



# Climate warming will affect the range dynamics of East Asian *Meehania* species: a maximum entropy approach

Bashir B. Tihamiyu<sup>1,2,3,6</sup>  · Boniface K. Ngarega<sup>4,5</sup> · Xu Zhang<sup>2,3</sup> · Huajie Zhang<sup>2,3</sup> · Lijuan Li<sup>2,3</sup> · Jiao Sun<sup>2,3</sup> · Tao Deng<sup>1</sup> · Hengchang Wang<sup>2,3</sup>

Received: 7 February 2023 / Revised: 11 January 2024 / Accepted: 20 April 2024  
© International Society for Tropical Ecology 2024

## Abstract

Global climate change is among the major anthropogenic factors impacting species distribution, with significant conservation implications. Yet, little is known about the effects of climate warming on the distributional shifts of East Asian species. In the current study, we used the maximum entropy model (MaxEnt) to determine present and possible future habitats for five *Meehania* species occurring in the East Asian region. Our objectives were to assess how climate change would influence the species' habitat under current and future climate scenarios (Representative Concentration Pathways 4.5 and 8.5). The mean area under the curve ranged between 0.896 and 0.973, while the TSS values for all species varied between 0.811 and 0.891. The modelled current habitat of the species corresponded with the recorded distribution localities, confirming the model's robustness. Analysis of variable contribution demonstrated that the distribution of the species had differential environmental requirements; however, isothermality, precipitation of driest month, and elevation variables were among the main influential variables. Based on present climatic conditions, the projected habitat suitability maps showed a total of 662,846.0 to 2,039,180.1 km<sup>2</sup> as suitable regions for the distribution of *Meehania* species. In addition, there was a substantial loss in habitat range under future climatic scenarios for all the species. While the East Asian region is rich in biodiversity, more attention should be given to its management conservation. The current findings provide a scientific foundation for the conservation of *Meehania* and other species' habitats in the region.

**Keywords** Climate change · East Asian biodiversity hotspot · Habitat suitability · *Meehania* · Spatial-temporal distribution, Species distribution modelling

## Introduction

Climate change has emerged as an apparent and developing global phenomenon in recent years, and severe effects on biotic components have been observed worldwide

(Bellard et al. 2012; Nzei et al. 2021). Both human populations and biodiversity have been affected by climate change (Shivanna 2022; Mkala et al. 2022); examples of the latter include changes in species distribution (Tihamiyu et al.

✉ Tao Deng  
dengtao@mail.kib.ac.cn

✉ Hengchang Wang  
hcwang@wbgcas.cn

<sup>1</sup> CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Yunnan International Joint Laboratory for Bioaffiliationersity of Central Asia, Chinese Academy of Sciences, Kunming 650201, Yunnan, China

<sup>2</sup> CAS Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, Hubei, China

<sup>3</sup> Center of Conservation Biology, Core Botanical Gardens, Chinese Academy of Sciences, Wuhan 430074, Hubei, China

<sup>4</sup> Centre for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun 666303, China

<sup>5</sup> Sino-African Joint Research Center, Chinese Academy of Sciences, Wuhan 430074, China

<sup>6</sup> Department of Plant Biology, University of Ilorin, 1515, P.M.B., Ilorin, Nigeria

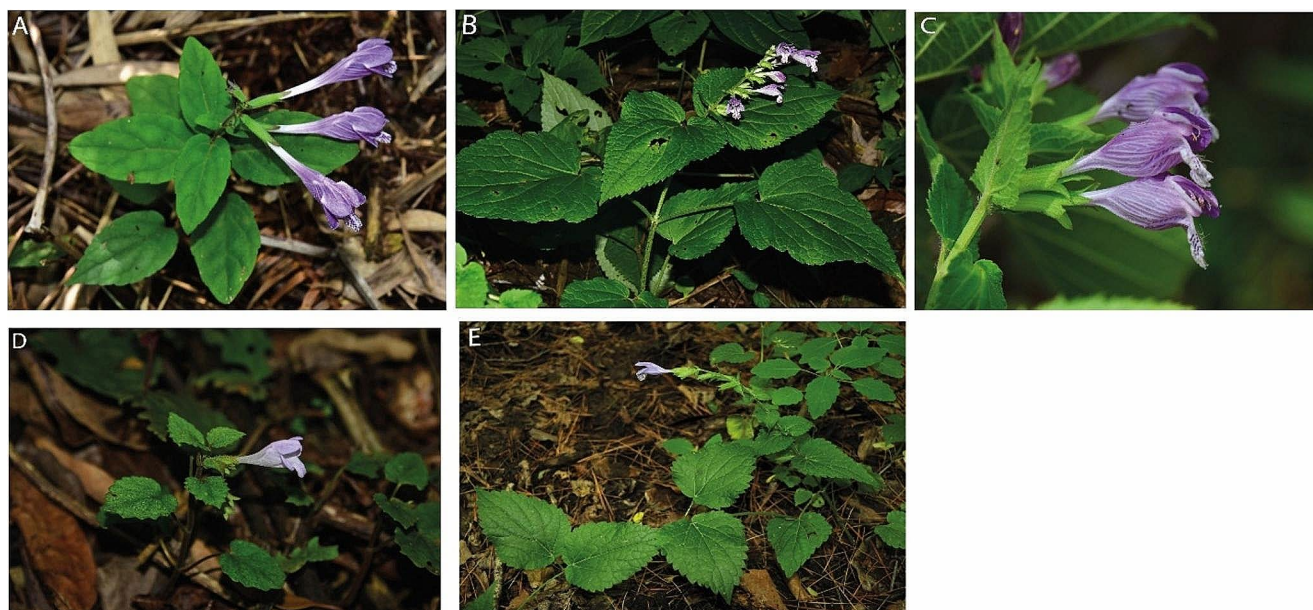
2021; Ngarega et al. 2022) and pest and disease outbreaks (Simons et al. 2019).

According to the Intergovernmental Panel on Climate Change (IPCC), global climate change is likely to persist, affecting the geographic range of numerous plant taxa (Sheldon 2019; Zellweger et al. 2020). Climate warming, for example, affects *Quercus petraea*, having a wide geographic distribution in various ways. This species has been observed to have a superior growing performance in the northern sections compared to the southern parts, as reported by Sáenz-Romero et al. (2017). Climate change may also decrease and reorganize the distributions of animal and plant species that contribute to natural community assembly and their functions and benefits (Tallis et al. 2008; Ali et al. 2021). Climate change effects on biodiversity may be assessed by linking precipitation and temperature trends with species distributional shifts (Weiskopf et al. 2020). In addition, predictions concerning the influence of climate change on species distribution could be used to address potential risks which might affect the distribution and abundance of these species (Fadrique et al. 2018). As a result, acquiring high-grade distribution data is critical for establishing measures and enforcing practical preventive actions. However, the lack of bio-geographical information typically slowdown conservation plans (Pearson et al. 2007; Wan et al. 2021), such as those of some species in the East Asian region, which remain largely unexplored.

*Meehania* Britton. is a small genus of herbaceous, evergreen plants in the Lamiaceae family with approximately seven species and five subspecies (Fig. 1, Li and Hedge

1994; Deng et al. 2015). The species are either annuals or perennials, displaying a characteristic pattern of the Arcto-Tertiary floristic disjunction with an altitudinal range of 300–3,500 m (Xiang et al. 2000; Takano et al. 2020). Members of this genus are endemic to the East Asiatic region, except for the *Meehania cordata* found in North America. It contains about 7 species (5 species in China) and 5 subspecies, mainly distributed in temperate to subtropical Asia and North America (Deng et al. 2015). Due to the narrow distribution of most of the members of this genus, some are considered endangered (*M. montis-koyae* Ohwi and *M. pinfaensis*), highly threatened species (*M. cordata* in the United States), and others have yet to be evaluated by the IUCN. *Meehania* species are typically found in highly humid, shady, mossy areas, valleys, forested hillsides, stream sides in mixed or pine forests, in mixed, coniferous forests, montane forests, and nonforested vegetation (e.g., steppe, grasslands) (Flora of China 2009; Deng et al. 2015; Takano et al. 2020). For instance, the population of *M. montis-koyae* is often threatened as a result of human activities such as illegal digging for commercial purposes and construction along rivers, which together may result in habitat disturbance and fragmentation, contributing to population declines in the species (Takano et al. 2020).

In China, some species (e.g., *M. henryi* and *M. urticifolia*) are used for culinary and as sources of traditional medicine for snake bites (Tanaka and Nakao 1976; Kunkel 1984). A recent biogeographic investigation of the genus *Meehania* showed that the genus is monophyletic and belonged to the tribe Menteeae (Deng et al. 2015). The solitary North



**Fig. 1** The morphological features of five *Meehania* species (A–E). (A) *Meehania faberi*, (B) *M. fargesii*, (C) *M. henryi*, (D) *M. montis-koyae*, (E) *M. urticifolia* (POWO 2022). The photographs (A, B, D)

were provided by Zhang C.; (C) by Zhu R. and (E) from <https://powo.science.kew.org/taxon/urn:lsid:ipni.org:names:21010-1/images>

American species, *M. cordata*, is sister to a clade that includes the rest of the Asian species. Besides, the Bayesian relaxed clock methods performed on the nuclear DNA sequence data indicated that divergence between the Asian clade and *M. cordata* occurred around 9.81 million years ago. Up to date, no study on the potential distribution using environmental variables of *Meehanian* species in East Asia has been carried out. Considering the narrow distribution of *Meehanian* species, habitat sensitivity and their vulnerability to climate change make them a good choice for this study. Therefore, investigating the relationships between *Meehanian* and environmental variables and related factors affecting their distribution is important and would benefit land-use managers and planners for conservation efforts.

