Article

Exploring the Potential Distribution of Relic *Trochodendron aralioides*: An Approach Using Open-Access Resources and Free Software

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Abstract: *Trochodendron aralioides* Siebold & Zucc. is a relic tree that is discontinuously scattered across the mountainous areas of Japan, Taiwan, and South Korea, but the origin of *T. aralioides* in South Korea is still unclear and debated. To confirm its distribution and explore its origins, we constructed a streamlined framework to examine potential species distribution using multiple open access data and free and open-source software, as well as employing maximum entropy principles to predict the potential distribution of *T. aralioides*. The results showed reasonably good discrimination and were used to examine and discuss the explicit distribution of *T. aralioides*. The potential distribution of *T. aralioides* in Japan extended from Iriomote Island to approximately 37° N in Honshu on the Pacific Ocean side. In Taiwan, the potential distribution of *T. aralioides* was more common than in Japan. It occurred at 1500–3000 m a.s.l. across the Central Mountain Range and decreased toward the northern and southern tips, correlating to the descending pattern of the cloud belt. Thermal and moisture conditions were important factors to determine the distribution of *T. aralioides*. The potential distribution indicated that Jeju island had high potential as a habitat for *T. aralioides*, and that may indirectly imply its existence and origins in South Korea, as some researchers have noted.

Keywords: *Trochodendron aralioides*; species distribution modeling; open-access resources; free software; MaxEnt

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1. Introduction

Trochodendron aralioides Siebold and Zuccarini (Trochodendraceae Prantl) is a distinctive broad-leaved tree without a vessel in the woody tissue and is the only living species of this genus [1,2]. Although *Trochodendron* was widely distributed in the Northern Hemisphere during the geological ages in the past [3–6], the distribution of relic *T. aralioides* is currently restricted to East Asia [2]. In general, *T. aralioides* is distributed in the prevalent cloud zones of temperate or subtropical mountains in East Asia, but only a few distribution maps of *T. aralioides* were found in the Angiosperm Phylogeny web-site (<http://www.mobot.org/MOBOT/research/APweb/>; accessed on 19 September 2021) and GBIF georeferenced data map (<http://www.gbif.org/species/4191567>; accessed on 19 September 2021). The spatially explicit distribution of *T. aralioides* still remains to be further explored.

Whether *T. aralioides* is a native species in South Korea is not clear due to the inconsistent descriptions of its natural distribution in different sources. It has been consistently described as a native species in Taiwan and Japan. In Taiwan, *T. aralioides* is moderately

common in the prevalent cloud forests of the Central Mountain Ranges at 2000–3000 m above sea level (a.s.l.) and, in the northern part at 500–1050 m a.s.l., sometimes forms pure stands [7]. In the range of 2000–3000 m a.s.l. in Taiwan, the zonal vegetation comprises mixed needle-broad-leaved forests, in which the *T. aralioides* and *Chamaecyparis* species are significantly important, which indicates the significance of the humid environment [8]. In Japan, *T. aralioides* was found in the temperate zone [9], including in the Ryukyu Islands [10,11]. Interestingly, some literature has described the natural distribution of *T. aralioides* only in Taiwan and Japan [2,7,12,13], but others have included South Korea [6,10,11,14–17]. However, this question may be addressed through species distribution modeling (SDM) based on niche theory and can explain the discontinuous distribution of *T. aralioides*.

Recently, SDM has proven useful in the fields of ecology and biogeography for theoretical and applied purposes [18–21]. Theoretically, SDM is based on the ecological niche theory, and it combines statistical or machine learning techniques and geographical information technology to simulate the species–environment relationship. Therefore, SDM is a progressively important tool in the prediction of the spatial distribution of a species [19,22], and it can be applied in the field of biological conservation [19,23,24]. Many articles concerning and utilizing SDM have emerged during the past two decades. For example, typing “species distribution model*” in the search box of Thomson Reuters’ Institute for Scientific Information (ISI) reveals only 439 related articles during 1991–2010, but there were 6766 related articles from January 2011 to June 2021. However, SDM studies were heavily relied on for geographical information science (e.g., [25–27]), and thus these geographical information system (GIS) tools to process SDM datasets are necessary for researchers.

