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Ensemble model-based analysis of the effects of environmental factors on the distribution and chemical composition of *Asparagus cochinchinensis* (Lour.) Merr.

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ABSTRACT

Asparagus cochinchinensis (Lour.) Merr., is a traditional Chinese herbal medicine with pharmacological effects such as cough and asthma suppression, anti-inflammation, and immunity enhancement. Currently, as a wild resource it is scarce and its distribution has not been well defined. Especially in the context of climate change, the effect of the environment on its chemical composition is also unknown. In this study, we constructed an ensemble model of species distribution for *A. cochinchinensis* to predict its current and future potential suitable habitat areas, and explored the relationship between its chemical composition and key environmental factor using statistical analysis. The results showed that the Mean Diurnal Range (Bio2) contributed 67.74% to the model and was the key environmental factor influencing the distribution of *A. cochinchinensis*. The current habitat of *A. cochinchinensis* was mainly distributed in south-central and southeastern China, such as Sichuan, Chongqing, Guangxi, Guangdong and Fujian. Under the influence of climate change, its potential habitat would gradually decrease, especially in highly suitable areas. The results of chemical analysis showed that the quality of *A. cochinchinensis* was higher in Neijiang than other locations, which might be related to the fact that Bio2 in Neijiang was most suitable for growth. In addition, the correlation results showed that 12 out of 36 chemical indicators had significant correlation with Bio2, and all of them except protein and Tyr had significantly negative correlation with Bio2, indicating that the environment affected the biosynthesis of chemical composition of *A. cochinchinensis*. The results of the study provide theoretical guidance for the cultivation, management, and sustainable use of *A. cochinchinensis* resources, as well as a theoretical basis for their quality improvement.

1. Introduction

The dried roots of *Asparagus cochinchinensis* (Lour.) Merr., a plant of the genus *Asparagus* in the family *Liliaceae*, are traditional Chinese medicine commonly used in clinical practice (Xue et al., 2022). Studies have shown that the chemical constituents of *A. cochinchinensis* mainly consist of saponins, polysaccharides, polyphenols, flavonoids, amino acids and lignans (Sun et al., 2021; Yunmam et al., 2023), which confer a variety of pharmacological effects, such as antioxidant, anti-tumor, antidepressant, immune function modulation, analgesic, and asthmatic (Luo et al., 2022). Wild resources of *A. cochinchinensis* have been gradually depleted with increasing demand in the pharmaceutical market and due to global warming, the natural habitat of the medicinal plant may be displaced, and its yield and quality may be affected (Yu et al.,

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2022; Applequist et al., 2020). Therefore, it is necessary to analyze the distribution of *A. cochinchinensis* resources to provide theoretical guidance for cultivation and to ensure its supply.

Species distribution models (SDMs) have been widely applied to discern the relationship between environmental factors and the potential distribution of species, and are powerful tools for predicting changes in the distribution of species under climate change (Fourcade et al., 2018). SDMs simulate and predict the geographic distribution of species in a study area based on known distribution points, data on environmental factors, and the calculated degree of influence of these factors on distribution (Elith and Leathwick, 2009; Wen et al., 2022). Currently, commonly used SDMs include MaxEnt, GLM, and RF (Li et al., 2020a, 2020b; Zhang and Wang, 2023). SDMs are known to be variable in their predictive outcomes and predictive performance, and no one model is consistently superior to the others (Hao et al., 2019), giving rise to the idea of combining the results of different models into a so-called ensemble (Araújo and New, 2007). Biomod2 is a widely used, free and open-source platform, based on the R language, which can easily accomplish ensemble modeling (Thuiller et al., 2009). Biomod2 has been applied in species distribution prediction of invasive (Fang et al., 2021), endangered (Xu et al., 2021), and economic species (Zhao et al., 2021), providing a practical significance reference for the management, control and conservation of these species. However, few studies have focused on its application in predicting suitable habitats for medicinal plants.

The biosynthesis and accumulation of chemical constituents in medicinal plants depend critically on environmental conditions (Yang et al., 2018) such as changes in light, which affect the content of alkaloids and phenols, and changes in temperature, which affect the content of sesquiterpene lactones, phenolics and fatty acids (Li et al., 2020a, 2020b). A medicinal plant grown in different environments can have different concentrations of metabolites. Some studies have correlated the chemical content of medicinal plants such as *Nardostachys jatamansi* (D. Don) DC (Wen et al., 2022), *Ligusticum chuanxiong* Hort. (Liu et al., 2023), and *Astragalus membranaceus* var. *mongholicus* (Yang et al., 2020) with the key environmental factors predicted by SDMs. However, despite the potential impact of environmental factors on the chemical composition of *A. cochinchinensis*, few studies have been conducted on this relationship.

In summary, the aims of this study were to construct an ensemble model using the Biomod2 platform to predict the potential distribution of *A. cochinchinensis* under current and future environmental conditions and to analyze the shifts in its distribution under climate change; to analyze the key environmental factor affecting its distribution from the modeling results; to determine the contents of five types of major chemical components including nutrients, minerals, vitamins, amino acids and active ingredients from different locations and to analyze the quality differences of *A. cochinchinensis* among different locations by statistical methods; and to investigate the potential relationship between the key environmental factor and chemical composition of *A. cochinchinensis* with Pearson correlation analysis in order to explore the environmental causes of the quality differences. The results of this study may provide a theoretical basis for the cultivation, resource management and quality improvement of *A. cochinchinensis.*

2. Materials and methods

2.1. Presence and pseudo-absence data

The presence records of *A. cochinchinensis* used in the study were collected from several public databases, including the Global Biodiversity Information Facility (GBIF, https://www.gbif.org/), the Chinese Virtual Herbarium (CVH, http://www.cvh.ac.cn/), and the Specimen Resources Sharing Platform for Education (SRSPE, http://mnh.scu.edu.cn/), as well as from relevant published literature (Chen et al., 2022; Xue et al., 2022). Google earth (version 7.3) was used to identify locations with known latitude and longitude, and to locate points for which latitude and longitude was unavailable. To avoid model overfitting caused by spatial autocorrelation between presence points, the 'spThin' package in R (version 4.3.0) was used to remove points that were too close or duplicated, keeping the distance between any two sample points greater than 10 km (Zhang, et al., 2018). Finally, a total of 228 presence point data for *A. cochinchinensis* were obtained (Fig. 1a). Biomod2 modelling also requires absence point data for a species. Due to the difficulty and subjective nature of their collection, Biomod2 provides several methods for generating absence points, called pseudo-absence points (PAs) (Barbet-Massin et al., 2012). In this study, two groups of 1000 PA points each were randomly generated using the 'random' method.

