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封面圖說／

短突紅螫蛛 (*Cheiracanthium insigne*) 成熟雄蛛。

(劉函景 攝)

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澎湖竹灣海域棲居於延繩式養殖牡蠣串之動物相

Fauna in Longline Oyster Farm in Jhuwan Waters, Penghu, Taiwan

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摘要

本研究為調查澎湖縣竹灣海域延繩式養殖牡蠣周遭的生物。採樣時間為2018年7-8月與2019年7-8月。結果發現2018年之採獲物種的組成共7門32科38屬49種生物，採獲頻率分析則以少見與稀有漁獲種類為主，共佔92%；2019年之採獲物種的組成共4門9科10屬11種生物。由此可知此生態系的主要組成為少見與稀有物種，而較為多元的組成特性物種間的可取代性

高，生態系亦較為穩定。比較2017年底與2018年底冬季海溫，發現前者皆大約較後者低，推測影響2019年物種數與量的原因在於，2018年的冬季不夠寒冷，無法在此海域以大型藻類累積冬季的營養鹽。

關鍵詞：澎湖、牡蠣、動物相

Abstract

This study was conducted to investigate the basic fauna information in the longline oyster farm in the Jhuwan waters of Penghu County, Taiwan. Samples were collected from July to August in 2018 and 2019, respectively. A total of 49 samples, including 49 species, 38 genera, and 32 families from seven phyla, were obtained in 2018. Analysis showed that rare and scarce species had the highest appearance frequency, making up 92% of total samples. A total of 11 samples, including 11 species, 10 genera, and nine families from four phyla were obtained in 2019. Analysis showed rare species had the highest appearance frequency, reaching 82% of total samples. We conclude that the main inhabitants in this ecosystem are rare and scarce species, and the high fauna diversity allowed replacements of species. The ecosystem was thus more resilient. Comparison of sea temperatures in late 2017 and 2018 showed that 2018 was warmer, which could have adversely impacted species numbers and population in 2019, as warmer climate caused reduced nutrients and therefore lower seaweed growth in the winter.

Key words: Penghu County, oyster, fauna

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前言

澎湖群島係由64個大小島嶼所組成，地理位置位於中國與台灣之間，附近有中國沿岸流、黑潮支流、南海季風流等不同

海流匯集，漁業資源豐富，且附屬離島眾多，提供良好避風所，具有先天地理與海域的優越條件，而周邊海域水質潔淨，適宜海水養殖，故發展出眾多箱網養殖漁場（王，2010）。



圖版1. 澎湖內灣海域（紅圈）&採樣地點（★）(23.625926°E, 119.521558°N)
（圖片來源: Google map）

澎湖之內灣海域是指位在本島中間之半封閉海域（陳等，2016）（圖版1）。內灣海域與周邊海域深度具有明顯差異，內海水深大多在15 m以淺，因深度較淺又受部分陸地遮掩，故受季風、海浪、海流之影響較小，形成海洋生物良好的生活與棲息場所，同時也是澎湖當地沿岸漁業及近海漁船活動頻繁之海域，如牡蠣養殖等（陳等，2016）。目前在內灣的養殖戶多以空汽油桶或保麗龍塊等製作浮標，並以雙纜於一定的間隔串連在海上，而牡蠣吊掛於纜繩下（陳等，2010）。內灣海域中，又以竹灣海域較為廣大、平靜且水深適中，而成為一天然的養殖港灣（澎湖縣

西嶼鄉公所，2017）。

在台灣所養殖的牡蠣主要為葡萄牙牡蠣 *Crassostrea angulata*，養殖方式有插枝式、垂下式、竹筏式、延繩式等4種，早期的牡蠣養殖主要以插枝式、垂下式為主，後來因沿岸汙染嚴重，而慢慢轉為較外海的竹筏式與延繩式，在澎湖地區主要盛行延繩式牡蠣養殖是因內灣海域風浪較小且場地較大（陳等，2010）。

牡蠣可透過濾食淨化海水，並經由有機合成碳酸鈣達到固碳的作用，在海洋生態系中提供很高的「生態服務」價值，而於蚵棚聚生的牡蠣，則為許多海洋生物棲息與覓食的場所，使海岸線得以穩定（蕭

等, 2011)。所謂的生態服務指的是群聚具有相當高的生產力, 提供給許多初級消費者食物來源, 而徐(2013)提及藻礁可將游離之鈣離子固定, 在經由生長後形成碳酸鈣(CaCO_3)。藻礁構成的複雜立體多孔隙結構能為許多不同種類之底棲生物躲藏以作為棲地之用(Steller et al., 2003; 徐, 2013); 相同還有利用具有多層次的立體空間人工藻場, 作為底棲生物躲藏的還有洗(2019)研究附著中國半葉馬尾藻*Sargassum hemiphyllum* var. *chinense*藻苗之藻繩增加海洋生物棲息環境場域, 對漁業生物誘集的效益相當高。藻繩甚至可以作為新型放流遠海梭子蟹之利用(澎湖海洋生物研究中心, 2020)可見多層次的立體空間也可應用於養殖方面上。

由上述得知, 立體多孔隙結構以及多層次的立體空間之空間利用對於海洋生物幼苗可提供相當的棲息與成長的環境並達到生物誘集之效益, 也藉此成為一個小型生態系。本研究的牡蠣串上的牡蠣與牡蠣之間存在許多縫隙, 這些縫隙除了可以增加牡蠣的濾食作用外還可以提供大部分生物無論是成體或幼生躲藏以及成長之環境, 對於周遭海洋生態中的生物提供了避風港。

目前對於牡蠣之研究, 大多注重於幼生發育觀察、附苗基質、密度、淡水浴、疾病、附著物等(許與陳, 1989; 陳等, 2017; 鄧等, 2017; 簡等, 2018)。其中根據許與陳(1989)於附著物的研究中顯示出附著生物彼此間是具交互作用的, 上層靠近水面之生物, 易受溫度影響, 在水表層水溫變化明顯且劇烈生活的生物, 是需要

能容忍這種快速變化的, 而水流與水沫也集中於此, 生物亦須能耐得住水流衝擊, 多以水螅為主。另外, 簡等(2018)發現養殖密度高會使扁蟲大量聚集。

本研究目的為了瞭解延繩式養殖牡蠣串上的物種組成進而探討其作為海洋生物幼生的育苗場以及牡蠣串周遭所形成之小型生態系, 調查選定竹灣海域作為採樣地點, 並以螺貝類、頭足類、甲殼類、魚類等為主要之採集對象, 希望可建立基礎資料, 有助於日後海洋資源之管理與應用。

材料與方法

一、採樣時間、地點、頻率及方法

(一) 採樣時間

研究期間為2018年7月、8月及2019年的7月、8月, 分別為5: 00-9: 00及15: 00-17: 00。

(二) 採樣地點

位於澎湖縣西嶼鄉竹灣港, 自港口向海外海延伸約300-1000公尺的延繩式牡蠣串(23.625926°E, 119.521558°N)(圖版2)。

(三) 採樣頻率

為配合蚵農收成時間及判斷累計採樣曲線, 因此2018年為17次; 2019年為8次。

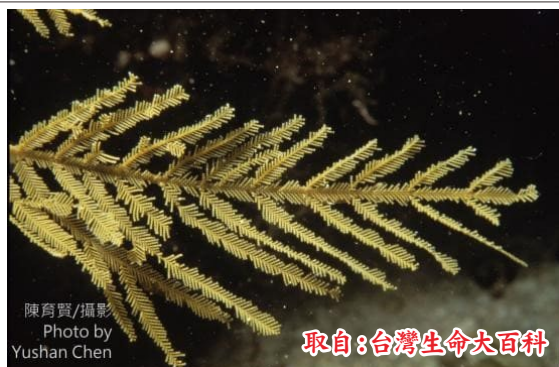
(四) 採樣方法

為將牡蠣串拉上竹筏, 此時以徒手採集掉落於船板與附著於牡蠣串上之生物, 並將之放置於水桶, 以便回到港口後, 進行紀錄。

二、樣本處理與鑑定

(一) 紀錄方法

以數位防水相機(Olympus Stylus TG-4



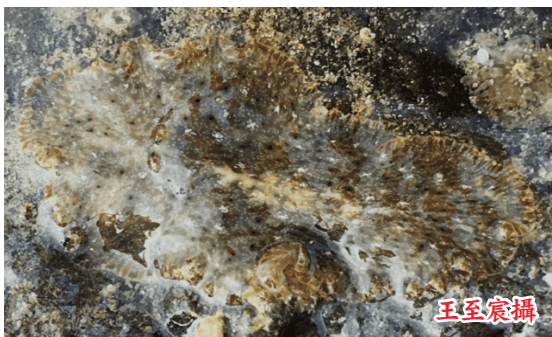
a. 柏狀羽螅
Aglaophenia cupressina #



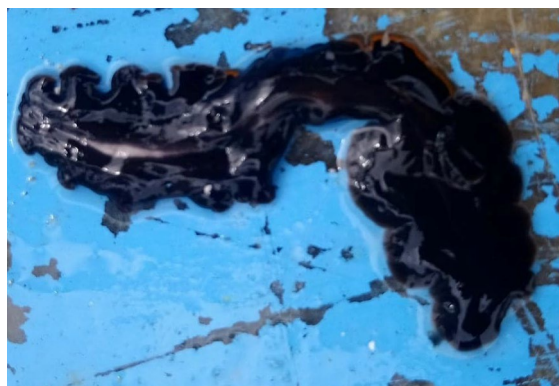
b. 白羽鞘水螅
Aglaophenia whiteleggei #



c. 大盤扁蟲 *Discoplana gigas* #



d. 網平渦蟲 *Planocera reticulata* #



e. 橙緣美麗海扁蟲
Calliplana marginata



f. 齒輪鐘螺 *Trochus sacellus*

圖版2. 澎湖竹灣牡蠣串上採獲物種
#:目視紀錄

a. 毛法螺 *Cymatium pileare*b. 花麥螺 *Pyrene scripta*c. 長蛸 *Octopus variabilis*d. 綠殼菜蛤 *Perna viridis*e. 黑蝶珍珠蛤 *Pinctada margaritifera*f. 牛角江瑤蛤 *Atrina pectinata*

圖版2-2. 澎湖竹灣牡蠣串上採獲物種



a. 尖角江瑤蛤 *Pinna muricata*



b. 旗幟江瑤蛤 *Atrina vexillum*



c. 沙蠶的一種 *Nereis* sp.



d. 模里西斯鎧甲蝦 *Galathea mauritiana*



e. 銳齒蟬 *Charybdis acuta* #
取自：澎湖的蟹類



f. 近親蟬 *Charybdis affinis*

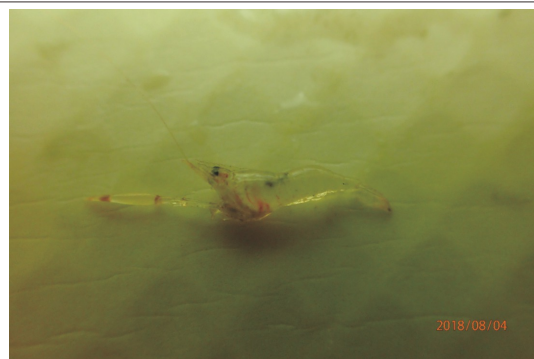
圖版2-3. 澎湖竹灣牡蠣串上採獲物種
#:目視紀錄

a. 安汶蟬 *Charybdis amboinensis*b. 善泳蟬 *Charybdis natator*c. 東方蟬 *Charybdis orientalis*d. 底棲短槳蟹 *Thalamita prymna*e. 雙額短槳蟹 *Thalamita sima*f. 皺紋花瓣蟹 *Liomera rugata*

圖版2-4. 澎湖竹灣牡蠣串上採獲物種



a. 印痕新近扇蟹 *Neoxanthias impressus*



b. 岩蝦的一種 *Pariclimenes* sp.



c. 短脊槍蝦 *Alpheus brevicristatus*



d. 日本龍蝦 *Panulirus japonicus*



e. 錦繡龍蝦 *Panulirus ornatus*



f. 矛形岩瓷蟹 *Petrolisthes hastatus*

圖版2-5. 澎湖竹灣牡蠣串上採獲物種



a. 平背蜞 *Gaetice depressus*



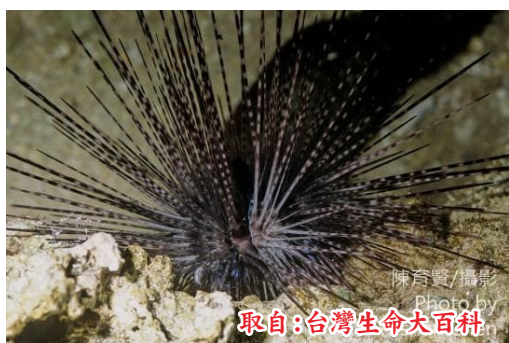
b. 扁跳蝦 *Orchestia platensis*



c. 史氏指蝦蛄 *Gonodactylus smithii*



d. 冠棘真頭帕海膽 *Eucidaris metularia* #



e. 沙氏冠海膽 *Diadema savignyi* #



f. 刺冠海膽 *Diadema setosum* #

圖版2-6. 澎湖竹灣牡蠣串上採獲物種
#:目視紀錄



a.環棘刺海膽 *Echinothrix calamaris* #



b.斑點毒棘海膽 *Pseudoboletia maculata* #



c.白棘三列海膽 *Tripneustes gratilla*



d.鉛筆海膽 *Heterocentrotus mammillatus* #



e. 三齒躉魚 *Phrynelox tridons*



f. 青石斑魚 *Epinephelus awoara*

圖版2-7. 澎湖竹灣牡蠣串上採獲物種
#:目視紀錄



a. 點帶石斑魚 *Epinephelus coioides*



b. 玳瑁石斑魚 *Epinephelus quoyanus*



c. 六線雞魚 *Pelates sexlineatus*



d. 短頭跳岩鰻 *Petroscirtes breviceps*



e. 褐籃子魚 *Siganus fuscescens*



f. 中華單棘魨 *Monacanthus chinensis*

圖版2-8. 澎湖竹灣牡蠣串上採獲物種

Tough)進行拍照紀錄物種之體色與外觀形態特徵，並記錄種類與數量，最後帶回實驗室製成標本。

(二) 樣本處理

帶回之物種浸泡保存於95%酒精中，並以標籤紙標示物種學名、採樣時間、地點，將其貼上對應之標本瓶，以便日後尋找及辨識。鑑定方法為參閱各式圖鑑及文獻（何，1994；李與陳，1994；洗與鄭，2005；彼得•當斯，1996；施等，2010；陳與游，1993；陳，2001；陳，2003；黃與游，1997；賴，2005；中央研究院，2001；中央研究院數位文化中心&中央研究院生物多樣性研究中心，2001；Keiji et al., 2009）以確認物種名稱。