In the past two decades, the “free software” movement initialized a novel way of considering information technologies, especially those used in scientific research, and it suggested a more cost-effective method for the future of scientific research, rather than continuing to rely on proprietary third-party software. In this paper, “free” does not mean “free of charge”, but rather it refers to “freedom”. There are four essential freedoms involved in “free software”: (1) the freedom to use the software; (2) the freedom to study how it works and modify it to meet the needs of the user, which also means that it is open-source; (3) the freedom to redistribute the original software; and (4) the freedom to redistribute any user-modified source code (Free Software Foundation, <https://www.fsf.org>; accessed on 19 September 2021). Furthermore, the free software movement also helped to pave the way for data sharing, such as the recent open-data idea. For GIS tools, there are several free, modern GIS desktop software, such as GRASS (Geographic Resources Analysis Support System) GIS (<http://grass.osgeo.org>; version 7.2.3) and QGIS (<https://qgis.org>; version 3.2). Unlike the ArcMap and ArcDesktop series, most of the free GIS software are platform independent, i.e., usable on either a Windows, GNU/Linux, MacOS, or even BSD operating system. There are also several online open databases for biodiversity and ecological research, such as global biodiversity information facility (GBIF, URL: <http://gbif.org>; accessed on 19 September 2021), WorldClim climate database (URL: <https://worldclim.org>; accessed on 19 September 2021) [28] and free high-resolution global climate database CHELSA (URL: <https://chelsa-climate.org>; accessed on 19 September 2021) [29]. Access to these freely available online resources has made scientific research easier to complete [30–33]. Moreover, the prevalence of smart phones has engaged citizen scientists in data collection via crowd-sourcing using platforms, such as iNaturalist [34], which employs a “research grade” to lower the risk of errors (e.g., non-captive/cultivated species with more than two user-community identifications with two-thirds of the community members in concordance); the platform’s aggregated data automatically export and integrate into the GBIF databases. In this study, we addressed the following topic and hypotheses: (1) propose an approach of using open-access data and free software, as well as other free tools, to process GIS data for species distribution models, and (2) determine the spatial distribution patterns of *T. aralioides* in East Asia, and which important variables have determined its distribution.

2. Materials and Methods

2.1. Target Species

Trochodendron aralioides Siebold & Zucc. (Trochodendraceae), more commonly referred to as an “evergreen” tree, is 5–25 m tall and glabrous with stout branches and terminal buds with paper-like scales. The leaves are crowded at the ends of the branches, almost whorled, 5–15 cm × 2–8 cm, broadly ovate to lanceolate–elliptic or rarely elliptic, and are dark lustrous green adaxial surface with a pale abaxis. Flowers are bisexual, 1–2 cm in diameter, without petals, and with the radiative-spreading of 40–75 stamens surrounding the 5–11 carpels. They flower in March–June. The fruits mature in late August. More detailed descriptions have been reported by Watson and Dallwitz [35], Li and Chaw [7], Andrews [14], Fu and Endress [1], among others.

2.2. Target Area

Given that the natural distribution of *T. aralioides* has been restricted to East Asia, the study area ranged from 119° E to 146° E and 21° N to 46° N. The modeling area covered all distributions denoted in the related literature (e.g., [1,2,7,14]), including Taiwan, Japan (excluding Hokkaido), and South Korea, but excluding China (see Figure 1 for occurrences and distribution area).

Figure 1. Study area and verified occurrences (806 points) of *Trochodendron aralioides*.

2.3. Open-Access Resources and Free Software

Many open-access resources can be accessed via the Internet, including geographical data and software. In this paper, we used the following five freely available online resources (Table 1) to model the distribution of *T. aralioides*. Figure 2 shows the flowchart of the integrated applications.

2.3.1. Species Occurrences

Since the number of occurrences in Japan was relatively small in the Global Biodiversity Information Facility (GBIF) database, we merged it with the occurrence data from the Phytosociological Relevé database (PRDB). PRDB is a phytosociological database composed of relevé data throughout Japan, while the original data sources were digitized from a variety of published and unpublished literature [36]. GBIF was established by recommendation from the Organization for Economic Cooperation and Development in

