

CHAPTER 1

SAFING the world used to be the job of experience

But now, with billions of novel and untested species being introduced

It's down to an exact science

What are the risks?

It's the same old story: it's not the numbers that matter

It's how you use them. The numbers are meaningless

until we know how the species will fit in with us.

What we need is a way to make predictions

based on the information we already have

And the fledgling science of ecology

has been working on the job without much success for a long time

Take the case of invasive species, for example

It's a puzzle that is being solved only

slowly. It's not as simple as examining reproductive strategies

and dispersal and comparing them to local species

and adaptations of plants, zoology are now turning to field studies

that can explain patterns in nature and help predict how ecosystems will react to change

Arno Friedl, New Scientist 18 August 2001

Introduction

The current concerns about global warming has stimulated considerable interest in species distributions, especially the knowledge of how their current distributions may change. The urgency to acquire this knowledge is augmented by the existence of numerous IPCC reports to the fact that the global climate is changing at an unprecedented rate, most likely due to anthropogenic activities, and that these changes in climate are causing severe, and possibly irreversible, changes in physical and biological systems (<http://www.ipcc.ch>). Since in the past, large-scale extinctions and species introductions were precipitated by major climatic changes (Gates 1993; Roy *et al.* 1996), it is critical for us to use our understanding of distribution pattern drivers to predict how future climatic change will affect species distributions and biological processes. Acquisition of this knowledge should not be delayed until a complete understanding of the mechanisms determining species distributions patterns has been achieved. Some form of environmental change (human induced habitat destruction, global climate change) will

*" SAVING the world used to be the job of superheroes.
 But now, with millions of plant and animal species facing extinction,
 it's down to us mere mortals.
 Where do we begin?
 We don't even know how many species are out there.
 And even if we did, the numbers are meaningless
 until we know how the different species interact...
 What we need is a way to make predictions
 based on the information we already have.
 But the fledgling science of ecology
 has struggled to describe the natural world, let alone understand it.
 Like early astronomers, ecologists are faced with
 a unique system that doesn't lend itself
 to scientific methods such as experimentation, replication or manipulation.
 However, just as stargazers learnt to predict eclipses
 and alignments of planets, ecologists are now starting to build models
 that can explain patterns in nature and help predict how ecosystems will react to change "*

Arran Frood, New Scientist 18 August 2001

The current concerns about global warming has stimulated considerable interest in species distributions, especially the knowledge of how their current distribution, may change. The urgency to acquire this knowledge is augmented by the existence of numerous IPCC reports to the fact that the global climate is changing at an unprecedented rate, most likely due to anthropogenic activities, and that these changes in climate are causing severe, and possibly irreversible, changes in physical and biological systems ([http:// www.ipcc.ch](http://www.ipcc.ch)). Since in the past, large-scale extinction, and species movements were precipitated by major climatic changes (Gates 1993; Roy *et al.* 1996), it is crucial for us to use our understanding of distribution pattern drivers to predict how future climatic change will affect species distributions and biological processes. Acquisition of this knowledge should not be delayed until a complete understanding of the mechanisms determining species distributions patterns has been achieved. Some form of environmental change (human induced habitat destruction, global climate change) will

likely have precipitated considerable species losses in the interim (Chown and Gaston 1999).

The importance of climate to explain animal and plant distribution was recognised as early as the 18th century (Guisan & Zimmermann 2000) and a vast body of literature from past and current field experiments exists in support of this. The relationships between sensitivity of species to climate change and their ecological properties has also been reported in current literature (Thuiller *et al.* 2005) while the primary importance of climatic factors in explaining the link between latitude and the spatial pattern of human pathogens has also been reported (Guernier *et al.* 2004). With the looming global climate change, the issue is not how climate defines the current distribution of species but how the current distribution will react to climate change. There is no alternative to long – term field studies to provide proof for such a hypothesis. But what does one do when the issues are very complex or the scale is unmanageably large, and the time is forthcoming? How then can we be anticipatory, if no meaningful physical experiment can be performed? (Schneider 1992) and in this case no fieldwork can be done? We can turn to a surrogate lab, not a room with bunsen burners, but a small box with transistors and microchips. We can build mathematical models and perform our “experiments” in computers. Although models are not usually faithful simulations of the full complexity of reality, they can tell us the logical consequences of explicit sets of assumptions (Schneider 1992).