三、數據分析

(一) 累計採獲曲線

黃(2012)指出採獲曲線開始平緩為一判斷採樣次數的依據，表示已採獲大多數種類，以此可推斷出較有代表性的採樣頻

率。

(二) 採獲種類組成

依照生物分類法對所有物種進行排序與表列，以顯示出延繩養殖牡蠣之生物相組成，並計算物種數量。

(三) 採獲頻率分析

參考前人研究（廖，2017）將採獲頻率分為以下四大類：

1. 經常漁獲種類(Very common)：調查期間內物種出現的次數佔採樣次數的80%以上。
2. 一般漁獲種類(Common)：調查期間內物種出現的次數佔採樣次數的50%-79%。
3. 少見漁獲種類(Rare)：調查期間內物種出現的次數佔採樣次數的11%-49%。
4. 稀有漁獲種類(Scarce)：調查期間內物種出現的次數佔採樣次數的10%以下。

公式：採獲頻率＝物種出現次數／採集次數（四捨五入法至小數點後第2位）×100%。

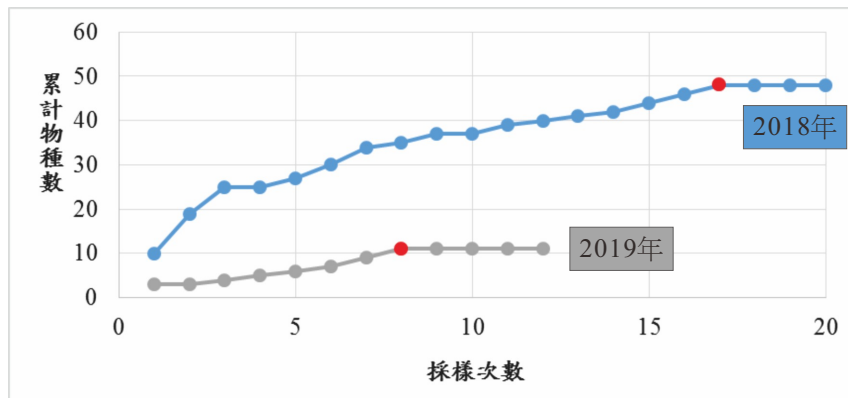


圖1. 累計採獲曲線。

表1. 2018年竹灣海域延繩養殖牡蠣串採獲之生物列表

Cnidaria	Mollusca	Arthropoda	Arthropoda	Chordata
Aglaopheniidae <i>Aglaophenia cupressina</i> ** <i>Aglaophenia whitelegget</i> ** Total: 2 species, 1 genus, 1 family	Octopodidae <i>Octopus variabilis</i> *** Mytilidae <i>Perna viridis</i> * Pteriidae <i>Pinctada margaritifera</i> * Pinnidae <i>Atrina pectinata</i> ** <i>Perna muricata</i> ** <i>Streptopinna saccata</i> * Total: 9 species, 9 genera, 7 families	<i>Charybdis lucifera</i> ** <i>Charybdis natator</i> ** <i>Charybdis orientalis</i> *** <i>Thalamita pyrama</i> **** <i>Thalamita sima</i> *** Xanthidae <i>Lionera rugata</i> * <i>Neoxanthus impressus</i> * Palaeonidae <i>Pariclimenes</i> sp. ** Alpheidae <i>Alpheus brevicristatus</i> ** Palinuridae <i>Panulirus japonicus</i> ** <i>Panulirus ornatus</i> * Porcellanidae <i>Porolithes hastatus</i> * Grapsidae <i>Gaetice depressus</i> ** Talitridae <i>Orcestia platensis</i> ** Gonodactylidae <i>Gonodactylus smithi</i> **	Total: 19 species, 12 genera, 10 families Echinodermata Cidaridae <i>Eucidaris metularia</i> * Diademidae <i>Diadema savignyi</i> * <i>Diadema setosum</i> ** <i>Echinolirix calamaris</i> ** Toxopneustidae <i>Pseudoboletia maculata</i> ** <i>Tripaneustes grailla</i> ** Echinometridae <i>Heterocentrotus mammillatus</i> * Total: 7 species, 6 genera, 4 families	Antennariidae <i>Phrynelox tridons</i> * Serranidae <i>Epinephelus awoara</i> * <i>Epinephelus coioides</i> ** <i>Epinephelus quoyanus</i> ** Teraponidae <i>Pelates sexlineatus</i> ** Blenniidae <i>Petroscirtes breviceps</i> ** Siganidae <i>Siganus fuscescens</i> ** Monacanthidae <i>Monacanthus chinensis</i> * Total: 8 species, 6 genera, 5 families
Mollusca Trochidae <i>Trochus sacellus</i> ** Cymatidae <i>Cymatium pileare</i> ** Columbellidae <i>Pyrene scripta</i> **	Arthropoda Galatheididae <i>Galathea mauritiana</i> ** Portunidae <i>Charybdis acuta</i> * <i>Charybdis affinis</i> * <i>Charybdis amboinensis</i> **			

(****: 經常漁獲種類、***: 一般漁獲種類、** : 少見漁獲種類、* : 稀有漁獲種類)

表2. 2019年竹灣海域延繩養殖牡蠣串採獲之生物列表

(****：經常漁獲種類、***：一般漁獲種類、**：少見漁獲種類、*：稀有漁獲種類)

Platyhelminthes	Arthropoda
Leptoplanidae <i>Discoplana gigas</i> ** Total: 1 species, 1 genus, 1 family	Talitridae <i>Orchestia platensis</i> ** Total: 5 species, 4 genera, 3 families
Mollusca	Chordata
Trochidae <i>Trochus sacellus</i> ** Columbellidae <i>Pyrene scripta</i> ** Octopodidae <i>Octopus variabilis</i> ** Total: 3 species, 3 genera, 3 families	Serranidae <i>Epinephelus awoara</i> ** Siganidae <i>Siganus fuscescens</i> ** Total: 2 species, 2 genera, 2 families
Arthropoda	
Portunidae <i>Charybdis amboinensis</i> ** <i>Charybdis lucifera</i> ** <i>Thalamita sima</i> *** Alpheidae <i>Alpheus brevicristatus</i> *	

結果

一、累計採獲曲線

2018年7、8月的採樣，於第17次時，坡度已明顯趨於平緩，往後的3次採樣中均未再發現新物種；而隔年2019年7、8月的採

樣，僅於第8次時，坡度就已明顯趨於平緩，往後的4次採樣中均未再發現新物種（圖1）。

二、採獲物種的組成

(一) 2018年

2018年共進行20次採樣，平均海溫為

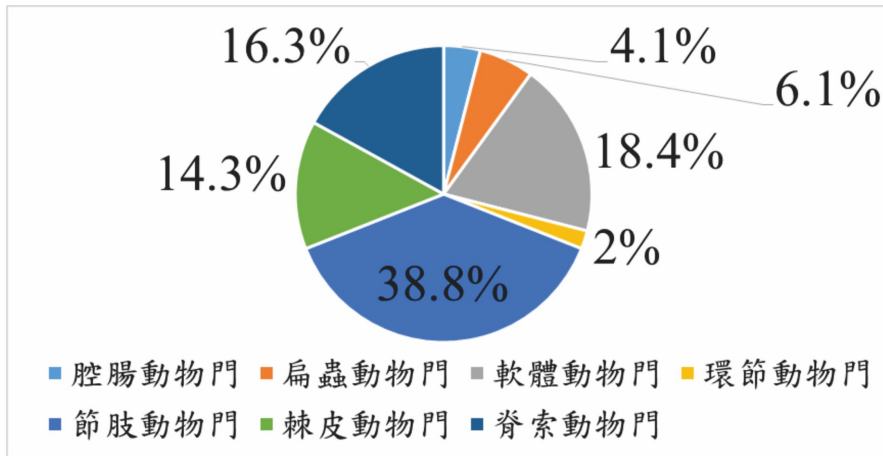


圖2. 2018年澎湖竹灣海域延繩養殖牡蠣串各動物門比例。

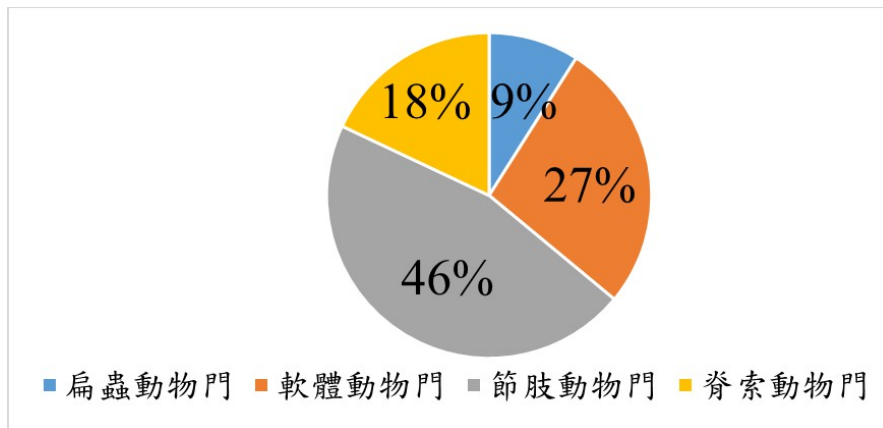


圖3. 2019年澎湖竹灣海域延繩養殖牡蠣串各動物門比例。

28.6°C (澎湖氣象站, 2019)。共採獲7門32科38屬49種生物 (表1)，上述生物分別有腔腸動物門Cnidaria、扁蟲動物門Platyhelminthes、軟體動物門Mollusca、環節動物門Annelida、節肢動物門Arthropoda、棘皮動物門Echinodermata、脊索動物門Chordata，其中以節肢動物門為

最多，共計10科12屬19種，佔38.8%；而環節動物門則為最少，僅1科1屬1種，佔2%。

(二) 2019年

2019年則進行12次採樣，平均海溫為28.5°C (澎湖氣象站, 2019)。共採獲4門9科10屬11種生物 (表2)，上述生物分別有扁蟲動物門、軟體動物門、節肢動物門、

脊索動物門，其中以節肢動物門為最多共3科4屬5種，共佔46%；而扁蟲動物門則為最少，為1科1屬1種，佔9%（圖3）。這些種類均出現於2018年的採樣記錄中。

三、採獲頻率分析

(一) 2018年

1. 經常漁獲種類

共有1門1科1屬1種，佔所有物種的2%，分別為節肢動物門中的底棲短漿蟹 *Thalamita prymna*。

2. 一般漁獲種類

共有2門2科2屬3種，佔所有物種的6%，分別為軟體動物門中的長蛸 *Octopus variabilis*；節肢動物門中的東方螳 *Charybdis orientalis* 以及雙額短漿蟹 *T. sima*。

3. 少見漁獲種類

共有7門22科26屬30種，佔所有物種數的61%，分別為腔腸動物門的柏狀羽螅 *Aglaophenia cupressina*與白羽鞘水螅 *A. whiteleggei*；扁蟲動物門的大盤扁蟲 *Discoplana gigas*、網平渦蟲 *Planocera reticulata*、橙緣美麗海扁蟲 *Calliplana marginata*；軟體動物門中的齒輪鐘螺 *Trochus sacellus*、毛法螺 *Cymatium pileare*、花麥螺 *Pyrene scripta*、牛角江瑤蛤 *Atrina pectinata*、尖角江瑤蛤 *Pinna muricata*；環節動物門中的沙蠶的一種 *Nereis* sp.；節肢動物門中的模里西斯鎧甲蝦 *Galathea mauritiana*、安汶螳 *C. amboinensis*、晶瑩螳 *C. lucifera*、善泳螳 *C.*

natator、岩蝦的一種 *Pariclimenes* sp.、短脊槍蝦 *Alpheus brevicristatus*、日本龍蝦 *Panulirus japonicus*、平背蜆 *Gaetice depressus*、扁跳蝦 *Orchestia platensis*、史氏指蝦蛄 *Gonodactylus smithii*；棘皮動物門中的刺冠海膽 *Diadema setosum*、環刺棘海膽 *Echinothrix calamaris*、斑點毒棘海膽 *Pseudoboletia maculata*、白棘三列海膽 *Tripneustes gratilla*；脊索動物門中的點帶石斑魚 *Epinephelus coioides*、玳瑁石斑魚 *E. quoyanus*、六線雞魚 *Pelates sexlineatus*、短頭跳岩鰩 *Petroscirtes breviceps*、褐籃子魚 *Siganus fuscescens*。

