




# Emergence and Potential Spread of Rust Disease on *Wisteria floribunda* and *Corydalis incisa* Influenced by Climate Change in Korea

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## ABSTRACT

Global climate change influences the emergence, spread, and severity of rust diseases that affect crops and forests. In Korea, the rust diseases that affect *Wisteria floribunda* and its alternate host *Corydalis incisa* are rapidly spreading northwards. Through morphological, molecular, phylogenetic, and pathogenicity approaches, *Neophytopella kraunhiae* was identified as the causal agent, alternating between the two host plants to complete its life cycle. Using the maximum entropy model (Maxent) under shared socioeconomic pathways (SSPs), the results of this study suggest that by the 2050s, *C. incisa* is likely to extend its range into central Korea owing to climate shifts, whereas the distribution of *W. floribunda* is expected to remain unchanged nationwide. The generalized additive model revealed a significant positive correlation between the presence of *C. incisa* and the incidence of rust disease, highlighting the role that climate-driven expansion of this alternate host plays in the spread of *N. kraunhiae*. These findings highlight the profound influence of climate change on both the distribution of a specific plant and the disease a rust fungus causes, raising concerns about the potential emergence and spread of other rust pathogens with similar host dynamics.

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## 1. Introduction

Rust diseases, increasingly emerging and causing damage to major crops and trees, are on the rise across the globe [1–4]. This increase is primarily linked to climate change, as it often establishes favorable conditions for rust fungi, posing threats to food security and natural ecosystems, such as forests [5–7]. However, the specific mechanisms by which climate change contributes to the emergence and spread of rust diseases remain poorly understood. This lack of understanding stems from all rust fungi being obligate biotrophs, meaning that they require a living host to complete their life cycles. Additionally, the complex life cycles of many rust species, which alternate between two unrelated host plants add to the lack of understanding of their epidemiology and dynamics [8].

*Wisteria* spp. (Fabaceae) are woody vines that are native to East Asia and North America. They are cultivated globally as ornamental trees because of their showy inflorescences and climbing growth habits. *Wisteria floribunda* is a popular wisteria with

many commercially available cultivars. In Korea, the vine is distributed nationwide and grown for ornamental purposes and as a natural shade tree in various public spaces, such as gardens, parks, and schools. In addition, they are planted to stabilize artificially cut slopes and reduce the risk of landslides [9].

To date, few fungal diseases have been reported on *W. floribunda* globally. These include rust (caused by *Neophytopella kraunhiae*), powdery mildew (*Erysiphe polygoni* and *Erysiphe trifoliorum*), leaf spot (*Cercospora muelleriana* and *Pseudocercospora wisteriicola*), and anthracnose (*Colletotrichum destructivum*) [10]. The rust affecting *W. floribunda* was initially associated with *Ochropsora kraunhiae* (= *N. kraunhiae*) in Japan [11]. This fungus is a heteroecious species that alternates between two different hosts during its life cycle, forming uredinal and telial stages on *Wisteria* spp. Later, Hiratsuka and Kaneko [12] verified *Corydalis* species (Papaveraceae) as a spermogonial and aecial host of *Aecidium corydalinum* based on a pathogenicity test. This epithet is now recognized as synonymous with *N. kraunhiae*.

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In Korea, the emergence of rust disease on *W. floribunda* was first reported in September 2016. Both uredinial and telial symptoms of the disease were found on the leaves of *W. floribunda* in an arboretum in Jeju, Korea. By April 2019, *Corydalis incisa*, growing near the infected wisteria began showing signs of infection, including spermogonial and aecial symptoms. Since these initial discoveries, the rust disease has consistently affected these two species. Global warming is fueling the spread of *C. incisa* across Korea [13,14]. The expansion of this alternate host could potentially enhance the occurrence and spread of wisteria rust, particularly in the central regions of the Korean Peninsula. Therefore, a predictive model is required to assess the effects of *C. incisa* expansion on the occurrence and spread of its rust agent under the influence of climate change. Although existing predictive models offer valuable information on some rust species [15–17], developing more refined predictive models remains vital to thoroughly comprehend their epidemiology.

The goal of this study was to identify the rust agent on *W. floribunda* and *C. incisa* based on morphological characteristics, molecular sequence data, and a pathogenicity assay. Additionally, this study aimed to investigate the potential spread of wisteria rust in Korea by simulating how climate change could affect the distribution of *W. floribunda* and its alternate host, *C. incisa*, and exploring the correlation between the climate change-driven distribution of these hosts and the occurrence of wisteria rust.

## 2. Materials and methods

### 2.1. Rust samples

Rust occurrence on *W. floribunda* and *C. incisa* was investigated through extensive field surveys conducted across Korea from 2016 to 2022. The confirmed presence of rust was charted geographically to generate a distribution map. All collected voucher specimens were housed at the Korea University Herbarium (KUS) and Kunsan National University Herbarium (KSNUH) in Korea (Table 1).

### 2.2. Morphological analysis

The rust symptoms and sorus structures on freshly infected leaves were observed under a dissecting microscope (M205C; Leica, Wetzlar, Germany). Specific characteristics, such as the shape and size of spores were analyzed and photographed under a differential interference contrast light microscope (Axio Imager 2; Carl Zeiss, Oberkochen, Germany). Length, width, and wall thickness measurements

were obtained from 50 spores in each sample, and the results were reported as maximum, minimum, and mean values. Additionally, microscopic details, such as sorus shape and spore wall ornamentation, were observed and photographed using a scanning electron microscope (S-4800 + EDS; Hitachi, Tokyo, Japan).

### 2.3. Molecular phylogenetic analysis

For molecular phylogenetic analysis, genomic DNA was extracted from rust-infected leaves using a MagListo 5M Plant Genomic DNA Extraction Kit (Bioneer, Daejeon, Korea). PCR amplification was performed for the internal transcribed spacer (ITS) and large subunit (LSU) rDNA regions using primer pair ITS5u/ITS4rust [18,19] and LRust1R/LRust3 [18], respectively. The PCR products were purified using AccuPrep<sup>®</sup> PCR/Gel Purification Kit (Bioneer, Daejeon, Korea) and sequenced by a DNA sequencing service (Macrogen, Seoul, Korea) with the primers used for amplification. The resulting sequences were edited using DNASTAR software version 7 (Lasergen, Madison, WI, USA) and deposited in GenBank (Table 1). To compare the sequences, we performed a BLASTn search against the reference sequences of *Neophytopella* species available in GenBank. The ITS and LSU sequences were aligned using MAFFT version 7 [20]. A phylogenetic tree was reconstructed using the maximum-likelihood method based on the Tamura-Nei model in MEGA 7 [21]. The robustness of the individual branches was estimated by bootstrapping 1000 replicates.

