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Infection risk assessment of flower yellowing disease in *Zanthoxylum armatum* DC. under projected climate change in Southwest China

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Abstract Research on the infection risk of Flower yellowing disease (FYD) is crucial for promoting the sustainable cultivation of *Zanthoxylum armatum* DC. This study aimed to assess the potential distribution of FYD under current (1970–2000) and future (2041–2060 and 2061–2080) climate conditions across four Shared Socioeconomic Pathway scenarios (SSP126, SSP245, SSP370, and SSP585). A total of 80 occurrence records of FYD associated with *Z. armatum* were collected from Southwest China, together with 19 bioclimatic variables, one elevation variable, and eight edaphic variables. The MaxEnt model, optimized using the ENMeval package, was applied to predict the potential distribution of FYD. The results showed that all optimized models achieved a $\Delta AICc$ value of 0 and AUC values exceeding 0.90, indicating excellent predictive performance. Precipitation of the driest month (Bio_14), annual temperature range (Bio_7), precipitation seasonality (Bio_15), and elevation were identified as the dominant environmental factors influencing the potential distribution of FYD. Compared with the current period, future climate change is projected to markedly expand the area of high-suitability habitats for FYD, with major expansion concentrated in eastern Yunnan, southern Guizhou, and northern Sichuan. These findings suggest that enhanced field surveys, long-term monitoring, and targeted prevention strategies should be prioritized in projected expansion areas to reduce the potential risks of FYD to *Z. armatum* cultivation.

Keywords Flower yellowing disease; Potential distribution; Southwest of China; MaxEnt model; Climate change

Introduction

Zanthoxylum armatum DC. is an evergreen shrub or small tree belonging to the genus *Zanthoxylum* in the family Rutaceae. Its fruits are rich in bioactive compounds with notable pharmacological activities, including antioxidant, antitumor (Tian et al., 2017), antibacterial, and hypoglycemic effects (Alam et al., 2018), which confer high economic and medicinal value to this species. In 2019, a newly emerging disease, Flower yellowing disease (FYD), was first reported in *Z. armatum* plantations in Chongqing, China. Since then, FYD has caused

substantial yield losses, and with the continuous expansion and aging of plantations, the affected area has increased progressively (Cao et al., 2019), posing a serious threat to the sustainable development of the *Z. armatum* industry.

In recent years, FYD has become widespread in major *Z. armatum* cultivation regions of Southwest China, including Yunnan, Guizhou, and Sichuan provinces, as well as Chongqing municipality. Typical symptoms of FYD include the formation of abnormal male flowers, severe pistil abortion, leaf chlorosis, and a marked reduction in fruit yield (Cao et al., 2019; Yu et al., 2023). Field investigations conducted in Guanling County, Guizhou, have shown that infected plants may die within 1–2 years after symptom onset (Chen et al., 2024). Despite its destructive impact, the pathogenic mechanisms and transmission pathways of FYD remain poorly understood (Cao et al., 2019).

Previous studies suggest that FYD may be associated with phytoplasma infection (Qin, 2018) or caused by reverse-transcribing DNA and RNA viruses (Cao et al., 2019; Xu et al., 2021). Notably, Cao et al. (2019) identified a virus associated with FYD in *Z. armatum* from Chongqing, designated *Green Sichuan pepper nepovirus* (GSPNeV), a member of the genus *Nepovirus* in the family *Secoviridae*, providing the first evidence that FYD is induced by viral or subviral agents. Subsequent studies further detected additional viruses closely associated with FYD, including *Green Sichuan pepper idaeovirus* (genus *Idaeovirus*, family *Mayoviridae*) and *Grapevine vein-clearing virus* (genus *Badnavirus*, family *Caulimoviridae*) (Cao et al., 2019; Xu et al., 2019). Moreover, Yu et al. (2023) reported that viruses belonging to the genus *Carlavirus* may act as causal agents of FYD in *Z. armatum* populations in Yunnan.

Plant DNA and RNA viruses exhibit diverse transmission pathways (Ghoshal & Sanfaçon, 2015; Kumar et al., 2025), including dissemination by insect vectors, pollen, wind, rain, and agricultural practices (Whitfield et al., 2015; Bragard et al., 2013). For example, viruses in the genus *Nepovirus* can be transmitted through seeds and/or pollen (Ghoshal & Sanfaçon, 2015). In addition, Cao et al. (2019) demonstrated that GSPNeV could be transmitted via grafting by inoculating virus-free *Z. armatum* saplings with infected materials. The coexistence of multiple transmission routes substantially increases the complexity and potential risk of FYD spread.

Virus occurrence and spatial distribution are closely linked to environmental conditions. Species distribution models (SDMs) are widely applied to predict potential distribution areas by integrating occurrence records with environmental variables (Anderson, 2013; Guo et al., 2020). Among various SDMs, the maximum entropy (MaxEnt) model is particularly suitable for predicting the potential distribution of plant viruses due to its strong predictive performance and robustness when dealing with presence-only data and complex environmental

conditions. The MaxEnt model has been successfully applied to assess the potential distributions of *Tomato brown rugose fruit virus* (Zheng et al., 2025), *Tomato yellow leaf curl virus* (TYLCV) (Ramos et al., 2019), and *Watermelon mosaic virus* (de Brito Reis et al., 2025), providing valuable guidance for disease surveillance and management. However, studies on the potential distribution of FYD in China, especially under future climate change scenarios, remain scarce.

Climate is a fundamental driver shaping species distribution at regional and global scales (Do et al., 2025). Ongoing climate change can induce a range of physiological and ecological responses in organisms, directly influencing their survival, reproduction, and dispersal, and ultimately altering their distribution patterns (Willis & Bhagwat, 2009). Changes in key climatic variables, particularly temperature and precipitation, may modify the habitats of plant viruses, their hosts, and associated vectors (Jones, 2016), thereby affecting virus transmission dynamics. The BCC-CSM2-MR model developed under the sixth Coupled Model Intercomparison Project (CMIP6) represents a substantial improvement over CMIP5 models, incorporating more complex physical processes (Shi et al., 2020) and exhibiting strong performance in simulating future climate patterns in China (Wu et al., 2019). Consequently, it is well suited for predicting the potential occurrence and spread of FYD in *Z. armatum* under future climate scenarios in Southwest China.

Therefore, in this study, FYD occurrence records from major *Z. armatum* cultivation regions were compiled and integrated with CMIP6 bioclimatic data, as well as elevation and soil variables. An optimized MaxEnt model implemented with the ENMeval package was used to (i) predict the potential suitable distribution of FYD under different climate scenarios, (ii) identify key environmental factors influencing its spatial distribution, and (iii) provide a scientific basis for the monitoring, prevention, and management of FYD in *Z. armatum* plantations in Southwest China.

Materials and Methods

Acquisition of FYD distribution data and environmental variables

Based on pathogens associated with FYD in *Z. armatum* identified in our preliminary investigations and previous reports (Table 1), a total of 112 occurrence records were obtained through systematic field surveys and targeted data retrieval from the International Committee on Taxonomy of Viruses (ICTV; <https://ictv.global/report/genome>) and the China National Knowledge Infrastructure (CNKI; <https://www.cnki.net>). To reduce spatial sampling bias, a spatial filtering procedure was performed using

ArcGIS (version 10.8), whereby a buffer radius of 5 km was applied and only one occurrence point was retained within each 10 km×10 km grid cell (Shan et al., 2024). After filtering, a total of 80 valid distribution points were retained. These points were mainly concentrated in the four principal *Z. armatum* cultivation regions—Yunnan, Chongqing, Guizhou, and Sichuan—in Southwest China (Fig. 1).

