

Article

BIOCLIM Modeling for Predicting Suitable Habitat for Endangered Tree *Tapiscia sinensis* (Tapisciaceae) in China

Chunping Xie ^{1,†} , Lin Chen ^{2,†} , Meng Li ² , Chi Yung Jim ^{3,*}  and Dawei Liu ⁴

¹ Tropical Biodiversity and Bioresource Utilization Laboratory, Qiongtai Normal University, Haikou 571127, China; xcp@mail.qtnu.edu.cn

² Co-Innovation Center for the Sustainable Forestry in Southern China, College of Life Sciences, Nanjing Forestry University, Nanjing 210037, China; clinechen@njfu.edu.cn (L.C.); limeng@njfu.edu.cn (M.L.)

³ Department of Social Sciences and Policy Studies, Education University of Hong Kong, Tai Po, Hong Kong, China

⁴ Key Laboratory of State Forest and Grassland Administration Wildlife Evidence Technology, Nanjing Police College, Nanjing 210023, China; dwliu@nfpcc.edu.cn

* Correspondence: cyjim@eduhk.hk

† These authors contributed equally to this work.

Abstract: Climate change jeopardizes species survival, particularly for endangered species. This risk extends to the endangered Chinese endemic tree *Tapiscia sinensis*. The factors underpinning *T. sinensis*'s habitat distribution are poorly understood, and its potential response to future climate scenarios remains unclear. With six shortlisted climate factors and 117 occurrence records, we modeled *T. sinensis*'s potential distribution across China using the BIOCLIM model. We applied principal component analysis to examine the primary climate factors restricting its geographical range. The findings indicate that *T. sinensis*' range is principally located in China's middle subtropical climatic zone at low–mid altitudes. The principal component analysis identified two critical factors representing temperature and precipitation. Temperature was the most critical factor limiting *T. sinensis* distribution, especially the effect of temperature seasonality and isothermality. The habitat suitability model generated by BIOCLIM under current climate conditions demonstrated strong concordance between the predicted suitable areas and the present actual distribution range. These results verify that the model can reliably identify habitats conducive to *T. sinensis* growth and survival. However, under a hypothetical future climate scenario of doubled atmospheric CO₂ concentrations for 2100, the model indicates a precipitous reduction and fragmentation in the areas with excellent suitability conditions. This predicted decline highlights the considerable threats posed by climate change to the long-term survival of this endangered species in China. Our habitat modeling yields critical insights that inform the development of science-based strategies and best practices to improve conservation management plans for research, protection, nursery cultivation, and sustainable planting in China. Habitat suitability knowledge could aid introduction and cultivation efforts for *T. sinensis* globally in places with analogous climates.

Keywords: *Tapiscia sinensis*; endangered species; geographical range; bioclimatic factor; suitable habitat; climate change scenario



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1. Introduction

Climate is the primary factor shaping the geographical distribution of species and one of the key factors that limit species reproduction and growth [1]. Understanding the correlation between species geographical distribution and climate can help us in grasping the macro patterns of threatened status, endemism, diversity, evolution, and development, and provide valuable clues for predicting future distribution patterns [2]. Global warming has led to the fragmentation of plant habitats and a sharp decrease in suitable habitats, which has driven some species to the brink of extinction [3]. Some species have responded

to environmental changes by migration to modify distribution areas [4]. Therefore, studying the impacts of current and future climate conditions on species geographical patterns is crucial to ensure timely planning and implementing effective conservation strategies [5].

Species distribution models (SDMs) have been developed to analyze the evolution of species distribution patterns. SDMs have been widely applied in quantitative ecology to evaluate species patterns, which has become a research hotspot [6]. They have been used to formulate practical problem solutions and scientific hypotheses [7]. SDMs are also known as habitat or niche models, bioclimatic envelopes, and resource selection functions. They describe the observed distribution patterns of specific species using environmental and geographical data [8]. Their ability to process diverse data, including occurrence records in museums and herbaria, has permitted widespread applications [9].

In assessing climate change's effects on species distribution evolution, SDM predictions can extend beyond the regions supplying the original training samples [10]. For example, the MaxEnt model can explore the suitable distribution range of *Mentha pulegium* L. in Tunisia and identify the main ecological factors limiting its distribution. The findings provide critical information that will help us to develop management strategies to protect and conserve the species [11]. The coupling of geographic information system (GIS) technology and data analysis has promoted new modeling methods and applications [12]. These range from simple environmental matching techniques, to complex nonlinear relationships between environment and species occurrence, and maximum entropy modeling [13]. The currently used SDMs include MaxEnt, GLM, GAM, BRT, BIOCLIM, DOMAIN, GARSP, etc., each with advantages and disadvantages [14–16]. For example, the popular MaxEnt model shows good predictive performance for small levels of sample data [17], but queries have been raised regarding the credibility of its predictive results [18].

The BIOCLIM model, created by Nix and Busby late in the last century, is characterized by its early development, simple algorithm, ease of operation, and good generality. It is still widely used for predicting species distribution and studying the impacts of environmental factors on species distribution [16]. BIOCLIM is based on the principle of generating a series of climate parameters that are biologically significant to describe a species' distribution area [19,20]. They include general climate, extreme climate, and seasonal climate variables in relation to the species' known distribution area. A bioclimatic envelope (file or profile) is then calculated using a digital elevation model (DEM) for the studied species [21]. In each grid, the variables of the study area are compared with those of the bioclimatic envelope to predict suitable habitats for the species [22]. If all climate variables in the area fall within the species' bioclimatic envelope, that area is rated suitable for its survival [23].

Generally, a species' marginal and core bioclimatic envelopes are classified into levels 0 (100%) to 5 (95%) [24]. However, this definition has a pitfall in assuming the maintenance of stable populations even under extreme environmental conditions [25]. While a species may survive such stressful conditions, it cannot sustain a continuous population. To reduce the impact of extreme values on model performance and improve its predictive ability, samples with extreme values (e.g., the highest 5%) are selected from all variables in all samples before defining the boundaries of multidimensional hyperrectangles [14]. The extreme values of these environmental variables are averaged to obtain the boundary of the hyperrectangle and estimate the species' potential distribution area [15]. For example, using the BIOCLIM to predict the distribution of *Garcinia indica* in India indicated that it could grow in Maharashtra, Goa, and Karnataka. The results are useful for the large-scale planting and sustainable utilization of this species [26].

Tapiscia sinensis Oliver, within the Tapisciaceae family, is a unique Tertiary relict plant in China [27]. It is an ecologically and evolutionarily important species that plays a significant role in maintaining biodiversity in China's forests [28]. This species is important in studying subtropical flora and the evolution of angiosperm breeding systems in China [29,30]. *T. sinensis* is sparsely distributed in the broad subtropical regions of China, ranging from Sichuan, Shaanxi, and Guizhou provinces in the west to Zhejiang, Fujian, and Guangdong provinces in the east. Due to its poor breeding performance and natural regeneration ability,

as well as its widespread damage by deforestation and reclamation [31], the species' small and widely scattered wild population demands enhanced protection [32]. The decline in the population of *T. sinensis* due to habitat loss and fragmentation has significantly degraded forest ecosystems, making it an important species to study from a conservation perspective. The extensive collection of specimen occurrence data can improve our understanding of the geographical distribution and biogeographical dynamics of *T. sinensis*.

The species was included in the IUCN Red List of Threatened Species in 1998 as vulnerable, raising its threat status from the rare category (<https://www.iucnredlist.org/species/32455/9708341>, accessed on 6 May 2013). It is described as showing "continuing decline in area, extent and/or quality of habitat". The population is described as severely fragmented, beset with the continuing decline of mature individuals. *T. sinensis* has received much research attention due to its unique functionally androdioecious breeding system, thus presenting an important case for studying the evolution of the angiosperm reproduction mechanism [27,29]. It was listed as a third-class key protected plant in China in the 1990s [33]. Furthermore, the species is an important genetic resource for developing new drugs and bioproducts [34]. However, due to recent changes in China's evaluation criteria for rare and endangered plants, this species was not listed in the latest list of national key protected plants [35]. Whether this treatment is appropriate remains to be assessed and debated.