Environmental considerations are important in determining plant species distribution (Ngarega et al. 2021; Nzei et al. 2021). Ecological Niche Models (ENMs) of a species incorporate environmental covariates with occurrence data and display them on distribution maps that illustrate the species' potential range (Phillips et al. 2006; Elith et al. 2011). In addition, the models also indicate potential habitat suitability under future climate scenarios, indicating where a particular species has expanded or lost its potential ranges (Wan et al. 2021). As a result, ENMs are critical for understanding the many environmental conditions that influence niche localisation for different plant species (Buonincontri et al. 2023; Salako et al. 2021). ENMs can assess the relationship between species occurrence records and native habitat parameters (Cerrejón et al. 2022). Among the most popular species distribution models is the MaxEnt modelling technique. The maximum entropy (MaxEnt) is preferred for presence-only models and has been successfully used to forecast the distribution of many species (Elith et al. 2011; Nzei et al. 2021; Chukwuma et al. 2023).

According to previous studies, MaxEnt has been shown to perform better than other algorithms and regression models for predicting species distribution (Elith et al. 2011; Kaky et al. 2020; Ahmadi et al. 2023), and could account for the multifaceted interactions between geographical features (Phillips et al. 2006). It can predict the distribution of suitable habitats for range-restricted or endemic species with a distinct natural history spanning various habitats (i.e., terrestrial, or aquatic, e.g., Ancillotto et al. 2019; Tiamiyu et al. 2021; Ngarega et al. 2022). MaxEnt also has the ability to avoid commission and omission errors when projecting species distribution (Townsend et al. 2007). It has been used for species with small geographic distributions (Radomski et al. 2022). Much prior research has employed it for modelling the distributional range of genera and species such as *Ottelia* (Ngarega et al. 2022), water lilies (Nzei et al. 2021), and baobab (Wan et al. 2021).

Using the MaxEnt model and the Coupled Model Inter-comparison Project Phase 5 (CMIP5) data, we aimed to forecast the potential geographical distribution of five *Meehanian* species in East Asia. Specifically, the objectives of this study were to (i) predict the current and future habitat suitability distributions of *Meehanian* species in relation to environmental variables and future climate change scenarios (Representative Concentration Pathways {RCP}); RCP 4.5 and RCP8.5 respectively, for the year 2050) and (ii) determine the most important environmental variables controlling the distribution of the species in the region.

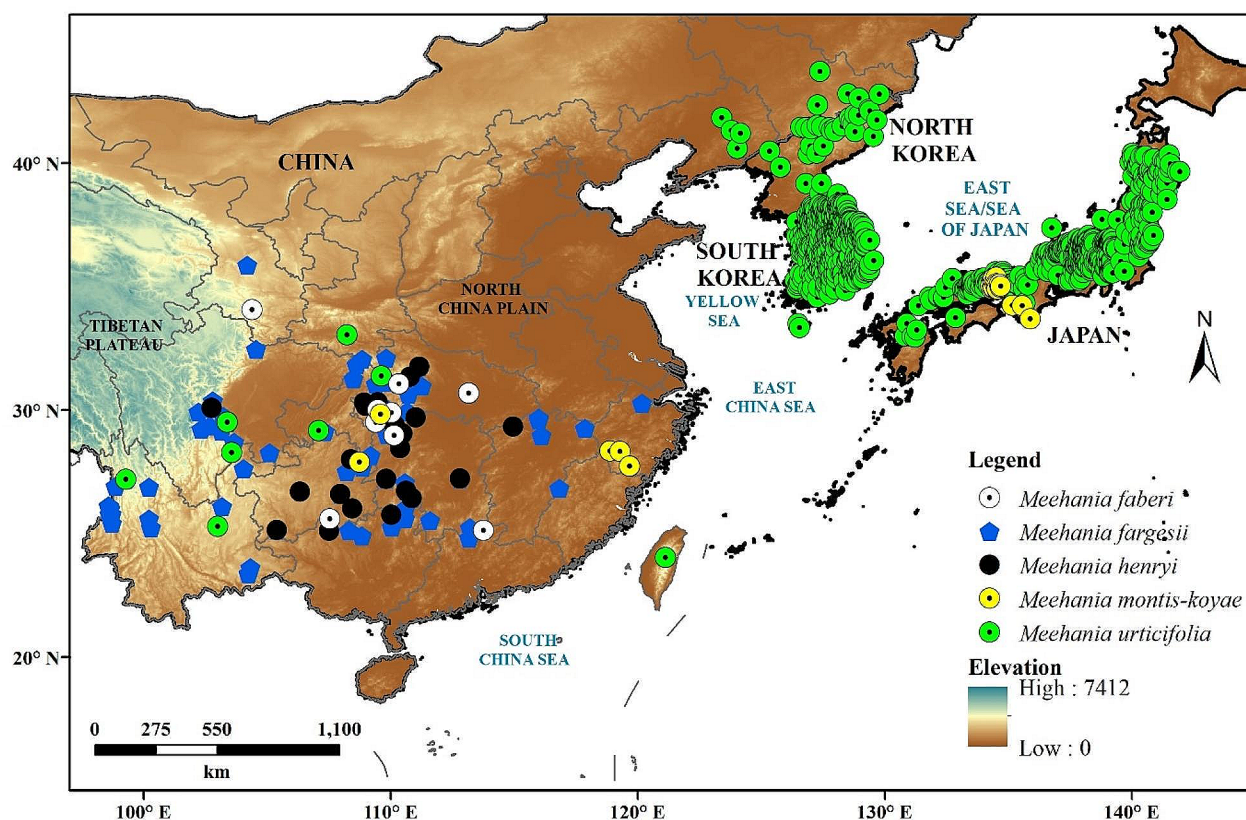
## Materials and methods

### Occurrence distribution data

The study area included China, Japan, Korea, and South Korea, with a total surface area of approximately 7,092,321 km<sup>2</sup>. It encompassed the East Asian geographical ranges of the five *Meehanian* species (Li and Hedge 2000) that we evaluated for our study, but not the entire range. The occurrence localities data for *Meehanian* were obtained from online sources, including the Global Biodiversity Information Facility (GBIF, <http://www.gbif.org/>; accessed on 10 January 2022), the Chinese Virtual Herbarium (CVH, <http://www.cvh.org.cn/>), past literature and the authors' field notes. Occurrence data was restricted to the years 1970–2022. Data lacking precise geographical coordinates were assigned to them using locality descriptors in Google Earth. Duplicate and invalid records were manually filtered in excel sheets. In addition, a spatial rarefaction was performed using the *spThin* package in R v.3.6.2 to screen the records for spatial autocorrelation, minimize spatial biases and ensure occurrence independence (Aiello-Lammens et al. 2015). Following this analysis, the records were reduced to 9 for *Meehanian faberi*, (with small geographic distributions), 93 for *M. fargesii*, 27 for *M. henryi*, 26 for *M. montis-koyae*, and 905 for *M. urticifolia* and a total of 1,060 occurrence points were used to develop ENMs in the subsequent analyses (Fig. 2).

### Environmental variables

As for the initial set of predictor variables, we employed the 19 bioclimatic variables from the WorldClim2.1 database (<https://www.worldclim.org/data/worldclim21.html>, Table S1; Fick and Hijmans 2017) with a 2.5 arc-min spatial resolution of ( $\approx 5$  km the equator). This dataset is based on monthly consensus climatologies spanning 1970 to 2000. We removed four data layers (bio 8–9 and bio18–19) because they have been reported to contain artefacts that



**Fig. 2** Study area and distribution of *Meehanian* species in East Asia

cause variances between neighbouring pixels (Bede-Fazekas and Somodi 2020). In addition, we checked for variable autocorrelation of the remaining variables using the VIF procedure. This analysis was carried out using the *usdm* package in R v.3.6.2. For future scenarios, we obtained climatic layers from WorldClim future climate data (<http://www.worldclim.org/CMIP5v1>) with a spatial resolution of 2.5arc-min (Hijmans et al. 2005). Two representative pathway scenarios (RCPs) representing the moderate and high greenhouse gas emission scenarios RCP4.5 and RCP8.5, respectively, for the year 2050 (average for 2041–2060) were considered (Van Vuuren et al. 2011). One global circulation model (GCM) from the Intergovernmental Panel on Climate Change's Fifth Assessment Report (IPCC; <https://www.ipcc.ch/report/ar5/wg2/>): The National (Beijing) Climate Center Climate System Model (BCC-CSM2-MR) was selected due to improved simulation performance in terms of the annual mean climate distribution of precipitation in China (Xin et al. 2019; Wang et al. 2023). This GCM was chosen because it is among the most accurate and relevant models currently used to estimate the influence of increasing greenhouse gas concentrations on biodiversity. They

have previously been used to give realistic ENMs for East Asia (Hijmans et al. 2005).