2.2. Environmental variables

A total of 26 environmental variables including three categories of climate, soil and topography were initially selected as pre-modelling environmental variables, all with a spatial resolution of 2.5 minutes (approximately 21 km^2). Nineteen climate variables and elevation were downloaded from the WorldClim database (version 2.1, https://www.worldclim.org/). Six soil variables were downloaded from the Harmonized World Soil Database (version 1.2, http://webarchive.iiasa.ac.at/Research/LUC/External-World-soil-database/HTML/). The aspect and slope were both extracted from elevation. The 'raster' package in R was used to bulk clip the environmental variables to the Chinese territory. To prevent multicollinearity between environmental variables from affecting the model predictions, Pearson coefficients between rasters of environmental variables were calculated using the 'ENMTools' package in R (Dormann et al., 2013). When pairs of environmental variables were highly correlated ($|r| > 0.8$) (Yi et al., 2016), that which contributed less to *A. cochinchinensis* distribution was removed. Finally, 14 environmental variables were selected for modelling (Table 1).

The second-generation Beijing Climate Centre Climate System Model (BCC-CSM2-MR), which is widely used in China, was selected for modelling future climate data (Wu et al., 2019). The model includes four shared socioeconomic pathway (SSP) scenarios, SSP126, SSP245, SSP370 and SSP585, under different green gas (GHG) emission concentrations and social development levels (Riahi et al., 2017). In this study, changes in the distribution of *A. cochinchinensis* under these four SSPs are projected for the years 2041–2060 and 2061–2080.

2.3. Ensemble modelling

The nine models used in Biomod2 in this study include the generalized linear model (GLM), the generalized additive model (GAM), the generalized boosting model (GBM), classification tree analysis (CTA), surface range envelop (SRE), flexible discriminant analysis (FDA), multiple adaptive regression splines (MARS), random forest (RF), and maximum entropy (MAXENT). Presence points and environment variable data were imported into the Biomod2 platform and the corresponding parameters were selected to generate the PAs. To construct individual models, 75% of the presence-absence data was randomly assigned to training data to calibrate the models, and the remaining 25% was used to evaluate the models. The importance of each environmental variable was assessed three times. Each model run was set to repeat 10 times, and the final number of models was 180 (i.e the product of the number of individual models selected, the number of times PAs were generated, and the number of model repetitions).

The area under the curve (AUC) of the receiver operating characteristic (ROC) curve and the true skill statistics (TSS) were selected to assess the performance of the models (Allouche et al., 2006). The ROC curve has the false positives rate (1 − specificity) on the x-axis and the true positives rate (sensitivity) on the y-axis, and the AUC value, a commonly used metric for model assessment, summarizes the diagnostic accuracy of the test (Hallgren et al., 2019). An AUC value ranges from

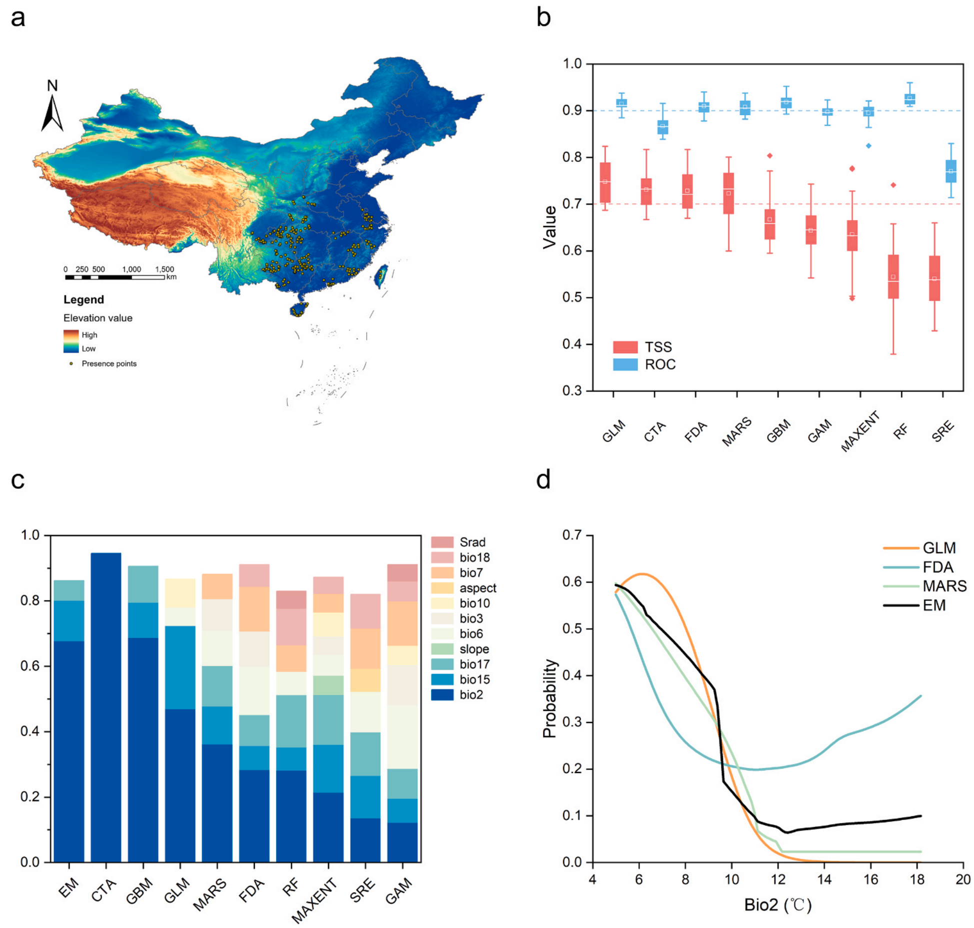

Fig. 1. Prediction results of species distribution modeling. Presence points distribution of *A. cochinchinensis* (a). Values of evaluation metrics for individual and ensemble models (b). Percentage of environmental factors importance in individual and ensemble models (only importance greater than 5% are shown) (c). The response curves of Bio2 for the ensemble model and the better performing individual model (d).

Table 1
Description of the selected environmental variables used for modeling.

Type	Code	Description
Climate	Bio2	Mean Diurnal Range (Mean of monthly (max temp-min temp)) (℃)
	Bio3	Isothermally (Bio2/bio7) (× 100)
	Bio6	Min Temperature of Coldest Month (℃)
	Bio7	Temperature Annual Range (Bio5-Bio6) (℃)
	Bio10	Mean Temperature of Warmest Quarter (℃)
	Bio15	Precipitation Seasonality (C of V)
	Bio17	Precipitation of Driest Quarter (mm)
	Bio18	Precipitation of Warmest Quarter (mm)
	Srad	Solar radiation (KJ m^{-2} day^{-1})
Soil	T_BS	Topsoil Base Saturation (%)
	T_ESP	Topsoil Sodicity (%)
	T_PH_H2O	Topsoil pH (H_2O) (-log H^+)
Topography	Aspect	Aspect (∘)
	Slope	Slope (∘)

0 to 1, with a higher value indicating better prediction of the model. Generally, prediction is considered acceptable for an AUC of 0.7–0.8, excellent for an AUC of 0.8–0.9, and outstanding for an AUC >0.9 (Hu et al., 2020). TSS considers both omission and commission errors but in contrast to KAPPA, corrects for the dependence on prevalence (Allouche et al., 2006). TSS is calculated as sensitivity + specificity − 1, and also takes a value in the range 0–1 (Fourcade et al., 2018), wherein 0.7–0.9 is considered a moderate, and >0.9 is considered a good model fit. Individual models with AUC>0.9 and TSS>0.7 were selected to construct an ensemble model through a weighted mean approach. The ensemble model predictions were imported into ArcGIS Pro (version 3.0) for visualization. The current and future potential habitat areas of *A. cochinchinensis* were classified according to their suitability using the natural breakpoint method, and the areas were calculated.