A total of 28 environmental variables were initially considered, including eight soil variables, nineteen bioclimatic variables, and one elevation variable. The soil variables were obtained from the Harmonized World Soil Database (HWSD, version 1.2; FAO, 2012; <https://www.fao.org/soils-portal/en>) (Table 2). The bioclimatic and elevation variables were downloaded from the WorldClim database (<https://www.worldclim.org>). Soil data in HWSD.bil format were converted to Tagged Image File Format (TIFF) using ArcGIS software (version 10.8). To ensure consistency among datasets, all environmental layers were resampled to a spatial resolution of 2.5' × 2.5' using the “Resampling” tool in ArcGIS (version 10.8). Subsequently, the TIFF files were converted to American Standard Code for Information Interchange (ASCII, .asc) format using the “Raster to ASCII” tool for compatibility with the MaxEnt model.

Future climate projections were derived from the BCC-CSM2-MR model under the CMIP6. This model has been widely used in regional climate studies in China and exhibits high simulation reliability (Wu et al., 2019). Four Shared Socioeconomic Pathway (SSP) scenarios—SSP126, SSP245, SSP370, and SSP585—were selected to represent different greenhouse gas emission trajectories. Climate projections were analyzed for two future periods, 2041–2060 and 2061–2080. All future climate layers were standardized to a spatial resolution of 2.5'×2.5' and converted to .asc format for subsequent analyses.

Screening of environmental variables

Preliminary screening of environmental variables was conducted using MaxEnt software (version 3.4.4). Variables with zero contribution rates were first excluded. Environmental values corresponding to the retained distribution points were then extracted in ArcGIS and subjected to Pearson correlation analysis using SPSS software (version 19.0). For pairs of variables with a high correlation coefficient ($|R|>0.85$), the variable with the lower contribution rate was removed to reduce multicollinearity. Ultimately, six environmental variables were retained for model construction: annual temperature range (Bio_7), precipitation of the driest month (Bio_14), precipitation seasonality (coefficient of variation; Bio_15), precipitation of the warmest quarter (Bio_18), elevation (Elev), and cation exchange capacity of clay in the topsoil (T_CEC_CLAY).

Optimization and construction of MaxEnt model

To optimize model parameterization, reduce model complexity, and minimize overfitting, the ENMeval package (version 2.0.0) in R was used to optimize two key MaxEnt parameters: the regularization multiplier (RM) and feature combination (FC). The RM was tested over a range from 0.5 to 5.0 at increments of 0.5 (Muscarella et al., 2014). Six FC combinations—L, LQ, H, LQH, LQHP, and LQHPT (where L=linear, Q=quadratic, H=hinge, P=product, and T=threshold)—were evaluated (Muscarella et al., 2014; Yang et al., 2022a). The optimal RM and FC values were determined based on overall model performance.

Model performance was assessed using the corrected Akaike Information Criterion difference ($\Delta AICc$) and the 10% training omission rate (or.10p.avg). Lower values of both metrics indicate reduced overfitting and improved predictive accuracy, with a $\Delta AICc$ value of 0 representing the optimal model (Muscarella et al., 2014; Zhang et al., 2024). Seventy-five percent of the occurrence points were randomly selected as training data, while the remaining 25% were used for model testing. The jackknife resampling method was applied to evaluate the contribution and relative importance of each environmental variable, with the maximum number of iterations set to 5000 (Li et al., 2024). An environmental variable was considered to be within a suitable range when the predicted probability of presence for that single variable exceeded 0.5 (Tian et al., 2025).

The predictive performance of the optimized MaxEnt model was evaluated using the receiver operating characteristic (ROC) curve. The area under the ROC curve (AUC) was used as a quantitative indicator of model accuracy (Elith et al., 2006). An AUC value < 0.6 indicated poor predictive performance, whereas an AUC value between 0.9 and 1.0 indicated excellent model performance (Lai et al., 2025a).

Classification of suitable areas and centroid migration analysis

Based on the optimized MaxEnt model outputs, the potential distribution of FYD was classified into four suitability categories using the natural breaks (Jenks) method in ArcGIS according to the predicted probability of presence (P): unsuitable ($0 < P < 0.14$), low suitability ($0.14 \leq P < 0.39$), moderate suitability ($0.39 \leq P < 0.70$), and high suitability ($0.70 \leq P < 1.00$). The areas corresponding to each suitability class under different climate scenarios were calculated using the “Raster to Polygon” tool, and spatial distribution maps were generated accordingly.

Centroid migration of suitable habitats was analyzed using the “Spatial Statistics Tools” in ArcGIS to assess shifts in the geographic center of FYD distribution under future climate scenarios. In addition, the average

elevation of highly suitable areas was calculated using the “Zonal Statistics” tool to further characterize altitudinal distribution patterns.

Results

Model performance and accuracy evaluation

Based on the occurrence records and environmental variables, a total of 48 model parameter combinations with different FCs and RMs were evaluated using cross-validation. Under current climatic conditions, the model with FC=H and RM=0.5 achieved the optimal performance, yielding a $\Delta AICc$ value of 0, a training AUC of 0.991, and a test AUC of 0.982 (Fig. 2), indicating excellent predictive accuracy.

For future climate scenarios (SSP126, SSP245, SSP370, and SSP585) during both periods (2041–2060 and 2061–2080), all optimized models maintained $\Delta AICc$ values of 0, with training and test AUC values consistently exceeding 0.90 (Table 3). These results demonstrate the robustness and high reliability of the optimized MaxEnt model for predicting the potential suitable distribution of FYD under both current and future climate conditions.

Dominant environmental variables affecting FYD distribution

The relative importance of environmental variables was evaluated based on contribution rates and permutation importance. The results showed that Bio_14, Bio_7, Bio_15, and Elev were the dominant factors influencing the potential distribution of FYD. Together, these four variables accounted for 90.1% of the total contribution.

Response curve analysis indicated unimodal relationships between FYD suitability and Bio_14, Bio_7, and Bio_15, with optimal ranges of 8.95–23.16 mm, 23.65–27.69 °C, and 67.69–91.79, respectively. In contrast, Elev exhibited a bimodal response pattern, with two optimal ranges at 250–575 m and 1000–3125 m (Fig. 3; Table 4).

Potential distribution for FYD under current climate conditions

Under current climate conditions, the total area of potential suitable habitat for FYD in Yunnan, Chongqing, Guizhou, and Sichuan was estimated at 535,500 km². Among these, highly suitable habitats covered 159,800 km², accounting for 29.85% of the total suitable area. The areas of high-suitability habitat in Yunnan, Chongqing,

Guizhou, and Sichuan were 39,100 km², 4,600 km², 45,200 km², and 70,900 km², respectively. Spatially, high-suitability regions were mainly concentrated in northeastern and central Yunnan, western Chongqing, southwestern Guizhou, and eastern Sichuan (Fig. 4).