### 2.4. Pathogenicity test

For the pathogenicity test, aeciospores were harvested from rust-infected leaves of *C. incisa* using a spore collector (Tallgrass Solutions Inc., Manhattan, NY, USA) and then placed onto 1 cm<sup>2</sup> sections of moistened filter paper (CHM Lab, Barcelona, Spain). Each paper section contained av. 500 aeciospores and three sections were placed on the lower surfaces of three healthy leaves of *W. floribunda* in Petri dishes. Three non-inoculated leaves served as controls. Inoculated and non-inoculated leaves were kept in an incubator at 90% humidity and 20°C for 3 weeks.

### 2.5. Distribution modeling of rust and host plants

To predict the potential distribution of *N. kraunhiae*, we employed the maximum entropy model (Maxent)

**Table 1.** The information on *Neophytopella kraunhiae* specimens used for morphological and phylogenetic analysis.

Host plant	Herbarium specimen	Locality in Korea	Coordinates	Date	GenBank accession no.	
					ITS	LSU
<i>Wisteria floribunda</i>	KUS-F29420	Jeju; Halla Arboretum	35° 2'48.24"N, 126°42'38.82"E	Sep 06, 2016	—	—
	KUS-F29606	Mokpo; Mt. Yudalsan	34°47'30.75"N, 126°22'20.48"E	Oct 20, 2016	—	—
	KUS-F29648	Naju; Jeongyeolsa Shrine	35° 2'48.24"N, 126°42'38.82"E	Nov 03, 2016	OR524168	OR512006
	KUS-F30156	Jeju; Halla Arboretum	33°28'11.74"N, 126°29'35.68"E	Oct 12, 2017	OR524169	OR512007
	KUS-F30308	Seoul; Hongneung Arboretum	37°35'35.05"N, 127°2'37.26"E	Nov 04, 2017	—	—
	KUS-F30410	Jeju; Mt. Sarabong	33°31'4.26"N, 126°32'41.87"E	Nov 23, 2017	OR524170	OR512008
	KUS-F30822	Jeju; Halla Arboretum	33°28'11.74"N, 126°29'35.68"E	Oct 18, 2018	—	—
	KUS-F30830	Jeju; Halla Arboretum	33°28'11.74"N, 126°29'35.68"E	Oct 18, 2018	—	—
	KUS-F30857	Mokpo; Mt. Yudalsan	34°47'30.75"N, 126°22'20.48"E	Nov 15, 2018	OR524171	OR512009
	KUS-F32102	Seoul; Mt. Namsan	37°33'11.48"N, 126°59'4.74"E	Oct 25, 2020	OR524172	OR512010
	KUS-F32536	Wanju; Gosan Recreation Forest	35°57'35.00"N, 127°14'8.00"E	Oct 15, 2021	—	—
	KUS-F32583	Naju; Jeongyeolsa Shrine	35° 2'48.24"N, 126°42'38.82"E	Nov 01, 2021	—	—
	KUS-F33805	Dongducheon; Mt. Soyosan	37°56'46.87"N, 127°4'10.52"E	Sep 19, 2023	—	—
	KUS-F33814	Seoul; Buamdong	37°35'37.28"N, 126°58'6.70"E	Sep 23, 2023	—	—
	<i>Corydalis incisa</i>	KUS-F30855	Jeju; Halla Arboretum	33°28'11.74"N, 126°29'35.68"E	Apr 16, 2019	OR524167
KUS-F32708		Wanju; Songgwangsa Temple	35°53'4.26"N, 127°14'34.82"E	Apr 11, 2022	OR524173	OR512011
KUS-F32745		Wanju; Gosan Recreation Forest	35°57'35.00"N, 127°14'8.00"E	Apr 22, 2022	OR524174	OR512012
KUS-F32751		Wanju; Sanggwan Recreation Forest	35°44'22.75"N, 127°12'24.43"E	Apr 23, 2022	OR524175	—
KSNUH1814		Wanju; Songgwangsa Temple	35°53'4.26"N, 127°14'34.82"E	May 09, 2022	OR524166	OR512004
KUS-F32800		Wanju; Songgwangsa Trail	35°53'9.63"N, 127°14'26.29"E	May 09, 2022	—	OR512013

to create distribution models for rust disease and two host plants, *C. incisa* and *W. floribunda* [22]. The occurrence records of these plants in Korea were retrieved from the Global Biodiversity Information Facility (GBIF.org [July 05, 2023] GBIF Occurrence Download <https://doi.org/10.15468/dl.gwfwf3> for *C. incisa*; GBIF.org [July 05, 2023] GBIF Occurrence Download <https://doi.org/10.15468/dl.x5vcd> for *W. floribunda*). Fourteen occurrences of *N. kraunhiae* were utilized for rust distribution modeling (see Table 1).

To construct the distribution model, we used 19 bioclimatic variables [23] and a 90 m digital elevation model (DEM). These bioclimatic variables were derived from monthly temperature and precipitation data supplied by the Korea Meteorological Administration (KMA) and processed using the QGIS software 3.32.2 version. Pearson's correlation test was performed using R software (4.2.2 version; R Foundation for Statistical Computing, Vienna, Austria) to assess the presence of multicollinearity.

The variables selected for each distribution model are shown in Table 2. The models were constructed using four different combinations of features (H, LQ, LQH, and LQHP), along with the selected variables. "ENMTools" package in R [24] was utilized to compare each model, aiming to determine the optimal ones. The optimal models identified were evaluated using bootstrapping and 10-fold cross-validation methods. In addition, the significant and influence of variables within the models were assessed by Jackknife test. With the selected models, we projected the potential distributions for the future (2050s) under two different SSP scenarios, SSP245 and SSP585, as provided by the KMA.