2.4. Sample preparation

A total of 12 batches of *A. cochinchinensis* root samples were collected for the determination of chemical content, including 6 from Neijiang (Sichuan), 2 from Suining and Luzhou (Sichuan), and 4 from Chongqing, Guizhou, Yunnan and Guangxi, and three biological replicates were collected from each location. Samples were dug out and washed, steamed in boiling water for 20–30 min before peeling manually, and were then dried in an oven at 65 ℃ for 13–15 hours. The dried samples were pulverized and passed through a 50-mesh sieve (355 ± 13μm aperture) to provide off-white or light-yellow powders.

2.5. Chemical determination

The content of five chemical component categories in *A. cochinchinensis* was determined, including nutrients, vitamins, minerals, amino acids, and active ingredients. Nutritional components include moisture, ash, dietary fiber, starch, fat, protein and total carbohydrates. Moisture, ash, dietary fiber, starch, fat, and protein were determined using the Chinese National Standards: GB 5009.3–2016, GB 5009.4–2016, GB 5009.88–2014, GB 5009.9–2016, GB5009.6–2016, and GB 5009.5–2016, respectively. Total carbohydrate content was calculated by subtracting the sum of protein, fat, moisture, and ash from

100 (carbohydrate = 100−protein−fat−moisture−ash). Vitamins including niacin, vitamin B_1, vitamin B_2, vitamin B_6, vitamin C, vitamin E, folic acid, pantothenic acid, biotin, and vitamin K_1 were tested according to the Chinese National Standards GB 5009.89–2016, GB 5009.84–2016, GB 5009.85–2016, GB 5009.154–2016, GB 5009.86–2016, GB 5009.82–2016, GB 5009.211–2014, GB 5009.210–2016, GB 5009.259–2016, and GB 5009.158–2016, respectively. The content of 18 minerals in *A. cochinchinensis* was determined, Mg and Ca according to GB 5009.241–2017 and GB 5009.92–2016, respectively, and all other elements according to GB 5009.268–2016. Analyses were performed by inductively coupled plasma mass spectrometry (ICP-MS) and inductively coupled plasma optical emission spectrometry (ICP-OES). Amino acid analysis was performed according to GB 5009.124–2016. Total saponins, total flavonoids, crude polysaccharides and total polyphenols were identified and quantified by spectrophotometry.

2.6. Data analysis

All chemical contents were determined three times and the average value was calculated. The compositions of *A. cochinchinensis* samples from 12 locations was analyzed by principal component analysis (PCA), ANOVA analysis and cluster analysis using SIMCA software (version 14.1.0).

The key environmental factor for each location were extracted by ArcGIS Pro3.0. The correlation between chemical content and key environmental factor was calculated by SPSS 26.0. The variables were tested for normality before calculating the correlations.

3. Results

3.1. Models performance and environmental variables importance

Modelling of data on distribution points and environmental variables for *A. cochinchinensis* revealed differences in performance between individual models (Fig. 1b). GLM gave the best overall performance, with mean AUC and TSS values of 0.914 and 0.748, respectively, and better stability over multiple modelling sessions. The next best performers were FDA and MARS, with mean AUC and TSS values of 0.909 and 0.728 for FDA, and 0.907 and 0.723 for MARS, respectively. The worst performer was SRE, with mean AUC and TSS values of 0.770 and 0.540, respectively. Compared to the individual models, the ensemble model constructed from the well-performing individual models had a higher prediction accuracy with an AUC value of 0.951 and a TSS value of 0.809. Therefore, the prediction results of the ensemble model were selected for subsequent analyses.

Environmental variables with importance greater than 5% in the individual and ensemble models are shown in Fig. 1c. In the ensemble model, environmental variables with importance greater than 5% were Bio2, Bio15 and Bio17, with 67.74%, 12.39% and 6.12% importance, respectively. Bio2 plays a crucial role in almost all individual models and its share in the ensemble model is also the highest, and was considered a key environmental variable influencing the distribution of *A. cochinchinenesis*. Response curves are plotted during the model run based on the species' growth probability values and the corresponding environmental variables. Trends in the response curves for the three best-performing individual models for Bio2 are broadly consistent (Fig. 1d). *A. cochinchinensis* growth probability was maximized when Bio2 was around 5 ℃ and minimized when Bio2 was over around 12 ℃, indicating that the mean diurnal range suitable for its growth was around 5–12 ℃, and its growth probability tended to decrease with increasing temperature.

3.2. Current and future potential distribution of A. cochinchinensis

The potential distribution area of *A. cochinchinensis* under current climatic conditions is shown in Fig. 2a. The total current suitable area is 199.5017×10^4 km^2, containing 89.7691×10^4 km^2 of highly suitable area, 62.5139×10^4 km^2 of moderately suitable area and 47.2187×10^4 km^2 of generally suitable area (Fig. 2b). The highly suitable areas are mainly distributed in eastern Sichuan, Chongqing, southwestern Hubei, Guizhou, western Hunan, Guangxi, Hainan, Guangdong, Fujian, central Taiwan, and small parts of Zhejiang, Jiangxi, and Anhui. Moderately suitable areas are mainly distributed in southern Shaanxi, central Hubei, eastern Anhui, most parts of Jiangxi, and surrounding some highly suitable areas. The generally suitable areas are mainly distributed in southeastern Gansu, southwestern Shanxi, eastern Shandong, eastern Jiangsu, central Hunan, northeastern Taiwan, and surrounding some moderately suitable areas (Fig. 2a).

Both the potential distribution area of *A. cochinchinensis* and their size change under future climate conditions (Fig. 3). For the current, 2041–2060 and 2061–2080 periods, the generally suitable area showed a trend first unchanged and then increasing, the moderately suitable area showed an increasing and then unchanged trend, and the highly suitable area showed a decreasing trend with time. In summary, the total suitable area decreased over time (Fig. 2b). In the period 2041–2060, only the SSP245 scenario shows an increase in total suitable area compared to the current, while all other scenarios show a decrease. Among the four future climate scenarios, the generally, moderately, and highly suitable areas are highest under SSP370, SSP585, and SSP245 scenarios, respectively, and lowest under SSP585, SSP126, and SSP370 scenarios, respectively (Fig. 2c). In the period 2061–2080, the total suitable area under the four climate scenarios still increases only in the SSP245 scenario and decreases in the other scenarios compared to the current. In this period, the scenarios in which the area of each class of suitable area peaked were the same as in the 2041–2060 period, while the area of each class of suitable area was lowest under the SSP126, SSP245, and SSP370 scenarios, respectively (Fig. 2d). Taken together, the most suitable climate scenario for the distribution of *A. cochinchinensis* under climate change is SSP245, and the least suitable is SSP370.