4. 稀有漁獲種類

共有4門13科14屬15種，佔所有物種的31%，分別為軟體動物門的綠殼菜蛤 *Perna viridis*、黑蝶珍珠蛤 *Pinctada margaritifera*、旗幟江瑤蛤 *Streptopinna saccata*；節肢動物門的銳齒螳 *C. acuta*、近親螳 *C. affinis*、皺紋花瓣蟹 *Liomera rugata*、印痕新近扇蟹 *Neoxanthias impressus*、錦繡龍蝦 *P. ornatus*、矛形岩瓷蟹 *Petrolisthes hastatus*；棘皮動物門的冠棘真頭帕海膽 *Eucidaris metularia*、沙氏冠海膽 *D. savignyi*、鉛筆海膽 *Heterocentrotus mammillatus*；脊索動物門中的三齒躉魚 *Phrynelox tridons*、青石斑魚 *E. awoara*、中華單棘魷 *Monacanthus chinensis*。

(二) 2019年

1. 經常漁獲種類

無採獲經常漁獲種類。

2. 一般漁獲種類

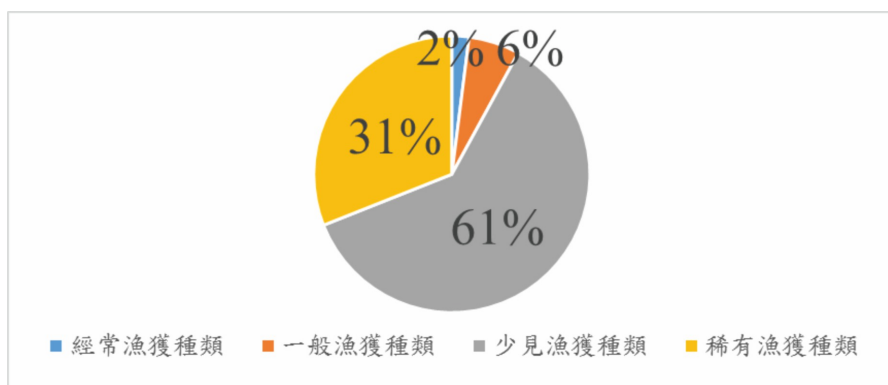


圖4. 2018年澎湖竹灣海域延繩養殖牡蠣串生物採獲頻率分析。

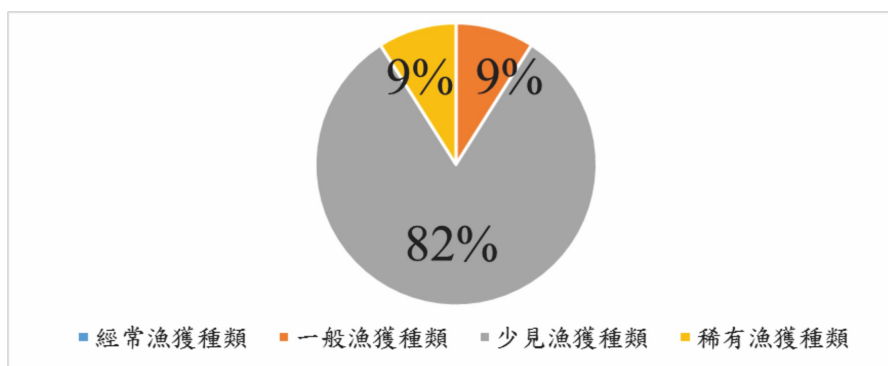


圖5. 2019年澎湖竹灣海域延繩養殖牡蠣串生物採獲頻率分析。

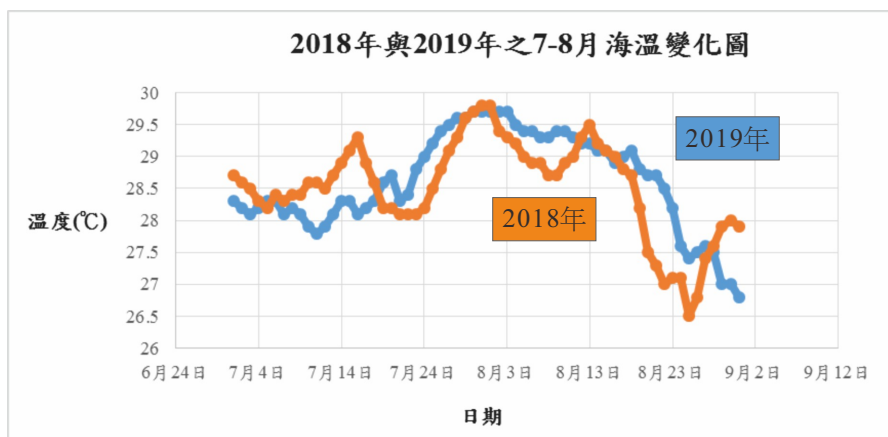


圖6. 2018年與2019年的7-8月海溫圖。

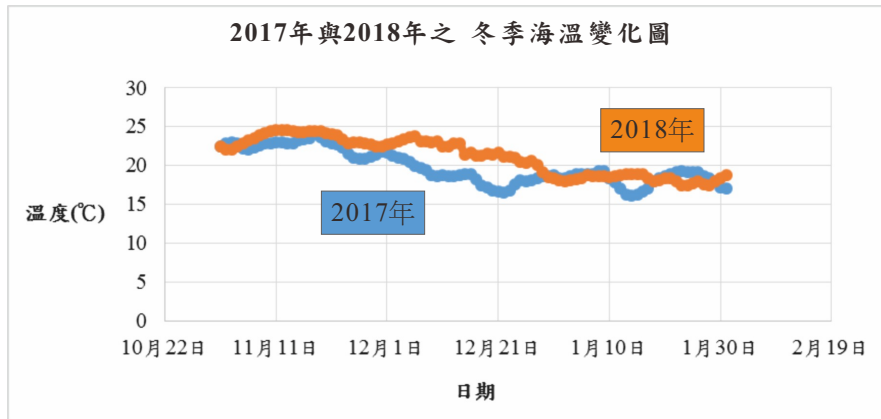


圖7. 2017年與2018年的冬季海溫圖。

共有1門1科1屬1種，佔所有物種的9%，為節肢動物門中的雙額短槳蟹 *T. sima*。

3. 少見漁獲種類

共有4門8科9屬9種，佔所有物種的82%，分別為扁蟲動物門中的大盤扁蟲 *D. gigas*；軟體動物門中的長蛸 *O. variabilis*、齒輪鐘螺 *T. sacellus*、花麥螺 *P. scripta*；節肢動物門中的安汶蟬 *C. amboinensis*、晶瑩蟬 *C. lucifera*、扁跳蝦 *O. platensis*；脊索動物門中的褐籃子魚 *S. fuscescens*、青石斑魚 *E. awoara*。

4. 稀有漁獲種類

共有1門1科1屬1種，佔所有物種的9%，為節肢動物門中的短脊槍蝦 *A. brevicristatus*。

討論

一、採獲頻率分析探討

本調查依2018年的採獲頻率結果分為

經常、一般、少見、稀有等四類漁獲種類，但以少見漁獲種類為最多，佔61%；次之為稀有漁獲種類，佔31%；而一般漁獲種類，佔6%；經常漁獲種類則為最少，佔2%（圖4）；而2019年僅一般、少見及稀有漁獲三類，仍以少見漁獲種類為最多，佔82%；次之同為一般與稀有漁獲種類，均佔9%（圖5）。

可知，生物相的組成以少見與稀有漁獲種類為主。根據多樣性-穩定性假說 (diversity-stability hypothesis)，一個種數越高的生態系統，透過種間的交互作用，表現出較高的生產力，能量的使用效率亦高，對於外來的干擾也具有較強的緩衝力，亦即生物多樣性高，則系統穩定性高（廖與周，2000）。

另外，透過上述得知，少見與稀有物種的種類數為未來採樣得以參考的重要指標，倘若在未來的採樣中，觀察到少見與稀有漁獲種類所佔比例下降，則表示生態系中的物種不如以往多元，物種間的可取代性也不高，生態系的穩定性相對較低。

本調查探討2018與2019年數據具差異之因素有二：一為冬季海溫相異。大型藻類由於環境中的水溫，光週期...等環境因子呈現「季節性」變化，且多以冬、春兩季為生長繁盛期（曾等，2005；曾等，2006），這些大型藻在春末夏初逐漸死亡後釋放出的有機碎屑及營養鹽，將影響春夏間浮游動、植物的生長。而浮游藻類屬初級生產者，因此浮游藻類的豐度變化影響著海洋漁業資源，及其可透過溶解有機質傳遞到後生動物食物網，進而影響後續海域的生產力（李與范，2005），因此冬季大型藻生長越旺盛，越可累積更多的營養鹽。以本調查的結果觀之，2018年與2019年的7-8月海溫（圖6），雖無明顯差異，但由該2年的冬季海溫（圖7）可得知兩年的溫差甚至可達 $3.5 - 4^{\circ}\text{C}$ ；由李等（2009）在2008年澎湖寒害調查數據中得知2008年2月的澎湖水域水溫較前12年（1996-2007年）低了 7°C ，並發現大型藻如礁膜 *Monostroma nitidum*、石蓴 *Ulva lactuca*、石髮 *Ulva* spp.等，因當年冬季持續的低溫造成當年生物量倍增，而2009與2008年相較下即因海水回歸正常導致生物量明顯減少。另外，方等（2002）在2001年與2002年的海藻覆蓋率調查中，發現2002年覆蓋率低於2001年，推測是2002年之月平均氣溫較往年為高所致。其次為，捕食浮游動物的掠食者減少可能也有些許關係，如李等（2009）提到2008年3月過後澎湖內灣海域的浮游動物個體數量高達 $670,003 \text{ ind./1000m}^3$ ，並推測可能是因寒潮之後捕食浮游動物的族群死亡所導致。綜上所

述，推測本研究調查年度中，2018年的低水溫使大型藻類大量生長且可能造成部分浮游動物之掠食者減少，因此造成2018年夏季（經歷較低溫的冬季）的物種數高於2019年夏季（經歷較高溫冬季）的主因。

二、生物聚集原因之探討

廣大的大洋缺乏可依附、潛居或躲藏之物體；而海域內的牡蠣串，相較於前者，則屬較易生活的地方（Alastair et al., 2004）。依據本研究於採樣時的觀察，將生物依據聚集之原因大致分為覓食及掩蔽。以下將進行說明。

（一）無脊椎動物

1. 腔腸動物門

本次採集共計1科1屬2種。其中柏狀羽螅 *A. cupressina*，以觸手捕捉浮游動物為食，其群體上常有蜘蛛蟹科的箭蟹 (*Hyastenus bispinosus*) 或藻蝦 (*Hippolyte* sp.) 和疣蛇尾 (*Ophiothela* sp.) 共生，天敵為海蛞蝓 *Doto ussi*（陳，2014）

2. 扁蟲動物門

本次採集共計3科3屬3種。僅發現嗜食牡蠣的扁蟲但未發現蚵螺 *Thais clavigera*，陳等（2019）提及澎湖與臺灣西部沿海的養殖牡蠣其差異在於養殖深度與環境不同，扁蟲因為日照關係、潮汐、表水層水溫導致大量出現，而蕭等（2013）提及蚵螺 *T. clavigera* 可耐潮差與乾燥之環境，推測此為未採集到蚵螺 *T. clavigera* 原因之一。

3. 軟體動物門

本次採集共計7科9屬9種。二枚貝會選擇合宜之環境，以足絲附著於硬物或石

縫，貝殼與固著基底合為一體，不再移動，屬終生固著型，進行濾食行為（行政院農業委員會，2012）。特別的是，江瑤蛤科的物種普遍生長於沙底中（陳，2003），不過採集中發現江瑤蛤會以足絲附於牡蠣串上。另外高階的掠食者如長蛸 *O. variabilis*，章魚會將八條腕伸進岩石縫隙中主要捕食甲殼類、軟體動物和魚類，而陽隧足動物、多毛類動物等其他動物皆是章魚的食物(Nixon, 1987; 伯爾尼, 2002; López-Uriarte et al., 2008)。

4. 環節動物門

本次採集共計1科1屬1種。常發現於沙子的洞穴中或與棲息於貽貝和藤壺當中，沙蠶屬的吻部具有顎齒可捕食獵物(Woodin, 1977)。伯爾尼(2002)也提到多毛類喜生活在永久的管子或洞穴之中，除可躲避天敵外，亦可透過其修長且柔軟的身體，向管外或洞外收集任何可以吃的東西為食。

5. 節肢動物門

本次採集共計10科12屬19種。

十足目：

依其腹部形態分為長尾類、短尾類、異尾類，以下分別介紹：

長尾類：龍蝦科共計1屬2種。龍蝦喜歡藏身在岩礁的洞隙中，晝伏夜出（游等，1996）。牡蠣間的凹槽、縫隙對於小龍蝦而言，不僅可以藏身，避免被天敵捕食，亦可於這些凹槽、縫隙中尋找食物（螺貝類等），甚至體型較小的牡蠣，也可做為龍蝦的食物。