## 2.6. Statistical analysis

To assess the correlation between rust occurrence, environmental variables, and the presence of the two host plants (*C. incisa* and *W. floribunda*), we performed Pearson's correlation analysis. This analysis

**Table 2.** List of environmental variables using distribution models.

Species	Environmental variable	Description	Unit
<i>Corydalis incisa</i>	BIO1	Annual temperature	°C
	BIO7	Temperature annual range	°C
	BIO12	Annual precipitation	mm (millimeter)
	BIO19	Precipitation of coldest quarter	mm (millimeter)
	DEM	90m digital elevation model	m (meter)
<i>Wisteria floribunda</i>	BIO1	Annual temperature	°C
	BIO3	Isothermality (BIO2/BIO7) × 100	percentage (%)
	BIO12	Annual precipitation	mm (millimeter)
	BIO19	Precipitation of coldest quarter	mm (millimeter)
	DEM	90m digital elevation model	m (meter)
<i>Neophysopella kraunhiaie</i>	BIO1	Annual temperature	°C
	BIO3	Isothermality (BIO2/BIO7) × 100	Percentage (%)
	BIO12	Annual precipitation	mm (millimeter)
C_incisa	Presence	probability of <i>Corydalis incisa</i>	Probability (0.0–1.0)
W_floribunda	Presence	probability of <i>Wisteria floribunda</i>	Probability (0.0–1.0)

used rasterized data, which were projected based on the current records of the two host plants and rust occurrence data. Pearson's correlation analysis was executed using the "ENMTools" package in R [24]. Additionally, the generalized additive model (GAM), a recognized method for delineating nonlinear relationships [25], was employed to construct response curves linking the occurrence of wisteria rust with bioclimatic variables and the distribution of the two hosts. This analysis was carried out using the "mgcv" R package [26].

### 3. Results

#### 3.1. Morphological study

The rust symptoms on *C. incisa* appeared as chlorotic spots on the upper leaf surfaces, with spermogonia and aecia forming on the corresponding lower leaf surfaces (Figures 1(A,B)). Spermogonia were hypophyllous, densely scattered over the entire

surface of the leaf, orange, round, and measured 100–250 µm in diameter (Figures 1(C,F)). Aecia were hypophyllous, scattered or grouped, bright orange, typical Aecidium-type with peridia, and measured 200–500 µm in diameter (Figures 1(D,G)). Aeciospores were subglobose to ellipsoidal, pale yellow, and measured (16.2–)17.6–20.0(–21.7) × (13.2–)14.6–17.1(–19.7) µm (mean, 18.87 × 15.88 µm), with a verrucose wall surface (Figures 1(E,H)).

On *W. floribunda*, symptoms at the uredinial stage appeared as yellowish and chlorotic spots on the upper surfaces of the infected leaves (Figure 2(A)), whereas uredinial pustules formed on the lower leaf surfaces (Figure 2(B)). Uredinia were hypophyllous, mostly scattered, bright yellow to orange, round, and measured 100–200 µm in diameter (Figures 2(C,F)). Urediniospores were subglobose to obovate, yellowish, with two germ pores, and measured (16.3–)18.1–21.7(–23.7) × (12.1–)13.5–15.9(–17.1) µm (mean, 19.96 × 14.72 µm), with an echinulate wall of 1–1.5 µm thick (Figures 2(D,G,H)). Teliospores were hypophyllous, epidermal, two or three-celled, oblong, and measured 28–33 × 8–12 µm, with a thin wall of 0.5–1.0 µm thick (Figure 2(E)). All morphological characteristics matched well with previous data for *N. kraunhiaie* (spermogonial and aecial stages of *A. corydalinum*, and the uredinial and telial stages of *O. kraunhiaie*) [12,27].

