

1. EXECUTIVE SUMMARY

Risk assessment of the impact of climate change on human health and well-being



This project aims to provide a realistic assessment of the impact of climate change on human & animal health. It begins by considering all known pathogens, and then filters for those that have significant impact on human and animal health, affect or threaten Western Europe, and are sensitive to weather/climate and may therefore be affected by climate change. Questions asked include: How realistic is the threat to human & animal health from climate change's effects on infectious diseases? Will most diseases respond or just a few? Will there be a net increase or decrease in disease burden? Is it possible that the diseases 'that matter most' are the least likely to respond to climate change? How will society respond to these threats? What do we think will really happen?

A database of all human & animal pathogens (the Enhanced Infectious Disease Database, EID2) was completed; this includes 1907 pathogens of the 50 human and animal hosts under consideration. EID2 has been built using automated methods to extract information from online databases. Pathogens are labelled with information on where they are found and when they were isolated. This information is linked to map systems and Google Earth (Figure 1), and enables us to select pathogens that are present in the target region, Europe. Of the 1907 pathogens, 795 are present in Europe. Of these, 159 are animal-only, 383 are human-only and 253 infect both. EID2 also stores information on those pathogens that infrequently cause disease (in, eg,

Figure 1. Example output from EID2 - the distribution of rabies virus according to the NCBI nucleotide database. Red colour indicates sequences of rabies virus in the NCBI nucleotide database from the appropriate country; red border, 1-9 sequences; red fill, 10 or more sequences.



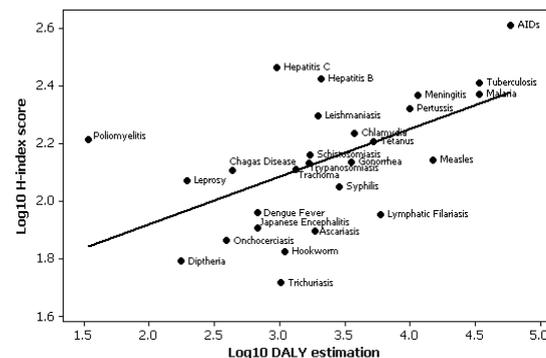
immunocompromised individuals), or have unknown pathogenicity. The 795 pathogens affecting ENHanCE hosts in Europe comprise 334 (42%) bacteria, 140 (18%) fungi, 119 (15%) helminths, 64 (8%) protozoa and 138 (17%) viruses.

Climate data are present in the database at 0.25° spatial resolution. This includes seasonal and annual mean temperature and rainfall for the entire globe, for 1950-2000. The climate data can be related to pathogen data. For example, we can compare the climate of countries where a pathogen is present with that of countries where it is absent.

The 795 pathogens in Europe were prioritised for further consideration using a major innovation – the *H-index*. a rapidly obtained and objective indicator of societal interest. The H-index derives from both the quantity and quality of scientific work published on a pathogen. For high H-index pathogens, there is a significant correlation between H-index and a true measure of impact, the Disability Adjusted Life Year or DALY (Figure 2). Also, the H-index is significantly correlated with scores obtained from 9 of 12 other prioritization exercises.

The 795 pathogens in Europe were prioritised for further consideration using a major innovation – the *H-index*. a rapidly obtained and objective indicator of societal interest. The H-index derives from both the quantity and quality of scientific work published on a pathogen. For high H-index pathogens, there is a significant correlation between H-index and a true measure of impact, the Disability Adjusted Life Year or DALY (Figure 2). Also, the H-index is significantly correlated with scores obtained from 9 of 12 other prioritization exercises.

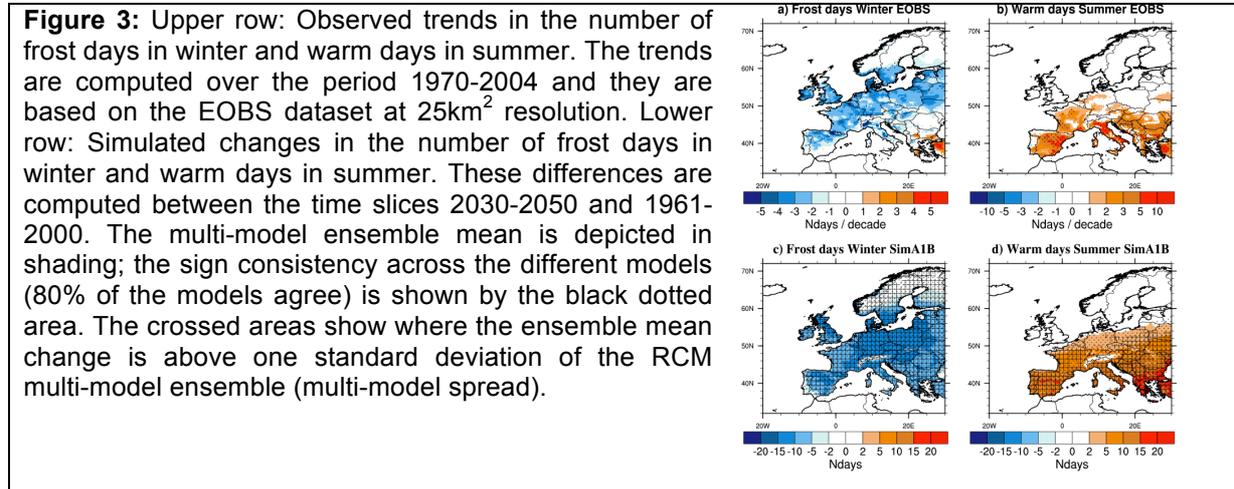
Figure 2. Relationship between burden of disease in log-transformed disability-adjusted-life-years (DALY) and H-index. It is constrained to high DALY diseases, as few diseases have DALY estimates. By contrast, the H-index takes seconds to obtain. The figure provides a visual picture of the meaning of *neglected diseases*: those well below the line receive less scientific attention than is due according to their impact.