短尾類：梭子蟹科的種類為肉食性或雜食性，其螯腳掌節較為粗壯，指節呈交

叉狀，可降低獵物脫逃的機會；扇蟹科的種類指節末端大都為匙狀，可藉以刮食藻類或有機碎屑。

異尾類：岩瓷蟹具1對粗壯的大螯，而第3顎足特化成具網狀結構可以濾食浮游生物及有機碎屑，除濾食外岩瓷蟹也會以大螯攝食食物；鎧甲蝦其身體縱扁且腹部伸長並有一對大螯，時常被認為是長尾類的蝦類，但其第5步足與岩瓷蟹相同萎縮退化。

口足目：

蝦蛄依其第2顎足所特化之大鉗型態，可大概分為鐮刀型與垂直型。本次採集僅採到1種指蝦蛄屬的垂直型史氏指蝦蛄 *G. smithii*，此類型蝦蛄大都以特化之棒槌型第2顎足敲擊獵物進行獵食行為。

6. 棘皮動物門

本次採集共計4科6屬7種。

毒棘海膽科 *Toxopneustidae* 與冠海膽科 *Diadematidae* 之物種；兩者會攝食附著其上的藻類與小型附著生物（中央研究院，2007）。

(二) 脊椎動物

1. 脊索動物門

本次採集共計5科6屬8種。

鰐魚科：僅有1種，三齒鰐魚 *P. tridons* 其胸鰭特化成臂狀可用於海底爬行，頭頂上還有第1背鰭棘所特化的吻觸手，其頂端還有發達的餌球，猶如釣竿一樣可以誘騙小魚靠近並吞食。

鮎科：具有1屬3種。石斑魚性情兇猛會獵食礁區的生物，於生態系中屬較高等的生物。

鰻科：僅1種，六線雞魚 *P.*

*sexlineatus*屬肉食性魚類，常以小魚、甲殼類、多毛類為食。

鰯科：僅1種，短頭跳岩鰯 *P. breviceps* 以藻類、碎屑和小型無脊椎動物為食，雄魚會使用貝殼來築巢，甚至使用圓口的空罐。（中央研究院數位文化中心 & 中央研究院生物多樣性研究中心，2001）。

藍子魚科：僅1種，褐藍子魚 *S. fuscescens*：具群居性，屬雜食性偏藻食性，亦會食用無脊椎動物跟甲殼類。採集時常可觀察到成群包圍牡蠣串，啄食牡蠣串上表面的附著生物。

單棘魷科：僅1種，中華單棘魷 *M. chinensis*，受驚嚇時會以背棘上之大棘卡於石縫中避免攻擊，其牙齒堅硬，常以貝類、小型甲殼類為食，有時也會以藻類或小鱼為食。

牡蠣串上表面皆充滿附著藻與小型附著生物，這些附著藻與小型附著生物吸引著肉食性、藻食性、雜食性者前來攝食，進而吸引更大型肉食性者前來掠食，形成一食物鏈。例如，採樣時發現，一串牡蠣串(2.0± 0.5m)，最多可採集到4-5顆毒棘海膽科 *Toxopneustidae* 與冠海膽科 *Diadematidae* 之物種；兩者會攝食附著其上的藻類與小型附著生物（中央研究院，2007），本研究亦採獲大量短槳蟹，一串牡蠣串採獲的數量可高達20隻，推測冠海膽科的數量多寡，可能也是短槳蟹選擇棲息的誘因之一。而牡蠣串上的空殼或凹槽，恰符合以上這些生物所喜愛的棲身之所，除可避敵外，亦可確保食物的穩定量。例如二枚貝中以江瑤蛤科 *Pinnidae* 為最

多，這些殼薄的二枚貝以足絲附著於牡蠣間的凹槽、縫隙，藉牡蠣的厚殼得到較佳的掩蔽，同時可順利進行濾食。

而本調查之牡蠣串養殖時間由每年9-10至隔年8-10月，總養殖時間約為11-12個月。對於大部分物種皆未到達其成熟體型，所採集的大部分生物體型尚小，推測是因牡蠣串養殖時間僅約莫1年導致，時間短未能使大部分生物生長至性成熟的體型。而每種物種由浮游階段(meroplankton)至底棲階段的時間不一，依附於牡蠣串的時間皆不相同，因此本調查僅以覓食或掩蔽作為棲息的大概依據。除此之外，亦有許多原因使其依附於牡蠣串上或是周圍環境，例如：生殖等諸多原因，皆會是誘集生物生活於此的可能因素，如未來能以長時間觀察牡蠣串之生物相變化，對於海洋環境資源保育會有所幫助。

唯本調查可惜之處為以下：

1. 未能完整記錄牡蠣串養殖過程生物相之時空變化，僅有2018、2019兩年7-8月之紀錄。
2. 未記錄到於牡蠣串周圍環境停留或短暫停留之大型掠食者。
3. 採集之生物體型小或是未達成熟體型，鑑種難度十分高。
4. 未記錄到生物與生物之間的共生行為，若有，則能使物種數更豐富。很多海洋生物彼此會有共棲關係，例如短腕岩蝦 *Periclimenes brevicarpalis*、白斑拖蝦 *Thor amboiensis*、以及紅斑新岩瓷蟹 *Neopetrolisthes maculatus* 等常與大型海葵共生；魔鬼海膽則會有海膽針蝦

Stegopontonia commensalis、固著性的櫛水母*Coeloplana bannwarthi*、裸掌盾牌蟹*Percnon planissimum*、天竺鯛Apogonidae幼魚與其共生或藉以掩蔽掠食者(黃, 2015)。另外, 中華蚶豆蟹*Arcotheres sinensis*與牡蠣共棲且比例可達10%, 而雄性多具游泳功能可自由進出不同的宿主(Christensen and McDermott, 1958; 陳, 2008) 因此牡蠣串有一定的機率會採集到雄蟹。而李(2019)甚至發現中華蚶豆蟹*A. sinensis*腹甲內也會住著中華淺鰓虱 *Rhopalione sinensis*。因此除了生物與生物的共生行為外, 在這之中還有存在寄生關係。Pontonine shrimps時常會與很多海洋生物共棲, 如多孔動物門Porifera、腔腸動物門、軟體動物門、棘皮動物門、被囊動物亞門Tunicata (Miyake and Fujino, 1967; Lee and Ko, 2013), 而Lee and Ko (2013)所發表的*Conchodytes nipponensis*會與牛角江瑤蛤*A. pectinata*共棲, 但本調查未檢視江瑤蛤殼內部, 因此未有數據。

經本調查結果可得知牡蠣串之生物相豐富, 而於長期浸泡於海水中的牡蠣串中, 除了為生物提供掩蔽物之外還提供大量食物來源, 儼然成為一小型生態系, 顯見牡蠣串的功能對生物誘集具有正面的效益, 使生物相走向多元化, 相信對於海洋生物棲息環境場域具有一定的影響力, 雖目前對於牡蠣串生物相的相關研究可能不及珊瑚礁、藻礁眾多, 但如未來有更深入的相關研究, 或許會發現牡蠣串之生態服務功能與珊瑚礁、藻礁相同具有一定的價

值。而與牡蠣串相同以繩索掛於海面上作為藻床的藻繩, 如洗(2019)利用中國半葉馬尾藻進行大型藻藻床之利用, 發現藻床的多層次的立體空間及依附性的生物, 可以誘集許多甲殼類、螺類, 以及多種魚類之幼魚覓食及棲息於周圍。未來如欲增加海洋生物棲息環境場域以豐富漁業資源, 或許在養殖經濟與永續環境利用之間, 牡蠣串的生態服務可以達到沿近海資源復育之利用。

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台灣新歸化禾本科植物—鉤毛草

Pseudechinolaena polystachya (Kunth) Stapf—A newly naturalized Poaceae in Taiwan

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摘要

鉤毛草(*Pseudechinolaena polystachya* (Kunth) Stapf)原產中南美洲、非洲和亞洲的熱帶山地林下。本種為小草本，小穗成熟時內穎表面密生開展的鉤狀剛毛的特徵與台灣原生的其

他種類明顯不同。本文報導鉤毛草歸化於台灣中部低海拔地區的果園道路邊緣和荒廢地，描述其外部形態特性，生育地環境和共同伴生之植物。

關鍵詞：鉤毛草、禾本科、歸化植物、台灣

Abstract

Pseudechinolaena polystachya (Kunth) Stapf, belonging to the grass family, is widely distributed in America, Africa and Asia. This species is characterized by its upper glume of spikelet densely covered with long hooked-hair in fruiting stage. In a recent plant survey, we found a wild naturalized population of *Pseudechinolaena polystachya* in Central Taiwan. A detailed description with color photographs, linedrawing and habitat information is provided in this paper.

Key words: *Pseudechinolaena polystachya*, Poaceae, naturalized plant, Taiwan

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前言

禾本科是廣布全球的植物，約含有768屬11,506種(Soreng et al., 2017)。鉤毛草屬(*Pseudechinolaena*)有6種，其中5種僅分布於非洲的馬達加斯加島，但有1種鉤毛草(*Pseudechinolaena polystachya* (Kunth) Stapf)廣布於非洲南部、中美洲至南美洲，在亞洲廣布中國、印度、泰國、越南、馬來西亞、印尼和新幾內亞等國家(Clayton et al., 2006)。本種為纖細一年生或多年生草

本，小穗成熟時內穎表面脈間密生開展的長鉤狀剛毛的特徵(金, 1990)，使本種容易辨識。鉤毛草廣布於中國南方各省，台灣植物誌中記載台灣禾本科有118屬289種1亞種39變種8型，但並未有本種分布之紀錄(Hsu et al., 2000)。禾本科與人類生活關係密切，在各地有很多歸化種，台灣有90種歸化種(Wu et al., 2010)，近年來陸續有多種禾本科歸化植物之報導，但也無鉤毛草歸化之報導。

作者最近於台灣中部山區採獲一種新歸

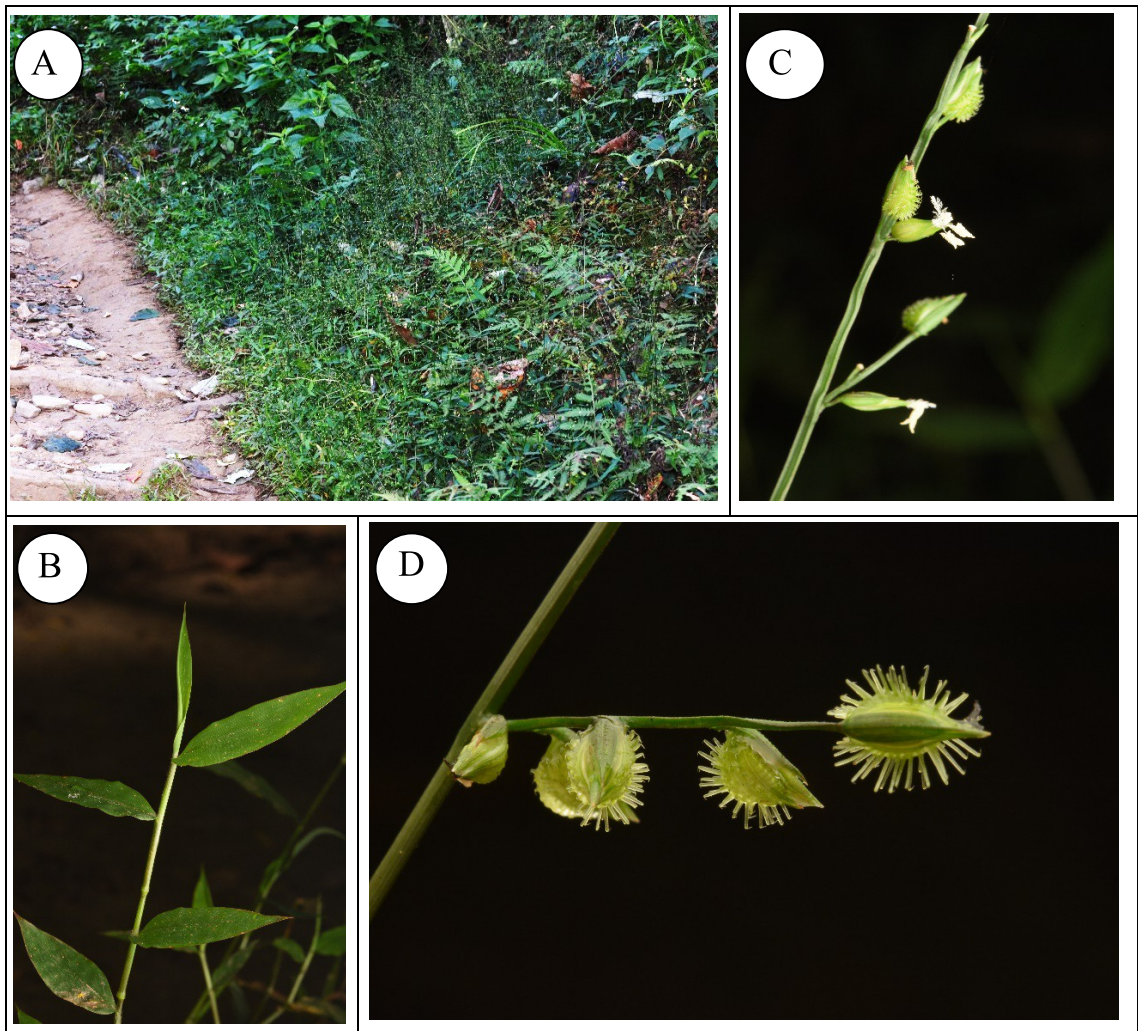


圖1. 鈎毛草的生育地(A)、植株形態(B)、開花(C)和成熟穎果具長鈎毛(D)。

Fig. 1. Habitat(A), habit (B), flowers(C) and mature fruits with long hooked-hairs of *Pseudechinolaena polystachya* (Kunth) Stapf from Taiwan(D).