2001 to encourage free and open access to biodiversity data. Through a global network of countries and organizations, GBIF promotes and facilitates the mobilization, access, discovery, and use of biodiversity information across spatial and temporal scales. Therefore, many researchers (e.g., Guralnick et al. [37]; Porretta et al. [38]) have used records sourced from GBIF search results to represent species occurrence samples, and many front-end interfaces have been developed with programming languages R, Python, and Ruby to access GBIF occurrence data [39]. Since the data were collected by different methods and the data quality would be important for accurate modeling, we adopted the data-cleaning framework employed by Maletic and Marcus [40], which included three steps: (1) to define error types, (2) to identify error instances, and (3) to correct the defined errors. Chapman (2005) also introduced several data-cleaning principles for biodiversity spatial data, such as verifying georeferences against other information, and checking spatial accuracy against other information using GIS, etc. In this study, we defined three error types: (1) occurrence data out of the target area, such as occurrences in the United Kingdom; (2) impossible locality, such as for occurrences in the Pacific Ocean; and (3) duplicate entries. We used QGIS to test for and remove the aforementioned errors to ensure the accuracy of the data used for modeling.

2.3.2. Environmental Variables

High-resolution climate data are essential for ecological studies at a global or regional scale, and interpolation methods are typically required with meteorological station data, such as PRISM, WorldClim [28], and CHELSA [29], etc. Many researchers have used WorldClim layers as environmental variables, such as Ashraf et al. [41], Meneguzzi et al. [42], Porto et al. [43], and Rupprecht et al. [44]. However, the CHELSA datasets integrate wind and topological factors to correct for bias, which is why they are considered more robust and accurate than WorldClim datasets [29]. CHELSA provides global climatic layers down-scaled to 30 arcseconds (~1 km), which are therefore more precise than the other free global climate databases, such as CliMond [45], for ecological modeling and geographic information system. The climate conditions data include monthly precipitation; mean, minimum, and maximum temperature, as well as altitude; and 19 bioclimatic layers; however, some of the environmental factors are estimated [44]. Therefore, the most common method of variable selection for SDM was based on pairwise Pearson correlation coefficients [46,47]. We excluded bioclimatic variables that had a correlation coefficient > 0.75. However, the determining climatic variables of *Trochodendron aralioides* were still unclear, so we also used jackknife resampling analysis (a leave-one-out resampling technique to evaluate the environmental variables) to assess the most important variables for model building.

Table 1. Open-access resources used in this study for species distribution modeling.

Data or Tool	URL ¹	Service	License/Access
GBIF	https://www.gbif.org/	Supplying biodiversity data as species dataset	CC0 ² , CC BY or CC BY-NC
iNaturalist ³	https://inaturalist.org/	Crowdsourcing biodiversity occurrences	CC BY, CC BY-NC
WorldClim	https://www.worldclim.org/	Supplying high-resolution bioclimatic and elevation layers as environment datasets	Free download. No distribution
CHELSA	https://chelsa-climate.org	Supplying high-resolution bioclimatic and elevation layers as environment datasets	CC BY 4.0
GRASS GIS	https://grass.osgeo.org/	GIS data processing	General Public License (GPL)
QGIS	https://qgis.org/	GIS data processing	GPL version 2
PostGIS	https://postgis.net	GIS data processing (integration with QGIS)	GPL version 2
R	https://www.r-project.org	Statistical computing and data preprocess/postprocess	GPL version 2/3
MaxEnt	https://biodiversityinformatics.amnh.org/open_source/maxent/	modeling the species distribution through species-environment relationships	MIT License

¹ Accessed on 19 September 2021. ² CC = Creative Commons License; CC0 = public domain; CC BY = CC attribution; NC = non-commercial.

³ The “research grade” observations periodically exported to GBIF.

Figure 2. Flowchart of modeling species distribution through an integrated application of open-access resources.

2.3.3. GIS: GRASS GIS and QGIS

GRASS GIS is a free GIS software used for geospatial data management and analyses, image processing, cartographic production, spatial modeling, and visualization. GRASS has been developing for more than 34 years, and it includes many geographical algorithms that have been used regularly for environmental modeling [48]. QGIS is also a free GIS desktop software; in addition to its tools for vector and raster processing, the most advanced feature is that it can function as a wrapper of third-party GISs (e.g., call the function or programs of GRASS GIS, Saga GIS, PostgreSQL/PostGIS or even R programs while working inside QGIS). In this study, we used QGIS as the main GIS processing tool and called GRASS functions by a GRASS plugin.