The use of geographical predictive models to predict the distribution of both plants and animals species has recently gained importance not only as a research tool in autecology but also as a tool to assess the impacts of accelerated land use and other environmental change on the distribution of organisms (for review see Guisan & Zimmermann 2000). These models, though static and comparative often remain the only approach for studying the possible consequences of a changing environment on species distribution since only very few species have been studied in detail in terms of their dynamic responses to environmental change (Woodward & Cramer 1996). In response to the inevitable climate change and a call for assessment of impacts, adaptations and vulnerability by IPCC

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(IPCC 2001), various studies have attempted to predict the current and future distribution of species based on major environmental factors that influence their distribution. In this issue in which the projected climate change impacts on Africa were elucidated, the health and agricultural sectors were among those that were reported to show high vulnerabilities. This is not only as a result of limited or deteriorating infrastructure in the public health system but also because insect-vector diseases and water-borne diseases are prevalent in Africa and their distribution is influenced by climate. Climate change may alter the distribution of vector species—increasing or decreasing the ranges, depending on whether conditions are favourable or unfavourable for their breeding places (e.g., vegetation, host, or water availability).

The World health organisation report on the effect of climate change on health sector in Africa reported that climate plays an important role in vector-borne diseases -- a major cause of illness and death in tropical countries. Insects such as mosquitoes, ticks, sandflies and tsetse flies transmit these diseases. These cold-blooded vectors are sensitive to direct effects of climate such as temperature, rainfall patterns and wind. Temperature alone directly influences the reproduction and maturation rate of the infective agent within the vector organism, as well as the survival rate of the vector organism, thereby further influencing disease transmission (IPCC (TAR) 2001). Climate also affects their distribution and abundance through its effects on host plants and animals". WHO (2001) (<http://www.who.int/mediacentre/factsheets>).

Accurate and verified models that translate these physiological climate-related processes into more detailed maps of disease distribution are scarce. Such maps and models are necessary to set the baseline of current levels and limits of transmission against which projected impacts of climate change can be measured (IPCC 2001). Also it is clear in this report that the assessment of the response of vectors and vector-borne diseases to climate change has been attempted but mainly in human related vectors as opposed to vectors that transmit pathogen to livestock and other wild animals. And yet ticks alone are exposed to more than 80% of the world's cattle population resulting in global annual losses of up to US \$7 billion (McCoster 1979). This is because ticks exceed any

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arthropod groups in being pests, parasites and vectors both in the tropics and temperate regions. They are very successful vectors because they transmit a greater variety of microorganisms to humans and livestock than any other arthropods, (Sonenshine 1991).

In Africa, East Coast fever (ECF), devastating disease of livestock transmitted mainly but not exclusively by a tick *Rhipicephalus appendiculatus*, threatens over 25 million cattle, costing farmers more than US\$170 million a year in direct losses. This loss may be underestimation since most devastation from ticks is in remote areas in Africa where pastoralists continue to move their herds in search of green pastures. For instance in 2001, 120 cattle died daily per sub-county from various tick-borne diseases in Kotido District in the Northern part of Karamoja, North Eastern Uganda. (<http://www.cahnet.com>). Under climate change accentuated by insufficient mitigation options and inadequate health facilities, Africa may suffer under the heavy burden of these livestock diseases. Currently, the main form of control by use of chemicals to target either the parasite or the habitat may not be sufficient if the future world is a world more suitable for ticks. Predicting the suitability of areas for ticks may solve the pressure and urgency that goes with chemical control and may also save the control agents time and resources because the actions will be targeted to already identify specific areas. Also this traditional chemical control of ticks may benefit from new ecological approaches to tick control by including the knowledge of the preferred and reservoir hosts of the vector and the pathogen respectively. It was under this background that this study was initiated to explore the impacts of climate change on the distribution of ticks and their hosts in Africa, deduce how the predicted change in distribution may impact tick-borne diseases.

