

Research article

MODELING THE CURRENT AND FUTURE DISTRIBUTION OF BRUCELLOSIS UNDER CLIMATE CHANGE SCENARIOS IN QINGHAI LAKE BASIN, CHINA

Temitope Emmanuel AROTOLU^{1,2,3}, HaoNing WANG⁴, JiaNing LV³, Kun SHI⁵, LiYa HUANG⁶, XiaoLong WANG^{1,2,3*}

¹Northeast Forestry University, Center of Conservation Medicine & Ecological Safety, Harbin, Heilongjiang province, P. R. China; ²Key Laboratory of Wildlife Diseases and Biosecurity management, Harbin, Heilongjiang province, P. R. China; ³Northeast Forestry University, College of Wildlife and Protected Area, Harbin, Heilongjiang province, P. R. China; ⁴Harbin University, School of Geography and Tourism, Harbin, Heilongjiang province, P. R. China; ⁵Beijing Forestry University, Wildlife Institute, Beijing, P. R. China; ⁶Changbai Mountain Academy of Sciences, Antu, Jilin province, P. R. China.

(Received 08 April, Accepted 16 August 2023)

Brucellosis is a bacterial disease caused by various *Brucella* species, which infect primarily cattle, swine, goats, sheep, and dogs. The disease is typically transmitted to humans through direct contact with diseased animals, consumption of contaminated animal products, or inhalation of airborne pollutants. The majority of cases are caused by consuming unpasteurized goat or sheep milk or cheese. Based on observed Brucellosis occurrence data and ecogeographic variables, a MaxEnt algorithm was used to model the current and future distribution of Brucellosis in Qinghai Lake basin, P.R. China. Our model showed the Brucellosis current distribution and predicts suitable habitat shifts under future climate scenarios. In the new representatives; SSP 2.6 and SSP 4.5 for the year 2050s and 2070s, our model predicts an expansion in the current suitable areas. This indicates that under the possible climate changes in the future, the living space of Brucellosis in Qinghai Lake basin China will expand significantly. Ecogeographic variables that contributed significantly to the distribution of Brucellosis in Qinghai Lake basin are revealed by our model. The results of our study will promote comparisons with future research and provide a new perspective to inform decision-making in the field of public health in Qinghai province.

Keywords: Climate change, Brucellosis, Bioclimatic variables, future scenarios, Habitat suitability, Qinghai, China

*Corresponding author: e-mail: wxlhrb@outlook.com

INTRODUCTION

Brucellosis is an infectious bacterial disease. People can become infected if they come in contact an infected animal or contaminated animal products [1]. Animals that are primarily infected include sheep, cattle, dogs, goats, and pigs, among others [2]. The defining characteristic of Brucellosis as a zoonosis is that it is completely zoonotic: a disease transmitted exclusively from animals to humans. Human-to-human transmission has occurred, but it is extremely uncommon [3]. Brucellosis is a contagious disease; consequently, it is also known as contagious abortion. It is transmitted by bacteria of the genus *brucella*, such as *B. abortus* (cattle), *B. melitensis* (goat), *B. suis* (swine), *B. neotomae* (desert wood rat), *B. ovis* (sheep), and *B. canis* (dogs) [4] each with its principal host [5]. Moreover, wildlife is prone to *Brucella* infection. *Brucella* species have been isolated from a wide range of wildlife species, including bison (*Bison bison*), elk (*Cervus canadensis*), wild boar (*Sus scrofa*), fox (*Vulpes vulpes*), hare (*Lepus europaeus*), and caribou (*Rangifer tarandus*) [6].

Brucella is found globally and is a significant economic problem due to the diseases they cause in domestic animals, wildlife, and humans. Lack of strict control over the movement of animals from one area to another, lack of basic hygienic measures, and poor husbandry management significantly influence the increase of Brucellosis prevalence [2]. *Brucella* are relatively resistant to environmental conditions, especially in the presence of protein and when shielded from sunlight [7]. *Brucella abortus* can live for up to six months in shaded fetuses [8]. Most clinical manifestations involve the reproductive tract, involving abortion or the birth of nonviable offspring, as well as orchitis, epididymitis, and infertility [9]. When an outbreak of brucellosis is found in a herd, flock, area, or country, international veterinary standards prohibit animal transportation and trade, resulting in enormous economic losses.

The economic losses connected with a *Brucella* outbreak include a decrease in milk output, the loss of calves, and culling. Depending on the timing of therapy and the severity of the disease, the duration of recovery might range from a few weeks to several months. Mortality due to brucellosis is uncommon, occurring in less than 2% of cases.

The bacterial load of dairy products at the moment of consumption can vary. A product's rate of bacterial death depends on its pH, salinity, water content, temperature, and fat content. At higher storage temperatures, *Brucella* species perish; refrigeration protects *Brucella* organisms. The survival of *Brucella* spp. is jeopardized at even greater temperatures. *Brucella* dies when the pH falls below 4 ($\text{pH} \leq 4$) [10]. *Brucella* spp. does not grow in the pH range of 5 to 6, but they also do not die. The amount of water also influences bacterial burden. The shorter the survival duration, the lower the water content [10].

Climate changes have been identified as a primary cause of abundance and distributional declines in numerous species [11,12]. Inadvertently, a move towards

warmer temperatures could have a substantial impact on disease dynamics, leading to severe outbreaks [13]. A rise in vector-borne diseases is anticipated due to the impending movement of humans into endemic regions [14].

The complexity of vector-borne diseases' transmission hosts renders them very sensitive to climatic change [15]. Since the vast majority of disease vectors (e.g., insects and mites) are arthropods, climatic change is likely to affect the distribution, density, seasonality, and prevalence of diseases [16,17].

This study employed ecological niche modelling techniques to produce a map (output) of the predicted ecological niche of the species on a scale of 0 to 1 and lowest suitability to highest suitability, respectively [18]. The objective was to get an understanding of the history and future distribution of Brucellosis based on environmental characteristics of known occurrence sites. One of the top species distribution modelling methods for assessing presence-only data is the MaxEnt model [19]. When compared to other presence-only models, this approach typically produces solid predictive models and is especially well-suited to handle the limited availability of presence-only data [20].

The Intergovernmental Panel on Climate Change's (IPCC) fifth assessment report, published in 2014, confirms that recent climate change brought on by higher concentrations of greenhouse gases produced by human activity has had an impact on both human and natural systems [21,22]. Therefore, we adopted the niche modeling method to assess the future distribution of Brucellosis for Qinghai Lake basin, based on existing presence records. In addition, our modeling took into account the possibility of habitat expansion caused by climate change. This enabled predictions to be made for future distribution for the decades 2050s and 2070s under two shared socioeconomical pathways (SSP 2.6 and SSP 4.5). We used the assumptions of future climate conditions to account for the uncertainty of global climate change.