2.3.4. MaxEnt

MaxEnt is a machine-learning method based on maximum entropy principles, and its presence-only method is suitable for species investigation datasets [49]. Although there are many SDM techniques [19,20,50], MaxEnt was selected to model the potential distribution of *T. aralioides* for the following two reasons. First, the accuracy associated with occurrences has been a common concern when using location data [51,52]. The spatial positions of *T. aralioides* in GBIF have often been in error. MaxEnt is more robust than other methods, especially in regression-based modeling, in spatial errors of species occurrence [53]. Second, the sample size (occurrence records) of *T. aralioides* is relatively small in the scale of East Asia. MaxEnt has performed better than other methods with small sample sizes [44,54,55].

2.4. Model Building and Validation

We developed the SDMs with MaxEnt, version 3.4.1, using nine important environmental variables and cleaned data. Before predicting our model, we used the ENMeval package of R to evaluate and test a range of parameters to optimize MaxEnt's model parameters [56,57]. We randomly created 10,000 background points and applied a checkboard2 algorithm to create spatial blocks in order to avoid model-overfitting issues in MaxEnt. A set of features including linear (L), quadratic (Q), product (P), threshold (T), and hinge (H) as well as regularization multipliers (RMs) from 0.25 to 1.5 with 0.25 intervals were tested in the ENMevaluate function and to calculate the corrected Akaike information criterion (AICc) and determine an optimized model. Furthermore, in order to achieve statistical significance, we also executed 100 replications with 5000 iterations per replication in MaxEnt to obtain the mean probability of the potential distribution map.

We used the area under the receiver operating characteristics curve (AUC); a threshold-independent method that characterizes the performance of a model at all possible thresholds by a single number to evaluate the modeling performance [49]. The modeling performance was categorized into three classes, as described by Swets [58]: poor discrimination ($0.5 < \text{AUC} < 0.7$), reasonable discrimination ($0.7 < \text{AUC} < 0.9$), and very good discrimination ($0.9 < \text{AUC} < 1.0$). However, several studies reported that the AUC would not be a good measure of performance in SDMs [59,60], so we also used the AICc from the ENMeval package to increase the discrimination of the model.

3. Results

3.1. Species Dataset

The numbers of *T. aralioides* records contained in the PRDB and GBIF database obtained in July 2018 were 529 and 1729, respectively (Table S1 from Supplementary Materials). Among them, only 943 records had been georeferenced. We excluded 214 occurrences based on a point-in-polygon check (i.e., joining attributes by location in QGIS) and data-cleaning procedures (e.g., remove duplicates, doubtful records, etc.) available in the QGIS and PostgreSQL databases. Besides the outliers of occurrences, there were several plots located in residential areas, such as in a garden or a park. Therefore, we had 806 occurrence records of *T. aralioides* with verified coordinates as the species dataset, with 308 records in Taiwan, 498 records in Japan, and none in South Korea (see Figure 1). The species-occurrence samples were exported from the PostgreSQL database via a comma-separated-values (.csv) file, which served as the input data for MaxEnt. The 806 samples were located within an area of occurrence spread across 683 modeling environmental grids (with a resolution of 30 arcseconds) due to the occurrence of several records in the same grid. Table 2 presents the statistical summary of the bioclimatic layers in our modeling area and in the occurrence grids.

3.2. MaxEnt Modeling and Performance

The ENMevaluate results revealed that the lowest AICc (18,897.19) was the combination of LQ and LQPT features with an RM = 0.25 (Figure S1). The average tested AUC was 0.8821, and the trained AUC was 0.8873. The distribution modeling by MaxEnt for *T. aralioides* obtained reasonable discrimination with an AUC mean value of 0.8577 (0.6738–0.9733) for the training data and 0.8588 (0.8555–0.8619) for the testing data. The modeling distribution map of *T. aralioides* is shown in Figure 3. The highest probabilities of predicting hot spots were in the Central Mountain Range in Taiwan (including the low elevation areas of the northern and southern tips that include winter northeast monsoon-facing slopes); the mountainous ranges of Honshu, Shikoku, Kyushu, Yakushima Island, and Iriomote Island in Japan; and Jeju Island in South Korea. Figure S2 shows the results of the jackknife test and the training gains for evaluating the relative contributions of the predictor environmental variables for the MaxEnt *T. aralioides* model. The estimates of the relative contributions of five environmental variables are given in Table S2. Based on the permutation importance, the most important variables were BIO5, BIO12, and BIO1, explaining 36.4, 30.8, and 12.7

of variation in the distribution of *T. aralioides*, respectively. The aforementioned three variables contributed to almost 80% of our model; the other variables had relatively low contributions in terms of permutation importance. The response curves, shown in Figure 4, further detailed how each of the environmental variables altered the model prediction.

