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# Predicting potential distributions of *Monochamus saltuarius*, a novel insect vector of pine wilt disease in China

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*Monochamus saltuarius* Gebler was first identified as a new vector of pine wilt disease in Northeast China in 2018, and monitoring of *M. saltuarius* has become a key strategy to prevent and control the disease in this region. However, the potential distributions of *M. saltuarius* in China are unclear. In this study, we clarified bioclimatic environmental variables affecting the distribution of *M. saltuarius*, predicted the geographically suitable habitats of *M. saltuarius* in current and future climate conditions, and determined changes in the spatial pattern of a suitable distribution area of *M. saltuarius* under current and future climate conditions. This is the first study to use the optimized maximum entropy model and ArcGIS to accurately predict suitable geographical areas for *M. saltuarius* based on different climatic conditions in China. and the average area under the receiver operating characteristic curve reached  $0.954 \pm 0.0024$ . Of the 32 bioclimatic variables, temperature seasonality, precipitation of wettest month, precipitation seasonality, maximum temperature of the warmest month, and elevation played significant roles in determining the potential distribution of *M. saltuarius*, with contribution rates to the model of 32.1, 31.8, 11.5, 7.5, and 6.5%, respectively. Under the current climate scenario, the predicted suitable areas for *M. saltuarius* were mainly at latitudes north of 33° in China, and larger suitable areas were mainly distributed in Northeast China and North China, with areas of  $87.04 \times 10^4$  and  $73.15 \times 10^4$  km<sup>2</sup>, respectively. Using future climatic scenarios SSP126 and SSP585, the predicted suitable areas of *M. saltuarius* will continue to expand from that of 2040, 2070, and 2100, with highly and moderately suitable areas showing larger increasing trends but low suitable distribution areas will decrease to varying degrees. The potential suitable areas of *M. saltuarius* may increase greatly in Northwest, Central, and Eastern China. This study provides important scientific theoretical knowledge for effectively controlling and preventing *M. saltuarius* and pine wilt disease in northern China.

## KEYWORDS

pine wilt disease, *Monochamus saltuarius*, *Bursaphelenchus xylophilus*, MaxEnt, climate change

## 1. Introduction

*Bursaphelenchus xylophilus* (Steiner and Buhner) Nickle can cause pine wilt disease (PWD), which systematically infects and causes wilting of healthy pines (Sun, 1982; Mamiya, 1983). *Bursaphelenchus xylophilus* leads to high mortality of conifer trees, including of *Pinus* plants and non-*Pinus* plants such as *Picea*, *Larix*, *Abies*, and *Cedrus* (Nunes et al., 2013; Foit et al., 2019). PWD was first discovered in 1982 in *Pinus thunbergii* Parl. in Nanjing, Jiangsu province of China (Sun, 1982). Since then, it has become one of the most destructive forest quarantine pests, causing very large economic and ecological losses (Gao et al., 2017; Ye and Wu, 2022). As of February 2023, PWD had spread to 700 county-level administrative regions in 19 provinces of China (Figure 1) and continuously spread to the northern and western parts of China (Li et al., 2022; Ye and Wu, 2022; Zhang et al., 2022; Zong and Bi, 2022).

As a plant parasitic nematode, *B. xylophilus* lives in the xylem of host pines, and its natural transmission relies on insect vectors that are transported from infected host plants to healthy plants (Aikawa, 2008; Li M. et al., 2021). Currently, the main vector insects that can carry *B. xylophilus* are beetles in the genus *Monochamus* (Cerambycidae) (Linit et al., 1983; Kobayashi et al., 1984; Linit, 1988; Li et al., 2020; Li M. et al., 2021). The 4th dispersal juveniles of *B. xylophilus* attach to the surface respiratory trachea and reproductive systems of the vector insect before eclosion (Pan et al., 2020). When vector insects eclose from pines killed by *B. xylophilus*, they feed on a new healthy host plant and release *B. xylophilus*, which then infects the healthy host tree (Balestrini et al., 2009; Zhao et al., 2013; Zhang et al., 2020). Therefore, vector

insects are an important link in the PWD infection system, and efficient control of vector insects is the most important measure for preventing PWD (Linit et al., 1983; Kobayashi et al., 1984; Linit, 1988; Li et al., 2020, 2022; Li M. et al., 2021; Ye and Wu, 2022).

*Monochamus saltuarius* is among the main vector insects of *B. xylophilus* in Southeast Asia, including China, South Korea, and Japan (Takizawa and Shoji, 1982; Sato et al., 1987; Jikumaru and Togashi, 1995; Kim et al., 2006; Koo et al., 2013; Han et al., 2016; Yu and Wu, 2018; Li et al., 2020; Li M. et al., 2021). Before 2016, *Monochamus alternatus* was the only insect vector of *B. xylophilus* in China and was widely distributed south of the Yellow River; its northern boundary was Dalian, Liaoning province (Li et al., 2007; Wu et al., 2013; Gao et al., 2023). However, in recent years, *M. saltuarius* has been considered as a novel vector of *B. xylophilus* in PWD-infected pines in high-latitude and newly invaded areas of China, including in Jilin and Liaoning provinces (Yu and Wu, 2018; Li et al., 2020; Li M. et al., 2021). *Monochamus saltuarius* plays a key role in carrying, spreading, and assisting the pathogen *B. xylophilus* to enter its host, and in its transmission efficiency and harmful effects (Ye, 2019; Li et al., 2022; Ye and Wu, 2022).

*Monochamus saltuarius* is a native species that is widespread in northern China and was a common pest in Shanxi, Inner Mongolia, Liaoning, Jilin, and Heilongjiang provinces before being identified as a new vector insect of *B. xylophilus* in these areas (Ye, 2019; Li M. et al., 2021; Figure 2). Moreover, by feeding on host plants, *M. saltuarius* can enable full-scale invasion of *B. xylophilus* and directly threaten healthy host trees in northern China (Chen et al., 1959; Wang, 2014; Yu et al., 2019). However, studies predicting *M. saltuarius* invasion in China have not been