### Ecological niche modelling

ENMs were constructed to assess the distribution of five *Meehanian* taxa using the maximum entropy modelling approach (MaxEnt v.3.4.4; Phillips et al. 2006). MaxEnt predicts the likelihood distribution for a given species by determining the maximum entropy probability distribution given a set of constraints representing the input known occurrence data (Phillips et al. 2006). The models were run on default parameters with a max of 5000 iterations. 25% of the occurrence data was utilized to evaluate model accuracy, while 75% was used for training. In each training partition, ten duplicates were generated, and the results were averaged. We evaluated several regularisation multiplier values (RM) and observed that the default value performed exceptionally without overfitting the model (RM = 1, Merow et al. 2013). The clamping function was activated to fade out the predicted areas needing clamping. A rigorous statistical test to determine if models can forecast independent subsets of occurrence data better than random expectations is a critical

**Table 1** Evaluation values for model performance for the selected *Meehanian*

| Species                       | AUC (SD)      | TSS   |
|-------------------------------|---------------|-------|
| <i>Meehanian faberi</i>       | 0.896 (0.049) | 0.811 |
| <i>Meehanian fargesii</i>     | 0.913 (0.010) | 0.857 |
| <i>Meehanian henryi</i>       | 0.965 (0.007) | 0.884 |
| <i>Meehanian montis koyae</i> | 0.973 (0.005) | 0.891 |
| <i>Meehanian urticifolia</i>  | 0.932 (0.002) | 0.862 |

AUC- Area under the curve; SD- Standard deviation; TSS- True Skill Statistics

first step in evaluating the study results. For our case, we utilized the area under the receiver operating curve (AUC) and the true skill statistics (TSS) to evaluate the model's predictive capacity. The true skill statistic (TSS) comprises omission and commission errors. It varies from  $-1$  to  $+1$ , with  $+1$  indicating perfect classification and numbers less than zero indicating performance no better than random (Allouche et al. 2006). The AUC values, on the other hand, range between 0 and 1, with an AUC score of approximately 0.5 indicating that the distribution model is not superior to a random model in terms of prediction effects, whereas a value of 1 indicates that the information regarding species distribution is in excellent agreement with appropriate predictions (Phillips et al. 2006). After calibrating models for current conditions, predictions of future potential distributions for the 2050s were generated using the two climate change scenarios, RCP 4.5, and RCP 8.5. With a reference to the classification proposed by Yang et al. (2013), five classes of potential habitats were regrouped: unsuitable (below 0.2), lowly-suitable (between 0.2 and 0.4), moderately-suitable (between 0.4 and 0.6), highly-suitable (between 0.6 and 0.8), and very highly-suitable ( $>0.8$ ).

### Distributional changes for *Meehanian* range

All the averaged logistic output ASCII files (current and future) were converted into a binary presence-absence format using the SDMtoolbox 2.5 in ArcMap 10.5. For this selection, we used the threshold that maximised sensitivity and specificity (MTSS; Liu et al. 2016), as it is the most extensively used (e.g., Ngarega et al. 2021; Tiarniyu et al. 2021) and among the most accurate ones (Liu et al.

2016). These binary maps were utilized to analyze the distributional changes of *Meehanian* under two RCP scenarios- RCP4.5 and RCP8.5 for the 2050s (Brown et al. 2017).

## Results

### Model evaluation

The validation value of the data obtained on the AUC and TSS acquired after modelling the distribution of *Meehanian* species in east Asia was  $>0.811$ , suggesting that the models had a high level of predictive potential (Table 1).

### Contribution of variables

According to the percentage contribution of variables in the final models generated for the *Meehanian* species, two variables were observed to have the highest levels of contribution; the mean diurnal range (Bio2), which strongly influenced the distribution of *M. faberi* (78.7%) and *M. fargesii* (34.9%), and precipitation of driest month (Bio14) strongly affecting the distribution of *M. henryi* (63.2%), *M. montis-koyae* (84.7%), and *M. urticifolia* (63.2%). The contribution of the elevation variable varied from 0.1% for the *M. faberi* model to 17.2% for the *M. henryi* model. Isothermality (Bio3), on the other hand, contributed the most to the *M. fargesii*, *M. henryi* and *M. urticifolia* models, accounting for 18.2, 9.9, and 16.7% of the total contribution, respectively (Table 2).

### Current and future potential distribution of *Meehanian*

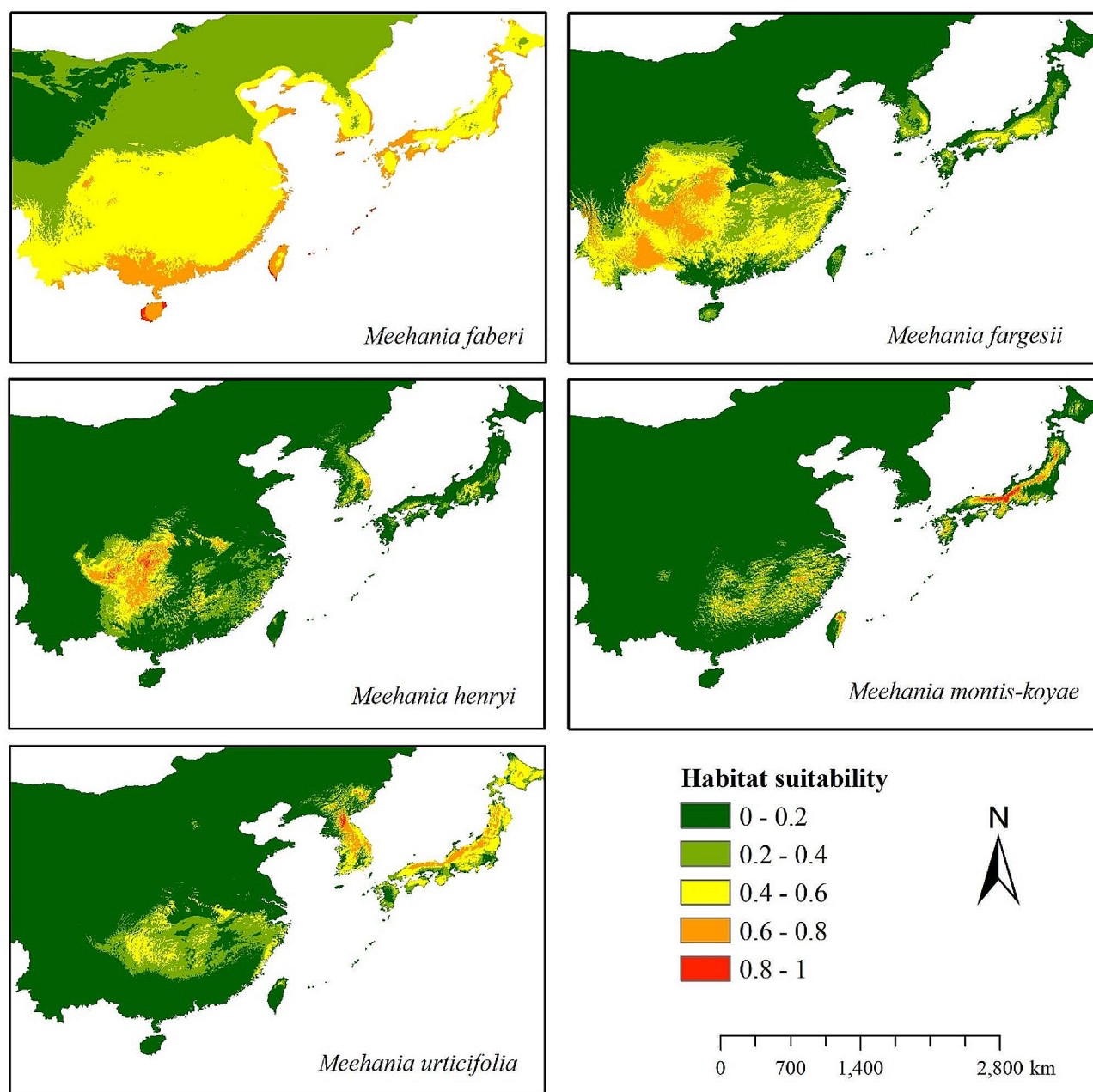
#### *Meehanian faberi*

China, South Korea, and Japan are projected to be suitable areas for the distribution of *Meehanian faberi*. The northernmost provinces of China and North Korea were projected to have a low occurrence. *M. faberi* can be found in locations ranging from  $18^{\circ}\text{N}$  in China to about  $35^{\circ}\text{N}$  in Japan (Fig. 3).

**Table 2** Mean relative variable contribution to the final model fitting of the studied species

| Species                       | Bio2        | Bio3        | Bio8        | Bio13 | Bio14       | Elev        |
|-------------------------------|-------------|-------------|-------------|-------|-------------|-------------|
| <i>Meehanian faberi</i>       | <b>78.7</b> | 3.4         | <b>17.5</b> | 0.3   | 0.1         | 0.1         |
| <i>Meehanian fargesii</i>     | <b>34.9</b> | <b>18.2</b> | 5.5         | 4.1   | <b>22.2</b> | <b>15.2</b> |
| <i>Meehanian henryi</i>       | 0.4         | 9.9         | 7.1         | 2.3   | <b>63.2</b> | <b>17.2</b> |
| <i>Meehanian montis koyae</i> | 1.9         | 5.1         | 1.8         | 1.4   | <b>84.7</b> | <b>5.0</b>  |
| <i>Meehanian urticifolia</i>  | 4.6         | <b>16.7</b> | <b>10.2</b> | 0.4   | <b>63.2</b> | 5.0         |

*Note* The variables in bold are the top three most important variables for each species. Bio2 = mean diurnal range ( $^{\circ}\text{C}$ ), Bio3 = isothermality (%), Bio8 = mean temperature of the wettest quarter ( $^{\circ}\text{C}$ ), Bio13 = precipitation of the wettest month (mm), Bio14 = driest month precipitation (mm), Bio18 = precipitation of warmest quarter (mm), Elev = Altitude above sea level



