically positive sheep or goats showed any clinical signs of BT. In a flock of sheep and some goats examined over a long period from April to the following January 59.2% of sheep (28/50) and 100% of goats (4/4) previous negative for BTV became positive. The animals became positive from August to October, and the rate was based the total number of sero positive animal, but the animals only exhibited slight changes of body temperature and WBC. BTV was isolated by cell culture, inoculation of egg embryos and inoculation of naïve sheep. However, the experimentally infected sheep also showed mild symptoms.

In Shanxi province (31 – 39ºN), which is located north of the Yellow River, BT was reported in 1992 among 56 farms, of 5160 sheep; 428 became sick and 98 died, the incidence rate was 8.2% and lethality was 22.89%. In 1993, the disease occurred in another county in three flocks of small ruminants, among 133 sheep and 16 goats, 56 sheep shoed clinical symptoms and 9 died, the incidence rate was 32.6% and lethality was 9%. The serotype of these two outbreaks was proved to be BTV1. The disease was prevalent mainly in August and September and the end of the outbreak coincided with the end of the activity of its vector—*Culicoides.* A serological survey in the province suggested the infection rate of goats, sheep and cattle 35%, 8.27% and 7.8% was respectively. Unfortunately, the identity of *Culicoides* was unknown. In Shaanxi province, from 1981-1991, 152,567 sheep and goats were examined by serological methods and the results suggested that the average infection rate was 3.8%. Another investigation of 965 sera from sheep and goats in 2002 indicating that the infection rate of sheep was 1.5 % (with female 0.85% while male 5.9%), and that of goats was 7.0%. The infection rate of local goats was 6.2%, and infection rate of the exotic goats imported from outside China grazing or kept in same area was as high as 20%.

In Xinjiang (latitude 34ºN), a serological survey in 1986 demonstrated that BT was prevalent in the province, the infection rate of sheep of goats in some flocks was more that 50%. Another survey was conducted in 1989 and 149,402 sheep, goats, yaks and deer were examined with agar diffusion test. It was found that the infection rate of goats, sheep, cattle, yak and deer was 34.5% (927/2680), 2.45% (418/17096), 1.34% (567/42828), 0% and 0% respectively. In one flock of sheep and goats, the infection rate of sheep was 4.08% while that of goats was 52.8%, which suggested that goats were more susceptible than sheep. The reason for this difference has not been considered.

In Tibet (lattitue 29 – 31ºN, 1023 sheep, goats, cattle, yak and pianniu (hybrid of yak and cattle) were examined with agar diffusion test and demonstrated that in Rikeze city, infection rate of sheep, goats and pianniu, yak and cattle was 3% (3/141), 0.83% (1/121), 1.055 (1/95), 0% (0/89), 0% (0/103) respectively, in Bailang county the infection rate of sheep, goats yak and cattle was 3.39% (4/118), 5.88% (7/139), 1.85%(2/108) and 0.84% (1/119) respectively..

4.7 Transmission and Vector.

Bluetongue virus is transmitted between its ruminant hosts almost entirely via the bites of certain species of *Culicoides* biting midge, which act as true biological vectors. The transmission is limited to those times of the year when adult vector are active. In epizootic areas this usually means during the late summer and autumn when vector abundance is highest.

Before 1998, only the major Old World vector *C. imicola* Kieffer was implicated in transmission and all BTV outbreaks occurred within its distribution in southern Europe, as brief periodic incursions, affecting mostly one or two countries. After 1998, however, a new epidemic of BTV started involving several countries in southern Europe. Initially all of these occurred within the known northern range limit of the main Afro-Asian Vector *C. imicola.* However, subsequently outbreaks also occurred for the first time beyond the distribution of *C. imicola*. In these regions *C. obsoletus* was the most abundant species complex of *Culicoides*. *C. obsoletus* has long been suspected of being a vector, mainly on the basis of BTV isolations from this species made in Cyprus in the 1970s and African horse sickness virus isolation from

