

East Coast Fever (ECF) in space and time

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**CHAPTER FOUR**

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Key words: ECF, sub-Saharan Africa, *R. appendiculatus*, predictive species modelling

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##### ABSTRACT

East Coast Fever (ECF), caused by a protozoan parasite *Theileria parva*, is one of the most important livestock diseases in Africa. For its transmission it depends on the tick *Rhipicephalus appendiculatus* Neuman 1901, which parasitises mainly cattle. The distribution of ECF is therefore restricted to those areas where cattle and *R. appendiculatus* coexist. The failure of tick chemical control programs in Africa, the lack of sufficient knowledge on the ecology of ECF and the lack of proper diseases surveillance has put a heavy burden on the livestock industry. These concerns and the implications of climate change for the diseases, necessitates exploration of other means of disease management. An ability to predict the current and future potential locations of ECF and its vectors would be a valuable development. In this sub-Saharan study, a predictive species distribution model and a nested regional climate model DARLAM was used to predict the present and future potential distribution of ECF. Kolmogorov-Smirnov test and a proportional overlap test were used to compare the current and future predictions of both ECF and *R. appendiculatus*. 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. These results serve as a caution to other areas in Africa where the tick is known to occur. Constant country-specific surveillance of ticks and the resultant disease is necessary so that changes are known at local scales. This paper also calls for a more active role for control agencies in Africa to provide more resources for proper monitoring.

## INTRODUCTION

Ticks (Acarina, Metastigmata) are obligate blood feeders. Although only 10% of ticks parasitise humans and their livestock, they are of particular concern because they transmit pathogenic microorganisms. In fact ticks are vectors of more kinds of microorganisms than any other single arthropod taxon, including mosquitoes (Diptera: Culicidae) (Oliver, 1989). Some of these microorganisms are known to cause diseases in humans and their livestock. East Coast Fever (ECF), caused by a protozoan parasite *Theileria parva* is one of the most important livestock diseases in Africa (Lessard *et al.*, 1988; Muraguri *et al.*, 1999). It depends on the tick *Rhipicephalus appendiculatus* Neuman 1901, a three-host tick, which has been collected mainly from cattle for its transmission. The distribution of ECF is therefore restricted to those areas of East and southern Africa where cattle and ticks coexist (Norval *et al.*, 1992). This area extends south from southern Sudan to eastern South Africa and as far west as the Democratic Republic of Congo (DRC). The disease kills 1.1 million cattle and causes an economic loss of \$168 million annually (Norval *et al.*, 1992). Mortality is higher (up to 100%) in the more expensive exotic cattle than in the indigenous Zebus, where the average mortality is estimated at 10% (Lawrence *et al.*, 1988). If uncontrolled, ECF can cause over 90% mortality of susceptible cattle following its introduction into a region (Lawrence *et al.*, 1988).

Apart from direct losses due to cattle mortality in endemic areas where chronic ECF occurs, other less quantifiable effects of the disease are apparent including poor weight gain, low fertility rates, reduced growth and milk production, paralysis, and secondary attacks from other parasites (Pegram *et al.*, 1989). ECF is therefore a major reason for tick control in most African countries. A main form of control, the use of acaricide, is however complicated by its high cost, development of tick resistance (Cox, 1991), stock movement during drought, inefficient supervision of ECF quarantines, abundant tick-carrying wildlife and lack of adequate dipping facilities; not to mention concerns about the potential environmental consequences of this control program (Cox, 1991). Other socio-economic factors such as inadequacy of the main tick control facilities make individual farmers undertake fewer control efforts than are optimal for the society at

#### 4. East Coast Fever (ECF) in space and time

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large. The failure of tick chemical control programs in Africa is accentuated by the fact that annual fluctuations in tick abundance, ecology of the ticks, as well as their habitat preferences are largely unknown and thus do not currently inform decisions about appropriate chemical or other tick control measures (Sutherst, 1987a). With these concerns of lack of knowledge on ECF biology and the implications of climate change for the diseases, an ability to predict the current and future potential locations of ECF vectors would be a valuable development (Cox, 1991).

Despite these concerns, this disease does not rank among the most important emerging vector-borne diseases for a variety of reasons including the almost total eradication of the main tick vector *R. appendiculatus* in South Africa and other parts of Africa. It is also known that after prolonged infestations, cattle can acquire enough resistance to ticks resulting in controlled field populations and can limit *T. parva* infection rates in ticks and therefore reduce field challenge. These reasons form part of the general feeling among epidemiologists that ECF is well contained in the areas where it occurs. However, when considering parasite survival, ticks transmit the disease more rapidly when feeding on tick-resistant cattle (Lawrence *et al.*, 1988). In addition, the impacts of global climate change on cattle, ticks and ECF would disrupt the current contained nature of the diseases through invasion of pastures by pastoralists or translocations of game to new areas. Newly introduced cattle, whether exotic, Taurine (*Bos taurus*) or the indigenous Zebu (*Bos indicus*) and Sanga (*Bos indicus*) breeds, during displacement driven by climate change, are much more susceptible to ECF than cattle from endemic areas.

Furthermore, under conditions of global warming, there is a possibility that the current range of the main tick vector, *R. appendiculatus*, may expand or shift and together with the current reduction in available grazing land and the consequent cattle movements to greener areas, the introduction of ECF to new areas is inevitable. In addition to this, there is an increasing demand for livestock products in Africa (Thornton *et al.*, 2000) and consequently, there is a move by most African rural farmers from indigenous cattle breeds to exotic ones that are believed to produce more milk, but are more susceptible to ECF.

#### 4. East Coast Fever (ECF) in space and time

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Tick abundances are known to vary through space and time due to interactions of many factors, such as climate, host diversity (Norval & Lightfoot, 1982), levels of resistance of hosts, absence of tick control measures and management practices that affect host behaviour. More importantly, the seasonal activity and occurrence of ticks are known to fluctuate from species to species and country to country due to variations in photoperiod (Rechav, 1981; 1982; Minshull & Norval, 1982; Short & Norval, 1981; Norval *et al.*, 1992, Okello–Onen *et al.*, 1999). As far as *R. appendiculatus* is concerned, in southern Africa for instance, there are marked annual cycles of abundance of each life-stage, punctuated by near total absence for several months of each year (see Rechav, 1981). This is due to a behavioral diapause in the adult tick, which is controlled by photoperiod and allows it to survive during the long hot dry seasons (Rechav, 1981; Norval *et al.*, 1992).

Nearer to the equator these ticks usually feed throughout the year and numbers vary far less, but still show discernible seasonality especially in the immature stages (Randolph & Rogers, 1997). This is because developmental rates of *R. appendiculatus* are reported to be temperature dependant, while survival is humidity influenced (Tukahirwa, 1976; Okello–Onen *et al.*, 1999). These reported tick seasonal dynamics, which are a function of climate, exert a major influence on the dynamics of transmission of tick-borne pathogens (Randolph & Rogers, 1997). They determine not only seasonally variable vector-host ratios but also the time delay between acquisition and transmission of pathogens.

The effect that climatic factors exert on tick distribution and abundance is therefore well documented, but the way in which these parameters will change under possible climate change is still uncertain. Studies on European ticks have shown that ticks and tick-borne disease systems will shift or be disrupted following predicted climate change (Randolph & Rogers, 2000; Randolph, 2001). This may lead to the introduction of disease and disease vectors in new areas and may prove catastrophic if prior warnings are not issued. In South Africa, research on the effect of climate change on other animal species

#### 4. East Coast Fever (ECF) in space and time

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(Erasmus *et al.*, 2002) has illustrated that 25% of the species investigated showed more than 90% shifts in their range. This general pattern of species showing limited overlap between their existing distributions and predicted distributions is most marked in reptiles and invertebrates (van Jaarsveld *et al.*, 2000). Studies in the prediction of African tick distributions remain inadequate, but there is a general prediction that under global warming South African ticks are likely to retreat to the mountainous eastern region near the border of South Africa with Mozambique (Rogers and Randolph, 1993). This effect will be more drastic near the edge of their present ranges.