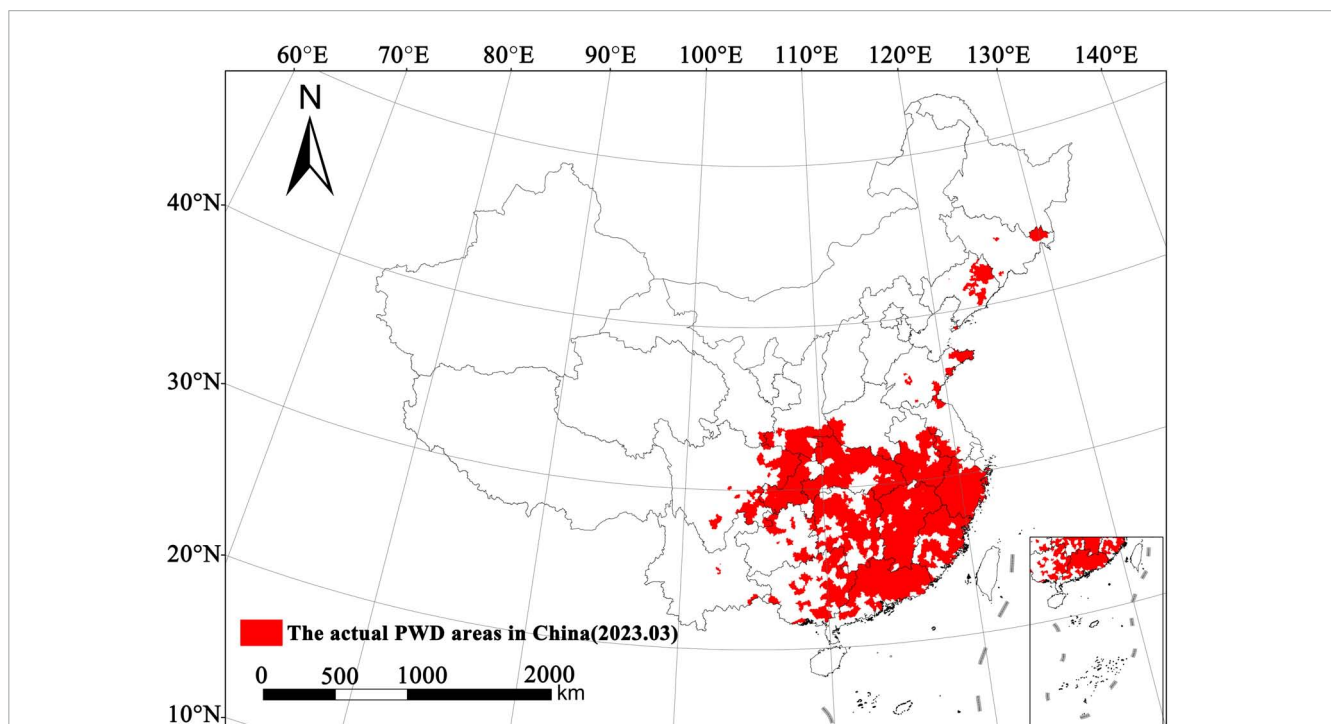


FIGURE 1

Actual epidemic distribution areas of pine wilt disease in China by March 2023 (Data obtained from the No. 7 bulletin of National Forestry and Grassland Administration [NFGA], 2023).

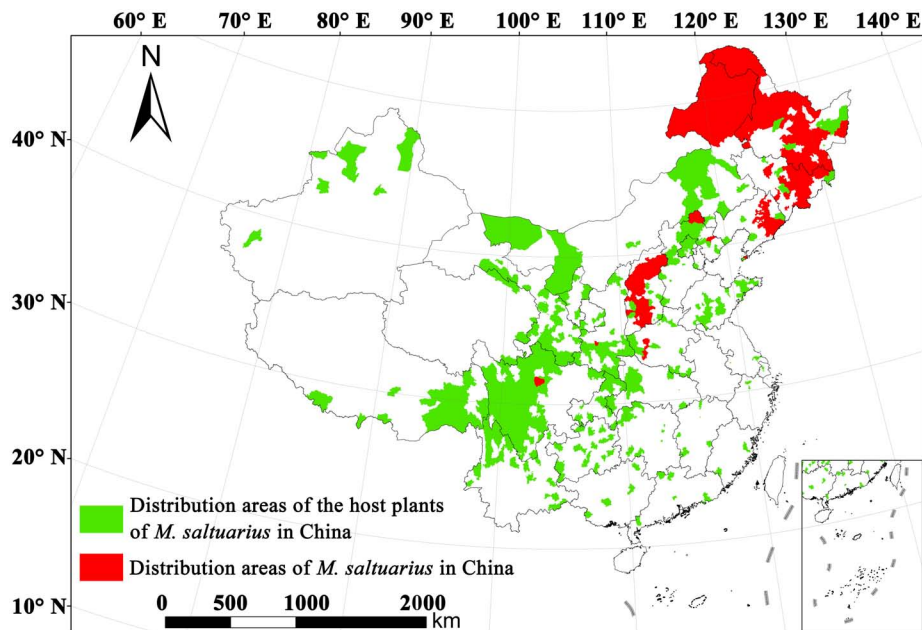


FIGURE 2  
Distribution areas of *Monochamus saltuarius* in China.

TABLE 1 The contribution rates of selected variables affecting the geographical distribution of *M. saltuarius*.

Code	Variables	Contribution rate/%
Bio4	Temperature seasonality (°C)	32.1
Bio13	Precipitation of wettest month (mm)	31.8
Bio15	Precipitation seasonality (mm)	11.5
Bio5	Max temperature of warmest month (°C)	7.5
Elev	Elevation (m)	6.5
Bio9	Mean temperature of driest quarter (°C)	6.0
Wind3	Wind speed in March (m/s)	2.8
Wind9	Wind speed in September (m/s)	1.8

performed, preventing accurate prevention and control measures for *M. saltuarius* and PWD.

There is an urgent need to carry out the research on the distribution and change of the potential suitable areas of *M. saltuarius* in China. An optimized MaxEnt model based on the 175 latest county-level geographical distribution points was used to predict a suitable distribution of *M. saltuarius* in China during different climatic conditions. The main objectives of this study were to (1) clarify the related bioclimatic environmental variables affecting the distribution of *M. saltuarius*, (2) predict geographically suitable areas for *M. saltuarius* under different climate conditions, and (3) determine changes in the spatial pattern of *M. saltuarius* in different climate conditions. This study provides important scientific theoretical knowledge for the effective control and prevention of *M. saltuarius* and PWD in northern China.

TABLE 2 The performance of MaxEnt model under default and optimized settings.

	Default	Optimization
RM	1.0	0.5
FC	LQHP	LQHP
Mean AUC	0.904	0.906
AUC <sub>DIFF</sub>	0.058	0.054
OR <sub>MTP</sub>	0.076	0.076
OR <sub>10</sub>	0.355	0.360
ΔAICc	39.274	0

RM means regularization multiplier, FC means feature combination, AUC means area under the ROC curve, AUC<sub>DIFF</sub> means the difference between the training AUC and the test AUC, OR<sub>MTP</sub> means the "Minimum Training Presence" omission rate, OR<sub>10</sub> means the 10% training omission rate, ΔAICc means Akaike information criterion.