The H-index was used to select the 100 highest impact pathogens of humans, and of animals, for more detailed consideration (157 in total, as some infect both types of host).

Having selected our pathogens, we needed to consider the effects of climate. We created a set of climate products that describe the recent climate of Europe, and provide simulations of future climate based on 12 European Regional Climate Models (RCMs). In addition to familiar variables like min, max and mean temperature, and total rainfall, we produced climate products of particularly relevance to health and disease modelling, such as 'number of days of rain', 'number of days of hot/cold weather', 'daily temperature range' etc. An example of our climate data is shown in Figure 3.



We sought evidence for the existence of climate drivers acting upon each of the 157 high H-index pathogens using automated literature searches; this generated 27,000 published papers which were prioritised, and then a proportion reviewed. Results suggest that 66% (103/157) of high impact pathogens have evidence of a climate driver. Most pathogens had relatively few climate drivers, whilst some had many more (Figure 4a). The most important driver was rainfall, followed in descending order by moisture, temperature, particle matter, 'other', extreme weather events, altitude, wind, oscillations and vegetation (Figure 4b). Protozoan and helminth parasite groups had more climate drivers than bacteria and viruses, perhaps indicative of their (often) more complex lifecycles. Transmission routes associated with climate drivers were (decreasing order of importance): vectors, ingestion, environment, fomite and inhalation, direct contact and sexual transmission routes.

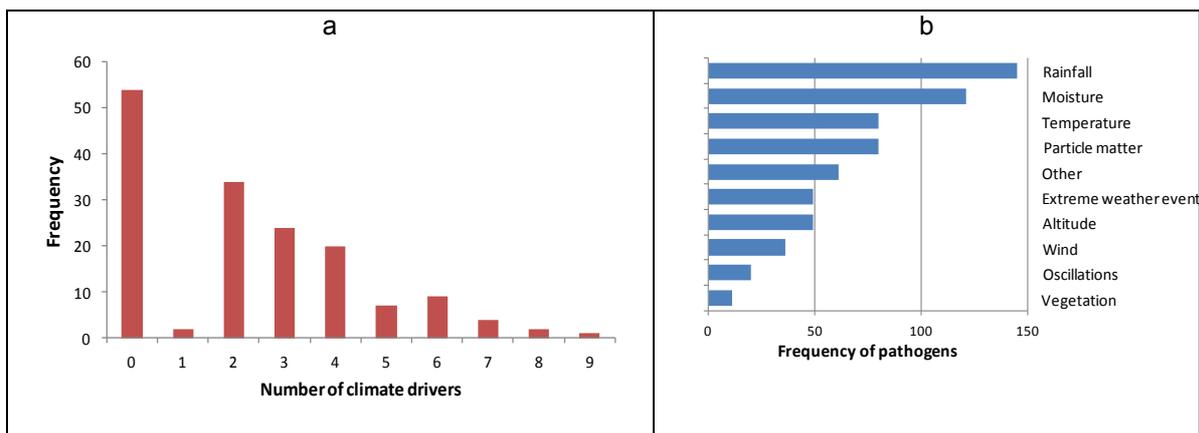


Figure 4. Number of climate drivers associated with 157 high impact human and animal pathogens: (a) the frequency of climate drivers; (b) the frequency of pathogens.

We developed complex, realistic models for the impact of climate change on one vector-borne disease (bluetongue, BT) and one disease vector (Asian tiger mosquito, *Aedes albopictus*) over Europe. For BT we modelled the risk of a disease outbreak. Figure 5 depicts the BT risk in late summer-early autumn for the recent past. Our model predicts that 2006 is the year of highest risk of a BT outbreak in northern Europe out of the previous 50 - the very year when the first outbreak occurred. We predict an increasing risk of BT in Europe until at least 2050.