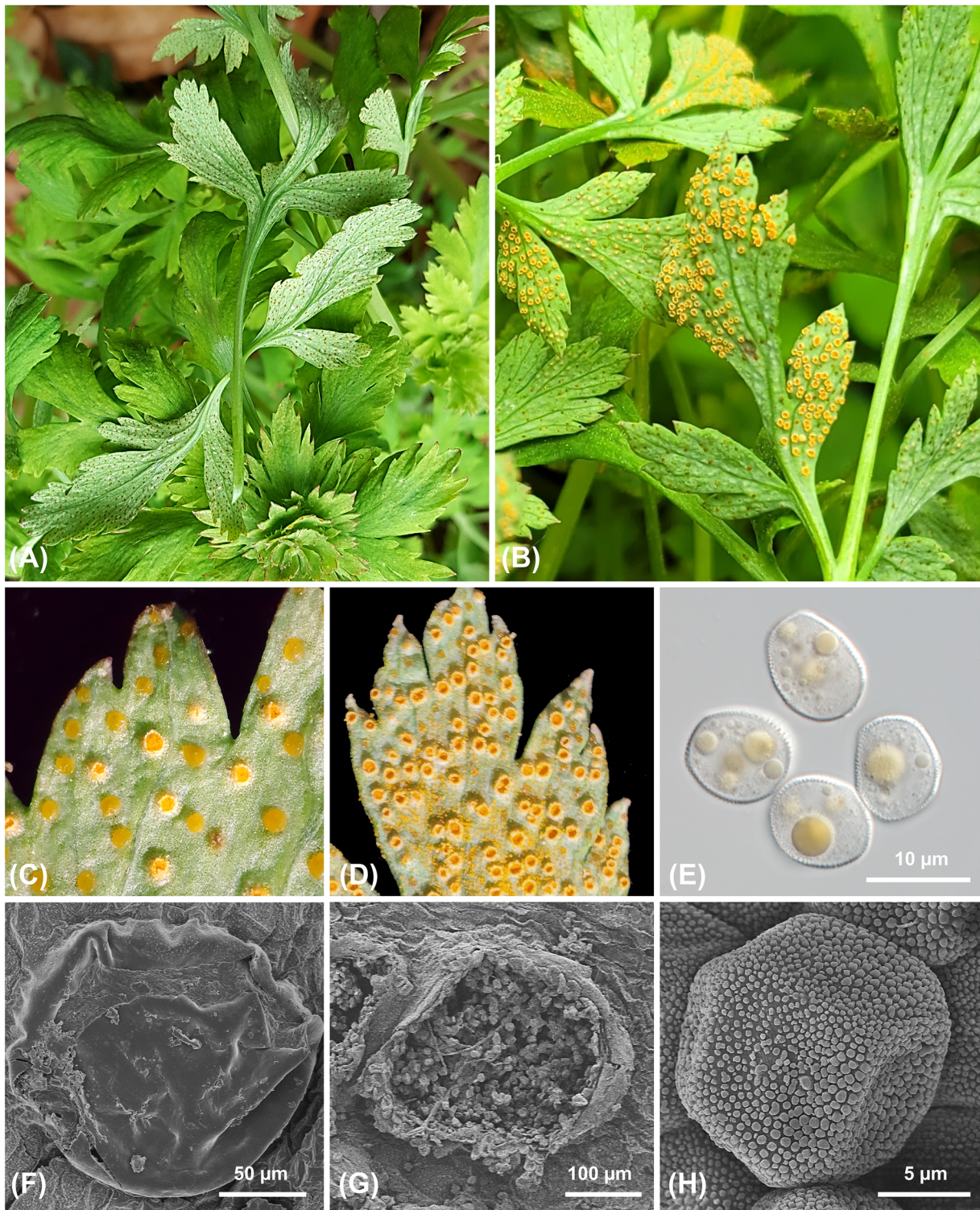
#### 3.2. Molecular phylogenetic study

A BLASTn search of the ITS sequences of Korean samples revealed a 100% match with two reference sequences of *N. kraunhiaie* from *W. floribunda* in Japan (LC492079–80), although there was a two-nucleotide difference when compared to another *N. kraunhiaie* sequence (LC492078). Except for one sample (KUS-F32102), the LSU sequences were identical to those of *N. kraunhiaie* isolated from *W. floribunda* (LC492084–5). The KUS-F32102 sample showed a 100% match with the LC492083 sequence obtained from another isolate of *N. kraunhiaie*. In the maximum-likelihood tree constructed using the ITS and LSU sequences (Figure 3), the Korean samples clustered with the reference sequences of *N. kraunhiaie*, supported by high bootstrap values of 99 and 100%, respectively.

#### 3.3. Pathogenicity test

In the pathogenicity test (Figures 4(A,B)), all leaves inoculated with aeciospores of *N. kraunhiaie* developed chlorotic spots on the upper leaf surface of *W. floribunda* after 3 weeks (Figures 4(C,D)) and





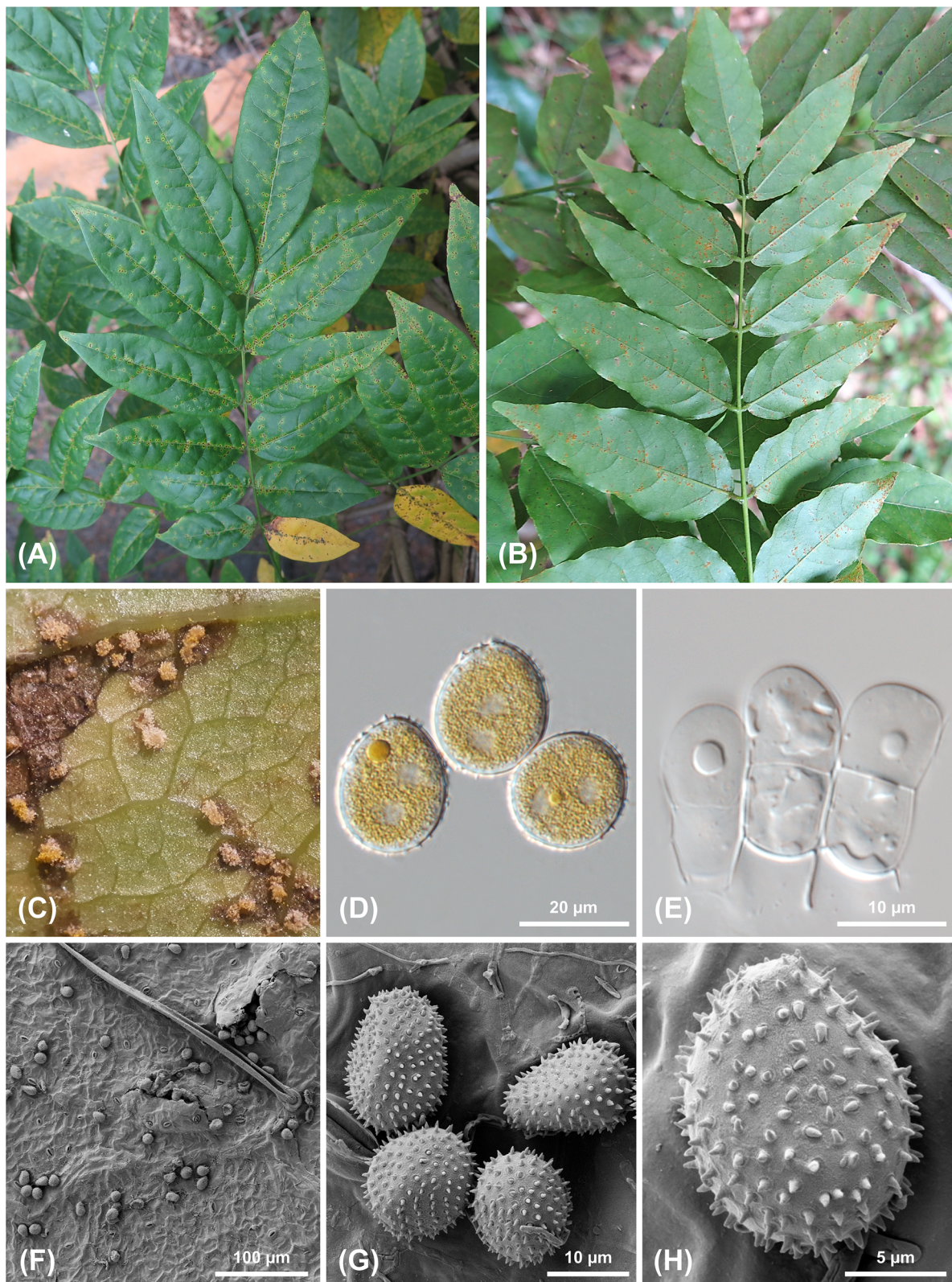
**Figure 1.** Rust disease caused by *Neophysopella kraunhiae* on *Corydalis incisa*. (A) Infected leaves of *C. incisa* with spermgogonial stage; (B) Infected leaves of *C. incisa* with aecial stage; (C) Spermgogonia; (D) Aecia; (E) Aeciospores under a differential interference contrast (DIC) microscope; (F) Spermgogonium under a scanning electron microscope (SEM); (G) Aecia under a SEM; (H) Aeciospore under a SEM.

immature uredinia on the corresponding underside (Figure 4(E)). Urediniospores were observed emerging from the uredinia (Figure 4(F)). Morphologically, the uredinia and urediniospores were identical to those initially found on *W. floribunda* in the field, thus fulfilling Koch's postulates. The control leaves remained symptom free.