Potential distribution for FYD during 2041–2060

Under the SSP126, SSP245, SSP370, and SSP585 scenarios for the period 2041–2060, the total areas of potential suitable habitats for FYD were predicted to be 748,600 km², 482,500 km², 785,800 km², and 921,700 km² (Fig. 5), respectively. Although the area of high-suitability habitat decreased in Yunnan and Chongqing under the SSP245 scenario, the total extent of high-suitability habitat across the four regions increased under all other scenarios. Compared with the current period, the area of high-suitability habitat increased by 90.16% (SSP126), 11.11% (SSP245), 88.79% (SSP370), and 188.60% (SSP585), respectively (Table 5).

Spatially, under SSP126, high-suitability habitats expanded in eastern Yunnan, extended from southwestern to southern Guizhou, showed minor expansion in southwestern Chongqing, and exhibited a northward extension from eastern Sichuan (Fig. 6a). Under SSP245, high-suitability habitats decreased markedly in Yunnan and Chongqing, remaining only in northeastern Yunnan (15,700 km²) and western Chongqing (100 km²), while expansion occurred in southern Guizhou and northern Sichuan (Fig. 6b). Under SSP370, high-suitability habitats expanded across all four regions, including eastern Yunnan, western Chongqing, southern Guizhou, and northern Sichuan (Fig. 6c). Under SSP585, high-suitability habitats exhibited substantial expansion, particularly in Yunnan (increase rate of 490.30%), forming a relatively continuous distribution across central and northeastern areas, while notable increases were also observed in Chongqing, Guizhou, and Sichuan (Fig. 6d).

Potential distribution for FYD during 2061–2080

For the period 2061–2080, the predicted total areas of potential suitable habitats under SSP126, SSP245, SSP370, and SSP585 were 751,900 km², 790,100 km², 495,400 km², and 820,900 km², respectively (Fig. 7). Although reductions in high-suitability habitat were observed in Chongqing under SSP245 and SSP370, and in Yunnan under SSP370, the overall area of high-suitability habitat across the four regions increased under all other scenarios. Relative to the current period, the area of high-suitability habitat increased by 92.33% (SSP126), 66.00% (SSP245), 24.07% (SSP370), and 103.02% (SSP585), respectively (Table 5).

Under SSP126, high-suitability habitats persisted in northeastern Yunnan, declined in central areas, and expanded eastward; remained concentrated in western Chongqing with scattered southern patches; expanded

from southwestern to southern Guizhou; and extended northward in Sichuan (Fig. 8a). Under SSP245, high-suitability habitats shifted eastward in Yunnan, decreased substantially in western Chongqing, expanded in southern Guizhou, and continued to extend northward in Sichuan (Fig. 8b). Under SSP370, high-suitability habitats were sharply reduced in Yunnan and entirely absent in Chongqing, while expansion occurred in southern Guizhou and northern Sichuan (Fig. 8c). Under SSP585, high-suitability habitats were distributed mainly in eastern and northeastern Yunnan, western and southern Chongqing, southern Guizhou, and northern Sichuan (Fig. 8d).

Centroid migration and elevation characteristics of high-suitability habitats

The centroid of high-suitability habitats for FYD exhibited distinct migration trajectories under different climate scenarios. From the current period to 2041–2060 and 2061–2080, centroid shifts varied among scenarios: under SSP126, the centroid moved northeastward and subsequently northward; under SSP245, it migrated northeastward initially and then shifted southwestward; under SSP370, a northward shift was followed by eastward migration; and under SSP585, the centroid moved northward initially and then southward (Fig. 9).

The mean elevation of high-suitability habitats showed no substantial variation across most climate scenarios compared with the current period (elevation of 1301.74 m), except for a noticeable increase under the SSP585 scenario during 2041–2060 (Table 5).

Discussion

Accuracy and reliability of the MaxEnt model

The AUC value is widely used as a robust indicator for evaluating the predictive performance of MaxEnt models (Elith et al., 2006; Lai et al., 2025a), while the $\Delta AICc$ value serves as an effective metric for model selection and parameter optimization (Muscarella et al., 2014). In this study, the MaxEnt model optimized using the ENMeval package exhibited $\Delta AICc$ values of 0 and AUC values exceeding 0.9 under both current and future climate scenarios, indicating excellent predictive accuracy and minimal overfitting (Warren et al., 2014).

Under current climatic conditions, the simulated core distribution areas of FYD were mainly concentrated in northeastern and central Yunnan, western Chongqing, southwestern Guizhou, and eastern Sichuan, which closely matched the reported field distribution of the disease. This strong spatial consistency suggests that the optimized MaxEnt model effectively captures the ecological niche characteristics of FYD. Previous studies have

demonstrated that parameter tuning using ENMeval can significantly improve the reliability of species distribution predictions (Macdonald et al., 2025). Therefore, the optimized model employed here provides a robust and objective framework for assessing the potential distribution of FYD and its response to environmental drivers.

Effects of environmental factors on the potential distribution of FYD

Based on contribution rates and response curve analyses, Bio_14, Bio_7, Bio_15, and Elev were identified as the dominant environmental factors shaping the potential distribution of FYD under current climatic conditions. Regions characterized by Bio_14 values of 8.95–23.16 mm, Bio_7 values of 23.65–27.69 °C, Bio_15 values of 67.69–91.79, and Elev of 250–575 m and 1000–3125 m were found to be suitable for FYD occurrence (Table 4).

Among these variables, temperature- and precipitation-related factors jointly accounted for 81.4% of the total contribution, highlighting their dominant role in determining FYD distribution. Similar patterns have been reported for other plant viral diseases; for example, Wei et al. (2022) demonstrated that temperature and precipitation are key determinants of the potential distribution of *Maize chlorotic mottle virus*.

Temperature is a fundamental regulator of plant physiology and metabolism. In this study, Bio_7 was the only temperature-related variable retained after screening and contributed 22.6% to the model, indicating its importance in shaping FYD distribution. This finding may be attributed to the temperature sensitivity of *Z. armatum*, the primary host of FYD (Xu et al., 2019), which indirectly constrains disease occurrence. In addition, several viruses associated with FYD, including members of the genera *Idaeovirus* and *Nucleorhabdovirus*, are transmitted by aphids (Demler et al., 1996; Walker et al., 2018). Temperature strongly affects aphid survival, reproduction, and dispersal (Gao et al., 2012; Ma & Ma, 2012), thereby influencing viral transmission efficiency. This result is consistent with previous findings that Bio_7 is a primary climatic factor affecting the distribution of TYLCV (Ramos et al., 2019).

Precipitation-related variables (Bio_14 and Bio_15) collectively contributed 58.8% to the model, indicating that moisture availability and variability play a critical role in regulating FYD distribution (Table 4). Precipitation influences virus occurrence indirectly by affecting host plant growth and geographic distribution (Jones, 2016; Wu et al., 2024). Although *Z. armatum* exhibits a certain degree of drought tolerance, its shallow root system renders it susceptible to both drought stress under low precipitation and waterlogging stress under excessive rainfall (Zhou et al., 2021; Deng et al., 2025). Either stress condition can impair host vigor, thereby

influencing FYD persistence and spread. The concentration of *Z. armatum* plantations in regions of Southwest China with moderate precipitation further supports this relationship (Xu et al., 2019). Notably, the suitable Bio_15 range for FYD identified in this study (67.69–91.79) closely matches that reported for *Z. armatum* (43.9–92.2), suggesting a strong environmental coupling between the disease and its host. Similar precipitation-driven patterns have also been observed for TYLCV (Ramos et al., 2019).