MATERIALS AND METHODS

Study area

Our study area is the Qinghai Lake basin in Qinghai province, Northwest China (98°37'-101°45' E and 36°33'-39°14' N) (Figure 1). The Lake is roughly 4,300 km², while the basin is about 29,600 km². The average depth of the water is 21 meters, and the water's surface is around 3,193 meters above sea level (m.a.s.l.). [23]. The location of Qinghai Lake is in a closed basin (29,661 km²) with no outflow of surface water. A high-altitude, cold, and semiarid climatic zone encompasses the entire watershed [24]. More than 40 rivers enter the Qinghai Lake, but the majority just seldom. Qinghai Lake, the biggest Salt Lake in China, is a worldwide wetland [25], a breeding site for migratory ducks, and a location for them to build their nests. Moreover, the Przewalski's gazelle, an endangered species, may find its final refuge in the highlands surrounding Qinghai Lake [26]. Humans and environment coexist peacefully in the Qinghai Lake basin, which has been recognized as a modern, highly productive

location for animal husbandry [27]. Over 110,000 people live throughout the entire watershed, mostly in the of the Qinghai Lake area [28]. Livestock farming serves as the foundation of the rural economy in China's Qinghai province, which includes the lake basin [29]. In addition to sheep, goats, and yaks, there are also horses, cattle, and donkeys. Household livestock numbers ranged from dozens to more than 1,000 [30]. The majority of animals are moved to elevated pastures (4850 to 4950 m.a.s.l.) in the spring or early summer, where milk is digested and herds gain weight. Upon returning to the homestead (3190 to 3300 m a.s.l.) in late summer, forage and crop remnants serve as the major feed, combined with stubble browsing and grassy spots near the winter residence [31]. About 63% of the region under study is covered by grassland [27]. The principal forms of vegetation are as follows: needleleaved forest in cold temperate, shrubs in plain valley, alpine shrubs, sandy shrubs, steppe in temperate, alpine steppe, alpine meadow, swamp meadow, subnival vegetation, etc. [32].

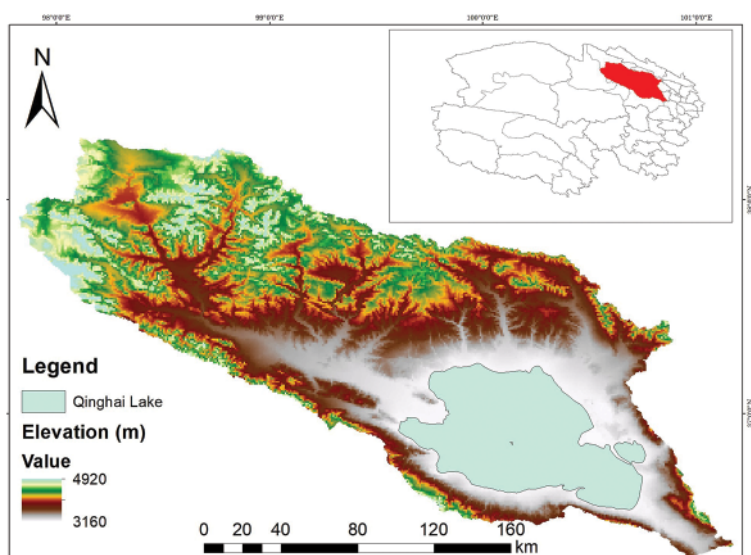


Figure 1. Study area: Qinghai Lake basin in Qinghai Province, People's Republic of China

Brucellosis occurrence data collection and pre-processing

We gathered the occurrence locations for Brucellosis ($n = 60$) from the publications and the world organization for animal health (WOAH founded as OIE) reports. In order to exclude records with geocoordinate errors, the data were modified and checked after being placed in a Microsoft Excel spreadsheet. To reduce any spatial autocorrelation (SAC), we filtered the presence points using the SDM Toolbox v1.1c [33] integrated with ArcGIS 10.6 [34]. Filtering was done by setting a minimum separation of 10 km between each pair of occurrence points [35,36]. This assisted in addressing issues with geographic sampling biases. The ideal filtering or thinning process keeps the occurrence points with the most insightful data while simultaneously

removing the fewest records required to significantly lessen the impacts of sampling bias [37]. The occurrence points were then stored as comma-separated values (CSV) and imported into ArcGIS (version 10.6 ESRI) for editing. They were transformed to UTM-WGS-1984 with conventional settings or resampled to 30 arc-seconds.

Environmental data preprocessing

An aggregate of 68 climatic, sheep population density, and human population density variables (S1 Table) were extracted from the WorldClim version 1.4 dataset from 1950–2000 at 30 arc-second resolution [38], the Gridded livestock of the world (GLW3) dataset from <http://www.fao.org/livestock-systems>, and the WorldPop dataset from www.worldpop.org. GLW3 is available in GeoTIFF and ASCII XYZ format with a 30 arc-second resolution. Also included are the unrestricted individual country population count files for 2000–2020. Principal component analysis (PCA) was utilized to reduce the number of continuous environmental variables [40–42]. We applied eigenvalues greater than 0.95 and the scree plot criterion for PCA in item level factoring (S1 Fig) during PCA [39–41]. During PCA, we used eigenvalues larger than 0.95 and the scree plot criterion for PCA in item level factoring (S1 Figure) [42]. To keep climatic variables, we performed suppression of superfluous loading and rotation of factor pattern [43] (S2 Table). Thirty-six (36) of the 68 factors initially examined for multicollinearity were omitted from further analysis, they were considered to be independent, the remaining factors were included in the study. The multicollinearity test was implemented using a social sciences statistical software (SPSS v22.0). In addition, the remaining bioclimatic variables, human population density and elevation, were analyzed in MaxEnt algorithm, two approaches; Jackknife test, and variable response curves were chosen to determine the relative contribution of predictor variables to the model. All variables contributing less than one percent were eliminated from the model.

S1 Table. Bioclimatic, elevation and classical meteorological variables used for initial modeling in maxent software (T – Temperature and P – Precipitation)

Label	Variable description	Units
1. Bioclimatic variables		
Bio1	Annual Mean T	°C
Bio2	Mean Monthly Diurnal Range (Tmax - Tmin)	°C
Bio3	Isothermally (BIO2/BIO7) x 100	Index
Bio4	T Seasonality (Standard Deviation)	°C
Bio5	Max T of Warmest Month	°C
Bio6	Min T of Coldest Month	°C
Bio7	T Annual Range (BIO5-BIO6)	°C
Bio8	Mean T of Wettest Quarter	°C
Bio9	Mean T of Driest Quarter	°C

cont. S1Table

Bio10	Mean T of Warmest Quarter	°C
Bio11	Mean T of Coldest Quarter	°C
Bio12	Annual P	mm
Bio13	P of Wettest Month	mm
Bio14	P of Driest Month	mm
Bio15	P Seasonality (Coefficient of Variation)	Fraction
Bio16	P of Wettest Quarter	mm
Bio17	P of Driest Quarter	mm
Bio18	P of Warmest Quarter	mm
Bio19	P of Coldest Quarter	mm

2. Elevation

Alt	Elevation	m a.s.l.
-----	-----------	----------

3. Classical meteorological variables

Monthly P	Monthly P (n=12)	mm
Monthly Tmean, Tmin, Tmax	Monthly mean, minimum and maximum T (n=36)	°C

4. Host

Population density	Sheep population density	Sheep/km ²
	Human population density	People/km ²

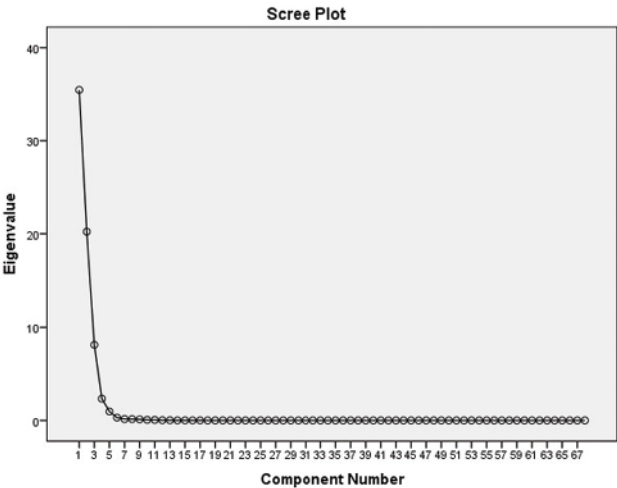


Figure S1.

