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Predicting the potential distribution of the cattle fever tick *Rhipicephalus annulatus* (Acari: Ixodidae) using ecological niche modeling

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Abstract

Rhipicephalus annulatus is a tick species of veterinary importance due to its potential to transmit babesiosis to cattle. This species has a Holarctic distribution with some Afrotropical records and is one-host species of veterinary importance. This study was carried out from September 2021 to February 2022 at 6 Egyptian collection sites, and a total of 1150 cattle were scanned randomly to collect ticks. A total of 1095 tick specimens were collected and identified as *R. annulatus* using taxonomic keys. Males were found on all parts of the cattle except the head and around the eyes, but females were found on all parts; in addition, the highest number of specimens was gathered from the udder, (neck and chest), and belly. Maximum entropy (MaxEnt) modeling was used to predict the potential global distribution of *R. annulatus*. The MaxEnt model performed better than random with an average test area under the curve (AUC) value of 0.96, and model predictions were significantly better than random and gave (AUC) ratios above the null expectations in the partial receiver operating characteristic (pROC) analyses ($P < 0.001$). Based on correlation analyses, a set of 9 variables was selected for species from 15 bioclimatic and 5 normalized difference vegetation index (NDVI) variables. The study showed that the current distribution of *R. annulatus* is estimated to occur across Asia, Africa, Europe, South America, and North America. Annual mean temperature (Bio1) and median NDVI had the highest effect on the distribution of this species. The environmentally suitable habitat for *R. annulatus* sharply increased with increasing annual mean temperature (Bio1). These results can be used for making effective control planning decisions in areas suitable to this vector of many diseases worldwide.

Keywords *Rhipicephalus annulatus* · Survey · Niche modeling · MaxEnt · Suitable habitat · Risk map

Introduction

Rhipicephalus annulatus (Say, 1821) is known as a cattle tick and could be considered a one-host tick in the genus *Rhipicephalus*; however, it is also collected from horses, sheep, goats, deer, and wild ungulates (Walker et al. 2003; Guglielmone et al. 2014). This species formerly belonged to

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the genus *Boophilus* until Murrell and Barker (2003) transferred it to the genus *Rhipicephalus*. This species is considered the vector for many diseases, such as bovine babesiosis (cattle fever) and bovine anaplasmosis (Samish et al. 1993; Miller et al. 2012). These protozoan and bacterial diseases are a significant threat to the cattle and beef industries and decrease meat and milk production (McCosker 1981; Bock et al. 2004). In Egypt, this species is distributed in different ecological zones and is considered the most important tick-infesting cattle throughout the country (Okely et al. 2021). Several pathogens were detected in this species from Egypt, such as CCHFV, lumpy skin disease virus, *Rickettsia* spp., *Anaplasma* spp., *Ehrlichia* spp., *Borrelia* spp., *Staphylococcus* spp., and *Babesia* spp. (Okely et al. 2022).

In terms of global geographic distribution, *R. annulatus* has a high abundance in tropical and subtropical regions (Graham and Price 1966; Estrada-Peña et al. 2006; Popara et al. 2013; Klafke et al. 2020). This tick is found in parts

of Africa with Mediterranean and savanna climates, southern countries of the former USSR, Southern and Western Europe, in the Near and the Middle East, South America, and Mexico and may be found in Texas or California (Hoogstraal 1956; Jongejan and Uilenberg 2004). The USA carried out eradication programs between 1906 and 1943 to eliminate *R. annulatus*, but recently, this vector has re-emerged again as a direct threat to cattle throughout the country (Lohmeyer et al. 2011; Giles et al. 2014).

There is an increasing need to understand the distribution pattern of vectors and species transmitting specific diseases (Peterson et al. 2004). In recent years, many studies have predicted the potential distribution of tick vectors using ecological niche modeling (Raghavan et al. 2016; Kessler et al. 2019; Pascoe et al. 2019; Boorgula et al. 2020; Zhao et al. 2021).

Previous studies have mapped the distribution of *R. annulatus* at local and regional levels. For Mediterranean countries, two studies focused on the distribution of this species by conducting environmental niche modeling (Estrada-Peña and Venzal 2007; Williams et al. 2015). In addition, one study focused on the distribution of this species on the island of Sicily (Torina et al. 2008). Other studies have estimated the habitat suitability for *R. annulatus* in the USA and Mexico (Estrada-Peña and Venzal 2006; Giles et al. 2014). To date, no study has evaluated the potential global distribution of this species.

Therefore, this work aims to survey *R. annulatus* in Egypt, in addition to estimating the potential distribution of this vector using an ecological niche modeling approach via the maximum entropy algorithm (MaxEnt).

Materials and methods

Sample collection

R. annulatus ($n = 1095$) was collected from September 2021 to February 2022 from a total of 6 collection stations in Egypt. A total of 1150 cattle were examined to collect ticks. Samples were preserved in vials containing 70% alcohol + 20% glycerol. Each vial was specific to an individual collection site and assigned information that indicated the site of collection, host, and GPS coordinates for each site.