Elevation integrates the effects of temperature and precipitation and thus indirectly influences the distribution of host plants and vector insects (Jones, 2016). The bimodal elevation suitability of FYD (250–575 m and 1000–3125 m) reflects the heterogeneous altitudinal distribution of *Z. armatum* across Southwest China. While *Z. armatum* is mainly distributed at 200–500 m in Sichuan and Chongqing, its cultivation elevation in northern Yunnan (e.g., Zhaotong) frequently exceeds 1000 m. Consequently, although the average elevation of highly suitable FYD habitats in Sichuan and Chongqing is relatively low (<800 m), the higher elevations of central and northern Yunnan and southwestern Guizhou (>1200 m) elevate the overall mean altitude of suitable areas (1212.32–1627.60 m).

Impact of future climate change on the potential distribution of FYD

Southwest China, encompassing the Sichuan Basin and the Yunnan–Guizhou Plateau, is characterized by complex topography and a climate jointly influenced by the Indian and East Asian monsoons, making it particularly sensitive to global climate change (Zhang & Wu, 2021). Recent projections indicate that China will experience rising temperatures and increased precipitation under future climate scenarios (Zhao et al., 2024), with Southwest China expected to undergo pronounced warming, higher total precipitation, and more frequent extreme precipitation events (Yang et al., 2022b; Yang et al., 2024; Lai et al., 2025b).

Our results indicate that under the BCC-CSM2-MR model, the area of high-suitability habitats for FYD during the periods 2041–2060 and 2061–2080 increases significantly across all SSP scenarios, with expansion rates ranging from 11.11% to 188.60% compared with the current period (Table 5). Several mechanisms may explain this trend. First, increased precipitation and extreme rainfall events may elevate flood risks and soil moisture, creating conditions conducive to viral survival and persistence (Jones, 2016). For example, Rua et al. (2014) reported a positive relationship between precipitation and the incidence of *Barley yellow dwarf virus* (BYDV) in tall fescue. Second, climate-driven increases in soil moisture can promote aphid population growth, thereby enhancing viral transmission (Simson et al., 2012). Third, rising temperatures may alter host plant susceptibility to viral infection (Chung et al., 2015). Finally, temperature increases can directly affect vector

dynamics, further facilitating viral spread, as demonstrated for BYDV (Rua et al., 2014). Similar climate-driven expansions have been projected for TYLCV in northern Europe (Ramos et al., 2019).

Consistent with broader ecological theory, climate change is expected to drive species distributions toward higher elevations (Sekercioglu et al., 2008; Li et al., 2022). Our results support this pattern for FYD. Compared with the current mean elevation of high-suitability habitats (1301.74 m), the projected mean elevation under the SSP585 scenario during 2041–2060 increases to 1627.60 m, representing an upward shift of 325.86 m. This elevation increase is particularly evident in central and northeastern Yunnan, southern Sichuan, and western Guizhou, indicating a climate-driven altitudinal migration of FYD. Similar elevation shifts have been reported for *Potato yellow vein virus* in the Andean region (Jones, 2014). In contrast, mean elevation changes under other SSP scenarios were relatively minor.

Overall, future climate change is expected to increase the outbreak risk of FYD in Southwest China. Consequently, enhanced disease surveillance, integrated pest management strategies, and cautious planning of *Z. armatum* plantation expansion are urgently needed. Notably, our results also indicate a contraction of high-suitability FYD habitats in central Yunnan under SSP126, SSP245, and SSP370 during 2041–2060, and under all scenarios during 2061–2080, suggesting that *Z. armatum* cultivation could be moderately expanded in these regions. In contrast, eastern Yunnan, southern Guizhou, and northern Sichuan are projected to become potential FYD expansion zones, while northeastern Yunnan, southwestern Guizhou, and eastern Sichuan are expected to remain persistently highly suitable for FYD (Figs. 4, 6, and 8). These regions should therefore be prioritized for long-term monitoring and targeted disease control.

Despite its strengths, this study has several limitations. First, the relatively small number of occurrence records (80 points) may not fully capture the complete geographic range of FYD, potentially introducing uncertainty into model predictions. Second, uncertainties associated with land-use change and the complex spatiotemporal dynamics of vector populations were not explicitly incorporated. Finally, occurrence data were limited to *Z. armatum*, although related viruses have been reported to infect multiple additional host species (e.g., *Betapartitivirus* infecting at least seven plant species; Lesker et al., 2013), which may lead to underestimation of FYD's potential distribution. Future studies should therefore integrate expanded field surveys, multi-host sampling, and vector data to further refine predictive models and improve climate-driven risk assessments.

CRedit authorship contribution statement Hongxia Liu: data curation, formal analysis, investigation, methodology, writing-original draft, writing-review and editing. Xue Song: data curation, formal analysis, investigation, methodology, writing-original draft. Jingwen Xu: data curation, investigation, writing-original draft. Chaobin Zhou: Conceptualization, formal analysis, investigation, methodology, writing-original draft, writing-review and editing, supervision. Weihong Sun: data curation, investigation, writing-original draft, writing-review and editing.

Conflict of interest The authors declare that there are no conflicts of interest.

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Data availability Data will be made available on request.

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Table 1 Pathogens associated with Yellow flowering disease in Southwest China

Family	Genus	Species (Virus name)	Data sources
<i>Secoviridae</i>	<i>Nepovirus</i>	<i>Nepovirus sichuanense</i> (Green Sichuan pepper nepovirus)	Cao et al., 2019
<i>Mayoviridae</i>	<i>Idaeovirus</i>	<i>Green Sichuanpepper idaeovirus</i>	Cao et al., 2019
<i>Solemoviridae</i>	<i>Enamovirus</i>	<i>Green Sichuan pepper enamovirus</i>	Cao et al., 2019
<i>Bromoviridae</i>	<i>Ilarvirus</i>	<i>Green Sichuan pepper ilarvirus</i>	Unpublished data ^a
<i>Rhabdoviridae</i>	<i>Nucleorhabdovirus</i>	<i>Green Sichuan pepper nucleorhabdovirus</i>	Cao et al., 2019
<i>Caulimoviridae</i>	<i>Badnavirus</i>	<i>Badnavirus venazanthoxyli</i> (Green Sichuan pepper vein clearing-associated virus)	Cao et al., 2019 Xu et al., 2019
<i>Caulimoviridae</i>	<i>Badnavirus</i>	<i>Badnavirus venavitis</i> (Grapevine vein-clearing virus)	Xu et al., 2019
<i>Mitoviridae</i>	<i>Duamitovirus</i>	<i>Duamitovirus_dapi1</i>	Unpublished data ^a
<i>Tombusviridae</i>	<i>Umbravirus</i>	<i>Yongqing green pepper-associated umbravirus</i>	Yu et al., 2023
<i>Betaflexiviridae</i>	<i>Carlavirus</i>	<i>Potato virus M, Potato virus H, Potato virus S</i>	Yu et al., 2023
<i>Partitiviridae</i>	<i>Betapartitivirus</i>	<i>Erysiphe necator associated betapartitivirus 1</i>	Unpublished data ^a

^aNote: Viral samples were collected from leaves of *Zanthoxylum armatum* DC. in Guanling County, Guizhou Province, China, and identification was conducted using a metaviromic methodology, with detailed results to be published separately.