S2 Table. Ranking of Principal Components by Eigenvalues

PC rank	Eigenvalues		
	Total	Variance %	Cumulative %
1	35.459	52.146	52.146
2	20.223	29.739	81.885
3	8.128	11.953	93.838
4	2.337	3.436	97.275
5	0.963	1.416	98.69

Future climatic variables

We retrieved the future climate variables from WorldClim version 2.1 for 2050 and 2070 at a resolution of 30 arc-seconds [38, 44]. The projected climate scenarios assumptions were obtained from the fifth IPCC assessment report (AR5). The Intergovernmental Panel on Climate Change (IPCC) combines climate research communities to generate a set of climatic scenarios for the twenty-first century. The “Representative Concentration Pathways” (RCPs), renamed “Shared Socioeconomic Pathway” (SSP), describe potential future greenhouse gas emissions based on certain assumptions [45]. In this research, we used the Euro-Mediterranean Centre on Climate Change Earth System Model version 2 (CMCC-ESM2) under two emission scenarios, “Shared Socioeconomic Pathway” (SSP) 1-2.6 (SSP1-2.6), and 2-4.5. (SSP2-4.5). Much lower projected greenhouse gas concentrations are predicted for smaller SSPs, such as 2.6, than for bigger SSPs, such as 8.5. SSP 4.5 provides a modest scenario for reducing greenhouse gas emissions [46].

Model development and evaluation

Using 100 replicates and a 70/30 ratio between the training and testing data sets, a MaxEnt model was trained. To give the models ample time for convergence at 0.00001 [47], the maximum iteration was set to 5000, and 90% sensitivity was set within the MaxEnt model to determine suitability. As a measure of the model’s efficacy, we looked at the area under the Receiver Operating Characteristics (ROC) [48]. The accuracy of the MaxEnt model was determined by calculating the Area Under the Curve (AUC) of the receiver operating characteristic plot [49]. For the future climate change model, we reclassified the MaxEnt spatial model output into four risk classes, namely high, moderate, low and none.

Estimates of suitable habitat under current and future climate change scenarios

Suitable area was calculated using raster calculator in spatial analyst tool in ArcGIS. The raster calculator tool allows one to create and execute a map algebra expression that will output a raster into either a suitable or unsuitable habitat.

RESULTS

Prediction of current Brucellosis distribution

The spatial rarefication of occurrence data selected 36 out of 60 occurrence records at a distance of at least 10 km apart from each other, after duplicates and outliers' points were removed. PCA analysis filtered the 68 environmental variables to 22 independent variables. The independent variables were fitted in the MaxEnt algorithms. After occurrence data filtering, PCA delivered mean diurnal range, Isothermality, Sheep population density, December precipitation, precipitation of the driest month, and June Precipitation as the predictor factors which remained (Table 1). For model validation, our model had a high AUC value of 0.961 and a standard deviation of 0.014, indicating that it had an excellent ability to predict the suitable areas for Brucellosis (Figure 2). Six variables contributed >1%, namely: mean diurnal range (31%), isothermality (26%), sheep population density (17%), December precipitation (13%), precipitation of the driest month (10%), and June precipitation (3%) (Figure 2). The response curves of the variables show that the mean diurnal range (<12°C), isothermality (<33), sheep population density (500 sheep/km²), December precipitation (1mm), precipitation of the driest month (1.0 – 2.5 mm), and June precipitation (>40mm) (Figure 3) can influence brucellosis.

Table 1. Summary of the Jackknife analysis performed to determine importance per environmental variable

Variable	Regularized training gain		Test gain		Test AUC	
	Without variable	With only variable	Without variable	With only variable	Without variable	With only variable
Mean diurnal range	1.56	0.84	1.7	1.02	0.95	0.93
Isothermality	1.7	0.78	1.8	0.9	0.96	0.88
Sheep population density	1.58	0.4	1.78	0.6	0.96	0.88
December precipitation	1.58	0.2	1.7	0.2	0.95	0.68
Precipitation of the driest month	1.7	0.1	1.78	0.12	0.96	0.55
June Precipitation	1.62	0.08	1.78	0.05	0.95	0.55

The Jackknife test of variables demonstrates that excluding any of these six variables influences the model's regularization gain, test gain, and AUC (Table 2). The mean diurnal range had the most significant training gain when each variable was examined as the single environmental variable. In contrast, June precipitation had the lowest values. Furthermore, the lowest training gain appeared when the mean diurnal range was excluded from the model, while the model had the highest gain when isothermality and precipitation of the driest month were excluded (Table 2).

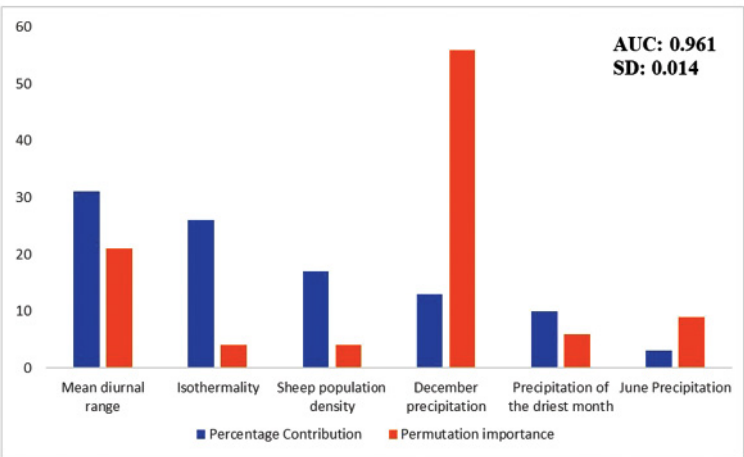


Figure 2. Contribution of the six environmental predictors to the current climate MaxEnt model

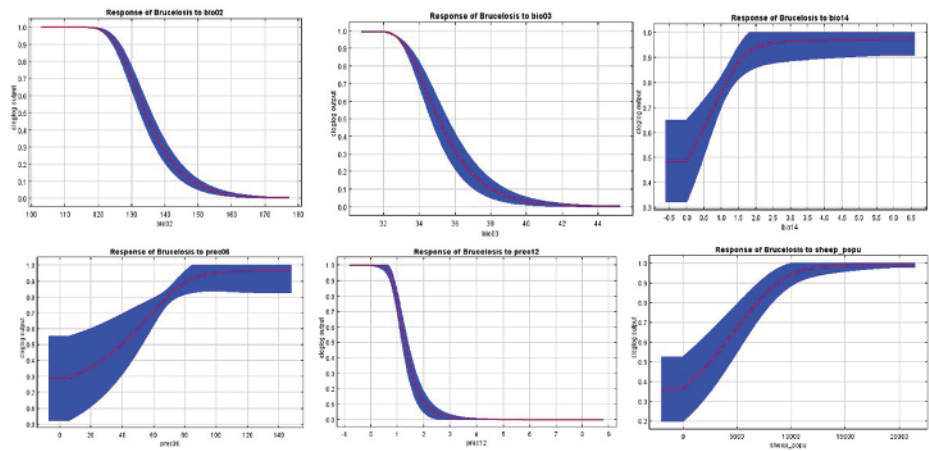


Figure 3. Response curve of Brucellosis under current climate

The mean diurnal range had the highest test gain when utilized as the single environmental variable, whereas June precipitation had the lowest test gain. Our model had the lowest AUC when the mean diurnal range was excluded from the model. Conversely, we had the highest AUC with the mean diurnal range when used as the only variable in the model.

Brucellosis high-risk areas in Qinghai Lake basin were predicted using the MaxEnt algorithm model (Figure 5). High-risk areas were distributed in the north and eastern part of the lake basin. While both low and high elevations were determined to be favorable for Brucellosis, it is of no consequence that the distribution has no distinct elevation preference.