This study aimed to systematically collect data on the natural distribution and bioclimatic factors of *T. sinensis* in order to explore the key climatic variables influencing its geographical occurrences. We applied principal component analysis to identify the most important bioclimatic predictors of *T. sinensis* distribution. We then developed a species distribution model using BIOCLIM to predict its potential range in China and examined how future climate change might modify its distribution pattern. The findings could provide a scientific foundation that will inform the conservation of wild *T. sinensis* populations, guide introduction and breeding programs, and sustainably develop its resource base.

2. Materials and Methods

2.1. Data Collection

Occurrence records for *T. sinensis* wild populations stretching from southwest to south and east China were compiled from extensive field surveys conducted in Anhui, Jiangxi, Zhejiang, and other provinces over several years. Additional occurrence data were gathered through a literature review of publications on flora, as well as checklists, articles, monographs, and reports. Online specimen databases were also consulted, including the Chinese Virtual Herbarium (CVH, <http://www.cvh.ac.cn/>, accessed on 10 May 2023), National Specimen Information Infrastructure (NSII, NSII; <http://www.nsii.org.cn/2017/home.php>, accessed on 12 May 2023), and Global Biodiversity Information Facility (GBIF, <http://www.gbif.org/>, accessed on 15 May 2023). Records lacking geographical coordinates or representing cultivated specimens were excluded. The initial compilation logged 1062 occurrence points for the species. After removing incomplete, incorrect and duplicated records, the spatial rarefaction occurrence data tool SDMtoolbox 2.0 was used to filter the points, retaining only one record per 5×5 km grid cell based on the resolution of bioclimatic data [36]. This method reduced spatial autocorrelation in the dataset. The final spatially filtered dataset contained 117 *T. sinensis* occurrence records suitable for BIOCLIM species distribution modeling, covering primarily from Zhejiang to Sichuan and Yunnan (Figure 1).

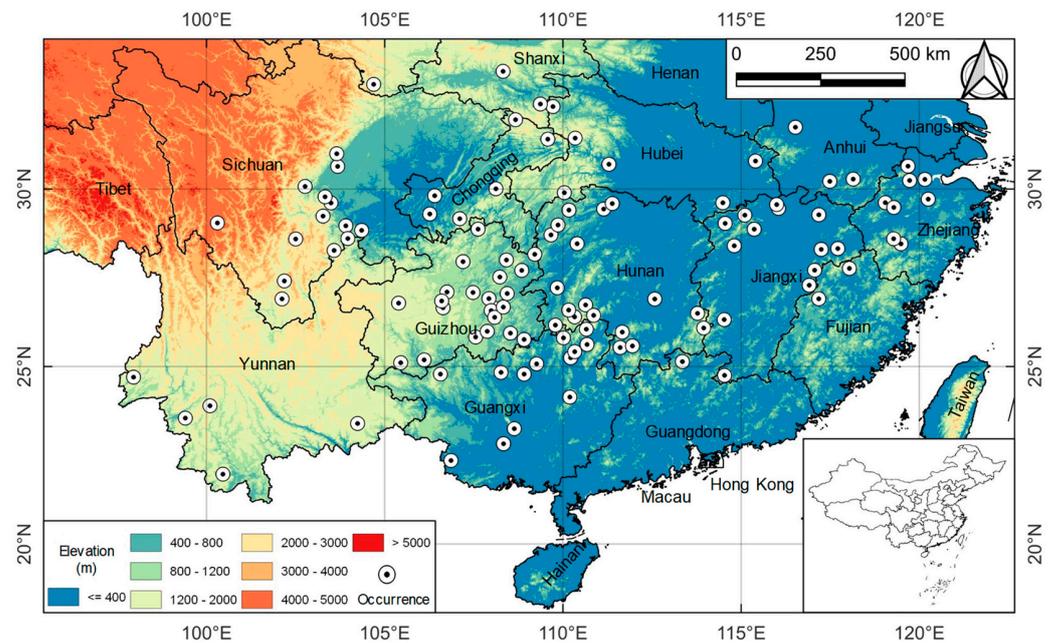


Figure 1. Locations of 117 spatially filtered occurrence records (shown by white circles) of *T. sinensis* in southwest to south and east China in relation to elevation.

2.2. Environmental Factors

The current climate data used in this study were downloaded from the Worldclim (<http://www.worldclim.org>, accessed on 15 May 2023) [37,38], containing a total of 19 bioclimatic variables, recorded as bio1~bio19 (Table 1). It is a set of global climate raster data generated by interpolating monthly meteorological information recorded by weather stations around the world from 1950 to 2000 [39]. The bioclimatic variables were selected based on their biological relevance and inclusion in similar studies. Specifically, the analysis focused on variables related to annual trends (e.g., annual mean temperature, annual precipitation), seasonality (e.g., precipitation in the warmest/coldest quarters), and extreme conditions (e.g., extreme high and low temperatures). Derived from monthly temperature and precipitation measurements, these factors broadly characterize the annual, seasonal, and extreme climatic conditions relevant to species distributions [40]. Future climate projections were generated by the National Center for Atmospheric Research's CCM3 model [41], which simulates the 2100 climate scenario with a doubling of atmospheric carbon dioxide concentrations. Both current and future climate data sets adopted a spatial resolution of 2.5 arcminutes.

Multicollinearity among predictor variables can lead to overfitting and reduced accuracy in ecological niche models [4,42]. To avoid introducing redundant information in model development, preliminary screening was conducted using principal component analysis (PCA) and the Spearman correlation coefficient (r) to identify the bioclimatic variables contributing the most to model gain [43,44]. The r values were calculated between all pairs of bioclimatic variables using PAST 4.12b to quantify collinearity [45]. If the absolute r value between two variables exceeded 0.8, indicating a strong correlation, only the variable with a greater contribution (higher PCA loading) was retained for further analysis, while the remaining one was removed. This selection process kept 11 uncorrelated bioclimatic variables (included in Figure 2) to maximize the unique informational content for the ensuing data processing. We conducted a second PCA using the 11 shortlisted variables. We then selected the factors that ranked in the top three for the simulation using the first and second axes of the principal components as the environmental variables [46]. A final set of six bioclimatic variables was selected for inclusion in the final ecological niche model (Table 1, shown in bold).

Table 1. Nineteen environmental variables were selected to predict the geographical distribution of *T. sinensis*. After screening to eliminate multicollinearity and factor selection by principal component analysis, the six variables shown in bold font were retained for BIOCLIM modeling. The bioclimatic variables are divided into three categories: (1) interannual variation factors, including bio1, bio3, bio7 and bio12; (2) seasonal variation factors, including bio2, bio4, bio8, bio9, bio10, bio11, bio15, bio16, bio17, bio18, and bio19; and (3) extreme climate factors, including bio5, bio6, bio13, and bio14.

Code	Bioclimatic Variable	Unit	Code	Bioclimatic Variable	Unit
bio1	Annual mean temperature	°C	bio11	Mean temperature of coldest quarter	°C
bio2	Mean diurnal range	°C	bio12	Annual precipitation	mm
bio3	Isothermality (Bio2/Bio7) ($\times 100$)	Index	bio13	Precipitation of wettest month	mm
bio4	Temperature seasonality	Index	bio14	Precipitation of driest month	mm
bio5	Max temperature of warmest month	°C	bio15	Precipitation seasonality	Index
bio6	Min temperature of coldest month	°C	bio16	Precipitation of wettest quarter	mm
bio7	Temperature annual range	°C	bio17	Precipitation of driest quarter	mm
bio8	Mean temperature of wettest quarter	°C	bio18	Precipitation of warmest quarter	mm
bio9	Mean temperature of driest quarter	°C	bio19	Precipitation of coldest quarter	mm
bio10	Mean temperature of warmest quarter	°C			

