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Old health risks in new places? An ecological niche model for *I. ricinus* tick distribution in Europe under a changing climate

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ABSTRACT

Climate change will likely have impacts on disease vector distribution. Posing a significant health threat in the 21st century, risk of tick-borne diseases may increase with higher annual mean temperatures and changes in precipitation. We modeled the current and future potential distribution of the *Ixodes ricinus* tick species in Europe. The Genetic Algorithm for Rule-set Prediction (GARP) was utilized to predict potential distributions of *I. ricinus* based on current (1990–2010 averages) and future (2040–2060 averages) environmental variables. A ten model best subset was created out of a possible 200 models based on omission and commission criteria. Our results show that under the A2 climate change scenario the potential habitat range for the *I. ricinus* tick in Europe will expand into higher elevations and latitudes (e.g., Scandinavia, the Baltics, and Belarus), while contracting in other areas (e.g., Alps, Pyrenees, interior Italy, and northwestern Poland). Overall, a potential habitat expansion of 3.8% in all of Europe is possible. Our results may be used to inform climate change adaptation efforts in Europe.

1. Introduction

Climate change has substantial impacts on human health (Costello et al., 2011; Frumkin et al., 2008; Haines et al., 2006; McMichael and Lindgren, 2011; Patz et al., 2005). Impacts on the European continent will likely include a higher frequency of extreme weather events, prolonged heat waves, changes in precipitation, reduction in biodiversity, and changes in the spatial distribution of various infectious diseases (Bittner et al., 2014; Confalonieri et al., 2007; Fischer and Schär, 2010; Nikulin et al., 2011; Parks et al., 2010; Semenza et al., 2012; Thuiller et al., 2005). In addition to a potential increase in food-borne infections with warmer mean temperatures (Thomas et al., 2012), the distribution and life cycle changes of rodents, arthropods, and other disease vectors present a major public health risk to Europe (Ciscar et al., 2011; Semenza and Menne, 2009; Semenza et al., 2012). Vector-borne diseases are transmitted by ticks (e.g., tick-borne encephalitis (TBE), Lyme borreliosis), mosquitoes (e.g., West Nile Virus, malaria, dengue), sandflies (e.g., leishmaniasis), rodents (e.g., plague, hantavirus), and other arthropods. While risks to Europe from emerging tropical diseases under a changing climate should not be dismissed, morbidity from tick-borne diseases is already a public health issue in Europe that may be exacerbated by climatic change (Jaenson and Lindgren, 2011; Massad et al., 2011; Semenza et al., 2012). In Europe's temperate climate, ticks are the primary disease vector (Capelli et al., 2012a), and assessing future perturbations in tick distribution under a changing climate is an imperative component of climate change adaptation and public health preparedness (Semenza et al., 2012).

1.1. Climate change effects on tick-borne diseases

Already endemic in northern and central Europe, ticks of the *Ixodes ricinus* (subsequently called *I. ricinus*) family act as both a reservoir and vector for lyme borreliosis and TBE pathogens (Jaenson and Lindgren, 2011; Jaenson et al., 2012; Lindquist and Vapalahti, 2008; Süss, 2011). Climate change affects vector-borne disease distribution and incidence through various paths (Gage et al., 2008; Kovats et al., 2001; Mills et al., 2010; Semenza et al., 2012). First, arthropod vectors such as ticks are ectothermic (cold-blooded) and therefore sensitive to changes in temperature (European Center for Disease Prevention and Control, 2012). Secondly, precipitation and humidity additionally affect reproduction and egg development, vector development, population density as well as biting activity (Gage et al., 2008; Harrus and Baneth, 2005; Knap et al., 2009). Pathogen load, pathogen development, abundance of host species and human behavior are also affected by climate factors (Kovats et al., 2001; Massad et al., 2011; Semenza

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and Menne, 2009; Zhang et al., 2008). *I. ricinus* spends all of its life stages outside and thus depends on a suitable combination of climate variables making them particularly vulnerable to changes in climate (Estrada-Peña, 2008; Gage et al., 2008). Milder winters and longer growing seasons could expand climate-sensitive vector ranges to higher altitudes and latitudes (Süss, 2011), while a hotter and drier climate in southern European countries might lead to a decrease in tick abundance in these regions (Semenza and Menne, 2009). Temperate environments have also been described as particularly at risk from global warming as low temperatures usually limit vector survival (Sutherst, 2004). European countries with lower mean temperatures are expected to experience an increase in climate-sensitive disease vectors in the near future (Semenza et al., 2012).

In recent years, the public health research community has become increasingly interested in future impacts of climate change on human health as shown by a larger output of research articles (Hosking and Campbell-Lendrum, 2012). Whereas future distribution of ticks in individual European countries has been modeled (Gray et al., 2009), transfer of these results of spatial epidemiological modeling into national adaptation policy has been slow. Limited information exists on changes in tick niche distribution on the European continent overall, a gap which this study attempts to fill. Based on our results of modeling current and prospective *I. ricinus* tick distribution in Europe, we discuss the potential implementation of our methods into European climate change adaptation strategies.