Table 2. Jackknife contribution of the environmental predictors to the future climate change MaxEnt model

Model	AUC	Variables	% Contribution
2050s SSP 2.6	0.81	Bio 3	33.6
		Bio 4	23
		Bio 15	10.1
		Bio 7	9.7
		Bio 18	7.9
		Bio 13	6.4
		Bio 5	4.9
		Bio 8	4.5
2050s SSP 4.5	0.81	Bio 3	28.6
		Bio 8	19
		Bio 5	16.1
		Bio 4	12.1
		Bio 13	8.1
		Bio 15	7.2
		Bio 18	4.5
		Bio 7	4.4
2070s SSP 2.6	0.82	Bio 3	26.2
		Bio 4	21.6
		Bio 8	18.2
		Bio 18	13
		Bio 5	11.5
		Bio 15	9.5
2070s SSP 4.5	0.8	Bio 3	35.5
		Bio 4	26.1
		Bio 15	13.5
		Bio 18	10
		Bio 8	7.6
		Bio 5	7.2

Distribution prediction under future climate scenarios

Four ecological niche models (2050 (SSP 2.6 & SSP 4.5) and 2070 (SSP 2.6 & SSP 4.5)) were produced to predict the potential risk areas for Brucellosis in the Qinghai Lake basin. A total of 19 bioclimatic variables and elevation variable were used in this study. After removing some variables that were found to have highly correlated with other variables, we have Bio 3 (Isothermality), Bio 4 (Temperature seasonality), Bio 5 (Max temperature of the warmest month), Bio 7 (Temperature annual range), Bio 8

(Mean temperature of the wettest quarter), Bio 13 (Precipitation of wettest month), Bio 15 (Precipitation seasonality), and Bio 18 (Precipitation of warmest quarter) for our final model (Table 2). Table 2 shows the relative contributions of 8 variables to all the models. We defined important variables are variables with a 10% contribution to the models. The two most important variables in the model were the Bio 3 and Bio 4 in all the models. In the 2050 RCP 2.6 model, the four most important variables are Bio3, Bio 4, Bio 15 and Bio 7. In the 2050 RCP 4.5 model, Bio 3, Bio 8, Bio 5, and Bio 4 were the most important variables. In 2070 RCP 2.6 model, the six most important variables are Bio 3, Bio 4, Bio 8, Bio 18, Bio 5 and Bio 15. Lastly, in RCP 4.5-year 2070, Bio 3, Bio 4, Bio 15, and Bio 18 are the most important variables in the model. The four models had similar AUCs for RCP 2.6 2050, RCP 4.5 2050, RCP 2.6 2070, and RCP 4.5 2070, which are 0.81, 0.81, 0.82, and 0.80, respectively.

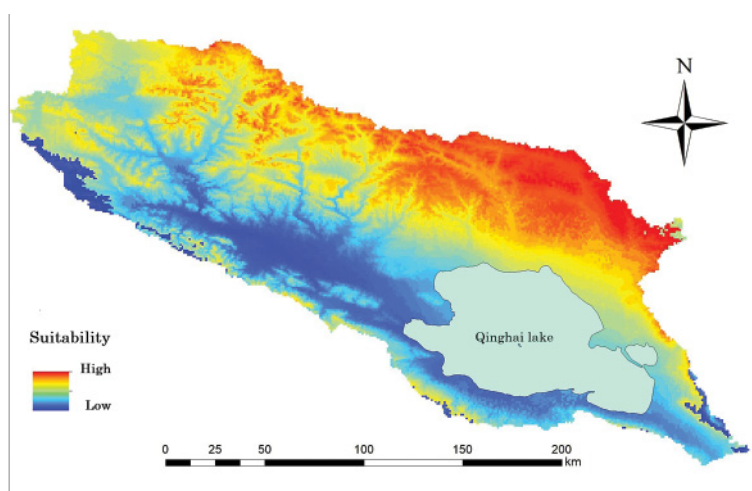


Figure 4. Potential distribution of Brucellosis under current climate

A suitability map of Brucellosis in the Qinghai Lake basin is shown in Figure 1. The red and blue areas indicated high and unsuitable area marked as none, respectively. Figures 1A&B are low emission representatives of the two years 2050 and 2070. A closer observation of the two figures suggests a marked expansion of the highly suitable area in our study area. The high elevated area marked unsuitable in the 2050 was suitable in 2070. Figures 1C&D represent RCP 4.5 for both years 2050 and 2070. The two figures showed a contraction of the high suitable areas from 2050 to 2070, which makes some highly suitable area moderates, and moderate to low suitable areas in our study area.

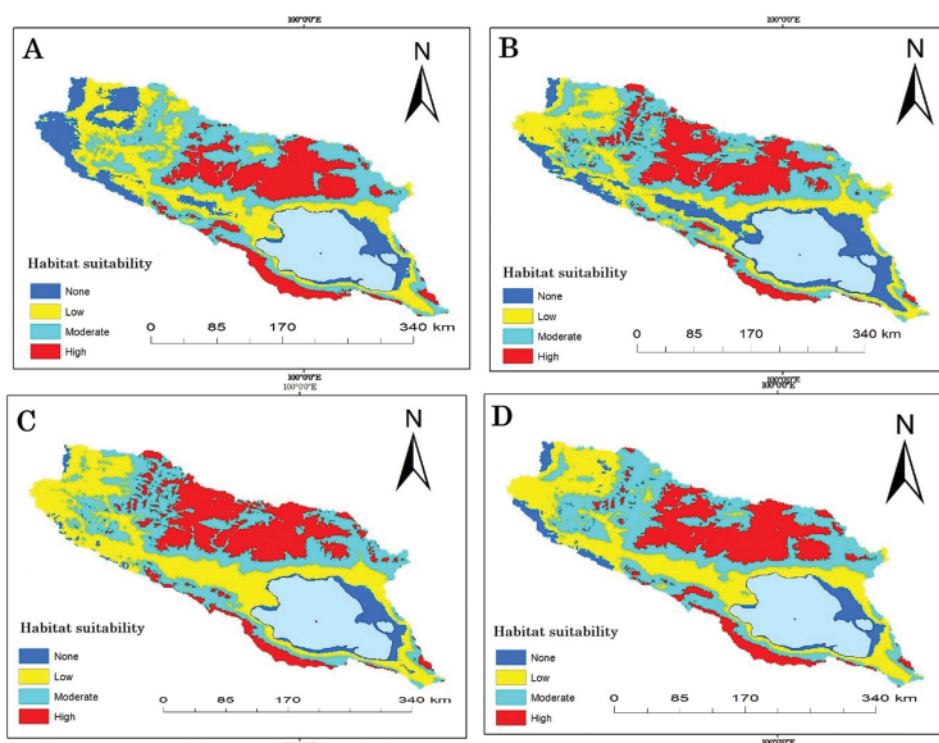


Figure 5. Potential distribution of Brucellosis under future climate: (a) year 2050 SSP 2.6, (b) year 2050 SSP 4.5, (c) year 2070 SSP 2.6 and (d) year 2070 SSP 4.5.

Estimates and comparison of suitable habitat under current and future climate change scenarios

The current habitat suitability map shows that the suitable area is about 21.71% of the study area. Similarly, most of the area exposed to Brucellosis are predicted to remain stable in future scenarios (Fig. 6), with about 16.74 – 21% increase in 2050 and 13.23 – 17.48% in 2070. The suitable area for Brucellosis will increase continuously under the two-greenhouse gas emission in 2050s and 2070s. However, habitat contraction would occur in the 2070s under SSP 2.6 and SSP 4.5 compared to the rapid expansion in the 2050s. The habitat estimation under SSP 4.5, 2050s is predicted to gain the most significant area with about 42.71% of the entire study area, which doubled the present Brucellosis distribution in the Qinghai Lake basin.

