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Survey data of benthic diatom resources in a Cijiawan Creek drainage basin in Wuling, Taiwan

武陵七家灣溪流域底棲矽藻資源調查資料

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Abstract

Background

Cijiawan Creek in Shei-Pa National Park of central Taiwan nurtures a unique and important natural resource, the Formosan landlocked salmon (*Oncorhynchus masou formosanus*). In order to conserve and restore the species population, many related researches are already underway, including long-term ecological monitoring. Benthic diatoms are the main basic producers of the food network of the stream ecosystem, and their species composition will directly or indirectly impact the entire ecosystem. This paper includes a list of benthic diatoms and related information surveyed in a Cijiawan Creek drainage basin in 2019.

New information

In the paper we provide a detailed dataset that contains 1,839 benthic diatom occurrences collected during a field campaign in 2019. A total of 55 diatom (Bacillariophyta) taxa belonging to 9 orders, 17 families, and 27 genera were collected. The frequency analysis indicated that *Planothidium frequentissimum*, *Cocconeis placentula* var. *euglypta*, and *Achnanthidium convergens* were the most common diatom species at the sampling stations. The second most common diatom species were *Nitzschia amphibia* and *Synedra ulna*.

摘要

本調查資料是 2019 年間，在七家灣溪流域各樣站所採集之矽藻物種鑑定、藻種電顯影像、分布位置及環境因子等資料進行建置，可供為未來各項相關研究利用參考。調查結果顯示，9 個樣站共鑑定出 27 屬 55 種矽藻。將各樣點所採集之藻類進行頻度分析 *Planothidium frequentissimum*, *Cocconeis placentula* var. *euglypta*, 和 *Achnanthidium convergens* 這三種在各樣點出現頻度最高 ，其次是 *Nitzschia amphibia* 和 *Synedra ulna*。

Keywords: Bacillariophyta, benthic diatom, Cijiawan Creek

關鍵字：矽藻門、底棲矽藻、七家灣溪

Introduction

Cijiawan Creek is the main tributary in the upper stretch of Dajia River in Taiwan and is located in Wuling, Heping District, Taichung City. This creek is under the jurisdiction of Shei-Pa National Park and is regarded as the only surviving habitat of *Oncorhynchus masou formosanus.* This type of salmon mainly feeds on aquatic insects (Lin et al. 1988; Wang 1994), and these insects feed on epiphytic algae in streams, where diatoms have the highest species diversity (Yu 2008). Both diatoms and aquatic insects can be used as a biological indicator of the stream environment (Chu et al. 2006). According to the Wuling Long-Term Ecological Research and Modeling research team, several biological groups in the ecosystem food webs have been observed (Lin et al. 2007), with epiphytic algae at the upper stretch of Dajia River identified as one of the primary producers. Generally, the biomass of epiphytic algae may alter the energy flow of food webs in river ecosystems (Kano et al. 2016). Epiphytes can also conserve and store energy and materials, and provide food and habitat to other aquatic organisms, thereby affecting the composition of such organisms (Lock et al. 1984). In the streams of Wuling, epiphytes are mostly diatoms (Yu et al. 2006). The analysis of diatom communities and their biodiversity is a useful tool to secure an ecological and sustainable use of the water resources and the correct elaboration of guidelines for their preservation, in particular, in specially protected natural areas (Falasco and Bona 2011; Falasco et al. 2012; Neplyukhina et al. 2022). Relevant investigations are mostly about the relationship between algae and environmental factors (Lin 2011; Su 2009; Wu 2010; Ye 2011) and there are few surveys on the classification and identification of diatoms. In the past, the identification of diatoms was mainly based on optical microscopy. However, due to the limitation of observation multiples, it is not easy to

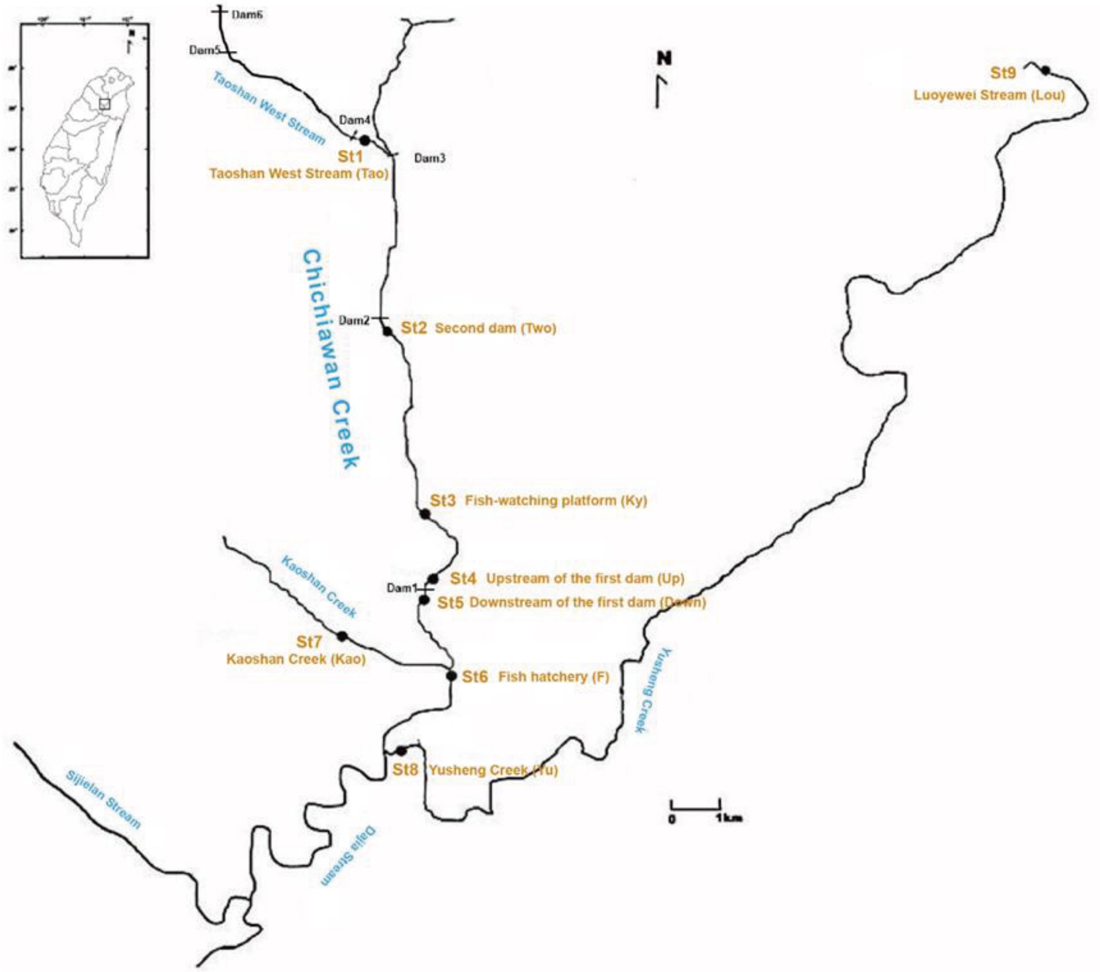

Fig 1. The sampling stations are shown in the Cijiawan Creek drainage basin. In Cijiawan Creek (from upstream to downstream) and its tributaries, nine sampling stations were installed. Characteristics of all the sampling stations are described in Table 1.

Table 1. Characteristics of sampling stations

Sampling station no.	Sampling station name	Code	Characteristics
St1	Taoshan West Stream	Tao	Located below the Wuling Suspension Bridge and divided into three mesohabitat units: riffles, run, and pools.
St2	Second dam	Two	Located nearly 100 m downstream of the damaged second dam and divided into two mesohabitat units: pools and runs.
St3	Fish-watching platform	Ky	An open sampling station located nearly 1 km downstream of the fish-watching platform and divided into three mesohabitat units: riffles, run, and pools.
St4	Upstream of the first dam	Up	An open terrain located 100 m upstream of the first dam. The river channel is located on the right bank, and the right-hand side is covered with little vegetation. Riffle and pool mesohabitat units are clearly observable, and a run unit is located downstream of the pool.
St5	Downstream of the first dam	Down	Located 100 m downstream of the first dam with steep rock walls on both sides. Compared with the upstream of the first dam, this sampling station is more shaded. Riffle and pool mesohabitat units are clearly observable, with the run unit being less marked.
St6	Fish hatchery	F	An open terrain where the riverway is widest among all sampling stations. Riffle and run mesohabitat units are clearly observable, and the pool unit is less marked and covered by gravel.
St7	Kaoshan Creek	Kao	A primary shaded sampling station where only a riffle unit is observable and the flow velocity is relatively high.
St8	Yusheng Creek	Yu	An area that is subjected to human-induced disturbances and agricultural activities and has a riffle unit with a relatively low flow velocity and relatively high nutrient concentration. The long-term monitoring results of the algal phase in this area considerably differ from those obtained at other sampling stations.
St9	Luoyewei Stream	Luo	The terrain on both sides of the strait is narrow and steep, thereby preserving the appearance of the primary forest and demonstrating high vegetation coverage on both sides.

distinguish diatoms in classification. In this investigation, electron microscope was mainly used to record the collected diatom morphology, so as to observe the diatom morphology more clearly for identification, and compile it into the database for reference with the data of the sampling station.

Project description

Title:

Survey data of benthic diatom resources in a Cijiawan Creek drainage basin in Wuling

Study area description:

A total of nine sampling stations were installed in the Cijiawan Creek watershed, as shown in Figure 1.

Sampling methods

Sampling description:

Sampling stations in the Cijiawan Creek watershed were divided into three mesohabitat units for separate sample collection: riffles, run, and pools. Depending on the size of the substrate in the sampling area, stones representative of the particle size of the sampling station were randomly selected. At least three stones of the same particle size were collected from each habitat. Diatom samples (with an area of 16–25 cm^2) were scraped off the collected stones on the river bank and placed into a sample collection container along with stream water from the site. The samples were then sent to the laboratory for acid-wash treatment for identification (Su 2009).

A total of five sampling events were performed in January, April, July, August, and October, 2019. For the final two sampling events, samples were collected after Typhoon Lekima to determine the effect of typhoons on epiphytes.

Quality control:

For diatom identification, a number of manuals were used (Taylor et al. 2007,

Wu et al. 201). Valid diatom taxon names were referenced according to Guiry and Guiry (2022).

Step description:

1.Collect samples from habitats.

2.The samples underwent acid-wash treatment for identification.

3.Photograph the samples with an electron microscope.

4.Convert paper-based records from the field and laboratory into an electronic data format (Excel spreadsheets).

5.Organize the datasets into a standardized format.

6.Export data as a Darwin Core Archive.

7.Generate dataset-level metadata.

Statistical analysis:

R programming language (version 4.0.3; R Foundation for Statistical Computing, Vienna, Austria) was used for Bray–Curtis dissimilarity testing and nonmetric multidimensional scaling (NMDS) for understanding the differences in diatom communities among the sampling sites. Because the Luoyewei Stream sampling station (St9) was sampled only once, it was excluded from the analysis (see Figure 2). The results indicated that the diatom species composition of the sampling stations of Cijiawan Creek's tributaries (i.e., Kaoshan Creek [Kao], Yusheng Creek [Yu], and Taoshan West Stream [Tao]) was considerably different from that of other sampling stations in Cijiawan Creek. The results also indicated large differences between the aforementioned three sampling stations, which agreed with previous long-term monitoring results of algal species in this area. This is because the habitat environment and water quality of these three sampling stations considerably differed from those of Cijiawan Creek (Yu and Lin 2009).

