Potential geographic distribution of *Rhipicephalus sanguineus* sensu lato in Tunisia: review and modelling

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Abstract

Rhipicephalus sanguineus sensu lato (*R. sanguineus* s.l.) is an important group of ticks that infest a large panel of animals' species and are vectors of multiple pathogens of medical and veterinary importance. As the biology of ticks is driven by abiotic factors, mainly temperature and humidity, climate changes are incriminated in increasing ticks and tick-borne pathogens incidence. The aim of this study was to map the current potential geographic distribution of *R. sanguineus* s.l. in Tunisia to help anticipating control measures to prevent tick-borne pathogens transmitted by these ticks. Extracted *R. sanguineus* s.l. occurrence records from the literature and a field survey across Tunisia were combined with environmental predictors using the maximum-entropy (MaxEnt) approach. The higher habitat suitability is expected for *R. sanguineus* s.l. along the coasts of Tunisia than in the

internal regions, in particular in the north-east and the north-west of the country. Nevertheless, suitability reaches the lowest level in the plateau of Kasserine district, center west. The probability of *R. sanguineus* s.l. occurrence is positively correlated to the mean temperature of the coldest quarter and the mean specific humidity of the least humid quarter. The Mediterranean climate which is prevalent in north and coastal Tunisian regions is favorable to *R. sanguineus* s.l. occurrence, while the harsh conditions of the southern and the central-west region is unfavorable for the presence of this tick. Getting a detailed view of *R. sanguineus* s.l. potential distribution is of paramount importance for public health and veterinary decision makers to implement adequate control measures in the present.

1 INTRODUCTION

Ixodid ticks are considered as the second most important disease vector to both humans and animals after mosquitos (1). Globally, their geographic distribution continues to expand inducing an increase in the tick-borne pathogens in both tropical and temperate regions nowadays (2). The main cause of this expansion is climate changes, which is affecting more severely the Northern rather than the Southern hemisphere (3). Mediterranean regions are considered as hotspots of climatic extremes with increased precipitation and drought in winter and summer, respectively (4). As a consequence of such climatic changes, it was shown that the geographic distribution of some tick species will increase in the Mediterranean countries in 2050 (5).

Depending on the geographic region, multiple tick species are threatening animal and human health, among them, *R. sanguineus* sensu lato (s.l.) is an important group of tick species including *R. sanguineus* sensu stricto (s.s.) which is considered as the most important tick species worldwide (6).

The *R. sanguineus* s.l. infest large panel of both domestic animals, including dogs, livestock (cattle, sheep and goats), and wild species, such as reptiles, insectivores and rodents (7). *Rhipicephalus sanguineus* s.l. are vectors of multiple pathogens such as *Ehrlichia canis*, *Anaplasma platys*, *Bartonella henselea*, *Mycoplasma canis*, *Mycoplasma ovis*, *Rickettsia rickettsii*, *R. conorii* and several *Babesia* species (1). Based on their geographic distribution, two main genetic lineages are described within this tick group: the tropical lineage, which comprises ticks from tropical countries such as Thailand and Brazil; and the temperate lineage, encompassing ticks from Spain, France and Italy (8,9).

Although *R. sanguineus* s.s. natural habitat is more commonly associated with the Mediterranean region, where it is active from spring to autumn (10), it was shown that the suitable area for its reproduction has dramatically expanded in Europe by 66% between 1960 and 2000 (11), with a marked expansion to the northern regions. Indeed, its geographic range extended to UK (12) and Slovakia (13), where it was reported for the first time in 2014 and 2017, respectively.

As the biology of ticks is driven by both biotic and abiotic factors (mainly temperature and humidity), mathematical models combining field, spatial and climatic data were shown to be good predictors of tick and tick-borne pathogens geographic distribution (14). Predicting the risk of tick infestation may improve the implementation of tick control by both animal and human health decision makers, and also by farmers (15).

Several methodologies were developed to estimate distributional areas on the basis of correlations on known occurrences with environmental variables (16). Ecological niche modelling (ENM) and species distribution modelling (SDM), have been were extensively used in the last 20 years to understand geographic distribution and mapping of disease vectors (17). While SDM focuses on the actual distribution of the species, the ENM involves more the estimation of invasive potential niche or assessment of environmental effects changes on species distribution potential (18).

Among the tools deployed for ENM, the maximum-entropy (MaxEnt) approach has a predictive performance considered as consistently competitive with the highest performing methods (19). Available since 2004, MaxEnt has been widely used in recent years for predicting the potential geographic distribution of several tick species under current and future conditions using different climate changes scenarios in several regions around the world (20–23).

Climate change is incriminated in increasing ticks and tick-borne pathogens incidence (24). As Tunisia is situated in a hotspot region for climate change (25), it's expected that ticks will shift their geographic distribution in the near future inducing an important modification of the epidemiological patterns of tick-borne diseases.

In Tunisia, *R. sanguineus* s.l. infest a wide range of animal species and transmit several pathogens of public health and veterinary (26–28) importance (29). As the geographic distribution of these ticks was not well documented in Tunisia, the aim of this study was to map their potential geographic distribution under current conditions. This work will provide a guide on the suitable geographic areas for *R. sanguineus* s.l., and help anticipating control measures to prevent pathogens transmitted by these tick species.

2 MATERIALS AND METHODS

2.1 Study Area

Tunisia, is located in North Africa, and is situated at the south of the Mediterranean basin with 1,445 km long coast that extends from the extreme north-west to the south-east.