### 3.4. Maxent model projection

Utilizing occurrence data of *N. kraunhiae* and its two host plants, we assessed several candidate models and selected individual optimal models: LQHP-1.5 (with an AUC value of 0.839) for *C. incisa*, LQHP-2 (0.693) for *W. floribunda*, and



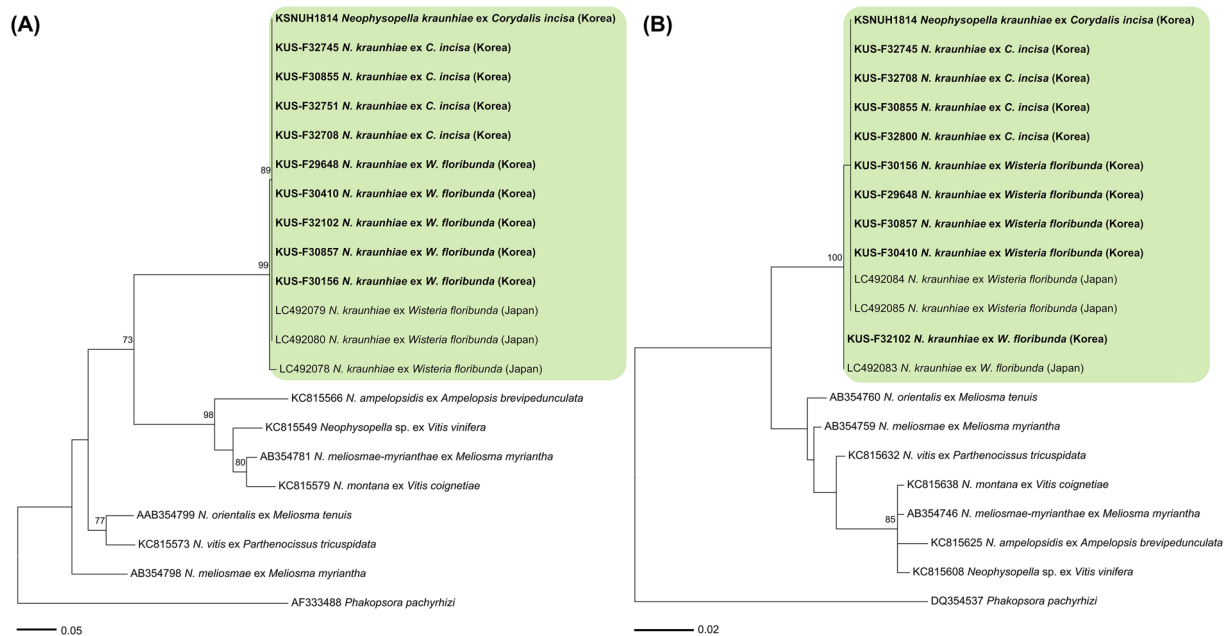


**Figure 2.** Rust disease caused by *Neophysopella kraunhiae* on *Wisteria floribunda*. (A) The chlorotic spots on the upper leaf surface of *W. floribunda*; (B) Uredinia on the lower leaf surface of *W. floribunda*; (C) Uredinia; (D) Urediniospores under a DIC microscope; (E) Teliospores under a DIC microscope; (F) Uredinia under a SEM; (G) Urediniospores under a SEM; (H) Wall surface of an urediniospore under a SEM.

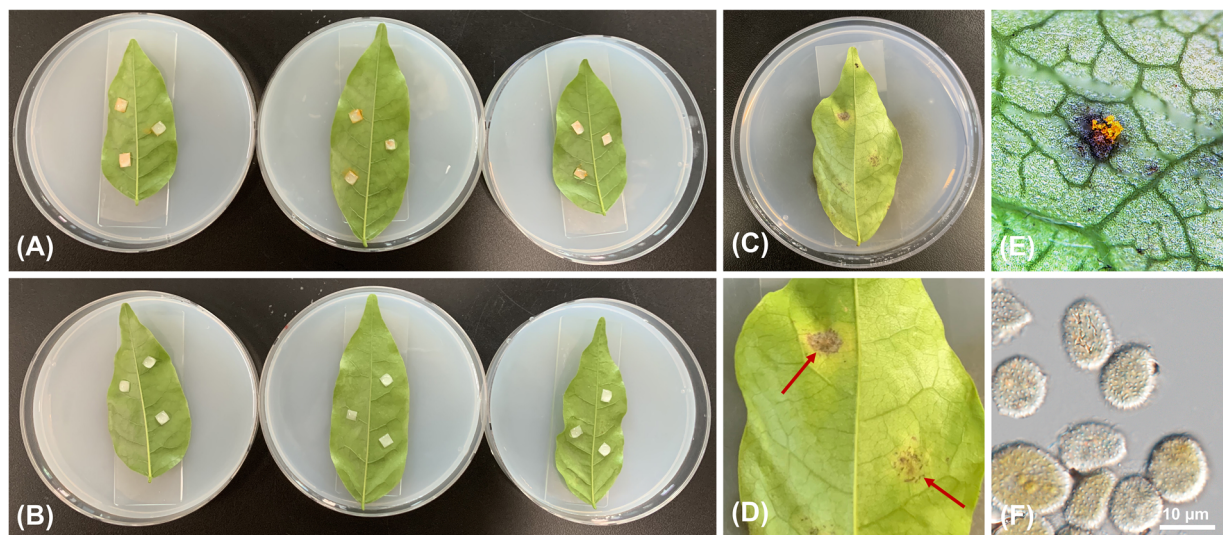
LQH-2 (0.893) for *N. kraunhiae*. In the variable contribution analysis of LQH-2, the distribution of *C. incisa* emerged as the most influential factor, accounting for 58.1% of the model's importance and

contributing 56.1% to the model's performance (Figure 5(A)). The Jackknife test further validated that it acted as an essential variable in regularized training gain (Figure 5(B)). On the other hand, the





**Figure 3.** Maximum likelihood tree of *Neophysopella* species based on the internal transcribed spacer (ITS) (A) and large subunit (LSU) (B) rDNA sequences. The bootstrapping values higher than 70% are given above the branches. The green box represents *Neophysopella kraunhiae*. The Korean specimens sequenced in the present study are shown in bold.