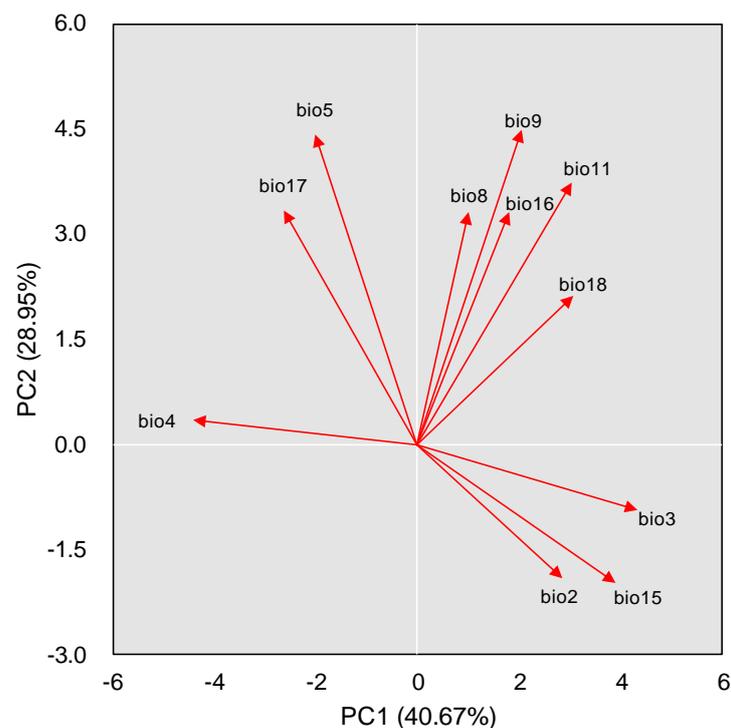


Figure 2. Principal component analysis (PCA) of 11 bioclimatic variables for the 117 occurrence records of *T. sinensis*. The first PCA axis accounts for 40.67% of the total variance, and the second PCA axis accounts for 28.95% of the total variance. The meanings of bioclimatic variables can be found in Table 1.

2.3. Models Analysis

BIOCLIM is one of the earliest and most widely used species distribution models developed for conservation applications [47]. It enlists the environmental envelope concept to define a species' climatic requirements, taking species occurrence locations and extracting the range of climatic values to delineate the climatic niche space [16]. This climatic envelope is then used to map habitat suitability across a landscape, relying only on climatic variables like annual means, extremes, and seasonality derived from temperature and rainfall data [21]. BIOCLIM is relatively simple and transparent, but relies on equilibrium

assumptions and unlimited dispersal. It pioneered the most easily interpretable climate envelope models, providing a foundation for more complex methods [16,47]. It is still considered to perform reasonably well, especially in ensembles, for mapping potential species distributions. However, it may overpredict compared to models incorporating additional predictors and species interactions [19].

Species distribution models for *T. sinensis* were developed using the BIOCLIM algorithms in the Modeling-Bioclim/Domain module of DIVA-GIS 7.5 software [38]. The generated habitat suitability maps were imported into QGIS 3.28.3 for analysis [48]. Suitable habitats were classified as excellent, very high, high, medium, low, or unsuitable based on different thresholds in each model. BIOCLIM defined thresholds from unsuitable to excellent as 0%–2.5%, 2.5%–5%, 5%–10%, 10%–20%, and 20%–46% habitat suitability [46]. Occurrence data were split, with 75% for model training and 25% for testing. Model accuracy was evaluated using the area under the receiver operating characteristic curve (AUC). AUC values near 1 indicate a higher prediction accuracy. Values of 0.5–0.6, 0.6–0.7, 0.7–0.8, and >0.9 represent fair, good, very good, and excellent predictions, respectively. AUC < 0.5 signifies a failed prediction [11,18].

3. Results

3.1. Geographical Distribution Pattern

The 117 valid natural occurrences of *T. sinensis* in China cover a horizontal range between circa 97°56' E–120°15' E and 21°57' N–33°18' N (Figure 1). Guizhou has the highest frequency (23), followed by Hunan (18), Jiangxi (14), Guangxi (14), and Sichuan (13). The frequency is less than 10 in Anhui, Fujian, Gansu, Guangdong, Hubei, Shaanxi, and Chongqing. The southernmost distribution is in Menghai (Yunnan), the northernmost is in Ningshan (Shaanxi), the easternmost is in Zhuji (Zhejiang), and the westernmost is in Wenshan (Yunnan). Therefore, the horizontal distribution of *T. sinensis* is focused on China's middle subtropical zone.

The elevational distribution of *T. sinensis* (Figure 1) shows a wide vertical range, from low elevations to above 2000 m. Based on specimen records, the highest occurrence is in Daocheng (>2000 m) in Sichuan, and the lowest is in Guangde (about 200 m) in Anhui. By altitudinal classes, the spreads at low (<500 m), mid (500–1000 m), mid–high (1000–2000 m), and high (\geq 2000 m) elevations are 57.26%, 25.64%, 17.09% and 0.01%, respectively. The low to mid elevations account for over 80%. Therefore, *T. sinensis* is a subtropical tree species distributed predominantly at low–mid elevations with a certain cold tolerance.

3.2. Restrictive Climatic Factors

Principal component analysis was performed on the 11 selected bioclimatic factors. The first four principal components had eigenvalues greater than 1.0, contributing 40.67%, 28.95%, 11.85% and 10.16%, respectively (Figure 2). The cumulative contribution of the first three principal components reached 81.47% (>75%), indicating that most of the original information was preserved in the reduced dimensional space [49]. The top four factors in the first principal component were the coefficient of variation of temperature seasonality (bio4, −0.44), isothermality (bio3, 0.43), precipitation seasonality (bio15, 0.39), and precipitation of warmest quarter (bio18, 0.31). This order indicates that excessive fluctuations in temperature have a greater impact on *T. sinensis*, which may be more suitable in areas with less annual temperature variation. The main factors in the second principal component were the maximum temperature of the warmest month (bio5, 0.44), the mean temperature of the driest quarter (bio9, 0.45), the mean temperature of the coldest quarter (bio11, 0.37) and precipitation of the wettest quarter (bio17, 0.33). This axis mainly reflects the influence of extreme seasonal temperatures and precipitation on *T. sinensis*, signifying the impact of extreme ecological conditions on species growth. The remaining principal components contained progressively less information, denoting the effects of minor factors.

Table 2 presents the descriptive statistics of the key bioclimatic parameters in the distribution areas of *T. sinensis* in China. The isothermality (bio3) range varied from 23.54

to 53.22, with a mean of 29.58 ± 5.89 and a coefficient of variation of 19.92. The 95% confidence interval for bio3 was 28.50 to 30.66. Temperature seasonality (bio4) showed greater variability, ranging from 341.12 to 916.92 and averaging 749.93 ± 117.73 . Its coefficient of variation was relatively high at 15.70, and the 95% confidence interval was 728.38 to 771.49. For the maximum temperature of the warmest month (bio5), the minimum and maximum values were 18.20 and 34.40 °C, respectively, with a mean of 31.21 ± 2.53 °C and a coefficient of variation of 8.10, which has a key influence on the distribution of *T. sinensis* [49]. The 95% confidence interval for bio5 was tight at 30.75 to 31.68 °C. The mean temperature of the driest quarter (bio9) had the widest range, from -3.43 to 16.28 °C, and the highest coefficient of variation at 40.62. The average bio9 was 8.43 ± 3.43 °C, with a 95% confidence interval of 7.81 to 9.06 °C. Similar patterns were observed for the mean temperature of the coldest quarter (bio11), which varied from -3.43 to 15.72 °C, with an average of 7.37 ± 2.95 °C and a coefficient of variation of 40.00. Its 95% confidence interval was 6.83 to 7.91 °C. For precipitation seasonality (bio15), the range was 44.71 to 122.97, with an average of 66.42 ± 15.11 and a coefficient of variation of 22.75. The 95% confidence interval for bio15 was 63.65 to 69.19. Overall, the data show considerable variability in key bioclimatic factors across the distribution areas of *T. sinensis* in China.

Table 2. Descriptive statistics of the main bioclimatic parameters in the distribution areas of *T. sinensis* in China.