Most ticks of the genus *Rhipicephalus* are generalists and therefore climate, and not host availability, is assumed to be the most important limiting factor. The host may be limiting factor where all climatic factors become suitable. Cattle are the preferred domestic hosts of all stages of development of *R. appendiculatus* (Norval *et al.*, 1982; Okello-Onen *et al.*, 1999). The preferred wild hosts of all stages of development are African buffalo (*Syncerus caffer*), eland (*Taurotragus oryx*), sable (*Hippotragus niger*) impala (*Aepyceros melampus*) and waterbuck (*Kobus ellipsiprymnus ellipsiprymnus*) (Horak *et al.*, 1983, 1995; Norval *et al.*, 1992). African buffalo are also the main wild reservoirs of *T. parva* infection, and may suffer clinical disease. The less specific the tick-host relationship, the less likely it is that hosts will be a limiting factor (Randolph, 2002), because such a tick can use any available host to complete its life cycle. For this reason, spatial distribution of ticks may be analysed by simple statistical methods that seek correlations between known tick presence/absence and climatic factors (Rogers & Randolph, 1993; Cumming, 2000c; Estrada-Pena, 1999; Estrada-Pena, 2003, 2005 & Olwoch *et al.*, 2003).

However, analysis of the spatial and temporal distribution of tick-borne diseases is more complex and multifaceted. It requires the analysis of tick and host distribution, pathogen reproduction, growth, development and mutation. It also requires the analysis of the nutritional conditions of the pastures, because they affect the ability of the host to withstand infection. A more robust and comprehensive biological model is needed to predict the effect of climate change on this complex system accurately. However such a

#### 4. East Coast Fever (ECF) in space and time

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biological system does not exist (Randolph, 2002). With the birth of predictive habitat distribution modelling (for review see Guisan & Zimmermann, 2000), and reliable climate data, the distributions of many insects, pests and pathogens have been predicted using their major climate drivers (Messenger, 1959; Meats, 1989; Sutherst & Maywald, 1985; Sutherst *et al.*, 1995; Perry *et al.*, 1990; Coakley *et al.*, 1999; Rogers & Randolph, 2000; Randolph & Rogers, 2000; Randolph, 2001; 2002; Harvell *et al.*, 2002; Erasmus *et al.*, 2000, 2002). Recently, a multivariate model has been used to predict the location of future climate envelopes of South African fauna (Erasmus *et al.*, 2002). These predictions have shown acceptable success rates in the way they predict known records.

In a previous study (Olwoch *et al.*, 2003), this multivariate habitat model and high resolution climate data simulated by a limited-area atmospheric model, DARLAM (Division of Atmospheric Research limited-area model) (Engelbrecht *et al.*, 2002) in combination with existing known tick distribution records provided potential distribution predictions for selected tick species. The same habitat model and DARLAM are used in this study to identify potential areas of *R. appendiculatus* distribution after possible climate change. Like all other vector-borne diseases, risk of infection of ECF depends on the degree of contact between cattle, the main host animal, and infected *R. appendiculatus* vectors determined by both biological and non-biological factors.

The aim of this paper is therefore to establish the present and potential future distribution of ECF based on the present and potential future distribution of the tick and cattle assemblage and to assess the impacts of these range shifts on tick-borne disease control by use of a predictive species model. The use of predictive distribution models in tick research is still in its infancy, especially in Africa where biological requirements of ticks are not sufficiently known. Consequently, robust mechanistic models that are reported to yield superior results (Pearson and Dawson, 2003) are not suitable for this study. Correlative models that make use of species-environment relations are more suitable and more specifically, profile models that rely only on presence data are preferred because of the uncertainty around true or false absence of *R. appendiculatus*. These models as represented by the modified multivariate technique (Erasmus *et al.*, 2000) have



#### 4. East Coast Fever (ECF) in space and time

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successfully predicted South African fauna (Erasmus *et al.*, 2002) and African ticks (Olwoch *et al.*, 2003).

### MATERIALS AND METHODS

#### Study area

This study covers Sub-Saharan Africa (Fig. 1). The study area was divided into 3000 grids cells of 60 x 60 km resolution. This resolution was determined by DARLAM climate data.

#### Tick Data

Point localities of recorded tick observations restricted to sub-Saharan Africa were obtained from Cumming (1999b). These data were compiled from various tick collections (see Cumming, 1999b for a detailed list of sources). Combining data sets from different sources invariably compounds identification and distribution errors. For this reason data comparison with Walker *et al.*, (2000) was used to assess data quality. This latter reference provides well-illustrated distributions of *Rhipicephalus* species. Synonyms provided in this reference also solved the common problem of species synonyms. The distribution of *R. appendiculatus* was used in this study as the main determinant of ECF transmission. There are other tick species that are capable of transmitting ECF but only under laboratory conditions and their distribution has therefore not been included in this study. The present distribution of *R. appendiculatus* (Fig. 2) was used as an input to the habitat model (Olwoch *et al.*, 2003). These point localities were used to assign each 60x60 km grid a tick presence or absence.

#### Cattle data

Cattle density data were obtained from Kruska *et al.*, (1995) (Fig. 2). This database is a result of International Livestock Research Institute's (ILRI) work in which country level

#### 4. East Coast Fever (ECF) in space and time

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cattle census data was collated to create a cattle density layer for Africa. The census figures are not usually conclusive because they are reported on the basis of administrative boundaries, which can vary widely in resolution (province, district, division). These figures were therefore improved by attaching an administrative boundary layer that was obtained from Food and Agricultural Organisation (FAO) (Kruska *et al.*, 1995). The best available cattle data from the census was attached to this administrative boundary layer. During this process, areas of zero cattle population such as protected areas and water bodies were not included in order to improve density calculations. Because of the variation in the quality of census data from country to country, additional attribute fields were added to the density database that included administration level information and date of the census (see Kruska *et al.*, 1995). The cattle density layer used includes both the indigenous and exotic breeds.

The purpose of the cattle data used was to refine the predicted current and future range of *R. appendiculatus* in order to predict ECF habitat suitability. It might be argued that the current density data for cattle would not suffice as a refinement of the future predicted distribution of the ticks, and instead a map of future cattle densities would have to be used. But predicting cattle distribution changes would need a comprehensive review of at least the following factors: human population distribution changes resulting from population growth and urbanization; economic changes affecting trade and market development; agro-ecological changes affecting livestock systems, including the impacts of climate change on feed supplies from pastures and crops; and estimation of the effects on livestock production of changes in grazing and land use caused by human use, and finally an ability to model people's behaviour. Such elaborate data does not exist at the moment and given the capabilities of the modelling approach used in this study, it is not possible at the moment to include all these factors. Furthermore, an analysis of the existing cattle records (FAO) showed that there was no marked increase in cattle numbers from 1990 to 2003. However this does not suggest that no change will take place over the long term, but at the moment there are no better available resources that indicate how cattle numbers will change in the future. The cattle distributions used for refining the predictions of ticks in the present and future were therefore kept constant.

#### 4. East Coast Fever (ECF) in space and time

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##### **DARLAM present and future climate data**

The Commonwealth Scientific and Industrial Research Organisation (CSIRO) in Melbourne, Australia has developed the high-resolution limited-area model DARLAM for use in both short-term mesoscale atmospheric studies and longer-term climate simulation experiments (Walsh & McGregor, 1995). In the present study ten separate 30-day simulations were performed for both January and July for different 10-year periods. The periods selected are the 1990's and 2020. The simulations were performed at a horizontal grid resolution of 60 km x 60 km using a domain of 100 x 100 grid points that cover sub-Saharan Africa. The monthly average of the ten simulations constitutes the model climatology for the month. The CSIRO Mark 2 GCM was used to force DARLAM at its lateral boundaries. The GCM was integrated for the period 1960-2100, with greenhouse gas forcing corresponding to the A<sub>2</sub> SRES (Special Report on Emission Scenario, issued by the Intergovernmental Panel on Climate Change) scenario. 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 climatological anomalies for the 2020s vs. the 1990s as predicted by DARLAM are shown in figure 3. January minimum and maximum temperatures are simulated to increase by more than 2°C over certain regions of the subcontinent. Much of the eastern regions are expected to become drier with an associated pattern of higher sea-level pressure, whilst the western subcontinent is expected to become wetter. An interesting feature of the July anomaly fields is that parts of the central subcontinent are simulated to become cooler and wetter.