Sample identification and mapping

Collected samples were identified in the laboratory using the appropriate taxonomic keys (Hoogstraal 1956; Walker et al. 2003; Okely et al. 2021). All specimens are preserved in the Ain Shams University tick collection. The sample collection locations were georeferenced using the ArcGIS software, version 10.3 (ESRI, Redlands, CA, USA).

Occurrence records

Primary occurrence records for *R. annulatus* were obtained from VectorMap (www.vectormap.org), previous literature (Loftis et al. 2006; Hassan et al. 2017; Aboelhadid et al. 2018; Okely et al. 2021), and field surveillance conducted by the first author. All records were included with geographic coordinates in the final dataset. Unique records were used in the final occurrence records by removing the duplicate records. We filtered these occurrences depending on a distance filter to remove all redundant records occurring in a single 2.5' pixel (~ 5 km) (Syfert et al. 2013). The final dataset was divided into two halves: 50% for calibrating the model and 50% for evaluating the model prediction.

Bioclimatic variables

Data from WorldClim (www.worldclim.org), including 19 bioclimatic variables, were used to assess the potential distribution; bio 8–9 and 18–19 were not used in the analyses due to spatial artifacts in these variables (Nasser et al. 2021). In addition to bioclimatic data, normalized difference vegetation index (NDVI) data were incorporated into the analysis. Monthly NDVI data values from 2012 to 2018 were averaged into the mean, median, minimum, maximum, and range using the Spatial Analyst tools function in ArcMap v10.3 (Okely et al. 2020a). All bioclimatic variables and 5 NDVI variables (Table 1) were submitted to a principal component analysis (PCA) to reduce the significant correlations among some of these variables (Kriticos et al. 2014). The first 6 principal components summarized approximately 99% of the overall variance and were used as components in our analyses.

Ecological niche modeling

The ecological niche of *R. annulatus* was predicted using the maximum entropy algorithm implemented in MaxEnt v3.3.3e (Phillips et al. 2006). MaxEnt estimates environmentally suitable habitats for species that vary from 0 (lowest suitability) to 1 (highest suitability) (Nasser et al. 2019). Additionally, response curves were generated for each variable. Finally, MaxEnt produced a jackknife to estimate the most important set of variables that had a greater contribution to species distribution (Khanum et al. 2013; Okely et al. 2020b). The current 15 bioclimatic and 5 NDVI variables were reduced to fewer variables after undergoing the test in SDMTools in ArcGIS 10.3 (Universal tool; Remove highly correlated variables) to remove variables with high correlations among them (Graham 2003). The Pearson correlation coefficient was used with $r > 0.7$ as a cutoff threshold

Table 1 Bioclimatic and normalized difference vegetation index variables used for the principal component analysis

Variable	Explanation	Source of data
Bio1	Annual mean temperature	WorldClim
Bio2	Mean diurnal range [mean of monthly (max temp − min temp)]	WorldClim
Bio3	Isothermality (Bio 2/Bio 7)($\times$ 100)	WorldClim
Bio4	Temperature seasonality (standard deviation $\times$ 100)	WorldClim
Bio5	Max temperature of warmest month	WorldClim
Bio6	Min temperature of coldest month	WorldClim
Bio7	Temperature annual range	WorldClim
Bio10	Mean temperature of warmest quarter	WorldClim
Bio11	Mean temperature of coldest quarter	WorldClim
Bio12	Annual precipitation	WorldClim
Bio13	Precipitation of wettest month	WorldClim
Bio14	Precipitation of driest month	WorldClim
Bio15	Precipitation seasonality (coefficient of variation)	WorldClim
Bio16	Precipitation of wettest quarter	WorldClim
Bio17	Precipitation of driest quarter	WorldClim
Minimum NDVI	Minimum normalized difference vegetation index	Copernicus Global Land Service archive
Maximum NDVI	Maximum normalized difference vegetation index	Copernicus Global Land Service archive
Range NDVI	Range normalized difference vegetation index	Copernicus Global Land Service archive
Mean NDVI	Mean normalized difference vegetation index	Copernicus Global Land Service archive
Median NDVI	Median normalized difference vegetation index	Copernicus Global Land Service archive

to determine the highly correlated variables (Dormann et al. 2013). The final set of nine variables was used in our analysis (Table 2). The calibration area (M) was estimated (Fig. 1) (Soberon and Peterson 2005; Barve et al. 2011) to project the model for the Old World, South America, and North America. The bootstrap function in MaxEnt was used to create 100 replicates for model analyses. To estimate the perfect model of *R. annulatus*, median values across all replicates were selected. The final model was thresholded to define habitat and nonhabitats (or unsuitable areas) for species based on a maximum allowable omission error rate of 5% ($E = 5\%$) (Peterson et al. 2008). We identified type I novelty (analogous and nonanalogous environments) in the

study area by comparing accessible area data vs. study area data using the extrapolation detection software Exdet tool V1.1 (Mesgaran et al. 2014).

