Evaluating the Impact of Climate Change on the Endangered Endemic Species *Thuja koraiensis* Nakai in Baekdudaegan, South Korea: An Ensemble Modelling Approach

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Thuja koraiensis Nakai (*Cupressaceae*) is an endangered conifer species that holds significant ecological importance as an endemic plant in Korea. To facilitate the adaptive management of ecosystems on the Korean peninsula in the face of climate change, the use of species distribution models (SDMs) can be instrumental in supporting climate-adaptive forest restoration programs. In this study, we collected occurrence and bioclimatic data from remote sensing to analyze the current and projected distribution of *T. koraiensis*. We employed four different SDMs, namely, the general additive model, generalized boosted model, general linear model, and random forest, to predict the potential distribution of *T. koraiensis* under both current and future climate scenarios. To assess the risk of extinction for this species, we utilized ensemble-averaged models to estimate the extent of area loss in currently suitable habitats for *T. koraiensis*, with a focus on stable true skill statistic (*TSS*) results exceeding 0.9. Encouragingly, our results indicate that *T. koraiensis* is likely to persist into the 2070s, specifically when considering the representative concentration pathway (RCP) 4.5 scenario for climate change on the Korean peninsula. These findings provide robust predictions regarding the future habitat occupancy probabilities of *T. koraiensis* populations across South Korea. Moreover, they contribute to the development of climate-adaptive forest restoration programs, taking into account long-term perspectives.

1. Introduction

Thuja koraiensis Nakai is a short and creeping evergreen shrub that reaches nearly 3 m in height and only grows in northeast China and the high mountains of Korea.[1] Climate change has progressed in recent years and natural populations of *T. koraiensis* have declined together with the competition with temperate species. Furthermore, the decline in the number of *T. koraiensis* might be related to inbreeding and inadequate environments for seed germination

within the natural habitats situated in restricted areas high atop mountains.[2] Currently, the studies of *T. koraiensis* are focused on the molecular mechanism of somatic embryogensis,[3] genetic variation,[4] habitat investigation and growth patterns[5] in terms of conservation efforts. The decrease in the habitats of *T. koraiensis* has emerged as a serious issue in terms of preserving the diverse species on the Korean peninsula.[6] Therefore, the endemic *T. koraiensis* has been designated as a rare and endangered tree species in Korea and a vulnerable species on the International Union for Conservation of Nature (IUCN) Red List of Threatened Species.[7]

Species distribution models (SDMs) are quantitative models of species–environment relationships typically developed using species location data and those environmental variables considered to affect the species distribution.[8] Commonly, SDMs are used to investigate the environmental suitability to estimate a species' current or future distribution.[9] Furthermore, many studies of future climate change use an ensemble modelling approach in which simulations of future conditions are produced with multiple climate models, rather than just one.[10] As a single algorithm can easily result in the overfitting phenomenon, this problem is eliminated after the ensemble.[11] Hence, ensemble modelling can significantly improve the modelling accuracy and reduce uncertainty compared with modelling using only a single model.[12] However, there is no research on the ensemble modelling of *T. koraiensis* species in Baekdudaegan (South Korea), which should be predicted with an assessment of their uncertainty, in accordance with the potential impact of climate change.

Therefore, in this study, we use ensemble algorithm SDM methods to evaluate the impact of climate change scenarios under representative concentration pathway (RCP) 4.5 on the endangered native *T. koraiensis* populations across the South Korean peninsula. Our findings would provide long-term insights into forest conservation and restoration strategies in response to climate change.

2. Materials and Methods

2.1 Location data for *T. koraiensis* in South Korea

To acquire data on *T. koraiensis* in South Korea, we employed databases serviced by Baekdudaegan National Arboretum, Korea Arboreta and Gardens Institute (Gonghwa, South Korea). Four additional field surveys were performed to confirm the current populations of *T. koraiensis* (Fig. 1). In total, 118 sites where *T. koraiensis* are present were identified, and maps with binary cell values of presence (1) and absence (0) were produced for each SDM using the threshold value of 0.5 (Fig. 2).