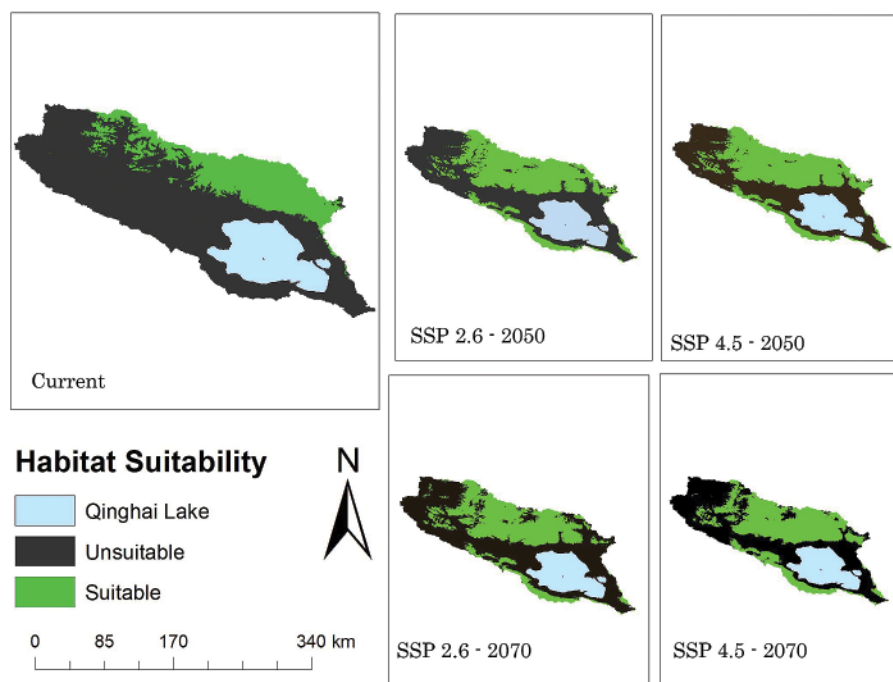


Figure 6. Comparison of suitable habitat under current and future climate change scenarios

DISCUSSION

This work utilized ecological niche modelling to predict the possible habitat distribution of Brucellosis in the Qinghai Lake basin. This is the first risk evaluation of environmentally suitable locations for Brucellosis in the Qinghai Lake basin, while similar work has been conducted at the provincial and national levels. In addition, many studies have explored the spatial distribution of Brucellosis in various countries including Azerbaijan [50], Italy [51], Nigeria [52], Germany [53], Pakistan [54], United States [55], Ecuador [56], and mainland China [57-59]. However, the most suitable study area for Brucellosis in the Qinghai Lake basin yet to be well-studied. Moreover, limited efforts have primarily focused on the environmental dynamics of Brucellosis occurrences [60]. To fill the gaps, this study systematically examined the spatial-temporal distribution of reported Brucellosis cases and incidence rates in the Qinghai Lake basin.

The probability of the presence of Brucellosis based on the MaxEnt model represents the extent of the similarity of ecogeographic conditions at each location to those most suitable for Brucellosis. The areas with a high estimated likelihood of presence may not always have a high number of previously reported cases. Consequently, they may have suitable conditions and, consequently, the potential for future occurrences [34].

The mean diurnal range is our model's most important predictive variable, with the highest percentage of contribution. This was in agreement with other research on modeling the future distribution of vectors in China [61]. According to previous study, Bio 2 (Mean diurnal range) and Bio 4 (Temperature seasonality) are the main factors driving the distribution of two species of mosquito which show different dependence on temperature conditions [62]. Our temperature and livestock population density findings agree with [63] and [64] that temperature influences the spread of infectious diseases in many ways. A lower temperature may favor the microorganism's survival in the environment for more prolonged periods causing outbreaks in the small ruminant population. Another previous study indicated that a higher temperature negatively affects the distribution of host animals [65].

Domesticated animals most often carry Brucellosis, and evidence from a model of animal- Brucellosis transmission shows that 90% of Brucellosis cases are small-ruminant derived in Mongolia [66]. In China, higher incidence rates of Brucellosis were positively associated with the density of sheep and goats [60] and approximately 84.5% of human cases were found to be infected by *B. melitensis* [67]. This agrees with our model which predicts sheep population density as one of the most important variables in Brucellosis distribution in Qinghai Lake basin. Therefore, small ruminant density is used as an indicator for the possibility of Brucellosis occurrences, and sheep and goats are combined to represent small ruminant densities when small ruminant density is unavailable. A study concluded that vaccinating adult sheep alone is insufficient in eradicating Brucellosis based on the prediction that Brucellosis would persist for an extended period, even though all sheep were supposedly vaccinated twice per year [68]. Since 2011, the government has required vaccinations for all sheep twice annually. Given that infected sheep are still common, especially among local herders, simultaneous disinfection and vaccination was suggested, and regular sheep surveillance which has been realized for some areas in China [68].

This study combined MaxEnt and geographic information system (GIS) techniques for Brucellosis's current and future analysis under multiple climate change scenarios in the Qinghai Lake basin. With the rapid spread of advanced spatial techniques and the fast-growing volume of Spatiotemporal high-resolution data, GIS and remote sensing (RS) have played an increasingly vital role in disease ecology and spatial epidemiology. GIS and RS provide a powerful toolset and diversity of data sources for modeling; MaxEnt model in turn has advanced conventional Spatio-temporal analysis by adding more mathematical and computational complexity. The three most important variables are Bio 3 (Isothermality), Bio 4 (Temperature seasonality) and Bio 8 (Mean temperature of the wettest quarter). Regarding future distribution, climate scenarios at different time horizons have indicated that the brucellosis niche will grow regardless of the scenario studied and the time horizon. Our model predicts an expansion in suitable areas in SSP 2.6 for the 2050s and 2070s. This indicates that Brucellosis's living space in Qinghai Lake basin, China will expand under the possible future climate changes.

Environmental modeling for Brucellosis is important, although Brucellosis occurrence is not entirely climate-driven as some infectious diseases, such as malaria [69, 70] and

dengue fever [71] among other diseases. However, varying environmental conditions act as proxies and can influence the lack of water or grass in pasturing areas, increasing disease susceptibility in low-resistance animals. Other environmental factors, such as altitude, can play a vital role in the types of vegetation that can grow in certain areas, precipitation levels, temperature ranges, and other environmental conditions important to the survival and transmission of *Brucella*. Additionally, Brucellosis is capable of being transmitted by fomites. The *Brucella* organism can survive for several months in water, aborted fetuses, manure, hay, contaminated equipment and clothes, and especially in conditions with high humidity, low temperature, and no sunlight [72]. Similar environmental impacts have been revealed by a macro-level study, where lower temperature and less sunshine in winter and spring, and a 1–2-month incubation period have been associated with epidemic peaks from March to August, especially in May [60]. Inhabitants of Qinghai also spend more time working outside during epidemic months than during the harsh winter months, increasing their exposure to Brucellosis infection.