Model evaluation

The area under the curve (AUC) was used to evaluate model performance. AUC is a measure of model performance and varies from random discrimination to perfect discrimination (Swets 1988). Additionally, our model was evaluated using the partial receiver operating characteristic (*p*ROC) function in the ENMGadgets package in R (Peterson et al. 2011). We chose *p*ROC for testing the model to prevent errors obtained from the traditional ROC (Lobo et al. 2008).

Results

Overall, 16 nymphs, 76 males, and 1003 females were collected and identified as *R. annulatus* from 6 collection sites in Egypt. The sex ratio between males and females was 0.075:1. The individual geographic collection locations for previous literature data, vector map data, and new field surveys were georeferenced and are displayed in Fig. 2.

The distribution of *R. annulatus* on different body parts of the cattle varied among nymphs, males, and females (Fig. 3). Nymphs were found only at three sites. Males were found on all parts except the head and

Table 2 Percent contributions of the bioclimatic and NDVI variables in the MaxEnt models for *Rhipicephalus annulatus*; values shown are averages over 100 replicate runs

Variable	Percent contribution (%)
Bio1	30.2
Median NDVI	20.5
Bio15	16.3
Bio12	10.9
Minimum NDVI	7.1
Bio14	7
Maximum NDVI	4.4
Bio2	2.4
Range NDVI	1.2

Fig. 1 The accessible area (M) for *Rhipicephalus annulatus* with occurrence records of this species derived from various sources after data cleaning
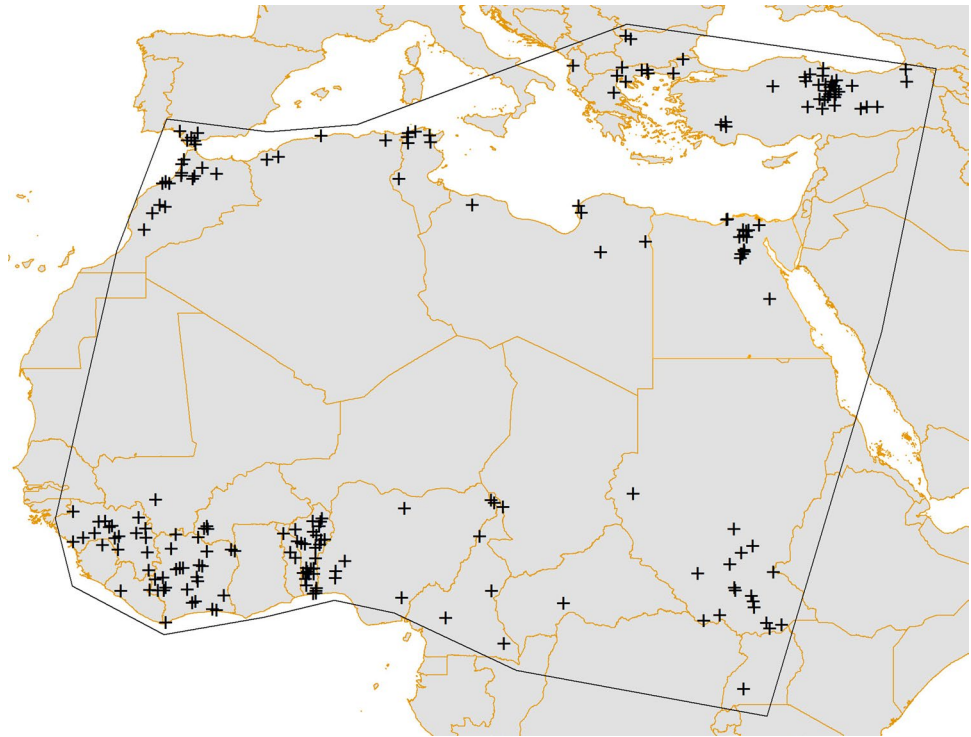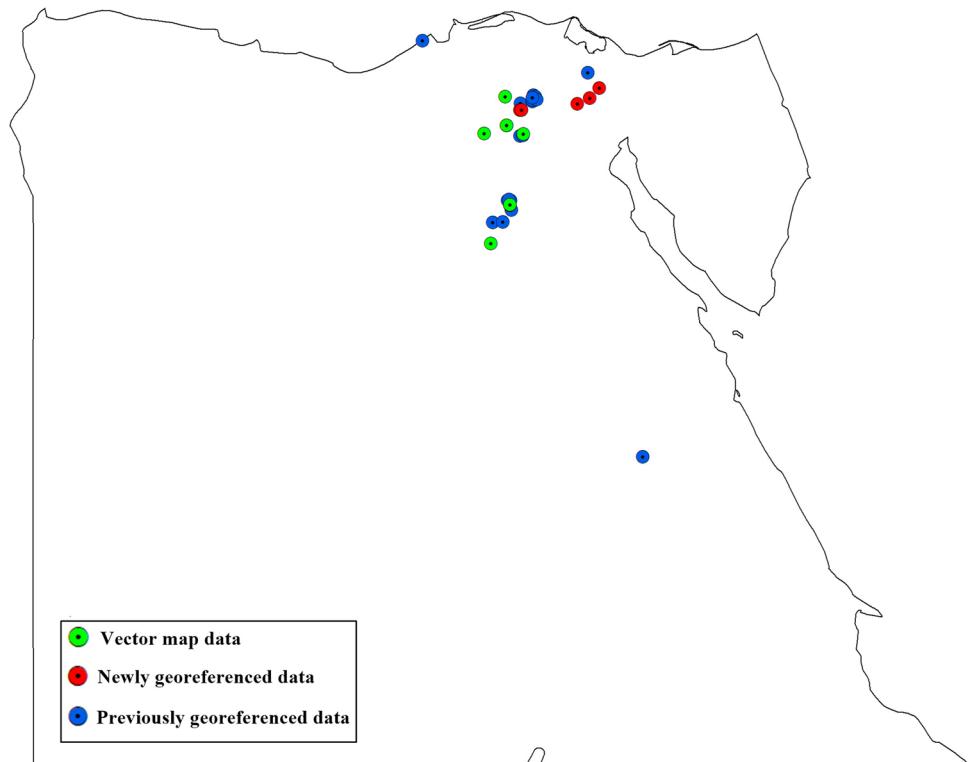

