

Climate change and species distribution: possible scenarios for thermophilic ticks in Romania

Cristian Domșa, Attila D. Sándor, Andrei D. Mihalca

Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Romania

Abstract

Several zoonotic tick-borne diseases are emerging in Europe due to various factors, including changes of the cultural landscape, increasing human populations, variation of social habits and climate change. We have modelled the potential range changes for two thermophilic tick species (*Hyalomma marginatum* and *Rhipicephalus annulatus*) by use of MaxEnt® and 15 climatic predictors, taking into account the aptitude for future climatic change in Romania. Current models predict increased temperatures, both in the short term (up to 2050) and in the long term (up to 2070), together with possible changes also of the other climatic factors (e.g. precipitation), and may lead to higher zoonotic risks associated with an expansion of the range of the target species. Three different models were constructed (the present, 2050 and 2070) for four representative concentration pathways (RCPs) of greenhouse gas scenarios: RCP2.6, RCP4.5, RCP6, and RCP8.5. The most dramatic scenario (RCP8.5) produced the highest increase in the probable distribution range for both species. In concordance with similar continental-wide studies, both tick species displayed a shift of distribution towards previously cooler areas of Romania. In most scenarios, this would lead to wider ranges; from 9.7 to

43.1% for *H. marginatum*, and from 53.4 to 205.2% for *R. annulatus*. Although the developed models demonstrate a good predictive power, the issue of species ecology should also be considered.

Introduction

Ticks are blood-sucking arthropods considered to be the most important vectors of both human and animal disease in the temperate areas of Europe. Due to various factors, including changes of the cultural landscape, increasing human populations, variation of social habits and climate change, several zoonotic tick-borne diseases are emerging in Europe (Gray *et al.*, 2009). The distribution range of these ticks is influenced by complex interactions that include both biotic (the prevailing type of vegetation, host specificity, host community structure and abundance) and abiotic, climatic factors. Knowledge of tick ranges and their likely distribution changes are needed for the projection of future threats and this information is needed for the formulation of a suitable epidemiologic policy with respect to ticks (Campbell-Lendrum *et al.*, 2015). The distribution of the *Hyalomma marginatum* and *Rhipicephalus annulatus* ticks is mainly determined by the temperature and the availability of large animal hosts, particularly ruminants although the larval stages of *H. marginatum* also commonly feed on small homeotherms, e.g. birds [European Centre for Disease Prevention and Control (ECDC, 2015)]. Both tick species present a southern distribution in Europe with noted range expansions in the last few decades (Estrada-Peña *et al.*, 2012, 2013). Field data collections have shown that their distribution in Romania is influenced by temperature (the tick species under study have appeared in new, now warmer areas only at present). Currently, both species are mostly found in the southern and western regions of the country (Mihalca *et al.*, 2012). *H. marginatum* is considered to be the most important vector for the Crimean-Congo hemorrhagic fever virus in Europe and Asia (Hoogstraal, 1979; Ergonul and Whitehouse, 2007). In addition *Rickettsia aeschlimannii* has been detected in specimens collected from migratory birds in several European countries (Rumer *et al.*, 2011; Chochlakis *et al.*, 2012; Hornok *et al.*, 2013; Movila *et al.*, 2013; Tomassone *et al.*, 2013). A number of other viruses (Dhori, Bahig, Matruh) have also been found in *H. marginatum*, but its vectorial capacity for these viruses is not yet defined (Converse *et al.*, 1974; Moussa *et al.*, 1974; Filipe and Casals, 1979). The immature stages *H. marginatum* readily feed on migratory birds, while the adults prefer large herbivores, which makes the tick prone to be carried over large distances (Jameson *et al.*, 2012). *R. annulatus*, on the other hand, feeds specifically on cattle and is an important vector for economically important pathogens as *Babesia bigemina*, *B. bovis* and *Anaplasma marginale* (Walker *et al.*, 2000).

Current climate models predict a continuous increase in temperatures, both in the short term (up to 2050) and in the long term (up to

Correspondence: Attila D. Sándor, Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine, Cluj-Napoca, Calea Mănăstur 3-5, 400372 Cluj, Romania.
Tel. +40.264.596384 - Fax: +40.264.593792.
E-mail: attila.sandor@usamvcluj.ro

Key words: Climate change; Modelling; *Hyalomma marginatum*; *Rhipicephalus annulatus*; Romania.