In addition to environmental and biological determinants of the organism, different cultural and livestock management practices among communities in the highlands might impact differences in risk factors, but these differences warrant additional epidemiological field work before they can be confirmed. The probability of presence for Brucellosis represents the extent of the similarity of ecogeographic conditions at each location to those most suitable for Brucellosis. The locations with high predicted probability of presence do not necessarily have a large number of reported cases in the past. They may just have suitable conditions and, consequently, the potential for future occurrences. Pilot surveillance programs should be launched to determine if any under reporting or reporting biases exists at those locations. Another limitation of the study is the quality of disease data that were available (as is the case with most ENM and SDM research [73–75] because the true occurrence locations were not available. Therefore, predicting the high-risk areas of Brucellosis requires knowledge of the locations where people are most likely infected.

Our study on the niche modeling of Brucellosis in QLB does have some limitations. Firstly, there are relatively few occurrence records of Brucellosis so we could only use a small sample size. We therefore chose to use the MaxEnt model as it has shown advantage in terms of predictive performance for use with small sample sizes [76]. Among modeling algorithms that using presence-only records, MaxEnt is relatively insensitive to the sample size (which can be as small as 5) [77, 78].

This study provides a new direction for Brucellosis research and greatly contributes to our knowledge of the roles that various environmental and socioeconomic factors play in the distribution of Brucellosis in Qinghai Lake basin. Moreover, the output of this study will promote comparisons with future research and provide a new perspective to inform decision-making in the field of public health in Qinghai. This study also serves as a predecessor to broader and more in-depth studies of Brucellosis in Qinghai province.

CONCLUSION

The main conclusions of this study are as follows:

1) Brucellosis occurrences in the Qinghai Lake basin exhibit a spatial trend gradually changing from west to east, with the incidence rates in the east far higher than those of other regions; 2) The major variables contributing to the model include mean diurnal range, isothermality, sheep population density, temperature seasonality, December precipitation, mean temperature of wettest quarter, precipitation of the driest month, and June precipitation; 3) The predicted suitable areas cut across all elevation ranging from high to low. 4) The future suitability under lower greenhouse gases emission (SSP 2.6) reveal an expansion in the suitable area for the year 2050 and 2070i

Acknowledgments

We are grateful for the support of the Qinghai provincial administration of forestry and grasslands during sampling and data collection. Thanks to Dr. Hein van Gils for his advice and guidance during the course of data collection, formatting and interpretation.

Funding

This study was supported by State Key Laboratory of Veterinary Biotechnology Foundation (Grant no. SKLVBF201904). The APC was funded by the Northeast Forestry University, Harbin, P. R. China.

Authors' contributions

XL. W and A.T. E. conceived and designed the study, and wrote the manuscript together with HN. A.T. E., HN. W, S. K, JN. L, and LY.H participated in software, validation, formal analysis, and data curation. XL. W. supervised the study and funding acquisition. All authors have read and agreed to the published version of the manuscript.

Declaration of conflicting interests

The authors declare that they have no conflict of interest with respect to the research, authorship, and/or publication of this article.

Abbreviation

MaxEnt – Maximum entropy; SSP – Shared Socioeconomic Pathway; ESRI – Environmental systems research institute; IPCC – Intergovernmental Panel on Climate Change; GIS – Geographic Information System; AUC – Area Under the Curve; ROC – Receiver Operating Characteristics; ISRIC - International Soil Reference and Information; USDA – United States Department of Agriculture; SPSS - Statistical Package for Social Sciences; PCA – Principal Component Analysis; QLB – Qinghai Lake basin.

REFERENCES

1. Marvi A, Asadi-Aliabadi M, Darabi M, Abedi G, Siamian H, Rostami-Maskopae F: Trend Analysis and Affecting Components of Human Brucellosis Incidence During 2006 to 2016. *Med Arch (Sarajevo, Bosnia and Herzegovina)* 2018,72(1):17-21.
2. Morwal S, Sharma S: Bacterial Zoonosis-A Public Health Importance. *J of Dairy Vet and Anim Res* 2017,5(2):56-59.
3. WHO: Brucellosis 2020 [cited 2022]. Available from: <https://www.who.int/news-room/fact-sheets/detail/brucellosis>.
4. Doganay M, Demiraslan H: Human anthrax as a re-emerging disease. *Rec Pat Anti Drug Dis* 2015,10(1):10-29.
5. Dean AS, Bonfoh B, Kulo AE, Boukaya GA, Amidou M, Hattendorf J, Pilo P, Schelling E: Epidemiology of Brucellosis and Q Fever in Linked Human and Animal Populations in Northern Togo. *PLoS One* 2013,8(8):e71501.
6. Godfroid J: Brucellosis in wildlife. *Rev Sci Tech* 2002,21(2):277-286.
7. Corbel MJ, Wray C: The Effect of Natural Infection with *Salmonella Urbana* on the Serological Status of Cattle in Relation to Tests for Brucellosis. *Br Vet J* 1975,131(3):324-334.
8. Jones TC.: *Infectious Diseases of Animals. vol. 1 and vol. 2, Diseases Due to Bacteria.* A. W. Stableforth and I. A. Galloway, Eds. Academic Press, New York; Butterworths, London, 1959. 396 pp.; 414 pp. Illus; 2 vols. *Sci* 1960,132(3418):30-31.
9. Thorne ET, Honess RE: *Diseases of wildlife in Wyoming.* 1982.
10. Corbel, M.J: *Brucellosis in humans and animals.* WHO 2006, Geneva.
11. Olabimi IO, Ileke KD, Adu BW, Arotolu TE: Potential distribution of the primary malaria vector *Anopheles gambiae* Giles [Diptera: Culicidae] in Southwest Nigeria under current and future climatic conditions. *JoBAZ* 2021,82(1):63.
12. Araújo MB, Guisan A: Five (or so) challenges for species distribution modelling. *J of Biogeo* 2006,33(10):1677-1688.
13. Pounds JA, Bustamante MR, Coloma LA, Consuegra JA, Fogden MP, Foster PN, La Marca E, Masters KL, Merino-Viteri A, Puschendorf R, Ron SR, Sánchez-Azofeifa GA, Still CJ, Young BE: Widespread amphibian extinctions from epidemic disease driven by global warming. *Nature* 2006,439(7073):161-167.
14. Woodward A, Smith KR, Campbell-Lendrum D, Chadee DD, Honda Y, Liu Q, Olwoch J, Revich B, Sauerborn R, Chafe Z: Climate change and health: on the latest IPCC report. *The Lan* 2014,383(9924):1185-9.
15. Parham PE, Waldock J, Christophides GK, Hemming D, Augusto F, Evans KJ, Fefferman N, Gaff H, Gumel A, LaDeau S: Climate, environmental and socio-economic change: weighing up the balance in vector-borne disease transmission. *Philosophical Transactions of the Royal Society B: Biol Sci* 2015,370(1665):20130551.
16. Mills JN, Gage KL, Khan AS: Potential influence of climate change on vector-borne and zoonotic diseases: a review and proposed research plan. *Env health pers* 2010,118(11):1507-1514.
17. Rosenthal J: Climate change and the geographic distribution of infectious diseases. *EcoH* 2009,6(4):489-495.
18. Phillips SJ, Elith J: POC plots: calibrating species distribution models with presence-only data. *Ecol* 2010,91(8):2476-2484.