The climate in Tunisia consists of three Köppen-Grieg patterns (30) (Figure 1). The northern, mountainous (maximum altitude 1203 meter above the sea level) and forestall region is characterized by a Mediterranean climate with mild, rainy winters and hot, dry summers, where the average annual precipitation reaches 1,500 mm. During winter, the temperature can decrease to 10°C in the Kroumirie Mountains (Districts of Jendouba, Béja and Bizerte).

The south is occupied by the desert, with an average summer temperature in July and August reaching 40°C and precipitations in winter below 100 mm (31). The eastern coastal border has an arid steppe climate where temperature ranges from 10°C in winter (December to February) to 27°C in summer (June-August) in northern part. In central western regions, temperature ranges from 11°C in winter to 32°C in summer, drought can be frequent (32).

FIGURE 1. Köppen-Geiger climate classification map for Tunisia (1980-2016) at 1 km resolution (30)

2.2 Tick Collection and Identification

Between April 2018 and January 2020 repeated cross-sectional trimestral visits were performed to 15 small and extensively managed sheep flocks randomly selected from six Tunisian localities. A total of 459 ear-tagged yearling and ewes were monitored. Sheep are reared in mixed flocks with goats, cows, mules and dogs, and graze all the year-round on natural range-lands and cereal stubbles in summer. This survey was part of a large study on ticks and tick-borne pathogens in sheep in Tunisia.

During each visit, animals were clinically examined and all attached ticks were collected and stored in identified tubes (one tube per animal) containing 70% ethanol. Ticks were identified under a stereomicroscope according to the key of Walker et al. (33).

As mentioned by Nava et al. (34), studies on several specimens from the *R. sanguineus* complex, showed that they are morphologically and genetically very close, suggesting that 12 *Rhipicephalus* species could be considered as conspecific. For this reason, we pooled the three *Rhipicephalus* ticks found in Tunisia (*R. turanicus*, *R. camicasi*, and *R. sanguineus* sensu stricto), as *R. sanguineus* s.l.

2.3 *Rhipicephalus sanguineus* s.l. Data Sources and Data Preparation

2.3.1.1 Data sources

A total number of 16 peer-reviewed articles from PubMed database and 8 Tunisian doctor in veterinary medicine dissertations were reviewed from the Database of ticks in livestock species in Tunisia website (35) (Supplementary Material D). This database is managed by the International Center for Agricultural Research in the Dry Areas (ICARDA) and the National School of Veterinary Medicine of Sidi Thabet, Tunisia, it contains an exhaustive literature about ticks and tick-borne pathogens in Tunisia published since 1935. Additional records were included from the database published as supplementary material by Estrada-Peña and de la Fuente (36) to get totally 103 records (Table 1).

TABLE 1. *Rhipicephalus sanguineus* s.l. occurrence number and sources

2.3.2 Literature Selection

2.3.2.1 Inclusion criteria

All studies reporting *R. sanguineus* s.s., *R. camicasi*, *R. turanicus* the only species from the *R. sanguineus* s.l. present in Tunisia and collected from different host species (cattle, sheep, goats, and dogs) were selected. The included studies must indicate the geographic coordinates (latitude and longitude) of the sampled farms or at least the correct name of the smallest Tunisian administrative subdivision (it corresponds to village called in Tunisian Arabic “imada”).

2.3.2.2 Exclusion criteria

All the studies where not indicating one of the following information were excluded: GPS coordinates, a clear indication about the location name of the sampled farms or animals.

2.3.3 Occurrence Data Preparation

Each tick occurrence record was defined by its geographic coordinates (longitude and latitude in decimal degrees). From the selected documents, coordinates corresponding to *R. sanguineus* s.l. occurrence were extracted and checked in Google Earth (www.google.com) according to the recommendations of Hijman (37). For occurrences without georeferencing, the centroid coordinates of the smallest administrative subdivision of the mentioned locality was considered. As different published studies mentioned the same localities, all duplicated coordinates were considered once. The extracted records from the data of Estrada-Peña and de la Fuente (36), were combined with the retrieved data from the Database of ticks in livestock species in Tunisia website and those of the present field records by resulting in a total of 87 eligible records (Figure 2) (Supplementary Material E).

FIGURE 2. Map of Tunisia showing the location of *Rhipicephalus sanguineus* s.l. collection sites.

Circles: localities of the field work

Triangles: metadata derivative localities

Red polygon: calibration (M) area

To avoid model bias and overfitting resulting from spatial autocorrelation (38), we thinned the 87 records using a spatial distance filter of 15 km (spTthin package) (39). Several iterations on R using increasing thinning distance were tested. The 15 km filter distance was selected as the best in terms of having a good number of occurrence points to run the models.

Finally, a total of 45 occurrence points was used to model *R. sanguineus* s.l. potential distribution over Tunisia. The data was divided randomly into two sets: 50% for model calibration and 50% for model evaluation. Then, the full set of data was used for creating the final models (40).

2.3.4 Climatic Variables Selection and Preparation, and Calibration Area Definition

The effect of climate on tick distribution was well described in the literature, where temperature and humidity were identified to play a major role (10). Indeed, engorged larvae and nymphs enter in diapause phase at low temperatures whereas the molting period is shorter at higher temperatures (41). Thus, heat, humidity, and moisture are very important factors of tick survival and dispersion (42).

To prevent final models from bias, the accessible area (termed **M**) of the studied species is to be considered during tick modelling (43). This area describes the dispersal capacities of the tick species from established populations, by either their own movements or by the host-mediated movements (44). Assuming the latter play a key role in dispersing *R. sanguineus* s.l., the **M** area (study area, or calibration area) was delimited based on a 50 km buffer zone around the available occurrence points and used in model calibration (Figure 2). As far as it could be ascertained, there is no publication indicating the distance to be used for the calibration area, thus we performed several iterations on QGIS using increasing calibration area radius. The best calibration area was 50 km since it covers the whole country and we considered that this radius covers the distance reached by different mammal hosts.