Table 2 Eight selected edaphic variables from World Soil Database

Abbreviation	Variables (Units)	Abbreviation	Variables (Units)
T_GRAVEL	Topsoil gravel content (%vol.)	T_PH_H2O	Topsoil pH (H ₂ O) (-log[H ⁺])
T_REF_BULK_DEN	Topsoil reference bulk Density (kg·dm ⁻³)	T_CEC_CLAY	Topsoil CEC (clay) (cmol/kg)
T_REF_DEPTH	Reference soil depth (cm)	T_CEC_SOIL	Topsoil CEC (soil) (cmol/kg)
T_OC	Topsoil organic carbon (% weight)	T_CACO ₃	Topsoil calcium carbonate (% weight)

493 Table 3 FC, RM, AUC, $\Delta AICc$ and omission rate of potential distribution of Flower yellowing disease under
 494 different climate scenarios
 495

Table 3 FC, RM, AUC, $\Delta AICc$ and omission rate of potential distribution of Flower yellowing disease under different climate scenarios

Climate scenarios	FC	RM	Training data AUC	Test data AUC	$\Delta AICc$	Or.10p.avg
Current	H	0.5	0.991	0.982	0	0.193
SSP126(2041–2060)	LQH	0.5	0.992	0.988	0	0.125
SSP245(2041–2060)	LQH	0.5	0.995	0.990	0	0.313
SSP370(2041–2060)	LQHP	0.5	0.993	0.989	0	0.225
SSP585(2041–2060)	LQH	0.5	0.987	0.983	0	0.175
SSP126(2061–2080)	LQH	0.5	0.993	0.988	0	0.200
SSP245(2061–2080)	H	0.5	0.993	0.987	0	0.175
SSP370(2061–2080)	LQH	0.5	0.994	0.989	0	0.237
SSP585(2061–2080)	LQH	0.5	0.992	0.986	0	0.150

496

497 Table 4 Environmental variables affecting the suitable distribution of Flower yellowing disease and their
 498 contribution rates under current climatic conditions in Southwest China

Table 4 Environmental variables affecting the suitable distribution of Flower yellowing disease and their contribution rates under current climatic conditions

Environmental variables	Percentage	Permutation	Range
	Contribution	Importance	
	(%)	(%)	
Precipitation of the driest month (Bio_14)	42.4	51.1	8.95–23.16 mm
Temperature annual range (Bio_7)	22.6	21.9	23.65–27.69 °C
Precipitation seasonality(Bio_15)	16.4	21.0	67.69–91.79
Elevation(elev)	8.7	3.2	250–575 m, 1000–3125 m
Precipitation of the warmest quarter(Bio_18)	5.9	2.7	
Topsoil CEC (clay) (T_CEC_CLAY)	4.0	0.0	

Table 5 Altitudinal characteristics and area changes of potential high-suitability habitats for Flower yellowing disease

Table 5 Altitudinal characteristics and area changes of potential high-suitability habitats for Flower yellowing disease under different climate scenarios

Climate scenarios	Regions	Changes of high-suitability regions	Mean elevation (m)	Climate scenarios	Regions	Changes of high-suitability regions	Mean elevation (m)
SSP126 (2041–2060)	Yunnan	72.79%	1217.79	SSP126 (2061–2080)	Yunnan	80.78%	1238.05
	Chongqing	53.14%			Chongqing	55.68%	
	Guizhou	104.91%			Guizhou	115.73%	
	Sichuan	92.74%			Sichuan	86.16%	
	Total	90.16%			Total	92.33%	
SSP245 (2041–2060)	Yunnan	-59.83%	1212.32	SSP245 (2061–2080)	Yunnan	46.60%	1294.82
	Chongqing	-97.16%			Chongqing	-47.94%	
	Guizhou	45.58%			Guizhou	68.71%	
	Sichuan	35.35%			Sichuan	82.42%	
	Total	11.11%			Total	66.00%	
SSP370 (2041–2060)	Yunnan	92.12%	1213.83	SSP370 (2061–2080)	Yunnan	-42.23%	1245.49
	Chongqing	52.90%			Chongqing	-100.00%	
	Guizhou	78.38%			Guizhou	74.83%	
	Sichuan	95.94%			Sichuan	36.35%	
	Total	88.79%			Total	24.07%	
SSP585 (2041–2060)	Yunnan	490.30%	1627.60	SSP585 (2061–2080)	Yunnan	98.78%	1263.01
	Chongqing	51.15%			Chongqing	100.19%	
	Guizhou	26.32%			Guizhou	115.63%	
	Sichuan	134.79%			Sichuan	97.49%	
	Total	188.60%			Total	103.02%	

Fig. 1 Distribution points information of Flower yellowing disease of *Zanthoxylum armatum* DC. in Southwest China

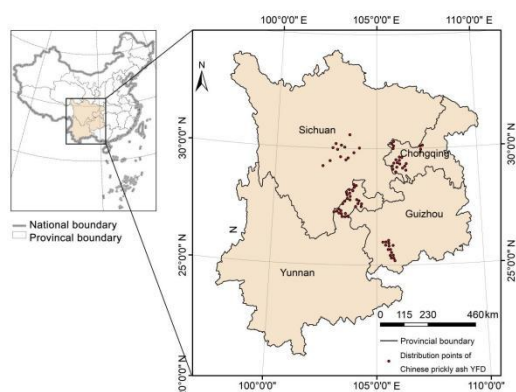


Fig. 1 Distribution data in Flower yellowing disease of *Zanthoxylum armatum* DC. in Southwest China

Note: The map was based on the Chinese standard map with the map content approval No. GS(2020)4619, and the base map was not modified. The same as below.

Fig. 2 ROC curve of the MaxEnt model for predicting distribution of Flower yellowing disease under current climatic conditions



Fig. 2 ROC curve of the MaxEnt model for predicting distribution of Flower yellowing disease under current climatic conditions

Fig. 3 Relationship between the potential distribution of Flower yellowing disease and dominant environmental variables