2. Materials and methods

2.1. Data sources

A total of 2097 georeferenced localities (presence-only) for *I. ricinus* were obtained from the Global Biodiversity Information Facility (2013). Most tick localities were recorded using handheld GPS, while coordinates for older records were documented using local maps and distance and azimuth (direction) from the nearest town. The majority of ticks (~97%) were collected from their observed presence on a host (e.g., human, dog), then mailed to a public health station or museum. The remaining ticks were observed and not collected. Absence data were not needed for the chosen method of modeling. More than one species was recorded at multiple locations, providing a rudimentary level of abundance. However, abundance was also not necessary for modeling and only one *I. ricinus* tick was needed per geographically unique location. GBIF is a global inventory of freely available species locality data that combines multiple datasets into one. Only data from European countries were used in this study and the original data sources include the Ohio State University Acarology Collection, Berlin Museum of Natural History, Illinois Natural History Survey, National Natural History Museum of Luxembourg, United Kingdom National Biodiversity Network, Danish Biodiversity Information Facility, Swedish Species Data Bank, Natural History Museum – University of Oslo, and Norwegian Species Data Bank.

The current distribution model utilized baseline climate data constructed of averages over the time period 1990–2010 and the future distribution model utilized the CSIRO SRES A2 emissions scenario for the time period 2040–2060. The A2 scenario was originally created by the CSIRO Marine and Atmospheric Research Laboratories Information Network in Australia (Collier et al., 2007; Gordon et al., 2002). Data were obtained from the Consultative Group on International Agricultural Research (CGIAR) Research Program on Climate Change, Agriculture and Food Security (CCAFS) global circulation model (GCM) data portal (Consultative Group on International Agricultural Research (CGIAR), 2013). The A2 emissions scenario uses global economic and industrial trend predictions to conceptualize a future climate influenced by a heterogeneous world where fertility patterns converge slowly across regions resulting in increasing population, while economic growth and technological change are regionally fragmented. Because the impact of these trends is expected to exacerbate current climate change tendencies, the A2 scenario is considered a "high" emissions scenario. Both the baseline climate data and A2 scenario climate data were processed and downscaled through the MarkSim pattern scaling technique, which groups over 9200 global weather stations into climate clusters based on monthly average rainfall and temperature figures from each station (Jones and Thornton, 2013).

Bioclimatic grids were created through the manipulation of monthly measures of solar radiation, precipitation, and temperature and included annual mean solar radiation, iso-thermality, annual total precipitation, precipitation of wettest quarter, and precipitation of driest quarter at a resolution of 5′ (~8 km) (Hijmans et al., 2005). Soil type was also used as a variable for modeling because of its importance in tick habitat suitability (Guerra et al., 2002). Soil data were obtained from the Harmonized World Soil Database (HWSD), which utilized the Soil and Terrain Database (SOTER) for Europe. Soil data were available at a resolution of 30″ (~1 km). All variables were resampled to a resolution of 8 km^2 (or 0.01°), and clipped to the boundary of Europe (excluding western Russia).

2.2. The GARP modeling approach

The Genetic Algorithm for Rule-set Prediction (GARP) was selected to create an ecological niche model (ENM) for *I. ricinus*. The GARP model was developed using the Desktop GARP version 1.1.3 open source software application (Scachetti-Pereira and Stockwell, 2002). GARP is a presence-only modeling tool that analyzes the relationship between locality data and the parameters of environmental variables in the same location through an iterative process of training and testing (Stockwell and Peters, 1999). A total of 50 rules are created from four main rule types (atomic, range, negated range, and logit rules) for each model run in a pattern matching process that finds non-random relationships between locality data and environmental parameters. Once a rule-set (i.e., the combination of all 50 rules in each model run) is created, then the relationship is applied to other areas of the landscape that have similar environmental parameters describing either presence or absence of the species. Validation occurs both internally and externally through a process of data splitting that is user-defined.

The GARP modeling approach is stochastic, or random, and consequently produces different outputs with each model run. Because of the variance between each model run output, it is important to produce multiple runs and utilize the best-subset technique of selecting the 10 best models that meet certain optimization parameters. Omission and commission thresholds are defined by the user to obtain a set of models that find a balance between sensitivity (absence of omission error) and specificity (absence of commission error) (Anderson et al., 2003). The resulting GARP output is a collection of grids that describe presence and absence of the species across the study area. These grids can be input in a Geographic Information System (GIS) and summated to find areas where higher and lower model agreement occurs. Presence or absence classification is more certain with increasing model agreement (Ron, 2005).

2.3. Application of GARP in this study

For this study, a total of 904 *I. ricinus* locations were found to be spatially unique and thus available for evaluation. Locations were spatially unique when they were not found in the same eight