Among the 19 bioclimatic variables, fourteen were removed for the following considerations:

(i) Variables with known spatial artefacts were removed (Bio8, Bio9, Bio18, and Bio19) (Bede-Fazekas and Somodi. 2020).
(ii) Variables expressing annual mean values (Bio1 and Bio12) were removed because the range of temperature between summer and winter in Tunisia is big.
(iii) Variables of extreme values (Bio5, Bio6, Bio13, and Bio14) were removed because activity of ticks is not conditioned by these extreme values which represent peaks and are not persistent in time.
(iv) Due to high correlation, variable expressed as a synthetic indicator of other bioclimatic variables (Bio3) was removed.
(v) Variables expressing seasonality (Bio4, and Bio15) were removed since they provide information about the whole season.

Five variables were considered in modelling; three related to temperature (BIO2, BIO10 and BIO11) and two related to humidity (BIO16 and BIO17) (Table 2). This set of five bioclimatic variables were retrieved from MERRAclim dataset (45), which contains three different version of the same 19 bioclimatic variables corresponding to the last three decades (1980s, 1990s and 2000s), presented as minimum, maximum and mean values, and available at three resolutions (2.5, 5 and 10 arc-minutes) (45). Contrarily to the commonly used Worldclim dataset (www.worldclim.org), whose variables derive from spatially interpolated climate surfaces as obtained from ground weather stations, MERRAclim uses satellite-based observations (46).

To match our sampling dates (extending from 1999 to 2016) with climatic information, the dataset for the 2000 decade was considered at 2.5 arc-minutes resolution corresponding to approximately 4 km. The predictors were masked to the **M** area, then combined to generate five candidate sets to improve model calibration, with one predictor removed in each dataset except the set 1 (Table 2). Indeed, using various candidate sets of predictors improves the model calibration (40).

TABLE 2. Predictors used in the maximum entropy for *Rhipicephalus sanguineus* sensu lato modelling (46)

2.4 *Rhipicephalus Sanguineus* sensu lato Distribution Modelling

2.4.1 Ecological Niche Modelling

We used maximum entropy (MaxEnt) that is implemented in MaxEnt (49). All implementation was performed with R software, using the “kuenm” package (50). By combining R and MaxEnt softwares, the “kuenm” package allows model calibration, final model selection, evaluation and extrapolation risk analysis through a simple processing (40).

Here, the ODMAP protocol was used to document all the key steps for producing the final model ((51); Supplementary material A).

2.4.2 Model Calibration

For model calibration, we tested 15 combinations among linear (l), quadratic (q), product (p), and hinge (h) features and 17 regularization multiplier values (Supplementary materials B). In turn, each feature-regularization multiplier combination was tested separately for each environmental dataset. Candidate models were tested and evaluated based on the statistical significance of the partial receiver operating characteristic (ROC) at $\alpha < 0.05$ (52) and omission rate ($E < 5\%$) thresholds (38). Finally, among significant, low-omission models, we estimated the Akaike Information Criterion corrected for small sampling sizes (AICc) (53) and delta AICc (ΔAICc). We retained 7 models as the best candidates (ΔAICc < 2) to be included for modelling the potential geographic distribution of *R. sanguineus* s.l. in Tunisia (Figure 3).

FIGURE 3. Calibration result and best selected models used for modelling the potential geographic distribution of *Rhipicephalus sanguineus* s.l. in Tunisia

2.4.3 Final Models

Seven models were finally retained having ΔAICc<2 to model the potential geographic distribution of *R. sanguineus* s.l. in Tunisia (Figure 3). For each final model, we used a 50% bootstrap with 10 replicates to quantify the uncertainty associated with the available occurrence data, and transferred the model prediction throughout the whole study area. In particular, the geographic representation of the final models was obtained by using the median value of the relative occurrence rate (ROR) among the bootstrapped replicates from each spatial unit (40).

An extrapolation process was necessary to predict the potential geographic distribution of *R. sanguineus* s.l. outside the calibration area. To this aim, we used ‘free extrapolation’ by assuming the species-environment relationship as observed within the calibration area to remain constant outside the calibration area itself (54).

3 RESULTS

3.1 Calibration models

From total of 2,635 candidate models, 1,948 were statistically significant ($P \leq 0.05$). Seven were identified as the best models based on their AICc (ΔAICc<2), but none of them met the omission rate criteria (OR ≤ 0.05; Table 3). All best models were characterized by the "product" feature class accounting for interaction among the predictors. One of the seven models was selected based on variables in Set 1, while the remaining models were chosen based on variables in Set 5 (Table 2).

TABLE 3. Best models after model calibration

In the seven retained models, three variables (Bio2, Bio11, and Bio17) were positively correlated with tick occurrence probability in the study area (Figure 4).

FIGURE 4: Mean responses of *Rhipicephalus sanguineus* s.l. to the Bio2, Bio10, Bio11, Bio16, and Bio17 predictors in the 7 models after 10 replicates

3.2 Current potential distribution

Current predictions for *R. sanguineus* s.l. showed higher suitability along the coasts of Tunisia than in the internal regions. In particular, higher suitability was observed in the north-east and north-west of the country specially in two districts (Jendouba and Nabeul) and two islands (Kerkennah and Djerba), respectively. Low suitability areas were observed as the distance increased from the coastal areas inside to Central and West Tunisia, in which reaching the lowest level in Kasserine district (Figure 5).