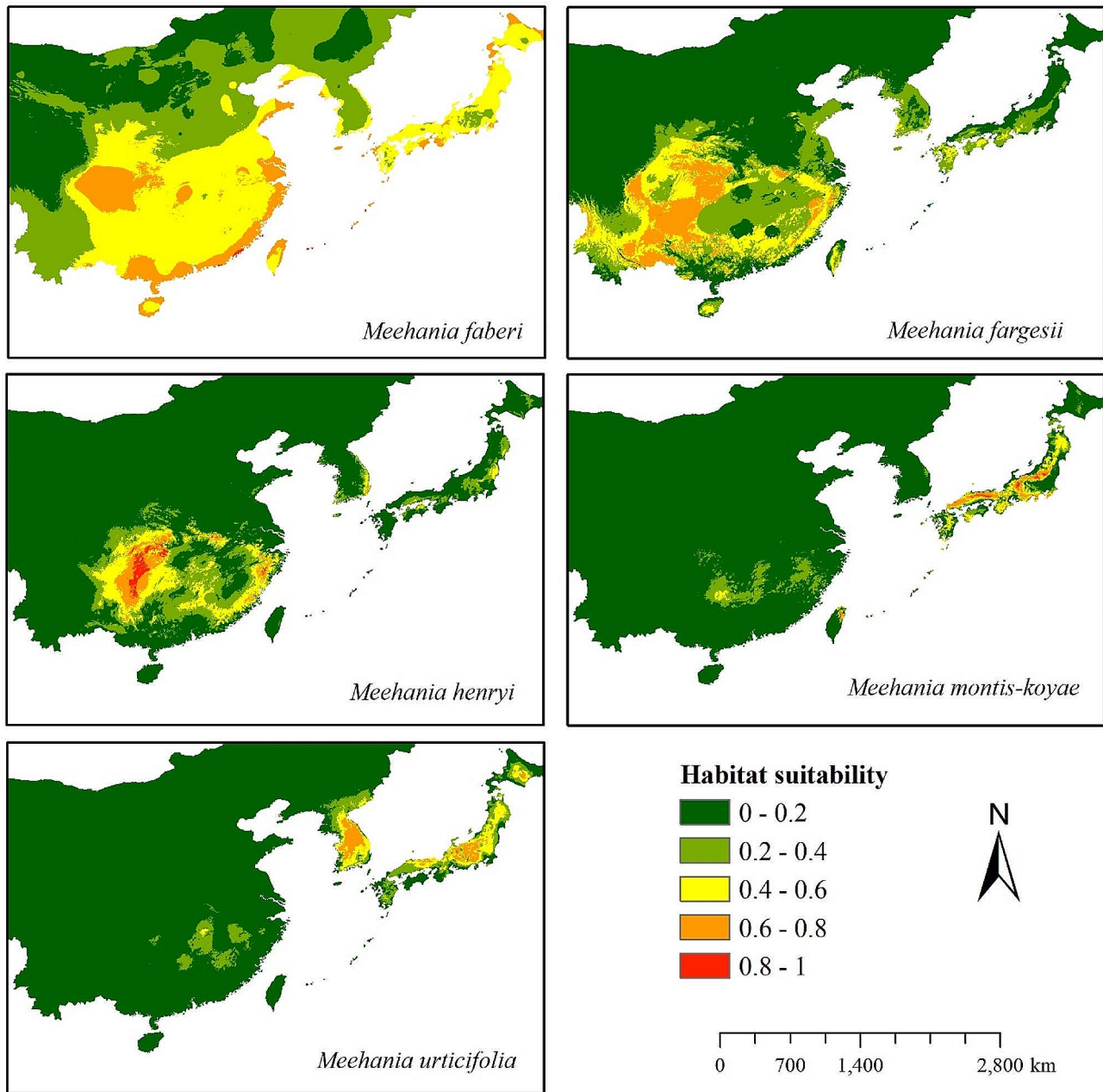
**Fig. 3** Potential climatically suitable habitats for *Meehanian* species in East Asia under current climate conditions. Threshold of classification was as follows, ‘not potential’ (<0.2), ‘low potential’ (0.2–0.4), ‘mod-

erate potential’ (0.4–0.6), ‘high potential’ (0.6–0.8), and ‘very high potential’ (>0.8) habitat

Under the moderate emissions scenario (RCP 4.5), climate change projections for *M. faberi* suggest that the species will shift northward in China (Figs. 4 and 6), with a total range gain of about 317,769 km<sup>2</sup> (Table 3). For the RCP 8.5 scenario, similar results were noted; the gain of the suitable habitat range for *M. faberi* was slightly higher, with an approximate range gain of 329,437 km<sup>2</sup> (Fig. 5; Table 3).

The suitability for *M. faberi* occurrence was predicted to decrease gradually in China, Japan, and South Korea under

the two climate change scenarios (RCP 4.5 and RCP 8.5). On the other hand, the potential region for species’ existence in China increased northwards (Fig. 6). Nevertheless, the overall lost habitat range for both scenarios exceeded the total gained habitat range (Table 3).



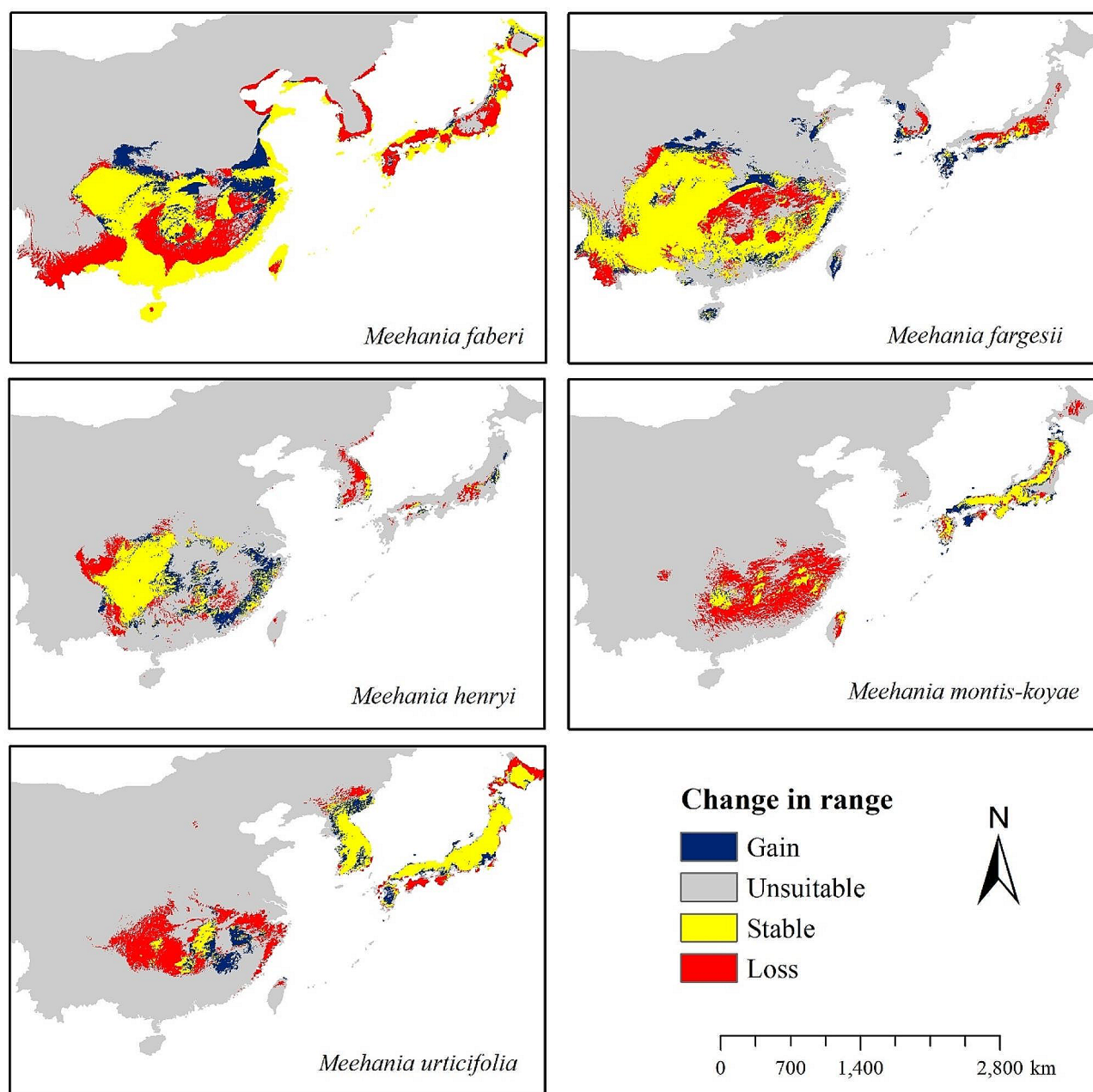
**Fig. 4** Potential climatically suitable habitats for *Meehania* in East Asia under the RCP4.5—moderate climate warming ( $4.5 \text{ W/m}^2$ ) in the 2050s. Threshold of classification was as follows, ‘not potential’

(<0.2), ‘low potential’ (0.2–0.4), ‘moderate potential’ (0.4–0.6), ‘high potential’ (0.6–0.8), and ‘very high potential’ (>0.8) habitat

#### *Meehania fargesii*

Most of China’s climatic conditions, including central, southeast, and southwest China, were favourable for the distribution of *Meehania fargesii* (Fig. 3). However, high suitability areas were only predicted in large portions of central and southwest China with a high fragmentation pattern. The regions projected to gain suitable habitats for *Meehania fargesii* under the RCP 4.5 climatic scenario would be

found in China, South Korea, and southern parts of Japan (Figs. 4 and 6), with an approximately gained suitable range of  $302,517.3 \text{ km}^2$  (Table 3). Furthermore, projected reductions in the suitable habitat of about  $458,186.4 \text{ km}^2$  were predicted in China, Japan, and Korea. Under the RCP 8.5 climate scenario (Fig. 5), the total gained distribution areas would reach  $274,472 \text{ km}^2$ , while the suitable range may decrease by approximately  $430,528 \text{ km}^2$ .