化的鈎毛草屬植物（圖1），經比對文獻及標本後後鑑定為鈎毛草(*Pseudechinolaena polystachya* (Kunth) Stapf)，分類地位為禾本科(Poaceae)/黍亞科(Panicoideae)/黍族

(Paniceae)(Soreng et al., 2017)，此新歸化植物為小草本，小穗成熟時內穎表面脈間密生開展的長鈎狀剛毛的特徵與台灣原生的其他種類明顯不同（圖1, 2），此紀錄亦為台灣增加一個新歸化屬。本文根據文

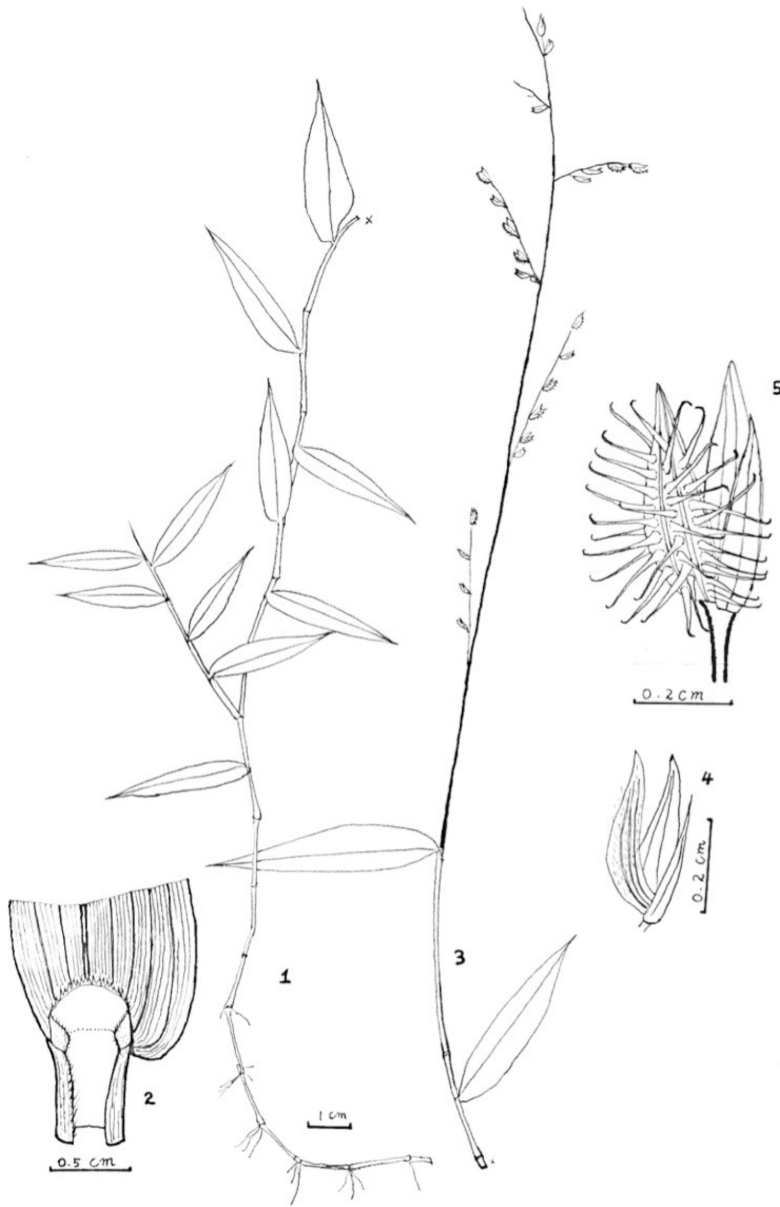


圖2. 鉤毛草手繪圖。1.習性；2.葉舌；3.開花枝條 4.小穗開花期； 5.小穗結果期具長鉤毛。

Fig. 2. *Pseudechinolaena polystachya* (Kunth) Stapf. 1.Habit; 2. Ligule; 3. Inflorescence a racemose racemes; 4.Spikelet in flowering stage; 5. Spikelet with long hooked-hairs in fruiting stage.

獻、標本和野外實地調查說明本種的特徵、分布及其相關特性。

分類處理

Pseudechinolaena Stapf. in Prain, Fl. Trop. Africa. 9: 495. 1919; Chen and Philips. Fl. China 22: 500. 2006. 鈎毛草屬

種類描述(以下描述根據台灣植物標本)

Pseudechinolaena polystachya (Kunth) Stapf. in Prain, Fl. Trop. Africa. 9: 495. 1919; Chen and Philips. Fl. China 22: 500. 2006. 鈎毛草(圖1、2)

Echinolaena polystachya Kunth. Nov. Gen. et Sp. 1: 119. 1816.

Annual or perennial. Culms slender, erect, often stoloniferous at lower part, rooting on nodes, 30-60 cm tall. Leaf alternative, leaf blades lanceolate, 3.5-6.5 cm long, 0.9-1.1 cm wide, slightly pilose on adaxial surface, glabrous on abaxial surface; leaf sheath 1.2-5 cm long, margin densely pilose; ligule membranous, 1-2 mm long, apex ciliate. Inflorescence a racemose racemes, bearing 4-7 loosely, ascending racemes with distant spikelets. Spikelets bisexual, ovate or oblong, 5-7 mm long, with 1-1.5 mm long pedicels. Lower glume lanceolate, acute, 4 mm long, 1 mm wide, 3-veined. Upper glume thicker, navicular, 3.5-

4 mm long, 1.5-2 mm wide, 7-veined, with tubercle-based hooks between the veins. Lower floret neutral, upper floret fertile. Lower lemma broadly ovate, 4 mm long, 2 mm wide, 5-7 veined. Lower palea lanceolate, 4 mm long, 0.5 mm wide. Upper lemma ovate, navicular, 3 mm long, 1 mm wide, subcoriaceous, glabrous and shining on the surface. Upper palea elliptic, 2.5 mm long, 0.5 mm wide, subcoriaceous, glabrous and shining on the surface. Lodicules 2, membranous, tiny; Anthers 3. Caryopsis fusiform, 2.5 mm long.

Flowering stage: September to December

Chromosome number: $n=18$ (Mehra, 1982), $2n=36$ (Pohl & Davidse, 1971; Christopher & Abraham, 1975)。

一年生或多年生細小草本；秆直立，下部常平臥，節上生根，高30-60 cm。葉互生，葉身披針形，葉基歪斜不等大小，長3.5-6.5 cm，寬0.9-1.1 cm，上表面疏被長毛，下表面無毛或疏被毛；葉鞘長1.2-5 cm，邊緣一側密被絨毛，另一側光滑無毛或在近葉舌處疏被毛；葉舌膜狀，長1-2 mm，先端疏被毛。花序頂生，4-7個總狀分枝，稀疏排列成圓錐花序；小穗排列稀疏，多排列於同一側；小穗卵形或橢圓形，長5-7 mm，小穗具柄，長1-1.5 mm；外穎披針形，先端漸尖，長4 mm，寬1 mm，具3脈；內穎較厚，寬卵形，舟狀，長3.5-4 mm，寬1.5-2 mm，具7脈，果熟時脈間密被基部瘤狀的直立鈎毛，長1 mm。

內有2朵花，下位小花大多中性，上位小花兩性；下位外稃寬卵形，長4 mm，寬2 mm，5-7脈；下位內稃披針形，長4 mm，寬0.5 mm；上位外稃卵形，舟狀，長3 mm，寬1 mm，亞革質，平滑光亮；上位內稃橢圓形，長2.5mm，寬0.5 mm，亞革質，平滑光亮；鱗被2，細小膜質；雄蕊3枚，花藥白色；花柱2裂，柱頭羽毛狀。穎果紡錘形，長約2.5 mm。

花果期：9-12月

染色體數： $n = 18$ (Mehra, 1982), $2n = 36$ (Pohl & Davidse, 1971; Christopher & Abraham, 1975)。

分布：廣泛分布於中南美洲、非洲和亞洲的熱帶山地林下。在亞洲廣布中國、印度、泰國、越南、馬來西亞、印尼和新幾內亞等國家。台灣目前歸化於中部台中市和平區的低海拔山區。

觀察標本：台中市(Taichung city)：和平區(Heping District)，松鶴，唐麻丹山，海拔約800公尺，13 Nov 2020, M. C. Chiang s. n.；20 Nov 2020, M. C. Chiang and T. H. Hsieh s. n. (NUTN, 國立台南大學生態科學與技術系標本室)

生態習性

鉤毛草生育地環境多在森林底層 (Ghosh & Bhattacharyya, 2018)，目前歸化於台灣中海拔約800公尺山區，該環境大致為森林邊緣與人為開墾環境之道路邊緣及工寮周遭潮濕處。該區主要種植咖啡和檸檬，喬木主要為俄氏柿 (*Diospyros*

oldhamii Maxim.)、白柏 (*Triadica cochinchinensis* Lour.)、白匏子 (*Mallotus paniculatus* var. *paniculatus*)、筆筒樹 (*Sphaeropteris lepifera* (J. Sm. ex Hook.) R.M. Tryon)，林下伴生植物常見有裏白鰓頭果 (*Glochidion acuminatum* Müll. Arg.)、冷清草 (*Elatostema lineolatum* var. *majus* Wedd.)、假蹄蓋蕨 (*Deparia petersenii* (Kunze) M. Kato)、大屯求米草 (*Oplismenus aemulus* (R. Br.) Roem. & Schult.)、藤竹草 (*Panicum sarmentosum* Roxb.)等。

對本種周遭環境出現的植物進行調查，共紀錄36種，其中原生種30種，外來種6種。外來歸化植物有發現假澤蘭 (*Austroeupatorium inulifolium* (Kunth) R.M. King & H. Rob.)、三角葉西番蓮 (*Passiflora suberosa* L.)、大花咸豐草 (*Bidens alba* var. *radiata* (Sch. Bip.) R.E. Ballard ex Melchert)、菁芳草 (*Drymaria diandra* Blume)、紫花藿香薷 (*Ageratum houstonianum* Mill.)以及多穗雀稗 (*Paspalum paniculatum* L.)。外來物種數雖然不多，但附近人為開墾痕跡明顯，且搜尋該區域附近自然林下都沒有其他鉤毛草族群出現，本種在果實成熟期特徵明顯非常容易辨識，應不難發現，但過往均未發現 (Hsu, 1978; Hsu et al., 2000)。因此就本次新發現的紀錄而言，筆者認為屬於歸化植物的可能性較高。不過就地理分布上來說，中國的福建、廣東、廣西、海南、雲南和西藏的山區皆有分布，台灣也很可能在本種的自然分布範圍內。此外本種的植株和葉形與求米草屬 (*Oplismenus*) 相類似，

且會共域混生，在未開花時不易分辨，但在果實期則容易區別，若將來發現有其他族群則可再更進一步評估本種是否為原生植物。本種果實成熟時小穗基部的關節有離層很容易掉落，加上內穎具直立鉤毛會黏著在經過的動物或是人類衣服上藉以傳播，未來可能會持續擴張。

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氣候變遷下入侵雜草與農業生產的空間衝突性評估

Accessing the spatial conflict of invasive plant and agricultural production under climate change in Taiwan

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摘要

生物入侵是造成農業環境劣化與經濟損耗的主要原因，瞭解入侵生物可能構成威脅的空間資訊，有助於入侵問題的預防與管理。本研究挑選具高度侵略潛力之5種外來入侵雜草作為目標種，運用生態棲位模式預測各物種當前及未來氣候變遷情境下(RCP2.6與RCP8.5，2060~2080年)的棲地適宜性，並透過與農業生產價值圖資的空間交集分析，評估兩者的潛在空間衝突性。研究結果顯示，溫度變項是驅使入侵雜草改變地理分布範圍的主因，所分析之5種入侵雜草未來皆將受益於氣候變遷，除增加整體的適宜棲地範圍外，亦將對農業生產帶

來程度不一的影響，其中合果芋、大花咸豐草與落葵等3種當前之明顯衝突區，在未來將往北發生轉移，應可將防治重點調整至高緯度的衝突區；相反地，美洲含羞草與含羞草等2種，則須持續關注當前的明顯衝突區。總結而言，本研究透過空間交集分析，可明確指出入侵雜草與農業生產價值的潛在的空間衝突區位與程度，得以為防治優先性的規劃提供具體的參考資訊。

關鍵詞：生物入侵、生態棲位模式、氣候變遷、空間交集分析、防治優先性

Abstract

Biological invasion is the main cause of agricultural environmental degradation and economic loss. Understanding the spatial information that invading organisms may pose a threat is helpful to the prevention and management of invasion problems. In this study, five invasive weed species with high aggressive potential were selected as target species, and the ecological niche model was used to predict the habitat suitability for current and future climate change scenarios (RCP2.6 and RCP8.5, 2060~2080). Through the spatial intersection analysis with the agricultural production value map, the potential spatial conflicts between the two are identified. The results showed that temperature variables are the main cause of changes for geographic distribution of invasive weeds. All five invasive weed species will benefit from climate change in the future. They not only increase the range of suitable habitats, but also have varying degrees of impact on agricultural production. We found that the conflicts among the three species, such as *Synгонium podophyllum*, *Bidens pilosa* var. *radiata*, and *Basella alba*, will shift to the north. We therefore considered that it should be possible to adjust the effort to high-latitude conflict zones. On the contrary, for *Mimosa diplotricha* and *Mimosa pudica*, we must continue to pay attention to the current locations where have conspicuous conflicts. In conclusion, this study can clearly express the extent of potential spatial conflicts between invasive weeds and agricultural production value using spatial intersection analysis to aid the prioritizing management.

