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Research article

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

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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

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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 (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 km^2, while the basin is about 29,600 km^2. 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: needleaved 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].

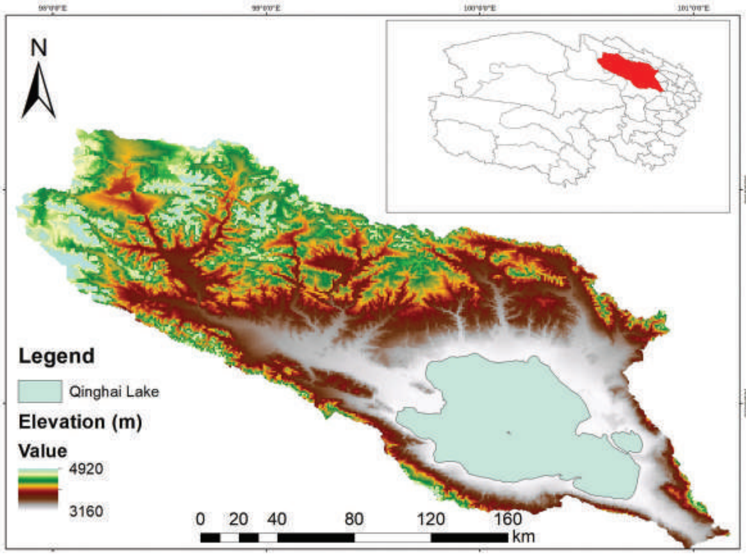

Figure 1. Study area: Qinghai Lake basin in Qinghai Province, People's Republic of China

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

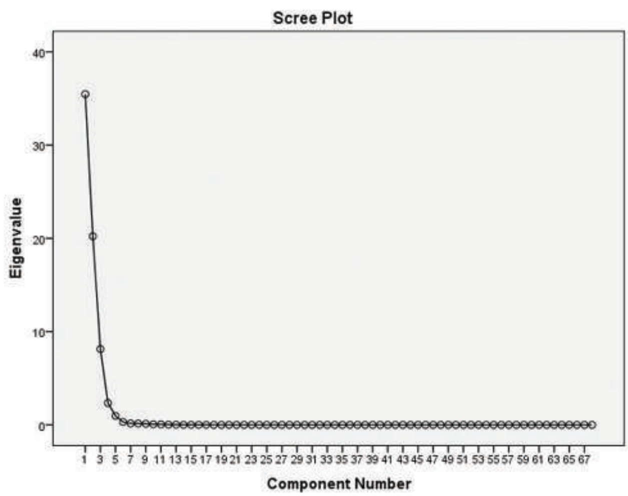

Figure S1.

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 (<12ºC), isothermality (<33), sheep population density (500 sheep/km^2), 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).

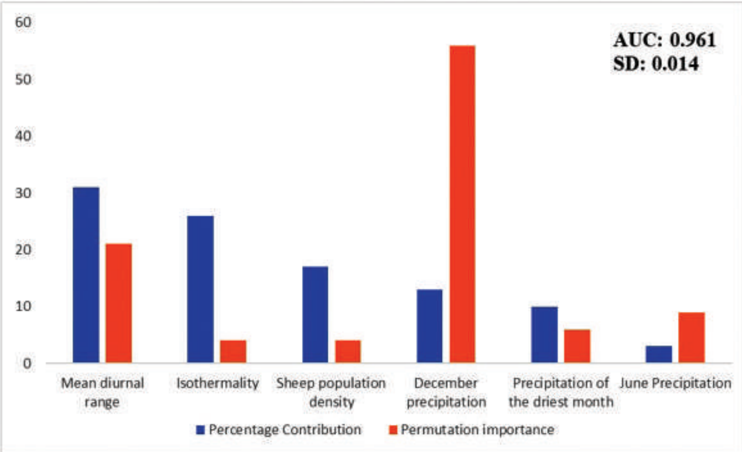

Figure 2. Contribution of the six environmental predictors to the current climate MaxEnt model

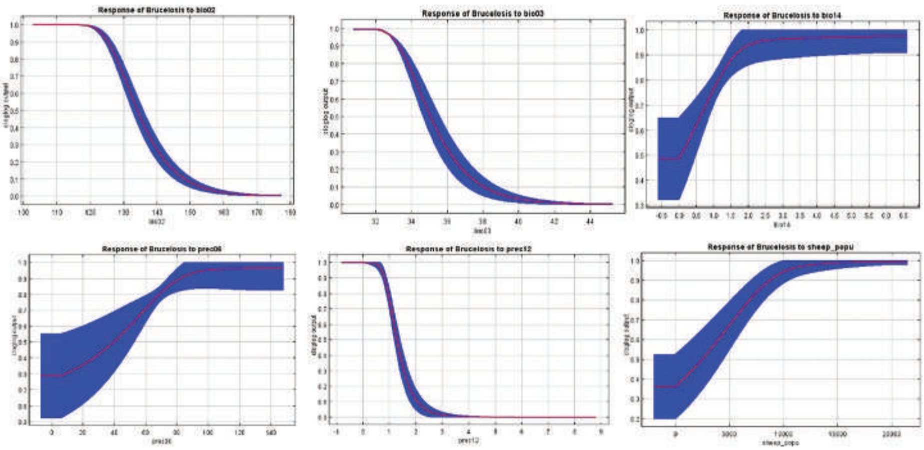

Figure 3. Response curve of Brucellosis under current climate

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.