Bioclimatic Variable	Minimum	Maximum	Mean \pm SD	Coefficient of Variation	95% Confidence Interval
bio3 Isothermality	23.54	53.22	29.58 ± 5.89	19.92	28.50–30.66
bio4 Temperature seasonality	341.12	916.92	749.93 ± 117.73	15.70	728.38–771.49
bio5 Max. temperature of warmest month	18.20	34.40	31.21 ± 2.53	8.10	30.75–31.68
bio9 Mean temperature of driest quarter	-3.43	16.28	8.43 ± 3.43	40.62	7.81–9.06
bio11 Mean temperature of coldest quarter	-3.43	15.72	7.37 ± 2.95	40.00	6.83–7.91
bio15 Precipitation seasonality	44.71	122.97	66.42 ± 15.11	22.75	63.65–69.19

3.3. Current and Future Potential Distribution

The BIOCLIM model predicted current and future suitable habitat areas for *T. sinensis* in China. Six suitability categories were defined, ranging from excellent to unsuitable (Table 3). Under current climate conditions, the excellent suitability habitat was predicted to be 12,440 km², while very high, high, medium, low, and unsuitable habitats covered 34,710 km², 37,910 km², 42,310 km², 66,640 km², and 235,210 km², respectively (Figure 3). The total area of suitable habitat (excellent to low suitability) was estimated at 193,005 km². Under future climate projections, the excellent suitability habitat is predicted to decrease substantially to 6370 km², representing a 48.77% reduction compared to current patterns (Figure 4). The very high and high suitability areas are expected to decrease slightly to 34,620 km² (−0.27%) and 34,800 km² (−8.22%), respectively. However, the medium and low suitability habitats are forecasted to increase to 50,110 km² (+18.42%) and 72,320 km² (+8.52%), respectively. The unsuitable habitat area will change little, with a −1.78% decrease to 231,010 km². Overall, the total suitable habitat for *T. sinensis* is projected to decline to 198,220 km² in future climate conditions, a 2.47% reduction compared to the current suitable habitat. The results suggest *T. sinensis* may face habitat losses in current excellent suitability areas, but gain habitat in medium and low suitability areas. Adaptation measures may be needed to facilitate *T. sinensis* persistence as climate shifts.

Under current climatic conditions, the excellent suitability habitat (20%–45%) for *T. sinensis* shows a semi-elliptical distribution pattern, covering circa 25 °N–32 °N and 104 °E–120 °E (Figure 3). Starting from northern Fujian, it runs through southeastern Jiangxi, northern Guangdong, southern and western Hunan, northern Guangxi, southeast-

ern Guizhou, and southwestern and eastern Sichuan. Taking excellent habitat suitability as the center of the species range, very high, high, medium, and low habitat suitability and unsuitable areas are distributed toward the periphery in approximately contiguous sequential belts. These sites are mainly found in provinces and regions besides those mentioned above, such as Yunnan, Hainan, Anhui, Jiangsu, and Taiwan. In addition, most areas south of the Tropic of Cancer ($23^{\circ}26'$), mainly covering the coastal and low-elevation zones of south and east China, are unsuitable or have lower suitability levels.

Table 3. Predicted suitable areas (km^2) for *T. sinensis* under the current and future climate scenarios are classified into six suitability categories generated by the BIOCLIM model.

Suitability Category	Current (10^4 km^2)	Future (10^4 km^2)	Area Change Ratio (%)
Excellent	12.44	6.37	−48.77
Very high	34.71	34.62	−0.27
High	37.91	34.80	−8.22
Medium	42.31	50.11	18.42
Low	66.64	72.32	8.52
Unsuitable	235.21	231.01	−1.78

Under the climate scenario of doubled CO_2 concentration in 2100, the area of suitable habitat of *T. sinensis* will change significantly (Figures 4 and 5). The optimal habitat will decrease sharply by nearly 50% (Table 3). Firstly, the current excellent habitat with an obvious semi-elliptical shape will fragment and contract notably in 2100. Pronounced area reductions will occur, especially in Fujian, Guangdong, Guangxi, and Sichuan provinces. Secondly, the excellent habitat areas in southeastern Zhejiang and western Hunan will show increasing trends. The fragmentation and shrinkage of suitable habitats for *T. sinensis* will become more acute in the future (Figure 5). Therefore, against the general background of climate warming, the suitable habitats of *T. sinensis* will demonstrate pronounced area losses.

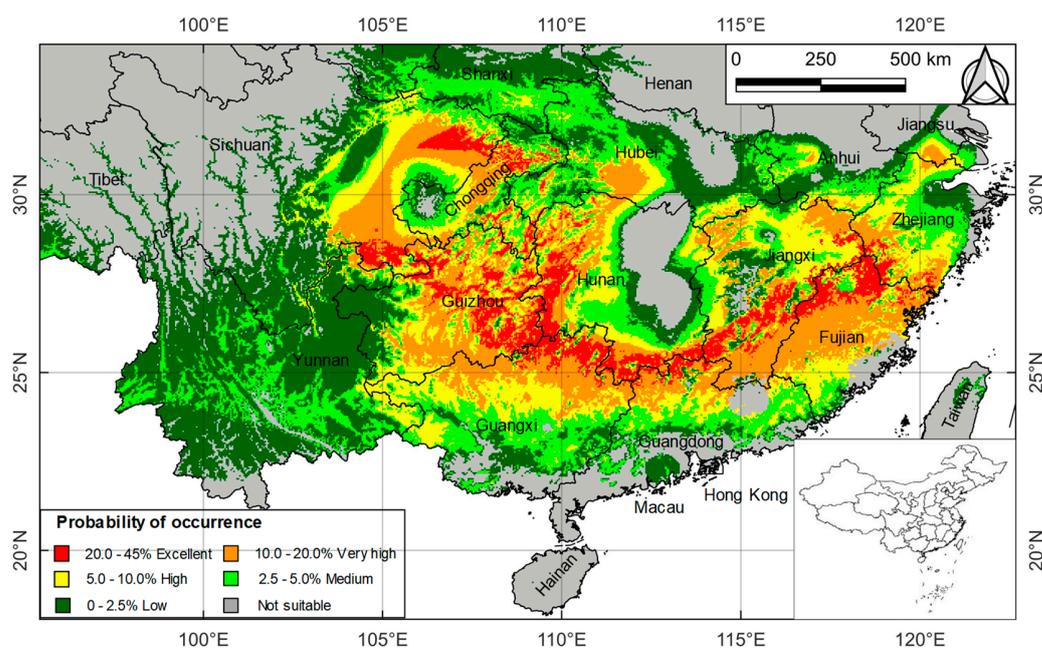


Figure 3. Potential suitability areas of *T. sinensis* under the current climate scenario (1970–2000) generated by the BIOCLIM model. They are divided into six categories based on the calculated habitat suitability index, as explained in the legend.

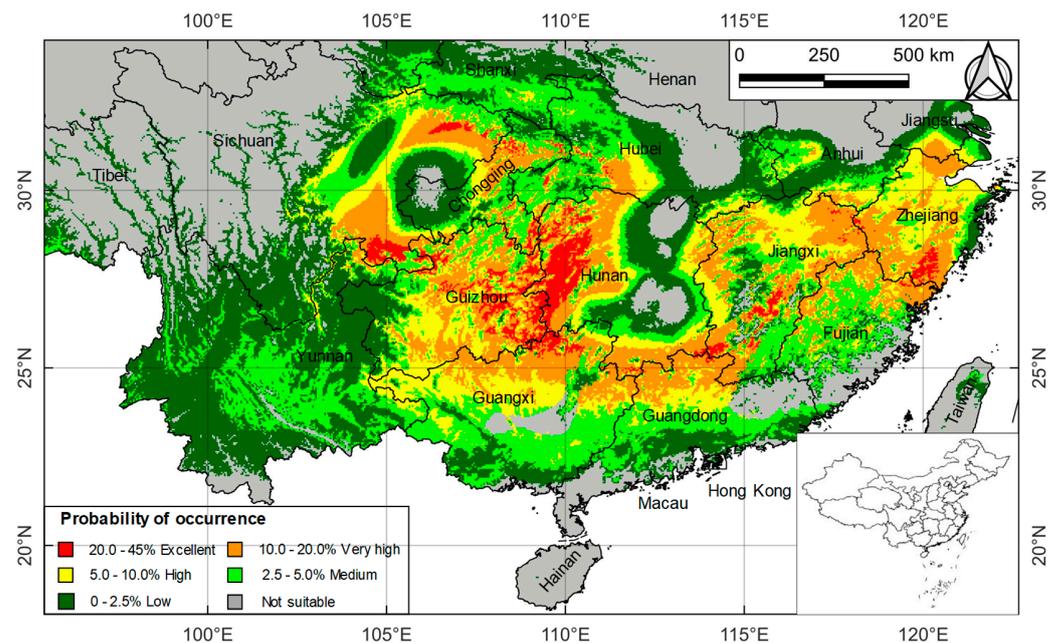


Figure 4. Potential suitable habitats of *T. sinensis* under the climate change scenario (double CO₂ concentration) in 2100 generated by the BIOCLIM model. The six categories of potential suitability habitats are explained in the legend.