Fig. 2 Map of Egypt showing georeferencing data of *Rhipicephalus annulatus* in Egypt from different sources

● Vector map data
● Newly georeferenced data
● Previously georeferenced data

around the eye, but they were collected more from the anus and under the tail than from other sites. On the other hand, females were found on all parts, and the highest number of specimens was gathered from the udder, neck, chest, and belly (Fig. 3). More than half of the females were semiengorged, followed by fully engorged females, and unfed females were collected throughout the study (Fig. 4).

Fig. 3 The number of *Rhipicephalus annulatus* specimens of nymphs, females and males collected from each body site of the cattle
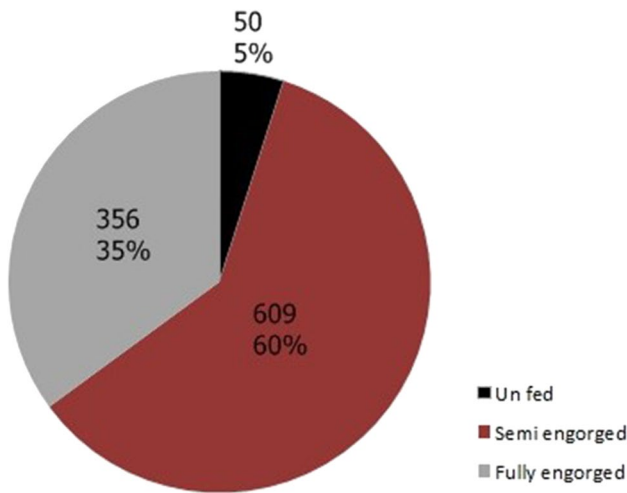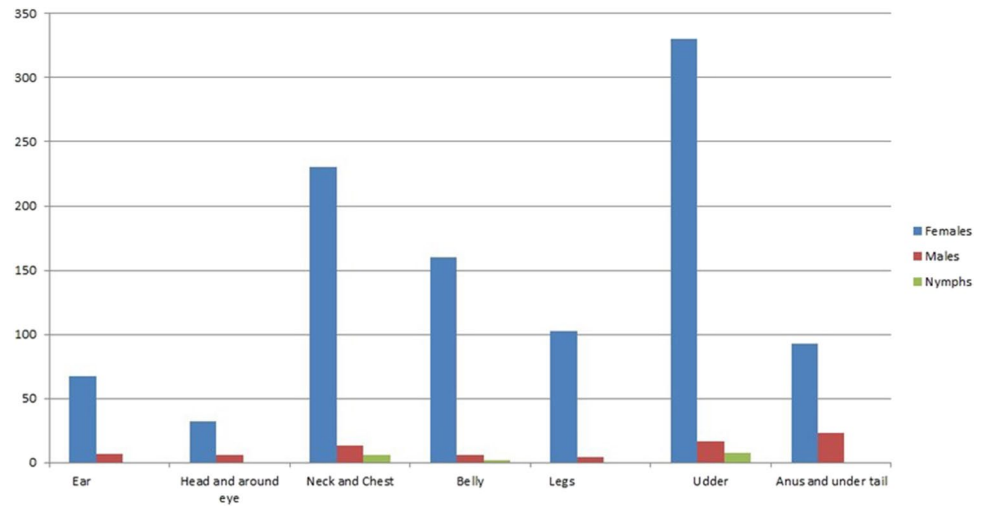

Fig. 4 The number and percentage of female *Rhipicephalus annulatus* specimens collected (unfed, semiengorged, and fully engorged)

The MaxEnt model for *R. annulatus* gave satisfactory results with an AUC value of 0.96, and model predictions were significantly better than random values and gave (AUC) ratios above the null expectations in the *p*ROC analyses ($P < 0.001$), where the minimum, maximum, and mean *p*ROC values were 1.69, 1.92, and 1.85, respectively. Annual mean temperature (Bio1) and median NDVI were the most important predictors of *R. annulatus* habitat distribution (Fig. 5); these factors had the highest influence on the model, with contributions of 30.2 and 20.5%, respectively (Table 2). The probability of the presence of *R. annulatus* increased with an increase in annual mean temperature (Bio1); additionally, the suitability of habitat for this species increased with the increase in annual precipitation (Bio12) (Fig. 6). *R. annulatus* increased their distribution in suitable a habitat with a low-median NDVI value and decreased their distribution in a habitat with a high-median NDVI value (Fig. 6).