FIGURE 5. Potential distribution of *Rhipicephalus sanguineus* s.l. in Tunisia based on MaxEnt modelling (Black dots corresponds to districts)

4 DISCUSSION

The present study aimed, for the first time, to model the current potential geographic distribution of *R. sanguineus* s.l. ticks, using MERRAclim variables. When compared to other algorithms applied to species distribution modelling (e.g. generalized linear models and generalized additive models), MaxEnt was the best for tick distribution modelling (20). Indeed, since its development in 2004, MaxEnt was improved markedly by adding several options (55,56). We performed the most up-to-date MaxEnt methodology in ecological niche modelling using the kuenm R package (40), which allows model calibration and selection, final model creation, and evaluation in a unified way from within the open source R environment. The candidate model performances are evaluated based on the significance of partial ROC, which is better than the full area under the ROC curve (52,57,58).

Models' performance was also evaluated by estimating the omission rate, which denotes how well a model based on the training data is able to predict the occurrences in the testing dataset. The fact that all final models showed 8.7% omission rate (a value slightly higher than the selected 5% threshold) could be due to the low number of occurrences in the training data (n=22), but does not compromise the good performance of the models. Indeed, we believe that our model is performant, also because we used remotely sensed predictors (eg. MerraClim) that allows better model performance than interpolated ground derived measurements (eg. Worldclim) as argued by Estrada-Peña et al. (14,59). However, considering that MaxEnt algorithm is performant to manage collinearity (48) we did not remove predictors with multicollinearity and having ecological significance to *R. sanguineus*, which potentially could hamper the analysis.

Although animal hosts play an important role in geographic distribution of ticks, we did not consider this factor because *R. sanguineus* s.l. species could be collected from a wide range of animal hosts, moreover, data regarding the geographic distribution of different domestic mammals are not available in Tunisia. This omission represents a limitation in the present work. Moreover, there is possibly a sampling bias due to using occurrence data with different sampling strategies and efforts, which could hamper the performances of modelling (60).

Assuming that *R. sanguineus* s.l. species behave equally to climatic variables, could possibly introduce another limitation to the present study. It was not possible to consider this aspect in the discussion because of the scarcity of data gathered through natural or experimental observations regarding the effect of temperature and humidity on *R. sanguineus* species other than *R. sanguineus* s.s. The difficulty of considering separately the behavior of *R. sanguineus* s.l. species may impact also the accessible area (M) determination which already suffers from the lack of objective criteria and detailed protocol for its estimation. Moreover, personal observation of one of the co-authors showed that in Southern Tunisia, there are probably a wild population of *R. sanguineus* linked to desertic wild animals (foxes, rodents…). This *R. sanguineus* wild population displays a different biological natural cycle than does the domestic population. This observation needs further investigations at the field. In addition, there are two reported lineages for *R. sanguineus* s.l. in the world depending on the geographic regions. Indeed, *R. sanguineus* s.l. temperate lineage is present in areas where the land surface temperature ranges between 10 and 20°C (9,61). Whereas, the tropical lineage of these ticks is more adapted to a higher land surface temperature, ranging between 20 and 30°C (9). Although there is no information about the type of lineage present in Tunisia, it seems that it's more likely to be a temperate lineage as in Spain, France and Italy (62).

In the present study, we estimated *R. sanguineus* s.l. potential geographic distribution in Tunisia, the coastal regions, showed the highest suitability. These areas have a temperate climate, according to the classification of Köppen-Geiger (30). Furthermore, high habitat suitability is also predicted in both Kerkennah archipelago and Djerba island despite their Köppen-Geiger classification as arid and desertic, respectively, possibly due to the tempered effect of sea in these islands (30). These islands are small in area (the maximum radius does not exceed 18 km for Djerba island), so they benefit of the moderation effect of the sea on both temperature and humidity. The geographic distribution we mapped overlays to the results obtained by Estarda-Penã and Venzal (63), and Alkishe et al. (23) for *R. turanicus* and *R. sanguineus* s.l., respectively, showing a high suitability of both of these ticks to northern and central-east coastal regions of Tunisia.

The high suitability of *R. sanguineus* s.l. in coastal region is concordant with the finding of Beugnet et al. (2009) for *R. sanguineus* s.s., where a weather research and forecasting (WRF) meteorological model was used and showed that the best combination of temperature and humidity was 20-30°C and 50-100%, respectively for *R. sanguineus* s.s. in terms of ability to attach to hosts, take blood meals and reproduce (activity index). The same model also evidenced how the combination of higher temperatures (30-35°C) and humidity (above 60%) leads to a lower activity index that varies between 60 and 80% (15).

The very low to low suitability in the central-western regions of Tunisia (Kasserine and Gafsa districts) could be explained by the big distance to the sea leading to unsuitable climatic conditions in addition to the limiting effect exercised by the variable Bio11 (mean temperature in the coldest quarter of the year), which appears to be among the main ecological variables driving habitat suitability for *R. sanguineus* s.l. in Tunisia. In this region the dry period is very long, it extends from April to September with high summer temperatures during long periods (reaching 43°C in August) and long cold periods in winter (reaching -4°C in January) (64,65). Based on our filed survey from April 2018 to January 2020, no tick was found in Sebeitla (Kasserine district) during two winter seasons (January 2019 and January 2020) (Supplementary Material C), where the mean temperatures recorded in both periods, ranged between 8 and 10°C, respectively (66). These temperatures are below the theoretical minimal threshold necessary to the tick to initiate molting, which is estimated to 10.8 and 13.9°C for *R. sanguineus* s.s. larvae and nymphs, respectively (67). Such a limiting factor for ticks' development could have been grasped by Bio11, whose mean response curve indicates increased habitat suitability when mean temperature exceeds 14°C. This behavior is consistent with the ecology of the species where the long-term low temperature is the major limiting factor for the establishment of *R. sanguineus* population in cold regions (68).