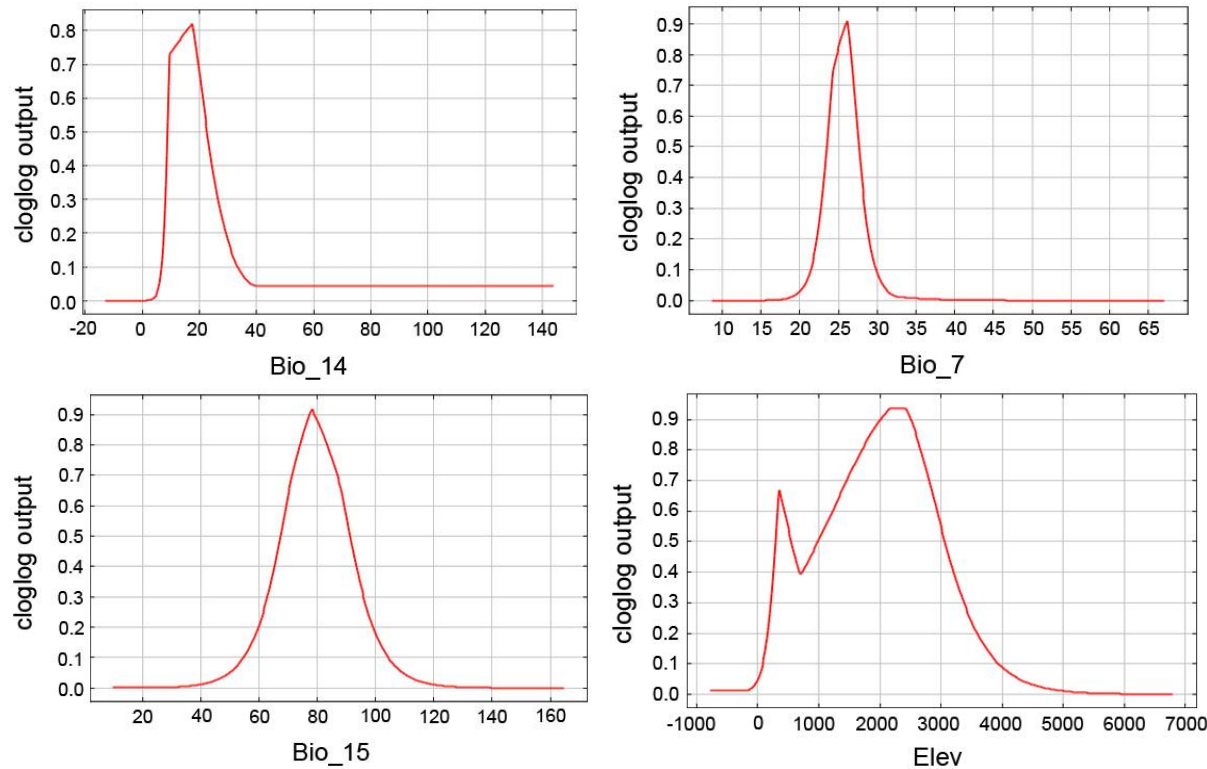


Fig. 3 Relationship between the potential distribution of Flower yellowing disease and dominant environmental variables

Fig. 4 Potential distribution of Flower yellowing disease under current climatic conditions in Southwest China

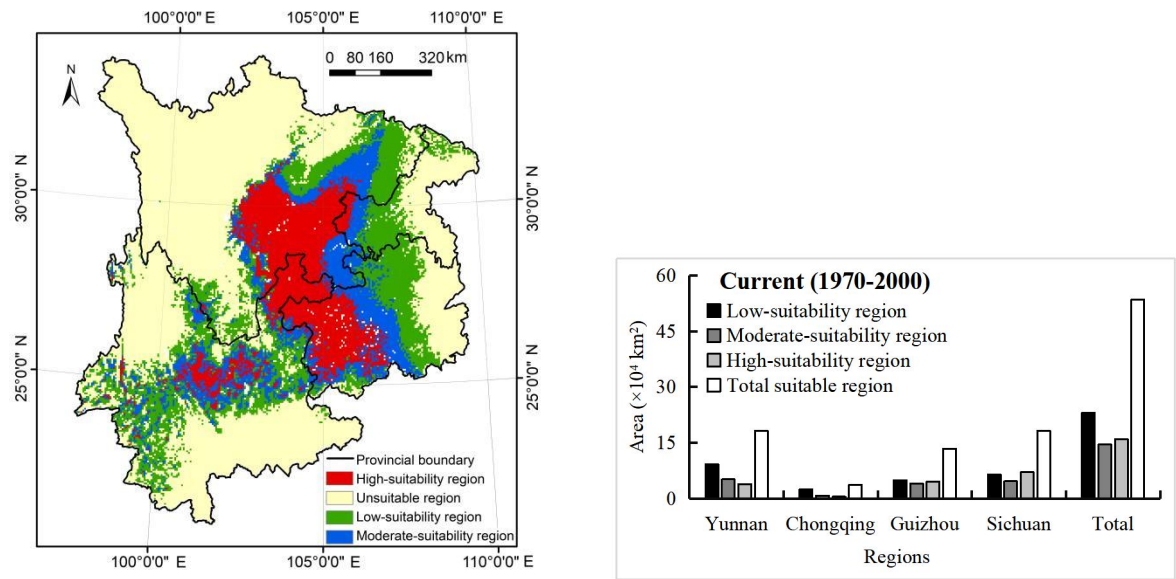


Fig. 4 Potential distribution and area of Flower yellowing disease under current climatic conditions in Southwest China

522 Fig. 5 Area of potential suitable habitats for Flower yellowing disease under different
523 Shared Socioeconomic Pathway scenarios during 2041–2060
524

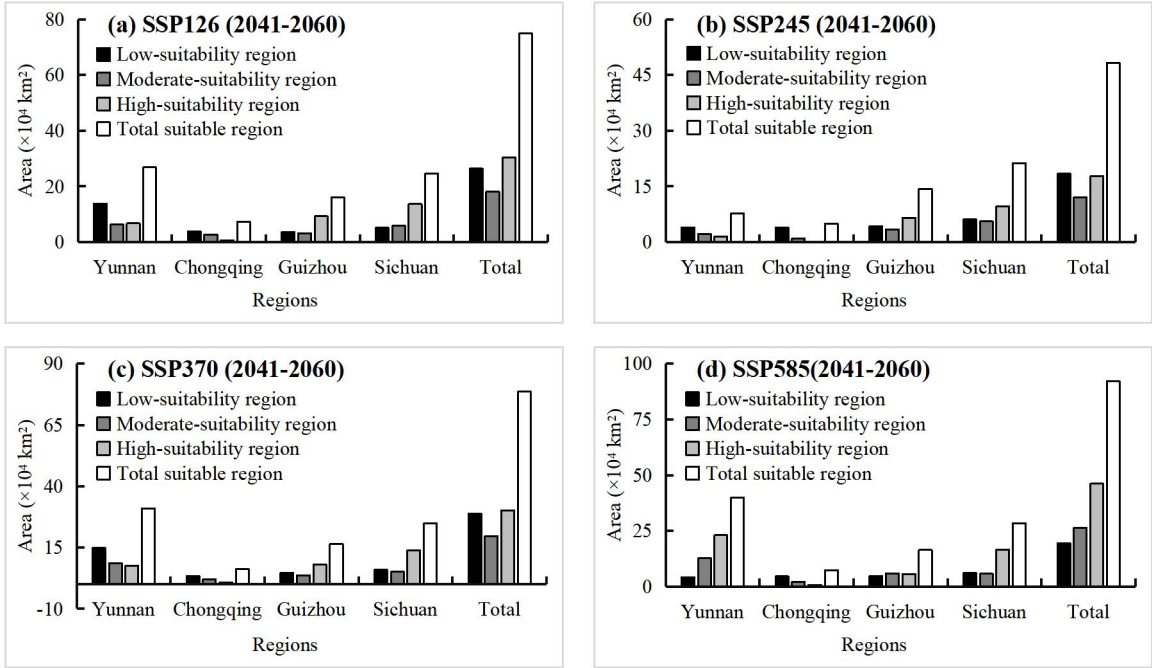


Fig. 5 Area of potential suitable habitats for Flower yellowing disease under different Shared Socioeconomic Pathway scenarios during 2041–2060

526 Fig. 6 Potential distribution characteristics of Flower yellowing disease during 2041–2060
527 in Southwest China
528