mixed pools of *C. obsoletus* and *C. pulicaris* made in Spain in the 1980s. However, vector competence studies on a British population of *C. obsoletus* carried out at that time suggested that this species of midge was likely to be only a minor or inefficient vector of BTV. Since then BTV has been isolated on several occasions from *C. obsoletus* spp. in Italy (Savini *et al.*, 2003) and from *C. pulicaris* spp in Sicily (Caracappa *et al.*, 2003) showing that in the current series of incursions of BTV into Europe these two species complexes are acting as fully competent vectors. Even more recently in 2006, Meiswinkel and his colleagues (*personal communication*) and then Mehlhorn *et al*., (2007) have recorded BTV infections in Obsoletus complex midges by real time PCR in The Netherlands and Germany, respectively suggesting that species within or associated with this complex are the vectors of BTV in north-central Europe. No other species of *Culicoides* have recoded positive BTV in these parts of Europe. These findings strongly support that the BTV epidemic, in north-central Europe is mediated mainly by virus transmission by midges of the *C. obsoletus* complex. Another widespread and abundant Palearctic species *C. pulicaris* may also be involved the transmission of BTV in Europe in more limited areas.

In China, investigation on the transmission of BTV by vectors has been carried out in some provinces. In Shizong county, where the first evidence of BT was reported and in Longqing County, Yunnan province, 600 midges were trapped, and seven species of *Culicoides*, *C. halonostictus*, *C. homotomus*, *C. tenuipalpis*, *C. holcus*, *C. arakawae*, *C. circumscriptus* and *C. actoni*, were identified, and it was believed that *C. actoni* might be the vector of BTV in these areas. In another survey in Anhui province, 12 species of *Culicoides*, *C. schultrei*, *C. homotomus*, *C. nipponensis*, *C. arakawae*, *C. mihensis*, *C. actoni*, *C. maculates*, *S. sigaensis*, *C. pulcaris. C. matsuzawai* and two unidentified *Culicoides* species, have been found in the epidemic areas, and *C. schultzei*, *C. homotomus* and *C. nipponensis* were the dominant ones. It was speculated that *C. homotomus* probably the vector of BTV in Anhui province. However, the result of investigation by Yunan Tropical and Subtropical Animal Disease Laboratory suggested that *C. actoni*, *C pallidipennis* (= *C. imicola*) *and C. variipennis* were the major vectors of BTV in China. However, in some parts in northern China where *Culicoides* have not yet been recorded goats have been infected with BTV. The vectors of BTV in these areas need to be further studied.

It would be easier, when comparing BTV outbreaks in China with those in Europe, if the latitudes of the locations where virus was being transmitted could be included. At the moment it is difficult to determine at what latitudes BTV transmission is occurring in China and when during the year transmission occurs in each of the different provinces. This information, together with some idea of temperature range when transmission was and was not occurring and vector seasonality, is not available. Also speculation on the overwintering mechanism in the more northerly areas has not been considered.

5. Conclusions

Many European reports document the changing climate within Europe through the 20th century, and the predictions for continued changes in the 21st century. In summary, between now and 2100, air temperatures are likely to increase further with particular increases in the winter. This means that cold winters are projected to disappear almost entirely by 2080 and hot summers are projected to become much more frequent. Warmer winter temperatures may have an important impact on vectors such as midges and mosquitoes, since it may enable such vectors to persist year-round, and may provide a mechanism for overwintering of livestock viruses in more northerly lattitudes. In northern Europe it will rain more, but in southern Europe a decrease in precipitation is likely to occur. It is likely that, by 2080, droughts as well as intense precipitation events will become more frequent. Weather extremes in temperature, precipitation, wind etc. will occur more frequently, but likely to affect the regions of the EU differently.

The European Environment Agency (EEA 2005) have assessed the vulnerability of Europe to climate change on a regional basis. They identify South-Eastern Europe, the Mediterranean and central Europe as most vulnerable to climate change, while Northern and some western regions of Europe may experience benefits. This could form the basis of breaking Europe up in to regions for livestock disease risk assessment.

Below, the risks of vector borne viruses entering and establishing within Europe due to climate change are summarised. Specific details can be found in the relevant sections of the Hazard Identification. Although these conclusions have been drawn generically, it is essential that any risk assessment incorporates the impact of climate change at a regional level, if not on a smaller scale. The vectors and viruses considered are set out in Table 9.