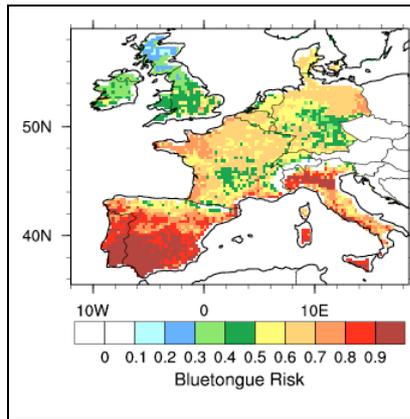


Figure 5: Simulated mean BT risk over western Europe based on the EOBS high resolution observed climate dataset for the season August-October for 1961-2008. BT risk (derived from R_0 , the basic reproduction number) is arbitrarily scaled to range between 0 and 1.

Consistent with epidemiological field measurements, the mean BT risk is high over Spain, Portugal, south western France, Sardinia and Sicily.

The Asian tiger mosquito has spread to many parts of the world, including Europe. It is a vector of many pathogens. Dengue was transmitted in France by this species in 2010, and Chikungunya in Italy since 2007. Several methods were used to model and map

the climatic suitability of this mosquito for recent past and future climates.

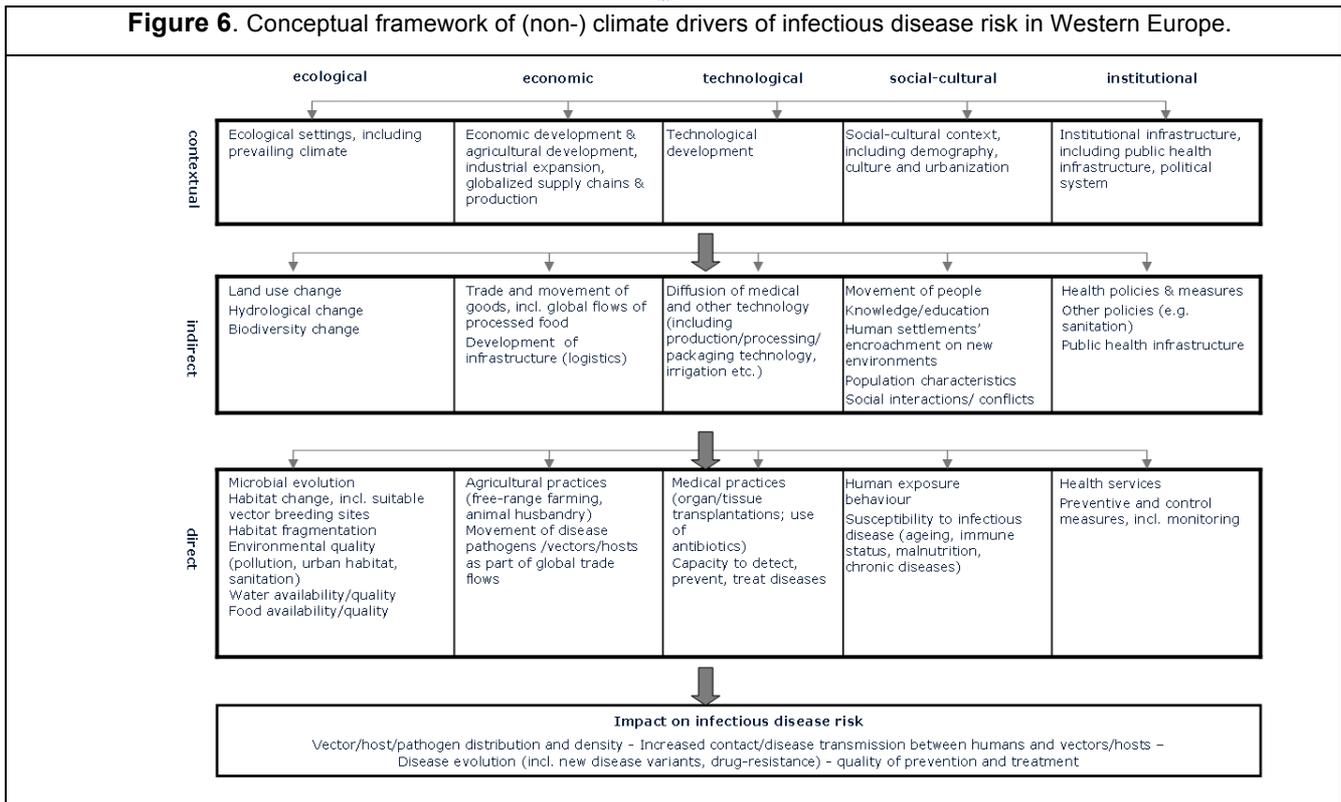
Finally, we investigated the effects of the North Atlantic Oscillation (NAO), an index of climate variability, on disease outbreaks. Data on outbreaks of 114 infectious diseases in 36 countries during 1950-2009 were analysed. NAO variation influenced outbreak occurrence of 11 infectious diseases. Seven diseases (adenovirus infection, measles, Q fever, gastroenteritis, tularaemia, shigellosis and trichinosis) were associated with winter NAO positive phases, and two (enterovirus and hantavirus) with summer or spring NAO negative phases, in Northern Europe. Two were associated with NAO phases in Southern Mediterranean countries; hepatitis A with summer negative phases and typhoid fever with summer positive phases.