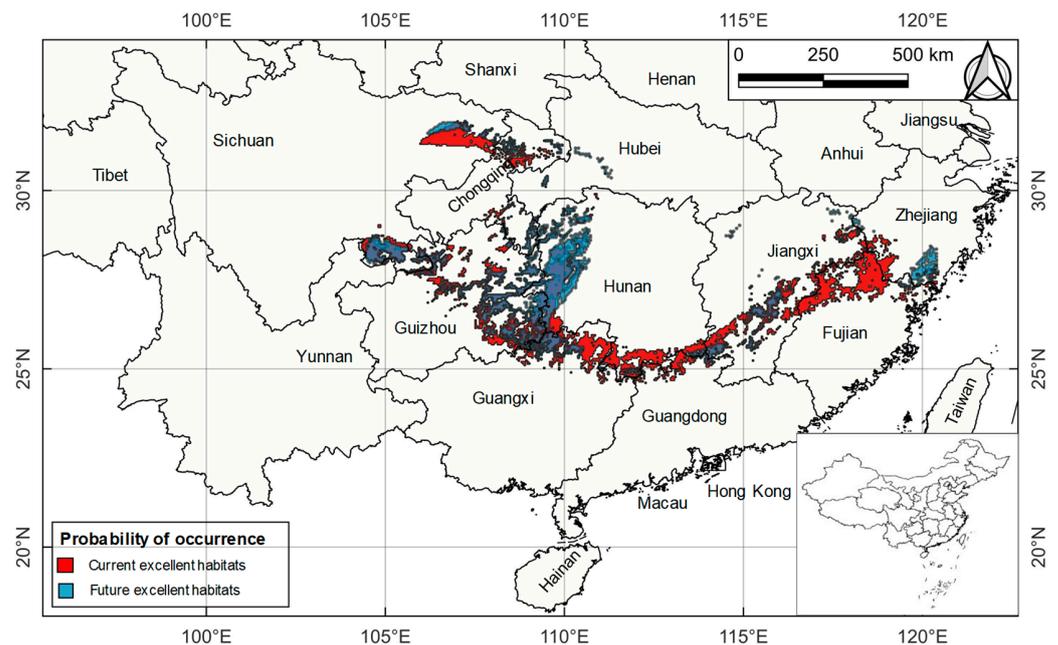


Figure 5. The differences in the distribution of excellent suitable habitats of *T. sinensis* under current and future climate change scenarios (double CO₂ concentration).

3.4. Model Accuracy

Habitat suitability models for *T. sinensis* in China were developed using BIOCLIM under current and future climate scenarios. The models demonstrate high predictive accuracy based on area under the receiver operating characteristic curve (AUC) values (Figure 6). The AUC was 0.893 for the current climate and 0.881 for future climate projections. The AUC values were significantly higher than the null model value of 0.5, indicating excellent prediction performance. The high AUC values suggest a close correspondence between the predicted potential distribution and the empirically observed distribution of *T. sinensis*.

in China. The habitat suitability maps are considered valid representations of this species' distribution under present and future climate conditions. The modeling approach and interpretations demonstrate the scientifically sound methodology and reasoning.

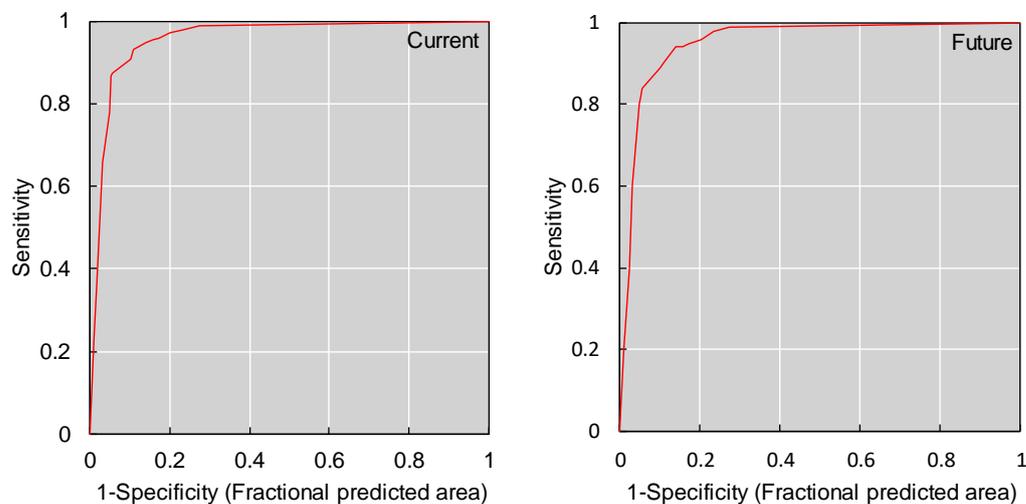


Figure 6. Prediction validation with receiver operating characteristic (ROC) curve in BIOCLIM.

4. Discussion

The species distribution model simulation can reveal the distribution of suitable habitats for species from a macro perspective, which will inform species occurrence mapping and conservation [50]. However, the accuracy of simulation results depends on model construction and algorithms, as well as the quality of geographical distribution data [6,8]. The predictive performance of species distribution models typically decreases with reduced sample size [17,20]. First, the level of uncertainty associated with parameter estimation (e.g., means, modal, median, predicted probability of occurrence) decreases with increasing sample size [51]. With a small sample size, outliers have a higher weight in the analysis than they would with a large sample size, which would provide more data to buffer the anomalous effects of outliers [17]. In addition, due to the high dimensionality and complexity of species' ecological niches, a large sample size can embrace a wider range of conditions under which a species can develop.

Empirical research shows that species' responses to environmental gradients can be skewed or multi-modal [52]. Interactions between environmental variables are important in assessing "species–environment" relationships. The number of interaction–effect parameters to be estimated increases exponentially with the number of predictor variables [53]. Therefore, a large amount of data can better describe complex relationships and interactions. In some cases, models performing well with a large sample size do not necessarily perform well with a small sample size [18]. This issue requires investigations into the possible trade-offs between sample size and model complexity. The sample size in this study exceeded 100 valid distribution records, and the AUC values reached a good level (Figure 6), indicating that our potential distribution predictions for *T. sinensis* based on the BIOCLIM model are reliable.

Climate is the primary factor limiting the natural distribution of species [49]. The growth and reproduction of plants not only require a certain amount of water, but more importantly, they have demands related to thermal conditions. Only when the heat reaches a certain level can species complete a series of reproductive activities such as flowering, pollination, and fruiting [54]. The PCA results show that the temperature seasonality coefficient of variation (bio4) and isothermality (bio3) had the greatest impact on the first principal component (Figure 2). Bio4 refers to the standard deviation of temperature seasonality, with a negative value. It indicates that wider seasonal temperature differences, and thus larger standard deviations, were detrimental to the distribution of *T. sinensis*. In contrast, bio3 is

the ratio of the mean diurnal temperature range (monthly mean) to the annual temperature range, with a positive value. It shows that a stable temperature environment was conducive to *T. sinensis* growth. The current and predicted distribution areas of *T. sinensis* were both located within the subtropical monsoon climate zone (Figures 3 and 4), indicating that its distribution was greatly influenced by subtropical monsoon climate. The subtropical monsoon climate has obvious monsoon characteristics, with significant changes in water and thermal condition [55]. Therefore, the two important factors reflect that temperature variability was a key limiting factor for *T. sinensis* distribution. Based on occurrence data, *T. sinensis* was mainly distributed south of the Qinling Mountains–Huai River and north of Lingnan (Figure 1). Besides a few occurrences in southwest Yunnan and Sichuan, most were found east of the Sichuan Basin. This pattern was found within China’s subtropical range, indicating an environment with predominantly “no severe coldness in winter, no intense heat in summer” [56]. No natural distribution points of *T. sinensis* were found outside this range.