##### **Predictive species modelling**

A simple climate envelope model was used to predict the future distribution of the focal species. (Erasmus *et al.*, 2000; 2002). The input data comprised 3000 grid cells of 60 x

#### 4. East Coast Fever (ECF) in space and time

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60 km size covering sub-Saharan Africa populated with climate variables. There were 548 known presence records of *R. appendiculatus* and the present climate values at these locations were used to construct a climate envelope, using a principal components-type analysis. This climate envelope represents the range of climates within which the tick is known to occur, and as such, can be interpreted as the realised niche, as defined purely by climate. To arrive at a predicted distribution under a climate change scenario, the existing climate envelope is applied to a climate surface representing future climates, and a new geographical interpretation of distribution is derived (see Erasmus *et al.*, (2000, 2002) and Olwoch *et al.*, (2003) for a more detailed explanation). Both the predicted current and future distributions were obtained using this predictive species model and 6 climate variables of current and future mean maximum temperature, mean minimum screen temperature and mean rainfall of January and July.

The perceived main draw back of this method is that it is based on the current species-environment relationships and may not be a reliable guide of the future interactions. Also most of the tick data used (*with exception of few new records, Horak private collection*) were collected at a different time scale from the cattle data. Furthermore, most of the climate data available for predictive species modelling is at a much coarser scale than the site-specific conditions in which the ticks and other vectors operate. However with the evolution of climate data used in predictive studies from long-term climate datasets (Hutchinson *et al.*, 1996) to GCMs (General circulation models) and to RCMs (Regional Climate models) such as DARLAM, we are confident that these results are useful. When this method was evaluated on how it predicts the current distribution of South African birds (Erasmus *et al.*, 2003) and African ticks (Olwoch *et al.*, 2003) relatively accurate results were obtained. It is the same confidence that we attach to the predicted future distribution. However caution should be exercised when interpreting these results because of the model and data gaps. Thus a record of ECF for at least two centuries is needed to evaluate these results. Proper monitoring and experimental research on vector borne diseases is necessary to comprehend future predictions.

#### 4. East Coast Fever (ECF) in space and time

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**Predicting the current and future distribution of *R. appendiculatus* and ECF** and the future were analysed by using Klotzwey's Simulacra (two examples) from StarSoft, Inc. From the 548 known distribution records of *R. appendiculatus*, the predicted current distribution was initially obtained using six variables of the current climate as an input into the model. This is useful because it represents a valuable comparison of how the model predicted distribution compares with the known records (see Olwoch *et al.*, 2003 for details). To obtain the future predictions, the grid cells are populated with future climate. In order to predict the potential current and future distribution of ECF, the predictive species model was used to get an idea of where the ticks could survive currently and in the future based on current and future climatic variables, and then refined these by adding the ranges of cattle. The predictive modelling was executed in S-Plus (S-Plus 2000) while maps of the results were drawn in ArcView GIS. The resultant potential distributions are maps of probability of occurrences per 60 km by 60 km grid cell based on climate. A simplified diagram representing this methodology is shown in figure 4.

#### **Comparison of the predicted present and future distribution of *R. appendiculatus* and ECF**

Several analyses were performed to compare the predicted current and future distributions of *R. appendiculatus*. These included: 1) a comparison of the probability of occurrence values per grid cell between current and future predictions; 2) an analysis of range contraction, expansion and shift; 3) an assessment of overlap between current and future distributions. These analyses were done for the entire study area, per region and per country. By using only the areas where *R. appendiculatus* is currently distributed three regions were defined and assessed: Southern Africa which includes; South Africa, Botswana, Zimbabwe, Zambia, Malawi, Angola and Mozambique; Central Africa which

#### 4. East Coast Fever (ECF) in space and time

includes Democratic Republic of Congo (DRC), Rwanda and Burundi; and East Africa which includes Uganda, Kenya and Tanzania.

The comparison in the probability values of tick occurrence between the present and the future were analysed by using Kolmogorov-Smirnov two-sample test (StatSoft, Inc. (2001)). This was done for all probability values and then a comparison was made between the number of grid cells in various probability classes in the current and future predictions. These probability classes were: 0-<20%, 20- <40%, 40 - <60%... 80-100%. Range changes between the current and the potential future distribution of *R. appendiculatus* were assessed. The predicted current or future potential distribution was taken as the number of grid cells where the probability of occurrence is equal or greater than 50%. This threshold has been used before (Beard *et al.*, 1999; Erasmus *et al.*, 2002; van Staden *et al.*, 2003; and Walker, 1990 for even lower thresholds). The difference in grid cells between the predicted current distribution (CD) and predicted future distribution (FD) constitutes distribution range change (DC). These range changes may either be range contraction or range expansion. There is range expansion if  $FD > CD$  and there is range contraction if  $FD < CD$ . Maps of range shifts were obtained by overlaying the number of grid cells with probability values  $> 50\%$  before climate change with the number of grid cells with probability values  $> 50\%$  after climate change. The number of grid cells outside the intersection constitutes range shifts in a specified direction.

Finally, the degree of proportional overlap between the predicted current and the predicted future distributions of *R. appendiculatus* was assessed by means of proportional overlap method (Prendergast *et al.*, 1993 and Reyers *et al.*, 2000). In this case the proportional overlap was calculated as  $N_c / N_s$ , where  $N_c$  is the number of common grid cells between a pair of areas under comparison and  $N_s$  is the number of grid cells in the smallest set of areas containing data for both groups or the number of grid cells in the smallest set minus the number of grids that are not common in these two sets.

These assessments of future range changes done for the tick distribution were then repeated for ECF distribution. The present and potential future ranges of ECF were

#### 4. East Coast Fever (ECF) in space and time

obtained by superimposing the distribution of cattle with the predicted current and predicted potential future distribution of *R. appendiculatus*. Again cells with a probability greater or equal to 50% that fell within the current cattle distribution were assigned a presence value for ECF. The degree of range change was been calculated as outlined above.

## RESULTS

### *R. appendiculatus* predicted distribution

Under the current and future climates, the predicted probability values of *R. appendiculatus* distribution based on the current and future climate are shown in Fig. 5. These values range from 0-1 (0% - 100%). The probability that the area will be climatically suitable for ticks decreases as one moves from 1-0. Visually, the current and future predicted distributions are not clearly differentiated, but when the number of grid cells in various probability classes was compared statistically, a significant difference between the current and future probability values was found (Kolmogorov-Smirnov two sample test,  $p < .005$ ). When the number of grid cells falling into different probability classes were analysed for the whole of sub-Saharan Africa (Table 1), there were no major changes in the number of grid cells in the lower probabilities (0-20%). The biggest change in the number of grids occurred in the 20 – 40% and 40 - 60% probability classes. This tick suitability class showed increases of 31 and 33 grid cells respectively in the future (Table 1). Also of interest was the reduction in the number of grid cells grid cells with a probability greater than 80% for the predicted future distribution.

Regional analysis of probability classes for predicted *R. appendiculatus* distribution revealed that the East Africa is predicted to be most affected region. There is greater than 100% increase in the number of grid cells in the 60-80% probability class. In the other regions (Central and South) there were no major changes for the current and future distributions (Fig. 6a). A further analysis of probability classes for individual countries revealed that in most of the countries tick suitability would stay the same. However, the

#### 4. East Coast Fever (ECF) in space and time

following exceptions were noted: Burundi, Kenya, Rwanda, Zambia, Zimbabwe and Uganda showed significant increases in the number of grid cells with higher probabilities (60-80%) (Fig. 6b) while DRC showed increases in the number of grids in the 20-40 % probability classes in the future (Fig. 6b).