2.2 Environmental parameters

Current climate data, including 19 bioclimatic variables in the World Climate data, were used to predict the change in the distribution of potential land suitable for *T. koraiensis* populations.[13] In particular, bioclimatic variables were considered suitable for investigating the species distributions under current or possible future conditions by applying the SDMs.[14,15] Four (max
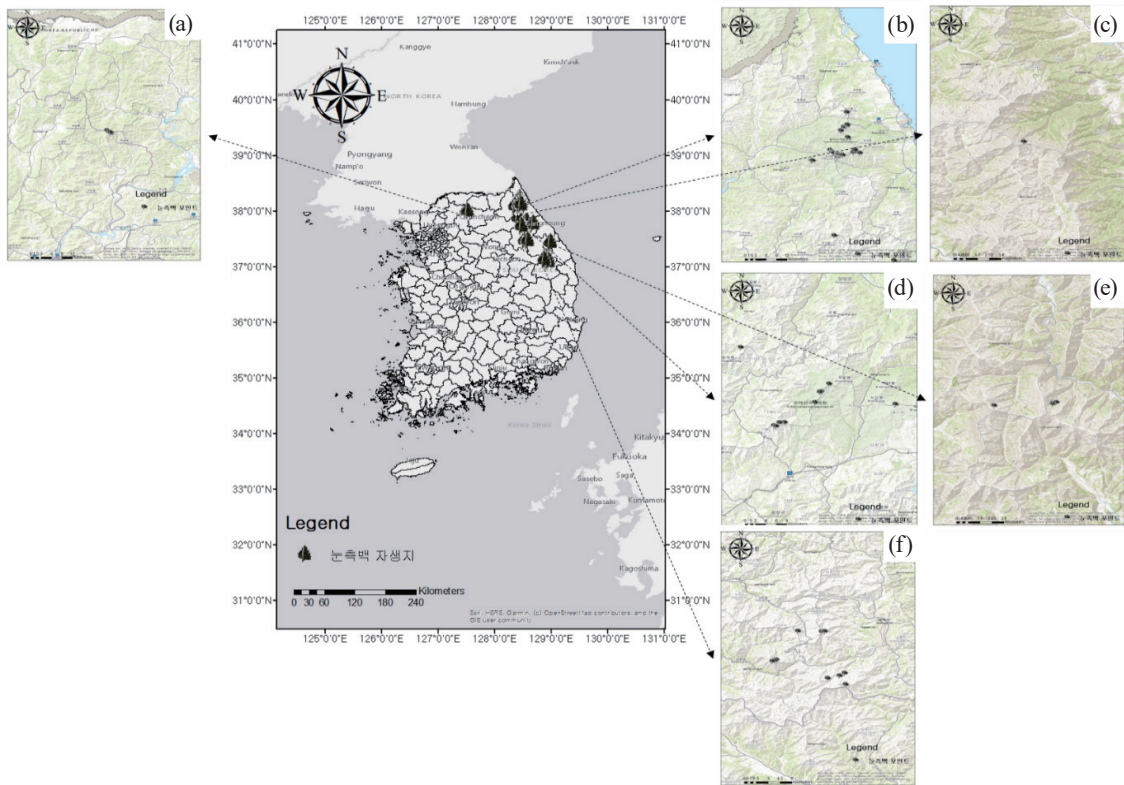
Fig. 1.   (Color online) Distribution of *T. koraiensis* on Korean peninsula (a) Chokdaebong, (b) Seoraksan National Park, (c) Donghae-si, (d) Odaesan National Park, (e) Pyeongchang and Jeongseon, (f) Undaebong (Taebaek).