In Southern Italy, where the climate is similar to northern Tunisia, *R. sanguineus* s.s., is influenced by the Mediterranean climate in natural conditions but behaves differently in spring, summer and autumn (10). It was observed that the number of eggs laid by female ticks is positively correlated with humidity and negatively correlated to temperature during spring, which indicates the vital role of relative humidity when associated to high temperature. This situation is similar to what we see in Northern and coastal Tunisian regions, where *R. sanguineus* activity starts in spring and continues during the summer (69). Indeed, the north-west is characterized by a maximal temperature below 35°C in August, tempered by the proximity to the sea and the rain during the winter. However, in Southern Tunisia, during the same period, the maximum temperature reaches 45.8°C (Tataouine district), combined with a low relative humidity, decreases the suitability for *R. sanguineus*. The harsh climate in Southern Tunisia, is concordant with the scarcity of *R. sanguineus* s.l. in this region, confirmed by the absence of ticks in July 2018, during our field survey. Nevertheless, in July 2019, we collected in the same region 40 specimens of *R. sanguineus* s.l. from 19 sheep probably due to the particular climate of 2019, that was cold and relatively rainy in winter and spring, associated to a hot summer classified as the third hottest one since 1950 (66). Despite the low suitability in Tataouine district, the presence of *R. sanguineus* s.l. could be also explained by the behavior of these tick species. *R. sanguineus* withstands the low relative humidity rates (67,70) and on the other hand, *R. sanguineus* free stages have both endophilic and exophilic behaviour, they hide in refuges, under stones and wall crevasses when temperatures increases (71).

Other factors than temperature and humidity, can determine *R. sanguineus* s.l. distribution such as host availability and abundance. In the review by Estrada-Peña et al. (7), multiple animal species are reported to serve as host for *R. sanguineus* s.l. Indeed, among the 478 *R. sanguineus* s.l. collected in the western Palearctic and recovered between 1975 and 2010, 37% were represented by carnivores, 35% by insectivores, 24% by rodents, 13% by sheep, and 12% by equids. In our case, no accurate data on the distribution of the major host species in Tunisia was available and no information related to hosts could be included into the model we built. Furthermore, the extent of urban area was identified as a key factor for *R. sanguineus* s.l. distribution in China, which could be possibly associated with the presence of dogs (72).

5 CONCLUSIONS

Getting a detailed pattern of *R. sanguineus* s.l. geographical distribution is of paramount importance for public and animal health point of view in order to implement adequate control measures in the present and to identify new areas of expansion under different climate change scenarios. Indeed, due to global warming, the geographic distribution of *R. sanguineus* is extending to new regions. This extension was reported in northern Europe and southern America (13,73,74).

The high adaptative capacity of *R. sanguineus* to different biotopes and its vector role increase the importance of studying its geographic distribution. The dual endophilic and exophilic behaviour of *R. sanguineus* makes their survival possible in large range of environmental conditions, excepting in very cold regions.

Species distribution modelling showed its efficacy to predict *Rhipicephalus* spp. potential distributions both under current and future abiotic conditions in several regions of the world including Africa (75). However, spatial predictions from such models must be validated by field observations, which is often hampered by the paucity of the collected data mainly in developing countries. As many limitations (tick collection efforts, sampling bias, accuracy of occurrence records…) could affect modelling performance, interpretation should be made carefully to avoid misunderstanding of such models. To circumvent this limit, we strongly encourage the creation of a regional network for tick and tick-borne pathogens monitoring in North Africa with an online free database. In this system, new tick records should be always georeferenced and climatic data collected with optimal resolution (76). Citizen science should be encouraged through different channels (direct reporting, GSM transmission…) to improve the knowledge about different tick species phenology mainly in remote African regions (Sahara, Savannah…).

6 CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

7 AUTHOR CONTRIBUTIONS

MKK participated to field investigation, to data curation and to modelling, wrote the manuscript and finalized it. EV contributed to data analysis, manuscript writing—review and editing. AA performed the modelling, contributed in manuscript review and editing. EH performed the literature data extraction. RR and LS carried out the field investigation. MR was in charge of the conceptualization, the funding acquisition, the project administration at ICARDA, and contributed in manuscript review and editing. MG was responsible of the conceptualization, the project administration at the national school of veterinary medicine, the supervision, the validation of results, and contributed in manuscript review and editing. All authors read and approved the final version.

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10 SUPPLEMENTARY MATERIAL

A. The ODMAP protocol

B. Parameters of the candidate models

C. *Rhipicephalus sanguineus* s.l. collected during two-years filed visits in 6 localities in Tunisia

D. Occurrences records sources

E. Final occurrences records coordinates used for modelling

11 DATA AVAILABILITY STATEMENT

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/supplementary material.