As shown in Figure 3, the frequency analysis indicated that *Planothidium frequentissimum*, *Cocconeis placentula* var. *euglypta*, and *Achnanthidium convergens* were the most common diatom species at the sampling stations. The second most common diatom species were *Nitzschia amphibia* and *Synedra ulna*.

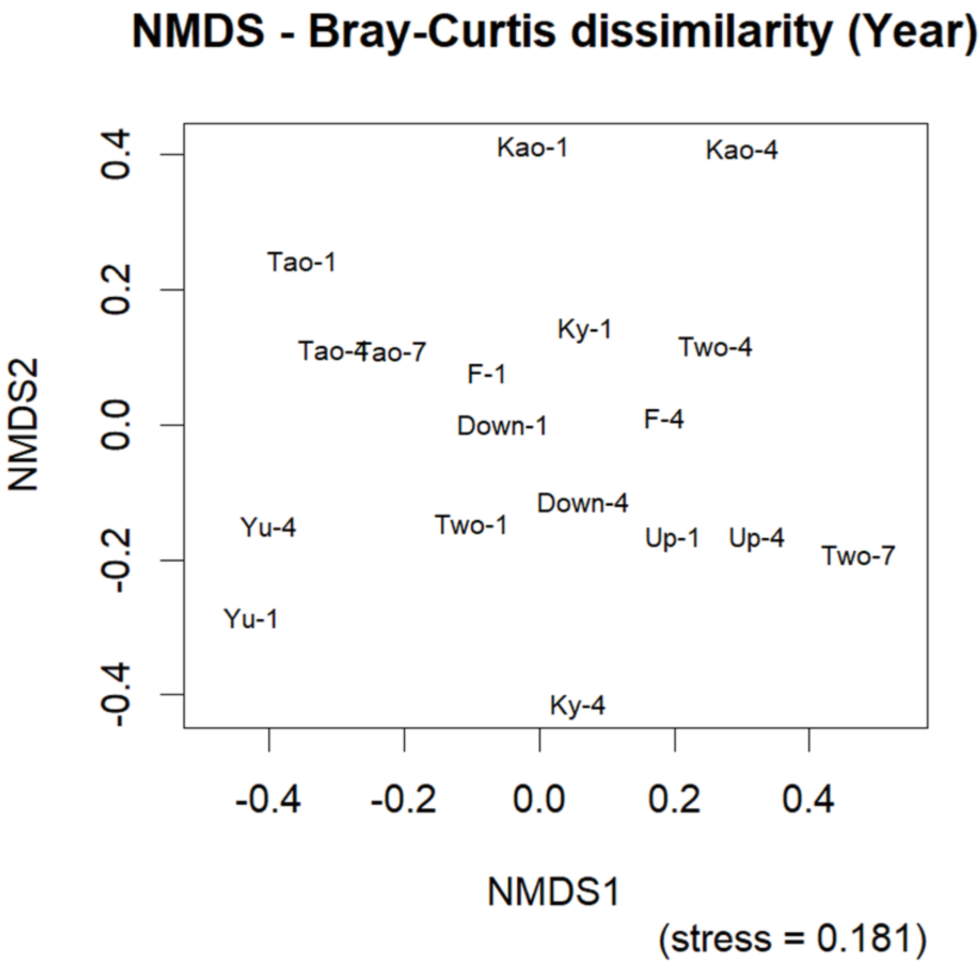

Fig. 2. The result of the diatom species composition of the sampling stations of the Cijiawan Creek drainage basin. Number 1 stands for riffle; number 4 stands for run; number 7 stands for pool.

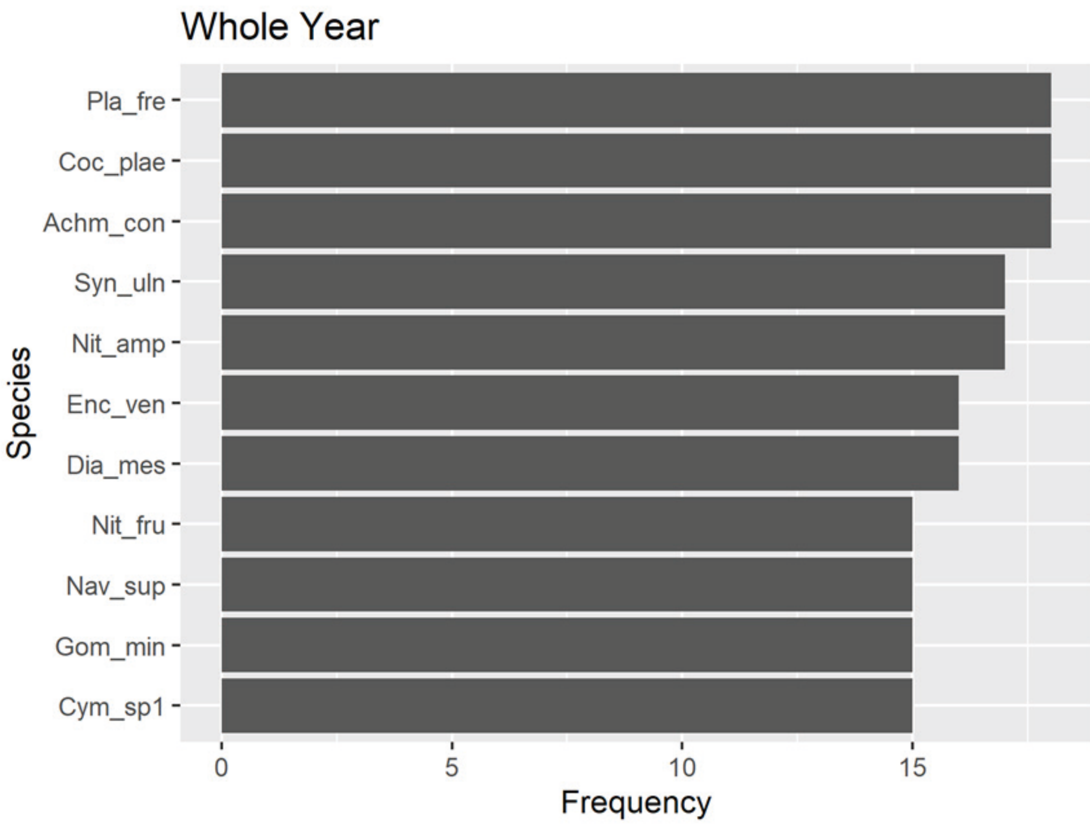

Fig. 3. The frequency of occurrence of diatom species in the Cijiawan Creek sampling stations in the whole year.

(Pla_fre= *Planothidium frequentissimum*；Coc_plae= *Cocconeis placentula* var. *euglypta*；Achm_con= *Achnanthidium convergens*; Syn_uln= *Synedra ulna*；Nit_amp= *Nitzschia amphibian*；Enc_ven= *Encyonema ventricosum*；Dia_mes= *Diatoma mesodon*；Nit_fru= *Nitzschia frustulum*; Nav_sup= *Navicula suprinii*；Gom_min= *Gomphonema minutum*；Cym_sp1= *Cymbella* sp.1)

Geographic coverage

Description:

Cijiawan Creek drainage basin, Shei-Pa National Park, Heping District, Taichung City, Taiwan.

Coordinates:

Sampling station no.	Sampling station name	N	E
St1	Taoshan West Stream	24.39802	121.3075
St2	Second dam	24.382139	121.310111
St3	Fish-watching platform	24.37083	121.31055
St4	Upstream of the first dam	24.36355	121.31163
St5	Downstream of the first dam	24.36383	121.31163
St6	Fish hatchery	24.35447	121.31383
St7	Kaoshan Creek	24.3587	121.3075
St8	Yusheng Creek	24.347773	121.310494
St9	Luoyewei Stream	24.39455	121.35119

Taxonomic coverage

Description:

All diatoms were identified to the genus or species level. In total, 55 species taxa were identified belonging to two classes, nine orders, 17 families, and 27 genera. The taxonomic coverage of the diatoms found in studied material is given in Table 2.

Table 2. Taxonomic coverage of diatoms from studied samples.

Orders	Families	Genera	Species
Achnanthales	2	5	12
Bacillariales	1	2	7
Cymbellales	3	7	15
Fragilariales	1	2	2
Melosirales	1	1	1
Naviculales	5	6	13
Licmophorales	1	1	1
Rhabdonematales	2	2	3
Thalassiophysales	1	1	1

Table 3. List of diatom species found in sample stations. (*presence)

	St1			St2			St3		St4		St5		St6		St7		St8		St9	
	Riffle	Run	Pool	Riffle	Run	Pool	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle
Achnanthes brevipes Agardh		*	*	*	*		*				*				*					
Achnanthes exigua Grunow in Cleve & Grunow																	*			
Achnanthes rupestoides Hohn	*	*	*										*		*				*	
Achnanthidium biasolettianum (Grunow) Round & Bukhtiyarova	*	*	*		*	*					*		*				*			
Achnanthidium convergens (Kobayasi) Kobayasi	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Achnanthidium minutissimum (Kützing) Czarnecki	*	*	*	*	*		*	*	*	*	*	*		*			*	*	*	
Amphora pediculus (Kützing) Grunow	*	*	*		*		*	*			*		*	*	*	*		*		
Amphora sp.1							*	*												
Caloneis bacillum (Grunow) Cleve	*	*	*	*	*	*		*												
Cocconeis pediculus Ehrenberg	*	*	*	*			*											*		*
Cocconeis placentula Ehrenberg	*	*	*	*	*			*	*											
Cocconeis placentula var. *euglypta* (Ehrenberg) Grunow	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Cocconeis placentula var. *lineata* (Ehrenberg) Van Heurck	*	*	*	*			*						*	*	*	*			*	*
Cymbella affinis Kützing	*	*	*	*	*	*	*	*			*		*					*		
Cymbella turgidula Grunow in A.W.F.Schmidt	*	*	*	*	*	*	*	*			*	*	*				*	*		*
Cymbella sp.1	*	*	*	*	*	*	*	*	*	*	*	*	*	*				*		
Diatoma mesodon (Ehrenberg) Grunow	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				*
Diatoma vulgaris Bory		*		*											*		*	*		
Diploneis elliptica (Kützing) Cleve														*						

Table 3. Cont.