19. Phillips SJ, Anderson RP, Schapire RE: Maximum entropy modeling of species geographic distributions. *Eco Mod* 2006,190(3):231-259.
20. Elith J, Phillips SJ, Hastie T, Dudík M, Chee YE, Yates CJ: A statistical explanation of MaxEnt for ecologists. *Diver and Distr* 2011,17(1):43-57.
21. Boral D, Moktan S: Predictive distribution modeling of *Swertia bimaculata* in Darjeeling-Sikkim Eastern Himalaya using MaxEnt: current and future scenarios. *Eco Proc* 2021,10:26.
22. IPCC. Climate Change 2014: synthesis report. Switzerland: IPCC, 2014.
23. Xiao F, Ling F, Du Y, Feng Q, Yan Y, Chen H: Evaluation of spatial-temporal dynamics in surface water temperature of Qinghai Lake from 2001 to 2010 by using MODIS data. *J of Ari Land* 2013,5(4):452-464.
24. Ma Y, Li X-Y, Liu L, Li Z, Hu X, Wu X, Yang X, Wang P, Zhao S-J, Zhang G-H, Liu B-Y: Measurements and Modeling of the Water Budget in Semiarid High-Altitude Qinghai Lake Basin, Northeast Qinghai-Tibet Plateau. *J of Geo Res: Atm* 2018.
25. Wang J, Tian J, Li X, Ma Y, Yi W: Evaluation of concordance between environment and economy in Qinghai Lake Watershed, Qinghai-Tibet Plateau. *J of Geo Sci* 2011, (5):949.
26. UNESCO. Qinghai Lake: World Heritage tentative lists. 2017(10th April 2019.).
27. Gong J, Li J, Yang J, Li S, Tang W: Land Use and Land Cover Change in the Qinghai Lake Region of the Tibetan Plateau and Its Impact on Ecosystem Services. *Int J Env Res Pub Health* 2017,14(7):818.
28. Wu Y-N, Ma Y-J, Liu W-L, Zhang W-Z: Modeling the Spatial Distribution of Plateau Pika (*Ochotona curzoniae*) in the Qinghai Lake Basin, China. *Animals (Basel)*. 2019,9(10):843.
29. Miller D: The importance of China's nomads. *Rang J* 2002,24(1):22.
30. QSB: Qinghai statistical yearbook. Beijing, China: China Statistics Press, 2010.
31. Kreutzmann H: The tragedy of responsibility in high Asia: modernizing traditional pastoral practices and preserving modernist worldviews. *Pas: Res, Pol and Prac* 2013,3(1):7.
32. Gui-chen C, Min P: Types and Distribution of Vegetation in Qinghai Lake Region. *Ch J of Plant Eco* 1993,17(1):71-81.
33. Brown JL. SDMtoolbox: a python-based GIS toolkit for landscape genetic, biogeographic and species distribution model analyses. *Meth in Eco and Evo* 2014,5(7):694-700.
34. Fekede RJ, van Gils H, Huang L, Wang X: High probability areas for ASF infection in China along the Russian and Korean borders. *Trans Emerg Dis* 2019,66(2):852-864.
35. Arotolu TE, Wang H, Lv J, Shi K, Gils Hv, Huang L, Wang X: Modeling the environmental suitability for *Bacillus anthracis* in the Qinghai Lake Basin, China. *PLoS One* 2022,17(10):e0275261.
36. Pearson R, Raxworthy C, Nakamura M, Peterson A: Predicting species distributions from small numbers of occurrence records: a test case using cryptic geckos in Madagascar. *J of Biogeo* 2007,34:102-117.
37. Arotolu TE, Afe AE, Wang H, Lv J, Shi K, Huang L, Wang X: Spatial modeling and ecological suitability of monkeypox disease in Southern Nigeria. *PLoS One* 2022,17(9):e0274325..
38. Hijmans RJ, Cameron SE, Parra JL, Jones PG, Jarvis A: Very high resolution interpolated climate surfaces for global land areas. *Int J of Clim* 2005,25(15):1965-1978.
39. Cruz-Cárdenas G, López-Mata L, Villaseñor JL, Ortiz E: Potential species distribution modeling and the use of principal component analysis as predictor variables. *Rev Mex de Bio* 2014,85(1):189-199.

40. Moriguchi S, Onuma M, Goka K: Spatial assessment of the potential risk of avian influenza A virus infection in three raptor species in Japan. *J of vet med sci* 2016,78(7):1107-1115.
41. Zeng Z, Gao S, Wang H-N, Huang L-Y, Wang X-L: A predictive analysis on the risk of peste des petits ruminants in livestock in the Trans-Himalayan region and validation of its transboundary transmission paths. *PLoS One* 2021,16(9):e0257094.
42. Bernstein IH: Applied multivariate analysis. Garbin CP, Teng GK, editors. New York: Springer-Verlag 1988.
43. Wade A. 1: A handbook of statistical analyses using SPSS. Sabine Landau and Brian S. Everitt, Chapman & Hall/CRC, Boca Raton, 2004. ISBN: 1-58488-369-3. *Stat in Med* 2005,24(20):3236-3237.
44. Fick SE, Hijmans RJ: WorldClim 2: new 1-km spatial resolution climate surfaces for global land areas. *Int J of Clim* 2017,37(12):4302-4315.
45. van Vuuren DP, Stehfest E, den Elzen MGJ, Kram T, van Vliet J, Deetman S, Isaac M, Klein Goldewijk K, Hof A, Mendoza Beltran A, Oostenrijk R, van Ruijven B: RCP2.6: exploring the possibility to keep global mean temperature increase below 2°C. *Clim Change* 2011,109(1):95.
46. Kopp RE, Horton RM, Little CM, Mitrovica JX, Oppenheimer M, Rasmussen DJ, Strauss BH, Tebaldi C: Probabilistic 21st and 22nd century sea-level projections at a global network of tide-gauge sites. *Eart Fut* 2014,2(8):383-406.
47. Young N, L. C, Evangelista P. A: MaxEnt Model v3.3.3e Tutorial (ArcGIS v10)2011 http://ibis.colostate.edu/webcontent/ws/coloradoview/tutorialsdownloads/a_maxent_model_v7.pdf. Accessed 28th October, 2020.
48. Skowronek S, Van De Kerchove R, Rombouts B, Aerts R, Ewald M, Warrie J, Schiefer F, Garzon-Lopez C, Hattab T, Honnay O: Transferability of species distribution models for the detection of an invasive alien bryophyte using imaging spectroscopy data. *Int J of app earth obs and geo* 2018,68:61-72.
49. Li Y, Li M, Li C, Z. L: Optimized maxent model predictions of climate change impacts on the suitable distribution of *cunninghamia lanceolata* in China. *Forests*. 2020,11(3):302.
50. Abdullayev R, Kracalik I, Ismayilova R, Ustun N, Talibzade A, Blackburn JK: Analyzing the spatial and temporal distribution of human brucellosis in Azerbaijan (1995 - 2009) using spatial and spatio-temporal statistics. *BMC Infec Dis*. 2012,12(1):185.
51. Mancini FR, Bella A, Graziani C, Marianelli C, Mughini-Gras L, Pasquali P, Pompa MG, Rizzo C, Rizzuto E, Busani L: Trends of human brucellosis in Italy, 1998-2010. *Epid and infec* 2014;142(6):1188-1195.
52. Yunusa K, Saidu s, Kudi A, Il I, Jacob R, Buhari H, Baba Y: Geo-Spatial Distribution of *Brucella melitensis* Infection in Selected Local Government Areas of Katsina and Sokoto States, Nigeria. *Nig vet J* 2019,95-103.
53. Al Dahouk S, Neubauer H, Hensel A, Schöneberg I, Nöckler K, Alpers K, Merzenich H, Stark K, Jansen A: Changing epidemiology of human brucellosis, Germany, 1962-2005. *Emerg Infec Dis* 2007,13(12):1895-1900.
54. Saeed U, Ali S: Prevalence and Spatial Distribution of Animal Brucellosis in Central Punjab, Pakistan. *Int J Environ Res Public Health* 2020,17(18).
55. Chomel BB, DeBess EE, Mangiamale DM, Reilly KF, Farver TB, Sun RK, Barrett LR: Changing trends in the epidemiology of human brucellosis in California from 1973 to 1992: a shift toward foodborne transmission. *J of infec dis* 1994,170(5):1216-1223.