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TABLE 1. *Rhipicephalus sanguineus* s.l. occurence number and sources

Source	Occurrence records
Our field survey	22
DVM dissertation and peer-reviewed articles	48
Estrada Peña and de la Fuente (2016)	33
Total	103

TABLE 2. Predictors used in the maximum entropy for *Rhipicephalus sanguineus* sensu lato modelling (46)

Description	Bioclimatic variable	Set 1	Set 2	Set 3	Set 4	Set 5
Mean diurnal range (mean of monthly (max temp - min temp))	BIO2	x	x	x	x	x
Mean temperature of warmest quarter	BIO10	x	x	x	x	
Mean temperature of coldest quarter	BIO11	x	x	x		x
Specific humidity (mean of most humid quarter)	BIO16	x	x		x	x
Specific humidity (mean of least humid quarter)	BIO17	x		x	x	x

TABLE 3. Best models as resulting from model calibration

N°	Regularization multiplier	Variable set	Mean AUC ratio	Partial ROC	Omission rate at 5%	AICc	ΔAICc	Parameters
1	0.3	Set 5	1.042	0.00	0.087	772.683	0.000	2
2	0.4	Set 5	1.049	0.00	0.087	772.707	0.023	2
3	0.5	Set 5	1.042	0.00	0.087	772.736	0.053	2
4	0.6	Set 5	1.040	0.00	0.087	772.772	0.089	2
5	0.7	Set 5	1.047	0.00	0.087	772.815	0.132	2
6	0.8	Set 5	1.035	0.00	0.087	772.864	0.181	2
7	1	Set 1	1.031	0.00	0.087	772.989	0.305	2

AUC = area under the curve.

ROC = receiver operating characteristic.

AICc = Akaike information criterion corrected for small sample size.

FIGURE 3. Köppen-Geiger climate classification map for Tunisia (1980-2016) at 1 km resolution (30)

FIGURE 4. Map of Tunisia showing the location of *Rhipicephalus sanguineus* s.l. collection sites.

Circles: localities of the field work

Triangles: metadata derivative localities

Red polygon: calibration (M) area

FIGURE 3. Calibration result and best selected models used for modelling the potential geographic distribution of *Rhipicephalus sanguineus* s.l. in Tunisia

FIGURE 4: Mean responses of *Rhipicephalus sanguineus* s.l. to the Bio2, Bio10, Bio11, Bio16, and Bio17 predictors in the 7 models after 10 replicates

FIGURE 5. Potential distribution of *Rhipicephalus sanguineus* s.l. in Tunisia based on MaxEnt modelling

Figures

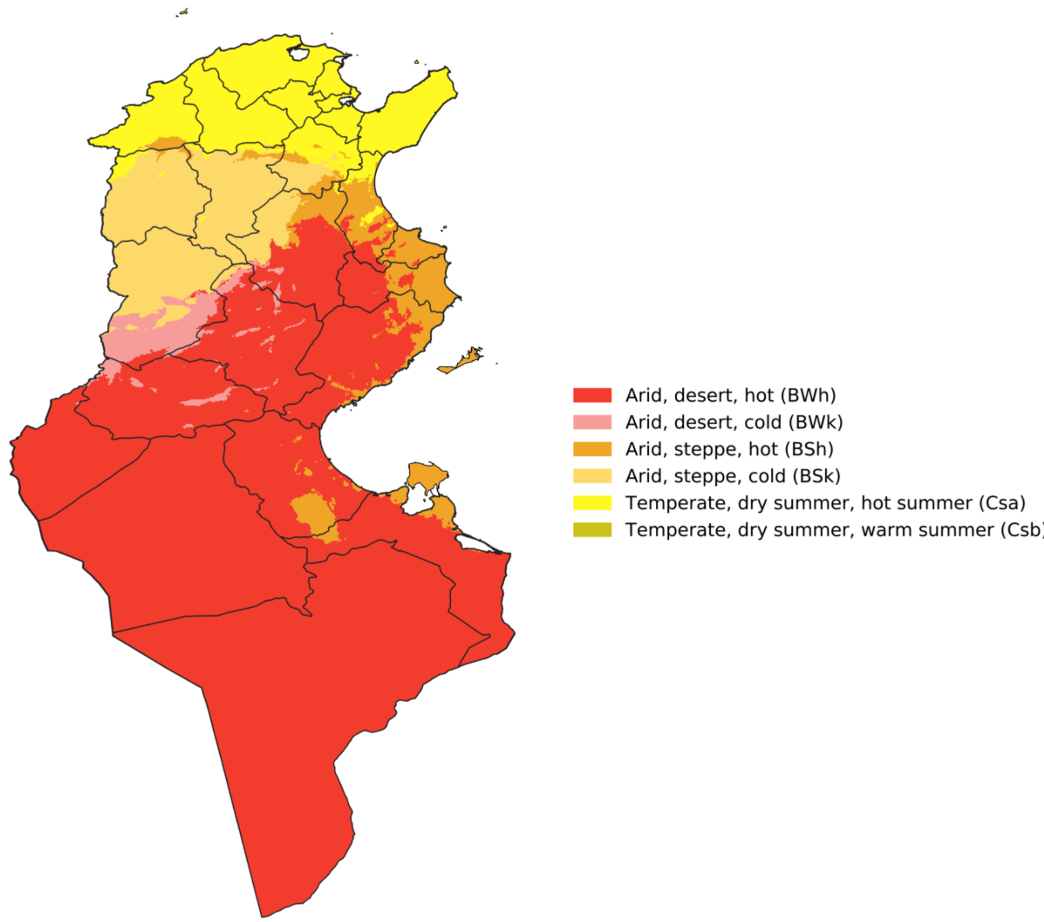

FIGURE 1.