**Fig. 6** Geographical distribution of *Meehania* species under the moderate climate change scenario — RCP 4.5 for the 2050s. Green color indicates areas to be gained by the species, gray color indicates areas

predicted to be stable for the species absence, blue color indicates areas to be stable for the species presence, and red color indicates areas to be lost by the species

### *Meehania henryi*

The current potential distribution of *Meehania henryi* was projected in central China, Japan, and South Korea occupying approximately 688,500 km<sup>2</sup> (Table 3). For the future scenarios, our results indicated an overall increase in suitable areas for *M. henryi*, with an eastward shift of the potential distribution regions (Figs. 6 and 7). The largest range expansions for the species were recorded in mainland China.

### *Meehania montis-koyae*

Stable, suitable conditions for *Meehania montis-koyae* were the dominant pattern in comparisons of current and future potential distributions. Projections of future habitat suitability for *Meehania montis-koyae* varied depending on the climate change scenario (Figs. 6 and 7). According to the MaxEnt models, approximately 190,400 km<sup>2</sup> and 319,000

**Table 3** An estimated area for each *Meehanian* species and habitat suitability category for the two future projections RCP4.5 and RCP8.5 for the climate 2070s (average for 2060–2080)

| Species                       | Current area(km <sup>2</sup> ) | Habitat RCP4.5 |                         |                       | Habitat RCP8.5 |                         |                       |
|-------------------------------|--------------------------------|----------------|-------------------------|-----------------------|----------------|-------------------------|-----------------------|
|                               |                                |                | Area (km <sup>2</sup> ) | Percentage Change (%) |                | Area (km <sup>2</sup> ) | Percentage Change (%) |
| <i>Meehanian faberi</i>       | 2,039,180.1                    | Loss           | 826,686.1               | 40.54                 | Loss           | 800,451.3               | 39.25                 |
|                               |                                | Gain           | 317,769.6               | 15.58                 | Gain           | 329,437.4               | 16.15                 |
|                               |                                | Stable         | 1,211,949.0             | 59.43                 | Stable         | 1,238,184.3             | 60.72                 |
| <i>Meehanian fargesii</i>     | 1,761,878.0                    | Loss           | 458,186.4               | 26.01                 | Loss           | 430,528.3               | 24.43                 |
|                               |                                | Gain           | 302,517.3               | 17.17                 | Gain           | 274,472.6               | 15.58                 |
|                               |                                | Stable         | 1,303,692.6             | 73.99                 | Stable         | 1,331,350.2             | 75.56                 |
| <i>Meehanian henryi</i>       | 688,536.2                      | Loss           | 240,892.7               | 34.99                 | Loss           | 144,686.8               | 21.01                 |
|                               |                                | Gain           | 213,779.3               | 31.05                 | Gain           | 326,731.3               | 47.45                 |
|                               |                                | Stable         | 447,643.3               | 65.01                 | Stable         | 543,849.3               | 78.99                 |
| <i>Meehanian montis-koyae</i> | 662,846.0                      | Loss           | 472,384.5               | 71.27                 | Loss           | 343,811.1               | 51.87                 |
|                               |                                | Gain           | 52,873.7                | 7.98                  | Gain           | 137,710.7               | 20.78                 |
|                               |                                | Stable         | 190,461.5               | 28.73                 | Stable         | 319,034.8               | 48.13                 |
| <i>Meehanian urticifolia</i>  | 861,425.6                      | Loss           | 469,994.7               | 54.56                 | Loss           | 514,117.7               | 59.68                 |
|                               |                                | Gain           | 171,448.7               | 19.90                 | Gain           | 164,947.1               | 19.14                 |
|                               |                                | Stable         | 391,413.3               | 45.43                 | Stable         | 347,290.4               | 40.31                 |

km<sup>2</sup> of the study area were considered suitable habitats for the species under RCP 4.5 and RCP 8.5, respectively.

### *Meehanian urticifolia*

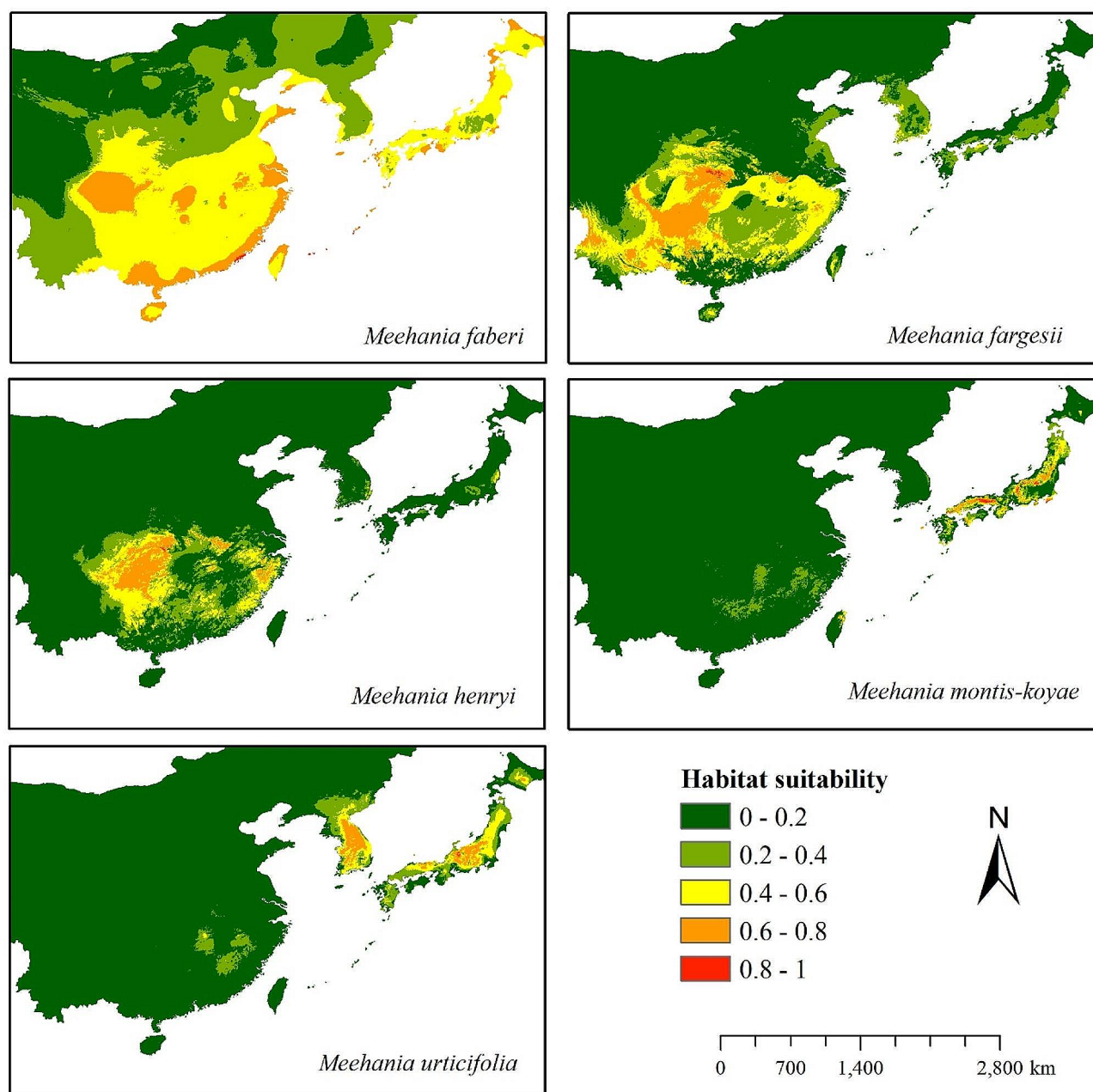
Across our calibration region, under present-day conditions, models showed high suitability for *Meehanian urticifolia* in Korean peninsula and Japan. Furthermore, small portions of suitable habitats were also recorded in south China. Future model projections showed that *Meehanian urticifolia* was highly vulnerable to climate change irrespective of the scenario (Table 3; Figs. 6 and 7). Under both scenarios, we observed a northward latitudinal shift for the species in South Korea and an eastward longitudinal shift for the range in China (Figs. 6 and 7). According to the future projections, the species' suitable habitats were primarily located in Japan and South Korea (Fig. 6).

## Discussion

It is widely established that global climate change will alter species' geographic distributions globally (Salako et al. 2021; Oyebanji et al. 2021; Ngarega et al. 2022). Knowledge of these changes in the distribution of species is crucial for plant and animal for conservation purpose. *Meehanian* species have a general worldwide distribution, although most occur in the Asian continent (Takano et al. 2020; Deng et al. 2015). Studies reporting the distribution of *Meehanian* in the Sino-Asiatic region remain relatively scarce. This is the first attempt to predict the geographical distribution of this relatively known genus in relation to the environmental dataset.

Rana et al. (2021) suggested that AUC alone does not reflect the absolute model performance. Therefore, model accuracy was assessed by combining two metrics, the AUC (threshold-independent) and TSS (threshold-dependent) values as model performance measures. For all the scenarios, the average AUC values (0.896–0.973) while the TSS values (0.811–0.891) were greater, indicating high confidence in the reliability of the models (Table 1) and were not significantly different from previous studies (Idohou et al. 2017; Nzei et al. 2021). So, the models were judged as descriptive and reliable for this study.