Acknowledgements: the research was funded by POSDRU grant no. 159/1.5/S/136893 with title: *Parteneriat strategic pentru creșterea calității cercetării științifice din universitățile medicale prin acordarea de burse doctorale și postdoctorale – DocMed.Net_2.0*. The work of ADS was funded by PN-II-RU-TE-2014-4-1389, while ADM was beneficiary of UEFISCDI Grant PCE IDEI 236/2011. This paper was published under the frame of EurNegVec COST Action TD1303.

Received for publication: 10 October 2015.

Revision received: 21 January 2016.

Accepted for publication: 21 January 2016.

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Geospatial Health 2016; 11:421

doi:10.4081/gh.2016.421

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2070) (IPCC, 2007). Together with the potential change of other climatic factors, e.g. precipitations, this change could lead to a higher zoonotic risk as such climatic changes may support an expansion of the range of vectors under study (Williams *et al.*, 2015). We used the currently known distribution data (presence only) for the two tick species studied, first to model the present distribution, using available ecological data. Then, using the projected climate scenarios, the present models were expanded in order to fit the projected changes of environmental variables. To model the distribution we used the maximum entropy approach as described by Phillips *et al.* (2006), Porretta *et al.* (2013) and Signorini *et al.* (2014). We choose to model the impact of the perceived climate change on the distribution of *H. marginatum* and *R. annulatus*, both distributed in the warmer areas of southern and southeastern Romania (Mihalca *et al.*, 2012). All four available representative concentration pathways (RCPs) of climate scenarios: RCP2.6, RCP4.5, RCP6, and RCP8.5 (Weyant *et al.*, 2009) were used with both time periods (2050 and 2070). For this paper, we used the Community Climate System Model, version 4 (CCSM4) of climate change (Gent *et al.*, 2011). CCSM is a coupled climate model used to simulate Earth's climate system. It is composed of four separate models simultaneously simulating different components (atmosphere, ocean, land surface and sea/ice) and one central coupler component (that binds the different parts together).

Materials and Methods

Tick distributions

The tick distribution data used for this study were compiled from the published literature, downloaded from a freely accessible georeferenced database (<http://www.geo-parasite.org>) (Figure 1). The species selected (*H. marginatum* and *R. annulatus*) show a limited distribution in Romania, occurring principally in the South and the Southeast. Their distribution is likely limited by climatic factors as their main hosts (large herbivores for adults and rodents/birds for larvae and nymphs) are common and occur continuously all over the territory of Romania. The number of available records varied. The numbers of *H. marginatum* records were relatively high (n=171), while those of *R. annulatus* were much fewer (n=35). We attempted to develop models for both species even if there were comparatively low number of the latter.

Environmental data

The models were built using climatic data provided by the WorldClim database (<http://www.worldclim.org>), which are presented as high-resolution, interpolated rasters. We used the bioclimatic dataset to construct the current and future probable distribution for both species. Environmental data were downloaded from WorldClim database with the highest resolution provided (which is 30 arc-seconds, i.e. one pixel=0.6 km²). The bioclimatic variables, derived from the monthly temperature and rainfall values in order to give the most biologically meaningful variables (Table 1), were downloaded and processed. Since our aim was not to evaluate the contribution of each variable to the

Table 1. Variables used for creating the models.

Variable	<i>H. marginatum</i> (% contribution)	<i>R. annulatus</i> (% contribution)
BIO1	4.8	5.1
BIO3	1.7	0
BIO6	1.8	0.2
BIO8	0.5	0.3
BIO9	0.1	0.2
BIO10	11.7	1.2
BIO11	29.6	0.4
BIO12	6.4	0.1
BIO13	0.1	1.8
BIO14	2.3	0.1
BIO15	29.6	77.4
BIO16	0.8	1.2
BIO17	0.1	3.7
BIO18	3.9	8.3
BIO19	6.6	0.1