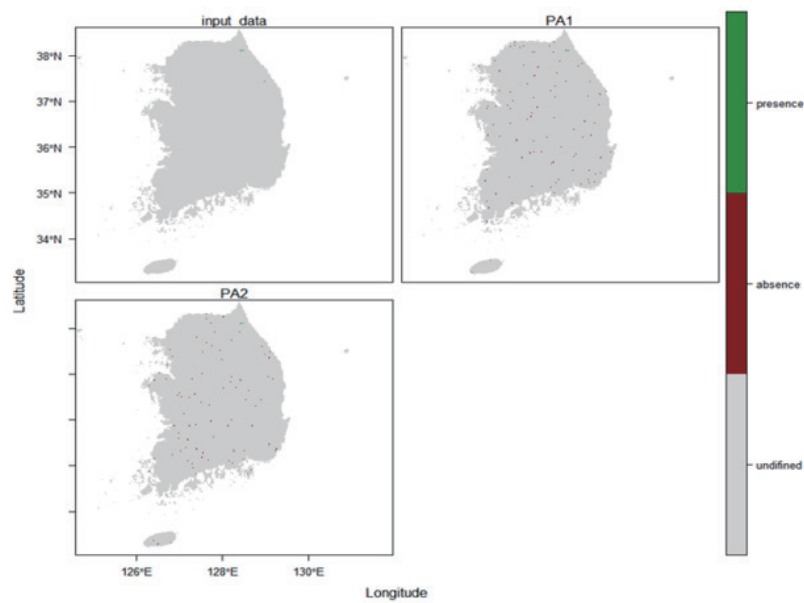

Fig. 2.   (Color online) Results of presence and absence mapping of *T. koraiensis* ($n = 59$ presence, $n = 500$ absence).

temperature of warmest month: bio 5, temperature annual range: bio 7, mean temperature of the coldest quarter: bio 11, prediction of the coldest quarter: bio 19) of the 19 BioClim variables were considered when applying the SDMs (Table 1). For future climate data, we referred to the HadGEM2-AO climate model constructed by the National Institute of Meteorological Science for the publication of the Intergovernmental Panel on Climate Change (IPCC) Assessment Report 5 (AR5) for the 2050s (2041–2060) and 2070s (2061–2080) under the RCP 4.5 emission scenario (RCP 4.5). The HadGEM2-AO climate model is a general circulation model (GCM) with a spatial resolution of 135 km, and its bioclimatic variables were downscaled to a spatial resolution of 30 arcsec using version 1.4 of WorldClim for the actual analysis conducted for our detailed climate forecast in South Korea.

2.3 Species distribution ensemble modelling

BIOMOD2 provides an ensemble platform of ten SDM algorithms, and we initially used four of these as ensemble candidates. To model the potential land suitability for *T. koraiensis* in the future, the ensemble modelling was designed to consist of three different regression models [general additive model (GAM), generalized boosted model (GBM), and general linear model (GLM)] and a machine learning model [random forest (RF), provided by the BIOMOD2 package in R statistical language (Fig. 3).[16] We built individual models using default settings provided by BIOMOD2 version 3.4.1 and ensembled the outcomes of SDM simulations with true skill statistics (*TSS*) values over 0.8 to reduce the uncertainty of SDMs. This evaluation metric is an

Table 1
Bioclimatic variables used for species distribution models to predict the potential future distribution of targeted species.