Tick data was obtained mainly from three sources (Cumming 1999b; Walker *et al.* 2000, I. G. Horak private collection). The hosts' data was obtained from Boitan *et al.* 1999). The multivariate predictive distribution modelling procedure developed by Erasmus *et al.* (2000) was employed throughout the current study and current and future climate data was provided by DARLAM (Division of Atmospheric Research limited-area model climate data). DARLAM is a high resolution limited area model that was developed by the Commonwealth Scientific and Industrial Research Organisation (CSIRO) in

Melbourne, Australia for use in both short-term mesoscale atmospheric studies and longer-term climate simulation experiments (Walsh & McGregor, 1995). The model is a two-time-level, semi-implicit, hydrostatic primitive equations model. It uses an Arakawa staggered C-grid (Mesinger & Arakawa, 1976) and semi-Lagrangian horizontal advection (McGregor, 1993) with bi-cubic spatial interpolation, and has 18 horizontal sigma (σ) levels in the vertical (Phillips, 1957). DARLAM employs a wide range of physical parameterization schemes to represent atmospheric processes such as cumulus convection that exist at sub-grid scale. A one-way nesting technique (Davies, 1976) is used with lateral boundary conditions supplied by the CSIRO-9 Mk 2 GCM with R21 spectral resolution.

In the present study nine separate 30-day simulations were performed for both January (representing mid-summer conditions) and July (representing mid-winter conditions). The monthly average of the nine simulations constitutes the model climatology for the month. Engelbrecht *et al.* (2002) illustrated that DARLAM is capable of simulating the regional characteristics of atmospheric variables like near-surface temperature, low-level wind patterns and rainfall over sub-Saharan Africa with considerable detail. The model does; however, tend to overestimate rainfall totals over regions with a steep topography. The DARLAM simulations used in this study were performed by my colleagues at the Laboratory for Research in Atmospheric Modelling (LRAM) in the Meteorology Department at the University of Pretoria on a Pentium III workstation with two 550 MHz processors. It took approximately 11-minutes (CPU time) to simulate a model day at the specified model resolutions. The climate variables employed in this study were mean maximum temperature of January and July, mean minimum of January and July, and mean rainfall of January and July.

The predictive species model used was originally developed by Jeffree & Jeffree (1994, 1996). It was used as a standard base for predicting species (ticks and vertebrate hosts) current and future distribution patterns and for evaluating the relative performance of the different climate data sets. This model was recently modified to accept multivariate inputs to yield probability of occurrence maps for species (Erasmus *et al.*, 2000). The original model was adapted to incorporate a variety of climatic predictor variables. Not

only does this improve the original model, but it also allows the production of a probability surface of suitability for each species (Erasmus *et al.*, 2000), rather than merely a presence-absence distribution model. This multivariate modelling approach uses the values of selected climate variables for each cell where a species had been recorded. These are plotted on an n -dimensional scatter plot (for the n -climate variables), and mean climate values subtracted to center values around the origin of the multidimensional scatter plot. An $n \times n$ covariance matrix is calculated and this matrix is used as an input to calculate eigen values and eigen vectors for the covariance matrix. These eigen vectors form the orthogonal principle axes of an n -dimensional hyperspace with the origin representing the theoretical core of the species' fundamental niche, as defined by the predictor climate variables (also see Robertson *et al.*, 2001).

The climate variables (temperature and rainfall) values of all grid cells are then transformed into this eigen vector space. These transformed climate variables are subsequently divided by the eigen values and in the resulting n -dimensional hyperspace, the distance of any particular unsampled grid cell from the origin represents a measure of the suitability of that locality for the specific species (Robertson *et al.*, 2001). According to Austin & Meyers (1996), the fundamental niche of an organism follows a broad Gaussian distribution. Such a Gaussian distribution is best approximated by a normal distribution but given that the distance from the origin of the hyperspace is calculated by the sum of the squared eigen vector axis scores, and that a squared normal distribution is equal to a chi-square distribution, the probability of any grid cell to be suitable for the selected species, can be read off a chi square probability table at the appropriate degrees of freedom (m , the number of climatic variables) (Robertson *et al.*, 2001).

