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Vector-Borne Diseases: Impact of Climate Change on Vectors and Rodent Reservoirs
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Modeling and prediction of habitat suitability for ticks.

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Ticks are a serious pest of domestic animals, and a threat for human health. Efforts continue at global, regional, and local scales to understand the major factors governing tick distribution, as a necessary step in the development of sound, ecologically based, control measures. The need for models in tick research arose from the problems associated with the use of acaricides in Australia, because of the development of resistance by the cattle tick. With the arrival of the computer age and the use of robust statistical methods to test the feasibility of the model's output, we have at hand a new set of tools devoted to understanding the effect of environmental factors on the tick's ability to colonize a site. This article is not a review of the different models built around the ticks and tick-borne diseases, but a personal insight into the main developments in this field, and how these models could help to protect humans by providing information about the "hot spots" by ticks.

In the last few years, models built around the main features of the life cycle of ticks have been produced, which not only provided information about the main demographic processes of ticks at a given site, but also allowed new insights into the sometimes complex regulation of the tick populations. At geographical scales beyond experimentation, empirical models provide one of the only ways to develop and test hypotheses about ecological features affecting tick distribution. It is a central premise of biogeography that climate exerts a dominant control over the natural distribution of species. Like many other arthropods, ticks are sensitive to climate features, these climate variables promoting, enhancing, or even stopping different and more or less critical parts of their life cycle. Models exploring the relationships between species occurrence and sets of predictor variables produce two kinds of useful outputs: (1) estimates of the probability that a species of tick might occur at given unrecorded locations and (2) an area's suitability for the species. Probabilities of occurrence could be interpreted as estimates of the probability that the species might find a suitable habitat in a given area.

A number of modeling strategies for predicting the impacts of climate on tick distribution have been developed. These have focused on the identification of the "bioclimate envelope" (alternatively termed climate space) through methods that correlate current species distribution with climate variables. The bioclimate envelope modeling approach has its foundations in the ecological niche theory, defined as the fundamental ecological niche as comprising those environmental conditions within which a species can survive and grow. The fundamental niche would completely define the ecological properties of a species: a conceptual space whose axes include all of the environmental variables affecting that species. Bioclimate envelopes can be defined as constituting the climatic component of the fundamental ecological niche. The validity of the bioclimatic envelope approach has been questioned by pointing to many other factors that play an important part in determining tick species distribution and their dynamics over time such as hosts, landscape patterns of vegetation, or even the competition between tick species for resources (hosts in this case). It has been proposed that continental-scale distributions of ticks are principally determined by climate, and it is therefore suggested that many species distributions can in fact be considered to be in equilibrium with the current climate at the macroscale.

Genetic adaptation of species is rarely considered, being range shifts frequently seen as the expected response to the climate. It is usually expected that evolutionary change occurs only on long time scales and that the tolerance range of a species remains the same as it shifts its geographical range. However, studies have shown that climate-induced range shifts can involve not only migration into newly suitable areas, but also selection against phenotypes that are poorly adapted to local conditions. The potential impact of rapid evolutionary change means that the climatic tolerances of a tick may alter from the original founders, making the fundamental niche unstable over time. It has been reported that tick species distributed over large areas display very different climate preferences. Therefore, the development of models for the whole distributional range would produce biased predictions. The erection of models applied on partial ranges (population-derived models) seems to be a better approach to this trouble.

However, the predictive mapping of the so called “climate suitability” (rather than the widely used habitat suitability, as commonly only climate is involved in calculations) is not necessarily a straightforward door to the understanding of ticks dynamics. Nor is the better way to discern the somewhat complex patterns behind epidemic processes of tick-borne diseases. These diseases are commonly the result of complex transmission patterns, the presence and abundance of important reservoir hosts, and, perhaps most important, the dynamics, social changes and behavior of humans in the vicinity of tick foci. At high resolution, vegetation, landscape pattern, and connectivity between patches of suitable vegetation and climate are the major determinants of tick distribution and abundance. Ticks spent most of their life cycles in sheltered microhabitats in the ground, and only a small part feeding on hosts. Acquisition and transmission of pathogens are therefore separated by long periods of free-living existence during which the tick develops from one stage to the next.

Much concern exists currently about the possibility of spread of some prominent tick species, restricted to the Mediterranean region because climate limiting factors into northern latitudes. The rational behind is that warmer winters could provide a more adequate environment for those species. However, as explained before, climate is not the only limiting factor in the spread of a tick population, as barriers to dispersion, lack of adequate hosts, or inadequate temporal synchrony between hosts and parasites would make the invasive event unlikely. Efforts should be addressed towards the evaluation of process-based models. Such an effort must to be based on the knowledge of microclimatic requirements for tick survival and development, in terms of temperature and moisture conditions, obtained from laboratory experiments under controlled conditions or long-term field work must to be obtained and applied to the development of models describing the different patterns of life cycles. These models should be aimed to understand the development and mortality processes behind the observed pattern of tick dynamics. The most important feature to obtain from these models should be the determination of R0, the basic reproduction rate of a disease. This is a pivotal feature in the understanding of the dynamics of any tick-borne disease and the best way to determine the potential impact of the many factors (and not only climate) involved on the transmission rates of such a disease.