H. marginatum, *Hyalomma marginatum*; *R. annulatus*, *Rhipicephalus annulatus*; BIO1, annual mean temperature; BIO3, isothermality (BIO1/BIO7)*100; BIO6, minimum temperature of coldest period; BIO8, mean temperature of wettest quarter; BIO9, mean temperature of driest quarter; BIO10, mean temperature of warmest quarter; BIO11, mean temperature of coldest quarter; BIO12, annual precipitation; BIO13, precipitation of wettest period; BIO14, precipitation of driest period; BIO15, precipitation seasonality; BIO16, precipitation of wettest quarter; BIO17, precipitation of driest quarter; BIO18, precipitation of warmest quarter; BIO19, precipitation of coldest quarter.



Figure 1. Occurrence points for the modelled species in Romania: A) *Hyalomma marginatum*; B) *Rhipicephalus annulatus*.

model but to construct reliable, general models, we used all available variables. For the estimated future climate conditions we used the Community Climate System Model version 4 (CCSM4) (Gent *et al.*, 2011), for two different time periods: 2050 (average for the years 2041-2060) and 2070 (average for the years 2061-2080). The outcome of the four available greenhouse gas scenarios, *i.e.* RCP2.6, RCP4.5, RCP6 and RCP8.5 (Weyant *et al.*, 2009) was examined for each period. Thus, we had a succession of three different, probable distribution models for each scenario, *i.e.* for the present, for 2050 and for 2070.

Modelling methods deployed

The MaxEnt software (<https://www.cs.princeton.edu/~schapire/max-ent/>) was used since it has been found to perform better than many other modelling methods (Phillips *et al.*, 2006; Porretta *et al.*, 2013). This technique utilizes presence-only records to estimate the potential distribution of the species based on the environmental variables and presents the results as a probability distribution (Phillips *et al.*, 2006).

Present and projected future probable distributions for the two target species were built with the presence data for the tick species in question and the climatic variables using a maximum entropy algorithm. We used 75% of the occurrence points to construct the model (training data) and the remaining 25% to test it (Pearson *et al.* 2007; Nenzén and Araújo, 2013; Pedersen *et al.*, 2014). In our case, the MaxEnt model output was logistic, which provided an estimated relative probability of presence for any given location ranging from 0 to 1, where 0 signifies a very low probability of species presence and 1 a very high relative probability (Phillips *et al.*, 2006; Signorini *et al.*, 2014). For all the runs, the default parameters of MaxEnt were used.

To evaluate the accuracy of the developed models, we used the area under the curve (AUC) of the receiver operating characteristic (ROC) provided by MaxEnt (Peterson *et al.*, 2007; Porretta *et al.*, 2013). To calculate the future increase of the distribution area in respect to the present model, presence/absence maps using the minimum training

presence threshold were constructed using two geographical information systems (GIS) tools for analysis and management: QGIS (free software, <https://www.qgis.org/>) and SAGA (free software, <http://www.saga-gis.org/>). Differences in future distribution were calculated as percentages of the current distribution. Supplementary, the contribution of each environmental variable to the model, was calculated for both tick species under study (Table 1). These percentages have only informative value, since the highly correlated variable pairs were not accounted for. The raster data were processed and analyzed using the SAGA and QGIS softwares. The models were fitted using MaxEnt software. The final distribution maps were constructed using ArcGIS (ESRI, Redlands, CA, USA).

Results

Out of the four greenhouse gas scenarios, the highest degree of potential distribution change of range for both tick species was the most dramatic scenario (RCP8.5) both for 2050 and 2070 (range expansion and range shift in case of 2050 and mainly range shift in case of 2070). For *H. marginatum*, the AUC value was 0.880 indicating a good performance for our model. As reference for the calculation of the climatically suitable distribution area, the minimum training presence threshold provided by the model was 0.084. The variation of the climatically suitable distribution area for *H. marginatum* predicted by the model is presented in Table 2. The net area is given in km² and the difference from the present conditions as a percentage of the present area. The maps for the climatically suitable distribution areas predicted by our model (Figure 2) show an expansion of the range towards the northern and central parts of Romania. The most dramatic increase of the area was in case of RCP 8.5, for the time period 2050. However, the area decreased in the 2070 period in this scenario. Although the expan-