MaxEnt modelling approach was utilized in this study to estimate optimal regions for five *Meehanian* species under current and future environmental conditions. The pattern of distribution range under different scenarios and major contributory environmental factors was observed and depicted. Although the five *Meehanian* species had similar ecological preferences, these species showed varied responses to projected climate change using environmental variables. Overall, “temperature,” “precipitation,” and “elevation” variables were observed as important variables responsible for the distribution of species of the genus *Meehanian* in Asia (Table 2). In particular, the mean diurnal range and precipitation of the driest month were the most important predictors of species distribution, indicating each species' climatic preference. Environmental variables, including elevation, precipitation, and temperature, have been reported in various studies to affect the distribution of species with known distribution in the East Asiatic region (e.g., Guo et al. 2021; Kanagaraj et al. 2019). For example, precipitation is the major climatic factor determining the distribution of *Akebia quinata* in East Asia (Zhang et al. 2022). In addition, temperature, precipitation, and elevation (> 2300 m



**Fig. 5** Potential climatically suitable habitats for *Meehanian* in East Asia under the RCP 8.5— extreme climate warming ( $8.5 \text{ W/m}^2$ ) in the 2050s. Threshold of classification was as follows, ‘not potential’

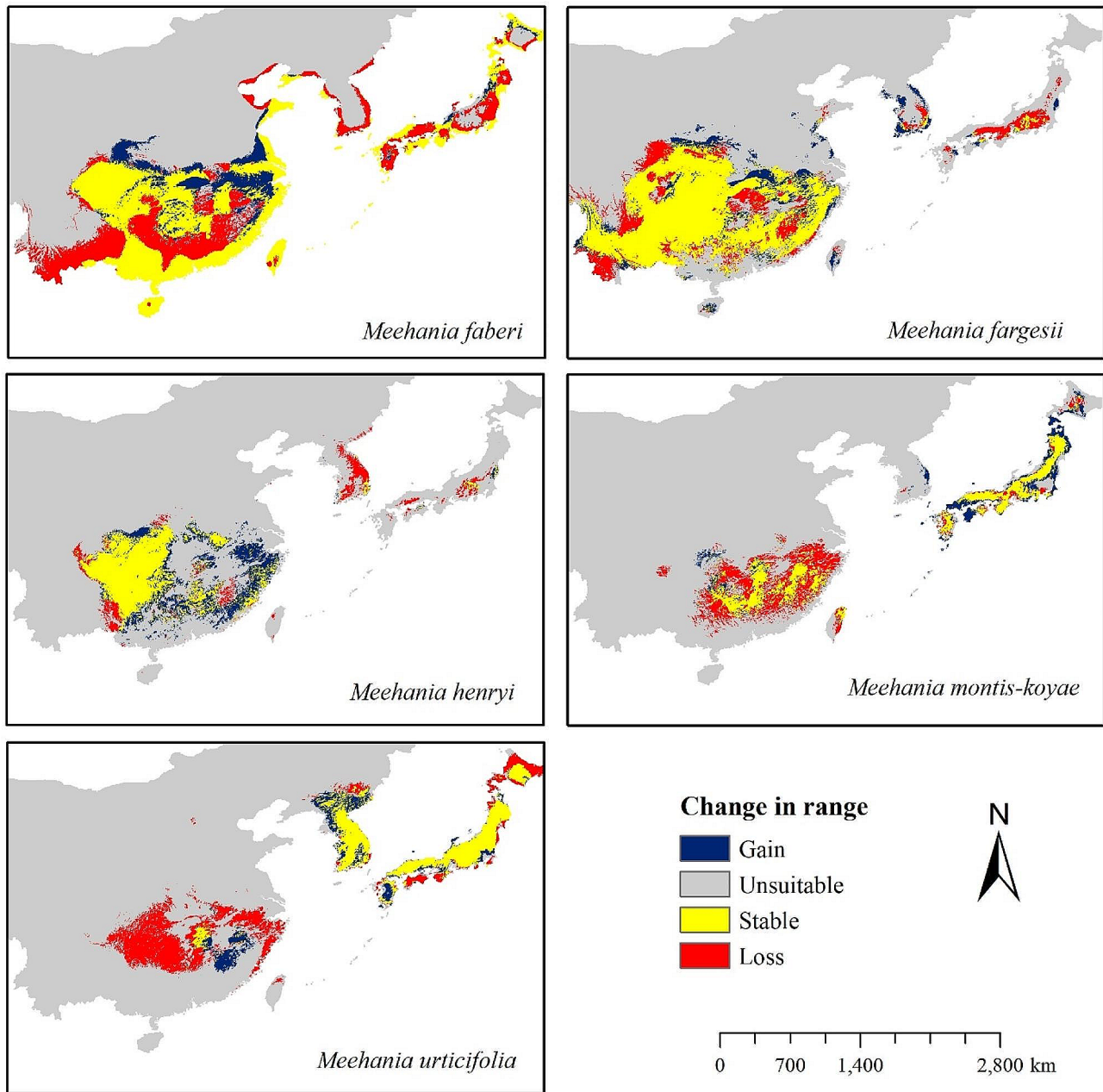
(<0.2), ‘low potential’ (0.2–0.4), ‘moderate potential’ (0.4–0.6), ‘high potential’ (0.6–0.8), and ‘very high potential’ (>0.8) habitat

as) account for a sizeable contributory influence in the distribution of *Garuga forrestii* found in Sichuan, Yunnan, and Guangxi (Tiamiyu et al. 2021).

Ecological niche models assume that species’ present native ranges and essential climatic tolerances are almost identical (Williams et al. 2009; Zhao et al. 2022). However, rapid evolution may change species’ adaptations to new climatic conditions in the future, enabling populations to persist in various locations amid changing conditions. Even

though fast evolution in the face of climate change has been widely established in several plant species (Ngarega et al. 2022; Nzei et al. 2021), it seems inadequate to counteract the high speed of present climate change (Franks et al. 2018).

Species with poor dispersal and range-filling ability might well be particularly vulnerable to current climate change since they are unlikely to move fast enough to keep up with shifting weather patterns (Erlandson et al. 2022;



**Fig. 7** Geographical distribution of *Meehanian* species under the extreme climate change scenario — RCP 8.5 for the 2050s. Green color indicates areas to be gained by the species, gray color indicates

areas predicted to be stable for the species absence, blue color indicates areas to be stable for the species presence, and red color indicates areas to be lost by the species

Ngarega et al. 2022). In other instances, their actual and projected ranges may diverge completely, subjecting these species to high extinction threats (Sax et al. 2013). As such, many endemics may be especially vulnerable, as their distributions often reflect past marginalisation by climate change (e.g., Pleistocene range dynamics), and their present range distributions are often constrained to odd habitats e.g., polar regions and high elevations (Erlandson et al. 2022). Therefore, the conservation of such species may necessitate aided

migration (see McLachlan et al. 2007). Based on our projections under future climate scenarios, the potential distribution of the *Meehanian* habitat range will generally shift northwards in China. Our findings are comparable to those of previous studies, supporting the assertion that climate warming will cause wide-ranging adjustments in biodiversity (Bellard et al. 2012; Fadrique et al. 2018). Besides, the loss of habitat recorded for species across China, Japan, and South Korea (Chang et al. 2007) is a problem that could

lead to the potential decrease in species populations in high suitability regions, which could be attributed to agricultural expansion, urbanization, and industrialization such as mining and hydropower constructions (Hughes 2017).

Environmental and occurrence data might not fully represent an organism's whole environmental/ecological need. As a result, predictions from predictive modelling research such as this must be sensibly considered, and the limits must be explicitly indicated. The outcomes of our study are also sensitive to the group of selected species and their significance in the East Asian ecosystem. As a result, the findings could have differed if a different group of organisms was selected. In the present study, we successfully modelled the distribution of *Meehanian* in East Asia. We, however, did not include the land use change factors and biotic interactions, which could have largely affected the outcomes of our study. Biotic interactions may be dynamic and complicated, and getting data to parameterize these relationships may be difficult. Furthermore, integrating such relationships necessitates a previous understanding of the species' biology as well as its community (Hof et al. 2012). Here, we advocate including biotic interactions and land use change variables in future research to investigate their implications on the habitat suitability of *Meehanian*. We also advocate integrating soil data in this research to determine the implications of climate change on *Meehanian* in the next decades.

## Conclusions

We presented the species distribution models for *Meehanian* in the East Asian region using environmental variables for the first time. Precipitation of the driest month (Bio14) indicated a high correlation with the distribution of *Meehanian henryi*, *M. montis-koyae*, and *M. urticifolia*, while Isothermality (Bio2) was strongly correlated with the distribution of *M. faberi* and *M. fargesii* in East Asian region. All the species were observed to be vulnerable to climate change, losing between 144,686 km<sup>2</sup> and 826,686 km<sup>2</sup> of their suitable range. Future research that assesses climate impacts using additional environmental covariates, such as land use, distance to roads, and land cover, will aid in understanding the mechanisms behind the distribution of herbaceous species and their responses to the changing climate. Such mechanistic understanding should help us forecast the climate change effects on species and their interactions.

**Supplementary Information** The online version contains supplementary material available at <https://doi.org/10.1007/s42965-024-00351-y>.

**Acknowledgements** Our appreciation is expressed to Zhang Cheng, College of Life Sciences, Beijing Normal University (BNU), and Zhu Renbin (XTBG) for the photographs.

**Authors' contributions** Conceptualization: Bashir B. Tiamiyu, Hengchang Wang and Tao Deng. Methodology: Bashir B. Tiamiyu, and Boniface K. Ngarega. Modelling and formal analysis: Boniface K. Ngarega. >Investigation, and resources: Xu Zhang, Huajie Zhang, Juan Lili and Jiao Sun. Data curation: Huajie Zhang, Xu Zhang and Jiao Sun. Writing—original draft preparation: Bashir B. Tiamiyu. Writing—review and editing: Bashir B. Tiamiyu and Boniface K. Ngarega. Project administration: Hengchang Wang. Funding acquisition: Hengchang Wang and Tao Deng. All authors have read and agreed to the published version of the manuscript.