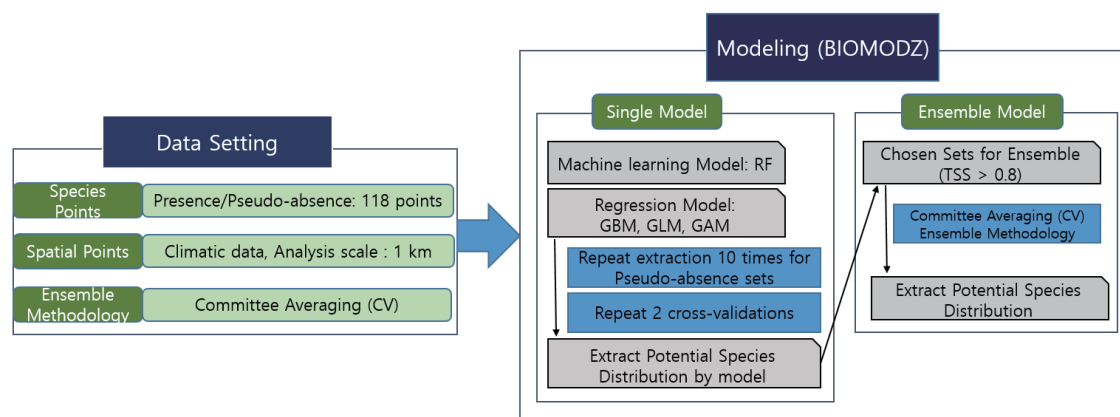| Factor	Variables	Meaning of Variables	Resolution
	Bio 5	Max Temperature of Warmest Month	
Climate factor	Bio 7	Temperature Annual Range (Bio 5-Bio 6)	30 arcsec
	Bio 11	Mean Temperature of Coldest Quarter	(1 km)
	Bio 19	Prediction of Coldest Quarter	

Fig. 3.   (Color online) Schematic representation of the ensemble species distribution modelling approach.

indicator of discrimination capacity and quantifies how well the model distinguishes presence from absence (or presence from background samples, when absence is unavailable). As held-out subsets of the original dataset are used for model evaluation (cross-validation) for partitioning data into subsets. SDM results represent the possibility of each species' occurrence in the form of a continuous distribution, implying the importance of the threshold in objectively determining the presence of a selected species for the integrity of the modelling results and their interpretation. In BIOMOD2, the cross-validation procedure was repeated two times for each of the 10 presence–absence groups.[17] The accuracy of a committee averaging (CV) ensemble methodology was evaluated using outer validation.

3. Results

3.1 Evaluation of the performance of various BIOMOD2 algorithms

The SDM platform and R package BIOMOD2 were used to explore the potential land suitability for *T. koraiensis* in the future. Also, by evaluating the performance of models, the receiver operating characteristic (*ROC*) and *TSS* were confirmed. The distribution habitats of *T. koraiensis* for both current and future climates were obtained by ensemble forecasting in the BIOMOD2 package by parameterizing *TSS* > 0.9 for individual models (Table 2). By comparing the *TSS* values, GBM, GLM, and RF (0.985 ± 0.011 − 0.988 ± 0.011) were found to perform better than the statistical GAM method (0.911 ± 0.109).

3.2 Contribution of the four predictor variables used to construct SDMs for *T. koraiensis*

As shown in Table 3, the importance of variables (environmental parameters) for SDM is presented. Among the four predictor variables under GAM and GLM, bio 5 (0.809 ± 0.066 and 0.997 ± 0.001, respectively) and bio 11 (0.977 ± 0.030 and 0.966 ± 0.054, respectively) contributed

Table 2
Mean and standard deviation of *ROC* and *TSS* for the models.

Model	*ROC* (0-1)	*TSS* (0-1)	*ROC* cutoff	Sensitivity	Specificity
GAM[1]	0.956 ± 0.055	0.911 ± 0.109	518.300 ± 200.352	93.333 ± 10.865	97.800 ± 27.800
GBM[2]	0.995 ± 0.006	0.985 ± 0.011	526.100 ± 174.66	100.000 ± 0.000	98.640 ± 1.117
GLM[3]	0.994 ± 0.007	0.985 ± 0.014	614.800 ± 213.223	100.000 ± 0.000	98.480 ± 1.432
RF[4]	0.995 ± 0.006	0.988 ± 0.011	329.600 ± 161.232	100.000 ± 0.000	98.760 ± 1.090

Table 3
Importance of variables (environmental parameters) for SDM.