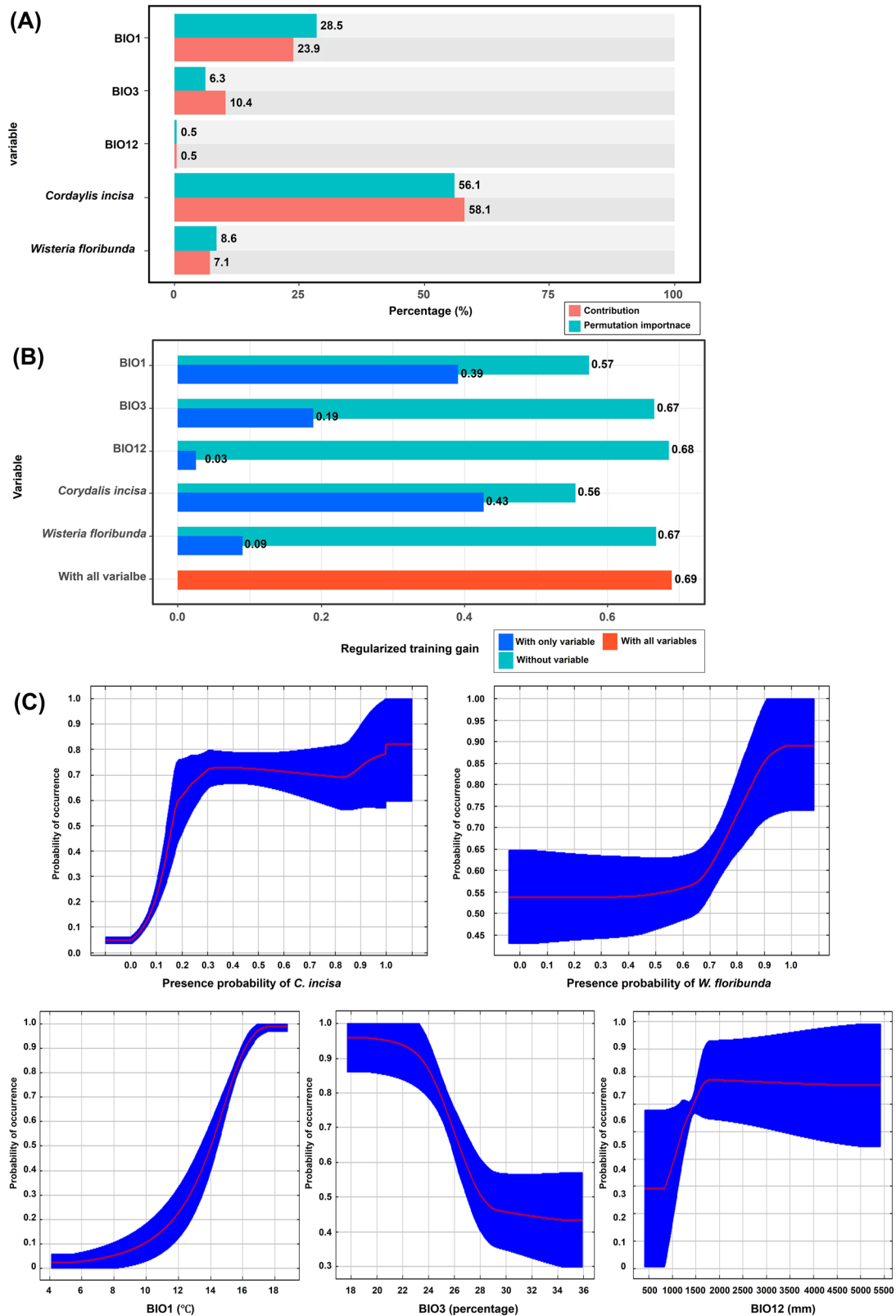


**Figure 4.** Pathogenicity test. (A) Inoculations of rust aciospores harvested from *Corydalis incisa* onto *Wisteria floribunda* leaves; (B) Controls; (C,D) A leaf with chlorotic spots three week after inoculation; (E) Uredinium; (F) Echinulate and immature uredinia.

distribution of *W. floribunda* exhibited minimal influence, with an importance of 8.6% and a contribution of 7.1%. Among the bioclimatic variables, BIO1 (annual temperature) exhibited significant importance (28.5%) and contribution (23.5%). Moreover, the analysis highlighted that all variables, except for BIO3, had a positive correlation with the model's response curves (Figure 5(C)).

*Corydalis incisa* is primarily distributed in the southwestern region of Korea, whereas *W. floribunda* is widespread across Korea (Figures 6(A,D)). Rust occurrence by *N. kraunhiae* in both hosts was noted in the southwestern region, mirroring the distribution pattern of *C. incisa* (Figure 6(G)).

In response to climate change predictions, we conducted modeling to predict the potential distributions of the two plants and rust pathogen. The projected current distributions of both hosts and rust pathogen, as shown by the model, closely aligned with the actual current distributions (Figures 6(A,D,G)). Future (2050s) climate scenarios suggested that *C. incisa* is likely to expand into the central regions of Korea (Figures 6(B,C)), whereas the nationwide distribution of *W. floribunda* will remain relatively unchanged (Figures 6(E,F)). The future distribution of *N. kraunhiae* (Figures 6(H,I)) showed a pattern like to one of *C. incisa*, expanding gradually northward.