**Funding** This study was supported by the Second Tibetan Plateau Scientific Expedition and Research program (2019QZKK0502), National Natural Science Foundation of China (32170215), the Key Projects of the Joint Fund of the National Natural Science Foundation of China (U1802232), International Partnership Program of Chinese Academy of Sciences (151853KYSB20180009), Yunnan Young & Elite Talents Project (YNWR-QNBJ-2019-033), the Ten Thousand Talents Program of Yunnan Province (202005AB160005) and the Chinese Academy of Sciences "Light of West China" Program.

**Data availability** The data that support the findings of this study are available from the corresponding author upon reasonable request.

## Declarations

**Ethics approval and consent to participate** Not applicable.

**Consent for publication** Not applicable.

**Competing interests** The authors declare that there is no conflict of interest.

## References

- Ahmadi M, Hemami MR, Kaboli M, Shabani F (2023) MaxEnt brings comparable results when the input data are being completed; Model parameterization of four species distribution models. *Ecol Evol* Feb 17(2):e9827. <https://doi.org/10.1002/ece3.9827>
- Aiello-Lammens ME, Boria RA, Radosavljevic A, Vilela B, Anderson RP (2015) *spThin*: an R package for spatial thinning of species occurrence records for use in ecological niche models. *Ecography* 38(5):541–545. <https://doi.org/10.1111/ecog.01132>
- Ali H, Din JU, Bosso L, Hameed S, Kabir M et al (2021) Expanding or shrinking? Range shifts in wild ungulates under climate change in Pamir-Karakoram mountains, Pakistan. *PLoS ONE* 16(12):e0260031. <https://doi.org/10.1371/journal.pone.0260031>
- Allouche O, Tsoar A, Kadmon R (2006) Assessing the accuracy of species distribution models: prevalence, kappa and the true skill statistic (TSS). *J Appl Ecol* 43(6):1223–1232. <https://doi.org/10.1111/j.1365-2664.2006.01214.x>
- Ancillotto L, Mori E, Bosso L, Agnelli P, Russo D (2019) The Balkan long-eared bat (*Plecotus kolombatovici*) occurs in Italy—first confirmed record and potential distribution. *Mammal Biol* 96:61–67. <https://doi.org/10.1016/j.mambio.2019.03.014>
- Bede-Fazekas Á, Somodi I (2020) The way bioclimatic variables are calculated has impact on potential distribution models. *Methods Ecol Evol* 11(12):1559–1570. <https://doi.org/10.1111/2041-210X.13488>
- Bellard C, Bertelsmeier C, Leadley P, Thuiller W, Courchamp F (2012) Impacts of climate change on the future

- of biodiversity. *Ecol Lett* 15(4):365–377. <https://doi.org/10.1111/j.1461-0248.2011.01736.x>
- Brown JL, Bennett JR, French CM (2017) SDMtoolbox 2.0: the next generation Python-based GIS toolkit for landscape genetic, biogeographic and species distribution model analyses. *PeerJ* 5:e4095. <https://doi.org/10.7717/peerj.4095>
- Corre  n C, Valeria O, Mu  oz J, Fenton NJ (2022) Small but visible: Predicting rare bryophyte distribution and richness patterns using remote sensing-based ensembles of small models. *PLoS ONE* 17(1):e0260543. <https://doi.org/10.1371/journal.pone.0260543>
- Chang CS, Choi DY, Kim H, Kim YS, Park TY (2007) Genetic diversity and mating system of the threatened plant *Kirengeshoma palmata* (Saxifragaceae) in Korea. *J Plant Res* 120(1):149–156. <https://doi.org/10.1007/s10265-006-0036-1>
- Chukwuma EC, Oyeibanji OO, Chukwuma DM, Ayodele AE, Tiamiyu BB, Bolarinwa KA, Adeyemi SB, Sagaya A (2023) Predicting the potential impact of environmental factors on the distribution of *Triplochiton scleroxylon* (Malvaceae): an economically important tree species in Nigeria. *Acta Ecol Sin* 43(6):1101–1111. <https://doi.org/10.1016/j.chnaes.2023.04.001>
- Deng T, Nie ZL, Drew BT, Volis S, Kim C, Xiang CL, Zhang JW, Wang YH, Sun H (2015) Does the Arcto-Tertiary biogeographic hypothesis explain the disjunct distribution of Northern Hemisphere herbaceous plants? The case of *Meehanian* (Lamiaceae). *PLoS ONE* 10(2):e0117171. <https://doi.org/10.1371/journal.pone.0117171>
- Elith JH, Graham CP, Anderson R, Dud  k M, Ferrier S, Guisan AJ, Hijmans R, Huettmann FR, Leathwick J, Lehmann A, Li J (2006) Novel methods improve prediction of species’ distributions from occurrence data. *Ecography* 29(2):129–151. <https://doi.org/10.1111/j.2006.0906-7590.04596.x>
- Elith J, Phillips SJ, Hastie T, Dud  k M, Chee YE, Yates CJ (2011) A statistical explanation of MaxEnt for ecologists. *Divers Distrib* 17(1):43–57. <https://doi.org/10.1111/j.1472-4642.2010.00725.x>
- Erlandson SK, Bellemare J, Moeller DA (2022) Limited range-filling among endemic forest herbs of Eastern North America and its implications for conservation with climate change. *Front Ecol Evol* 9:751728. <https://doi.org/10.3389/fevo.2021.751728>
- Fadrique B, B  ez S, Duque   , Malizia A, Blundo C, Carilla J, Osinaga-Acosta O, Malizia L, Silman M, Farf  n-R  os W, Malhi Y, Young KR, Cuesta CF, Homeier J, Peralvo M, Pinto E, Jadan O, Aguirre N, Aguirre Z, Feeley KJ (2018) Widespread but heterogeneous responses of Andean forests to climate change. *Nature* 564(7735):207–212. <https://doi.org/10.1038/s41586-018-0715-9>
- Fick SE, Hijmans RJ (2017) WorldClim 2: new 1-km spatial resolution climate surfaces for global land areas. *Int J Climatol* 37(12):4302–4315. <https://doi.org/10.1002/joc.5086>
- Franks SJ, Hamann E, Weis AE (2018) Using the resurrection approach to understand contemporary evolution in changing environments. *Evol Appl* 11(1):17–28. <https://doi.org/10.1111/eva.12528>
- GBIF, Occurrence Download (2021) The Global Biodiversity Information Facility. Available online: <https://doi.org/10.15468/dl.qfaum6> (accessed on 16 January 2022)
- Guo K, Yuan S, Wang H, Zhong J, Wu Y, Chen W, Hu C, Chang Q (2021) Species distribution models for predicting the habitat suitability of Chinese fire-bellied newt *Cynops orientalis* under climate change. *Ecol Evol* 11(15):10147–10154. <https://doi.org/10.1002/ece3.7822>
- Hijmans RJ, Cameron SE, Parra JL, Jones PG, Jarvis A (2005) Very high resolution interpolated climate surfaces for global land areas. *Int J Climatol: J Royal Meteorological Soc* 25(15):1965–1978. <https://doi.org/10.1002/joc.1276>
- Hof AR, Jansson R, Nilsson C (2012) Future climate change will favour non-specialist mammals in the (sub) arctics. *PLoS ONE* 7(12):e52574. <https://doi.org/10.1371/journal.pone.0052574>
- Hughes AC (2017) Understanding the drivers of southeast Asian biodiversity loss. *Ecosphere* 8(1):01624. <https://doi.org/10.1002/ecs2.1624>
- Idohou R, Assogbadjo AE, Kaka   RG et al (2017) Spatio-temporal dynamic of suitable areas for species conservation in West Africa: eight economically important wild palms under present and future climates. *Agroforest Syst* 91:527–540. <https://doi.org/10.1007/s10457-016-9955-6>
- Kaky E, Nolan V, Alatawi A, Gilbert F (2020) A comparison between Ensemble and MaxEnt species distribution modelling approaches for conservation: a case study with Egyptian medicinal plants. *Ecol Inf* 60:101150. <https://doi.org/10.1016/j.ecoinf.2020.101150>
- Kanagaraj R, Araujo MB, Barman R, Davidar P, De R, Digal DK, Gopi GV, Johnsingh AJT, Kakati K, Kramer-Schadt S, Lamichhane BR (2019) Predicting range shifts of Asian elephants under global change. *Divers Distrib* 25(5):822–838. <https://doi.org/10.1111/ddi.12898>
- Kunkel G (1984) Plants for human consumption. Koeltz Scientific Books, Koenigstein, pp 393–394
- Li XW, Hedge IC (1994) *Meehanian* Britton. In: Wu ZY, Raven PH (eds) *Flora of China*. Science Press, Beijing, China/Missouri Botanical Garden, St. Louis, MO, USA 17:122–124
- Liu C, Newell G, White M (2016) On the selection of thresholds for predicting species occurrence with presence-only data. *Ecol Evol* 6(1):337–348. <https://doi.org/10.1002/ece3.1878>
- Lowry DB, Willis JH (2010) A widespread chromosomal inversion polymorphism contributes to a major life-history transition, local adaptation, and reproductive isolation. *PLoS Biol* 8(9):e1000500. <https://doi.org/10.1371/journal.pbio.1000500>
- McLachlan JS, Hellmann JJ, Schwartz MW (2007) A framework for debate of assisted migration in an era of climate change. *Conserv Biol* 21(2):297–302. <https://www.jstor.org/stable/4620812>
- Merow C, Smith MJ, Silander JA Jr (2013) A practical guide to MaxEnt for modeling species’ distributions: what it does, and why inputs and settings matter. *Ecography* 36(10):1058–1069. <https://doi.org/10.1111/j.1600-0587.2013.07872.x>
- Mkala EM, Jost M, Wanke S, Ngarega BK, Hughes A, Mutinda ES et al (2022) How vulnerable are holoparasitic plants with obligate hosts to negative climate change impacts? *Ecol Inf* 69:101636. <https://doi.org/10.1016/j.ecoinf.2022.101636>
- Ngarega BK, Masocha VF, Schneider H (2021) Forecasting the effects of bioclimatic characteristics and climate change on the potential distribution of *Colophospermum mopane* in southern Africa using Maximum Entropy (Maxent). *Ecol Inf* 65:101419. <https://doi.org/10.1016/j.ecoinf.2021.101419>
- Ngarega BK, Nzei JM, Saina JK, Halmy MWA, Chen JM, Li ZZ (2022) Mapping the habitat suitability of *Ottelia* species in Africa. *Plant Divers* 44(5):468–480. <https://doi.org/10.1016/j.pld.2021.12.006>
- Nzei JM, Ngarega BK, Mwanzia VM, Musili PM, Wang QF, Chen JM (2021) The past, current, and future distribution modeling of four water lilies (*Nymphaea*) in Africa indicates varying suitable habitats and distribution in climate change. *Aquat Bot* 173:103416. <https://doi.org/10.1016/j.aquabot.2021.103416>
- Oyeibanji OO, Salako G, Nneji LM, Oladipo SO, Bolarinwa KA, Chukwuma EC, Ayoola AO, Olagunju TE, Ighodalo DJ, Nneji IC (2021) Impact of climate change on the spatial distribution of endemic legume species of the Guineo-Congolian forest, Africa. *Ecol Ind* 122:107282. <https://doi.org/10.1016/j.ecolind.2020.107282>
- Pearson RG, Raxworthy CJ, Nakamura M, Townsend Peterson A (2007) Predicting species distributions from small numbers of occurrence records: a test case using cryptic geckos in Madagascar. *J Biogeogr* 34(1):102–117. <https://doi.org/10.1111/j.1365-2699.2006.01594.x>
- Phillips SJ, Anderson RP, Schapire RE (2006) Maximum entropy modeling of species geographic distributions.