When assessing range changes, a tick was assumed present where the model predicted a probability value of  $\geq 50\%$ . On a sub-Saharan scale, the analysis revealed that there was a general reduction of 23.3% in *R. appendiculatus* range between predicted present (CD=1263 grid cells) and predicted future (FD = 969 grid cells) (Table 2) (Fig. 7). Range shift was mainly from west to east with most of the range reduction-taking place in the west. Regional analysis revealed less than 1% decrease of *R. appendiculatus* range in all regions. The country analysis showed that Botswana, Malawi, South Africa and Zimbabwe are predicted to show increases while Mozambique, Tanzania, Uganda, DRC and Zambia show slight decreases. The countries that are predicted to show no change are Burundi, Rwanda and Kenya (Table 3). Analysis of the spatial congruence between predicted current and future *R. appendiculatus* ranges by means of the proportional overlap method showed high congruency between current and future predicted distributions. On a sub-Saharan scale there was 89% congruence between current and future predicted distribution of *R. appendiculatus* (Table 2). On a regional scale, there is 90% congruence in Central and East with 87% congruence in the South (Table 2). Country proportional overlaps vary from 77% for Botswana, 78% for south Africa, 85% Zimbabwe and 87% DRC. The rest show 90% apart from Rwanda, Burundi, and Malawi that show 100% congruency (Table 3).

Once the cattle distributions were superimposed on the present and future potential tick distribution, an analysis of the change in potential ECF distribution was possible. On a sub-Saharan scale, there was a slight increase in ECF range between present and future (Table 4). The difference between the maps (Fig. 8) of ECF predicted range under the current climatic conditions and future climate scenarios showed that 100 grid cells which were suitable for ECF under the current climatic conditions become unsuitable in the future while 102 grid cells which were unsuitable in the current climate become suitable



#### 4. East Coast Fever (ECF) in space and time

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in the future. Visually, most of the south western African countries of Angola, Namibia, western and southern Botswana, western Zambia and central DRC are predicted to become unsuitable for East Coast Fever in the future. Regionally, there is a predicted increase of ECF in Southern and Central Africa while East Africa stays the same (Table 4). An analysis of individual country ECF changes revealed that the range is predicted to increase in Botswana, DRC, Malawi, and South Africa. Predicted decrease in ECF is expected in Tanzania and Uganda (Table 5). ECF in the rest of the countries (Burundi, Kenya, Mozambique, Zambia and Zimbabwe) stays the same. Analysis of the predicted ECF ranges for the present and future using proportional overlap method showed the lowest congruency in Kenya, followed by Botswana and South Africa (Table 5).

## DISCUSSION

### Implications of the findings

#### Changes in *R. appendiculatus* distribution

The climate predicted by DARLAM in the future renders the western arid regions of Africa unsuitable for *R. appendiculatus*. I propose here that increase in temperature in an already hot and dry area limits population increase, and any further rise in temperature may result in slowing down developmental rates and later limit or halt survival due to water loss under dry conditions. Angola, Namibia, southern DRC become climatically unsuitable for *R. appendiculatus* infestation. However the northern and eastern Cape provinces of South Africa as well as Botswana, Zambia and eastern DRC that are currently unsuitable are rendered climatically suitable for *R. appendiculatus* under future climate scenarios. This may be because of enhanced rainfall in these areas. Rises in temperature (especially the minima) as predicted over most of tropical Africa and southern Africa may contribute to the increases in suitability of *R. appendiculatus* in these regions. These effects would shorten generation time and may allow populations to pass through additional generations, possibly leading to higher pest populations in some cases. Increase in tick numbers, as well as shifts in the timing and duration of each

#### 4. East Coast Fever (ECF) in space and time

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generation time may overwhelm areas that may become more suitable for tick infestations. This would increase the absolute amount of production loss of cattle. Thus strategic dipping may not be a sufficient strategy in such an environment.

##### Changes in the range of East Coast Fever (ECF)

The predicted ECF range was mainly deduced from *R. appendiculatus* predicted distributions and cattle ranges. It will therefore follow the predicted range of these two factors. The slight increase in *R. appendiculatus* distribution in cattle inhabited areas leads to a slight increase in ECF on a sub-saharan scale. Minimum temperature is the main factor that influences tick abundance and length of generation time. The predicted general increase in minimum temperature in most areas therefore means an increase in tick density and a shorter generation time. This scenario is particular applicable to southern Africa which currently experiences only one generation of *R. appendiculatus* per year compared to the tropical African countries. Thus it is possible to say that southern Africa and central Africa are the regions predicted to show increases in ECF suitability in the future. Elsewhere, the climatic suitability of ECF in most of its core areas is predicted to stay the same. However at the edges of its range, there are observable changes in the suitability because the dynamics of any organism at the edge of its range are likely to be determined by a single limiting factor, while at the core of its range, an organism is more often subject to multivariate constraints (Randolph, 2001).

Country analysis of ECF changes show increases in ECF suitability in eastern DRC, Botswana, Malawi, and South Africa. The key factor linked to this response is the predicted decrease in temperatures during wetter winters (making conditions less harsh) (Botswana and Malawi), and increasing rainfall in the austral summer (South Africa and the eastern DRC). On the other hand, central Tanzania with its predicted future increase in rainfall and slight warming does not show the expected increase in ECF future suitability; a clear indication that although climate alone may be used to give acceptable biological explanations of the responses, more explicit models need to be developed to tackle such complex relationships. In this case other factors operating at local scales that

#### 4. East Coast Fever (ECF) in space and time

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are also crucial to tick seasonal dynamic such as the absence of the main hosts in this arid part of Tanzania may be responsible for the observable anomaly. Moreover it is important to note here that the reduction in ECF range does not necessarily mean reduction in the severity of the disease, because unfavorable climatic conditions may also render pastures unpalatable or not available and thus result in hosts with very poor nutrition conditions.

These underfed hosts are more prone to tick infections because cattle under stress appear to suffer more from each unit of tick attack (Sutherst, 1983). Studies in Australia have reported that the nutritional condition of cattle will decline in northern Australia due to reduced protein levels in pastures at high temperatures and carbon dioxide concentrations, leading to both heavier tick infestations and greater losses for each tick attaching under stressful conditions (Sutherst, 1983). An additional effect may be on the hosts' availability and well being. In this case, cattle may change their distribution and thereby disrupt the lifecycles of ticks. Other indirect effects may also come into play such as increases in the rate of evolution of the parasites thus the frequency of mutation. In such a case the hosts will be subjected to a multitude of new parasites at all times and the issue of resistant hosts does not arise (Harvell, 2002).

The assessment of biodiversity as a fundamental important factor in reducing the risk of exposure to tick-borne diseases (Ostefeld & Keesing, 2000) does not form part of this chapter but needs to be explored for East Coast Fever in future. The dependence of *R. appendiculatus* on different hosts to complete its life cycle means that changes in the population of those hosts within communities is a very important factor to consider when dealing with this tick-borne disease. Therefore, changes and proximity to wild host populations plays a great role in East Coast Fever transmission even more so for those hosts that act as reservoirs for this disease infection. Movement and displacement of some of these hosts as may happen after climate change may result in changes in host population and/or diversity which may lead to disruption in life cycles of the tick. This will influence the timing of tick borne infections and therefore place a huge burden on control programs. We suggest here that predicting the hosts' distribution would give an

#### 4. East Coast Fever (ECF) in space and time

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indication of the diseases prevalence. The use of changes in host numbers to predict disease outbreaks is being explored in the case of desert gerbils (*Rhombomys opimus*) and the plague in the Soviet Union. The findings of the gerbil study confirmed long held theory that plague and other infectious diseases erupt when host populations reach a critical threshold. For the plague, bigger populations of hosts make it easy for the vector to jump from one animal to another and the pathogen survives (Davies *et al.*, 2004).

The tick-host and disease relationships are very complex and are not fully understood at this moment. At the same time there are no equally complex models to deal with these relationships. However, there are good species distribution and climate data. With these, the distribution of vectors and diseases has been attempted using simpler climate envelope approaches. By using these models, it is now possible to understand the relationships between current climate, tick, host distribution and population in order to predict their future ranges. By doing this we provide a relatively acceptable picture of the disease's implications for the present and future. In Africa, economic crises and wars hinder proper surveillance of tick and host populations, but by observing changes in climatic conditions that are linked to vector and host reproduction and development, outbreak of diseases can be anticipated long before they occur. The tick *R. appendiculatus* being a three- host tick, the immature stages mainly depend on small hares to develop. These hosts respond quickly to heavy rains. Monitoring and predicting these hosts may be the practical key factor in the control and prevention of ECF in Africa. Understanding the dynamics of vector borne diseases rather than chemical control is the key. Moreover chemical control has proved unsuccessful partly because partial removal of one parasite results in invasion of others. For instance removal of *Glossina palpalis* in Cote d'Ivoire resulted in invasion of lesser dominant species, *Glossina pallicera* and *Glossina nigrofusca*. Also the eradication of *Boophilus decoloratus* in southeastern countries resulted in the invasion of its competitor, *B. microplus* (Sutherst, 2001).