	St1			St2			St3		St4		St5		St6		St7		St8		St9	
	Riffle	Run	Pool	Riffle	Run	Pool	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle
Encyonema ventricosum (Agardh) Grunow		*	*	*	*	*	*	*	*	*	*	*	*	*		*	*	*		*
Eolimna minima (Grunow) Lange-Bertalot & W.Schiller		*												*			*	*		
Epithemia cistula (Ehrenberg) Ralfs	*	*	*	*																
Fragilaria capucina var. *vaucheriae* (Kützing) Lange-Bertalot		*	*	*	*		*		*		*	*		*	*			*		*
Frustulia vulgaris (Thwaites) De Toni											*									
Geissleria decussis (Østrup) Lange-Bertalot & Metzeltin		*					*		*		*									
Gomphoneis sp.1				*	*	*								*			*		*	
Gomphoneis sp.2	*	*	*	*	*						*		*	*	*	*	*	*		*
Gomphonema clevei (Fricke) Gil							*													
Gomphonema lagenula Kützing				*	*	*												*		
Gomphonema lateripunctatum Reichardt & Lange-Bertalot	*		*	*	*	*						*				*		*	*	*
Gomphonema minutum (C.Agardh) C.Agardh	*	*	*	*		*	*	*			*	*	*	*	*	*	*	*	*	
Gomphonema sp.1			*	*								*	*				*	*	*	*
Grunowia tabellaria (Grunow) Rabenhorst	*	*	*	*	*	*				*			*				*			
Melosira varians Agardh	*	*	*	*	*	*	*	*	*	*	*			*						
Navicula cryptocephala Kützing	*	*	*	*		*		*					*							*
Navicula cryptotenella Lange-Bertalot. Dataset						*		*			*			*		*				
Navicula cryptotenelloides Lange-Bertalot	*	*	*	*	*			*												
Navicula germainii J.H.Wallace		*	*	*	*															
Navicula pseudobryophila Hustedt		*														*				
Navicula radiosa Kützing	*	*	*	*	*		*	*			*	*	*	*	*					*

Table 3. Cont.

	St1			St2			St3		St4		St5		St6		St7		St8		St9	
	Riffle	Run	Pool	Riffle	Run	Pool	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle	Run	Riffle
Navicula suprinii Gerd Moser, Lange-Bertalot and Metzeltin		*	*	*	*		*	*	*	*	*		*	*	*	*	*	*		
Navicula tripunctat (O.F.Müller) Bory de Saint-Vincent	*	*	*	*	*	*					*						*	*		
Nitzschia alpine Hustedt	*	*	*						*		*	*					*	*		
Nitzschia amphibia Grunow	*	*	*	*	*	*	*	*	*	*	*	*	*	*		*	*	*	*	*
Nitzschia frustulum (Kützing) Grunow	*	*	*	*		*	*	*	*		*	*	*	*	*		*	*		
Nitzschia inconspicua Grunow	*		*			*		*									*	*		
Nitzschia linearis (Agardh) W. Smith		*					*	*		*	*		*		*		*	*		*
Nitzschia palea (Kützing) W. Smith				*		*	*	*	*	*	*	*	*	*	*		*			
Pinnularia molaris var. *asiatica* Skvortzow		*	*																	
Placoneis gastrum (Ehrenberg) Mereschkowsky	*	*	*						*			*	*	*						
Planothidium frequentissimum (Lange-Bertalot) Lange-Bertalot	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Reimeria sinuata (W.Gregory) Kociolek & Stoermer			*	*	*	*	*	*	*	*	*	*	*	*			*	*		
Rhoicosphenia abbreviata (C.Agardh) Lange-Bertalot	*	*	*								*						*	*	*	*
Synedra ulna (Nitzsch) Ehrenberg	*	*	*		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
Ulnaria acus (Kützing) M.Aboal			*										*	*						

Temporal coverage

Notes:

Sample in January, April, July, August, and October, 2019.

Usage license

Usage license:

Data resources

Data package title:

Darwin Core Archive Survey Data of Diatoms in Cijiawan Creek

Resource link:

https://www.gbif.org/dataset/9e6bf53c-8dba-470a-9142-3607dfe21c41

Alternative identifiers:

https://doi.org/10.15468/rwjwkj

https://ipt.taibif.tw/resource?r=survey_data_of_diatoms_in_Cijiawan_creek

Data set name:

Survey Data of Diatoms in Cijiawan Creek

Data format:

Darwin Core Archive

Data format version:

1.6 published on September 30, 2022

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氣候變遷對高山受威脅植物川上氏忍冬地理分佈的潛在影響

Potential effects of climate change on the geographic distribution of the threatened alpine plant *Lonicera kawakamii*

呂明倫　黃靜宜 *

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摘　要

氣候變遷對高山的受威脅植物物種構成嚴重危機，川上氏忍冬 (*Lonicera kawakamii*) 為分佈在臺灣高山 (海拔 3,000-3,900 m) 的特有種植物，根據最新的 ” 臺灣維管束植物紅皮書名錄 ”，其被列為易危物種。本研究使用近年發展出的小模型集成法，預測川上氏忍冬的潛在分佈，以政府間氣候變化專門委員會第 6 次評估報告中的共享社會經濟途徑 (shared socio-economic pathway, SSP) 做為未來氣候變遷情境 (2085 年代)，預測適宜棲地之時空動態。研究結果顯示，氣候為影響川上氏忍冬分佈的主要因子，並且其適宜的氣候棲位包含低溫、日較差大和適度的降水量。根據輕度 (SSP126) 與重度 (SSP585) 暖化情境下的預測結果顯示，臺

灣的高山地區因氣候變暖，川上氏忍冬的適宜棲地大幅縮小，因此，該物種可能存在滅絕風險。本研究成果有助於鑑定未來適宜棲地的轉移，並提供因應氣候變遷的保育方針。

Abstract

Climate change leads to significant impacts on threatened plant species in mountainous regions. *Lonicera kawakamii (L. kawakamii)* is an endemic plant distributed across middle- to high-altitudes (3,000-3,900 m) in the mountainous Taiwan. This species has been currently listed as vulnerable in “The Red List of Vascular Plants of Taiwan.” In this study, a recently-developed ensemble of small models was used to predict the potential distribution of *L. kawakamii*. In order to project the spatiotemporal dynamics of suitable habitats, the shared socio-economic pathways (SSPs) from the Sixth Assessment Report of the Intergovernmental Panel on Climate Change was considered as various future climate change scenarios (in 2085). The results show that the geographic distribution of *L. kawakamii* was mainly affected by climatic factors, including low temperature, large diurnal range, and moderate precipitation. According to our predictions under mild (SSP126) and severe (SSP585) warming scenarios, the range of suitable habitat of *L. kawakamii* shrank significantly due to climate warming in the alpine regions of Taiwan. Therefore, the species may be at risk of extinction. These outcomes help to identify future shifts of suitable habitats and could provide reference for conservation strategies in response to climate change.

關鍵詞：特有種、易危、小模型集成、共享社會經濟途徑、滅絕風險

Keywords: endemic species, vulnerable, ensembles of small model, shared socio-economic pathway, extinction risk

緒　言

氣候變遷已被認為是本世紀無可避免的全球化現象，也可能是地球生物多樣性必須面對的最大威脅 (Warren *et al*. 2013, Urban *et al*. 2015)。氣候條件的改變與頻繁的人為活動，正驅動生態系中許多物種的地理分佈重新配置 (Pecl *et al*. 2017)， 據 Román-Palacios and Wiens (2020) 的分析，未來 50 年內全球大約有 1/3 的物種，都可能籠罩在滅絕的危機中。尤其長年生活在低溫環境的高山植物，若全球溫度持續暖化，恐對物種帶來巨大威脅 (Thuiller *et al*. 2005, Chou *et al*. 2011, Pauli *et al*.2012)，因此，有必要瞭解這些高山受威脅植物的地理分佈轉移，以識別其風險區及避難所的時空變化 (Baumgartner *et al*. 2018, Graham *et al*. 2019)。

為因應氣候變遷可能帶來的物種滅絕危機，預測受威脅種可能的潛在分佈，被視為是執行保育策略的首要任務 (Thomas 2010)。物種分佈模擬 (species distribution modeling, SDM) 可依據受威脅種存在位置與環境因子間的關聯性，預測潛在分佈範圍，配合氣候變遷情境更有助於瞭解動態發展，並製定適當的保育計畫 (Dhyani *et al*. 2021, Hoveka *et al*. 2022, Ceccarelli *et al*. 2022)。由於許多受威脅種通常也是族群數量相對稀少的物種，因此，SDM 的過程中，稀有種常因樣本數不足，使模型建構過程受到阻礙，另一方面，少量的樣本若配合多數的預測變項，可能導致模型過度擬合，從而影響預測的準確度 (Vaughan and Ormerod 2005)。為因應這些問題，近年研發出的小模型集成法 (ensemble of small models, ESM)，便是專為改善稀有物種分佈預測的新穎方法，其策略是將預測變項拆分成各種可能的雙變項配對組合，藉由這些小子集來構建以雙變項為主體的大量小模型，當有 n 個變項時，利用公式 $n(n-1)/2$，便可得知可生成的小模型數，每一模型經過測試後，再根據準確度進行加權平均，產生最終的集成預測結果。ESM 不僅能有效排除過度擬合問題，與標準的 SDM 方式相比，物種的樣本數量愈少，愈能突顯

準確度改善的程度 (Lomba *et al*. 2010, Breiner *et al*. 2015)。

忍冬屬 (*Lonicera*) 為忍冬科 (Caprifoliaceae) 下的一個屬，大概分佈於北半球溫帶與亞熱帶地區。目前為止，鑑定為臺灣原生的忍冬屬植物計有7種，其中，川上氏忍冬 (*Lonicera kawakamii*) 為落葉性的直立灌木，是分佈在臺灣高山 (海拔 3,000-3,900 m) 的特有種植物，目前野生的族群量不多，根據臺灣區域尺度的保育評估系統，將其列為受威脅種類中的 " 易危級 (Vulnerable)"(臺灣植物紅皮書編輯委員會 2017)。

臺灣是位處東亞太平洋上的亞熱帶島嶼，受氣候變遷影響甚鉅，根據 1911~2009 年統計，氣溫增溫約 1.4°C，遠高於全球平均值，足見臺灣的氣候暖化趨勢已相當明顯 (Shiu *et al*. 2009, 盧等 2012)。有鑑於此，原本就處於受威脅狀態的川上氏忍冬，正面臨嚴格的考驗，本研究即鎖定該物種為目標種，應用 ESM 建構預測模型，並從中瞭解影響物種潛在分佈的主要因子，進一步搭配政府間氣候變化專門委員會 (Intergovernmental Panel on Climate Change, IPCC) 最新的第 6 次評估報告中，所提出之氣候變遷情境，預測適宜棲地範圍的動態發展，研究成果可提供生態保育與經營管理之參考。

材料與方法

一、研究區概述

臺灣本島位於亞洲東部、太平洋西北側，西側緊鄰臺灣海峽，土地面積約 36,000 km^2。地形陡峭，多為山地與丘陵，平原及都市用地主要集中於西部沿海，形成東高西低的地勢，主要山脈有中央、玉山、阿里山、雪山及海岸等 5 大山脈，其中，玉山主峰為最高峰，標高 3,952 m；河川多發源於中央山脈，水系密布，大多分佈於西半部，流域長度最長的為濁水溪，面積最廣的為高屏溪；據中央氣象局資料顯示，年均溫約 21°C，年雨量約 2,500 mm，冬季有來自西伯利亞的大陸冷高壓，以東北季風為主，夏季則有來自太平洋的海洋高壓，以西南季風為主；據林務局第 4 次森林資源調