- Ecol Model 190(3–4):231–259. <https://doi.org/10.1016/j.ecolmodel.2005.03.026>
- POWO (2022) Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew. Published on the Internet; <http://www.plantsoftheworldonline.org/> Retrieved 24 August 2022
- R Core Team (2019) R: a language and environment for statistical computing (version 3.6. 1) [Computer software]. R Foundation for Statistical Computing. Vienna, Austria
- Radomski T, Beamer D, Babineau A, Wilson C, Pechmann J, Kozak KH (2022) Finding what you don't know: testing SDM methods for poorly known species. *Divers Distrib* 28(9):1769–1780. <https://doi.org/10.1111/ddi.13536>
- Rana SK, Rana HK, Luo D, Sun H (2021) Estimating climate-induced 'Nowhere to go' range shifts of the Himalayan *Incarvillea* Juss. Using multi-model median ensemble species distribution models. *Ecol Indic* 121:107127. <https://doi.org/10.1016/j.ecolind.2020.107127>
- Sáenz-Romero C, Lamy JB, Ducouso A, Musch B, Ehrenmann F, Delzon S, Kremer A (2017) Adaptive and plastic responses of *Quercus petraea* populations to climate across Europe. *Glob Change Biol* 23(7):2831–2847. <https://doi.org/10.1111/gcb.13576>
- Salako G, Oyeibanji OO, Olagunju TE, Howe GT (2021) Potential impact of climate change on the distribution of some selected legumes in Cameroon and adjoining Nigeria border. *Afr J Ecol* 59:959–975. <https://doi.org/10.1111/aje.12915>
- Sax DF, Early R, Bellemare J (2013) Niche syndromes, species extinction risks, and management under climate change. *Trends Ecol Evol* 28(9):517–523. <https://doi.org/10.1016/j.tree.2013.05.010>
- Sheldon KS (2019) Climate change in the tropics: ecological and evolutionary responses at low latitudes. *Annu Rev Ecol Evol Syst* 50:303–333. <https://doi.org/10.1146/annurev-ecolsys-110218-025005>
- Shivanna KR (2022) Climate change and its impact on biodiversity and human welfare. *Proc Indian Natl Sci Acad* 88:160–171. <https://doi.org/10.1007/s43538-022-00073-6>
- Simons RR, Croft S, Rees E, Tearne O, Arnold ME, Johnson N (2019) Using species distribution models to predict potential hot-spots for Rift Valley Fever establishment in the United Kingdom. *PLoS ONE* 14(12):e0225250. <https://doi.org/10.1371/journal.pone.0225250>
- Takano A, Sakaguchi S, Li P, Matsuo A, Suyama Y, Xia GH, Liu X, Isagi Y (2020) A Narrow Endemic or a Species Showing Disjunct Distribution? Studies on *Meehanian montis-koyae* Ohwi (Lamiaceae). *Plants* 9(9): 1159. <https://doi.org/10.3390/plants9091159>
- Tallis H, Kareiva P, Marvier M, Chang A (2008) An ecosystem services framework to support both practical conservation and economic development. *Proc Natl Acad Sci* 105(28):9457–9464. <https://doi.org/10.1073/pnas.0705797105>
- Tanaka T, Nakao S (1976) Tanaka's cyclopedia of edible plants of the world
- Tiamiyu BB, Ngarega BK, Zhang X, Zhang H, Kuang T, Huang GY, Deng T, Wang H (2021) Estimating the potential impacts of Climate Change on the spatial distribution of *Garuga Forrestii*, an endemic species in China. *Forests* 12(12):1708. <https://doi.org/10.3390/f12121708>
- Townsend PA, Papeş M, Eaton M (2007) Transferability and model evaluation in ecological niche modeling: a comparison of GARP and Maxent. *Ecography* 30(4):550–560. <https://doi.org/10.1111/j.0906-7590.2007.05102.x>
- Van Vuuren DP, Edmonds J, Kainuma M, Riahi K, Thomson A, Hibbard K, Hurtt GC, Kram T, Krey V, Lamarque J-F, Rose SK (2011) The representative concentration pathways: an overview. *Clim Change* 109(1):5–31. <https://doi.org/10.1007/s10584-011-0148-z>
- Wan JN, Mbari NJ, Wang SW, Liu B, Mwangi BN, Rasoarahaona JR, Xin HP, Zhou YD, Wang QF (2021) Modeling impacts of climate change on the potential distribution of six endemic baobab species in Madagascar. *Plant Divers* 43(2):117–124. <https://doi.org/10.1016/j.pld.2020.07.001>
- Wang C, Sheng Q, Zhao R, Zhu Z (2023) Differences in the suitable distribution area between Northern and Southern China landscape plants. *Plants* 12(14):2710. <https://doi.org/10.3390/plants12142710>
- Weiskopf SR, Rubenstein MA, Crozier LG, Gaichas S, Griffis R, Halofsky JE, Hyde KJ, Morelli TL, Morissette JT, Muñoz RC, Pershing AJ (2020) Climate change effects on biodiversity, ecosystems, ecosystem services, and natural resource management in the United States. *Sci Total Environ* 733:137782. <https://doi.org/10.1016/j.scitotenv.2020.137782>
- Williams JN, Seo C, Thorne J, Nelson JK, Erwin S, O'Brien JM, Schwartz MW (2009) Using species distribution models to predict new occurrences for rare plants. *Divers Distrib* 15(4):565–576
- Xiang QY, Soltis DE, Soltis PS, Manchester SR, Crawford DJ (2000) Timing the eastern Asian–eastern north American floristic disjunction: molecular clock corroborates paleontological estimates. *Mol Phylogenet Evol* 15(3):462–472. <https://doi.org/10.1006/mpev.2000.0766>
- Xin X, Wu T, Zhang J, Zhang F, Li W, Zhang Y et al (2019) Introduction of BCC models and its participation in CMIP6. *Clim Change Res* 15:533–539. <https://doi.org/10.12006/j.issn.1673-1719.2019.039>
- Yang XQ, Kushwaha SP, Saran S, Xu J, Roy PS (2013) Maxent modeling for predicting the potential distribution of medicinal plant, *Justicia adhatoda* L. in Lesser Himalayan foothills. *Ecol Eng* 51:83–87
- Zellweger F, De Frenne P, Lenoir J, Vangansbeke P, Verheyen K, Bernhardt-Römermann M, Baeten L, Hédal R, Berki I, Brunet J, Van Calster H, Chudomelová M, Decocq G, Dirnböck T, Durak T, Heinken T, Jaroszewicz B, Kopecký M, Máliš F, Macek M, Coomes D (2020) Forest microclimate dynamics drive plant responses to warming. *Science* 368(6492):772–775. <https://doi.org/10.1126/science.aba6880>
- Zhang JM, Song ML, Li ZJ, Peng XY, Su S, Li B, Xu XQ, Wang W (2022) Effects of climate change on the distribution of *Akebia quinata*. *Ecol Evol* 12:e8714. <https://doi.org/10.3389/fevo.2021.752682>
- Zhao Z, Xiao N, Shen M, Li J (2022) Comparison between optimized MaxEnt and random forest modeling in predicting potential distribution: a case study with *Quasipaa boulengeri* in China. *Sci Total Environ* 842:156867

Springer Nature or its licensor (e.g. a society or other partner) holds exclusive rights to this article under a publishing agreement with the author(s) or other rightsholder(s); author self-archiving of the accepted manuscript version of this article is solely governed by the terms of such publishing agreement and applicable law.