56. Ron L, Benitez W, Speybroeck N, Ron J, Saegerman C, Berkvens D, Abatih E: Spatio-temporal clusters of incident human brucellosis cases in Ecuador. *Spat Spatiotemp Epidem* 2013,5:1-10.
57. Zhang J, Yin F, Zhang T, Yang C, Zhang X, Feng Z, Li X: Spatial analysis on human brucellosis incidence in mainland China: 2004–2010. *BMJ Open* 2014,4(4):e004470.
58. Zhong Z, Yu S, Wang X, Dong S, Xu J, Wang Y, Chen Z, Ren Z, Peng G: Human brucellosis in the People's Republic of China during 2005-2010. *Int J of infec dis: IJID : official publication of the Int Soc for Infec Dis* 2013,17(5):e289-92.
59. Chen Z, Zhang W, Ke Y, Wang Y, Tian B, Wang D, Cui B, Zou W, Li S, Huang L, Song H: High-risk regions of human brucellosis in china: implications for prevention and early diagnosis of travel-related infections. *Clin infec dis: an official publication of the Infec Dis Soc of Ame* 2013,57(2):330-2.
60. Li Y-J, Li X-L, Liang S, Fang L-Q, Cao W-C. Epidemiological features and risk factors associated with the spatial and temporal distribution of human brucellosis in China. *BMC Infec Dis* 2013,13(1):547.
61. Liu B, Gao X, Ma J, Jiao Z, Xiao J, Hayat MA, Wang H: Modeling the present and future distribution of arbovirus vectors *Aedes aegypti* and *Aedes albopictus* under climate change scenarios in Mainland China. *Sci of Tot Env* 2019,664:203-214.
62. Liu B, Gao X, Ma J, Jiao Z, Xiao J, Hayat MA, Wang H: Modeling the present and future distribution of arbovirus vectors *Aedes aegypti* and *Aedes albopictus* under climate change scenarios in Mainland China. *Sci of Tot Env* 2019,664:203-214.
63. Arotolu TE, Wang H, Lv J, Kun S, Huang L, Wang X: Environmental suitability of *Yersinia pestis* and the spatial dynamics of plague in the Qinghai Lake region, China. *Vet med* 2022,67(11):569-578.
64. Assefa A, Tibebu A, Bihon A, Yimana M: Global ecological niche modelling of current and future distribution of peste des petits ruminants virus (PPRV) with an ensemble modelling algorithm. *Trans and emerg dis* 2020,00(n/a):1-10.
65. Qian Q, Zhao J, Fang L, Zhou H, Zhang W, Wei L, Yang H, Yin W, Cao W, Li Q: Mapping risk of plague in Qinghai-Tibetan plateau, China. *BMC infec dis* 2014,14(1):1-8.
66. Zinsstag J, Roth F, Orkhon D, Chimed-Ochir G, Nansalma M, Kolar J, Vounatsou P: A model of animal-human brucellosis transmission in Mongolia. *Prev vet med* 2005,69(1-2):77-95.
67. Deqiu S, Donglou X, Jiming Y: Epidemiology and control of brucellosis in China. *Vet micro* 2002,90(1-4):165-182.
68. Hou Q, Sun X, Zhang J, Liu Y, Wang Y, Jin Z: Modeling the transmission dynamics of sheep brucellosis in Inner Mongolia Autonomous Region, China. *Mat bio* 2013,242(1):51-58.
69. Ayala D, Costantini C, Ose K, Kamdem GC, Antonio-Nkondjio C, Agbor J-P, Awono-Ambene P, Fontenille D, Simard F: Habitat suitability and ecological niche profile of major malaria vectors in Cameroon. *Mal J* 2009,8(1):307.
70. Moffett A, Shackelford N, Sarkar S: Malaria in Africa: Vector Species' Niche Models and Relative Risk Maps. *PLoS One* 2007,2(9):e824.
71. Peterson AT, Martínez-Campos C, Nakazawa Y, Martínez-Meyer E: Time-specific ecological niche modeling predicts spatial dynamics of vector insects and human dengue cases. *Trans of the Roy Soc of Trop Med and Hyg* 2005,99(9):647-655.

72. Md SR, Roma RS, Falk M, Lisa DS, Heinrich N: Brucellosis in human and domestic animals in Bangladesh: A review. *Afri J of Mic Res* 2014,8(41):3580-3594.
73. Mischler P, Kearney M, McCarroll J, Scholte R, Vounatsou P, Malone J: Environmental and socio-economic risk modeling for Chagas disease in Bolivia. *Geo health* 2012,6:S59-66.
74. Escobar LE, Peterson AT, Favi M, Yung V, Pons DJ, Medina-Vogel G: Ecology and Geography of Transmission of Two Bat-Borne Rabies Lineages in Chile. *PLoS negl trop dis* 2013,7(12):e2577.
75. Medley KA: Niche shifts during the global invasion of the Asian tiger mosquito, *Aedes albopictus* Skuse (Culicidae), revealed by reciprocal distribution models. *Glob Eco and Bio* 2010,19(1):122-133.
76. Wisz MS, Hijmans RJ, Li J, Peterson AT, Graham CH, Guisan A, Group NPSDW: Effects of sample size on the performance of species distribution models. *Diver and Dis* 2008,14(5):763-73.
77. Hernandez PA, Graham CH, Master LL, Albert DL: The effect of sample size and species characteristics on performance of different species distribution modeling methods. *Ecog* 2006,29(5):773-85.
78. van Proosdij ASJ, Sosef MSM, Wieringa JJ, Raes N: Minimum required number of specimen records to develop accurate species distribution models. *Ecog* 2016,39(6):542-52.

MODELI SADAŠNJIH I BUDUĆIH DISTRIBUCIJA BRUCELOZE U ODNOSU NA KLIMATSKE PROMENE U BASENU QINGHAI JEZERA, KINA

Temitope Emmanuel AROTOLU, HaoNing WANG, JiaNing LV, Kun SHI, LiYa HUANG, XiaoLong WANG

Bruceloza je bakterijska bolest koju izazivaju različite vrste bakterije *Brucella*, koje inficiraju prvenstveno goveda, svinje, koze, ovce i pse. Bolest se obično prenosi na ljude direktnim kontaktom sa bolesnim životinjama tj. kliconošama, konzumiranjem kontaminiranih životinjskih proizvoda ili udisanjem konaminisanog vazduha. Većina slučajeva uzrokovana je konzumiranjem nepasterizovanog kozjeg ili ovčijeg mleka ili sira. Na osnovu uočenih podataka o pojavi bruceloze i ekogeografskih varijabli, MakEnt algoritam je korišćen za modeliranje trenutne i buduće distribucije bruceloze u basenu jezera Qinghaj, N. R. Kina. Naš model je pokazao trenutnu distribuciju bruceloze i predviđa odgovarajuća pomeranja staništa prema budućim klimatskim scenarijima. U novim predstavnicima; SSP 2.6 i SSP 4.5 za 2050-te i 2070-te godine, naš model predviđa ekspanziju u trenutnim pogodnim oblastima. Ovo ukazuje da će se u odnosu na moguće klimatske promene u budućnosti, geografska distribucija bruceloze u basenu jezera Qinghaj u Kini, značajno proširiti. Naš model ukazuje na ekogeografske varijable koje su značajno doprinele distribuciji bruceloze u basenu jezera Qinghaj. Rezultati naše studije promovišu poređenja sa budućim istraživanjima i pružaju novu perspektivu za donošenje odluka u oblasti javnog zdravlja u provinciji Qinghaj.