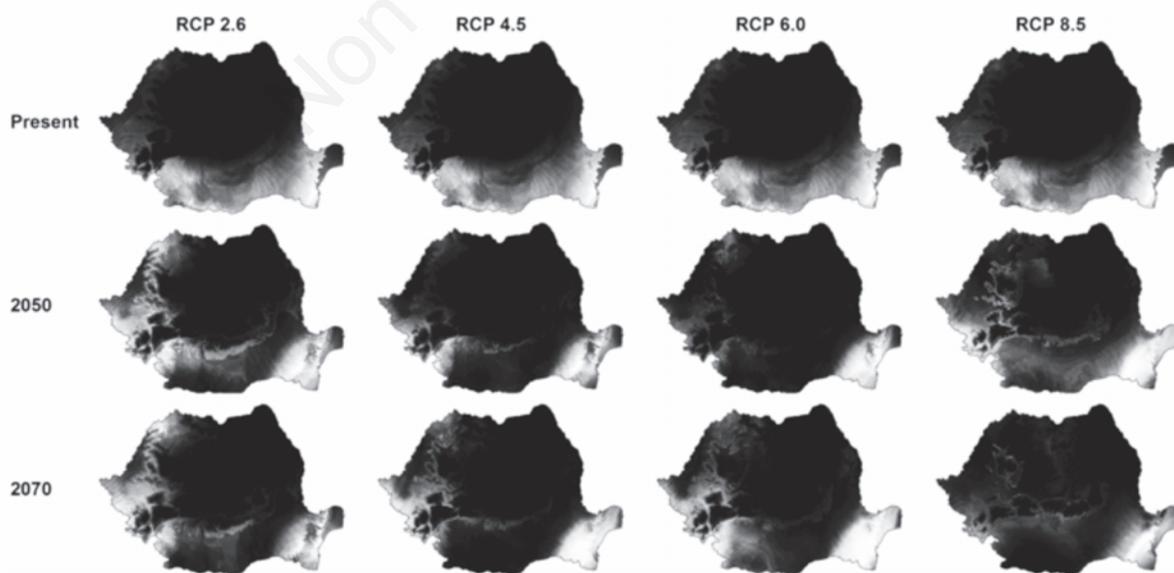


Figure 2. Maps of the distribution of *Hyalomma marginatum* in Romania according to the model. Probability of occurrence from close to 0 (black) to close to 1 (white).

sion of the area continued into the northern parts of Romania (Figure 2), the decrease was due to the fact that some areas in the southern part would become unsuitable in this scenario.

In the case of *R. annulatus*, the average value for AUC was 0.970, indicating a good performance for our model. As a reference, to calculate the climatically suitable distribution area, the minimum training presence threshold provided by the model was 0.053. The variation of the climatically suitable distribution area for *R. annulatus* predicted by the model is presented in Table 3. The net area is given in km² and the difference from the present conditions as a percentage of the present area.

The maps for the climatically suitable distribution areas, predicted by our model are shown in Figure 3. Also in case of this species, the most dramatic increase in the suitable area was in relation to RCP 8.5, both for 2050 and 2070 (there was no similar pattern with *H. marginata*-

tum, most of the southern areas remained suitable). There was an expansion of the range towards the southern and western parts of Romania for all models (but not to the central region, as in case of *R. annulatus*).

The MaxEnt software provides also an analysis regarding the contribution of each variable used for the construction of the model. Because we did not eliminate the highly correlated values, the results must be treated cautiously. For *H. marginatum* the most important variables were the mean temperature of the coldest quarter (28.6%) and the precipitation seasonality (24.4%) (Table 1). For *R. annulatus*, the most important variable was the precipitation of the warmest quarter (69.9%), followed by the precipitation of driest month (7.8%). There was also a difference in the distribution of variable contribution for the two species. Since the share of the variables was more evenly distributed for *H. marginatum* than in the case of *R. annulatus* where one

Table 2. The potential variation of the climatically suitable distribution area for *Hyalomma marginatum*.