The potential distribution of *R. annulatus* was estimated across Asia, Africa, Europe, South America, and North America. In Asia, the predicted distributional potential of this vector in Western Asia included Turkey, Lebanon,

Fig. 5 The jackknife test shows the most effective environmental variables and NDVI variables used in the analysis
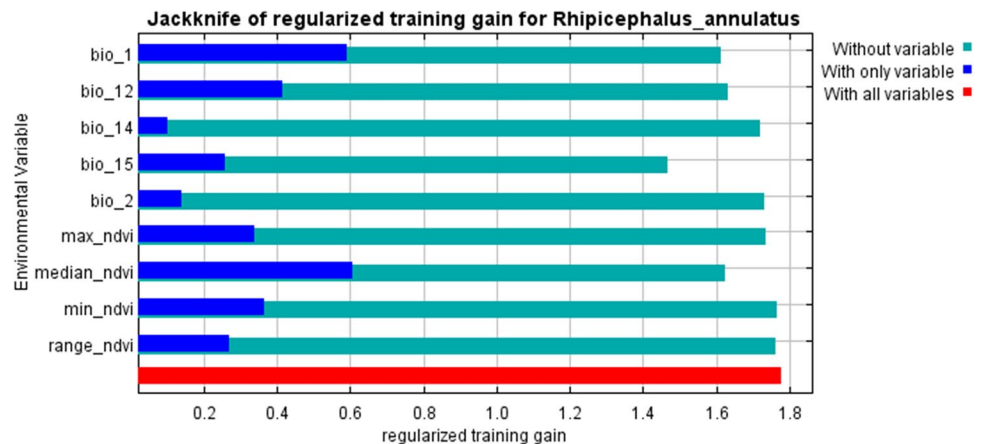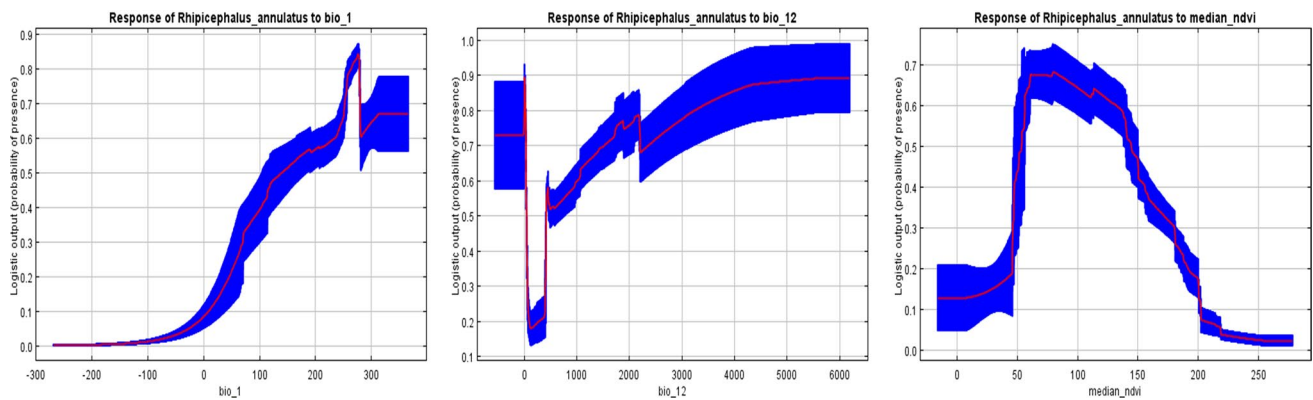
Fig. 6 Response curves showing the relationships between the probability of the presence of a species and top bioclimatic and NDVI predictors. These variables are; annual mean temperature (Bio1), annual precipitation (Bio12), and median-NDVI. values shown are average over 100 replicate runs

Palestine, Israel, Jordan, Syria, Iran, and the Arabian Peninsula (Oman, Saudi Arabia, and the United Arab Emirates). *R. annulatus* was also predicted to occur in Pakistan, India, Thailand, Vietnam, Cambodia, Laos, and China (Fig. 7). In Africa, the environmentally suitable areas for *R. annulatus* included Egypt, Libya, Tunisia, Algeria, and Morocco in North Africa, South Sudan and Sub-Saharan countries; however, its distributional potential is very limited in South Africa (Fig. 7).