The introduction experiments of *T. sinensis* showed that tree height growth was negatively correlated with temperature [28]. Height growth began around 12 °C in spring, entered a fast growth period above 15 °C, and slowed when the average temperature exceeded 25 °C [57]. This result indicates that *T. sinensis* seedlings preferred cool climates, with high temperatures being detrimental to height growth. Therefore, the year-round high temperatures in regions south of the Nanling Mountains in China are not conducive to *T. sinensis* growth, resulting in species absence in this area (Figure 1). This critical ecological trait illustrates that the numbers of excellent suitable habitats for *T. sinensis* will sharply decrease under future global warming (Table 3).

The dramatic climate changes over the past century have profoundly impacted species distribution patterns [58]. Climate change negatively affects plant species, especially those with a narrow ecological niche and a limited distribution range. For example, *Rosa arabica*, an endemic and protected plant in Egypt, has experienced severe population decline, becoming extremely endangered in recent decades. Species distribution models predict that its range may shift to higher elevations [4]. Similar changes have occurred in other species like *Adansonia digitata* [59] and *Melaleuca cajuputi* [37]. Additionally, to adapt to climate warming, some species have migrated westward and upward to higher elevations [4,36]. Comparing the changes in potential suitable habitat patterns of *T. sinensis* under current and future climate change scenarios, the fragmentation and loss of optimal potential suitable habitats are particularly obvious, trending toward concentration in mountainous areas in central and western China. These results should attract ongoing conservation efforts.

T. sinensis’ response to future climate change is characterized by the significant shrinkage and fragmentation of highly suitable habitats (Figures 4 and 5). Climate warming has caused remarkable ecological changes across the globe, threatening the fragmentation and loss of many plants’ habitats [3,37]. Such habitat waning will have widespread impacts on plant distribution and survival. First, endemic species dependent on specific climate conditions will suffer from the drastic shrinkage of their suitable habitats, precipitating endangerment and extinction risks [58]. Second, the pace of climate change far exceeds many plants’ migration and adaptation capacities, preventing them from successfully dispersing to more suitable environments via seed propagation, thus causing in situ extinction [60]. Third, habitat fragmentation will break up plant populations, hindering gene flow between disjointed subpopulations and reducing species genetic diversity, making them more vulnerable to extinction [3]. Fourth, climate change will give rise to new contacts and competitions between originally allopatrically distributed plant species, with some invasive species occupying dominant positions due to their greater adaptability, displacing or eliminating native species [61]. Finally, mutually beneficial relationships between plants and pollinator insects, seed disperser animals, and other species will be disrupted, destabilizing the critical interdependent relationships [62]. Although *T. sinensis* was once listed as a nationally key protected tree species [28,29], it is absent from the latest conservation list, even though its wild populations still face considerable threats. Therefore, future

conservation efforts should pay attention to protected areas and habitat losses, to be tackled by corresponding conservation measures.

The endangered status of *T. sinensis* results from interactions between intrinsic and extrinsic factors, including its inherent reproductive weaknesses and long sexual reproduction cycle [27,32,63], external disturbances, and climate change [33]. Thus, conserving this endangered species requires a multi-faceted approach. Some practical measures are suggested: (1) Strengthen ex situ conservation and promote the ornamental use of *T. sinensis* in horticulture. Its attractive form, large and fragrant inflorescences, and yellow autumn foliage offer excellent qualities for ornamental landscaping applications. The planting areas can be identified based on the most suitable areas predicted by our model, especially in highly suitable habitats. (2) Enhance in situ conservation by establishing protected areas for existing natural *T. sinensis* populations. Currently, *T. sinensis* is overlooked by relevant agencies and often mistakenly logged by local farmers for firewood. Many populations are small in number and area, fail to achieve dominance within the community, and are unable to nurture and sustain a minimum number of strong mother trees, making natural regeneration difficult [64]. Therefore, appropriate human intervention is an important means to facilitate population recovery. (3) Raise awareness about the scientific, ecological, and other types of importance of *T. sinensis*. It is an important species for studying the evolution of angiosperm reproductive systems. It has significant medicinal and economic value [29]. Public awareness about the species could be lifted by diverse means, such as the media and public education, bringing more attention to the species and enhancing its conservation.

Some limitations of this study could be assessed. The environmental factors influencing the geographical distribution of *T. sinensis* include not only climatic conditions, but also non-biotic factors such as soil, vegetation, topography, and human activities, as well as social factors like socioeconomic structure and production technology level [33]. Our model did not include these factors. The latitudes and longitudes of many *T. sinensis* distribution points used in the research were obtained by checking place name databases. The environmental conditions at these locations may not adequately represent detailed conditions at the actual distribution sites, especially for factors with drastic spatial variations like slope and aspect [65]. Sometimes, contradictory situations may even develop, limiting the use of some environmental factors with important influences on species distributions [66]. The interpolated environmental data may not fully represent the actual environmental conditions of the interpolated locations [23]. This study did not consider the effects of interspecific interactions. Explaining distribution patterns based on general ecological principles may include subjective judgments. Due to data constraints, this study only considered the impacts of two master climate variables, temperature and precipitation, on habitat suitability. Future work could model interactions between factors to improve the prediction.

Species distribution models offer valuable tools for identifying rare and endangered species habitats to inform conservation efforts [36,37,43]. The judicious application of these models can help us to effectively predict potential species distribution areas, facilitating policymaking to manage or protect them [18,50]. Additionally, forecasting future distributions based on environmental changes can allow the development of proactive conservation plans to preempt unnecessary habitat degradation and maximize species preservation [14,52]. However, practical limitations should be considered. Some models are overly reliant on algorithms lacking ecological grounding, while others depend heavily on subjective expert opinions [67]. Sample quality and size also strongly influence the prediction accuracy of some models [17,20]. Therefore, model selection should carefully match the underpinning algorithms and theories to the studied species. While species distribution models are useful for conservation, their limitations highlight the need for an informed modeling approach tailored to the species traits.

5. Conclusions

The known distribution of *T. sinensis* is concentrated primarily in China's middle subtropical climatic zone, exhibiting a geographical range typical of tree species native to the humid subtropical climate region of Central Asia. Our modeling results indicate that temperature factors have a greater influence than precipitation variables in delimiting *T. sinensis* distribution across China. In particular, temperature seasonality (bio4) and isothermality (bio3) emerged as the key climatic limitations restricting habitat range. Precipitation parameters reflected *T. sinensis*' preference for warm and humid conditions, though precipitation was not the primary limiting factor defining range boundaries. Species distribution modeling under current climate scenarios showed strong agreement between predicted potentially suitable areas and actual present-day distribution, validating the model's reliability. However, projections of future habitat suitability under climate change scenarios indicated sharp declines in areas classified as excellent habitats, along with the increasing fragmentation of remaining suitable areas. These findings underscore the urgent need for tailored conservation initiatives to reinforce protection and expand planting programs for *T. sinensis* in China. Given its ecological importance and endangered status, we recommend that *T. sinensis* be reclassified as a nationally protected plant species under Chinese law. Overall, proactive science-based management strategies are imperative to safeguard the long-term survival of this rare tree against mounting threats of climate change in its native range.