Key words: biological invasion, ecological niche model, climate change, spatial intersection, prioritization

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前言

農業生態系是陸域生態系的重要組成分，約占全球1/3土地總面積(The World Bank Group 2018)，直接供給人類所需糧食、飼料、生質能源、藥材等基本需求，對人類生活福祉至關重要(Power 2010)。然頻繁干擾與過度施肥的集約化經營，促使農地成為容易遭受生物入侵的土地利用型態(Fried *et al.* 2017)，入侵雜草通常透過資源競爭、毒他作用與寄生(Fried *et al.* 2017)，甚至作為病蟲害媒介(Klein and Smith 2020)等機制，對作物的品質與產量造成直接或間接的損失(Oerke 2006; Rockwell-Postel *et al.* 2020)，且其衍生的防治與控制成本更甚其他有害生物(Pimentel *et al.* 2000; Pimentel *et al.* 2005; Williams *et al.* 2010)。

近代更受矚目的議題是氣候變遷所帶來的衝擊，入侵雜草與許多原生種相同，兩者皆可能受氣候變遷的影響，改變其空間分布(Bradley *et al.* 2010; Koncki and Aronson 2015; Bellard *et al.* 2018)，但相較於原生植物，其生態幅度廣且對環境的適應力佳，經常能跨越原本的地理侷限，將分布範圍擴張至以往無法生存或繁衍的地區(Walther *et al.* 2009; Bradley *et al.* 2010; Carboni *et al.* 2018)，進而增強對農業生產的負面影響。因此，在氣候變遷與入侵雜草雙重威脅下，如何有效掌握其對原生生

態系可能構成威脅的空間資訊，將是防治策略施行成功與否之關鍵過程(Long *et al.* 2017; Rockwell-Postel *et al.* 2020)。

生態棲位模式(ecological niche model, ENM)係基於物種出現的位置與其對應環境變量間的關聯性，預測物種潛在空間分布或評估其棲地適宜性的有效工具(Phillips *et al.* 2006)，目前廣泛應用於生物地理、氣候變遷、保育生物、演化生物學等領域(Williams *et al.* 2009; Shrestha and Shrestha 2019; Guisan *et al.* 2013)，而高度棲地適宜性經常可導致生物入侵，許多入侵生物學家也嘗試利用ENM所推導之棲地適宜性，作為預測入侵成功與否的重要指標(Crall *et al.* 2013; Thuiller *et al.* 2005; Wan *et al.* 2018)，用以評估較大空間尺度的潛在入侵範圍與風險(Bradley *et al.* 2009; Allen and Bradley 2016; Slodowicz *et al.* 2018; Panda *et al.* 2018)，然而入侵生物對原生生態系所造成的影響評估，尚需考量空間相互作用(spatial interaction)。

過去的研究，除以入侵種出現與否的二元化圖資(binary)套疊欲關注的原生種棲地或地景要素，找出兩者共存的空間區位(Kariyawasam *et al.* 2017; Santana *et al.* 2019)外，亦有計算棲位相似性指數者(Baskaran *et al.* 2016; Holt *et al.* 2018)，惟兩方法往往過於粗略，以致無從明確得知入侵影響程度與區位；Vicente *et al.* (2013)基於兩物種空間衝突條件與動態，進

一步以組合模型的方法，獲取更詳細的入侵分布與動態訊息；Alaniz *et al.* (2018)則是將兩物種棲地適宜性資料適度分級後，直接導入交集分析模型內，因而得以確立詳細的空間衝突資訊，相較於Vicente *et al.* (2013)的組合模型法，此方法可說更為快速簡便，亦成功應用於生物防治、傳染病風險評估(Alaniz *et al.* 2017; Alaniz *et al.* 2020)等領域的空間防治規劃。儘管如此，目前尚無研究針對入侵雜草適宜性與農業生產潛力的空間衝突性進行分析者，無法為氣候變遷下農業地景的入侵防治提供有力的參考資訊。

臺灣位處歐亞大陸與菲律賓海板塊的交會處，地理位置特殊，以全球的視角來看，本質上即存在高度的生物入侵風險(Pyšek *et al.* 2012; Russell *et al.* 2017)，加上地狹人稠，島內生態系無可避免地會受外來雜草的入侵威脅。根據林業試驗所建置的「台灣外來入侵種資料庫」資料顯示，目前列屬入侵植物共計76種，在未來氣候變遷的影響下，其入侵熱點將有朝向高緯度或高海拔推移的趨勢(黃及呂 2018)，至於對農業生態系的具體影響則尚不明確。有鑒於此，本研究以臺灣本島為研究區，在先前研究的基礎下(Huang *et al.* 2020)，選擇5種在氣候變遷影響下，具高侵略潛力之外來入侵雜草為研究對象，運用ENM與地理資訊系統，進行空間分析與整合，評估瞭解氣候變遷對入侵雜草適宜棲地分布的影響，以及未來可能與農業生產構成空間衝突的區位，期研究結果能提供外來入侵雜草防治之參考。

材料與方法

一、研究區概述

臺灣本島位處位於太平洋海域西側及亞洲大陸邊緣，土地面積約36,000 km²，島內人口約2,300萬人。橫跨熱帶及亞熱帶氣候，境內高溫多雨，年均溫約21°C，年雨量約2,500 mm，具適宜農作物生長之優越氣候條件，惟因地形複雜，且地理位置特殊，氣候多變，每年農作遭受氣象災害之損失亦多(Lur *et al.* 1998)。區內地形陡峭，全島面積的2/3為山地及丘陵所覆蓋，地殼被擠壓抬升而形成的山脈，南北縱貫全臺，除最高峰玉山主峰(3,952 m)外，標高3,000m以上的高山有超過300座。在農業生產方面，依據農委會農業統計資料查詢系統顯示，農耕土地面積僅約79萬ha，雖不及全島1/4，然實際上有些耕地是屬集約化耕作，一年內可種植2~3種作物(Neszmelyi 2017)。整體農業部門生產之初級產品，以及所帶動相關產業之總產值與附加價值，約占全國國內生產毛額13%(林及張 2004)。

二、研究方法

(一) 入侵雜草資料

以未來氣候變遷情境下，選擇可能持續維持高度侵略性或大幅提升侵略性入侵雜草為目標種，包含合果芋(*Syngonium podophyllum*)、落葵(*Basella alba*)、大花咸豐草(*Bidens pilosa* var. *radiata*)、美洲含羞草(*Mimosa diplotricha*)及含羞草(*Mimosa pudica*)等5種(Huang *et al.* 2020)。物種調查點位來源為林務局生態調查資料庫系統，

調查期間為1998~2008年，座標格式為經緯度，本研究僅保留3位小數之資料，並統一將格式轉換為1997臺灣大地基準座標系統(Taiwan Datum 97)及橫麥卡托二度分帶座標格式，後續所採用之相關環境資料也以此系統與格式儲存，網格基本運算單元配合取得的環境資料，設定為 1×1 km，若一個網格內有重複記錄者以單筆計算，各物種整理過後的資料筆數如表1，供後續生態棲位建模使用。

(二) 環境資料

生態棲位模式之預測變項包含氣候、地形及土地覆蓋等3類，其中，氣候類乃從Hijmans *et al.* (2005)建立的全球氣候資料庫(WorldClim)，下載專為預測物種分布所產製之19種生物氣候變項(Hijmans and Graham 2006)；地形類由內政部取得數值高程模型(海拔高)，利用ArcGIS 10.6軟體製作坡度圖資，並參考Gessler *et al.* (1995) 與McCune and Keon (2002)的方法，分別產製代表濕度的複合地形指標(compound topographic index, CTI)及太陽輻射強度的熱負荷指標(heat load index, HLI)，共計4個變項。土地覆蓋類由美國Land Processes Distributed Active Archive Center取得2000~2009年Terra-MODIS衛星影像產品「MOD13Q，增揚植生指標(enhanced vegetation index, EVI)」，進一步製作該期間最大、最小、平均、中位數、全距和標準偏差等6種圖資，相較於常態化差異植生指標(normalized difference vegetation index)，EVI對於樹冠層的變異更為敏感(Huete *et al.* 2002)，最終，累計全部預測變

項共有29個，經最近相鄰法進行重取樣後，所有變項的空間解析力為 1×1 km。

為避免變項的多重共線性，以Pearson相關分析進行預測變項篩選，當兩變項相關係數大於0.7以上者，考量研究目的、與生物的關聯性及後續容易解讀等因素擇一適當變項(Kumar and Stohlgren 2009, Padalia *et al.* 2014)。

(三) 氣候變遷情境

假設所有被採用之氣候類變項，會隨聯合國氣候變遷政府間專家委員會(Intergovernmental Panel on Climate Change, IPCC)第5次評估報告所發布之氣候變遷情境而改變，其餘變項則保持恆定，據此模擬未來入侵雜草在不同情境下之棲地適宜性。IPCC第5次評估報告以代表濃度途徑(representative concentration pathway, RCP)定義變遷情境，其中RCP 2.6和8.5各表示輻射驅動力(radiative forcing)於1750~2100年間增加了2.6及8.5 Wm^{-2} ，換言之，RCP 2.6為暖化減緩之理想情境，RCP 8.5則是暖化加劇的情境(IPCC 2013)。未來的氣候資料是由全球氣候模式(global climate model, GCM)產生，前述的WorldClim資料庫，提供2050(2041~2060年的平均值)與2070年(2061~2080年的平均值)兩種時段的氣候資料，為突顯氣候變遷的影響程度，本研究選擇2070年適用於預測台灣氣候的CESM1-CAM5、CSIRO-Mk3-6-0、GISS-E2-R與MIROC5等4個GCM(Lin and Tung 2017)，生產的資料是藉由統計降尺度產生 1×1 km解析力的生物氣候變項，供預測入侵雜草未來之棲地適宜

性，每個GCM所獲得的預測結果取平均值，以消彌不確定性(Araújo and New 2007)。

(四) 生態棲位建模

生態棲位建模是依據最大熵(maximum entropy)理論，使用Phillips *et al.* (2006)所開發的MaxEnt (3.4.1版)，預測5種入侵雜草適宜棲地，該軟件為一種機器學習演算法，至今仍受到廣泛的應用。先將物種出現點位資料集逢機選取75%做為訓練集，25%為測驗集，並於研究區內產生10,000個逢機的背景點(background points)共同運算，採用bootstrap來測試模型性能，每物種重複運算10次，最終取平均值，輸出結果設定邏輯斯概率(logistic probability)轉換，使預測值域介於0~1，愈接近1者，代表入侵雜草於該網格出現的概率愈高，愈有可能為其適宜棲地。另模型的準確性評估應用接受者操作特徵(receiver operating characteristic)所產生之曲線面積(area under the curve, AUC)，AUC值域介於0.5~1，當值愈高代表模型預測出來的準確性愈佳，而高於0.7以上則達可接受標準(Swets 1988; Pearce and Ferrier 2000)。

(五) 空間衝突性分析

針對入侵雜草之適宜棲地性，採用MaxEnt所提供的「10th percentile of training presence」，即針對一組訓練集對應的概率，取概率分布低於10%的點位做為閾值，大於閾值的像元視為適宜棲地(Pearson *et al.* 2007; Koncki and Aronson 2015)，非適宜棲地網格視為無效，而適宜棲地範圍內之概率依據等距區分為低、中

及高等3類，並將網格重新配分，即無效=0、低=1、中=2、高=3，產生4種等級之離散圖，將此劃分標準套用於未來氣候情境下之適宜棲地性預測結果，以利後續比較分析。

本研究以具生產力之耕地，做為入侵雜草空間衝突性的分析對象，耕地範圍是參考台灣的農業發展條例第3條第10款所定義之耕地：依區域計畫法劃定為特定農業區、一般農業區、山坡地保育區及森林區之農牧用地。各分區的向量圖資由內政部營建署城鄉發展分署申請，並藉由以下公式計算每一1×1 km網格內之生產價值(P)：

$$P = \sum_{i=1}^m A_i \times S_i$$

式中 A_i 為分區 i 之面積大小， m 為分區總數， S_i 為分區 i 之配分，其中，特定農業區以優良農地為主，故設定為3，一般農業區為2，山坡地保育區及森林區為1，因這兩分區非以農業生產為主要目的。將上式計算結果，等距區分為低(1)、中(2)及高(3)，非耕地範圍則視無效(0)，產生耕地生產價值等級圖(補充圖1)。

為瞭解氣候變遷下，入侵雜草與耕地生產價值的空間衝突性，參考Alaniz *et al.* (2017)的空間交集方法，各別將當前與未來兩種氣候情境(RCP 2.6和RCP 8.5)的入侵雜草棲地適宜性等級圖與耕地生產價值等級圖相乘，獲取無效(0)、非常低(1)、低(2)、中(3及4)、高 (6)與非常高(9)等6種衝突程度，其值愈高者，入侵雜草入侵的風險愈高，耕地生產受到的影響也愈大。