In Europe, *R. annulatus* was predicted to occur in Spain, Portugal, Southern Italy, Sicily Island, Greece, some parts of Poland, Austria, Hungary, the Czech Republic, Slovakia, and Romania (Fig. 7). In the USA on the Atlantic coast, suitable habitat for this vector species was observed in much of South America in Brazil, Bolivia, Paraguay, Venezuela, and Argentina, and the environmentally suitable areas of *R. annulatus* included Central America and the Caribbean islands. In North America, suitable habitat was mainly in
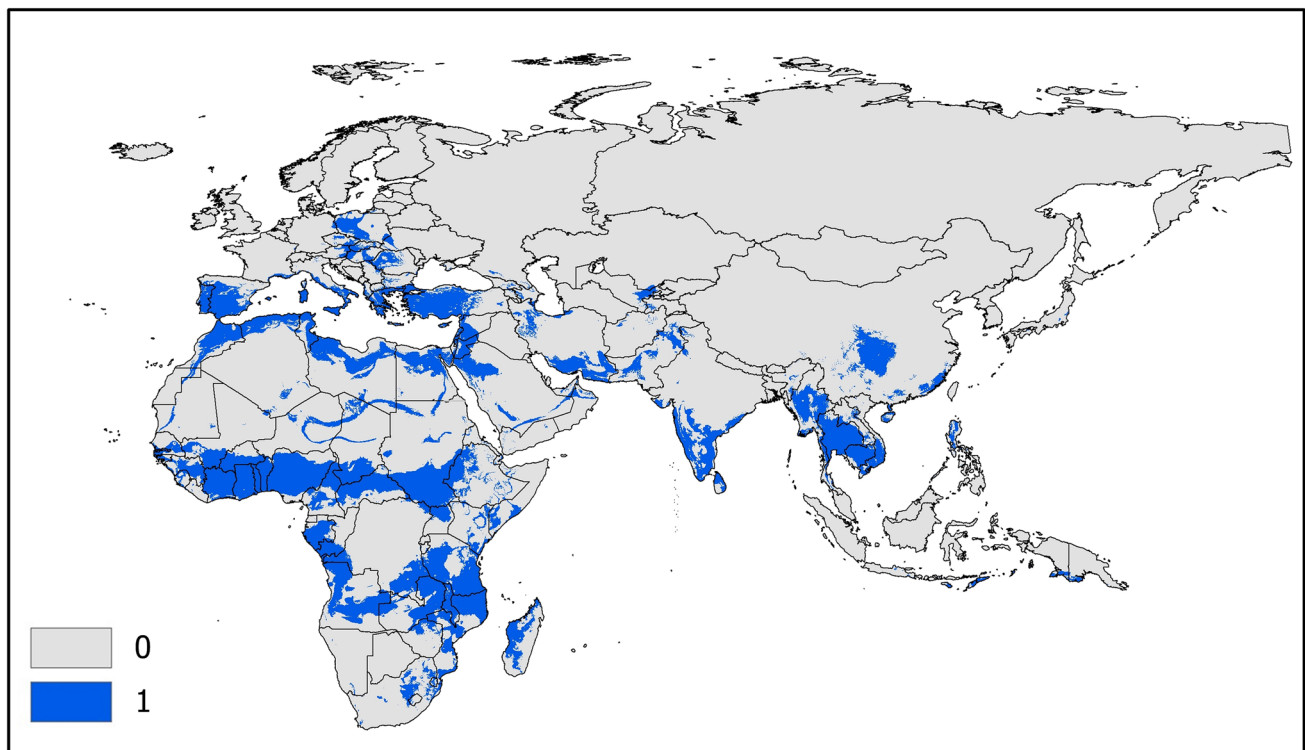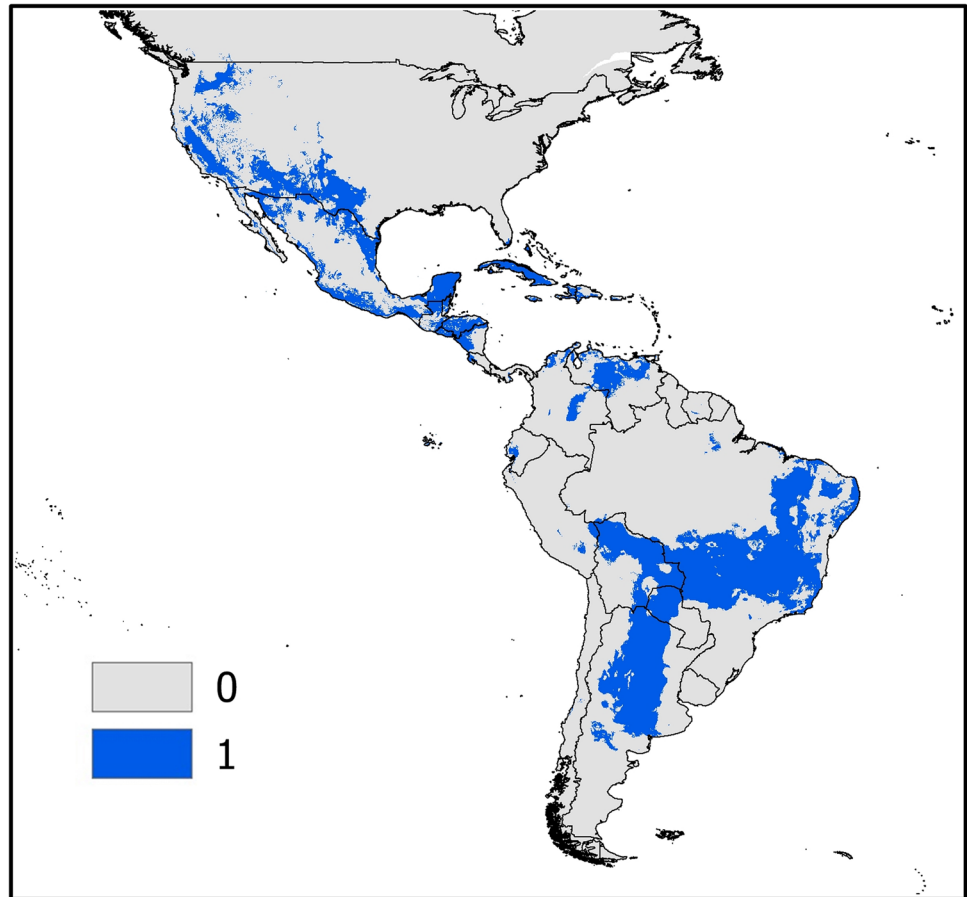