## 2. Materials and methods

### 2.1. Data collection

A total of 175 county-level geographical distribution points of *M. saltuarius* was obtained from four sources. First, 58 distribution points were obtained from field surveys of the distribution of *M. saltuarius* in different regions of China. Second, 69 distribution points were obtained from published references. Third, seven distribution points of *M. saltuarius* were obtained from the National Animal Specimen Database.<sup>1</sup> Fourth, 41 distribution points were obtained from the relevant databases and official websites. To remove the influence of spatial autocorrelation and

<sup>1</sup> <http://museum.ioz.ac.cn/index.html>

sampling bias, the distribution point data of *M. saltuarius* were imported into ArcGIS10.7, and the buffer analysis function in the software was used for sparse processing of distribution points to ensure that there was one *M. saltuarius* distribution point within areas of 25 km<sup>2</sup>.

## 2.2. Selection of variables

A total of 19 bioclimatic variables, 12 monthly average values about the wind speed as historical weather data and

terrain elevation were downloaded from the WorldClim website (Supplementary Table 1). Future climate data were simulated using SSP126 and SSP585 of Beijing Climate Central Climate System Model 2 Medium Resolution (BCC-CSM2-MR), and the simulated time periods included the years 2050, 2070, and 2100. To avoid autocorrelation between bioclimatic variables and overfitting (Sillero, 2011; Fotheringham and Oshan, 2016; Li X. et al., 2021; Gao et al., 2023), the 32 variables were screened and removed when the MaxEnt selected variables affecting the distribution of *M. saltuarius*. This step was performed to control the impact of redundant information

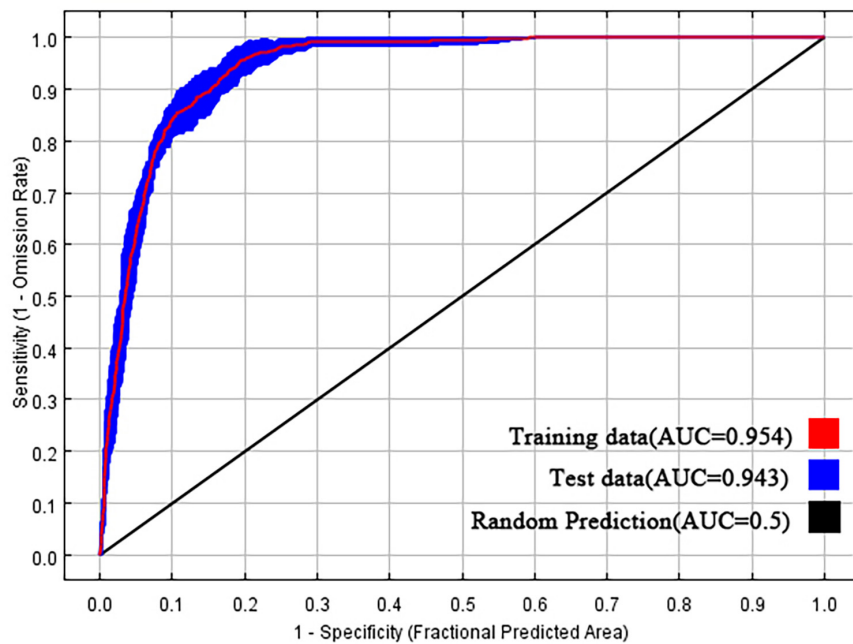


FIGURE 3 Receiver operating characteristic curve and areas under the curve for the optimized MaxEnt model.

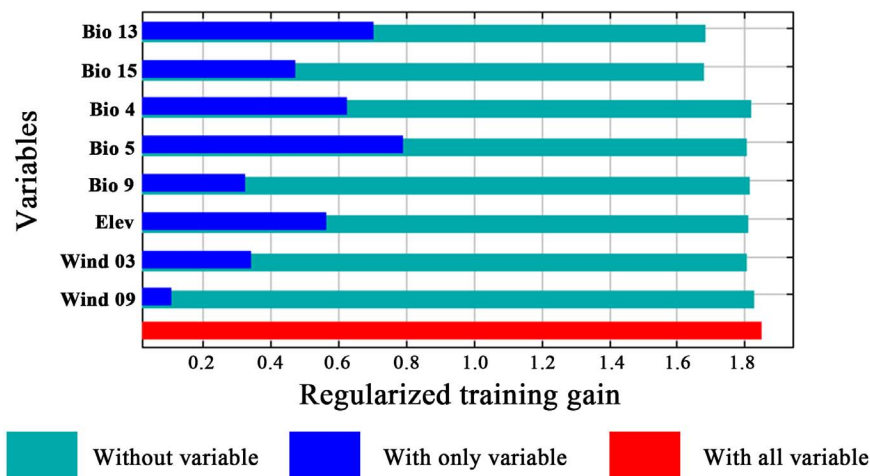


FIGURE 4 Importance of key bioclimatic variables in MaxEnt model for the distribution of *Monochamus saltuarius* determined using the Jackknife test. "Without variable" represents the regularized training gain of the model without this variable, "With only variable" represents the regularized training gain of the model with only this variable, "With all variable" represents the regularized training gain of the model with all variables.

on the simulation results and retain the environmental variables that limited the distribution of *M. saltuarius*. Initially, the MaxEnt was used to model the 32 variables, and the contribution rate of each variable was calculated. We continued to process bioclimatic variables using Pearson correlation analysis and removed variables with correlation coefficients higher than 0.8 (Supplementary Figure 1). Finally, eight variables were selected from 32 bioclimatic variables to predict the potential geographical distribution of *M. saltuarius* (Table 1).