3.3. Chemical determination and analytical results

The content of each chemical constituent of *A. cochinchinensis* from different locations is shown in Table 2. In this study, principal component analysis (PCA) was used to explore differences in sample quality between locations and to sort samples into groups (Fig. 4a). PCA extracted two principal components that cumulatively accounted for 56.9% of the total variance (PC1=40.1% and PC2=16.8%). The results showed that the 12 samples were divided into two groups. Six samples from Neijiang and samples from Suining were classified into group I, and samples from Luzhou and four outside Sichuan were classified into group II. The results indicated possible differences in the chemical composition between these two groups. From the loading diagram (Fig. 4b), it can be seen that the components causing quality differences between locations may include total carbohydrates, tyrosine, leucine, and proline. ANOVA analysis showed that the content of 19 components such as ash, protein, total carbohydrates, and crude polysaccharides were significantly different in these two groups, and the content of most of the indicators was higher in group I than group II. Cluster analysis results were basically the same as the PCA classification results, but were divided into three categories (Fig. 4c). Among them, SCNJ001, SCNJ002, SCNJ003 and SCNJ005 were clustered into one category, SCNJ004, SCNJ006 and SCSN008 were clustered into another, and GX00011, YN00010, CQ00009, SCLZ007 and GZ00012 were clustered into one further category. The results of PCA and cluster analysis corroborated each other, indicating differences in *A. cochinchinensis* quality among locations.

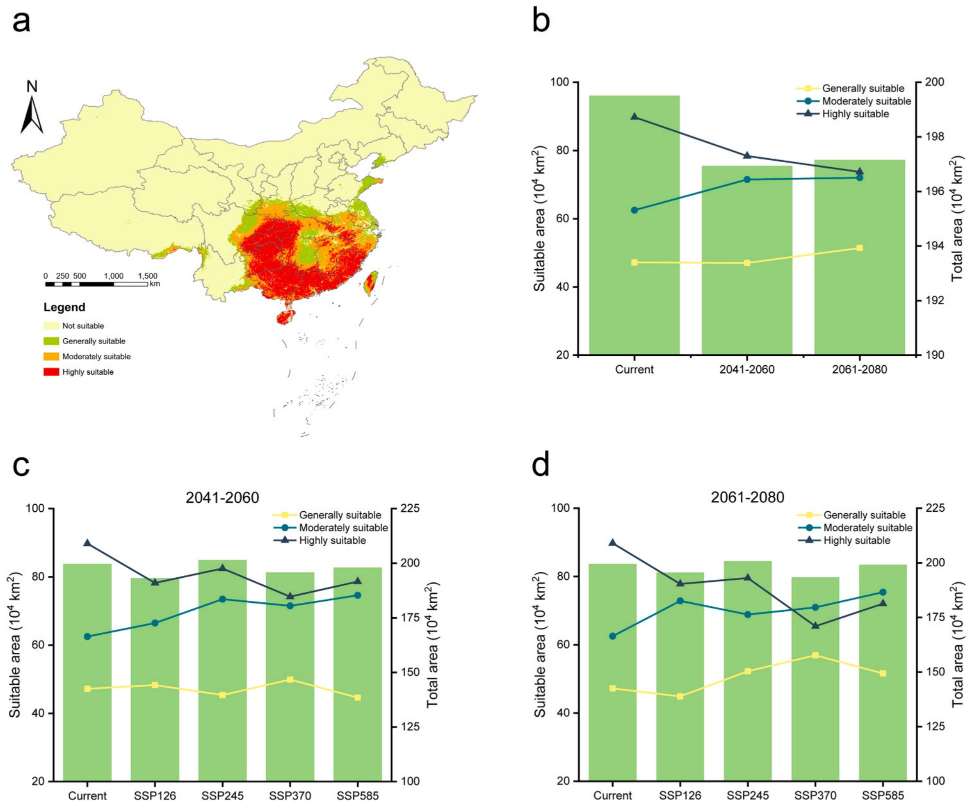

Fig. 2. Current potential distribution of *A. cochinchinensis* and suitable areas of current and future conditions. Current potential distribution of *A. cochinchinensis* (a). Average suitable area in different years (b). Different SSPs suitable areas of 2041–2060 (c). Different SSPs suitable areas of 2061–2080 (d).

3.4. Correlation between chemical composition and the key environmental factor Bio2

Correlation analysis of chemical composition with the key environmental factor showed significant correlations between Bio2 and a total of 12 chemical variables including ash, protein, total carbohydrates, Ca, K, B, Co, Val, Ile, Tyr, Lys, and crude polysaccharides (Fig. 4d). Among them, there were also significant correlations between chemical components. For example, ash was significantly correlated with protein, total carbohydrates, K, B, Co, Mo, Asp, Glu, Tyr, and crude polysaccharides, and crude polysaccharides were significantly correlated with ash, protein, total carbohydrates, K, B, Co, Ser, Val, Ile, and Tyr. The significant correlations between these chemical indicators also suggest a potential effect of Bio2 on some of the chemical indicators that are not directly and significantly correlated with it. Fig. 5. shows the specific linear relationships for these correlations. Nutrients, ash and protein showed significant negative correlation with Bio2, and total carbohydrates showed significant positive correlation with Bio2 (Fig. 5a). Minerals Ca, K, B and Co all showed significant negative correlation with Bio2 (Fig. 5b). Amino acids Val, Ile and Lys showed significant negative correlation with Bio2, while Tyr showed significant positive correlation with Bio2 (Fig. 5c). Among the active constituents, crude polysaccharides showed significant negative correlation with Bio2 (Fig. 5d). The results of the correlation analysis suggest that the environment plays a key role in the chemical biosynthesis of the medicinal plant *A. cochinchinensis*. The most of the chemical component contents were negatively correlated with Bio2, and a small portion was positively correlated. Combined with the response curve of Bio2, the negative correlation indicated that the higher the suitability of Bio2 the higher the content of chemical components, while the positive correlation indicated that the suitability of Bio2 had little effect on the content of chemical components.

4. Discussion

4.1. Analysis of key environmental factors

Currently, it has become a research trend to construct ensemble models to predict a species' habitat suitability (Fang, et al., 2021). Ensemble models can synthesize the real signals generated by individual models and separate out the noise generated by errors and uncertainties, thus providing higher accuracy (Hao, et al., 2019). Based on the prediction results of the ensemble model, Bio2 (Mean Diurnal Range) was selected as the key environmental factor influencing the distribution of *A. cochinchinensis*. The larger the Bio2, the lower the growth probability. Studies have shown that temperature is associated with productivity, species interactions and ecological specialization of medicinal plants, making it the most important predictor for modeling the distribution of medicinal plant species (Feng, et al., 2023). Bio2 provides information on the correlation of temperature fluctuations with different species. When the mean diurnal range (Bio2) is relatively large, the temperature is higher during the day (Gupta et al., 2020). However, higher temperatures can adversely affect plant photosynthesis, respiration, transpiration, membrane thermostability and osmotic regulation thereby constraining their distribution (Zhao et al., 2020). Actually, *A. cochinchinensis* is widely distributed in temperate regions (Luo, et al., 2022; Wang, et al., 2022), and in China is mainly found in the southern region and south of the Yangtze River (Liang, et al., 2018; Liu, et al., 2021). Accordingly, Bio2 values in these regions have a lower range, indicating higher suitability for growth and distribution of *A. cochinchinensis* than the high Bio2 values in northwestern China. This suggests that the actual growth conditions of *A. cochinchinensis* are basically consistent with the results predicted by the ensemble model.