This study does not suggest that climate is the only factor influencing the distribution of *R. appendiculatus* and ECF. Neither does it mean to imply that the distribution of *R.*

#### 4. East Coast Fever (ECF) in space and time

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*appendiculatus* and the presence of cattle are the only determinant factors for ECF transmission and prevalence. Other factors such as host population size and density, habitat modification, vector control programs and the social environments play a significant role. In Africa for instance, lack of enforcement of animal movement restrictions and invasion of game parks for grazing land play a very crucial role in ECF infection and spread. These results present the broad scale climatic limits within which finer scales operate and are therefore a valuable tool for understanding the relationship between ticks, tick-borne diseases and climate. In the absence of a more comprehensive and versatile model, these results are also the best alternative we have.

In an African context, predicted increase in ECF in areas such as Botswana, DRC and South Africa would be disastrous especially if other control measures arrive too late. A more active role for the control agencies is suggested especially in Africa to provide more resources for proper monitoring. Changes in human behaviour as well as tick-host distribution following a changed climate should also be included in future planning.

#### **Future direction**

These results can benefit from the inclusion of ECF distribution records over the last century. More importantly, research into the development of more comprehensive tick models that include both the biological and non-biological factors should be motivated so as to predict not only the distribution ranges but also their reproduction and developmental rates. Country surveillances of tick-borne diseases should be revived so that changes are known at local scales. Also increases in hosts that are linked to these vector borne diseases should also be reported for a better understanding of the interaction between vectors, vector-borne disease and their hosts.

## 4. East Coast Fever (ECF) in space and time

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Year	Number of 60km x 60km grid cells	Future no. of predicted grid cells	Change (grid cells)	Change (%)
1981	121	124	3	2%
1982	121	124	3	2%
1983	121	124	3	2%
1984	121	124	3	2%
1985	121	124	3	2%
1986	121	124	3	2%
1987	121	124	3	2%
1988	121	124	3	2%
1989	121	124	3	2%
1990	121	124	3	2%

Table 2. Number of 60km x 60km grids cells for which *R. appendiculatus* is present in the predicted current and future distribution at a sub-Saharan and regional scale. Proportional overlap values between current and future ranges are also shown. Proportional overlap is a threshold of 50%.

Year	Current no. of predicted grid cells	Future no. of predicted grid cells	Change (grid cells)	Change (%)
1981-1990	121	124	3	2%
1981-1990	121	124	3	2%
1981	121	124	3	2%
1990	121	124	3	2%

Table 3. Number of 60km x 60km grids cells for which *R. appendiculatus* is present in the predicted current and future distribution at a country scale. Proportional overlap

## 4. East Coast Fever (ECF) in space and time

values between current and future ranges are also shown. Presence assumed at a threshold

## TABLES

Table 1: Number of 60km x 60km grid cells falling into various probability classes for the presence of *R. appendiculatus* under the predicted current and future distribution.

Probability class	Current no. of predicted grid cells	Future no. of predicted grid cells	Common grids	Overlap
0-20%	1428	1486	1341	94%
20-40%	376	357	166	46%
40-60%	369	383	165	45%
60-80%	372	369	178	48%
80-100%	455	405	321	79%

Table 2: Number of 60km x 60km grids cells for which *R. appendiculatus* is present in the predicted current and future distribution at a sub-Saharan and regional scale. Proportional overlap values between current and future ranges are also shown. Presence assumed at a threshold of 50%.

Region	Current no. of predicted grid cells	Future no. of predicted grid cells	Common grid cells	Overlap
SUB-SAHARA	1233	969	867	89%
CENTRAL	437	403	373	93%
EAST	254	234	213	91%
SOUTH	572	563	490	87%

Table 3: Number of 60km x 60km grids cells for which *R. appendiculatus* is present in the predicted current and future distribution at a country scale. Proportional overlap

## 4. East Coast Fever (ECF) in space and time

values between current and future ranges are also shown. Presence assumed at a threshold of 50%.

Country	Current no. of predicted grid cells	Future no. of predicted grid cells	Common grid cells	Overlap
BOTSWANA	39	44	34	74%
BURUNDI	13	13	13	100%
KENYA	21	20	14	93%
MALAWI	35	38	35	100%
MOZAMBIQUE	156	119	114	93%
SOUTH AFRICA	86	78	61	78%
RWANDA	12	12	12	100%
TANZANIA	191	182	168	93%
UGANDA	42	32	31	91%
ZAIRE	283	250	231	87%
ZAMBIA	157	155	148	95%
ZIMBABWE	91	100	83	85%

Table 4: Number of 60km x 60km grids cells for which ECF is present in the predicted current and future distribution at a sub-Saharan and regional scales. Proportional overlap values between current and future ranges are also shown. Presence assumed at a threshold of 50%.

Region	Current no. of predicted grid cells	Future no. of predicted grid cells	Common grids	Overlap
SUB-SAHARA	739	741	639	86%
CENTRAL	90	102	88	98%
EAST	228	212	191	90%
SOUTH	401	410	347	87%



## 4. East Coast Fever (ECF) in space and time

Table 5: Number of 60km x 60km grids cells for which ECF is present in the predicted current and future distribution at a country scale. Proportional overlap values between current and future ranges are also shown. Presence assumed at a threshold of 50%

Country	Current no. of predicted grid cells	Future no. of predicted grid cells	Common grids	Overlap
BOTSWANA	39	44	34	77%
BURUNDI	12	12	12	100%
DRC	66	78	64	97%
KENYA	20	20	14	70%
MALAWI	28	31	28	100%
MOZAMBIQUE	45	45	43	96%
RWANDA	12	12	12	100%
SOUTH AFRICA	78	86	61	78%
TANZANIA	171	164	150	91%
UGANDA	37	28	27	96%
ZAMBIA	99	99	95	96%
ZIMBABWE	97	97	80	82%

## 4. East Coast Fever (ECF) in space and time

## FIGURE LEGENDS

**Figure 1:** Map showing the countries of sub-Saharan Africa that were included in this study

**Figure 2:** The relationship between recorded cattle density for sub-Saharan Africa and the recorded *R. appendiculatus* distribution.

**Figure 3:** DARLAMs climatological anomalies for the 2020s vs 1990s

**Figure 4:** Simplified diagram of how the current and future distribution of *R. appendiculatus* and East Coast Fever (ECF) were predicted

**Figure 5:** The current and future predicted probability values of *R. appendiculatus* obtained by using the predictive species model (Erasmus *et al.*, 2002) and DARLAM climate surfaces (a) Current (b) Future 2030

**Figure 6a:** Changes in number of 60kmx60km grid cells in various probability classes between the current and the future for different regions