Scenario	Present range (km ²)	Range in 2050 (km ²)	Change in 2050 (%)	Range in 2070 (km ²)	Change in 2070 (%)
RCP 2.6	97,992	134,823	37.6	131,554	34.2
RCP 4.5	97,992	107,465	9.7	126,716	29.3
RCP 6.0	97,992	91,181	-7.0	131,752	34.5
RCP 8.5	97,992	140,250	43.1	112,630	14.9

RCP, representative concentration pathway.

Table 3. The potential variation of the climatically suitable distribution area for *Rhipicephalus annulatus*.

Scenario	Present range (km ²)	Range in 2050 (km ²)	Change in 2050 (%)	Range in 2070 (km ²)	Change in 2070 (%)
RCP 2.6	28,181	43,236	53.4	31,145	10.5
RCP 4.5	28,181	50,481	79.1	43,517	54.4
RCP 6.0	28,181	27,835	-1.2	46,046	63.4
RCP 8.5	28,181	86,023	205.2	94,289	234.6

RCP, representative concentration pathway.

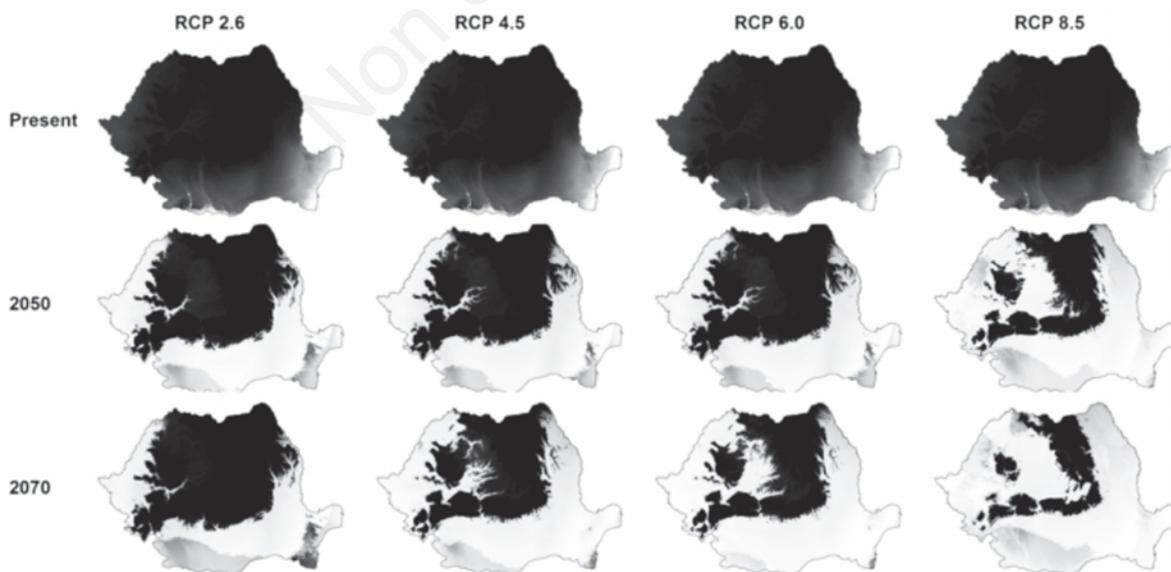


Figure 3. Maps of the distribution of *Rhipicephalus annulatus* according to the model. Probability of occurrence from close to 0 (black) to close to 1 (white).

variable (BIO18=precipitation of the warmest quarter) contributed more than 69%.

Discussion

Modelling the future distribution of animal organisms based on climate envelopes is useful for up-to-date studies of climate change adaptations and is often used for the formulation of epidemiologic policies (Pindyck, 2013). Predicting the geographical range changes caused by climate changes has become an important tool for nature conservation (Parmesan *et al.*, 2013), for developing climate-resilient agriculture practices (Howden *et al.*, 2007) or for health-related policies (Wardrop *et al.*, 2013). Range changes have been modelled from global to local scales for parasites and other infectious diseases (Khormi and Kumar, 2014; Lafaye *et al.*, 2013). Tick distribution studies are at the forefront of climate-related distribution modelling, with models built for global and regional distributions, *e.g.* for *H. marginatum* (Estrada-Peña *et al.*, 2012) and *R. annulatus* (Williams *et al.*, 2015), while there are no models built at the national scale.