Fig. 7 Potential distribution of *Rhipicephalus annulatus* in the Old World

Fig. 8 Potential distribution of *Rhipicephalus annulatus* in North and Latin America


Mexico and the western parts of the USA, including South Texas, New Mexico, Arizona, California, and Washington (Fig. 8).

The ExDet tool detected climatic novelty in our analysis for *R. annulatus* in Russia and North Canada and showed pixels corresponding to climatic novelty in Latin America and India (Fig. 9).

Discussion

According to previous literature (Hoogstraal and Kaiser 1960; Shoukry et al. 1993; El Kammah et al. 2001; Mazyad and Khalaf 2002; Okely et al. 2022) and our own observations, *R. annulatus* is considered the most abundant tick infesting cattle in Egypt. In this study, in comparison with

Fig. 9 Extrapolation detection (ExDet) output map for *Rhipicephalus annulatus* worldwide
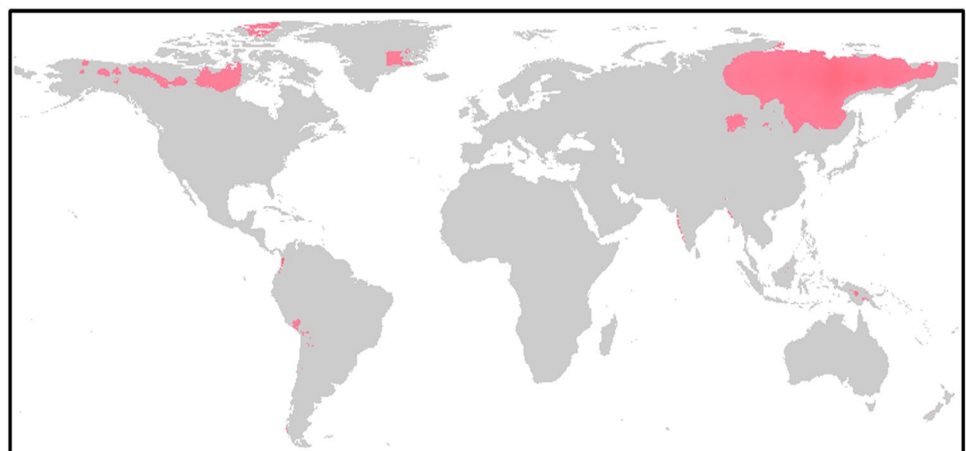
the number of males, a large number of females were collected. This was probably due to technical limitations, as the males were very small, and it was difficult to collect such samples compared to females; these findings agreed with those of previous studies (Lorusso et al. 2013; Kerario et al. 2017; Okely et al. 2021).

Our observations demonstrated that *R. annulatus* was collected from all the body sites of cattle, which agreed with the results of Gabaj et al. (1992). *R. annulatus* was collected mostly from the udder, neck, chest, and legs of the cattle, and these sites were mentioned previously as preferred sites for *R. annulatus* on the bodies of cattle (Walker et al. 2003). Previous literature indicated that the udders of cattle are classified as the most favorable site for infestation by this species (Gabaj et al. 1992). In this study, males were collected mostly from around the anus opening, and no studies discussed this observation previously. Our observations indicated that semiengorged females were collected more frequently than those that were fully engorged, which could be due to fully engorged *R. annulatus* female ticks usually laying eggs more quickly (Gindin et al. 2001) and thus dropping from their host for egg laying.