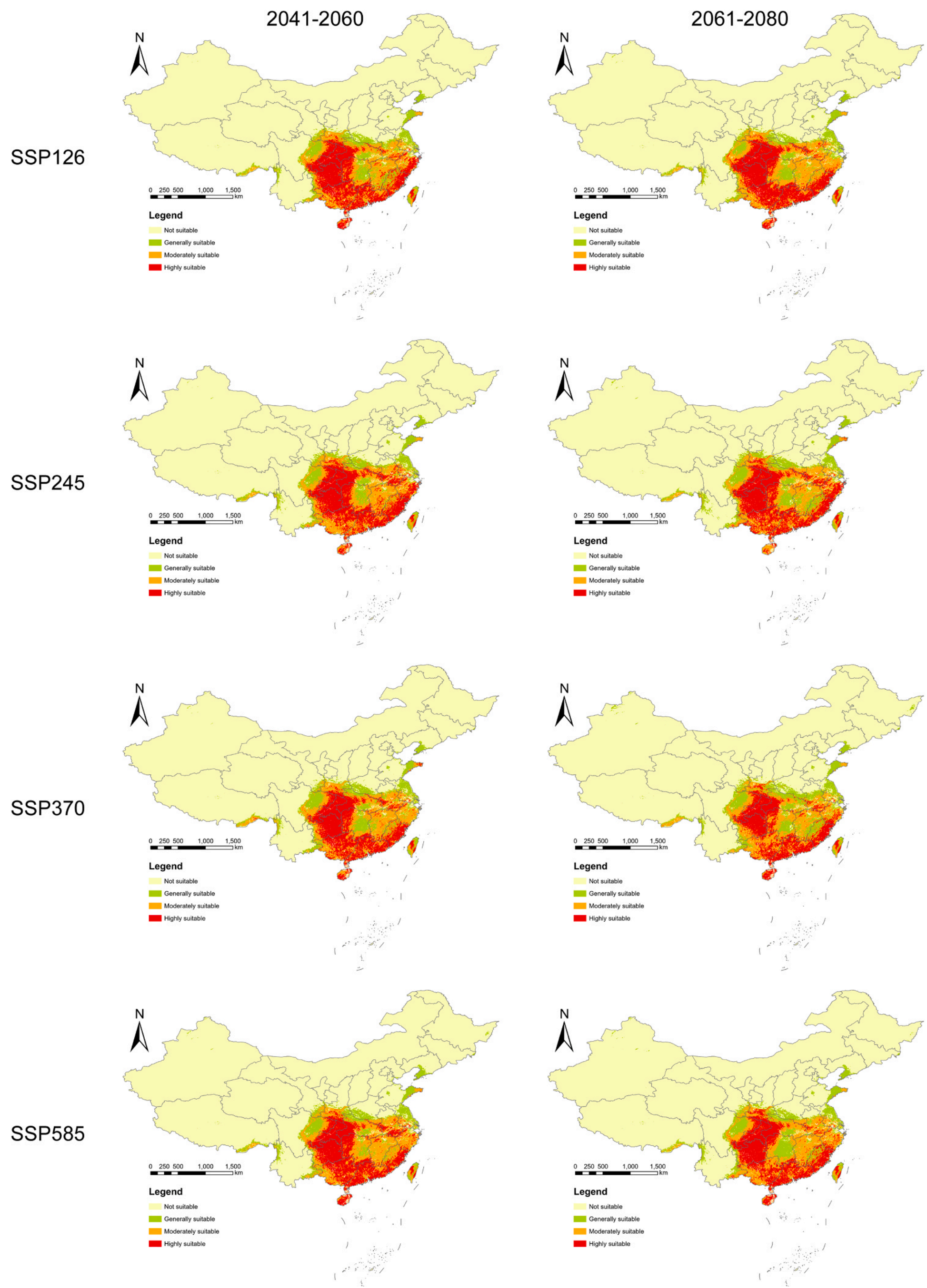

Fig. 3. Future potential distribution of *A. cochinchinensis* under different scenarios and different years.

4.2. Currently suitable habitats and future distribution shifts of A. cochinchinensis

In recent years, with growing appreciation of the medicinal and edible value of *A. cochinchinensis*, its market demand has risen, resulting in increasing pressure on its wild resources. However, studies are scarce on habitat suitability for *A. cochinchinensis* (Yu et al., 2022). Prediction results from the ensemble model show that the potentially suitable areas for *A. cochinchinensis* are mainly distributed in south-central and southeastern China. Highly suitable areas include Sichuan, Chongqing, Guizhou, Guangxi, Guangdong, Fujian and other provinces and municipalities, which is in general agreement with the main distribution of *A. cochinchinensis* reported in the literature (Liang et al., 2018; Xue et al., 2022). Therefore, these areas can serve as site selection references for the cultivation of *A. cochinchinensis*.

Climate change, global warming in particular, affects the biosynthesis of compounds in medicinal plants and can alter their phenology and distribution (Cahyaningsih et al., 2021). Studies have shown that, under the influence of climate change, the distribution of most species will shift to cooler temperatures and higher altitudes, resulting in a decrease in their distribution areas or even their classification as endangered (Li et al., 2020a,2020b; Wen et al., 2022). According to the future potential distribution of *A. cochinchinensis* predicted by the ensemble model, under future climate scenarios, the highly suitable area size shows a decreasing trend while the moderately suitable area size shows an increasing trend. Under future climate conditions, highly suitable areas become moderately or generally suitable areas, and there is a tendency to shift to areas with lower temperatures and higher

Table 2
Bio2 and chemical composition content of *A. cochinchinensis* from each sampling location.