Table 2. Statistical summary of environmental variables for modeling area and for all grids of *T. aralioides* occurrences.

Environmental Variable	Modeling Area		Occurrence Grids	
	Mean	SD	Mean	SD
BIO1 (annual mean temperature) *	13.5	3.5	13.1	3.4
BIO2 (mean diurnal range) *	5.9	1.5	5.0	1.6
BIO3 (isothermality) *	20.7	3.7	22.8	6.2
BIO4 (temperature seasonality)	774.3	133.32	593.5	182.0
BIO5 (max temperature of warmest month) *	27.5	2.56	24.0	3.5
BIO6 (min temperature of coldest month)	−0.6	5.3	1.8	5.4
BIO7 (temperature annual range)	28.1	4.7	22.2	6.2
BIO8 (mean temperature of wettest quarter) *	21.6	5.4	19.2	3.3
BIO9 (mean temperature of driest quarter)	5.1	6.0	6.6	5.4
BIO10 (mean temperature of warmest quarter)	24.4	2.7	21.3	3.6
BIO11 (mean temperature of coldest quarter)	2.9	4.9	5.0	4.8
BIO12 (annual precipitation) *	1724	542.8	2684.2	940.4
BIO13 (precipitation of wettest month)	281.3	99.4	426.4	170.9
BIO14 (precipitation of driest month) *	60.1	35.0	97.4	65.1
BIO15 (precipitation of seasonality)	51.4	21.0	48.7	17.6
BIO16 (precipitation of wettest quarter)	786.7	270.0	1180.7	449.6
BIO17 (precipitation of driest quarter)	192.5	107.7	312.1	203.8
BIO18 (precipitation of warmest quarter) *	667.5	230.1	937.4	342.8
BIO19 (precipitation of coldest quarter) *	232.8	153.4	364.7	233.9

* denotes the selected variables for modeling *T. aralioides* distribution in MaxEnt.

Figure 3. The potential distribution map of *Trochodendron aralioides* modeled by MaxEnt. (a) An enlarged map of Jeju Island in South Korea and (b) the enlarged map of Yakushima Island in Japan.

Figure 4. The response curves of logistic prediction changes of the environmental variables. The black curve represents the average of 100 replicates while the gray background indicates the range of values: (a–e) x -axis unit, °C and (f–i) x -axis unit, mm.

4. Discussion

4.1. Data Quality for Species Occurrence

GBIF was the largest single source of global biodiversity occurrence data. In this study, there were 1729 records of *T. aralioides* accessed from GBIF's online database, but 786 (~45%) records did not have georeferenced information. Most of these non-georeferenced records were obtained from herbariums and museums prior to the invention of global positioning systems and would likely have temporal sampling biases [61,62]. Comparatively, the PRDB data had better quality overall, as compared to the GBIF data (e.g., only 10 occurrences showed georeferenced errors, ~2%), particularly since most of the occurrence records were based on a phytosociological survey and were digitized from herbarium specimens with low geographical resolution. Furthermore, among the 943 GBIF records with georeferenced information, 444 (47%) records did not pass geographic validation tests or were determined to be duplicates through the data cleaning process in QGIS (Table S1). This determination

was made based on conditions noted by Yesson et al. [63], including undersea coordinates and georeferenced errors, as well as conditions considered in this study, including coordinates located in distinctly residential areas and improbable altitudes (e.g., ranging 300–3000 m a.s.l. in Taiwan) [1,7,64]. The spatial bias of the species records had been widely discussed regarding both theoretical errors and real cases [63,65–69]. Filtering out these biases in occurrence records would be a pioneering achievement as the bias data heavily influences the accuracy and reliability of the SDMs [70–72]. Of the 308 acceptable records in Taiwan, 217 (70.5%) were from vegetation diversity inventories and mapping plans (Chiou et al. [73]; also see Table S1, GBIF dataset key: 9edd4990-4138-11de-b28f-b8a03c50a862). Therefore, integrating vegetation inventory databases, such as the Global Index of Vegetation-Plot Databases (<http://www.givd.info>; accessed on 19 September 2021) with the 313 databases and 3,630,327 plots registered (date accessed: October 2021), into the GBIF database was a critical factor for broadening and refining biodiversity occurrence data [74,75].

