Climate change and tick-host relationships in Africa

by

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Abstract

The concerns that vectors and vector-borne diseases will expand, contract or shift their ranges in response to climate change revived investigations into the magnitude of these range alterations in worldwide species. By use of predictive species models and modelled or interpolated climate data, the current and future distribution of many insects, pests and pathogens in many parts of the world have been predicted using their major climate drivers. In sub-Saharan Africa studies on the impacts of climate change on the current distribution of vectors that transmit diseases to humans has also increased over the past few years but similar studies in vectors that transmit diseases in livestock or wild animals remains inadequate. Yet ticks and tick-borne diseases alone remain a burden to the livestock industry particularly the rural households whose livelihood may depend on a few heads of cattle. Under climate change conditions, the devastation is unknown and it needs to be investigated and incorporated in future control strategies. Furthermore, the current knowledge of the distribution and proximity of other domestic and wild animals to tick infested areas is inadequate and yet forms a vital role in proper management of ticks and tick-borne diseases since ticks use these hosts to complete their life cycles and tick borne disease pathogens reside in them.

This thesis addresses these concerns using a modelling approach in which current, future climate and tick/host distribution data were combined in a GIS environment. Different statistical methods were employed in the analysis of the predicted current and future distribution of various species of the tick genus *Rhipicephalus* and selected vertebrate species that act as hosts. A comparison of how different climate data sets predict the

current distribution of four Rhipicephalus species revealed different distribution per climate datasets. It is therefore important to assess the suitability of a climate data before use. The current and future prediction of 30 Rhipicephalus species showed that East Africa and 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 an increase in tick species richness in the south-western regions of the sub-continent. More than 20 % of the species experienced range shifts of between 50 and 100 %. The predicted impacts of climate change on the tick-borne disease, East Coast Fever (ECF) showed a potential increase in Northern Cape and Eastern Cape provinces of South Africa, Botswana, Malawi, Zambia and eastern DRC. Contraction was the main range alteration predicted for the vertebrate species that act as hosts of R. appendiculatus under climate change conditions. However, more generalist species expanded their ranges. It was also clear from the whole study that different tick species reacted differently to predicted changes in climate and different areas in Africa experienced varying degrees of impacts. The ability of tick and host species to shift their ranges depends on the degree of land degradation and transformation and not to mention the existing ecological interactions. The existing social, economic and environmental policies in individual counties will determine the actual vulnerability.

Key words: Climate change, sub-Sahara Africa, ticks, *Rhipicephalus* spp., tick-borne diseases, predictive species modelling, DARLAM, host assemblages

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Disclaimer

This thesis consists of chapters that have been prepared for submission to, or published in, a range of scientific journals. As a result styles may vary between chapters in the thesis and overlap may occur to secure publication entities. Figures have been added at the end of the respective chapters.

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