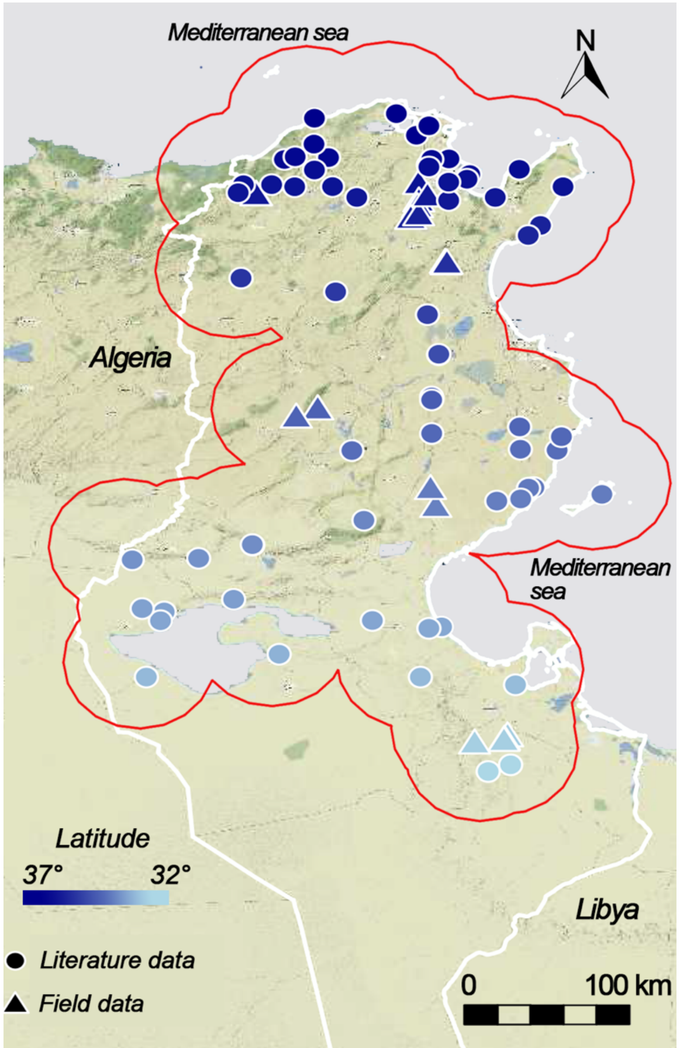
Mediterranean sea
N
Algeria
Mediterranean sea
Latitude
37°
32°
Libya
Literature data
Field data
0
100 km

FIGURE 2.

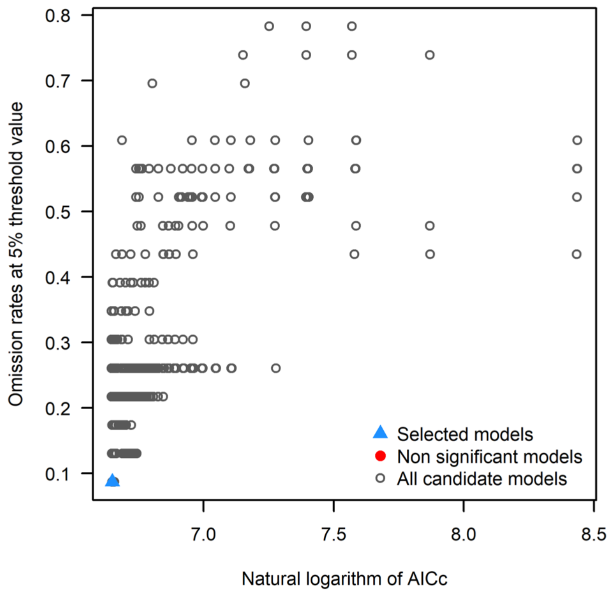
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
Omission rates at 5% threshold value
7.0
7.5
8.0
8.5
Natural logarithm of AICc
Selected models
Non significant models
All candidate models

FIGURE 3.

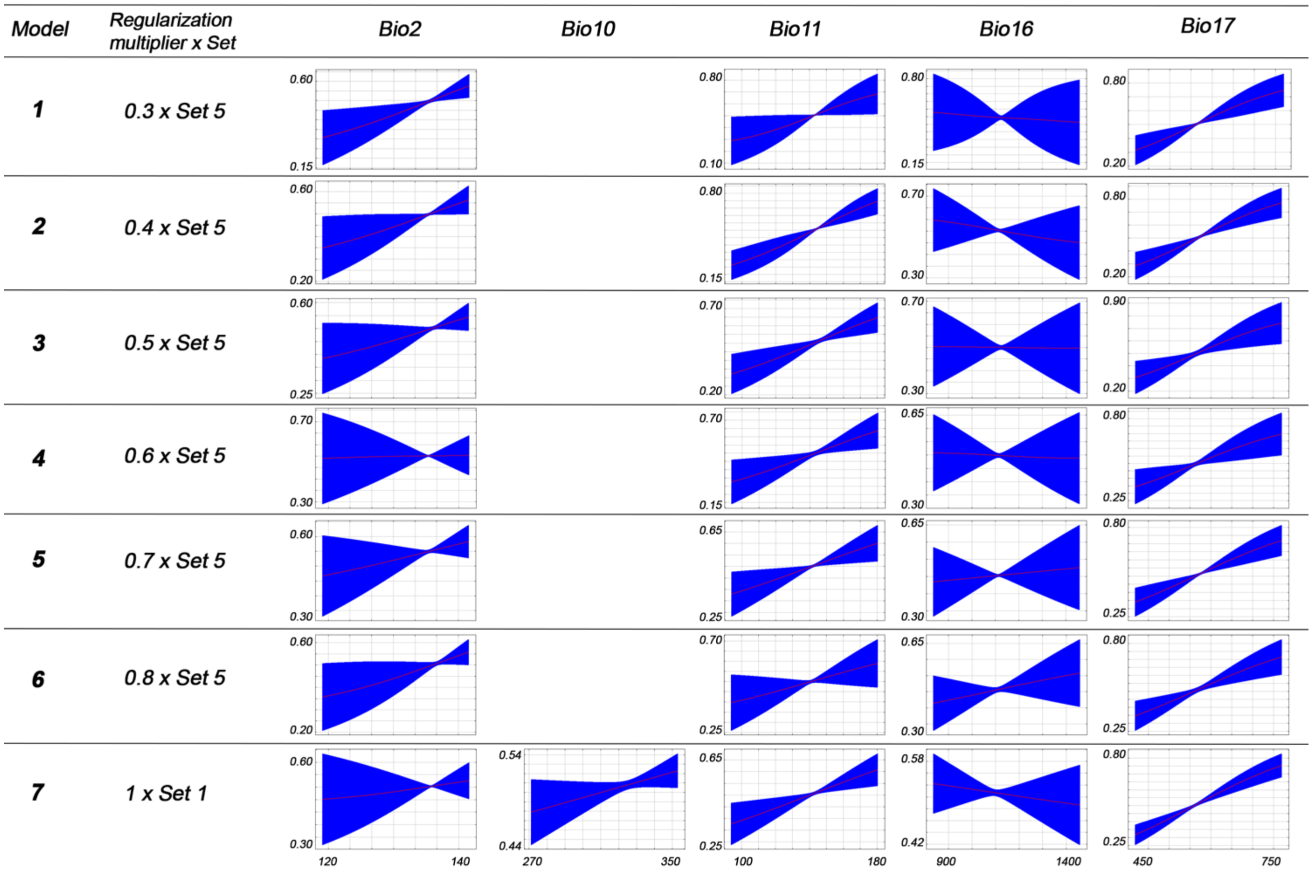
Model
Regularization multiplier x Set
Bio2
Bio10
Bio11
Bio16
Bio17
1
0.3 x Set 5
2
0.4 x Set 5
3
0.5 x Set 5
4
0.6 x Set 5
5
0.7 x Set 5
6
0.8 x Set 5
7
1 x Set 1
120
140
270
350
100
180
900
1400
450
750