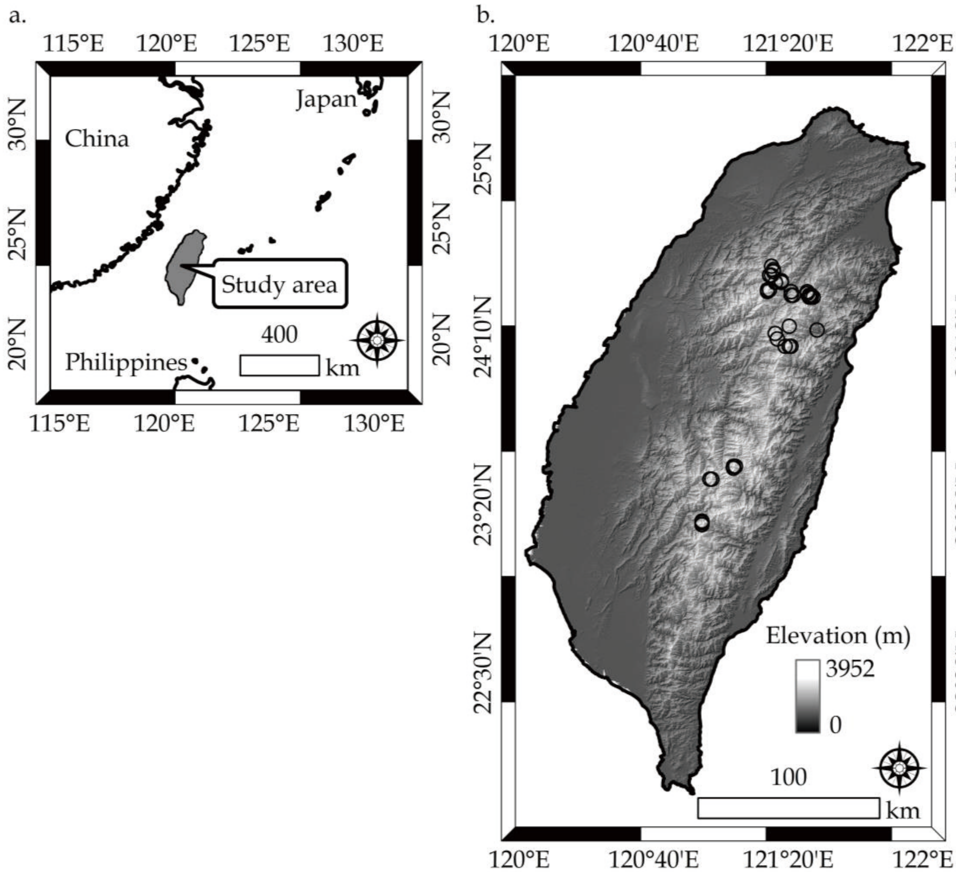

圖 **1.** (a) 研究區地理位置圖；(b) 物種出現點位 (黑色標記 ; n=36) 及數值高程模型 (digital elevation model)。

Fig. 1. (a) Geographical location of the study area; (b) Species occurrence records (black circle; n=36) and digital elevation model.

查報告，土地覆蓋型態以森林為主，占全島近 61% (圖 1)。

二、研究方法

(一) 物種存在資料

物種調查資料是來自生態調查資料庫系統 (ecollect.forest.gov.tw)，該批資料集是由林務局委託各大學院校和研究機構的專家及學者共同執行，屬全國性的官方自然資源普查計畫成果，本研究抽取忍冬屬物種的存在紀錄，座標格式為經緯度，僅使用 1981-2015 年期間的資料，以盡可能與環境資料的時間間隔匹配。考量到地理座

標的精確度，先刪除小數點不足 3 位的資料，進一步在 R 3.6.3 平台上，以軟件包 ”spThin” 進行空間過濾 (Aiello-Lammens *et al*. 2015)，減少空間自相關及地理取樣偏差的影響，為符合預測變項之空間解析力，設定各發生紀錄間的鄰近距離至少在半徑 1 km，經處理後剩下 36 筆的川上氏忍冬存在紀錄 (圖 1b)，另有 526 筆的非川上氏忍冬紀錄。

(二) 環境資料與變遷情境

氣候會影響生物的生理耐受性，土地利用與覆蓋 (land-use/land-cover, LULC) 則攸關其覓食、棲息或繁殖等行為，此外，由於地形對於高山植物的影響較不明顯 (黃 2019, Lu and Huang 2021)，因此，建模所使用之預測變項僅包含氣候和 LULC 兩類。現時的氣候資料是從 CHELSA V2.1 資料庫取得，涵蓋 1981-2010 年的全球氣象資料，本研究從中獲取 19 個 (BIO1-BIO19) 近 1×1 km 空間解析力之生物氣候變項 (Karger *et al*. 2017)，其源自每月的溫度 (℃) 和降水量 (mm)，包括年度趨勢、季節性變化及極端氣象特徵 (worldclim.org/data/bioclim.html)；LULC 方面是取自 Chen *et al*. (2022) 基於 Land-Use Harmonization 2 (Hurtt *et al*. 2020) 及 ESA-CCI 資料集 (www.esa-landcover-cci.org) 所建構的 2015 年全球 LULC 圖，包含森林、草地、農地、都市、荒地與水體等 6 種類別 (1×1 km 空間解析力)。由於植物在棲地間的傳播大多由動物所引導，常見的傳播距離約 1-10 km (Corlett 2009, Crossman *et al*. 2012)，考量到影響植物傳播的潛在範圍，本研究設定半徑 5 km 的移動窗，計算各 LULC 類別在移動窗內的覆蓋占比。總計共有 25 個預測變項，並將解析力重取樣為 1×1 km，為克服變項在統計上的多重共線性問題，以 R 軟件包 “virtual-species” 執行 Pearson 相關分析 (Leroy *et al*. 2016)，排除相關性高的變項，當相關係數大於 0.7 以上時擇一保留 (Dormann *et al*. 2013)。

對於未來的預測，本研究假設所有預測變項會隨 2021 年 IPCC 第 6 次

評估報告所發布的共享社會經濟途徑(shared socio-economic pathway, SSP)發生改變。本研究採用 SSP126 和 SSP585 兩種碳排放情境，也分別代表輕度和重度暖化情境，氣候類變項自前述 CHELSA V2.1 獲取 2085 年代(2071~2100 年的平均值) 兩種情境的生物氣候資料，包含 GFDL-ESM4、IPSL-CM6A-LR、MPI-ESM1-2-HR、MRI-ESM2-0 與 UKESM1-0-LL 等 5 種之大氣環流模型 (general circulation model, GCM)； 另 從 Chen *et al*. (2022) 取得相同年代的未來 LULC 變項，SSP126 與 SSP585 情境分別根據 IMAGE 和 REMIND-MAGPIE 兩種預測 LULC 變遷的綜合評估模型 (integrated assessment model, IAM)所產製。本研究使用 5 種 GCM 各別搭配兩種 IAM 為川上氏忍冬建模，並取其結果之平均數做為最終棲地適宜性，這種方式可排除模型間的不確定性 (Araújo and New 2007)。

(三) 小模型集成

ESM 是透過 R 軟件包 “ecospat” (Di Cola *et al*. 2017) 與 ”biomod2” (Thuiller *et al*. 2009) 共同執行，用來預測川上氏忍冬的適宜棲地。使用的演算法包括常見的彈性判別分析 (flexible discriminant analysis)、廣義相加模型 (generalized additive model, GAM)、廣義線性模型 (generalized linear model , GLM)、多變量適應迴歸 (multivariate adaptive regression splines, MARS) 和等 4 種統計迴歸模型；類神經網絡 (artificial neural networks, ANN)、增強迴歸樹 (boosted regression tree, BRT)、分類樹分析 (classification tree analysis, CTA)、最大熵 (maximum entropy, MaxEnt) 與隨機森林 (random forest, RF) 等 5 種機器學習演算法，由於所有演算法都需要背景點位 (或偽缺失點)，本研究將非川上氏忍冬的存在紀錄指定為背景點位，這是一種客觀的方法，可避免誤將未調查區視為非適合目標種棲息的點位 (Marshall *et al*. 2018, Williams *et al*. 2020)。模型性能使用 bootstrap 取樣法來評估，先逢機選取 70% 川上氏忍冬的存在紀錄做為訓練資料集，剩餘 30% 則做為測試資

料集，本研究使用 8 個預測變量，故在 ESM 的架構下，每一種演算法皆可產生 28 個小模型，進行 10 次的重複運算。

準確度評估依接受者操作特徵 (receiver operating characteristic) 所產生之曲線面積 (area under the curve, AUC)、真實技能統計值 (true skill statistics, TSS) 及 Boyce 指數 (Boyce index, BI, Boyce *et al*. 2002, Hirzel *et al*., 2006) 評估模型的性能。其中 AUC 值域介於 0.5~1，當值愈高代表模式推估出來的準確性愈佳，TSS 則落於 +1 至 -1，接近 1 表示模型幾乎完美，反之亦然 (Allouche *et al*. 2006)，當 AUC 與 TSS 分別高於 0.8 及 0.6 以上即達良好標準，若達 0.9 及 0.8 以上即達優越標準 (González-Ferreras *et al*. 2016)， BI 介於 -1 到 1 之間，正值表示預測模型與存在紀錄的分佈一致，接近零表示預測模型與隨機模型差距不大，負值表示預測結果不佳，即無物種出現的區域含有存在紀錄 (Hirzel *et al*. 2006)。所有小模型利用 Somers’D 進行加權，公式為 2×(AUC–0.5)，表現良好的模型將被賦予更高的權重，Somers' D 低於 0(AUC < 0.5) 的小模型則被排除 (Breiner *et al*. 2015)，最終，計算加權平均數後即可獲得介於 0-1000 的棲地適宜性圖。接著，參考最大 TSS 對應的適宜性做為閾值 (Liu *et al*. 2016)，並轉換為二位元 (binary) 的適宜 (1) 和非適宜 (0) 棲地圖，可用於觀察現時與未來之適宜棲地範圍變化。各預測變項對模型的重要性是透過 R 軟件包 ecospat 中的 “ecospat.ESM.VarContrib” 函數來衡量，其是將任一含有目標變項的模型，從所建構的 ESM 中抽離，計算抽離前後權重 (Somers’D) 加總的比值，當值大於 1 表示目標變項的貢獻度高於平均值。另反應曲線 (response curves) 則是觀察物種的適宜性與變項間之關係 (Elith *et al*. 2005)。

結　果

經相關分析後篩選出 8 個變項進行建模，模型性能的測試結果如 Table 1，所有演算法的 AUC 和 TSS 都達良好標準，其中 BRT、GAM 與 RF 更

表 **1.** 類神經網絡 (artificial neural networks, ANN)、增強迴歸樹 (boosted regression tree, BRT)、分類樹分析 (classification tree analysis, CTA)、彈性判別分析 (flexible discriminant analysis)、廣義相加模型 (generalized additive model, GAM)、廣義線性模型 (generalized linear model , GLM)、多變量適應迴歸 (multivariate adaptive regression splines, MARS)、最大熵 (maximum entropy, MaxEnt) 與隨機森林 (random forest, RF) 所獲得之接受者操作特徵曲線面積 (receiver operating characteristic, AUC)、真實技能統計值 (true skill statistic, TSS) 及 Boyce 指數 (Boyce index, BI)

Table 1. The area under the curve for the receiver operating characteristic (AUC), true skill statistic (TSS), and Boyce index (BI) generated by the artificial neural networks (ANN), boosted regression tree (BRT), classification tree analysis (CTA), flexible discriminant analysis (FDA), generalized additive model (GAM), generalized linear model (GLM), multivariate adaptive regression splines (MARS), maximum entropy (MaxEnt), and random forest (RF).