Projections of future disease risks can take many forms. Results can be presented for different time periods; risks can be quantitative or qualitative; disease models can be statistical or process-based; and simple and transparent, or complex; and outputs can be driven by climate change alone, or by other disease drivers as well. To adapt outputs for stakeholders we held a meeting with a number of national and international agencies; they were presented with a range of options and informed us of the format of project outputs that would be most useful to their agencies. The results are contained in a series of position papers. The 4th position paper presents a conceptual framework of climate and non-climate drivers of infectious disease risk in Western Europe (Figure 6). The description of the system resulting in infectious disease outcomes captured by this framework has provided insights into the potential linkages between the various factors involved in infectious disease risk.

An expert questionnaire was used to assess, qualitatively, policy responses to climate (and non-climate) change impacts on infectious disease risk. The first part assessed policy options: the results suggest that no one policy option is best, but the appropriateness of each policy option depends on the case at hand and which priorities are set for this case, such as cost-efficiency. The second part assessed priorities for spending on mitigation or adaptation measures. The results point to very diverse expert views on the optimal mix of adaptation and mitigation strategies, but with an average of 50% for each. This part also addressed the capacity and willingness of relevant organisations to respond to climate change induced infectious disease threats. The experts assigned high ratings to willingness to respond to NGO's, advocacy, funders, and charity; science; and environmental management and conservation. However, the capacity to respond of these actors was rated as moderate. National government/health authority was rated with high capacity to respond, but moderate willingness to respond. The final part of the questionnaire was concerned with the relative importance and degree of uncertainty of climate versus non-climate drivers of infectious disease risk. Indirect drivers were relatively more important. Direct ecological drivers were assigned the highest degree of uncertainty. Those non-climate drivers operating at an indirect and a direct level were overall perceived as being more important than climate change as a driver for infectious disease risk.

Finally, future scenarios of climate change's impact on disease risk were developed. Scenarios were developed in a participatory manner during two workshops. Scenarios were considered along two axes which represent a globalized versus a regionalized world, and a reactive versus a proactive governance or policy-making style. For the assessment of policy implications several issues were tackled, including the exploration of likely/potential overall policy strategies (e.g. emphasis on mitigation versus adaptation policies), and actions likely to be taken.

Figure 6. Conceptual framework of (non-) climate drivers of infectious disease risk in Western Europe.



Overall the scenario analysis and related participatory workshops helped to gain a more integrated insight into climate change and infectious disease risk, embedding the relationships within a broader context including economic, socio-cultural, technological, institutional, and ecological global changes. The outcomes obtained from previous research activities could be linked with other issues and placed within this context as well. The obtained scenarios present plausible future pathways for Europe's health and well-being under conditions of climate change centered around 2050.

Two important policy contributions of this project are as follows:

- Modelling of the risk of bluetongue provides strong evidence that this disease emerged in Europe in response to changing climate. The observed/recorded warming over recent decades, fed into a state-of-the-art disease model, leads to predictions that agree in both space and time with what is known to have occurred. For example, our model predicts that 2006 is the year of highest risk of BT in northern Europe out of the previous fifty, and this was the first year that it occurred in the region. This work provides the strongest evidence to date that climate change is driving the emergence and spread of BT and that it will continue to do so in future. Our modelling of the Asian tiger mosquito, indicates that this applies to other vectors/vector-borne diseases too. Policy makers need to be aware, that the effects of climate change on vector-borne disease are being felt already in Europe, and are expected to intensify in future
- Our larger-scale risk analysis of high-impact pathogens indicates that the majority are sensitive to one or more climate drivers, and so may respond to the effects of climate change. The most common climate drivers for these pathogens are rainfall and moisture: as there is considerable uncertainty over how these will be affected by climate change, and the effect is expected to vary by region, this points to significant uncertainty over the future of important climate-sensitive infections, some of which may expand while others retreat. The third most common driver was temperature, which is projected to rise across all of Europe, and which may act as a positive force for many infections. In answer to the overall aim of this project, our results indicate that a considerable proportion of important infections in Europe may be affected by climate change and, therefore, policy makers should take appropriate action.