Chemical composition	Locations					
	SCNJ001	SCNJ002	SCNJ003	SCNJ004	SCNJ005	SCNJ006
Key environmental factor						
Bio2 (℃)	6.31	6.41	6.44	6.67	6.57	6.44
Nutritional composition						
Moisture (g/100 g)	5.43±0.28	9.35±0.21	7.75±0.12	7.39±0.15	7.46±0.22	7.33±0.10
Ash (%)	4.17±0.06	4.20±0.10	3.83±0.06	2.83±0.06	4.03±0.06	3.43±0.15
Dietary fiber (g/100 g)	11.7±0.2	12.5±0.2	13.2±0.2	12.2±0.2	14.1±0.2	13.7±0.2
Starch (g/100 g)	0.622±0.022	0.849±0.006	0.843±0.011	0.964±0.011	1.19±0.04	0.940±0.015
Protein (g/100 g)	9.30±0.06	9.36±0.12	8.71±0.08	7.96±0.17	8.41±0.14	8.00±0.15
Total carbohydrates (%)	80.5±0.4	76.8±0.2	79.3±0.1	81.4±0.2	79.5±0.2	81.1±0.2
Vitamin						
Vitamin E (mg/100 g)	0.560±0.019	0.722±0.007	0.732±0.006	0.500±0.006	0.725±0.006	0.519±0.006
Pantothenic acid (mg/100 g)	0.327±0.012	0.508±0.006	0.862±0.006	1.04±0.01	0.462±0.004	0.519±0.005
Mineral composition						
Sodium (mg/100 g)	13.6±0.2	14.1±0.2	12.5±0.2	26.4±0.3	16.6±0.2	26.7±0.2
Magnesium (mg/100 g)	83.4±0.2	82.2±0.4	82±0.3	72.5±0.8	87.1±0.4	76.4±0.3
Calcium (mg/100 g)	380±12	406±20	399±11	310±10	405±10	329±8
Kalium (mg/100 g)	1717±25	1637±15	1530±20	1387±25	1513±25	1343±15
Manganese (mg/100 g)	1.78±0.04	1.45±0.07	1.59±0.05	1.04±0.09	1.49±0.06	1.03±0.08
Boron (mg/100 g)	1.64±0.16	1.52±0.06	1.51±0.08	1.09±0.06	1.51±0.04	1.07±0.07
Cobalt (mg/100 g)	0.0606±0.0031	0.0549±0.0013	0.0575±0.0007	0.0356±0.0007	0.0479±0.0013	0.0338±0.0016
Strontium (mg/100 g)	0.910±0.015	0.940±0.010	0.880±0.015	0.670±0.015	0.910±0.020	0.590±0.010
Molybdenum (mg/100 g)	0.0286±0.0011	0.0277±0.0012	0.0255±0.0006	0.0259±0.0022	0.0240±0.0015	0.0266±0.0011
Amino acids						
Aspartate (g/100 g)	1.23±0.03	1.33±0.03	1.27±0.01	0.904±0.005	1.23±0.04	0.832±0.022
Threonine (g/100 g)	0.0954±0.0031	0.0988±0.0004	0.108±0.002	0.151±0.004	0.111±0.004	0.139±0.002
Serine (g/100 g)	0.277±0.013	0.294±0.010	0.277±0.001	0.369±0.011	0.289±0.008	0.362±0.004
Glutamate (g/100 g)	1.59±0.06	1.73±0.04	1.68±0.01	0.910±0.007	1.53±0.06	0.850±0.016
Glycine (g/100 g)	0.0902±0.0025	0.0927±0.0028	0.0952±0.0010	0.128±0.001	0.0933±0.0042	0.115±0.001
Alanine (g/100 g)	0.139±0.004	0.147±0.004	0.151±0.001	0.242±0.003	0.150±0.005	0.225±0.003
Valine (g/100 g)	0.118±0.003	0.122±0.002	0.107±0.002	0.145±0.001	0.122±0.005	0.129±0.000
Methionine (g/100 g)	0.0305±0.0003	0.0274±0.0003	0.025±0.0005	0.0299±0.0008	0.0281±0.0010	0.0285±0.0010
Isoleucine (g/100 g)	0.0807±0.0021	0.0762±0.0021	0.0755±0.0001	0.0909±0.0028	0.0715±0.0025	0.0826±0.0010
Leucine (g/100 g)	0.106±0.002	0.112±0.001	0.0900±0.0016	0.156±0.004	0.0963±0.0026	0.129±0.003
Tyrosine (g/100 g)	0.0119±0.0001	0.0311±0.0006	0.0255±0.0004	0.0345±0.0006	0.0299±0.0013	0.0277±0.0008
Phenylalanine (g/100 g)	0.0590±0.0015	0.0715±0.0015	0.0672±0.0009	0.101±0.003	0.0737±0.0031	0.0795±0.0007
Lysine (g/100 g)	0.167±0.004	0.187±0.007	0.178±0.000	0.194±0.005	0.178±0.006	0.183±0.001
Histidine (g/100 g)	0.0652±0.0025	0.0691±0.0032	0.0605±0.0021	0.0762±0.0019	0.0661±0.0006	0.0587±0.0002
Proline (g/100 g)	0.278±0.013	0.298±0.011	0.267±0.003	0.163±0.001	0.279±0.012	0.139±0.006
Active ingredients						
Crude polysaccharides (mg/100 g)	1712±24	1250±15	1019±20	740±16	785±19	1557±17
Total saponins (mg/100 g)	1150±20	1180±22	1073±38	1306±28	1168±23	1140±14
Total flavonoids (mg/kg)	82.9±1.3	88.5±1.1	81.4±0.9	69.5±0.6	115.0±1.8	81.4±0.9
Total polyphenols (mg/kg)	834±7	634±19	1144±14	628±17	904±22	1216±24

Chemical composition	Locations					
	SCLZ007	SCSN008	CQ00009	YN00010	GX00011	GZ00012
Key environmental factor						
Bio2 (℃)	6.89	6.76	6.99	7.53	7.27	7.12
Nutritional composition						
Moisture (g/100 g)	6.28±0.08	6.75±0.08	7.18±0.13	5.93±0.22	5.61±0.16	6.24±0.10
Ash (%)	2.53±0.06	2.67±0.06	2.23±0.15	3.33±0.12	2.33±0.06	2.67±0.06
Dietary fiber (g/100 g)	12.6±0.2	16.6±0.2	16.8±0.2	11.2±0.1	10.7±0.1	14.2±0.2
Starch (g/100 g)	0.884±0.008	0.866±0.015	0.737±0.01	0.887±0.009	0.863±0.011	0.891±0.007
Protein (g/100 g)	5.35±0.09	8.36±0.14	4.18±0.05	7.34±0.13	7.17±0.16	6.54±0.18
Total carbohydrates (%)	85.4±0.1	81.9±0.1	86±0.1	83.3±0.2	84.5±0.2	84.3±0.1
Vitamin						
Vitamin E (mg/100 g)	0.576±0.007	0.886±0.006	0.463±0.004	0.612±0.008	0.571±0.006	0.988±0.006
Pantothenic acid (mg/100 g)	0.582±0.007	0.717±0.003	1.03±0.01	0.263±0.002	0.234±0.003	0.228±0.004
Mineral composition						
Sodium (mg/100 g)	7.23±0.15	25.3±0.2	4.05±0.17	11.4±0.2	18.6±0.1	4.91±0.14
Magnesium (mg/100 g)	57.7±0.3	76.0±0.6	56.5±0.5	88.3±0.8	73.8±0.4	98.1±0.6
Calcium (mg/100 g)	251±9	608±22	164±11	193±8	179±9	284±12
Kalium (mg/100 g)	844±9	636±11	778±13	1323±25	841±13	773±16
Manganese (mg/100 g)	0.895±0.020	1.103±0.030	1.09±0.02	0.618±0.038	2.28±0.08	1.29±0.04
Boron (mg/100 g)	0.930±0.012	1.09±0.07	0.766±0.021	0.734±0.009	0.627±0.013	0.750±0.012
Cobalt (mg/100 g)	0.0193±0.0005	0.0246±0.0008	0.0187±0.0006	0.0154±0.0002	0.0354±0.0009	0.0386±0.0011
Strontium (mg/100 g)	0.540±0.015	1.330±0.015	0.580±0.015	0.610±0.026	0.390±0.015	0.290±0.015
Molybdenum (mg/100 g)	0.00827±0.00032	0.0161±0.0007	0.0052±0.0001	0.0351±0.0003	0.00790±0.00075	0.00863±0.00080
Amino acids						
Aspartate (g/100 g)	0.971±0.019	1.15±0.01	0.605±0.011	1.51±0.02	0.833±0.013	0.963±0.017
Threonine (g/100 g)	0.0740±0.0024	0.126±0.002	0.0577±0.0015	0.119±0.002	0.109±0.000	0.086±0.000
Serine (g/100 g)	0.135±0.002	0.283±0.002	0.121±0.000	0.254±0.004	0.263±0.001	0.147±0.001