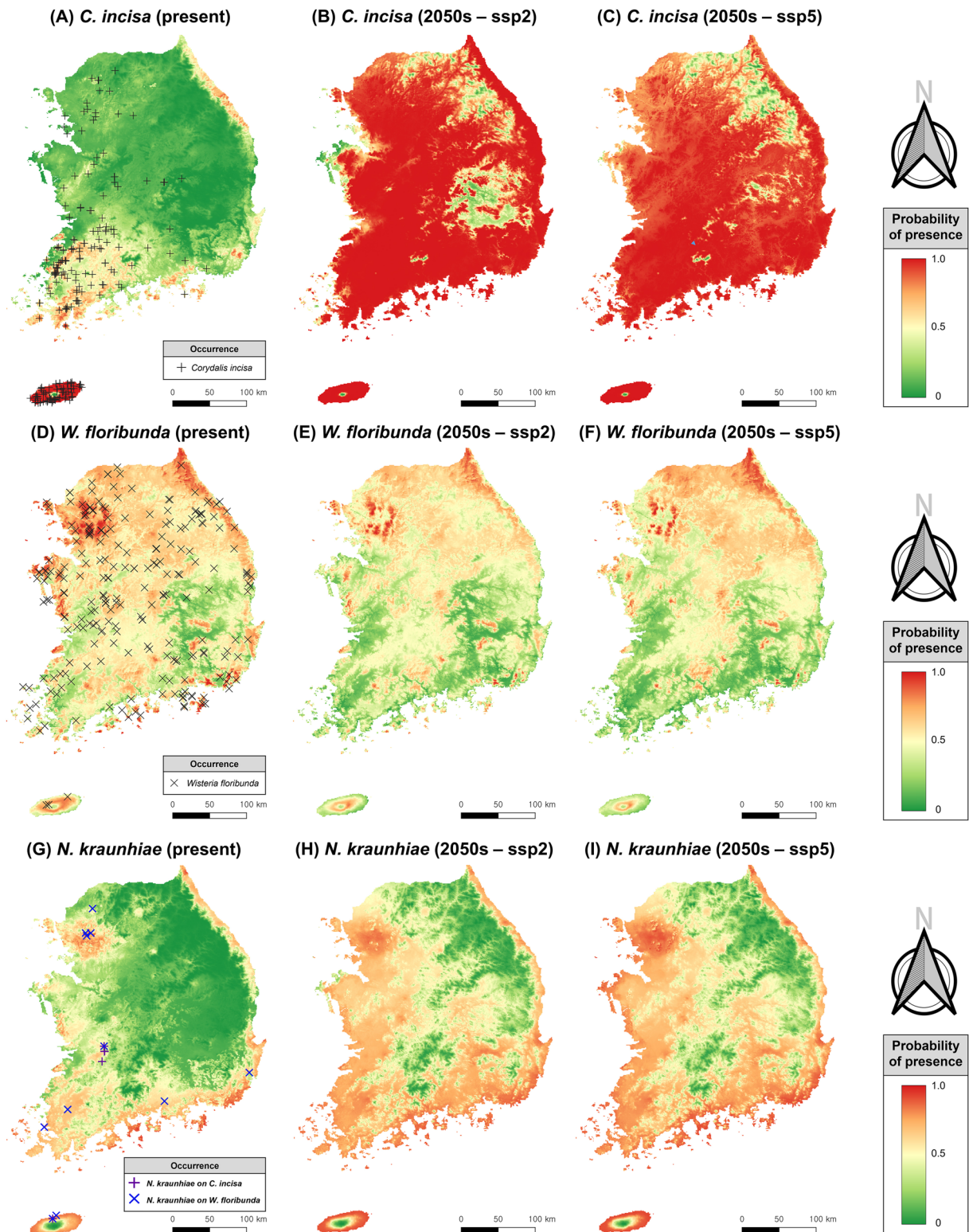
**Figure 5.** Evaluation of variables within LQH-2 model for *Neophysopele kraunhia*. (A) The permutation importance and contribution of environmental variables; (B) The results of the jackknife tests; (C) Response curves between the occurrence of wisteria rust and environmental variables.

### 3.5. Statistical analysis

Pearson's correlation analysis revealed that BIO1 showed a high positive correlation (0.76) with rust occurrences on *W. floribunda*, whereas BIO12

exhibited a weaker correlation ( $-0.06$ ) with rust presence (Figure 7(A)). The response curves generated from the GAM for BIO1 indicated an escalation in the rust disease on *W. floribunda* in response to increases in annual temperature, mirroring the

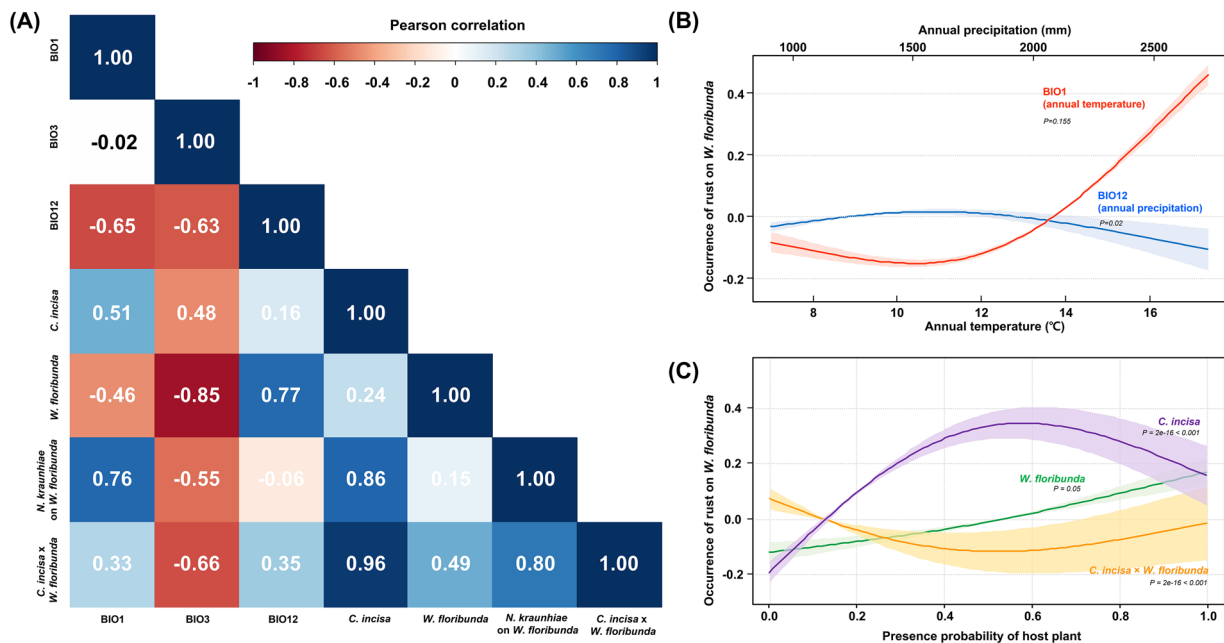




**Figure 6.** Projection for current and future (2050s) distributions of a rust fungus (*Neophysopelella kraunhiae*) and its two host plants (*Corydalis incisa* and *Wisteria floribunda*), utilizing the maximum entropy model (Maxent) under SSP245 and SSP585 scenarios. (A–C) *Corydalis incisa*; (D–F) *Wisteria floribunda*; (G–I) *Neophysopelella kraunhiae*.