Ecological niche modeling is an important technique for identifying geographic and ecological areas suitable for any species (Soberon and Peterson 2005). Throughout the present work, MaxEnt was used to predict the potential global distribution of *R. annulatus* based on climatic and NDVI variables. As *R. annulatus* is known for its role in the transmission of babesiosis and bovine anaplasmosis to cattle (Walker et al. 2003), the potential distribution maps of this species will be beneficial to vector surveillance programs for monitoring areas deemed to be highly suitable habitats for this species and to vector control programs, especially in countries where surveillance is unavailable.

The MaxEnt model performed better than random for predicting the distribution of *R. annulatus* with a high AUC value, which was greater than 0.95; additionally, partial *ROC* analysis was used to test the statistical significance of the model predictions, and the results were greater than the null hypothesis. In addition, ExDet (extrapolation detection) was included to understand the extrapolation of the results to different areas in the region of interest. In fact, the novel climate estimation confirmed the importance of using MaxEnt in anticipating ENMs for species, where prediction maps of MaxEnt anticipated these values only under analogous environmental conditions.

The obtained results indicated that annual mean temperature (Bio1), annual precipitation (Bio12), and median NDVI were the most important predictors of *R. annulatus* habitat distribution. This species preferred habitats with high temperatures and annual precipitation amounts (Estrada-Peña et al. 2006; Estrada-Peña and Venzal 2007), and the same results were acquired from the response curves (Fig. 3).

Additionally, the suitable habitats for *R. annulatus* decreased with increasing median NDVI values. This finding was consistent with that of Estrada-Peña et al. (2006), who indicated that the presence of this species in the Mediterranean region and the zone south of the Sahara Desert was associated with low NDVI values for much of the year.

The produced model estimated the suitable habitat for *R. annulatus* across the world. Our results predicted the presence of this vector in South Texas of the USA along the Texas–Mexico border, and this result overlapped in most cases with those of previously published studies (Estrada-Peña and Venzal 2006; Giles et al. 2014). Additionally, a previous study (Lohmeyer et al. 2011) indicated the presence of *R. annulatus* in Maverick, Kinney, and Webb Counties in southern Texas; this previous result concurred with our prediction in these regions. In California, this species is sometimes found (Spickler and Rovid 2007), which is similar to our result that predicted the potential distribution of *R. annulatus* in this region. No previous reports have indicated the presence of this species in New Mexico, Arizona, and Washington, although our model predicted its potential distribution in these states.

Our model predicted the presence of this vector in Brazil, Bolivia, Venezuela, and Argentina; however, previous studies interested in the surveillance of ticks in Brazil and Bolivia indicated that the presence of *R. annulatus* in these two countries was regarded as erroneous due to misidentification (Dantas-Torres et al. 2009; Mastropaolo et al. 2014). Hence, our study sheds light on performing de novo field surveillance for this vector in these regions.

In Africa, Estrada-Peña et al. (2006) predicted the distribution of *R. annulatus*. The results of our model overlap in most cases with the results of this study in areas with Mediterranean and savanna climates, especially in West and North Africa; however, our model showed an increase in suitable habitats in North Africa (Egypt, Libya, Tunisia, Algeria, and Morocco). Our map anticipated new suitable areas in Central Africa (Gabon, Central African Republic, and the Democratic Republic of Congo) and Eastern Africa (Tanzania), where the species was also identified (Kerario et al. 2017; Guglielmone and Robbins 2018). Our model was the first to focus on mapping the potential geographical distribution of this species in the Near East and Asia.

However, the present work predicts the potential current distribution of *R. annulatus* and has some limitations in anticipating the future distribution for species under climate change. We intentionally ignored predictions for future scenarios due to a lack of future data for NDVI variables, which made it difficult to project these models into the future. Finally, this study can guide control programs and surveillance priorities, which are primarily dependent on estimating suitable areas where a vector may occur. This study provided further details related to mapping the

potential current distribution of *R. annulatus* worldwide, improved the information on the potential distribution of *R. annulatus*, and identified several other regions at risk of invasions by this vector.

Author contribution Conceptualization: Mohammed Okely and Areej A. Al-Khalaf. Methodology: Mohammed Okely. Software: Mohammed Okely. Validation: Mohammed Okely. Formal analysis: Mohammed Okely and Areej A. Al-Khalaf. Investigation: Mohammed Okely and Areej A. Al-Khalaf. Resources: Mohammed Okely and Areej A. Al-Khalaf. Data curation: Mohammed Okely. Writing—original draft preparation: Mohammed Okely. Writing—review and editing: Mohammed Okely and Areej A. Al-Khalaf. Visualization: Mohammed Okely. Supervision: Areej A. Al-Khalaf. Project administration: Areej A. Al-Khalaf. Funding acquisition: Areej A. Al-Khalaf. All authors have reviewed and agreed to the published version of the manuscript.

Data availability Not applicable.

Declarations

Competing interests The authors declare no competing interests.

Ethics approval Verbal informed consent was obtained from all animal owners following a detailed explanation on the study purpose. Only tick samples were collected from live animals and no other medical intervention was undertaken on these animals for this study.

Consent to participate Not applicable.

Consent for publication Not applicable.

Conflict of interest The authors declare no competing interests.

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