Algorithm	AUC	TSS	BI
ANN	0.93	0.76	0.95
BRT	0.96	0.85	0.98
CTA	0.93	0.78	0.93
FDA	0.87	0.66	0.92
GAM	0.95	0.82	0.96
GLM	0.89	0.67	0.94
MARS	0.89	0.65	0.93
MaxEnt	0.90	0.70	0.97
RF	0.98	0.94	0.81

表 **2.** 各預測變項對於集成模型之貢獻度

Table 2. Contribution of each predictive variable to the ensemble model.

Variable	Contribution
Min temperature of coldest month (BIO6)	2.09
Mean diurnal range (BIO2)	1.45
Precipitation of coldest quarter (BIO19)	1.11
Precipitation of wettest quarter (BIO16)	0.89
Urban	0.85
Water	0.80
Grass	0.69
Barren	0.60

達優越標準，就 BI 的表現來看，以 BRT 最佳，GAM 也屬相對較佳，RF 則為所有演算法之末。經由 ESM 處理後，僅保留性能相對佳的模型進行加權平均，獲取川上氏忍冬的棲地適宜性。

由 ESM 生成的模型評估各變項的貢獻度，結果如 Table 2 所示，貢獻度高於 1 的計有 3 個氣候類變項，由高至低依序為最冷月最低溫 (2.09)、平均日較差範圍 (1.45) 與最冷季降水 (1.11)，其餘低於 1 的變項大多為 LULC 類，對模型的影響力相對較小。進一步觀察由 ESM 推導出的棲地適宜性與主要貢獻變項間的反應曲線 (圖 2)，本研究發現，當最冷月最低溫增加，川上氏忍冬的適宜性隨之降低 (圖 2a)；平均日較差範圍約在 6°C 以上，適宜性明顯上升 (圖 2b)；當最冷季降水介於 300-500 mm 時，適宜性維持高峰，但雨量低於 300mm 或高於 500mm，適宜性皆快速下降 (圖 2c)。

空間分佈的預測結果顯示，川上氏忍冬的適宜棲地主要位於高海拔山區，面積估算約 1192 km^2，占臺灣本島面積約 3%(圖 3)。以現時的適宜棲地做為基礎，分別與 2085 年輕度 (SSP126) 與重度 (SSP585) 暖化情境的預測結果套疊，預計可能減少的面積各為 677 km^2 和 871 km^2，反觀，可維持適宜棲地的面積各僅 544 km^2 及 350 km^2，另兩種情境可新增的適宜棲地則微乎其微。由此顯示，無論何種情境，未來氣候暖化將不利於川上氏忍冬，且隨暖化情勢的加劇，適宜棲地縮減的情況愈明顯。

討　論

SDM 為預測氣候變遷對受威脅種潛在分佈影響和保育規劃的有效工具，但前提是必須建立在高準確的模型基礎上 (Hernandez *et al*. 2006, Liu *et al*. 2011)。本研究建構過程採用 9 種演算法，由性能的表現來看，無論是機器學習或統計迴歸的演算法，各評估指標都呈現良好 (Table 1)，由此顯示，縱然演算法的原理有差異，但建構出的模型性能一致性高，應是穩定且無過度擬合的問題。為維持模型的穩定

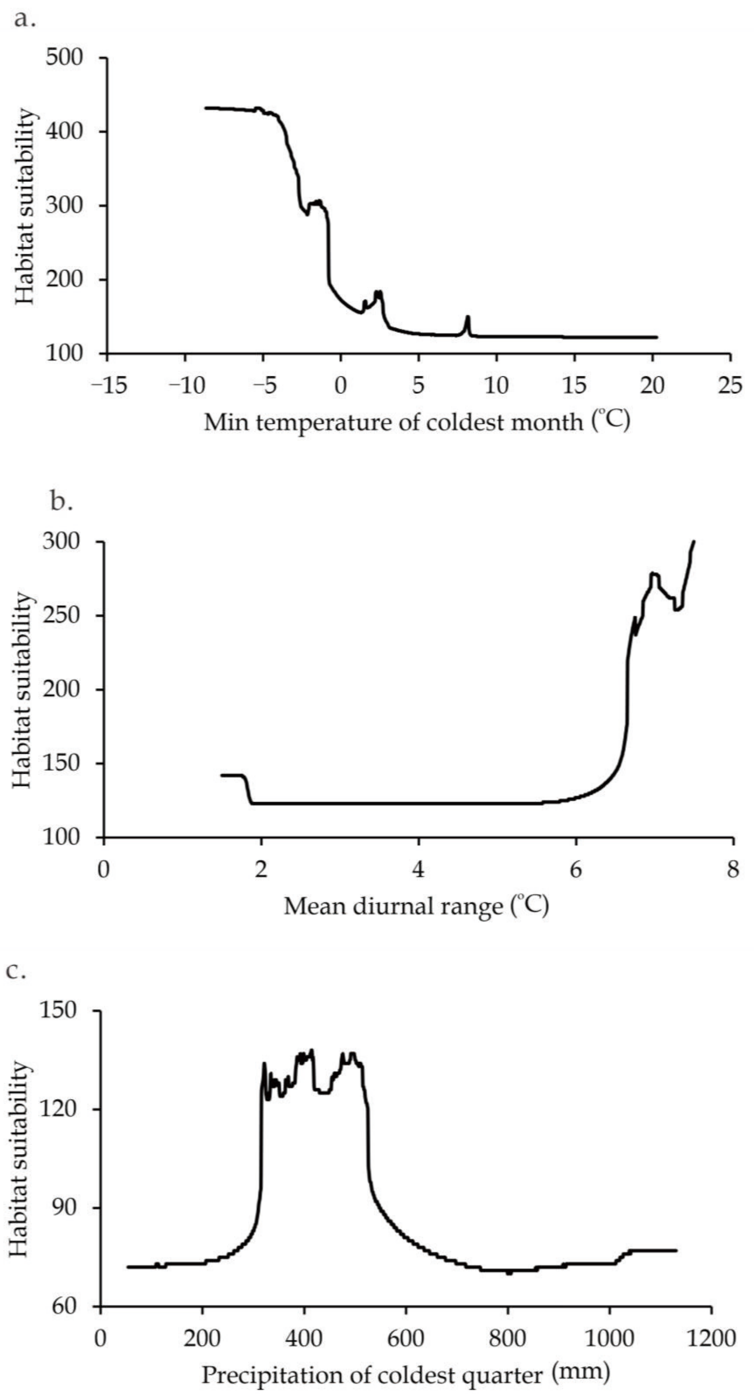

圖 **2.** 依據集成預測結果顯示主要貢獻變項之反應曲線；a、b 和 c 分別代表最冷月最低溫、平均日較差範圍與最冷季降水。

Fig. 2. Response curves of the primary contribution variables according to the ensemble prediction (a, b, and c represent the min temperature of coldest month, mean diurnal range, and precipitation of coldest quarter, respectively.

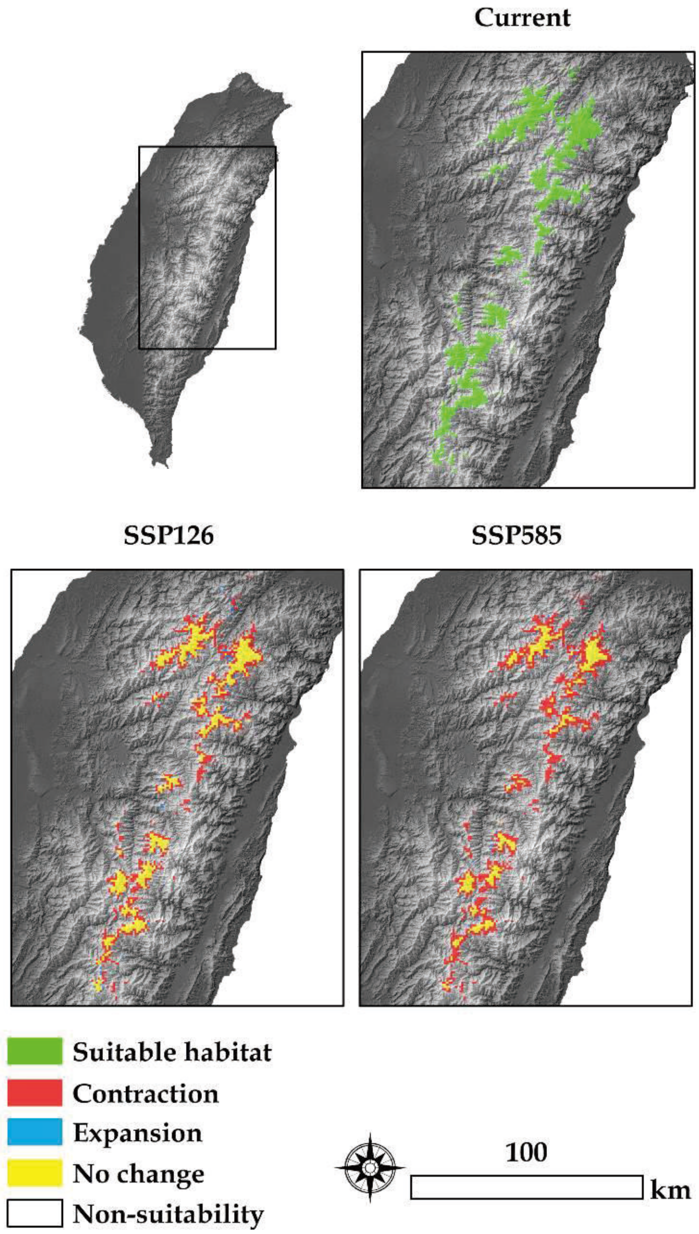

圖 **3.** 川上氏忍冬的適宜棲地預測。右上圖為現時分佈，下圖為 2085 年代兩個不同的氣候變遷情境輕度 (SSP126) 及重度 (SSP585) 碳排放預測分布結果。

Fig. 3. Prediction of the current suitable habitat for *Lonicera kawakamii*. The upper right panel shows the current distribution, and the bottom-left and bottom-right panels stand for SSP126 and SSPP585 emission scenarios, respectively, in 2085.