(continued on next page)

Table 2 (*continued*)

Chemical composition	Locations					
	SCLZ007	SCSN008	CQ00009	YN00010	GX00011	GZ00012
Glutamate (g/100 g)	1.02±0.03	1.62±0.02	0.590±0.007	1.76±0.03	1.11±0.01	0.980±0.025
Glycine (g/100 g)	0.0736±0.0025	0.103±0.008	0.0593±0.0015	0.0958±0.0020	0.111±0.001	0.0892±0.0020
Alanine (g/100 g)	0.0918±0.0027	0.155±0.001	0.0830±0.0015	0.145±0.001	0.173±0.002	0.132±0.003
Valine (g/100 g)	0.0776±0.0016	0.117±0.000	0.0658±0.003	0.0765±0.0005	0.0903±0.0012	0.0727±0.0015
Methionine (g/100 g)	0.0146±0.0010	0.0548±0.003	0.0213±0.0006	0.0416±0.0007	0.0338±0.0011	0.0187±0.0003
Isoleucine (g/100 g)	0.0497±0.0015	0.0707±0.0016	0.0497±0.0015	0.0579±0.0004	0.0645±0.0013	0.0568±0.0008
Leucine (g/100 g)	0.0742±0.0009	0.153±0.003	0.118±0.006	0.122±0.004	0.140±0.003	0.122±0.001
Tyrosine (g/100 g)	0.0328±0.0005	0.0479±0.0003	0.0517±0.0018	0.0503±0.0015	0.0562±0.0010	0.0420±0.0000
Phenylalanine (g/100 g)	0.0486±0.0010	0.0800±0.0004	0.0429±0.0009	0.0517±0.0008	0.0713±0.0015	0.0477±0.0008
Lysine (g/100 g)	0.142±0.001	0.195±0.002	0.131±0.004	0.149±0.003	0.151±0.003	0.137±0.004
Histidine (g/100 g)	0.0455±0.0014	0.0755±0.0010	0.0413±0.0042	0.0547±0.0015	0.0517±0.0015	0.045±0.001
Proline (g/100 g)	0.293±0.007	0.217±0.003	0.375±0.009	0.434±0.013	0.221±0.003	0.211±0.010
Active ingredients						
Crude polysaccharides (mg/100 g)	534±10	739±18	367±20	394±21	551±17	463±8
Total saponins (mg/100 g)	1767±24	1531±32	836±18	1340±17	1587±31	1504±26
Total flavonoids (mg/kg)	84.5±0.9	72.5±0.7	71.7±0.6	82.9±1.4	95.3±0.9	85.4±1.9
Total polyphenols (mg/kg)	588±17	825±11	838±10	741±16	770±22	555±21

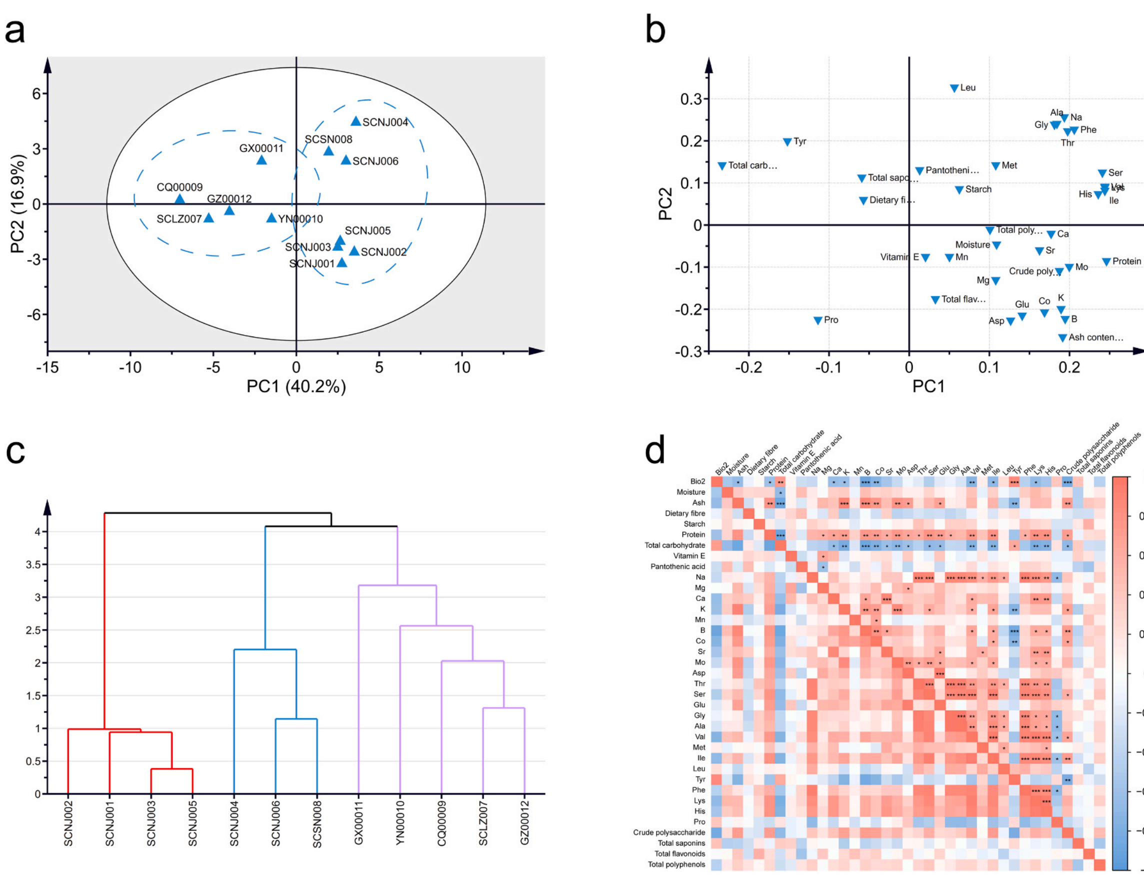

Fig. 4. Statistical analysis to chemical composition of *A. cochinchinensis*. Principal component analysis (a). Loading plot of PCA (b). Cluster analysis (c). Heatmap of correlation analysis between chemical content and the key environmental factor Bio2 (d).

altitudes. Therefore, climate change will have a negative impact on the potential distribution of *A. cochinchinensis* and measures should be taken to deal with this potential issue.