結果

一、模式性能與重要變數

由Pearson積差相關分析與相關係數小於0.7之門檻，可自29項環境因子中，選出年均溫(Annual mean temperature, BIO1)、平均氣溫日較差(Mean diurnal range, BIO2)、溫度季節性(Temperature seasonality, BIO4)、年降雨量(Annual precipitation, BIO12)、最暖季降雨量(Precipitation of warmest quarter, BIO18)、坡度、CTI、HLI、EVI最小值、EVI平均數、EVI標準偏差等11項做為MaxEnt模式之預測變項，以此所建立之入侵雜草ENM，其AUC介於0.74~0.91，平均值為0.84，標準偏差為0.02，模擬成效良好(表1)。

表1顯示，5種入侵雜草均以BIO1為最大貢獻量之變數，貢獻量落在49.20~69.38%之間。所有物種之前3項重要變項均為氣候因子，顯見氣候類變項，尤其溫度是驅動外來入侵雜草棲地適宜性變化的主要原因，所有物種將隨BIO1升高，提升其棲地適宜性，當BIO1介於24.4~25.2°C時，棲地適宜性可達到最高，隨後則持平或下降(補充圖2)。

二、適宜棲地範圍的變化

生態棲位模式的模擬結果(圖1)顯示，不論是當前氣候條件或未來氣候變遷情境下，均以大花咸豐草之適宜棲地分布最廣，其次為落葵。在未來兩種氣候變遷情境下，所有的物種除維持現有適宜棲地外，均將持續擴張其範圍，只是相較

RCP2.6情境，RCP8.5情境的擴張狀況更顯嚴峻。以當前適宜棲地面積為基礎，分別計算未來氣候情境下之棲地範圍變化率可以發現，當前分布最廣的大花咸豐草與落葵兩種物種升幅較小；而當前分布較為狹隘的合果芋、含羞草與美洲含羞草等3種升幅相對較高，其增幅在RCP8.5情境的情境下，均達80%以上。就擴張棲地的空間特徵而言，所有物種多為往高緯度或往高海拔方向擴張，惟在海拔的分布上似乎存在擴張侷限。

三、空間衝突性

由當前及氣候變遷情境下，入侵雜草適宜棲地與耕地生產等級的空間交集分級結果(圖2~4)可發現，所有物種在氣候變遷的影響下，與耕地產生衝突的強度與範圍皆有提升，其中較大程度增加適宜棲地的合果芋、含羞草與美洲含羞草等3種，雖在未來可能受益於新的氣候環境，提升棲地適宜性(圖1)，但新增棲地之適宜性尚不足以對耕地構成大規模的空間衝突，可能構成空間衝突的區位較侷限(圖2~4)。

當前氣候條件下，所有物種的主要衝突區位皆集中於屏東平原，而隨氣候暖化的情勢加劇，該些物種空間衝突性皆有往北伸張的趨勢，以致整個西部平原、淺山丘陵，甚至桃園台地將新增許多程度不一的衝突區位。將高度(high)與非常高度(very high)衝突兩等級，視為明顯衝突區，並就其在空間配置上的變化來看，大致呈現兩種型態，其一為：當前明顯衝突區衝突性逐漸減弱，並往高緯度大幅提升者，如合果芋、大花咸豐草、落葵等3種；其二為：當前明顯衝突區衝突性持續維持或增強，

表1. 入侵雜草生態棲位建模之參數統計

Table 1. Parameter statistics of niche modeling for invasive weed species

Species	Occurrences	AUC	SD	Contribution of the three important variables (%)					
				Variable 1		Variable 2		Variable 3	
<i>Syngonium podophyllum</i>	133	0.90	0.04	BIO1	49.20	BIO4	11.89	BIO18	11.30
<i>Basella alba</i>	618	0.81	0.02	BIO1	69.38	BIO4	13.12	BIO12	8.29
<i>Bidens pilosa</i>	1870	0.74	0.02	BIO1	67.46	BIO12	10.54	BIO4	9.59
<i>Mimosa diplotricha</i>	376	0.91	0.01	BIO1	61.73	BIO18	14.33	BIO2	9.57
<i>Mimosa pudica</i>	859	0.84	0.02	BIO1	62.93	BIO4	22.53	BIO12	6.33

AUC: area under the receiver operating characteristic curve

SD: standard deviation

僅往高緯度略為提升者，如同屬含羞草屬的美洲含羞草與含羞草等2種。

計算各物種明顯衝突區之面積與變化率(表2)，結果顯示不論當前或未來何種氣候變遷情境下，大花咸豐草與落葵兩物種，均為明顯衝突區分布面積最廣泛的物種；而相較於RCP8.5的情境，恐使5種入侵雜草分別再新增76.04~404.95%不等的明顯衝突面積，若將暖化情勢控制在RCP2.6情境，則可望將明顯衝突面積的增幅維持在20.25~215.92%。

討論

一、預測模式與重要變數

入侵雜草的潛在空間分布資訊是執行防治工作之重要依據，本研究利用氣候、地形與植被狀態等環境資料建立5種外來入侵ENM，預測結果皆達可接受標準。建模過程中所挑選的11個預測變項，有5個屬氣候

類因子，其中又以與溫度相關的變項對5種入侵雜草ENM貢獻度最高(表1)，為決定棲地適宜性的關鍵因子，此結果與許多外來入侵雜草研究的結果類似(Padalia *et al.* 2014; Wan and Wang 2019; Sintayehu *et al.* 2020)，事實上氣候狀態的改變，確實將影響入侵雜草種子萌芽、生長與繁殖等物候過程(Kathiresan *et al.* 2016; March-Salas and Pertierra 2020; Howell *et al.* 2020)，這也代表入侵雜草潛在空間分布，極可能受到氣候變異的影響，促使入侵範圍發生轉移(range shift)，讓原來未被入侵的區位遭到入侵，進而對當地的農業環境與社會經濟構成威脅(Ziska *et al.* 2011; Sintayehu *et al.* 2020)。

二、適宜棲地分布

適宜棲地將為外來植物提供適當的環境條件，有助於擴張潛在分布範圍。研究中

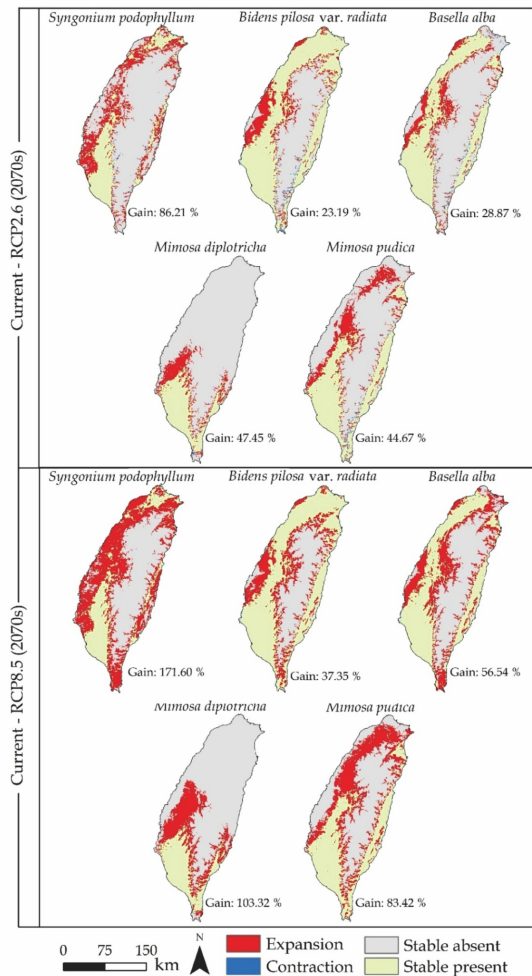


圖1. 未來氣候情境下5種入侵雜草適宜棲地的分布變化。

Fig. 1. Distribution changes of suitable habitat for five invasive weed species under future climate scenarios.

5種入侵雜草均將受益於新的氣候條件，除維持當前的適宜棲地外，亦以不同的擴張速率，持續增加未來適宜棲地範圍(圖1)。

合果芋是增幅最大的物種，概因這該物種在當前空間上的分布較為狹隘，推論未來的氣候條件，將處於有利生長與繁衍的範圍(Mortensen 1992)，因而得以大幅擴張其適宜棲地；至於大花咸豐草及落葵兩種，對溫度具有極大的耐受極限(Grubben *et al.* 1977; Reddy *et al.* 2014; Hou *et al.* 2014)，未來氣候仍將為其提供有利條件，只是可由不適宜轉為適宜棲地之區位所剩不多，以致面積增幅最少，即便如此，該兩物種無論在當前或未來均為適宜棲地分布最廣泛之物種。

從5種入侵雜草適宜棲地的空間擴張型態來看(圖1)，有朝向高緯度或高海拔擴張的趨勢，此與許多研究有一致的結果(Wasowicz *et al.* 2013; Pauchard *et al.* 2016; Shrestha and Shrestha 2019)，不過相較於緯度梯度，入侵雜草在海拔梯度上的擴張似乎進展緩慢，存在某種程度的侷限性，顯示海拔是入侵雜草擴張未來適宜棲地的限制因子，儘管氣候變遷可能加速入侵分布的進程(Petitpierre *et al.* 2016; Alexander *et al.* 2016)，但山區相形惡劣的環境條件，與短距離內迅速變化的多維環境梯度，仍將促使多數入侵雜草入侵山區的進程變緩，並在這些梯度上的某個位置，達到其分布極限(Becker *et al.* 2005)。

三、空間衝突

入侵雜草對耕地所構成的空間衝突，確實將在氣候變遷的影響下有所改變(圖2~4)，且改變的範圍或強度將無法單就適宜棲地範圍或增幅(圖1)進行推論。合果芋、大花咸豐草與落葵等3種，其主要衝突

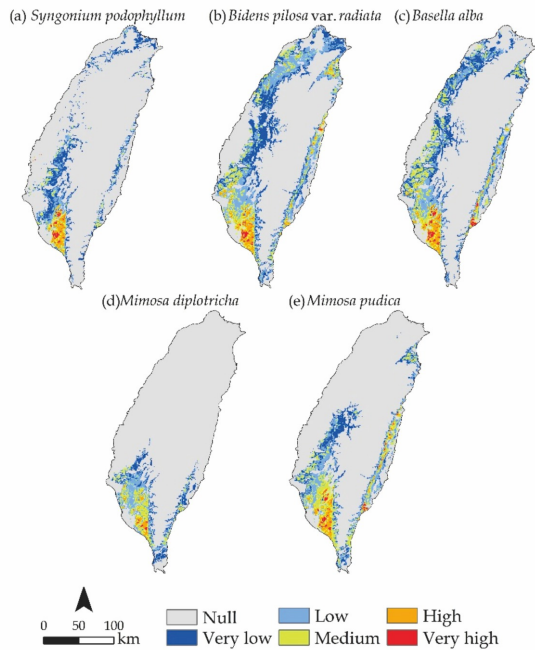


圖2. 當前氣候條件下入侵雜草對耕地產生的空間衝突性。

Fig. 2. Spatial conflicts of invasive weeds on cultivated land under current climate conditions.

區(屏東平原)之氣候條件在未來情境下，可能接近或逾越耐受極限，致衝突性稍有減弱，因此可將防治資源調控至嘉南平原等其他明顯衝突區位；相反地，美洲含羞草與含羞草兩種則在則應持續關注原明顯衝突區位。

值得一提的是，本研究係以棲地適宜性推論其空間衝突性，明顯衝突區可能存在尚未遭受入侵的極適宜棲地，在實務防治工作上，應積極防堵入侵者進駐，同時可選植親源或功能性狀相近的作物，使其優先成為優勢物種，從而成功抑制入侵者建

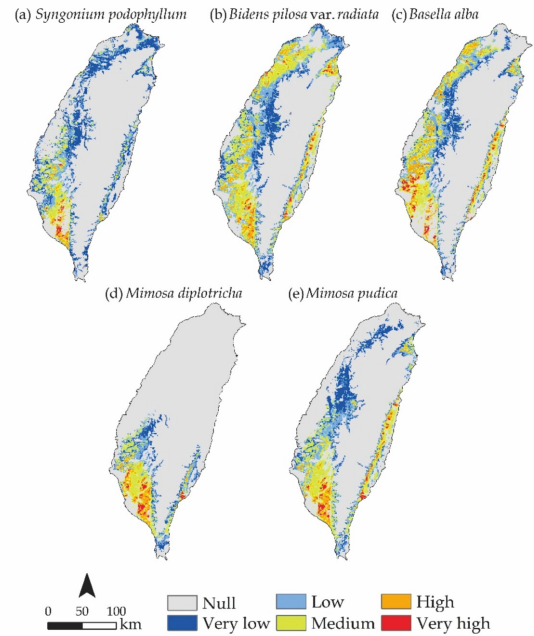


圖3. RCP2.6情境(2070年代)下入侵雜草對耕地產生的空間衝突性。

Fig. 3. Spatial conflicts of invasive weeds on cultivated land under the scenario RCP2.6 (2070s).