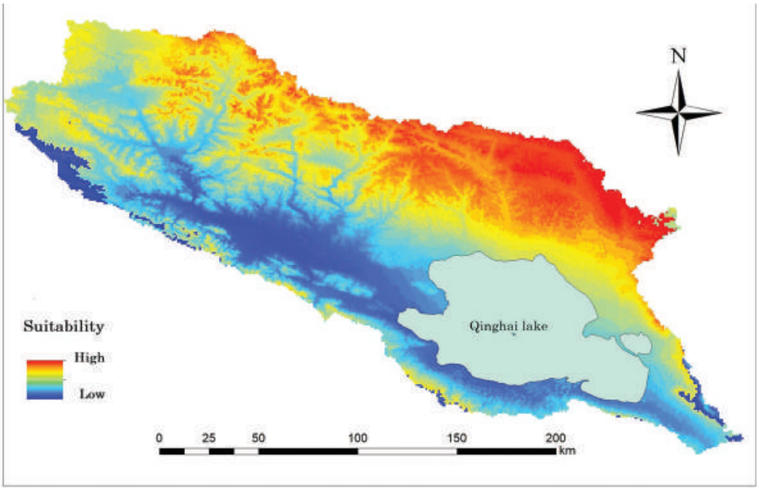

Figure 4. Potential distribution of Brucellosis under current climate

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.

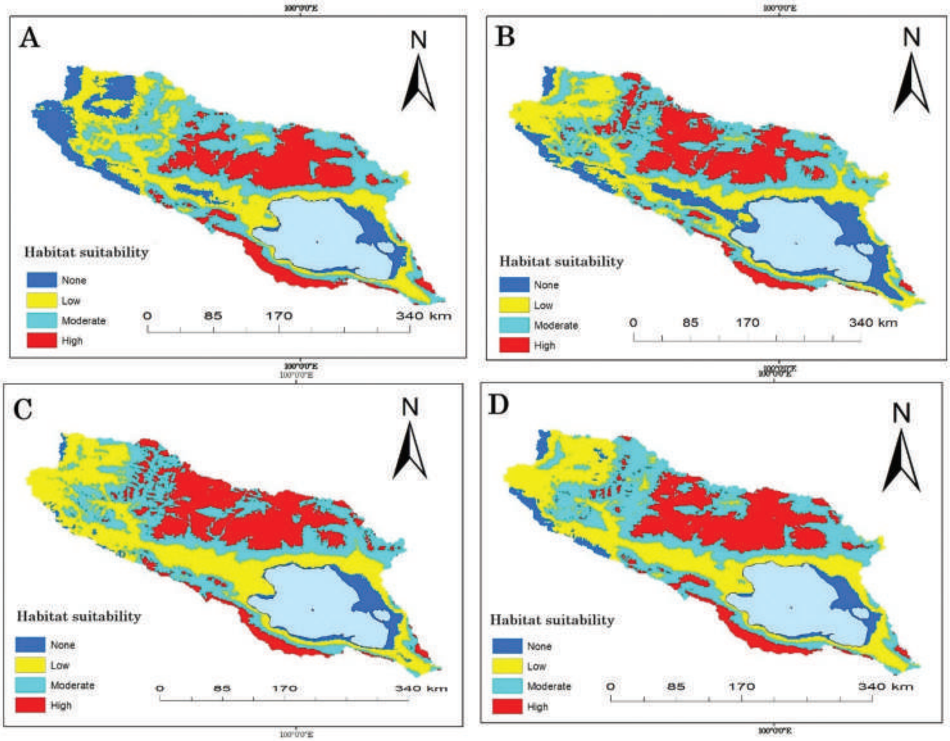

Figure 5. Potential distribution of Brucellosis under future climate: **(a)** year 2050 SSP 2.6, **(b)** year 2050 SSP 4.5, **(c)** year 2070 SSP 2.6 and **(d)** year 2070 SSP 4.5.

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.

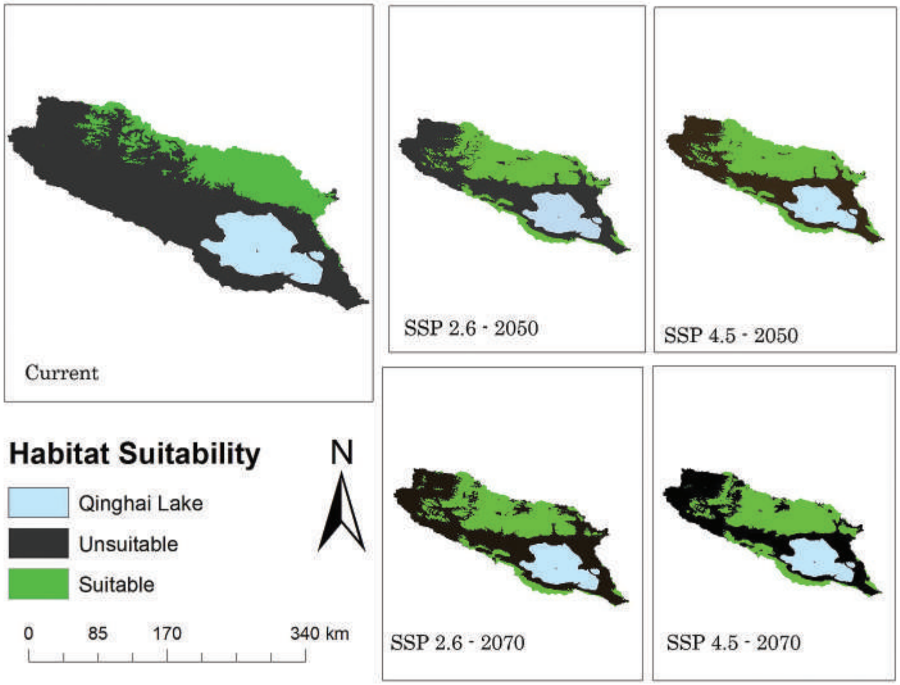

Figure 6. Comparison of suitable habitat under current and future climate change scenarios

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

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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.

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

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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 kontaminisanih 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.