The input data comprises 3000 grid cells covering sub-Saharan Africa populated with climate variables. Grid cells, in which particular tick /host species were recorded, are referred to as *known records* following Erasmus *et al.* (2002). Thus, on a scatter plot of climate variables (multivariate climate space), the values of climate variables from localities where species have been recorded are used to construct a confidence region where there is a high probability that the records reflect the core range of the species.

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Points falling within this confidence region are then mapped back to geographic space to represent an *interpolated distribution* (ID), represented as a probability of climate suitability (see Erasmus *et al.*, 2000 for a detailed model description. Each grid cell was assigned a tick presence, climate value and hosts as the analysis permitted. Geographic information system (GIS) analysis was conducted in ArcView ESRI (2000) and modelling was performed in S-Plus (2000). Throughout the various chapters, different methods of comparing the predicted distributions have been employed and discussed fully in the respective chapters. Also the implications of the results and the shortcomings of the methods used have been highlighted.

Recent developments in geographic information systems and easy accessibility of climate data from different climate models have fostered the development and use of many climate models in the exploration of the response of a changing climate on species distribution. Occasionally, the researcher is faced with a problem of selecting the best climate data for a particular study. To evaluate the impact different climate dataset have on the resultant predicted distribution, in chapter two three climate datasets (2 interpolated and 1 modeled) have been used to evaluate the relative performance of the climate datasets in simulating the present distributions of ticks in sub-Saharan Africa. In this chapter, distribution data of four tick species from the genus *Rhipicephalus* were used. The results showed that the use of data derived from high-resolution nested climate models (e.g. DARLAM) provided equal or even better species distribution-modelling performance (Olwoch *et al.* 2003). As the model is dynamic and process based, the output data are available at the modelled resolution, and are not hamstrung by the sampling intensity of observed climate datasets.

Genus Rhipicephalus is one of the largest genera and includes some of Africa's most economic important species. Chapter three focuses on the likely climate induced changes in the distributions of this genus. Analysis of predicted range contractions, shift and changes in species richness pattern were performed for the whole study area, per region and lastly an analysis of different aspects of range alterations were compared between the economic important ticks and non -economic ones. The latter was done to establish the

indirect effects of these range alterations to tick-borne diseases. The results showed that East Africa followed by South Africa are considered the most vulnerable regions on the continent to climate-induced changes in tick distributions and tick-borne diseases. More than 50% of the species examined show potential range expansion and more than 70% of this range expansion is found in economically important tick species. There is also a predicted increase in tick species richness in the southwestern regions of the sub-continent and more than 20 % of the species experienced range shifts of between 50 and 100 % under predicted climatic conditions.

One of the most devastating tick-borne diseases in sub-Saharan Africa is East Coast fever (ECF). It is transmitted by a protozoan parasite, *Theileria parva* that is transmitted by the brown ear-tick, *Rhipicephalus appendiculatus*. Since the results of chapter three revealed that economic important ticks were severely affected by climate change, in chapter four the potential present and future distribution of ECF based on the present and potential future distribution of the tick and cattle assemblage was assessed. The criticisms of this method were two fold: there are several different tick species that are vectors of ECF, and there are a number of different hosts, why use only *R. appendiculatus* and cattle? The available data and literature provides compelling evidence in support of the approach in this thesis. There are other species that have been mentioned as capable of transmitting the pathogen that causes ECF, but there is no evidence in the literature that these species are actually possible transmitters in the field. Whereas transmission clearly can occur via other tick species and probably does (Cummings pers.comm.), there is no evidence to date to support this. This thesis is therefore inclined to stay with the dominant view point that *R. appendiculatus* is the main, if not the only tick vector that is capable of transmitting the protozoan parasite *Theileria parva* that causes ECF in the field. The results obtained in this chapter are therefore based on the *R. appendiculatus* and cattle ranges only. The results show that the predicted general increase in minimum temperature has favoured the establishment of ticks and ECF. The Northern Cape and Eastern Cape provinces of South Africa, Botswana, Malawi, Zambia and eastern DRC are predicted to show increases in ECF prevalence.