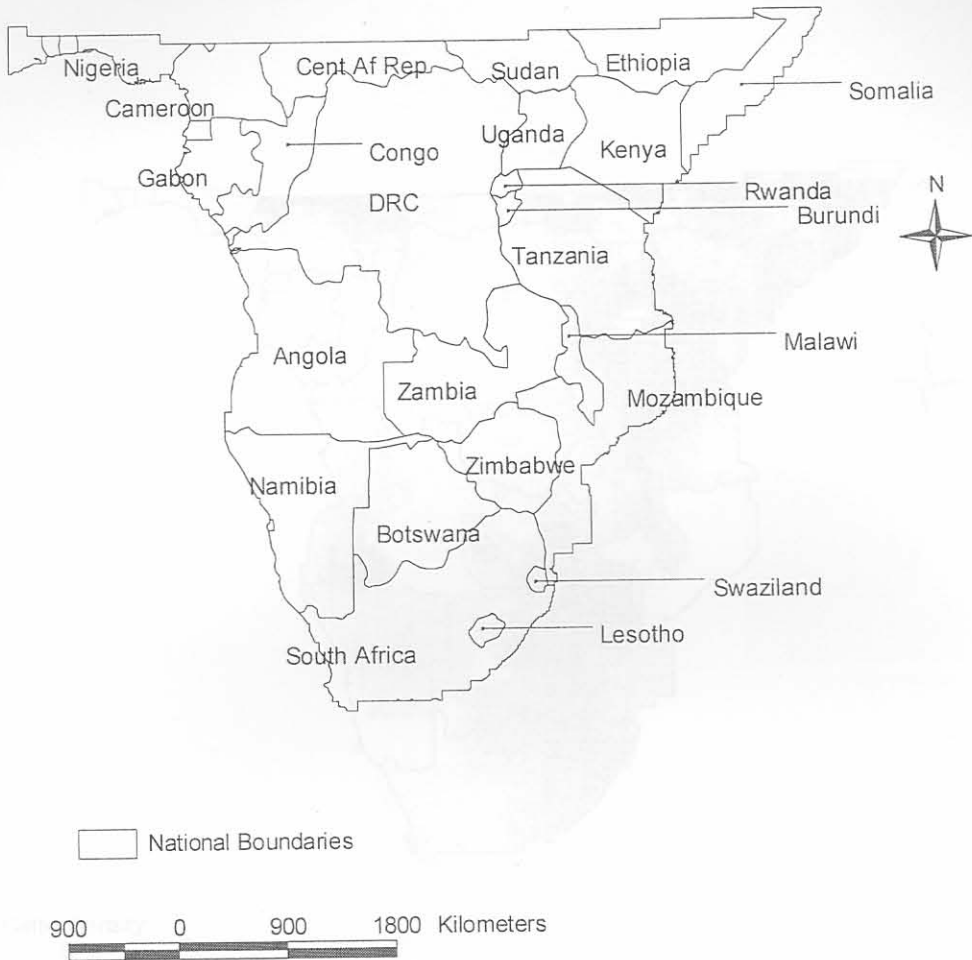
**Figure 6b:** Changes in the number of 60kmx60km grid cells in various probability classes between the current and the future for different countries

**Figure 7:** Predicted current and future *R. appendiculatus* distribution obtained by using the predictive species model (Erasmus *et al.*, 2002) and DARLAM climate surfaces (a) Current (b) Future. Presence assumed at a threshold of 50%.

**Figure 8:** East Coast Fever future risk map obtained by using by the predictive species model (Erasmus *et al.*, 2002) and DARLAM climate surfaces. Presence assumed at a threshold of 50% of *R. appendiculatus* and cattle presence.

#### 4. East Coast Fever (ECF) in space and time

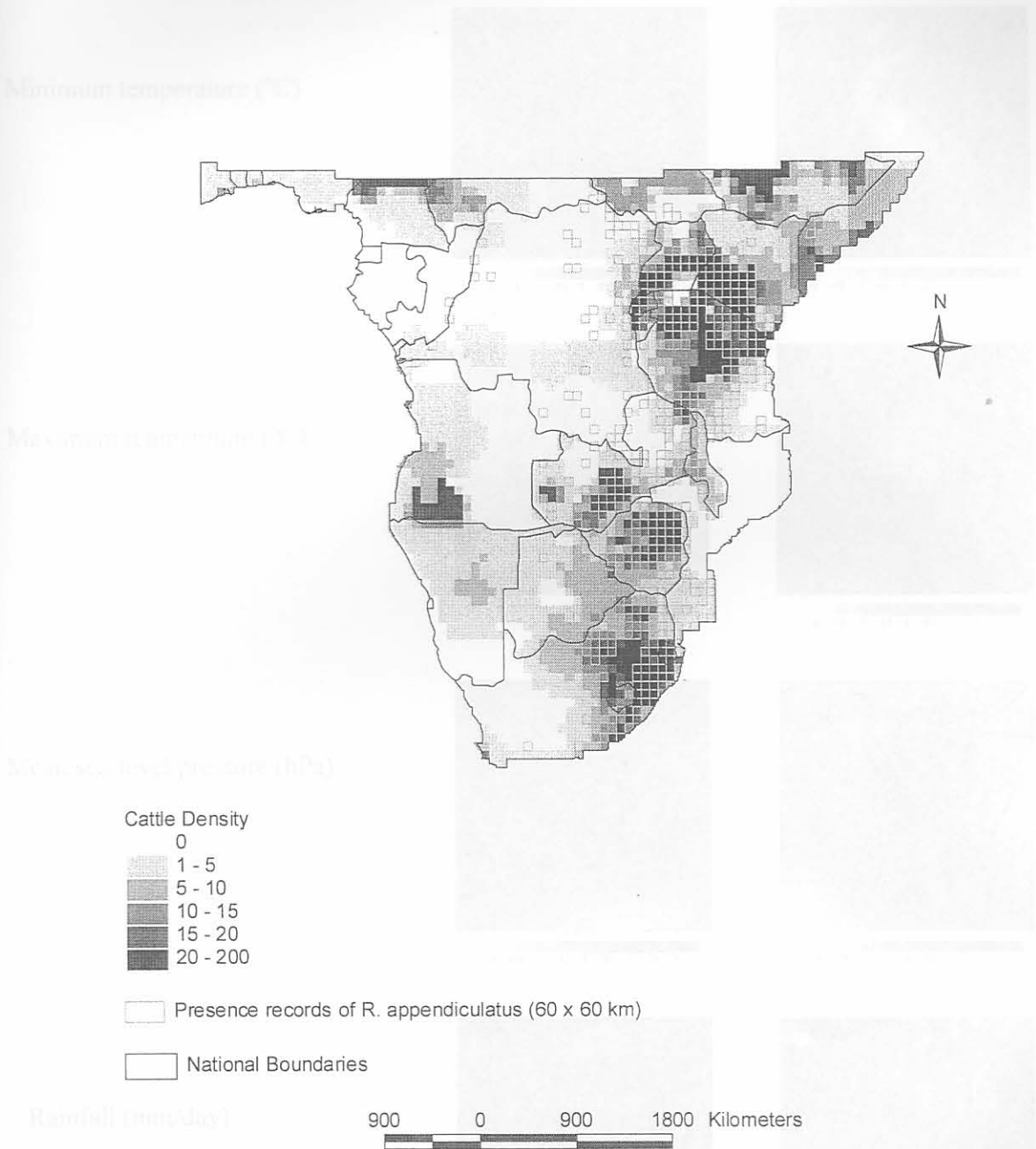
Figure 1



4. East Coast Fever (ECF) in space and time

Figure 3

Figure 2



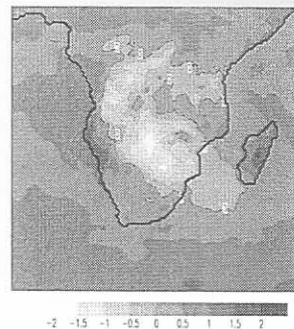
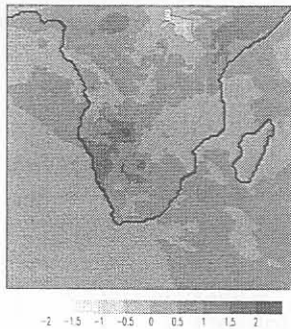
4. East Coast Fever (ECF) in space and time

Figure 3

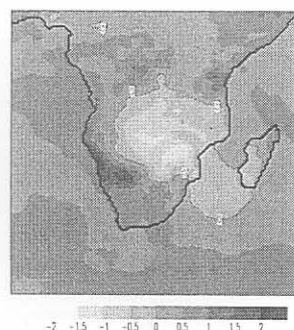
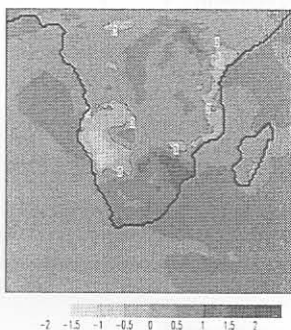
Figure 4

Simplified diagram of how the ECF transmission cycle is affected by climate change