性，僅保留高性能的模型進行 ESM，可提升後續動態預測的說服力，因此，本研究因應氣候變遷所建置的物種潛在分佈資訊，對於往後的保育計劃上提供了有效的科學依據。

預測變項對模型的影響力而言，氣候類明顯大於 LULC 類，因此，本研究以 ESM 構建的預測模型主要是由氣候因子所驅動，貢獻最大者為最冷月最低溫、平均日較差範圍與最冷季降水等 3 個變項 (Table 2)，是決定川上氏忍冬在空間上存在與否的關鍵。詳細的棲位特徵顯示 (圖 2)，該物種偏好 0ºC 以下的低溫及日較差明顯的寒冷環境，這也反映出其潛在分佈受限的原因，相反地，高溫環境非其適宜棲位，故暖化持續可能會造成巨大的衝擊。除了溫度外，高山地區的降水也是一個重要因子，不僅會關係著植物的生長，還會影響遺傳變 異 (Chaves *et al*. 2003, Manel *et al*. 2012)，本研究發現，冬季適度的降水有利於川上氏忍冬，大約 300-500 mm 範圍間最佳，超過該範圍反而會帶來負面影響。有關 LULC 類變項的貢獻相對低，應是臺灣的高海拔以天然林為主，自然就無法反映其他土地利用類型對模型模擬的效應，過往也有相似的研究結果可尋 (Eskildsen *et al*. 2013, Chitungo *et al*. 2022)。

由於植物生理和物候特徵上的差異，地理分佈狹窄的高山物種受到的潛在威脅會比廣泛種更大 (Thuiller *et al*. 2005, Pauli *et al*.2012)。誠如前段所述，川上氏忍冬的適宜棲地屬條件較嚴苛的環境，根據模型所預測的分佈結果發現，該物種的適宜棲地面積不大，並分佈在臺灣海拔最高的山區，如雪山、南湖大山及玉山等，比對過去的植群調查報告，所預測的分佈與實地現況大體一致 (呂及林 1990；歐等 2003；王等 2010)。然而，未來全球暖化恐導致高山生態系的溫度異常，有關臺灣氣候變遷的預測，大體是往暖化加劇的走向發展，與川上氏忍冬偏好低溫、日較差大和特定範圍的降水量等氣候棲位大相逕庭，如暖化的特徵會反映在空間格局，高山升

溫的幅度會比平原地區明顯 (Lin *et al*. 2015)；不僅如此，大部分地區的夜間溫度變暖，導致日較差減弱 (Tsai *et al*. 2022)；此外，乾濕季節的比例發生明顯變化，發生旱澇災害的風險增加，故降水的變異趨於極端 (Huang *et al*. 2012)。種種氣候變遷的跡象看來，臺灣未來的氣候型態將愈來愈不利川上氏忍冬，正如本研究的預測模型所示，SSP126 和 SSP585 兩種情境的預測結果，物種適宜棲地的面積都會大幅縮小 (圖 3)，殘存下來的零散棲地，則成了為數不多的避難所，故存在滅絕的風險。

生物多樣性面臨的最大威脅為棲地喪失，因此，保育行動最關鍵與最直接的方式便是保護棲地 (Pardini *et al*. 2017)。在本研究的研究結果基礎下，川上氏忍冬的保育策略可朝以下面向進行，第一，目前既有的就地保育系統，包括雪霸、太魯閣、玉山國家公園和丹大野生動物重要棲息環境等，皆是主要適宜棲地，可加強這些地區的氣候監測，必要時可根據物種適宜的氣候棲位輔助其引入到避難所。另一建議是加強遺傳面的試驗計畫，相關部門可配合宣揚忍冬屬植物的種質資源價值，以提升民眾的保育意識。

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低遺傳多樣性的易危植物濱槐之保育

Low genetic diversity of the vulnerable Ormocarpum cochinchinense (Fabaceae: Papilionoideae) in Taiwan and implications for its conservation

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摘要

濱槐 (*Ormocarpum cochinchinense* (Lour.) Merr.) 為豆科蝶形花亞科濱槐屬植物，在臺灣僅見於基隆和平島、綠島及蘭嶼，已被評為易危 (VU) 等級，為能確立其保育管理單位，本研究利用細胞核 internal transcribed spacer 及葉綠體 *trnH-psbA* 及 *trnL-trnF* 片段探討遺傳結構及分化，研究結果顯示分布在臺灣之濱槐遺傳多樣性極低，推測該物種曾受到基因漂變影響，喪失遺傳多樣性；族群間無分化推測可能與經由海流進行基因交流相關，而族群數量小及自花授粉亦為遺傳多樣性喪失原因之一。保育策略上建議應將 3 個族群視為 1 個管理單位，並以蘭嶼族群優先進行保育規劃，未來應收集種子與種苗進行域外保育，培育之個體可作為原生之景觀植物。

Abstract

Ormocarpum cochinchinense (Lour.) Merr. (Fabaceae: Papilionoideae) has been categorized as a vulnerable species in Taiwan, as its distribution is restricted in Heping Island, Green Island (Lyudao), and Lanyu. To establish a management unit for species conservation, the nuclear internal transcribed spacer, as well as the chloroplast *psbA-trnH* and *trnL-trnF* regions were applied to assess the genetic structure and the level of population differentiation of *O. cochinchinense*. Low genetic diversity was detected in all three populations in Taiwan, suggesting that genetic drift has reduced their genetic variations. No differentiation among populations may be attributable to a high level of gene flow via ocean currents. The loss of genetic diversity may be also related to their small population size and self-fertilization. Three populations of *O. cochinchinense* should be integrated as one management unit. The population of Lanyu should be protected in priority. Seeds and seedlings should be collected for *ex situ* conservation, and those cultivated individuals could be used as native landscape plants.

緒言

臺灣為一大陸型島嶼，其島嶼上的物種與鄰近大陸物種親緣相近，因地理隔離使得地理分隔之物種趨向分化，尤其以高山物種最為顯著 (Chiang and Schaal, 2006; Chiang et al., 2006; Huang et al., 2011)，然而對於海濱物種而言，水流為其重要之傳播方式之一，植物繁殖體如枝條、種子或果實等經由水流進行傳播，使得分隔兩地的物種或族群間產生基因交流 (Harwell and Orth, 2002; Nilsson et al., 2010)，如 Takayama et al., (2006, 2008) 研究分布太平洋及印度洋地區的黃槿 (*Hibiscus tiliaceus* L.) 族群均呈現低度分化；或是海流形成物理障蔽，使得不同側的物種或族群產生分隔，進而降低基因交流，如 Yamamoto et al., (2019) 研究分布西太平洋及印度洋地區的濱豇豆 (*Vigna marina* (Burm.) Merr.) 族群呈現

高度分化，推測因海流方向而產生地理隔離，進而造成族群分化。

物種族群間基因交流主要由花粉及種子傳播能力所影響，進而影響其遺傳結構，若基因交流受到阻礙，分隔的族群將趨向分化，反之若有頻繁之基因交流，即便長距離分隔的族群亦會有相似的遺傳組成 (Kudoh and Whigham, 1997)。被子植物的葉綠體片段主要為母系遺傳與種子傳播相關，而細胞核片段為雙系遺傳，與花粉及種子傳播相關 (Huang et al., 2011; Lee et al., 2018; Mccauley, 1994)，因此結合兩者分子標誌物將可了解花粉及種子傳播對於物種族群結構之影響。

受脅植物常因棲地破壞或過度採集等因素造成族群數量減少，使得基因漂變影響增大，易導致遺傳多樣性喪失，因此在面臨環境變遷下其適存度亦隨之降低，進而導致物種滅絕。受脅物種的保育應確認物種其分類地位及族群遺傳結構，在進行保育計畫時，應針對具高度遺傳多樣性，且為演化顯著單位 (Evolutionary Significant Unit, ESU) (Moritz, 1994, 1999) 的族群優先管理；相較於演化顯著單位著重在於演化歷史，管理單位 (Management Unit, MU) 則著重於現今的族群動態，侷限的基因交流造就成不同之管理單位 (Funk et al., 2012; Coates et al., 2018)。Wang (2020) 針對受脅特有種四川牡丹 (*Paeonia decomposita* Hand.-Mazz.) 進行遺傳結構分析，顯示其野生族群保有較低之遺傳多樣性，因有較高之基因交流導致族群間低度分化，並確認三個管理單位供後續保育管理；Lee et al., (2018) 評估受脅特有種烏頭屬植物 (*Aconitum austrokoreense* Koidz.) 之遺傳組成，顯示其遺傳多樣性低，且族群間呈現顯著遺傳分化，符合距離隔離模型 (isolation by distance)，推測該物種曾遭遇嚴重之瓶頸效應 (bottleneck effect)，持續的棲地破壞及侷限之傳播能力可能加速該物種滅絕。因此，在進行保育工作之前，除了瞭解物種現況之外，結合遺傳結構研究，並應用於管理策略的擬定上，有助於達成物種保育目標。

豆科濱槐屬植物，大約有 20 種，主要分佈在熱帶非洲，但也分佈在馬

達加斯加、非洲南部、阿拉伯南部到菲律賓、澳大利亞北部和斐濟 (Thulin and Lavin, 2001)，臺灣產濱槐 (*Ormocarpum cochinchinense* (Lour.) Merr.) 1 種，僅見於基隆和平島、綠島及蘭嶼等地，2017 臺灣維管束植物紅皮書名錄中將其列為易危 (VU) 等級 (Editorial Committee of the Red List of Taiwan Plants, 2017)。該物種萃取物具有藥用潛力，可用於抗癌及骨頭修復等 (Kumar et al., 2013; Gnanavel et al., 2017)，Lim et al., (2019) 指出該物種在新加坡已列入 Species Recovery Programme，藉由收集種子及枝條進行復育，並重新種回海岸地區以維持族群數量，唯缺乏族群遺傳結構方面研究。因此，本研究目的如下：

1. 探討分布於臺灣之濱槐葉綠體及細胞核片段遺傳組成差異。
2. 探討遺傳分化及族群遺傳結構。
3. 建立該物種之管理單位，並評估可行之保育策略。

材料與方法

採樣地點

本研究採樣地點分別為北臺灣的基隆市和平島、台東縣綠島鄉及蘭嶼鄉等地，取新鮮葉片 3-5 片以乾燥劑乾燥後帶回實驗室進行後續實驗。

DNA 萃取及定序

將乾燥之葉片以 cetyltrimethylammonium bromide (CTAB) 方式 (Doyle and Doyle, 1987)，萃取植物組織中的 genomic DNA。利用細胞核 internal transcribed spacer (nrDNA) (Chiang et al., 2001)、葉綠體 *trnH-psbA* (Shaw et al., 2005) 及葉綠體 *trnL-trnF* (Taberlet et al., 1991) 片段引子以聚合酵素 (Promega, GoTaq® Green Master Mix, USA) 在溫度循環器 (Appilied Biosystems, MiniAmp Plus Thermal Cycler, Singapore) 擴增出 DNA，在總體積 50μl 的反應液中加入 25 *m*L 聚合酵素，濃度 2μM 的引子各 5μl，最後加入 10ng DNA，以無菌水補足 50μl。聚合酵素反應在溫度循環機進行，共進行 30 個循環，每個循環流程為：92°C，45 秒，將 DNA 的雙股變性打

開 (denaturation)：55°C，1 分 15 秒，使 DNA 與引子結合 (annealing)：72°C，1 分 15 秒，進行 DNA 延伸反應 (extension)，最後在 72°C 作用 10 分鐘。PCR 結束後，取 5μl 的 PCR 產物加上 1μl 6 倍的染色溶液，在 1% 瓊脂凝膠中以 100 伏特電壓跑電泳約 30 分鐘，經過溴化乙啶螢光染劑 (BioVision, USA) 處理後，配合所選用的 DNA ladder 當分子大小的標記，並在紫外線燈下顯色及拍照。 選擇合適之片段送往生技公司以毛細管自動核酸定序儀 (Applied Biosystems, ABI 3730XL, USA) 進行定序。

序列及族群遺傳分析

將定序完成之序列以 Molecular Evolutionary Genetics Analysis (MEGA) X (Kumar et al., 2018) 進行比對及排列，比較彼此間鹼基對替換 (transition; 兩個嘌呤或嘧啶間的突變，A/G 或 T/C 突變) 及鹼基對顛換 (transversion; 嘌呤與嘧啶間的突變，T.C/A.G 突變) 的發生頻率及比值，來計算濱槐的序列變化。