Variable	GAM[1]	GBM[2]	GLM[3]	RF[4]
Bio 5	**0.809 ± 0.066**	0.197 ± 0.048	**0.997 ± 0.001**	**0.334 ± 0.026**
Bio 7	0.539 ± 0.025	**0.344 ± 0.027**	0.733 ± 0.131	**0.304 ± 0.030**
Bio 11	**0.977 ± 0.030**	**0.399 ± 0.039**	**0.966 ± 0.054**	0.292 ± 0.014
Bio 19	0.310 ± 0.050	0.086 ± 0.019	0.277 ± 0.080	0.147 ± 0.015

Each value is expressed as mean ± SD.

the most to the model predictions. In contrast, bio 19 contributed little to the predictive performance of the models among the four predictor variables under the four algorithms ($0.086 \pm 0.019 - 0.310 \pm 0.050$). Under GLM, bio 5 ($0.997 \pm 0.001$) and bio 11 ($0.966 \pm 0.054$) contributed the most to the model predictions, followed by bio 7 (0.733 ± 0.131). In summary, the dominant bioclimatic variables shaping the potential distribution of *T. koraiensis* are bio 5 and bio 11.

3.3.   Current and future potential distributions of *T. koraiensis* under RCP 4.5

The predicted distribution habitats of *T. koraiensis* for both current and future climates were revealed by the ensemble prediction (Fig. 4). The natural population of *T. koraiensis* currently spreads throughout Baekdu-degan including Gariwangsan, Gyebangsan, Jangsan, Taebaeksan, Hwahangsan, and Seoraksan. The predicted ensemble-averaged model showed the area loss of currently suitable habitats for *T. koraiensis,* yet the species is predicted to still exist in the future under RCP 4.5.

Under the RF models, the potential habitat distribution of *T. koraiensis* would be conserved under RCP 4.5 in the 2030s, 2050s, and 2070s. In particular, in the 2070s, an increase in the number of natural habitats of *T. koraiensis* is predicted. Similar to RF models, GLM models showed expanded natural populations of *T. koraiensis* throughout the Korean peninsula. Specifically, the areas near Mt. Halla on Jeju Island and Jirisan were identified as new potential habitats in the 2030s and 2050s. Yet, these predicted potential habitats of *T. koraiensis* were excluded in the 2070s owing to habitat loss across the Korean peninsula when considering the climatic conditions under RCP 4.5.
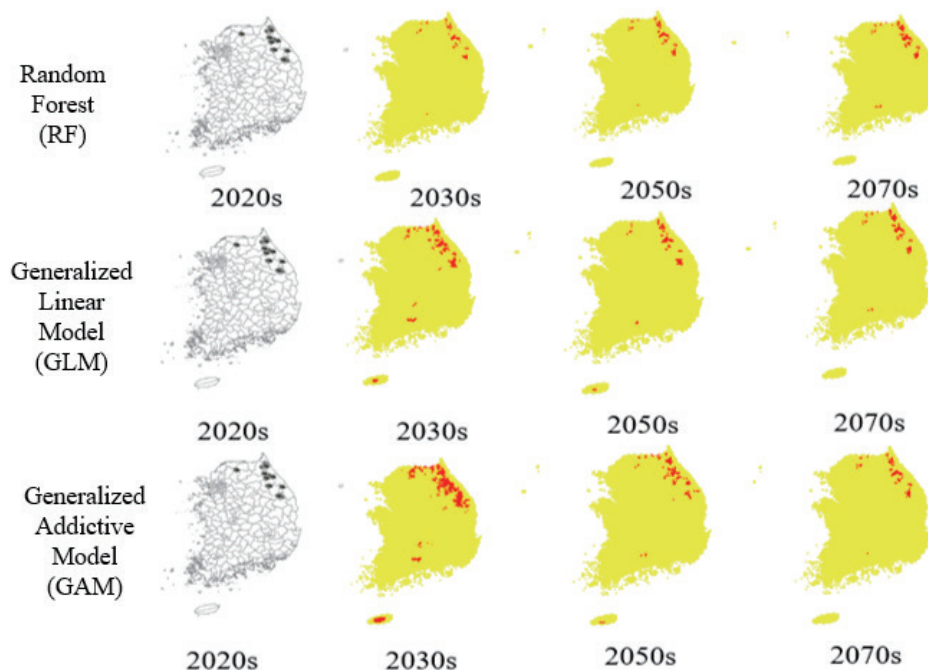

Fig. 4.   (Color online) Potential habitat distribution of *T. koraiensis* in the 2070s, predicted using single models under RCP 4.5.