Many of the emerging infections in wild life are usually caused by generalist pathogens transmitted by arthropods that “spill over” (Daszak *et al.* 2000) from other species, often from domestic animals and to a certain extent from human especially in cases where the population of other preferred hosts decline. The first three chapters relate the current and predicted future ticks distribution to climate. However, ticks exhibit a dual lifestyle in which they must constantly alternate between hiding in protected spaces and climbing up vegetation to quest for hosts (Londt & Whitehead 1972). Prediction of hosts, though very complicated (Estrada-Peña 2001b) forms an important part in establishing the prevalence of ticks and tick-borne diseases in a changing climate. Chapter five uses the same modelling approach on *R. appendiculatus* and its community of hosts to assess how the current host assemblage will be influenced by climate change. Furthermore it is now established that diversity in host communities can influence tick and tick-borne diseases through two pathways i) by increasing infection rates and ii) by increasing the density of vectors. Using predicted host ranges of *R. appendiculatus* for the current and future, the probable effect of that change on the current and future tick-host assemblages were analysed and conclusions were made regarding this change on tick abundance and infection rates of the pathogen that causes East Coast fever. Different host species reacted differently to climate change conditions. Although contraction was the main range alteration predicted, the future predicted distribution of the more generalist species expanded. The results also showed reduction in the range of the total host assemblage in the future climate. The predicted future range of the host assemblage intimately involved in ECF transmission was also altered at different degrees in different areas in sub-Saharan Africa. Increased probability of this assemblage was predicted in Tanzania, Angola and Mozambique.

Tick distributions are known to vary through space and time due to interactions of many factors, including climate, host diversity, levels of resistance of hosts, absence of tick control measures and management practices that affect host behaviour. The use of a simple climate model (as the one used in this study) often termed “climate envelope” or “correlative” as opposed to a more complex physiologically based model has therefore been reportedly not valid (Davis *et al.* 1998a, b). However, limitations regarding the use

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of physiologically based models exist especially where specific information regarding the species is sketchy (Pearson and Dawson 2003). On the other hand, relatively simple bioclimatic envelope models can provide a useful starting point when applied to suitable species and at appropriate spatial scales. In many cases, bioclimatic envelope models provide perhaps the best available guide for policy making at the current time (Hannah *et al.* 2002). The use of this simple model in this study is therefore appropriate since most areas in Africa are poorly sampled and the distribution of Africa ticks is relatively incomplete. Furthermore correlative /simple techniques do not require detailed physiological data about individual species; they can be applied to a large number of species as has been done in this study. This enables conclusions regarding the impacts of climate change on a wide range of species, thus habitat assemblages, to be made (Berry *et al.* 2002). Though not to be underestimated, model predictions should be interpreted with caution and should be viewed as first approximations indicating the potential magnitude and broad pattern of future impacts, rather than as accurate simulations of future species distributions (Pearson & Dawson 2003). The resultant predictive maps are also important because they fill in gaps in the primary observations and update the distributions as they shift with changing environmental conditions.

A tick - host - disease system is by no means a simple one. Unresolved viewpoint vis-à-vis host – tick relationships and limited knowledge concerning the relative importance of different hosts on tick and tick borne disease prevalence compounds this challenge. By use of a predictive species model and climate provided by DARLAM, this study has highlighted the importance of a suitable climate dataset in climate envelop studies. In addition, the study has identified the vulnerability of different areas in sub-Sahara Africa for ticks and tick-borne diseases under climate change conditions. The predicted ranges of vertebrate species that act as hosts of *Rhipicephalus appendiculatus* have complemented the climatic determinant of tick ranges. This approach neither disregards the need for more detailed and comprehensive eco-physiological approaches nor does it pretend to predict the future. What it does is define the role of climate as a factor in determining the potential for future vector establishment when all other factors are not included (Sutherst 2003). Therefore, what I present in this thesis is an initial but essential

step towards the production of tick risk maps for the current and future. Because vulnerabilities of specific areas are identified, these results also serve as a warning of the probable changes in tick distribution under a changed climate. They also serve to attract attention of tick-control agencies to those areas of tick expansions. Furthermore, these results serve as way of increasing awareness to the close relation between climate and vector distribution and the importance of all the parts of a tick-host-diseases system in selecting a tick control method. The results presented in this thesis must therefore be viewed as an initial step towards developing current and future tick risk maps for Africa and as base for more field oriented studies on the effect of climate change on African ticks.

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