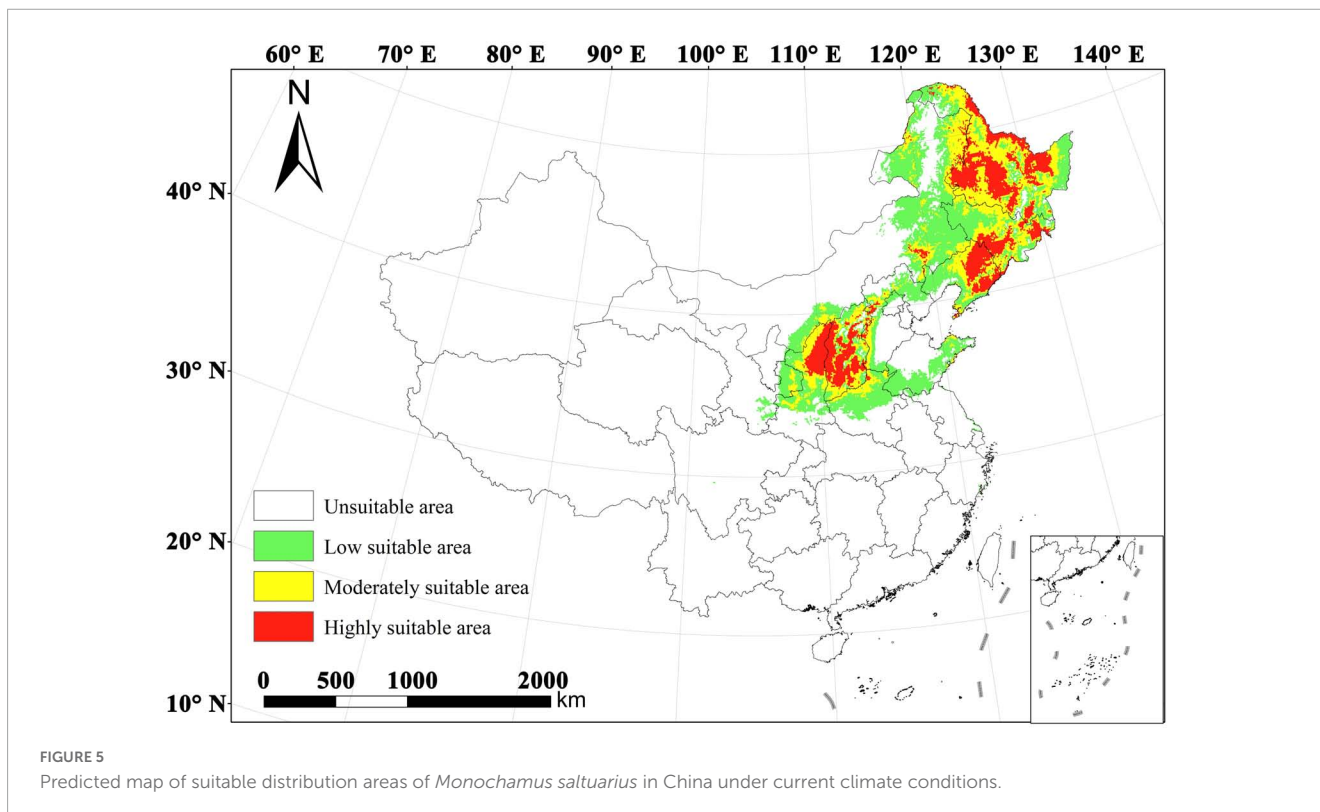
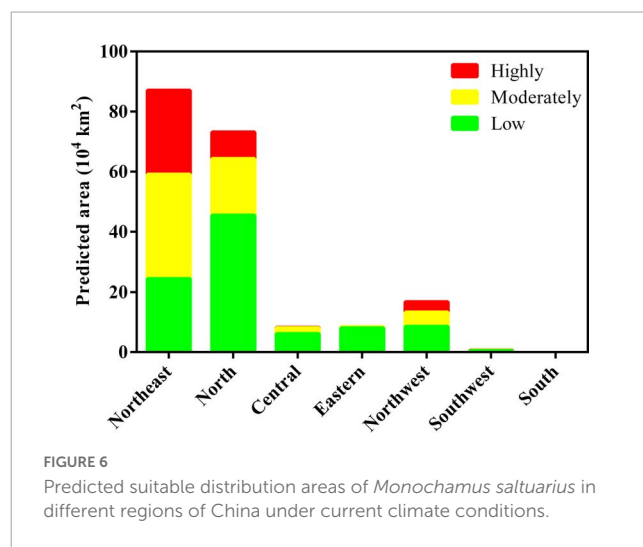
### 2.3. Model setting and analysis

The feature combinations and regularized multipliers of the model were optimized using the “ENMeval” package in R to screen the optimal combination and reduce the model complexity, and then randomly selected 75% of the data for model training and 25% for model testing. The regularization multiplier value of the MaxEnt model was set to change from 0.5 to 4 with an increase of 0.5 each time. Moreover, the accuracy of the MaxEnt was evaluated as the area under the receiver operating characteristic curve (AUC). A larger AUC value indicates higher model accuracy, and the evaluation criteria of the model were as follows: failure, poor, fair, good, and excellent. Finally, we used the Jenks’ natural breaks method (Qi et al., 2015; Ge et al., 2021) to reclassify the predicted suitable habitats for *M. saltuarius* into four categories, namely non-suitable (0–0.09), low suitable (0.09–0.28), moderately suitable (0.28–0.5), and highly suitable (0.5–1.00).

## 3. Results

### 3.1. Optimization and evaluation

The optimized MaxEnt parameters were adjusted to feature combination = LQHP, regularization multiplier = 0.5,  $\Delta AICc = 0$ , and  $AUC_{DIFF} = 0.054$  (Table 2). Evaluation of the optimized MaxEnt model showed that the average AUC ( $0.954 \pm 0.0024$ ) of the simulation run results of the MaxEnt model repeated 10 times was higher than 0.9 (Figure 3), demonstrating that the prediction results reached an high standard. Therefore, the MaxEnt model, which was set to optimize parameters.