4.2. Distribution of *T. aralioides*

4.2.1. Japan

As shown in Figure 3, *T. aralioides* was distributed across the mountains of Honshu, Shikoku, and Kyushu. The northeast occurrence of *T. aralioides* was on the Iwate Prefecture, but there was only one point that would need further validation. However, the probable northern limit of *T. aralioides* was near Yamagata City, Yamagata Prefecture, such as in Mount Funagata and Mount Zao, at approximately 38° N as denoted by Wu et al. [13]. Around 35° N, *T. aralioides* occurred on the piedmont slopes of Mount Fuji and the southern parts of the Akaishi and Kiso Mountains, but not on the alpine slopes where coniferous trees were dominant. In addition to the mainland of Japan, *T. aralioides* also occurred on the Izu [76] and Ryukyu Islands [6,7,10,14–16]. On Yakushima Island (30.2° N, 130.3° E, Figure 3b), which is one UNESCO's World Heritage Sites largely due to its unique vegetation, *T. aralioides* was a frequent feature in forest vegetation at 500–1800 m a.s.l., along with *Cryptomeria japonica* D.Don and *Tsuga sieboldii* Carrière [77–82].

Our results indicated that temperature-related variables, such as BIO5, were very important based on our models, and BIO5 was a limiting factor for the lower or southern distribution of *T. aralioides*. The potential distribution map (Figure 3) also showed the same pattern, while highly potential habitats were located on the Pacific side of the Honshu region. Figure 4d shows the probability of *T. aralioides* abruptly decreasing under BIO5 > 23 °C conditions. However, the precipitation-related variables, such as BIO12 (annual precipitation) also played important roles in the distribution of *T. aralioides* (see Figure 4f), but they required further research that was outside the scope of this study. Comparing the altitudinal ranges of *T. aralioides* in Japan and Taiwan (Huang et al. [83]; also see Table S1), *T. aralioides* in Japan (at high latitudes) occurred at lower altitudes than those in Taiwan (at low latitudes). Therefore, the thermal conditions were critical factors in *T. aralioides* distribution.

4.2.2. Taiwan

In contrast with the potential *T. aralioides* distribution in Japan, the distribution was relatively wide in Taiwan. It was moderately common in the mid-altitude forests of the Central Mountain Range [7], in the 1500–3000 m a.s.l. regions. Wu et al. [13] noted that central Taiwan was a probable refuge for *T. aralioides* during the last glacial periods due to those populations having the greatest genetic diversity. The altitudinal range of *T. aralioides* decreased considerably to the north and south [8,13,64,83,84]. As shown in Figure 3, the lowest altitude of *T. aralioides* distribution was at approximately 400 m a.s.l. in the northern region, then gradually increased up to 1300 m a.s.l. in the central region, and then finally descended to 500 m a.s.l. in the southern region. The altitudinal pattern of *T. aralioides* has been correlated with the position of cloud belts [8]. *T. aralioides* favor cool, humid habitats. In Japan, for example, *T. aralioides* tended to occur in steep slopes and

sometimes near bodies of water in the mountains, whereas in Taiwan, it had extended widely across the mountainous regions, where cloud belts are known to form. *T. aralioides* has been considered as an indicator for prevalent cloud zones where *Quercus* oak trees may also be found [8]. Within the cloud belt of the Central Mountain Range, *T. aralioides* is typically mixed with coniferous trees (e.g., *Chamaecyparis formosensis* Matsum. and *Cunninghamia konishii* Hayata) and other broad-leaved trees (e.g., *Quercus morii* Hayata and *Neolisteia* spp.; [8]). In the northern and southern regions of Taiwan, *T. aralioides* occurred in areas coinciding with cloud belts, but where coniferous trees were absent, suggesting that both were subject to thermal conditions. In this study, we used the novel effective warmth index (EWI), which associates the temperature sum with the thermal seasonality [85], to describe the *T. aralioides* habitat and applied the equal training sensitivity and specificity logistic threshold test [86] to classify our model predictions into suitable and unsuitable habitats. As shown in Figure 5, EWI = 160 isoline (yellow line) approximately matched the lowest limit of *T. aralioides* highly suitable habitat in the Central Mountain Range. Consequently, the distribution of *T. aralioides* was related to thermal variables and seasonal precipitation rather than to a simple climate factor.