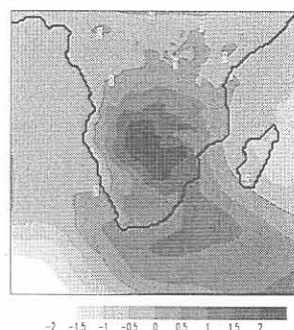
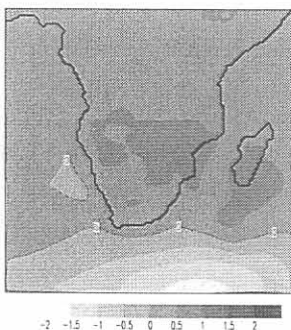
Minimum temperature (°C)



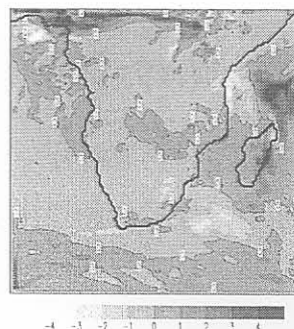
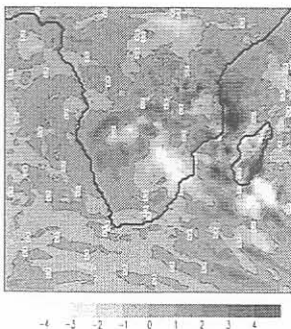
Maximum temperature (°C)



Mean sea-level pressure (hPa)



Rainfall (mm/day)

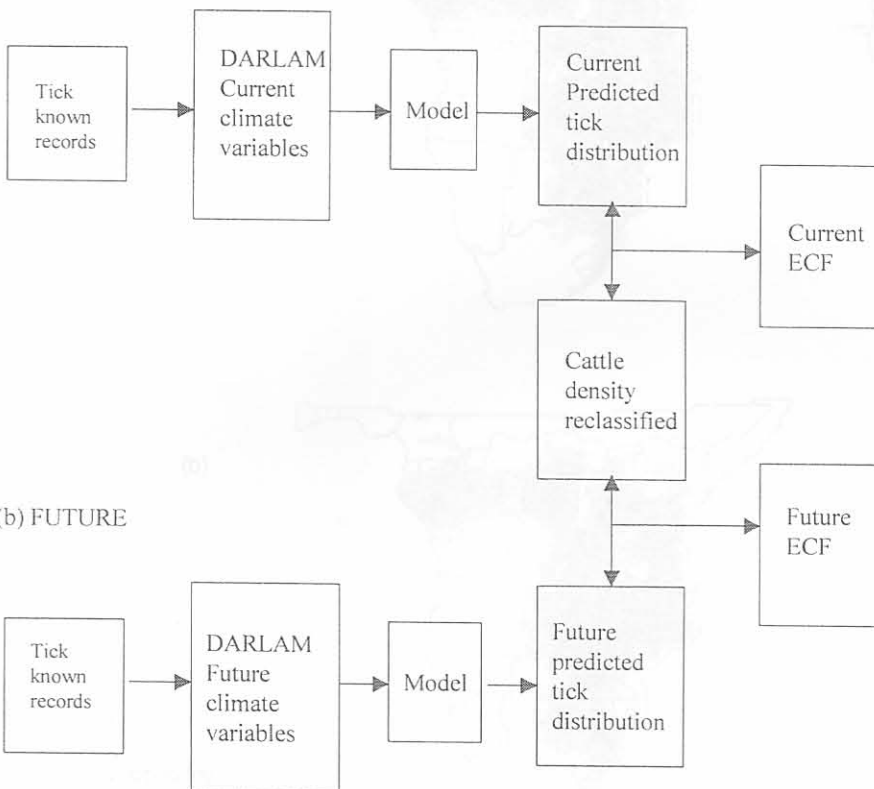


## 4. East Coast Fever (ECF) in space and time

Figure 4

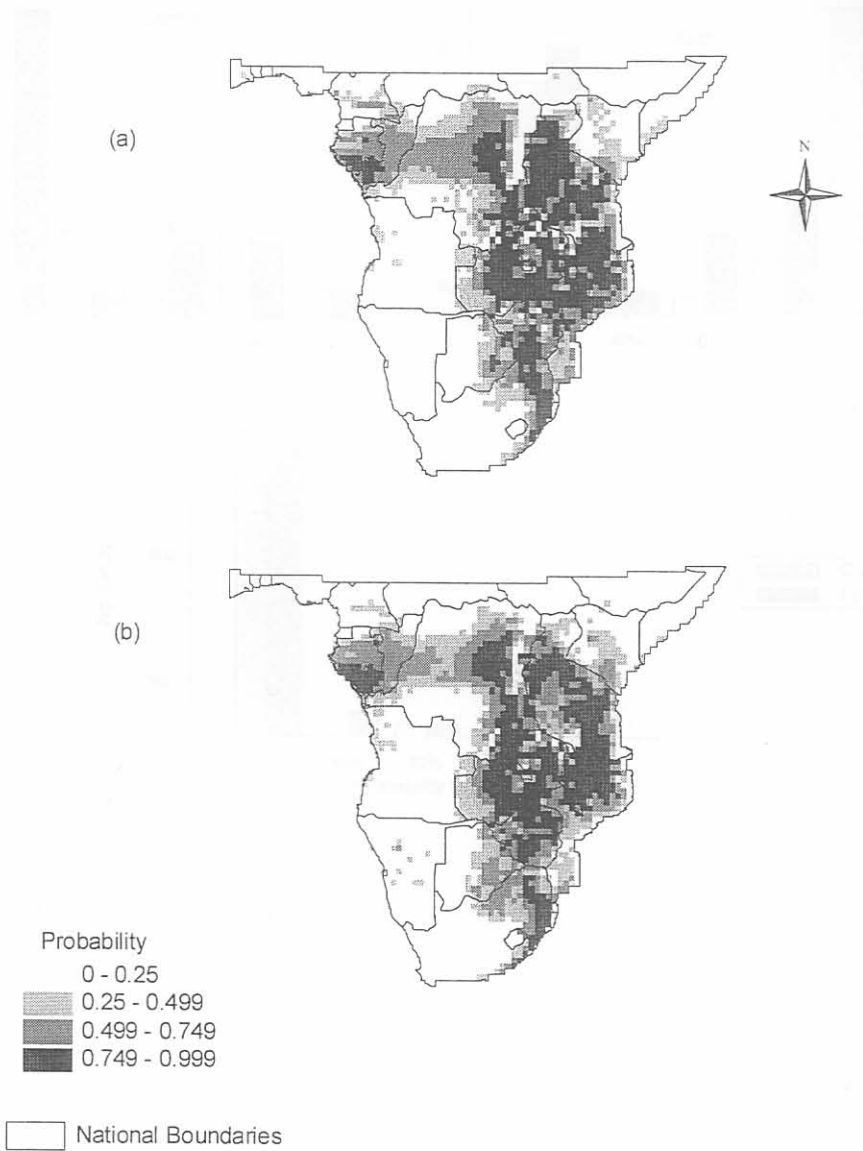
Simplified diagram of how the *R. appendiculatus* and ECF predicted current and future distributions were obtained