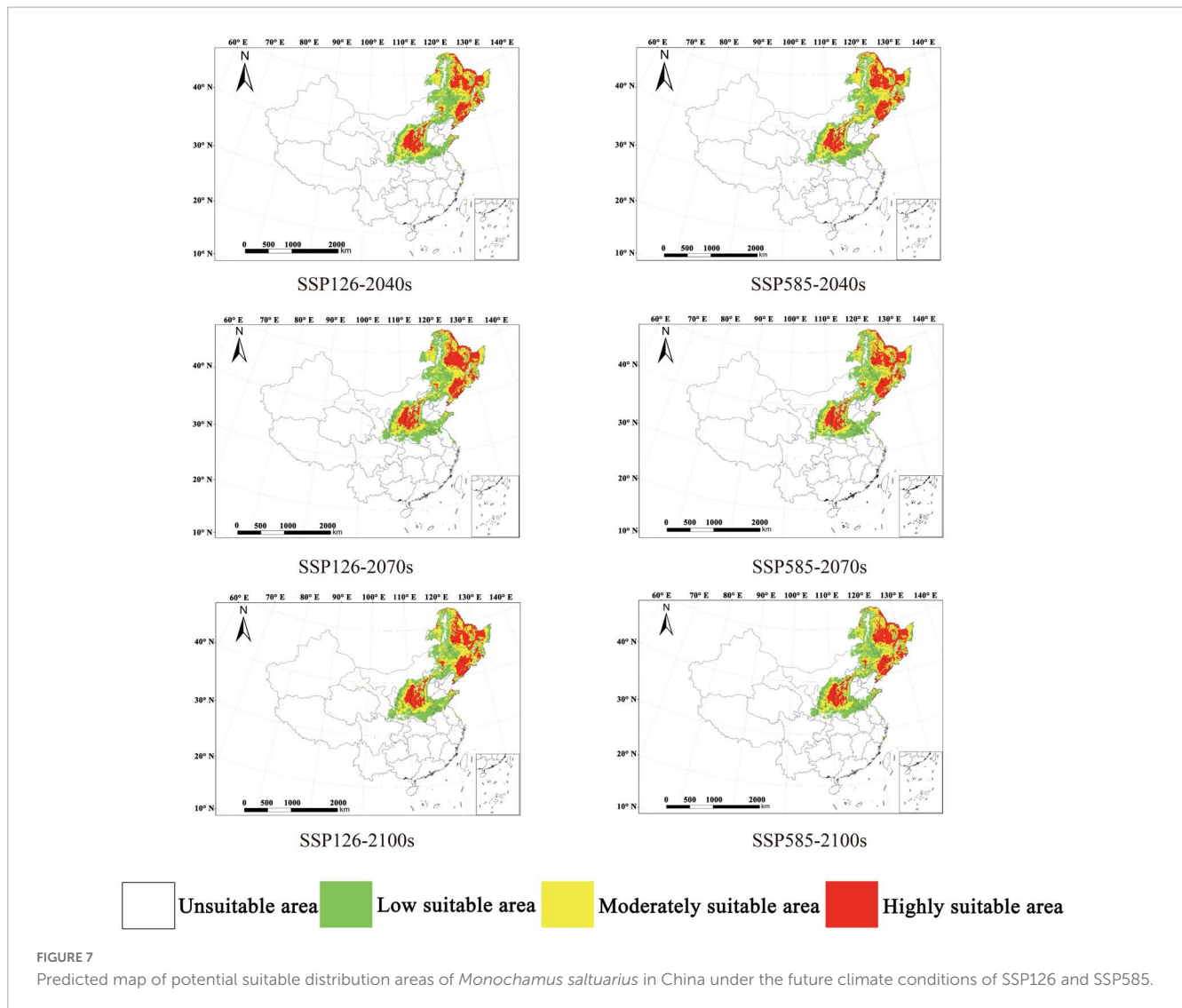


FIGURE 7

Predicted map of potential suitable distribution areas of *Monochamus saltuarius* in China under the future climate conditions of SSP126 and SSP585.

### 3.2. Key bioclimatic environmental variables

Eight variables were screened to predict the potential geographical distribution of *M. saltuarius*. Among them, the bioclimatic variables Bio4, Bio13, and Bio15 showed higher contribution rates, with a cumulative contribution rate of 75.4% (Table 2). Furthermore, the importance results of the selected bioclimatic variables using the Jackknife test showed that Bio4, Bio5, Bio13 and Elev were the variables with higher regularized training gains were when only one bioclimatic variable was used (Figure 4). Therefore, the key bioclimatic variables restricting the distribution of *M. saltuarius* were Bio4, Bio5, Bio13, Bio15, and Elev.

### 3.3. Current risk areas

Based on the historical climatic data and current distribution data, a suitable area for *M. saltuarius* was predicted using the current climate scenario (Figure 5), and the predicted total area was

approximately  $193.59 \times 10^4$  km<sup>2</sup>, accounting for approximately 20.10% of the total land area of China. The predicted areas of high, moderate, and low suitability for *M. saltuarius* were  $40.26 \times 10^4$ ,  $60.76 \times 10^4$ , and  $92.57 \times 10^4$  km<sup>2</sup>, accounting for 20.8, 31.38, and 47.82% of the total predicted suitable areas, respectively. The predicted suitable habitats of *M. saltuarius* were mainly at latitudes north of 33° in China, and the larger suitable areas were mainly distributed in Northeast and North China, with areas of  $87.04 \times 10^4$  and  $73.15 \times 10^4$  km<sup>2</sup>, respectively (Figure 6). There were some suitable distribution areas for *M. saltuarius* in Central, East, and Northwest China, with almost no predicted areas of *M. saltuarius* in Southwest and South China.

### 3.4. Future risk areas

We predicted the potentially suitable areas of *M. saltuarius* in 2040, 2070, and 2100 using future climatic scenarios (Figure 7). The predicted potentially suitable areas of *M. saltuarius* continued to expand in future climatic scenarios (Figure 8). Moreover, the center point of the suitable distribution area at different