將 NCBI 資料庫 (National Center for Biotechnology Information; https: // www.ncbi.nlm.nih.gov/) 濱槐屬植物及近緣物種之細胞核 internal transcribed spacer (nrDNA) 和葉綠體 *trnL-trnF* 片段與本研究之濱槐利用 RAxML (Kozlov et al., 2019) 程式以 Maximum likelihood 方式重建親緣樹狀圖。

以 DnaSP 6 (Rozas et al., 2017) 計算族群內及族群間的遺傳多樣性。以單型多樣性 (haplotype diversity)(Nei and Tajima, 1983) 及以核甘酸多樣性 (nucleotide diversity) (Jukes and Cantor, 1969) 估算族群內的遺傳多樣性。估算族群間的遺傳分化，並根據 $FST = 1/(1+2Nm)$ 的公式，估計族群間可能的基因交流，其中 N 中是表示族群中個體的有效族群量，m 表示個體的遷徙能力，當 FST 值愈高，族群間的遺傳分化程度就愈大。

結果與討論

臺灣濱槐之生育地環境及植株特徵如圖 1，本研究採集位置如圖 2，採樣數目分別為和平島 6 個、綠島 10 個和蘭嶼 12 個樣本，共 3 個族群 28 個樣本，利用 PCR 成功增幅細胞核 internal transcribed spacer (nrDNA) 及葉綠體 *trnH-psbA* 及 *trnL-trnF* 片段 (表 1)，其序列經比對後長度分別為 642、348 及 991 鹼基對，nrDNA、*trnH-psbA* 及 *trnL-trnF* 片段 GC content 比值分別為 57.3%、30.8% 及 33.3%。

將 NCBI 之濱槐屬植物及本研究之濱槐 nrDNA 片段共 19 個分類群以 Maximum likelihood 方式重建之親緣關係樹 (圖 3)，濱槐與 *O. orientale* (Spreng.) Merr. 最為近緣 (NCBI 編號：AF068159)，World Flora Online 指出 *O. orientale* 為濱槐之同物異名 (WFO, 2022)，確認分布於臺灣之濱槐分類地位。nrDNA 及 *trnH-psbA* 片段在種內均無變異，均僅有一個單型 (haplotype)，核苷酸及單型多樣性均為 0，比較族群間之遺傳多樣性及族群分化指數 (F_{ST}) 均為 0。*trnL-trnF* 片段在種內具有 2 個單型，核苷酸及單型多樣性分別為 0.00015 及 0.148，比較族群間之遺傳差異，臺灣濱槐族群間分化指數 (F_{ST}) 為 0 - 0.09 (表 2)；相較於和平島及綠島僅有 1 個單型，蘭嶼族群保有較高之遺傳多樣性。選用具有變異之 *trnL-trnF* 片段重建臺灣濱槐之親緣樹狀圖 (圖 4)，並以 NCBI 資料庫之 *Dalbergia oliveri* Gamble ex Prain (NCBI 編號：MN823694) 作為外群，結果顯示 3 個族群均聚在一起，僅蘭嶼族群具有變異。

遺傳多樣性探討

保育的目的在於維持物種之多樣性，維持其原生棲地及野生族群數量為重要課題之一，然而若棲地破壞及族群數量下降通常會導致物種之遺傳多樣性下降，一旦族群數量過低，近親交配及遺傳漂變將會導致遺傳多樣性降低 (Frankham et al., 2002; Spigler et al., 2017)。因族群小且棲地破碎化導致僅保有較低之遺傳多樣性，在遺傳多樣性喪失的情況下，可能導致物種適存度降低，無法適應環境變遷而滅絕 (Vranckx et al., 2012)。島嶼因地理位置的獨特性，保有較高之物種特有比例，但其物種可能都來自於少量之個體拓殖，這種奠基者效應 (founder effect) 下所移入之物種，通常僅保有較低之遺傳多樣性，因族群數量少且容易近親交配，產生較高之同型合子

比例，較容易累積有害之突變，引起近親衰退 (Hamabata et al., 2019)。濱槐在臺灣的分布侷限於北部基隆市和平島、東部台東縣綠島鄉及蘭嶼鄉，其分布較為狹隘，且野生族群數量相對少，本研究利用分子標誌物評估濱槐之遺傳多樣性，該種在細胞核或葉綠體片段均僅有 1-2 單型，顯示濱槐分布於臺灣之遺傳多樣性極低，推測該物種曾受到基因漂變影響，使得遺傳多樣性喪失，此一現象常見於受脅物種 (Szczecińska et al., 2016; Wang, 2020)。

族群分化及基因交流探討

比較臺灣之濱槐族群，nrDNA 及 *trnH-psbA* 均無變異，*trnL-trnF* 族群間之分化指數為 0- 0.09，顯示族群間無或低度分化，推測可能原因為：(1) 受到基因漂變影響，使得稀有對偶基因喪失，僅留下常見的對偶基因，造成族群間無分化；(2) 基因交流導致族群間無分化，海濱植物傳播通常與海流相關，並進行長距離傳播，使得地理分隔之族群呈現低度分化 (Harwell and Orth, 2002; Nilsson et al., 2010)；臺灣亦有相似案例，如津田氏大頭竹節蟲 (*Megacrania tsudai* Shiraki)，該物種僅分布於恆春半島及綠島，結果顯示族群全無遺傳變異，推論該物種源自一小族群或少數個體經由海流遷徙至臺灣 (Wu et al., 2012)；臺灣之濱槐族群間在 nrDNA 及葉綠體片段均呈現無或低度分化，代表不論是經由花粉或種子傳播方式，其族群間均有較高基因交流，推測可能與海流相關，即便分隔之族群間可能藉由海流進行長距離傳播，使得族群間無分化。此外，族群內低度分化可能與自花授粉機制有關 (Huang et al., 2019)，黃豬屎豆 (*Crotalaria micans* Link) 與濱槐同為蝶形花亞科 (Papilionoideae) 植物，因其蝶形花的龍骨瓣特徵，在缺少授粉者的狀態下，藉由改變雄蕊及雌蕊相對位置或同時成熟，可自花授粉並產生可孕之種子 (Etcheverry et al., 2003)。推測濱槐因族群數量少，可能缺乏授粉者的協助，該物種偏向以自花授粉方式繁衍，進而造成基因窄化現象。

保育策略建議及未來展望

保育目的在於維護生物多樣性，

確定管理單位為保育重要目標之一，應將具有不同之遺傳組成之族群視為不同之管理單位，本研究利用 nrDNA 及葉綠體片段進行分布於臺灣之濱槐遺傳組成分析，顯示現有三個分隔之族群間並無遺傳分化，在保育策略上建議應將其視為同一管理單位進行規劃，然而蘭嶼較其他兩個族群保有完整的二個葉綠體 *trnL-trnF* 基因型而有較多遺傳多樣性，應列為優先保育及復育之族群。濱槐已列為易危等級植物，後續可比照新加坡模式，收集根櫱苗、種子與種苗進行培育，培育之個體可作為原生之景觀植物，優先用於海濱地區造林等。未來應持續收集濱槐樣本，建立種原之遺傳資料庫。

相較於細胞核及葉綠體 DNA 片段，微衛星 DNA (simple sequence repeat; SSR) 與單核甘酸多型性 (Single nucleotide polymorphism; SNP) 等分子指紋 (DNA fingerprinting) 技術提供了幾近中性且代表整個基因體之分子標記，其對偶基因的特性更提供了估算族群中異型基因合子和遺傳變異以及族群間遺傳分化程度的可能；物種族群遺傳結構受繁殖策略及傳播模式所影響，有關濱槐生殖、種子及花粉傳播方式等仍需更多佐證資料，後續可針對濱槐族群進行微衛星 DNA 與 SNP 篩選、生殖及傳播模式試驗等，並應用於評估族群動態，提供更加完整的生態及遺傳資訊，用以後續修正並提出合適之保育策略。

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表 1. 分布於台灣之濱槐採樣資訊及遺傳多樣性。

Table 1. List of sampling locations, nucleotide diversities, and haplotype diversities of the *nrDNA*, *trnH-psbA*, and *trnL-trnF* regions sequences of *Ormocarpum cochinchinense* in Taiwan.

species	location	code	longitude	latitude	sample size	nrDNA nucleotide diversity	haplotype diversity	*trnH-psbA* nucleotide diversity	haplotype diversity	*trnL-trnF* nucleotide diversity	haplotype diversity
O. cochinchinense					28	0	0	0	0	0.00015	0.148
	和平島	HP	121.769	25.157	6	0	0	0	0	0	0
	綠島	LD	121.472	22.656	10	0	0	0	0	0	0
	蘭嶼	LY	121.550	22.044	12	0	0	0	0	0.00031	0.303

表 2. 以 *trnL-trnF* 估算濱槐的族群分化指數。HP: 和平島；LD：綠島；LY：蘭嶼。

Table 2. Pairwise F_{ST} between pairs of populations from *trnL-trnF* for *Ormocarpum cochinchinense.* HP: Heping Island; LD: Lyudao; LY: Lanyu.