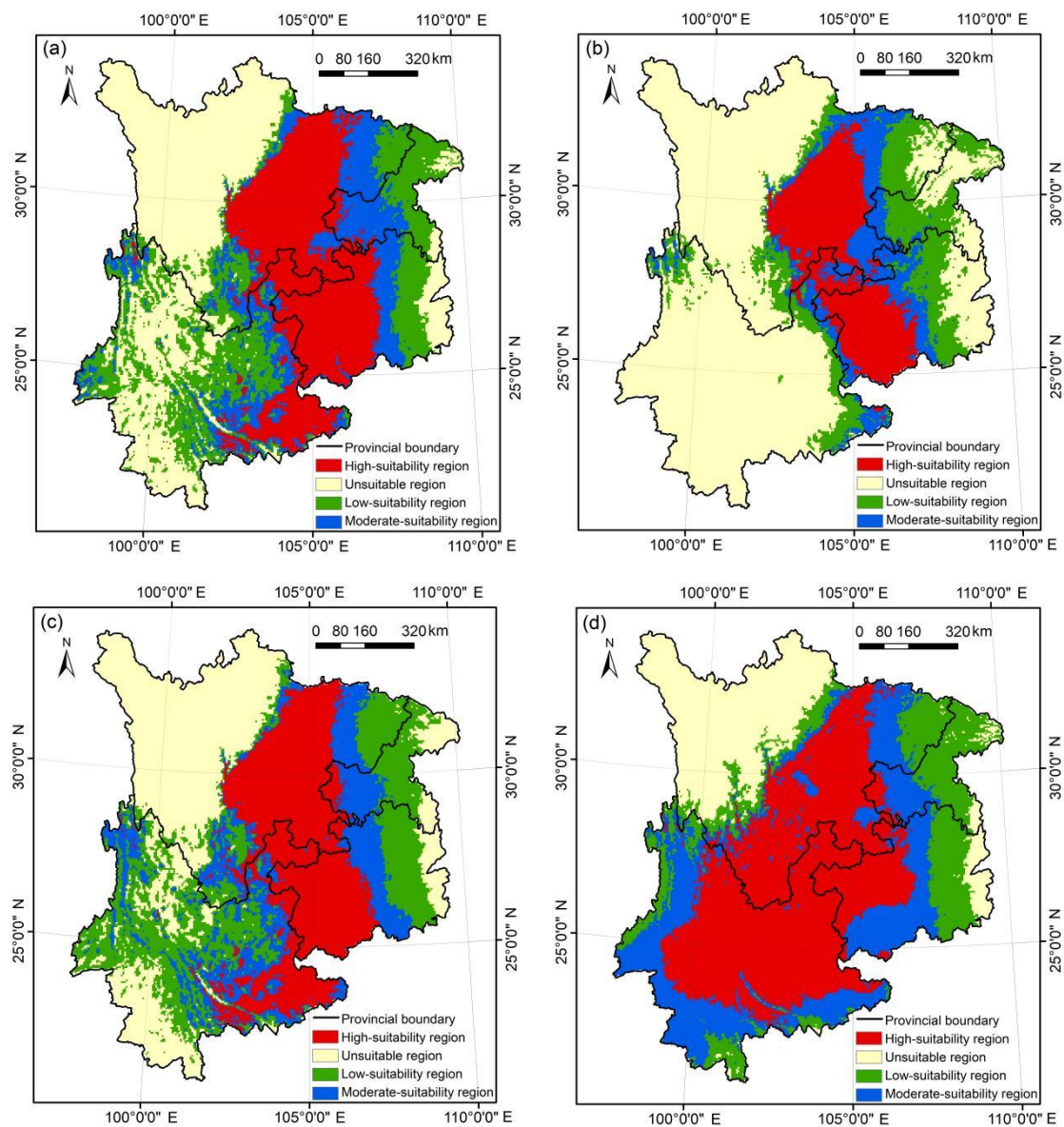


Fig. 6 Potential distribution characteristics of Flower yellowing disease during 2041–2060. (a) SSP126; (b) SSP245; (c) SSP370; (d) SSP585

530 Fig. 7 Area of potential suitable habitats for FYD under four Shared Socioeconomic
 531 Pathway scenarios during 2061–2080
 532

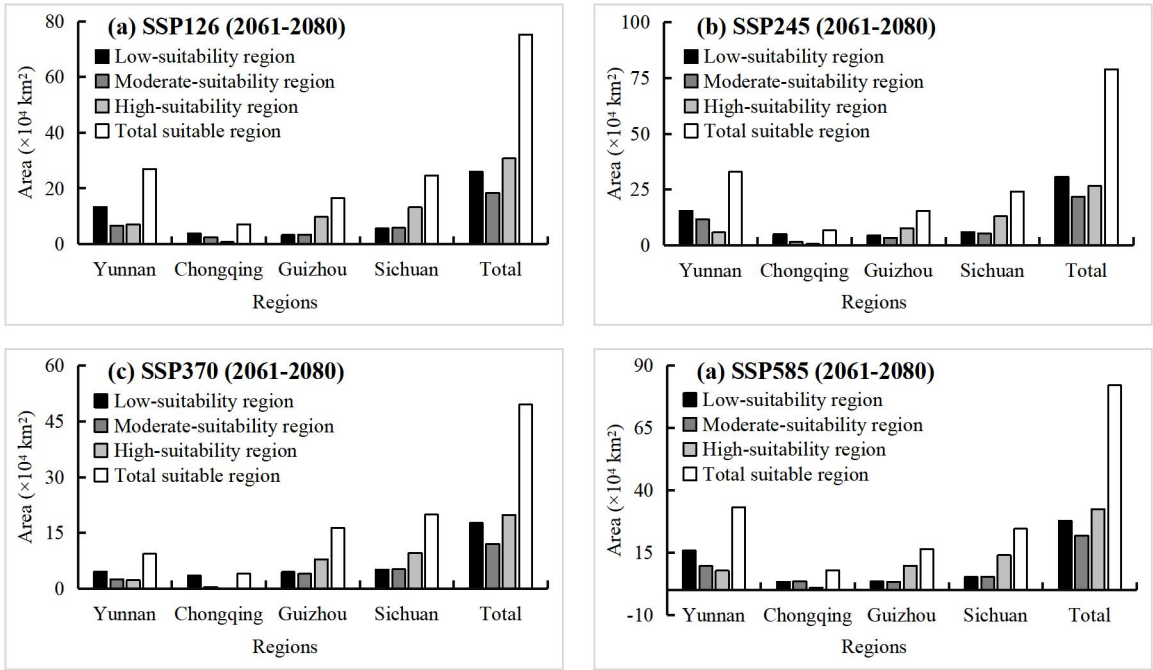


Fig. 7 Area of potential suitable habitats for FYD under four Shared Socioeconomic
 Pathway scenarios during 2061–2080

Fig. 8 Potential distribution characteristics of Flower yellowing disease during 2061–2080 in Southwest China