pattern observed in its Maxent response curve (Figure 7(B)). The correlation analysis also indicated a strong positive correlation (0.86) between the appearance of rust disease on *W. floribunda* and the presence of *C. incisa* (Figure 7(A)). However, there was a weak correlation (0.15) with the distribution of *W. floribunda* itself. Although there was a

moderately strong correlation (0.80) between the occurrence of wisteria rust and the interaction between both host plants; this was weaker than the correlation related to the probability of *C. incisa* being present. This suggested that wisteria rust is more strongly associated with the presence of *C. incisa* than with the interaction between the two



**Figure 7.** Statistical analysis of the interaction among rust disease (caused by *Neophysopelella kraunhia*), its two host plants (*Corydalis incisa* and *Wisteria floribunda*), and climate variables. (A) Pearson's correlation matrix displaying the correlations between the rust occurrence on *W. floribunda* and bioclimatic variables; (B) Response curves from the Generalized Additive Model (GAM), depicting the relationship between the occurrence of wisteria rust and two variables (annual temperature and precipitation); (C) Response curves from the GAM, illustrating the interdependence between the rust occurrence on *W. floribunda* and the distribution of the two hosts; 95% confidence intervals indicated by colored shading.

hosts. Furthermore, the GAM analysis displayed a pattern in which wisteria rust occurrence significantly increased with the increasing presence probability of *C. incisa* ( $p$ -value:  $2e-16$ ) (Figure 7(C)). In contrast, a weaker correlation was found between the probability of *W. floribunda* being present and the incidence of rust disease.

#### 4. Discussion

Rust (Pucciniales) is a notorious plant pathogenic group of ~8000 species [28]. These pathogens are unique in their intricate life cycles, and many rust species alternate between two unrelated plants [8]. Throughout this cycle, rust fungi produce different types of spores on each host plant, facilitating their dispersal and persistence, but also complicating control efforts. One well-documented rust pathogen is *Puccinia graminis*, responsible for wheat stem rust, which alternates its life cycle between wheat plants (*Triticum* spp.) and barberry (*Berberis* spp.) [1]. Therefore, understanding the complex life cycle, including identifying primary and alternate hosts, is essential for devising efficient control methods for harmful rust diseases. This study is the first to report the effects of the rust pathogen *N. kraunhia* on *W. floribunda* and *C. incisa* in Korea. We performed pathogenicity tests to verify *C. incisa* as a spermogonial and aecial host for *N. kraunhia*, which aligns with earlier research [12].

Although the connection between specific plant distributions and the onset of rust diseases is well-established [29–31], little is known about how climate-induced shifts in the distribution of a host plant, such as *C. incisa* influence rust outbreaks. In Korea, the distribution of *C. incisa* was limited to the southern islands and regions until around 2010. Our predictive models using the Maxent model under SSPs revealed that up to the 2050s, *C. incisa* will rapidly expand northward owing to accelerating climate change, encroaching on the central regions of Korea. However, the distribution of *W. floribunda* is likely to remain unchanged. The potential expansion of *C. incisa* is supported by our field surveys and other studies addressing the climatic impact [13,14].

The GAM model and statistical analysis revealed a robust correlation between the spread of *C. incisa* and the emergence of rust on *W. floribunda*. The climate-driven northward expansion of *C. incisa* poses a considerable threat to wisteria across Korea. These findings underscore the urgent need for further research aimed at devising targeted control strategies for wisteria rust disease, particularly in regions projected to experience significant shifts in the distribution of *C. incisa* due to climate change.

Remarkably, despite the worldwide distribution of *W. floribunda*, rust disease caused by *N. kraunhia* has previously been documented only in Japan and China, affecting specific *Wisteria* species: *W. brachybotrys* and

*W. floribunda* in Japan, and *W. sinensis* in China [10]. This localized occurrence can be attributed to the restricted distribution of its alternate hosts (*C. ambigua*, *C. decumbens*, *C. incisa*, and *C. pallida*) in East Asia, but is also aligned with our finding that *C. incisa* plays a pivotal role in the emergence of wisteria rust, shedding light on the potential spread of this rust pathogen. The recent invasion and rapid spread of *C. incisa* across other continents make this situation a cause for concern. In the United States, a weed risk assessment flagged this plant as an emerging invader with potential risks [32]. Given the ongoing disease development in Korea and our predictive analysis, there is a growing concern that the migration and spread of *C. incisa* could trigger a global surge in wisteria rust.

This study highlights the intricate interplay between host plants, rust pathogens, and climate change, emphasizing how climatic shifts influence plant distribution and related diseases. Research indicates that climate change may not only shift the distribution of host plants but also exacerbate the severity of diseases like rust, which poses substantial risks to both agriculture and forest ecosystems [17,33,34]. For instance, warmer temperatures and altered precipitation patterns have been linked to increased rust incidence of outbreaks. As such, monitoring rust pathogens with similar host interactions and significant economic value in agriculture and forest ecosystems is essential [7]. A deeper understanding of these interactions is essential for devising effective control strategies to counteract the adverse effects of rapid global climate change. Precise disease prediction models are invaluable and emphasize the urgent need to address climate-related challenges in disease management for future ecological and agricultural planning.

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### Author contributions

JSL: writing—review and editing, conceptualization, formal analysis, methodology; JHP: writing—review and editing, conceptualization, methodology; YJC: writing—review and editing, conceptualization, methodology, project administration; HDS: writing—review and editing, conceptualization, methodology.

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### Data availability statement

All sequence data used in this study are available in NCBI GenBank.

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