	HP	LD	LY
HP	-		
LD	0	-	
LY	0.09	0.09	-

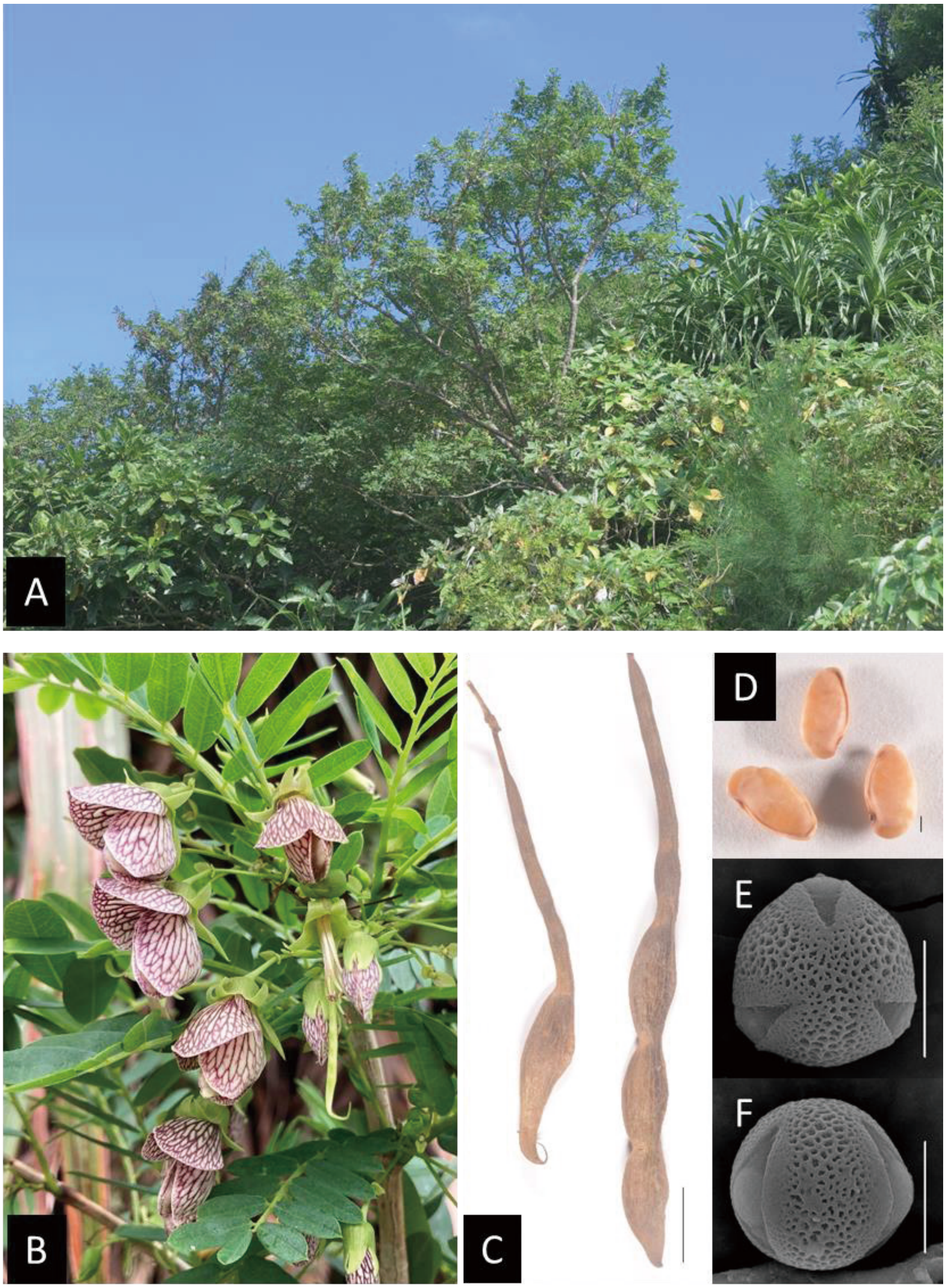

圖 1. 濱槐 A, 生育地 ; B, 花枝 ; C, 果 ; D, 種子 ; E, F, 掃描式電子顯微鏡之花粉 (比例尺 : C = 1 cm, D = 1 mm; E, F = 10 μm)。

Fig. 1. *Ormocarpum cochinchinense* (Lour.) Merr. A, habit; B, branch with flower; C, fruits; D, seeds; E, F, SEM photographs of pollen (scale bar: C = 1 cm, D = 1 mm; E, F = 10 μm).

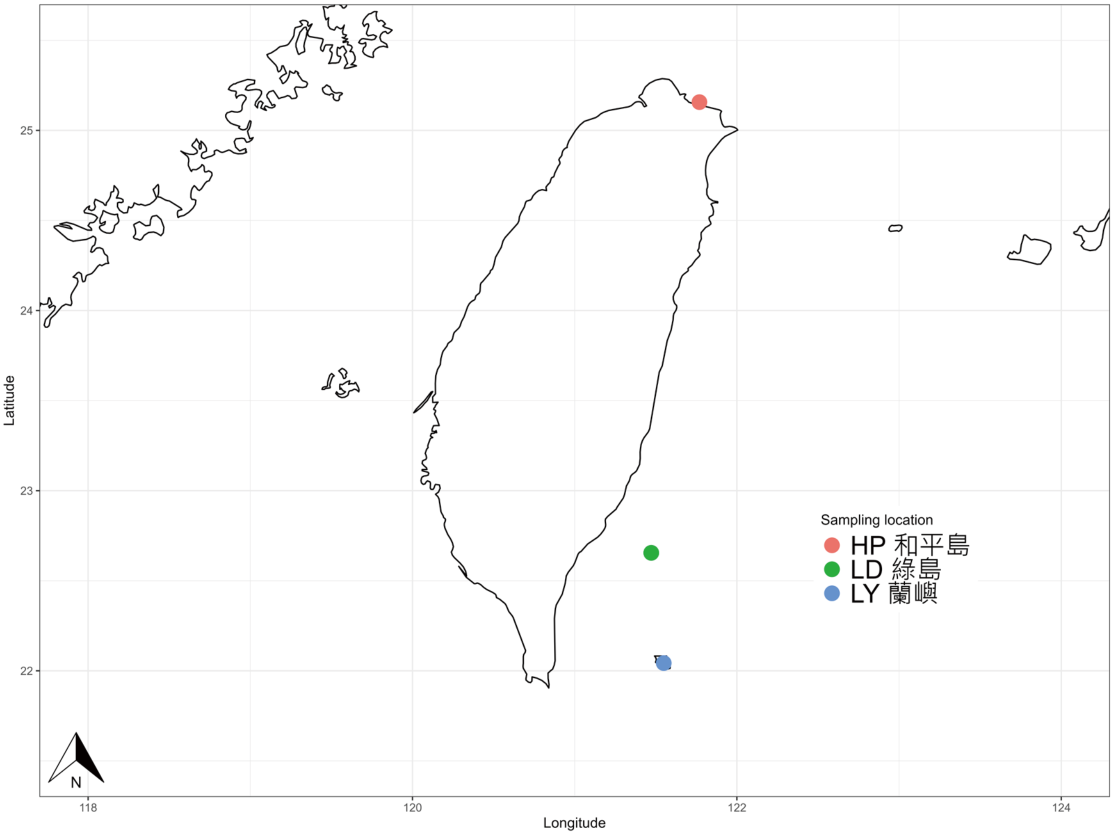

圖 2. 分布於臺灣之濱槐族群採樣位置。

Fig. 2. The sampling locations of *Ormocarpum cochinchinense* in Taiwan.

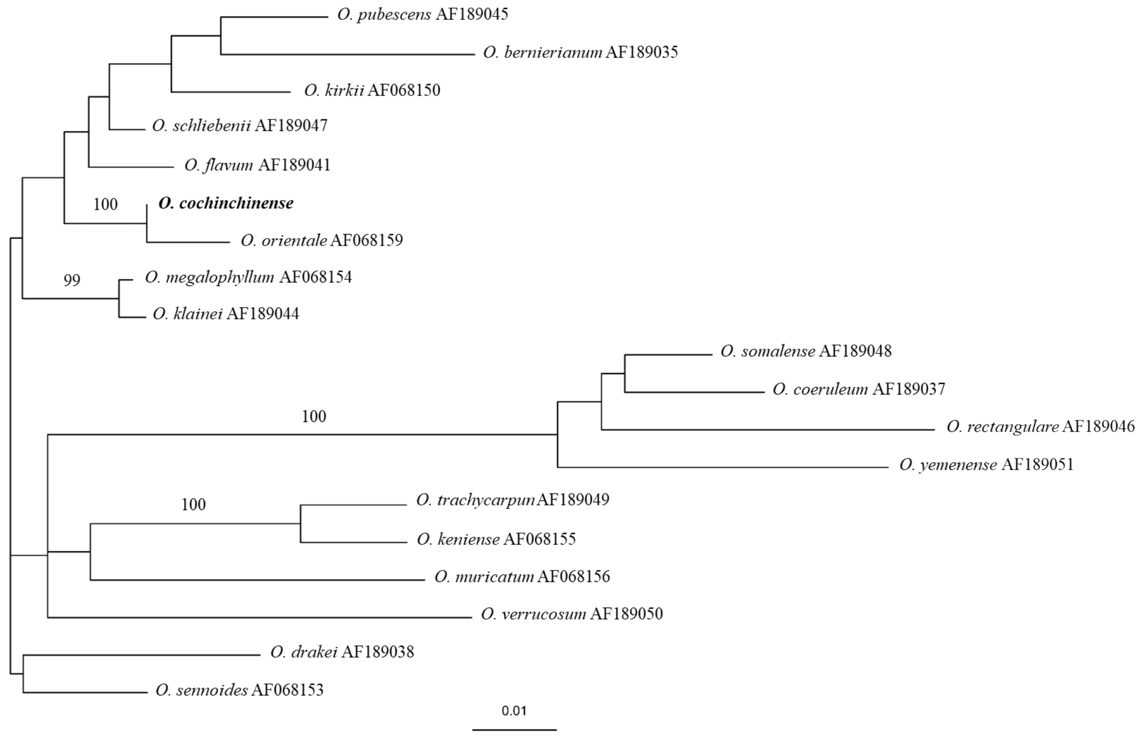

圖 3. 以 Maximum Likelihood 方式重建之濱槐屬植物親緣樹狀圖，分支數字為 bootstrap 值 (>70)，學名後面為 NCBI 資料庫編號。

Fig. 3. The maximum likelihood tree of nrDNA of *Ormocarpum*. Numbers at nodes indicate bootstrap value (>70).

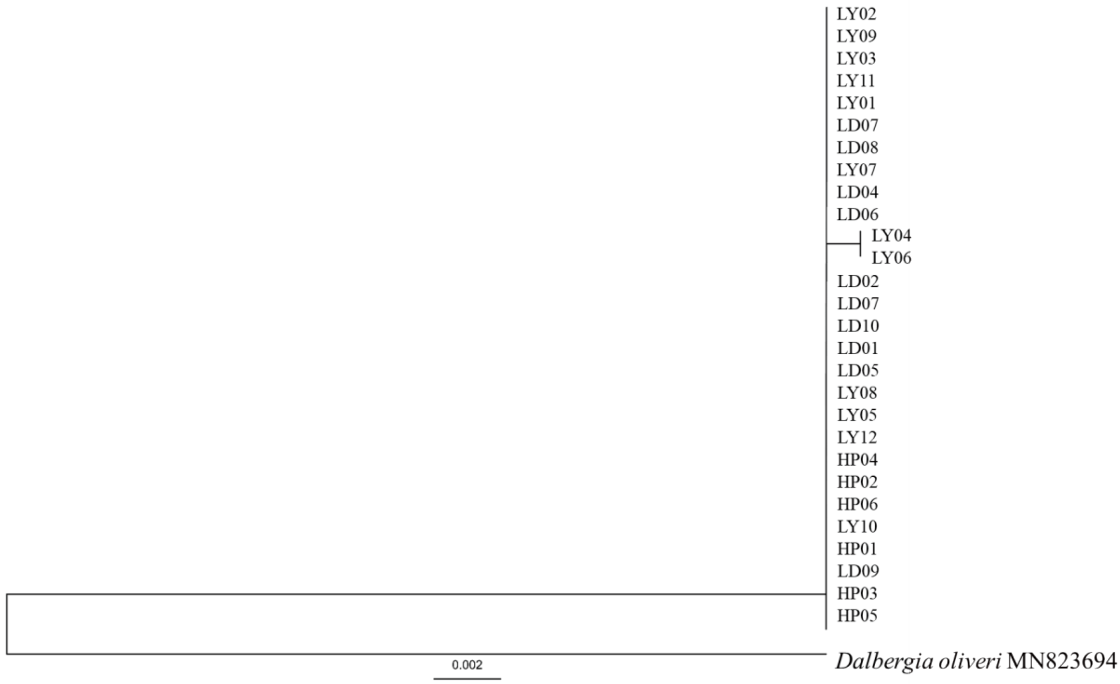

圖 4. 以 Maximum Likelihood 方式重建之濱槐屬植物親緣樹狀圖，以 *Dalbergia oliveri* 為外群。HP: 和平島；LD：綠島；LY：蘭嶼。

Fig. 4. The maximum likelihood tree of *trnL-trnF* of *Ormocarpum.* HP: Heping Island; LD: Lyudao; LY: Lanyu.

「台灣生物多樣性研究」稿約

壹、一般說明

一、《台灣生物多樣性研究》爲行政院農業委員會特有生物研究保育中心出版之學術期刊，歡迎國內外學者發表有關生物多樣性或自然保育之學術論文與有關物種出現資料之資料論文，但以未曾在其他刊物發表之原創研究及資料爲限。

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