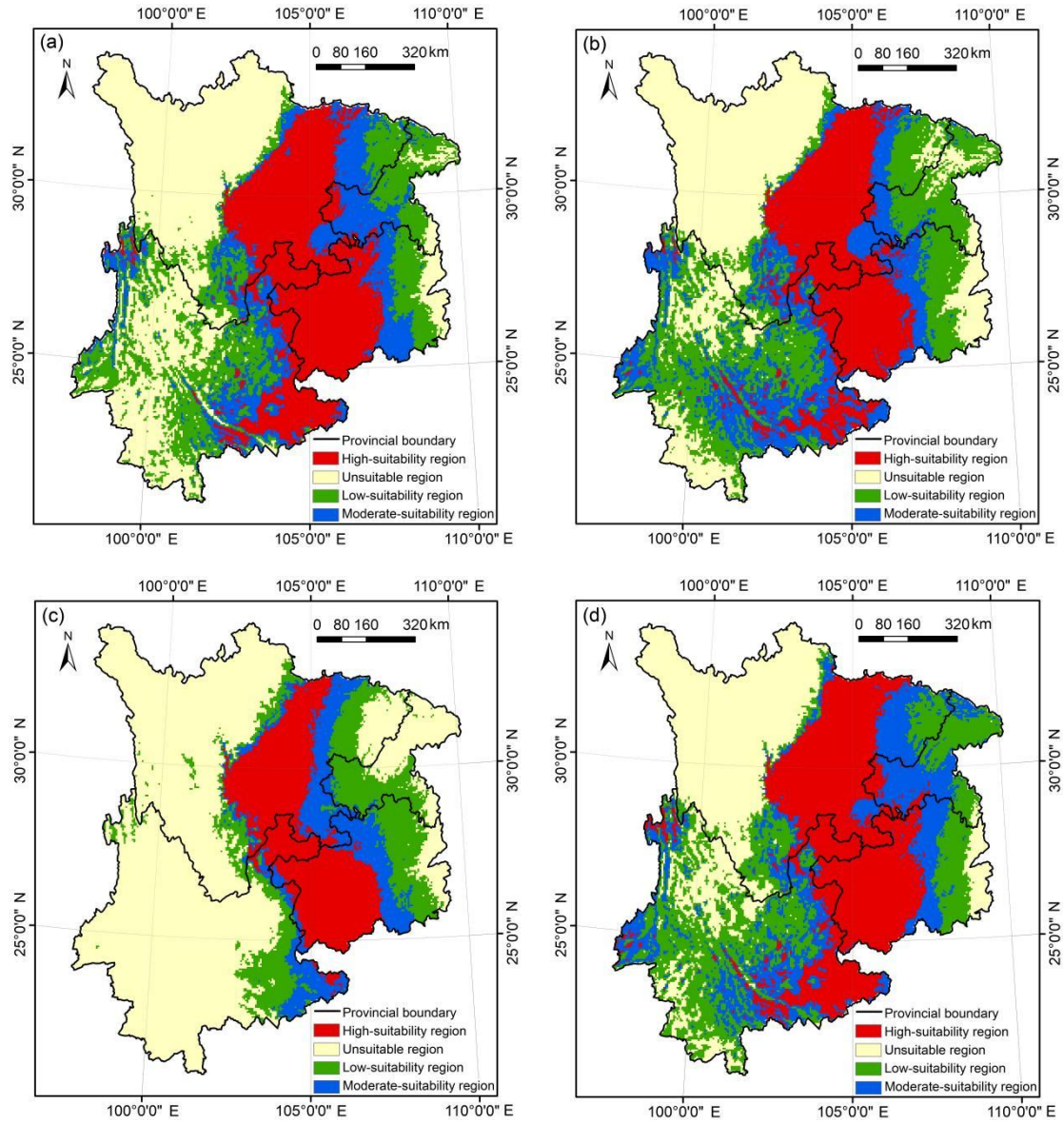


Fig. 8 Potential distribution characteristics of Flower yellowing disease during 2061–2080. (a) SSP126; (b) SSP245; (c) SSP370; (d) SSP585

538 Fig. 9 Centroid migrations of high-suitability habitats for FYD under future climate
539 scenarios
540

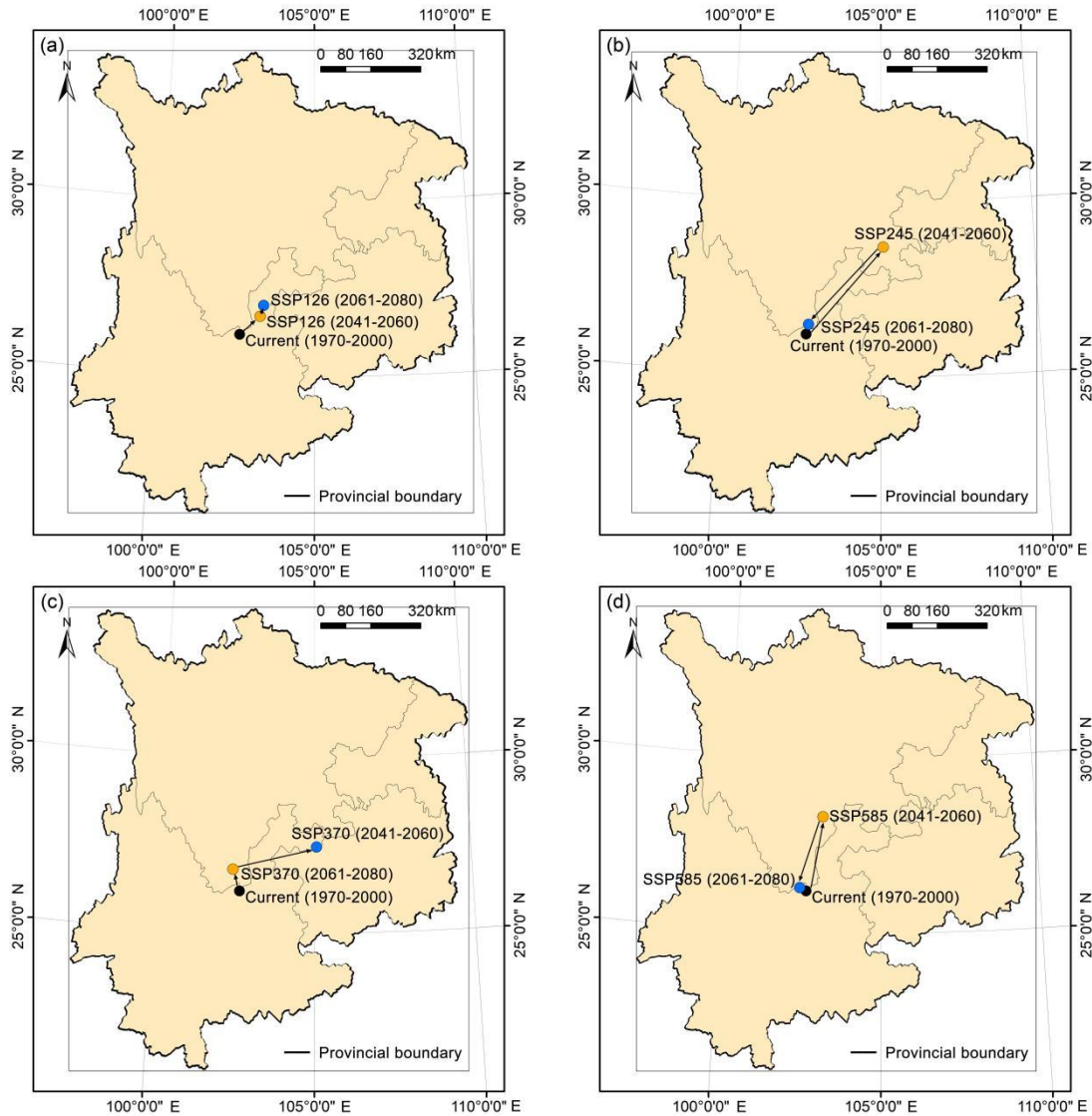


Fig. 9 Centroid migrations of high-suitability habitats for FYD under future climate scenarios