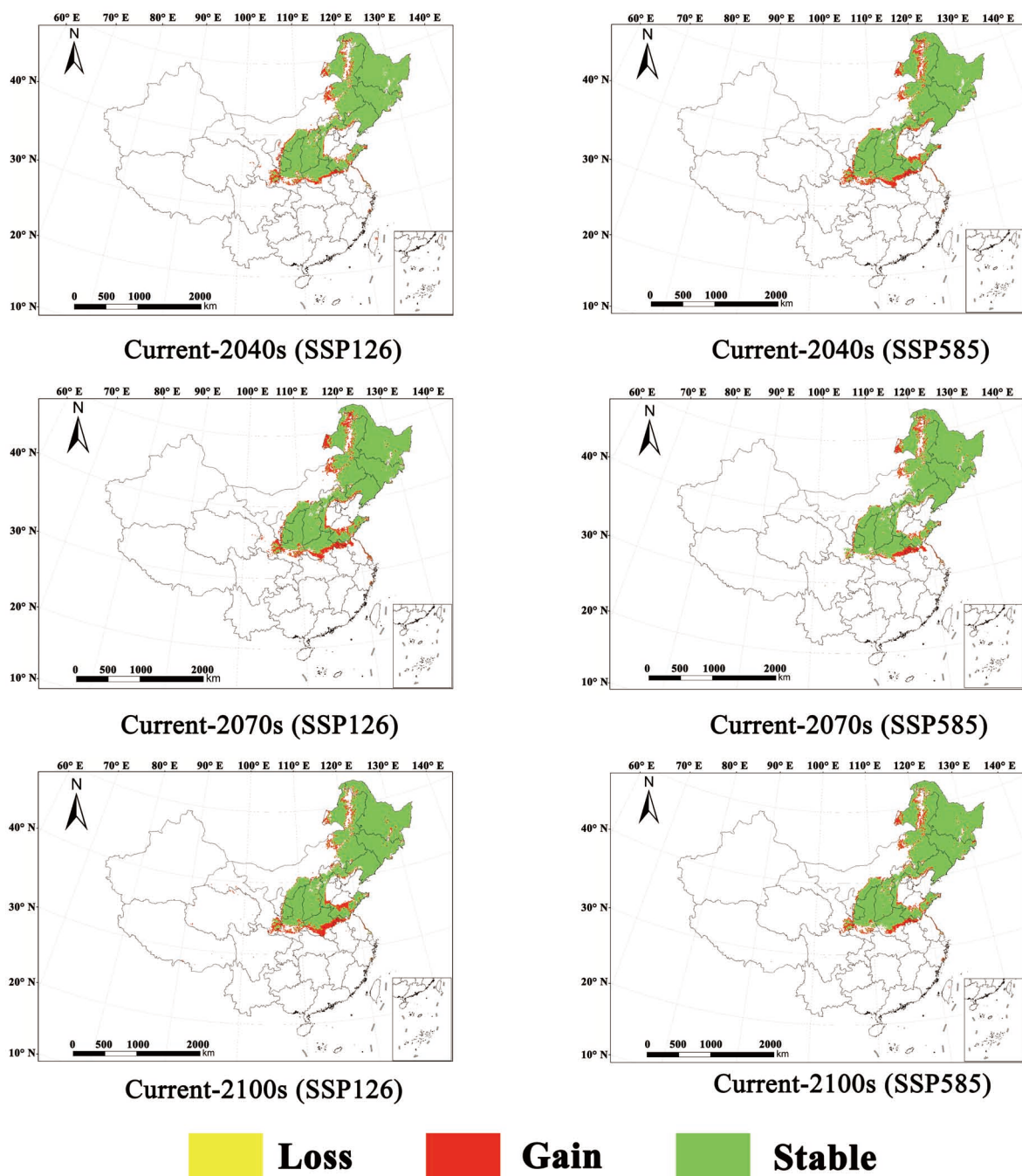


FIGURE 8

Changes in potential suitable areas of *Monochamus saltuarius* in different future climate conditions compared with the current areas.

times of *M. saltuarius* were predicted to shift with future climate change, showing an obvious spreading trend to the south and west (Figure 9). The range of centroid shifting occurred in Inner Mongolia. Moreover, highly and moderately suitable areas showed a larger increasing trend, but areas with low suitability distributions decreased to varying degrees (Table 3).

Similar to the current climate, the predicted areas of *M. saltuarius* under future climatic conditions are concentrated in Northeast and North China (Figure 10). In Northeast China,

highly suitable areas for *M. saltuarius* showed an increasing trend in future climatic conditions, whereas moderately and low-suitability areas generally showed a decreasing trend. In North China, highly suitable and moderately suitable areas for *M. saltuarius* showed a rising trend for future climatic conditions but low-suitability areas showed an overall decreasing trend. Moreover, there was a large increasing trend in the suitable distribution areas of *M. saltuarius* in Northwest, Central, and Eastern China (Table 4); however, there was almost no distribution area of *M. saltuarius* in Southwest and South China.

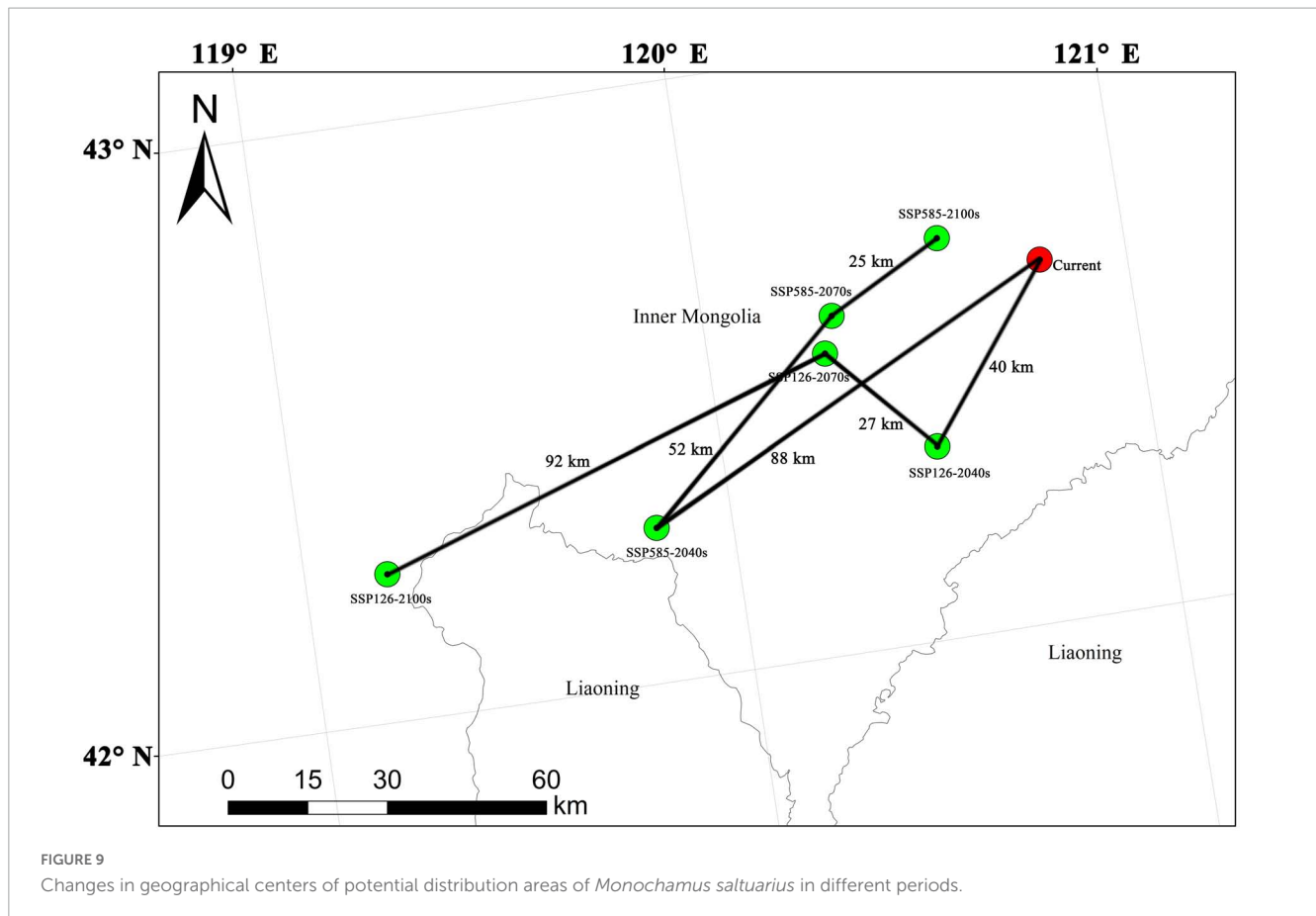


FIGURE 9 Changes in geographical centers of potential distribution areas of *Monochamus saltuarius* in different periods.