FIGURE 4

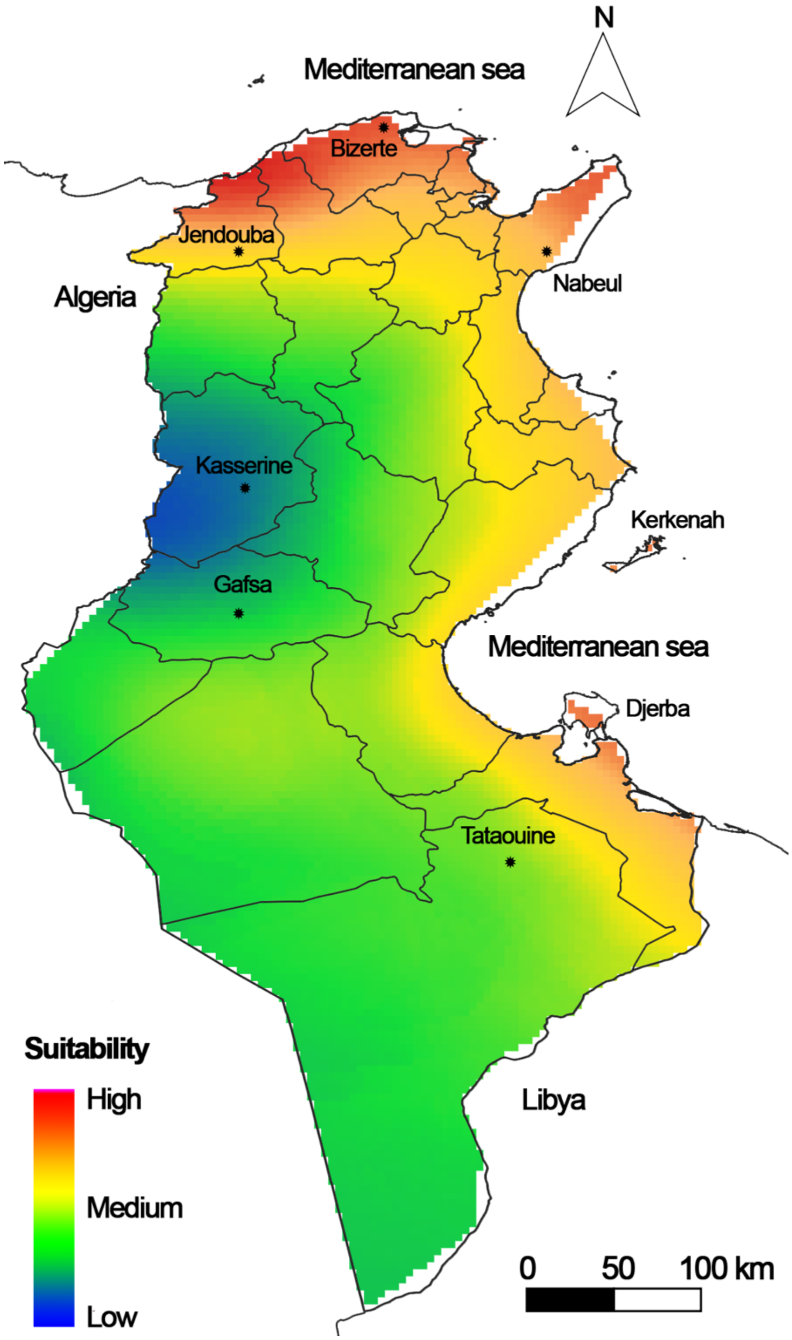
N
Mediterranean sea
Bizerte
Jendouba
Nabeul
Algeria
Kasserine
Kerkenah
Gafsa
Mediterranean sea
Djerba
Tataouine
Suitability
High
Medium
Low
Libya
0
50
100 km

FIGURE 5.