The prediction results obtained with GAM showed a trend different from those obtained with RF and GLM. GAM predicted that the potential habitat for *T. koraiensis* will greatly expand in the 2030s owing to climate change. However, this expansion of natural habitats of *T. koraiensis* would decrease in the 2050s and 2070s. Similar to GLM, predicted potential habitats such as Mt. Halla on Jeju Island and Jirisan would be excluded in the 2070s.

4. Discussion

Climate has been altering rapidly in South Korea. Specifically, it is predicted that by 2070, the average temperature will increase by 1.3 to 5.2 °C, and the average temperature will increase by up to 29.6%.[18] Climate change is an important factor that regulates the growth and survival of trees.[19] SDMs are widely used to support the climate-adaptive program of threatened species as they suggest potential translocation sites.[9]

Global warming is altering the natural habitat environments, threatening the natural populations of *T. koraiensis* in South Korea. In this study, we used the multiple SDMs for the ensemble average method and predicted that *T. Koraiensis* is vulnerable to future climate change. Several algorithms in this study performed well with our data, showing that the results of using the four methods converged successfully with stable *TSS* results. *TSS* provides a threshold-dependent measure of accuracy and is readily applied for presence–absence predictions.[20]

Climate projections using three different models (RF, GLM, and GAM) were used to assess the potential habitat of *T. Koraiensis* under RCP 4.5. On the basis of the results of the screening of the SDMs, RF is selected to construct a high-precision ensemble model as it showed the highest *TSS* (0.988 ± 0.011). The common finding obtained using the three models was that climate change in the Korean peninsula under RCP 4.5 has an impact on the natural habitat of *T. koraiensis*, as shown by the area loss of the potential population. Above all things, the species is predicted to still exist in the 2070s under RCP 4.5. These findings will provide meaningful insights for the forest conservation and restoration strategies in response to climate change.

The conservation of endangered species needs to take full consideration of the potential habitat of the species and plant saplings in the right locations.[21] By analyzing the potential habitat of *T. koraiensis* in ensemble models, we found that there is still a significant amount of land with good potential for restoration. In this study, only climate factors were considered in the analysis, but further research is needed to include topographic factors such as altitude and soil information, as well as the various environmental factors that are suitable for the growth environment characteristics of *T. koraiensis*. Additionally, in order to conserve the natural habitat of *T. koraiensis* on the Korean peninsula, it is necessary to establish spatial information data for regions with similar suitable environmental conditions for *T. koraiensis* as potential distribution areas. Using the established database, we must initiate efficient management strategies for the protection and nurturing of *T. koraiensis* in response to climate change.

5. Conclusions

Climate change will affect ecologically sensitive areas, so it is crucial to manage its impact on various species. *T. koraiensis* is an endangered and ecologically important conifer endemic to South Korea. SDMs can support climate-adaptive forest restoration programs by predicting the effect of climate change on the future dispersal and distribution of targeted species. In this study, we used multiple SDMs in the ensemble average method for predicting the changes in the endangered native *T. koraiensis* populations in response to climate change. The predicted ensemble-averaged model showed the area loss of currently suitable habitats of *T. koraiensis,* yet the species was predicted to still exist in the 2070s under RCP 4.5. Furthermore, several algorithms in the BiOMOD2 ensemble performed well with our data, showing that the four methods converged successfully, presenting stable *TSS* results. Our study suggests that common results from different SDMs can be used as the basis for developing conservation strategies to protect the native rare *T. koraiensis* in South Korea. These findings would provide a long-term perspective for preparing protective strategies of vulnerable species against climate change.

Acknowledgments

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