Table 9: Details of vectors and viruses considered

***Culicoides* biting midges**	**Mosquitoes**	**Ticks**	**Sandflies**
Bluetongue virus	West Nile virus	Crimean-Congo Haemorrhagic Fever (CCHF)	Rift Valley fever virus
African horse sickness virus	Rift Valley fever virus	African swine fever (ASF)	Vesicular stomatitis virus
Equine encephalosis virus	Japanese encephalitis virus	Tick Borne Encephalitis virus complex (TBEVs):	
Epizootic haemorrhagic disease virus	Eastern equine encephalitis virus	Central Siberian and Far Eastern TBE (Russian Spring Summer Encephalitis)	
Akabane virus	Western equine encephalitis virus	European TBE (Central European Encephalitis)	
Bovine ephemeral fever virus	Venezuelan equine encephalitis virus	Omsk Haemorrhagic fever	
	Wesselsbron disease virus	Louping ill	
		Thogoto virus	
		Dugbe virus	
		Nairobi sheep disease virus	

There are many ways in which incursion and hence establishment of a vector-borne virus can occur. Such risks can be directly (or indirectly) increased by climate change but are difficult to estimate. For example, it is very hard to predict future changes in fauna for the different vectors and hence presence or incursion of vector borne viruses to a particular region. The predictions carried out here have been done with climate as the dominant factor, at the broadest level, and factors such as topography and land cover types as well as biotic interactions and microclimate at the lowest level.

For the risk of incursion and establishment warmer temperatures and an increased windiness could be significant and, in particular could mean that:

- the distribution and/or abundance of vectors will change in Europe and in locations closer to Europe. Competent vectors of viral diseases of livestock may move more North.
- the vectors are more likely to become enzootic in locations closer to Europe.
- temperatures, for more of the year, will be suitable for survival and transport of midges, mosquitoes, sandflies and ticks, although there will be regional differences for example between central and southern Europe.
- it is also possible that vector species presently indigenous to southern Europe may become increasingly competent in supporting virus replication and transmission.
- in combination with warmer temperatures the increased windiness due to climate-change means that infected midges and even mosquitoes from these nearby infected regions will have enhanced likelihood of being blown into Europe and then surviving long enough to initiate an infection.

Of course these risks may be insignificant compared to other routes of introduction (e.g. animal movements, trade of food etc.). However even routes such as animal movements may be impacted, and act synergistically, with climate due to an increased risk of establishment if incursion via this route occurs.

The main conclusion for the section on *Culicoides* midges is that climate change means more midge-borne viruses will occur in livestock over a wider area for a longer time, which is already happening in the case of bluetongue virus. More specifically, there will be an extension in the northerly range of some midge vectors, a longer season for virus transmission, an increase in the number of effective vectors, and the ability to transmit to additional *Culicoides* species. Increased windiness will increase dispersion.

The conclusion from the section on mosquitoes is that the distribution of mosquito-borne viral diseases of livestock will move north, although factors due to human intervention will have a larger influence on the risk of transmission. Monitoring the distribution of the viruses and their vectors, together with increasing public awareness is important.

The conclusion from the tick section is that indigenous European tick species will be affected by climate change and the subsequent effects on vegetation, habitats and ecological niches. This will affect the geographical incidence of endemic tick borne viruses such as Louping Ill, Crimean-Congo haemorrhagic fever and tick-borne encephalitis. In addition, there are routes for introduction of exotic tick species into Europe. Current models are not yet sufficiently developed to predict the occurrence of tick-borne livestock disease viruses.

The focus on sandflies has been vesicular stomatis virus and Rift Valley fever virus. Although both those viruses are more likely to be introduced by mosquitoes, sandflies could play an important role in overwintering of the virus, and also in transmission from animal to animal.

Mongolia is of similar latitude from the south of Spain up to the Netherlands. Although some information has been collated on the outbreaks of bluetongue virus in China, little has been reported on Inner Mongolia itself. Vital information is missing on the latitudes of the locations where the virus is being transmitted, and when during the year transmission occurs in each of the different provinces. Furthermore, no data on the temperature ranges during which transmission occurred are available. There are no theories on the overwintering mechanism, and only speculation on the *Culicoides* vector.

From this work, it has been concluded that quantitative data on the distribution and abundance of vectors within the EU are not available. Due to this, it is a complex task to predict the influence of climate on vectors and therefore we recommend that appropriate quantitative data be collected.

At present the risk of incursion of bluetongue viruses is particularly under the limelight, but it is important that other viruses are monitored, since a changing climate will also affect these vectors. All of the viruses listed here are significant animal health diseases and many are listed as notifiable to the OIE. Therefore the consequences of incursion and establishment of these diseases to Europe would be highly significant and it is therefore important that risk managers are aware of these increasing risks.

6. References

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