Figure 5. The overlap map of the *T. aralioides* habitat and the effective warmth index (EWI, EWI = 100: black dotted line; EWI = 40: black line) approximately matched the lowest and highest limit of *T. aralioides* potentially suitable habitats in the Central Mountain Range. Black dots are occurrences.

4.3. *T. aralioides* in South Korea?

There were two opposing views regarding whether *T. aralioides* is native to South Korea or not. Most of the literature [6,10,11,15,16,87] has noted that the natural distribution of *T. aralioides* includes Taiwan, Japan, and South Korea. However, Wu et al. [13] and Andrews [14] opposed this point of view, as did Korean scientist Koh [88], all of whom agreed that *Trochodendron aralioides* did not originate on the Korean peninsula and its adjacent islands, though many foreign publications have suggested that this species could be found in the southern part of Korea. Furthermore, the flora identified in the Hallasan Natural Reserve in Jeju island did not include *T. aralioides* [89]. However, our results (Figure 3a) showed that Jeju Island in South Korea had a high probability (around 0.7–0.8) of *T. aralioides*. Nonetheless, whether *T. aralioides* is native to South Korea could not be determined and will require additional research.

On one hand, *T. aralioides* may not be native in South Korea. Our SDM was based on the concept of the realized niche [90] despite the arguments of Pearson and Dawson [91], as well as Soberón [92]. The probability of occurrence did not represent the real occurrence because the actual range was part of the potential range [93,94]. However, our SDM did not consider the potential effects of biotic exclusion, historical contingency, dispersal limitations, land usage, or species ranges that restrict the geographic expression of the fundamental niche [95,96]. Thus, Jeju Island may be a suitable habitat for *T. aralioides*; even so, *T. aralioides* may never have spread to there. On the other hand, *T. aralioides* may be native in South Korea. Brown et al. [97] noted that species tended to prosper in the center of their distribution and become rarer and more restricted to specific habitats towards the distribution margins. Our results indicated Jeju Island was a potential habitat of *T. aralioides*, but the presence of *T. aralioides* on the island has never been verified. However, an undiscovered or unrecorded species cannot prove a negative, i.e., that *T. aralioides* has never existed on Jeju Island. To answer the question about *T. aralioides*' native origins in South Korea, we could perhaps examine the surveys of Jeju island, especially the natural vegetation in Hallasan National Park. The discovery of a new species requires effort (e.g., vegetation surveys, specimen collections, time, etc.) and, in many cases, fortunate circumstances. In addition, it is possible that *T. aralioides* found refuge in central Taiwan during the last glacier period [13] and has not yet migrated to and settled in South Korea. Since one of the largest GBIF species occurrence datasets can be found in iNaturalist research-grade data, future research should consider further investigation concerning the origins and spread of *T. aralioides* in South Korea, namely on Jeju Island.

5. Conclusions

Trochodendron aralioides is an important indicator of prevalent cloud zones in Taiwan as well as *Chamaecyparis* species, whose disjointed distribution also reflects the historical impacts of prior climate changes. This study constructed a streamlined framework to predict the potential distribution of *T. aralioides* by applying species distribution modeling with multiple free software and open data sources. Our results showed that the most important environmental variables that influence the distribution of *T. aralioides* were BIO5 (maximum temperature of the warmest month), BIO12 (annual precipitation), and BIO1 (annual mean temperature), which implied that the maximum temperature of the warmest month would be the limitation factor and may be vulnerable to climate changes. In general, the distribution of *T. aralioides* in Japan was not common, except in the mountainous area of Yakushima Island. It was, however, common in the cloud zones in Taiwan. Therefore, conservation strategies can be developed based on the potential distribution probabilities of different countries. Regarding the uncertainty about the origins of *T. aralioides* in South Korea, we suggest that future research should consider examining Jeju island further, based on the results of our SDM, and develop a complete distribution map according to free, expansive data sources, such as iNaturalist.

Supplementary Materials: The following are available online at <https://www.mdpi.com/article/10.3390/f12121749/s1>, Table S1: The occurrence table of *Trochodendron aralioides*, Table S2: Average relative contribution and permutation importance of the environmental variables of the MaxEnt model, Figure S1: Delta AICc of regularization multipliers for optimization of models, Figure S2: Results of jackknife analyses of regularized training gain (a) and test gain (b) for *Trochodendron aralioides*.

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