4.3. The relationship between chemical content and the key environmental factor Bio2

A. cochinchinensis is widely distributed in China, but the types and contents of its metabolites vary in different habitats (Xue et al., 2022). Statistical analysis of the chemical composition of *A. cochinchinensis* from different locations reveals that the quality is better mainly in Neijiang, implying that the environmental conditions at this location are more suitable for the growth and the biosynthesis of its constituents. This was verified by subsequent analyses. Correlation analysis results show that the contents of some chemical indicators of *A. cochinchinensis* are significantly correlated with the key environmental factor Bio2, and that the correlation was consistent with the trend of the response curves of the key environmental factor. The response curve showed that Bio2 had an opposite trend to the growth suitability of *A. cochinchinensis*. A lower Bio2 indicates higher suitability for distribution, and the Bio2 value in Neijiang was relatively low. This indicates that the more suitable growth environment is more favorable for biosynthesis of chemical

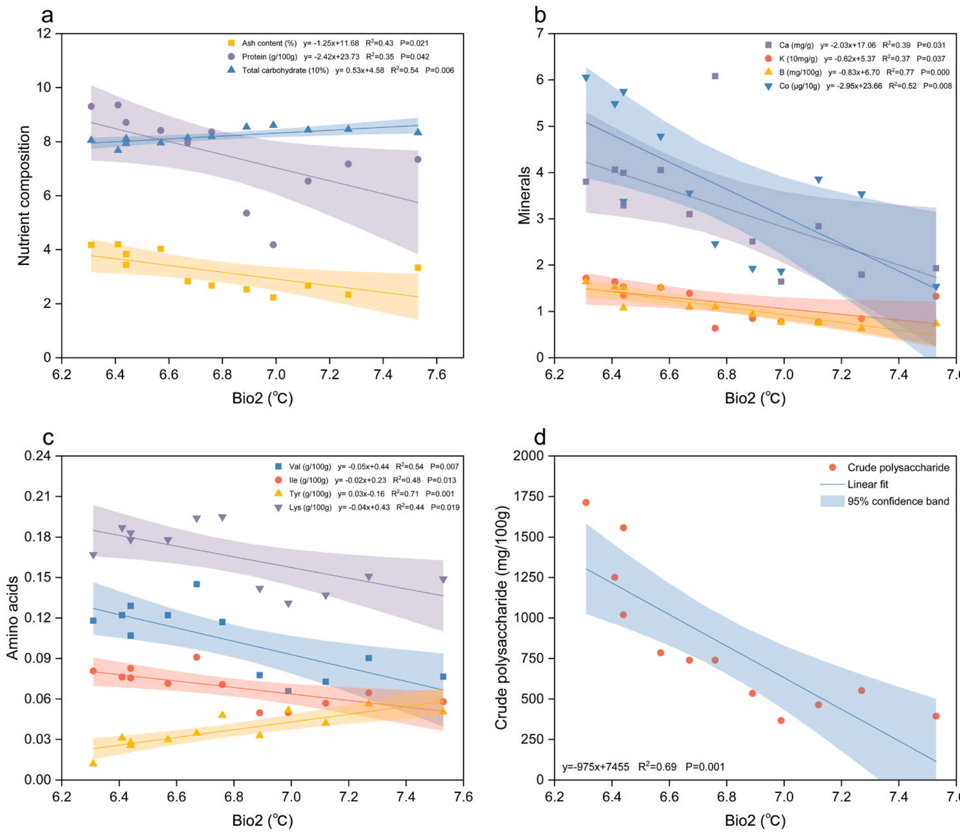

Fig. 5. Specific linear relationships between chemical composition and the key environmental factor Bio2. Nutrient composition (a). Minerals (b). Amino acids (c). Crude polysaccharides in the active ingredient (d).

indicators, which is consistent with previous reports (Li et al., 2020a, 2020b; Liu et al., 2023). As mentioned previously, Bio2 is a variable that is correlated with temperature fluctuations, with larger values making species more susceptible to high and low temperatures. However, high or low temperatures induce leaf senescence, membrane damage, degradation of chlorophyll, and denaturation of protein, thereby affecting the production of primary and secondary metabolites (Mahajan et al., 2020). At the molecular level, temperature regulates the expression levels of genes related to the plant's basic pathway or secondary metabolic synthesis pathway, which results in different chemical composition content of *A. cochinchinensis* from different locations (Li et al., 2020a, 2020b). In conclusion, the key environmental factor Bio2 affects not only the distribution of *A. cochinchinensis* but also its chemical composition. Therefore, the selection of suitable locations for cultivation plays an important role in the quality enhancement of *A. cochinchinensis*.

5. Conclusion

In this study, we successfully constructed an ensemble model for species distribution modeling of *A. cochinchinensis*. The prediction results showed the distribution of *A. cochinchinensis* in China under the current environmental conditions and a decreasing trend in the distribution area under future climate scenarios. The results of the importance of environmental factors showed that the key factor affecting the growth and distribution of *A. cochinchinensis* was the Mean Diurnal Range (Bio2). Principal component analysis, ANOVA analysis and cluster analysis showed differing chemical composition of *A. cochinchinensis* from different locations, with the highest quality of *A. cochinchinensis* from Neijiang. Correlation analysis showed significant correlations between the contents of some chemical indices of *A. cochinchinensis* and the key environmental factor Bio2. For example, the contents of Val, Ile and Lys in amino acids and crude polysaccharides in active constituents were significantly negatively correlated with Bio2, and the contents of total carbohydrates in nutrients and Tyr in amino acids were significantly positively correlated with Bio2, providing a rationale for the highest quality of *A. cochinchinensis* from Neijiang. In conclusion, environmental factors can influence the distribution and chemical composition of *A. cochinchinensis*. These results provide a scientific basis for the cultivation, the sustainable resources use, and the quality improvement of *A. cochinchinensis*.

CRediT authorship contribution statement

Tingting Zhang: Writing – original draft, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Lili Zhou:** Writing – review & editing, Methodology, Conceptualization. **Yang He:** Writing – review & editing, Supervision, Methodology, Funding acquisition, Formal analysis, Conceptualization. **Dan Liu:** Methodology, Formal analysis. **Chao Chen:** Methodology, Formal analysis, Conceptualization. **Jiawei Wen:** Methodology, Formal analysis, Conceptualization. **Wanqing Feng:** Methodology, Conceptualization. **Ying Han:** Methodology, Conceptualization. **Ya Yuan:** Resources, Methodology, Formal analysis.

Declaration of Competing Interest

We confirm that all competing interests, whether financial or non-financial, have been disclosed accurately and transparently. These potential competing interests have not influenced the design, conduct, or reporting of this research.

Data availability

Data will be made available on request.

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