(a) CURRENT



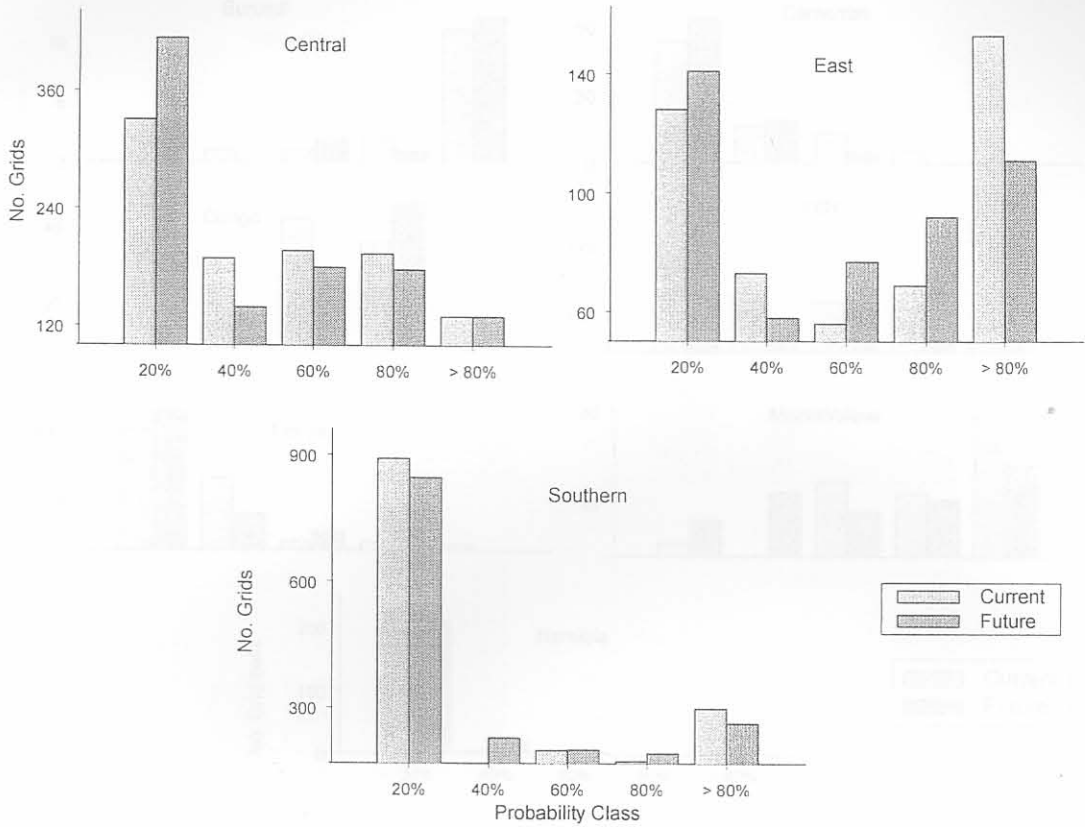
#### 4. East Coast Fever (ECF) in space and time

Figure 5



## 4. East Coast Fever (ECF) in space and time

Figure 6a

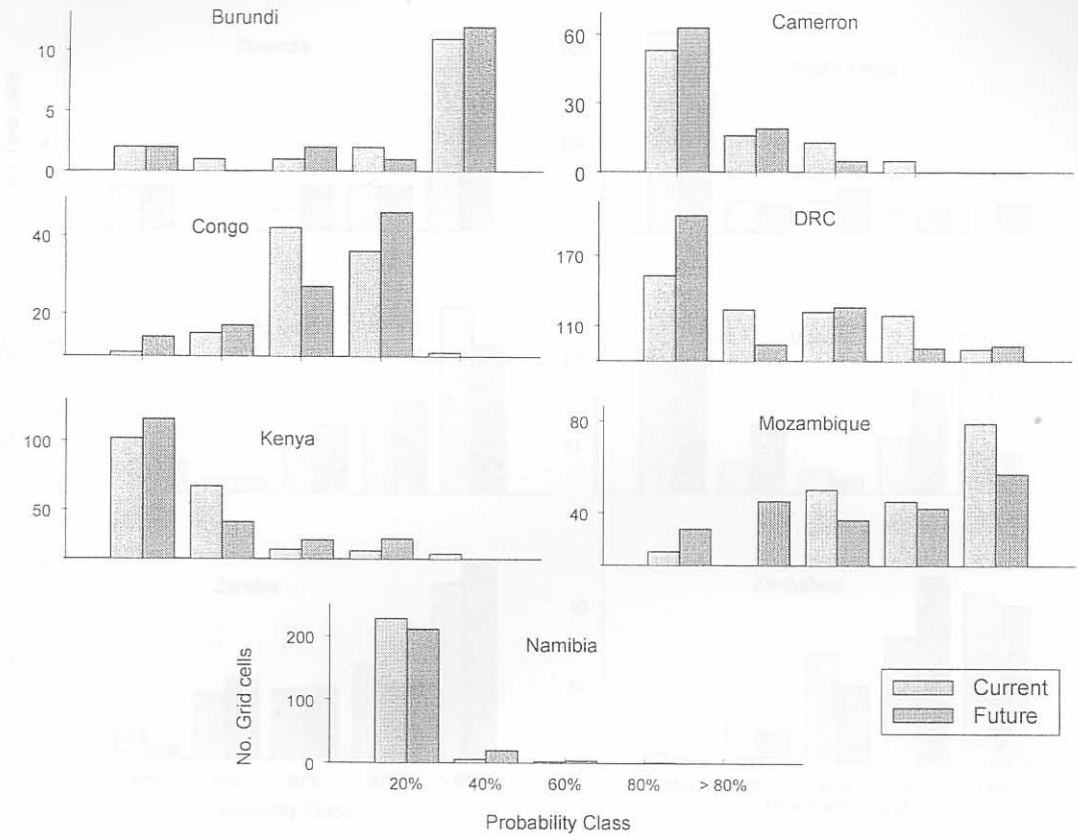




4. East Coast Fever (ECF) in space and time

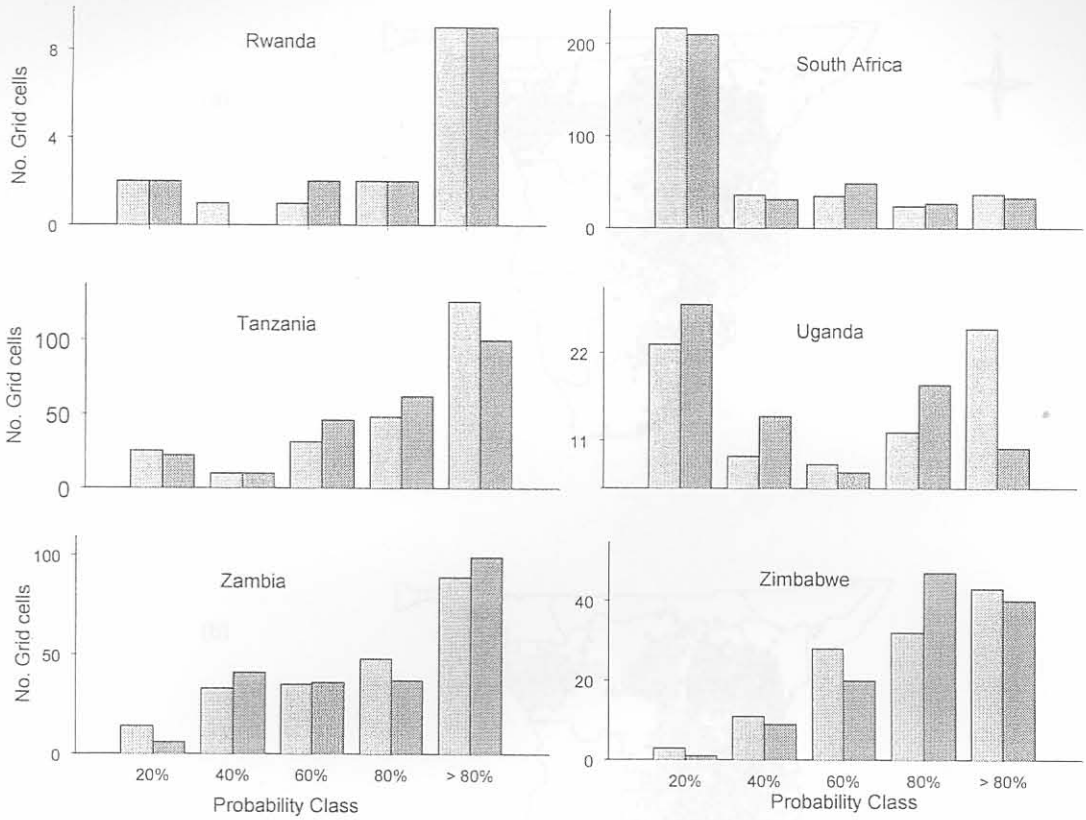
Figure 6b

Figure 6b continued



4. East Coast Fever (ECF) in space and time

Figure 6b continued



4. East Coast Fever (ECF) in space and time

Figure 7



#### 4. East Coast Fever (ECF) in space and time

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Figure 8