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References

1. Anderson, J.T.; Song, B.-H. Plant adaptation to climate change—Where are we? *J. Syst. Evol.* **2020**, *58*, 533–545. [[CrossRef](#)] [[PubMed](#)]
2. Wang, F.; Xiong, Z.; Yan, X.; Dai, X.; Wang, L.; Li, Y. Geographical distribution pattern of species diversity of the genus *Populus* L. *China Acta Ecol. Sin.* **2018**, *38*, 282–290. [[CrossRef](#)]
3. Meza-Joya, F.L.; Morgan-Richards, M.; Koot, E.M.; Trewick, S.A. Global warming leads to habitat loss and genetic erosion of alpine biodiversity. *J. Biogeogr.* **2023**, *50*, 961–975. [[CrossRef](#)]
4. Abdelaal, M.; Fois, M.; Fenu, G.; Bacchetta, G. Using MaxEnt modeling to predict the potential distribution of the endemic plant *Rosa arabica* Crép. in Egypt. *Ecol. Inform.* **2019**, *50*, 68–75. [[CrossRef](#)]
5. Domisch, S.; Friedrichs, M.; Hein, T.; Borgwardt, F.; Wetzig, A.; Jähnig, S.C.; Langhans, S.D. Spatially explicit species distribution models: A missed opportunity in conservation planning? *Divers. Distrib.* **2019**, *25*, 758–769. [[CrossRef](#)]
6. Elith, J.; Leathwick, J.R. Species distribution models: Ecological explanation and prediction across space and time. *Annu. Rev. Ecol. Evol. Syst.* **2009**, *40*, 677–697. [[CrossRef](#)]
7. Mellert, K.H.; Fensterer, V.; Küchenhoff, H.; Reger, B.; Kölling, C.; Klemmt, H.J.; Ewald, J. Hypothesis-driven species distribution models for tree species in the Bavarian Alps. *J. Veg. Sci.* **2011**, *22*, 635–646. [[CrossRef](#)]
8. Pecchi, M.; Marchi, M.; Burton, V.; Giannetti, F.; Moriondo, M.; Bernetti, I.; Bindi, M.; Chirici, G. Species distribution modelling to support forest management. A literature review. *Ecol. Model.* **2019**, *411*, 108817. [[CrossRef](#)]
9. Newbold, T. Applications and limitations of museum data for conservation and ecology, with particular attention to species distribution models. *Prog. Phys. Geogr. Earth Environ.* **2010**, *34*, 3–22. [[CrossRef](#)]
10. Syfert, M.M.; Smith, M.J.; Coomes, D.A. The effects of sampling bias and model complexity on the predictive performance of MaxEnt species distribution models. *PLoS ONE* **2013**, *8*, e55158. [[CrossRef](#)]
11. Soilhi, Z.; Sayari, N.; Benalouache, N.; Mekki, M. Predicting current and future distributions of *Mentha pulegium* L. in Tunisia under climate change conditions, using the MaxEnt model. *Ecol. Inform.* **2022**, *68*, 101533. [[CrossRef](#)]

12. Serra-Diaz, J.M.; Enquist, B.J.; Maitner, B.; Merow, C.; Svenning, J.-C. Big data of tree species distributions: How big and how good? *For. Ecosyst.* **2018**, *4*, 30. [[CrossRef](#)]
13. Bradie, J.; Leung, B. A quantitative synthesis of the importance of variables used in MaxEnt species distribution models. *J. Biogeogr.* **2017**, *44*, 1344–1361. [[CrossRef](#)]
14. Carpenter, G.; Gillison, A.N.; Winter, J. DOMAIN: A flexible modelling procedure for mapping potential distributions of plants and animals. *Biodivers. Conserv.* **1993**, *2*, 667–680. [[CrossRef](#)]
15. Lehmann, A.; Overton, J.M.; Leathwick, J.R. GRASP: Generalized regression analysis and spatial prediction. *Ecol. Model.* **2002**, *157*, 189–207. [[CrossRef](#)]
16. Booth, T.H.; Nix, H.A.; Busby, J.R.; Hutchinson, M.F. bioclim: The first species distribution modelling package, its early applications and relevance to most current MaxEnt studies. *Divers. Distrib.* **2014**, *20*, 1–9. [[CrossRef](#)]
17. Wisz, M.S.; Hijmans, R.J.; Li, J.; Peterson, A.T.; Graham, C.H.; Guisan, A.; Group, N.P.S.D.W. Effects of sample size on the performance of species distribution models. *Divers. Distrib.* **2008**, *14*, 763–773. [[CrossRef](#)]
18. Natale, E.; Zalba, S.M.; Reinoso, H. Presence—Absence versus invasive status data for modelling potential distribution of invasive plants: Saltcedar in Argentina. *Écoscience* **2013**, *20*, 161–171. [[CrossRef](#)]
19. Hijmans, R.J.; Graham, C.H. The ability of climate envelope models to predict the effect of climate change on species distributions. *Glob. Chang. Biol.* **2006**, *12*, 2272–2281. [[CrossRef](#)]
20. Duan, R.-Y.; Kong, X.-Q.; Huang, M.-Y.; Fan, W.-Y.; Wang, Z.-G. The predictive performance and stability of six species distribution models. *PLoS ONE* **2014**, *9*, e112764. [[CrossRef](#)]
21. Xu, T.; Hutchinson, M.F. New developments and applications in the ANUCLIM spatial climatic and bioclimatic modelling package. *Environ. Model. Softw.* **2013**, *40*, 267–279. [[CrossRef](#)]
22. Luoto, M.; Pöyry, J.; Heikkinen, R.K.; Saarinen, K. Uncertainty of bioclimate envelope models based on the geographical distribution of species. *Glob. Ecol. Biogeogr.* **2005**, *14*, 575–584. [[CrossRef](#)]
23. Kumar, P. Assessment of impact of climate change on *Rhododendrons* in Sikkim Himalayas using Maxent modelling: Limitations and challenges. *Biodivers. Conserv.* **2012**, *21*, 1251–1266. [[CrossRef](#)]
24. Rees, M.; Paull, D.J.; Carthew, S.M. Factors influencing the distribution of the yellow-bellied glider (*Petaurus australis australis*) in Victoria, Australia. *Wildl. Res.* **2007**, *34*, 228–233. [[CrossRef](#)]
25. Ward, D.F. Modelling the potential geographic distribution of invasive ant species in New Zealand. *Biol. Invasions* **2007**, *9*, 723–735. [[CrossRef](#)]
26. Palkar, R.S.; Janarthanam, M.K.; Sellappan, K. Prediction of potential distribution and climatic factors influencing *Garcinia indica* in the western Ghats of India using ecological niche modeling. *Natl. Acad. Sci. Lett.* **2020**, *43*, 585–591. [[CrossRef](#)]
27. Zhou, X.-J.; Ren, X.-L.; Liu, W.-Z. Genetic diversity of SSR markers in wild populations of *Tapiscia sinensis*, an endangered tree species. *Biochem. Syst. Ecol.* **2016**, *69*, 1–5. [[CrossRef](#)]
28. Zong, S.; Yang, Z.; Tao, J. A study on the ecological characteristics of *Tapiscia sinensis*. *Chin. J. Plant Ecol.* **1985**, *9*, 192–201.
29. Xin, G.-L.; Liu, J.-Q.; Liu, J.; Ren, X.-L.; Du, X.-M.; Liu, W.-Z. Anatomy and RNA-Seq reveal important gene pathways regulating sex differentiation in a functionally Androdioecious tree, *Tapiscia sinensis*. *BMC Plant Biol.* **2019**, *19*, 554. [[CrossRef](#)]
30. Lü, W.; Liu, W. Pollination biology in androdioecious species *Tapiscia sinensis* (Staphyleaceae). *Chin. Bull. Bot.* **2010**, *45*, 713–722. [[CrossRef](#)]
31. Zhang, J.; Li, Z.; Fritsch, P.W.; Tian, H.; Yang, A.; Yao, X. Phylogeography and genetic structure of a Tertiary relict tree species, *Tapiscia sinensis* (Tapisciaceae): Implications for conservation. *Ann. Bot.* **2015**, *116*, 727–737. [[CrossRef](#)] [[PubMed](#)]
32. Zhou, X.-J.; Wang, Y.-Y.; Xu, Y.-N.; Yan, R.-S.; Zhao, P.; Liu, W.-Z. De Novo characterization of flower bud transcriptomes and the development of EST-SSR markers for the endangered tree *Tapiscia sinensis*. *Int. J. Mol. Sci.* **2015**, *16*, 12855–12870. [[CrossRef](#)] [[PubMed](#)]
33. Xie, C. A review of research advances in rare and endangered plant *Tapiscia sinensis*. *Subtrop. Plant Sci.* **2006**, *35*, 71–74. [[CrossRef](#)]
34. Suryani, F.; Bakhtra, D.D.A.; Fajrina, A. Cytotoxic activity of endophytic fungus against HeLa Cells (cervical cancer cells): A article review. *Asian J. Pharm. Res. Dev.* **2022**, *10*, 25–28. [[CrossRef](#)]
35. Administration, F.a.G.; Affairs, M.o.A.a.R. The National Key Protected Wild Plants Catalogue. Available online: https://www.gov.cn/zhengce/zhengceku/2021-09/09/content_5636409.htm (accessed on 17 October 2023).
36. Sousa-Silva, R.; Alves, P.; Honrado, J.; Lomba, A. Improving the assessment and reporting on rare and endangered species through species distribution models. *Glob. Ecol. Conserv.* **2014**, *2*, 226–237. [[CrossRef](#)]
37. Wilson, C.D.; Roberts, D.; Reid, N. Applying species distribution modelling to identify areas of high conservation value for endangered species: A case study using *Margaritifera margaritifera* (L.). *Biol. Conserv.* **2011**, *144*, 821–829. [[CrossRef](#)]
38. Hijmans, R.J.; Guarino, L.; Cruz, M.; Rojas, E. Computer tools for spatial analysis of plant genetic resources data: 1. DIVA-GIS. *Plant Genet. Resour. Newsl.* **2001**, *127*, 15–19.
39. Fick, S.E.; Hijmans, R.J. WorldClim 2: New 1-km spatial resolution climate surfaces for global land areas. *Int. J. Climatol.* **2017**, *37*, 4302–4315. [[CrossRef](#)]
40. Wang, B.; Jin, C.; Liu, J. Understanding future change of global monsoons projected by CMIP6 models. *J. Clim.* **2020**, *33*, 6471–6489. [[CrossRef](#)]
41. Kiehl, J.T.; Hack, J.J.; Bonan, G.B.; Boville, B.A.; Williamson, D.L.; Rasch, P.J. The National Center for Atmospheric Research Community Climate Model: CCM3. *J. Clim.* **1998**, *11*, 1131–1149. [[CrossRef](#)]