TABLE 3 The difference in potential suitable areas for *M. saltuarius* under current and future climate scenarios.

Decade	Scenarios	Total	Predicted area (10 <sup>4</sup> km <sup>2</sup> )			Comparison with current (%)		
			Highly	Moderately	Low	Highly	Moderately	Low
Current	-	193.59	40.26	60.76	92.57			
2040s	ssp-126	216.10	54.60	70.73	90.77	35.62	16.41	-1.94
	ssp-585	221.58	58.14	77.79	85.65	44.41	28.03	-7.48
2070s	ssp-126	222.47	57.81	73.05	91.61	43.59	20.23	-1.04
	ssp-585	213.85	56.19	69.27	88.39	39.57	14.01	-4.52
2100s	ssp-126	218.78	58.12	73.22	87.44	44.36	20.51	-5.54
	ssp-585	216.60	58.12	71.39	87.09	44.36	17.50	-5.92

### 4. Discussion

*Monochamus saltuarius* Gebler was first identified as an insect vector of PWD in Northeast China in 2018 (Yu and Wu, 2018; Li et al., 2020, Li M. et al., 2021). Monitoring *M. saltuarius* has become a key strategy for the prevention and control of PWD in this region (Ye, 2019; Li M. et al., 2021, Li et al., 2022; Ye and Wu, 2022). Therefore, understanding the potential distribution of *M. saltuarius* can facilitate the prevention and control of *M. saltuarius* and PWD.

The MaxEnt model is a widely used species distribution model to predict the geographic spatial area of target species and exhibits highly accurate prediction when only the “existence only” distribution data of the target species are used (Ge et al., 2018; Raffini et al., 2020; Lee et al., 2021; Ramasamy et al., 2022;

Gao et al., 2023). The maximum entropy distribution of a species under environmental constraints in a specific area can be estimated using the accurate geographical location of species occurrence and related biological environmental variables (Jackson and Robertson, 2011; Mitchell et al., 2016; Cao et al., 2021). However, predicting species distribution may be limited when using the MaxEnt model. Setting the default parameters of the MaxEnt model may lead to excessive model fitting, (Warren and Seifert, 2011; Muscarella et al., 2014; Jin et al., 2022). Hence, the “ENMeval” packet in R software was used to optimize the default parameters of the MaxEnt model to reduce the fit degree of the model (Warren and Seifert, 2011; Muscarella et al., 2014; Porfirio et al., 2014; Yan et al., 2021). The MaxEnt model was optimized through ENMeval package, and it was found that when the feature combination = LQHP and the



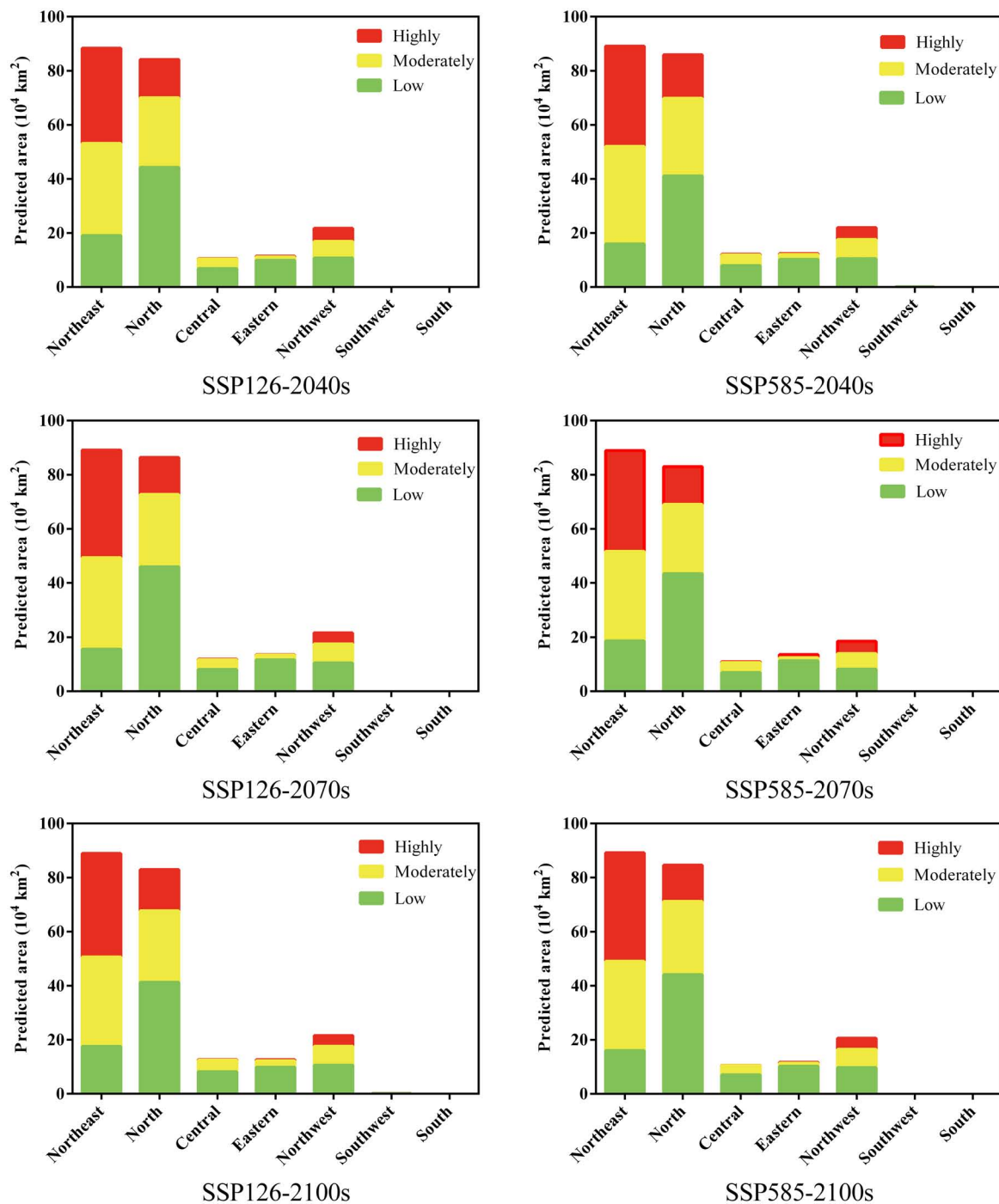


FIGURE 10

Predicted suitable distribution areas of *Monochamus saltuarius* in different regions of China under future climatic conditions.

regularization multiplier = 0.5, the model was the optimal model, and the predicted range of the suitable area of *Pinus sylvestris* var. *mongolica* was basically consistent with the actual distribution (Zhang et al., 2023).