This paper presents the first approach in Romania to model future distribution maps for tick species in the light of future climate scenarios. Our purpose was to predict the expansion of the risk zones for two thermophilic tick species in Romania using the predicted models based on the most up-to-date climate scenarios. Given the values for AUC provided by MaxEnt, our models demonstrate as good a predictive power that has been shown by other authors (Phillips *et al.*, 2006, Porretta *et al.*, 2013; Signorini *et al.*, 2014).

The general trend of areal expansion toward previously cooler zones is in line with other similar studies on different tick species (*Ixodes ricinus*, *I. scapularis*, *R. sanguineus*), both in Europe and North America (Ogden *et al.*, 2006; Gray *et al.*, 2009; Porretta *et al.*, 2013). In the case of *H. marginatum*, one of the clusters of its distribution extends from the Balkans (in the North) toward Turkey and Middle East. Analyses of the climate ecological niche for this species indicate a temperature-related limiting factor (Estrada-Peña, 2008).

The increase in temperature, which is predicted to occur in the near future (IPCC, 2007) is likely to affect the ecology and geographic distribution of many organisms, including ticks. In the case of *H. marginatum*, the most important climatic variables proved to be the mean temperature of the coldest quarter and the seasonality of precipitation (Estrada-Peña *et al.*, 2012). For all scenarios studied, we foresee an increase in the potential distribution areas of both *H. marginatum* and *R. annulatus*. The general trend of increase is more prominent in the northern and central parts of the country. The RCP 2.6 scenario predicted around 16% increase in the area for 2050, which would rise to 28% by 2070. An interesting evolution is shown in case of RCP 8.5: after a large increase projected for 2050, a decrease was noticed with respect to the extent of suitable areas for the year 2070. The explanation is that although we may observe an expansion of species range towards the north and centre, previously suitable areas in the south become unsuitable in the projected climate conditions. Hence, the net expanse of suitable areas should decrease by almost 30%. Furthermore, the tick vulnerability to drought according the Emergency Food Security Assessment - EFSA (2010) could have a negative effect on the species in southernmost part of its present range of distribution in Romania (as seen in our case in the 2070 / RCP 8.5 scenario).

In case of *R. annulatus*, the seasonality of precipitation was found to be the most important variable, which contributed massively to the model (more than 69%). Regarding the evolution of the distribution

range, the pattern is relatively similar. The general trend of area increase is shown to be more prominent in the southern and western parts of the country. All the scenarios predict a general increase. The most conservative one (RCP 2.6), however, predict a relative decrease in 2070 (still a net increase compared to the present), while the most dramatic increase (with around 40%) is predicted by the RCP 8.5 scenario both for 2050 and for 2070. In the latter case, the general pattern for *R. annulatus* was the expansion of the suitable distribution area combined with a levelling of the probability of occurrence throughout the range.

Having more data available usually increases the performance of species distribution modelling and also allows more data to be used for testing (hence better reliability for the predictions) (Phillips *et al.*, 2006). The lower number of data available with regard to *R. annulatus* may limit the significance of the conclusions for the species. Although the model performance in this case was high (AUC=0.970) due to the fact that most distribution records shared a homogenous set of climatic characteristics, this is not a global rule but an exception caused by high similarity of records in Romania.

Conclusions

The modelling of the geographical distribution patterns of vector species in ecological space, using presence data, maximum entropy approach and GIS tools, based on climatic and environmental data, is a useful tool for the understanding of the ecological requirements of the vectors, and hence the vectored pathogens. While vector pathogens require the presence of suitable reservoir hosts too, the assessment of their epidemiologic impact could not be decoupled from the geographic distribution of their vectors. Both studied species display a shift of their distribution towards presently cooler areas of Romania, in concordance with similar continental wide studies. Although the developed models demonstrate a good predictive power, the issue of species ecology should also be considered. The selected species, as well as all other ixodid ticks, depend for parts of their life on the availability of suitable hosts, so the climate is only one essential determinant of their occurrence. As the climate change will very likely affect the hosts as well, this in turn can affect the tick species distribution.

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