42. Mathur, M.; Mathur, P.; Purohit, H. Ecological niche modelling of a critically endangered species *Commiphora wightii* (Arn.) Bhandari using bioclimatic and non-bioclimatic variables. *Ecol. Process.* **2023**, *12*, 8. [[CrossRef](#)]
43. Yi, Y.-j.; Cheng, X.; Yang, Z.-F.; Zhang, S.-H. Maxent modeling for predicting the potential distribution of endangered medicinal plant (*H. riparia* Lour) in Yunnan, China. *Ecol. Eng.* **2016**, *92*, 260–269. [[CrossRef](#)]
44. Yoon, S.; Lee, W.-H. Methodological analysis of bioclimatic variable selection in species distribution modeling with application to agricultural pests (*Metcalfa pruinosa* and *Spodoptera litura*). *Comput. Electron. Agric.* **2021**, *190*, 106430. [[CrossRef](#)]
45. Hammer, Ø.; Harper, D.A. Past: Paleontological statistics software package for education and data analysis. *Palaeontol. Electron.* **2001**, *4*, 1.
46. Moya, W.; Jacome, G.; Yoo, C.K. Past, current, and future trends of red spiny lobster based on PCA with MaxEnt model in Galapagos Islands, Ecuador. *Ecol. Evol.* **2017**, *7*, 4881–4890. [[CrossRef](#)]
47. Booth, T.H. Why understanding the pioneering and continuing contributions of BIOCLIM to species distribution modelling is important. *Austral Ecol.* **2018**, *43*, 852–860. [[CrossRef](#)]
48. Gray, J. Quantum GIS: The open-source geographic information system. *Linux J.* **2008**, *2008*, 8.
49. Fang, J.; Lechowicz, M.J. Climatic limits for the present distribution of beech (*Fagus L.*) species in the world. *J. Biogeogr.* **2006**, *33*, 1804–1819. [[CrossRef](#)]
50. Ali, F.; Khan, N.; Khan, A.M.; Ali, K.; Abbas, F. Species distribution modelling of *Monothecha buxifolia* (Falc.) A. DC.: Present distribution and impacts of potential climate change. *Heliyon* **2023**, *9*, e13417. [[CrossRef](#)]
51. Naimi, B.; Hamm, N.A.S.; Groen, T.A.; Skidmore, A.K.; Toxopeus, A.G. Where is positional uncertainty a problem for species distribution modelling? *Ecography* **2014**, *37*, 191–203. [[CrossRef](#)]
52. Austin, M.P. Spatial prediction of species distribution: An interface between ecological theory and statistical modelling. *Ecol. Model.* **2002**, *157*, 101–118. [[CrossRef](#)]
53. Rao, K.; Zhang, X.; Yi, X.-J.; Li, Z.-S.; Wang, P.; Huang, G.-W.; Guo, X.-X. Interactive effects of environmental factors on phytoplankton communities and benthic nutrient interactions in a shallow lake and adjoining rivers in China. *Sci. Total Environ.* **2018**, *619–620*, 1661–1672. [[CrossRef](#)] [[PubMed](#)]
54. Bykova, O.; Chuine, I.; Morin, X.; Higgins, S.I. Temperature dependence of the reproduction niche and its relevance for plant species distributions. *J. Biogeogr.* **2012**, *39*, 2191–2200. [[CrossRef](#)]
55. Huan, Z.-q.; Geng, X.-m.; Xu, X.-r.; Liu, W.; Zhu, Z.-l.; Tang, M. Potential geographical distribution of *Michelia martinii* under different climate change scenarios based on MaxEnt model. *J. Ecol. Rural Environ.* **2023**, *39*, 1277–1287. [[CrossRef](#)]
56. Jiang, A. Discussion on the division of tropical and subtropical climatic zones in China. *Acta Geogr. Sin.* **1960**, *26*, 104–109.
57. Zhang, L.; Han, Y.; Liu, S.; Meng, Y.; Liu, Y.; Kong, D. Study on the growth rhythm of *Tapiscia siriensis* at seedling stage. *Guangdong Agric. Sci.* **2018**, *45*, 47–51.
58. Wiens, J.J. Climate-related local extinctions are already widespread among plant and animal species. *PLoS Biol.* **2016**, *14*, e2001104. [[CrossRef](#)] [[PubMed](#)]
59. Birhane, E.; Asgedom, K.T.; Tadesse, T.; Hishe, H.; Abrha, H.; Noulèkoun, F. Vulnerability of baobab (*Adansonia digitata* L.) to human disturbances and climate change in western Tigray, Ethiopia: Conservation concerns and priorities. *Glob. Ecol. Conserv.* **2020**, *22*, e00943. [[CrossRef](#)]
60. Christmas, M.J.; Breed, M.F.; Lowe, A.J. Constraints to and conservation implications for climate change adaptation in plants. *Conserv. Genet.* **2016**, *17*, 305–320. [[CrossRef](#)]
61. Walther, G.-R.; Roques, A.; Hulme, P.E.; Sykes, M.T.; Pyšek, P.; Kühn, I.; Zobel, M.; Bacher, S.; Botta-Dukát, Z.; Bugmann, H.; et al. Alien species in a warmer world: Risks and opportunities. *Trends Ecol. Evol.* **2009**, *24*, 686–693. [[CrossRef](#)]
62. Traill, L.W.; Lim, M.L.M.; Sodhi, N.S.; Bradshaw, C.J.A. Mechanisms driving change: Altered species interactions and ecosystem function through global warming. *J. Anim. Ecol.* **2010**, *79*, 937–947. [[CrossRef](#)] [[PubMed](#)]
63. Liu, W.; Kang, H.; Zheng, H.; Feng, Y. An investigation on the sexual reproductive cycle in *Tapiscia sinensis*. *J. Syst. Evol.* **2008**, *46*, 175–182. [[CrossRef](#)]
64. Zhang, J.; Chen, Y.; Liu, Z.; Wang, L.; Yang, S.; Liao, W. Study on the national rare and endangered key protected plants *Tapiscia sinensis* community in Taoyuandong National Nature Reserve, Hunan Province. *Ecol. Sci.* **2017**, *36*, 9–16. [[CrossRef](#)]
65. Graham, C.H.; Ferrier, S.; Huettman, F.; Moritz, C.; Peterson, A.T. New developments in museum-based informatics and applications in biodiversity analysis. *Trends Ecol. Evol.* **2004**, *19*, 497–503. [[CrossRef](#)] [[PubMed](#)]
66. Guisan, A.; Thuiller, W. Predicting species distribution: Offering more than simple habitat models. *Ecol. Lett.* **2005**, *8*, 993–1009. [[CrossRef](#)] [[PubMed](#)]
67. Beale, C.M.; Lennon, J.J. Incorporating uncertainty in predictive species distribution modelling. *Philos. Trans. R. Soc. B Biol. Sci.* **2012**, *367*, 247–258. [[CrossRef](#)]

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