In typical ectotherms, environmental variables can significantly affect the diversity, richness, and geographical distribution of insect species (Austin, 2002; Krefl and Jetz, 2007; Tang et al., 2021). The selected eight key bioclimatic variables in this study may significantly affect the distribution of

*M. saltuarius*. The results showed that Bio4, Bio5, Bio13, Bio15, and Elev played important roles in restricting the suitable distribution of *M. saltuarius*. In addition, Bio4 and Bio13 contributed relatively more to the distribution of *M. saltuarius*, indicating that *M. saltuarius* is highly sensitive to fluctuations in precipitation and temperature. The change in temperature is an important driving factor affecting the growth, development, and diffusion of *M. saltuarius*, and changes in temperature due to global warming will inevitably affect

TABLE 4 The difference in potential suitable areas for *M. saltuarius* in different regions of China under future climate scenarios compared with the current.

Decade	Scenarios	Northeast (%)			North (%)			Central (%)			Eastern (%)			Northwest (%)		
		Highly	Moderately	Low	Highly	Moderately	Low	Highly	Moderately	Low	Highly	Moderately	Low	Highly	Moderately	Low
2040s	ssp-126	26.27	-2.07	-21.84	59.82	36.49	-2.62	85.71	78.89	11.24	3,300	223.68	23.07	39.31	28.93	25.41
	ssp-585	32.94	3.94	-34.75	83.20	52.12	-9.61	242.86	96.98	29.32	3,000	394.74	27.06	25.43	50.31	22.13
	ssp-126	42.62	-2.88	-36.27	54.71	42.06	0.97	142.86	81.91	30.94	1,100	368.42	45.01	18.50	48.22	22.25
2070s	ssp-585	33.58	-4.92	-23.77	58.46	35.70	-4.49	257.14	86.93	12.54	11,300	200.00	40.52	29.48	34.17	6.56
	ssp-126	37.17	-4.84	-28.11	72.99	40.10	-9.24	171.43	115.58	33.06	4,100	536.84	22.19	15.03	46.33	24.00
	ssp-585	43.91	-5.01	-34.34	52.67	43.43	-3.06	57.14	72.86	14.01	3,000	194.74	27.43	18.21	41.51	13.82

its distribution region (Cornelissen et al., 2019; Daniel et al., 2020; Jin et al., 2022). In addition, the emergence period of adults of *M. saltuarius* is concentrated from May to August (Ochi, 1969; Jikumaru and Togashi, 1996; Han et al., 2007, 2009). This species is mainly active in the daytime, and its flight distance is generally not more than a few hundred meters (Ciesla, 2021); therefore, precipitation during this period affects the flight and dispersal of *M. saltuarius* (Gao et al., 2019; Zhao et al., 2021). Elevation was an important variable that significantly affected the potential distribution of *M. saltuarius*, possibly because of the close relationship between the host plant distribution and altitude, which also greatly affected the feeding and oviposition preferences of *M. saltuarius* (Zhao et al., 2021).

To predict the potential distribution areas of *M. saltuarius*, we previously obtained 175 distribution points of *M. saltuarius* from published references, authoritative databases, and official websites, and combined these data with field survey data. Each distribution point had accurate data sources. The prediction results of the MaxEnt model indicated that the potential distribution area of *M. saltuarius* under current climatic conditions included actual geographical distribution points, indicating that the optimized model was highly reliable and accurate (Lee et al., 2021; Gao et al., 2023).

Studies are urgently needed to accurately analyze and predict the natural distribution patterns and potential distribution areas of *M. saltuarius* in China. Under current climatic conditions, the predicted suitable habitats of *M. saltuarius* were mainly at latitudes north of 33°N in China, and the larger suitable areas were mainly distributed in Northeast China and North China. Moreover, in areas with large numbers of geographical distribution points of *M. saltuarius*, such as in Shanxi province, Heilongjiang province, Jilin province, Liaoning, and Inner Mongolia, the suitable areas for *M. saltuarius* will be further expanded under future climate conditions. Furthermore, the highly and moderately suitable areas of *M. saltuarius* have spread to the eastern Gansu province, northeastern Shaanxi province, northern Henan province, and southeastern Shandong province; currently, there is almost no geographical distribution of *M. saltuarius* in these areas. Therefore, local forestry departments should increase their monitoring efforts to prevent *M. saltuarius* from invading these areas. Our results also show that there are almost no suitable distribution areas for *M. saltuarius* in Southwest China and South China; however, *M. saltuarius* may occur in these areas in the future. Furthermore, the impacts of human activities and natural enemies on *M. saltuarius* should be considered when predicting potentially suitable distribution areas (Choi et al., 2017; Takahashi and Park, 2020; Gao et al., 2023).

As an insect vector of PWD in northern China, *M. saltuarius* can cause serious harm to the ecological environment and economic production in invaded areas (Yu and Wu, 2018; Li et al., 2020, Li M. et al., 2021). Previous studies showed that the effective control of *M. saltuarius* and other vector insects is among the most useful measures for preventing the occurrence of PWD (Linit et al., 1983; Kobayashi et al., 1984; Linit, 1988; Li et al., 2020, 2022; Li M. et al., 2021; Ye and Wu, 2022). Particularly, in areas where PWD is not currently occurring, *M. saltuarius* is a common insect, such

as Shanxi, Heilongjiang, Jilin, and Liaoning provinces, and PWD monitoring should be a focus when evaluating vector insects.

## Data availability statement

The original contributions presented in this study are included in the article/**Supplementary material**, further inquiries can be directed to the corresponding author.

## Author contributions

RG: conceptualization and writing-original draft preparation. LL, RL, SF, and JD: data curation. RG and LL: formal analysis. RG and LZ: writing-review and editing. All authors have read and agreed to the published version of the manuscript.

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## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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## Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/ffgc.2023.1243996/full#supplementary-material>

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