立群族(Emery 2007; Zheng *et al.* 2018; Fagúndez and Lema 2019)；至於已遭受入侵之區位，則儘可能將入侵者控制在已形成的範圍內，優先挹注防治資源，移除或控制景觀中連接度差的孤立或小型嵌塊體(Rohal *et al.* 2019; Eppinga *et al.* 2020)，隨後透過完善復育計畫，填補衝突區內的潛在生態棲位，重建能夠抵禦入侵的植物社會(Funk *et al.* 2008)。

四、研究方法的優勢與限制

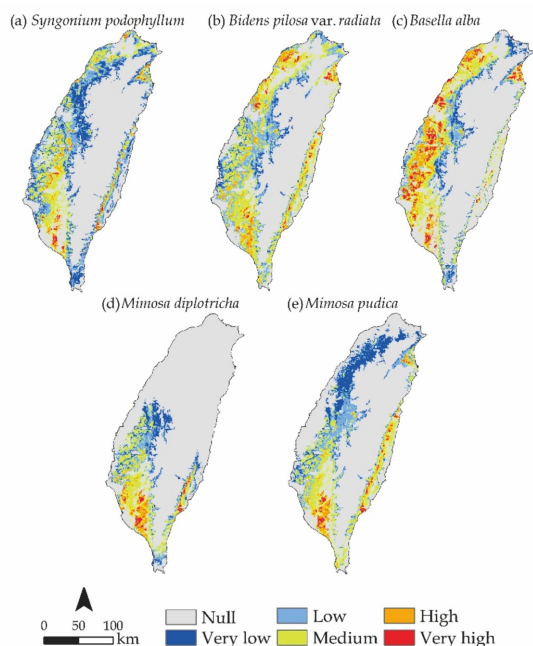


圖4. RCP8.5情境(2070年代)下入侵雜草對耕地產生的空間衝突性。

Fig. 4. Spatial conflicts of invasive weeds on cultivated land under the scenario RCP8.5 (2070s).

ENM所推導的棲地適宜性，具有物種出現機率的生態意涵，在有害生物危害或入侵風險的應用層面上，多以評估種間生態棲位匹配或重疊的研究為主(Alaniz *et al.* 2018; Naeem *et al.* 2018; Negrini *et al.* 2020)，較少著墨於對具高度功能價值土地利用的影響，尤其在農業生產系統上。本研究基於棲地適宜性與農地生產價值等級所建立的交集分析框架，可明確地提供兩衝突元素間的空間關聯訊息(圖2~4)，有助於突顯入侵雜草對具高生產價值區位的影響。儘管如此，由ENM獲取的結果未將擴散限制、生物相互作用，以及入侵雜草本身的進化潛力等生態過程納入考量，且未來氣候參數亦可能超出建模時的數據範圍，這些尚未突破的研究限制，皆可能為適宜性的推估增添不確定性(Phillips *et al.* 2006; Clements and Ditommaso 2011; Srivastava *et al.* 2019)，但研究架構至少可具體指出未來可能遭受入侵並構成威脅的位置與程度，得以作為防治優先性規劃的

表2. 氣候變遷情境下，5種入侵雜草與耕地產生明顯衝突之範圍變化

Table 2. Predicted range changes of conspicuous conflict for invasive weeds and cultivated land based on scenario RCP 2.6 and RCP 8.5, respectively

Species	Current	RCP 2.6 (2070s)		RCP 8.5 (2070s)	
	Range	Range	Change (%)	Range	Change (%)
<i>Syngonium podophyllum</i>	647	778	20.25	1,408	117.62
<i>Basella alba</i>	1,110	2,507	215.92	3,730	404.95
<i>Bidens pilosa</i> var. <i>radiata</i>	1,130	2,068	144.98	2,295	180.06
<i>Mimosa diplotricha</i>	366	1,236	134.47	1,302	144.67
<i>Mimosa pudica</i>	954	1,493	83.31	1,446	76.04

Range: Number of grid cells (1 km resolution) for high and very high levels

參考資訊，從而提高入侵防治的成本效益。

結論

本研究是台灣首次針對入侵雜草對農業生產的潛在空間衝突性進行評估，主要結果發現，氣候變暖情境下，所探討的5種入侵雜草未來的適宜棲地範圍皆會擴增，然就衝突強度來說，當前合果芋、大花咸豐草與落葵等3種之明顯衝突區，在未來可能轉移至較高緯度的耕地；而美洲含羞草與含羞草等2種，雖適宜棲地有往北擴張的趨勢，但適宜性尚不足以對耕地構成明顯衝突，未來明顯衝突區仍將維持在當前區位。因此，有關因應氣候變遷的防治策略，建議無論是當前或未來可能發生的高衝突地區，都有必要做進一步的控制與監測。

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**A newly recorded species of *Cheiracanthium* C. L. Koch,
1839 (Araneae, Cheiracanthiidae) from Taiwan**

臺灣產紅螯蛛屬蜘蛛之新紀錄種

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Abstract

This paper provides a morphological description of a newly recorded species from Taiwan, *Cheiracanthium insigne* O. Pickard-Cambridge, 1874, based on newly collected materials. Both male and female *C. insigne* specimens are analysed, redescribed, and photographed. We applied DNA barcoding validation for matching sexes and reviewed taxonomic issues of *C. insigne* with other related species. The results of maximum likelihood tree and Kimura two-parameter genetic distance confirm the correct matching of male and female *C. insigne* specimens from Taiwan (mean intraspecific distance as 1.15%). In addition, the phylogenetic analysis suggests that previous female specimens of *Cheiracanthium triviale* from Assam, India, could potentially be conspecific to *C. insigne* from Taiwan.

Key words: *Cheiracanthium insigne*; Cheiracanthiidae; new record; Taiwan

摘要

本報告依新採集標本及形態檢視，報告台灣產紅螯蛛屬蜘蛛之新紀錄種－短突紅螯蛛 (*Cheiracanthium insigne* O. Pickard-Cambridge, 1874)。雌、雄性皆重新描述及拍攝，同時運用基因條碼驗證本種正確之性別配對，並回顧與近緣種的分類問題。由maximum likelihood親緣關係樹及以K2P model計算之遺傳距離結果(平均種內遺傳距離為1.15%)皆驗證台灣產短突紅螯蛛的雌雄配對之正確性，並支持在過去研究中採集於印度阿薩姆的平庸紅螯蛛(*C. triviale*)雌蛛樣本應屬於本種。

關鍵詞：短突紅螯蛛、紅螯蛛科、新紀錄、台灣

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Introduction

Cheiracanthium C. L. Koch, 1839, the long-legged sac spiders, is the largest genus

of Cheiracanthiidae Wagner, 1887 and distributed worldwide (World Spider Catalog 2020). They are small to medium-sized spiders and generally yellowish in body

coloration. Long-legged sac spiders can be identified by the following characters: the leg I is conspicuously the longest, the male palp with well-developed papal tibial apophysis and distinctive backward-direction basal retrolateral spur on the cymbium, and the female epigyne with a central or posterior depression (Chen and Huang 2012).

To date, there are 218 valid species of the genus *Cheiracanthium* reported globally. However, the actual diversity of the genus remains unclear, and several new species from Asia were described recently (Barrion *et al.* 2013; Wang and Zhang 2013; Marusik and Fomichev 2016; Zhang *et al.* 2018; Li and Zhang 2019; Zhang *et al.* 2020). Yaginuma (1970) first noted *C. lascivum* Karsch, 1879 in Taiwan. A total of nine valid species of long-legged sac spiders have been reported successively (Chen and Huang 2004; Chen *et al.* 2006; Chen and Huang 2012). Recently, a newly recorded species, *Cheiracanthium insigne* O. Pickard-Cambridge, 1874, was discovered in Taiwan. The male *C. insigne* is distinguishable from congeneric species using the structure of palp organs, which have extremely well-developed tegular flanges. However, the identification of female is still unconfirmed.

The morphology of female *C. insigne* was first reported by O. Pickard-Cambridge

(1874) in India, then later noted in another study using samples from Myanmar (Gravely 1931). However, the delineation of epigyne was conspicuously inconsistent. Dankittipakul and Beccaloni (2012) examined the holotype of *C. truncatum* and supposed that the specimen of *C. insigne* examined by Gravely (1931) was actually *C. truncatum* because they could not find distinct differences between female genitalia of these two species. Therefore, the problem of female *C. insigne* identification remained unsolved. Due to cryptic habitat and the resembling appearances of *Cheiracanthium* species, to affirm correct sex-match is one of the challenges for taxonomic studies on the genus. For example, almost half of *Cheiracanthium* species are described from single sex: 38 species from males and 59 species from females (World Spider Catalog 2020). Therefore, the application of the molecular tools such as DNA barcoding is valuable for correct sex matching.

Hebert *et al.* (2003) proposed the common use of cytochrome c oxidase subunit 1 (*COI*) sequences on the mitochondrial gene in DNA barcoding techniques, which enable species identification in most animal phyla. The application of *COI* barcodes has been widely adapted in various animal groups and research purposes (Kress *et al.* 2015), such as species-level identification in immature

stages of rolled-leaf beetles (Garcia-Robledo *et al.* 2013), species identification in illegal trades or highly processed animal materials (Gonçalves *et al.* 2015; Janjua *et al.* 2017), the solution to certain taxonomic issues or the discovery of cryptic butterfly species (Hebert 2004), diet analysis for the ocean sunfish (Sousa *et al.* 2016), and the delimitation of species boundaries in Acridoidea (Huang *et al.* 2013). Similarly, DNA barcoding of spiders has been commonly used in taxonomic studies and relevant research in species identification or delimitation (Barrett and Hebert 2005; Candek and Kuntner 2015; Xu *et al.* 2015; Cao *et al.* 2016; Coddington *et al.* 2016). As morphological variation of spiders can be dependent on sex and life history stages, DNA barcode approach is effective to match sexes, life stages, or distinguish species with similar morphologies, which has been successfully used to rectify a previously mismatched male specimen in *Micrathena* genus in Brazil (Robinson *et al.* 2009; De Alvarenga *et al.* 2020). Also, it has ably overcome extent challenges of taxonomic and phylogenetic obstacles (Blagoev *et al.* 2016; Breitling 2019). Thus, the efficacy of DNA barcoding analysis illustrated its usefulness to correctly match sexes and identify species even if there was a lack of information on diagnostic features for one

sex or with few specimens available.

This study adds a new record of spider *Cheiracanthium insigne* for the Taiwanese spider fauna using both male and female specimens, assessed by morphological characteristics and through *COI* gene-based DNA barcoding validation to match sexes.

Materials and Methods

Sample collection and morphological examination

Specimens were preserved in 75% ethanol and deposited in the collection of Taiwan Endemic Species Research Institute (TESRI). The selected specimens were dissected to examine the palpal organs of the males and the epigyne of the females. To dissect the genital organs of the females, epigyna and inner genital structures were cleaned in the protein removal solution. Photographs were taken with a digital camera (Nikon D850), using a stereo microscope (Leica M125). For each specimen, Helicon Focus version 6 (Helicon Soft Ltd) was used for focus stacking. Scale bars were labeled on the digital images using ImageJ version 1.52k (National Institutes of Health) and Photoshop version 19.1.2 (Adobe Systems Corporation). All measurements of morphological structures were given in millimeters (mm), obtained by

a micrometer mounted on the eyepiece of the stereo microscope. The measurements of the pedipalp and leg were given as the total length (pedipalp: femur, patella, tibia, and tarsus lengths; leg: femur, patella, tibia, metatarsus, and tarsus lengths). Abbreviations addressed in this paper include: **A**, atrium; **AER**, anterior eye row; **ALE**, anterior lateral eye; **AME**, anterior median eye; **AW**, anterior width of MOA; **C**, conductor; **CD**, copulatory duct; **CS**, cymbial spur; **E**, Embolus; **MOA**, median ocular area; **MOA-L**, length of MOA; **PER**, posterior eye row; **PLE**, posterior lateral eye; **PME**, posterior median eye; **PW**, posterior width of MOA; **RTA**, retrolateral tibial apophysis; **S**, spermatheca; **TF**, tegular flange.

DNA extraction, PCR amplification, and sequencing

Tissues collected from one to four legs of the specimens were preserved in 95% ethanol and deposited in -20°C refrigerator until DNA extraction. DNA barcodes were subsequently obtained for molecular analyses and sex matching of conspecific. The partial cytochrome c oxidase subunit I gene (*COI*) was amplified using the primer pairs of LCO 1490 (Folmer *et al.* 1994) and Chelicerate R2 (Barrett and Hebert 2005). The polymerase chain reaction (PCR)

protocol was as follows: initial denaturation at 95 °C for 5 min; 35 cycles of denaturation at 95 °C for 30 sec, annealing at 45 °C for 30 sec, and elongation at 72 °C for 40 sec; and a final extension at 72 °C for 5 min. The 25-μL PCR reactions included 9.5 μL of double-distilled H₂O, 1 μL of each forward and reverse primer (10 μM), 1 μL of DNA template, and 12.5 μL *Taq* DNA Polymerase 2× Master Mix RED (with 1.5 mM MgCl₂ final concentration; Ampliqon, Herlev, Denmark). The PCR products were visualized by agarose gel electrophoresis (1% agarose). PCR products were sequenced by Genomics BioSci & Tech. Co., Ltd. (New Taipei City, Taiwan) using an ABI 3730xl DNA Analyzer.

Molecular data analysis and phylogenetic inference

The DNA sequences were trimmed and edited by Sequencher v.5.4.5 (DNA sequence analysis software, Gene Codes Corporation), then aligned with ClustalW in BioEdit v.7.0.5.3 (Hall 1999). For molecular analysis, the *COI* sequences of a closely related species, *Cheiracanthium triviale* (Thorell, 1895), were downloaded from GenBank (Benson *et al.* 2012) which were provided in Tyagi *et al.* (2019, 2020) as its epigynal characters were similar to *C. insigne* based on preliminary specimen

examination. To identify haplotypes and polymorphic sites, DnaSP v.6.12 (Rozas *et al.* 2017) was utilized, and the pairwise genetic distances (Kimura two-parameter [K2P]) were calculated using MEGA 7 (Kumar *et al.* 2016) to assess the genetic differences. Phylogenetic tree was reconstructed using maximum likelihood (ML) with GTR+G model, which was determined as the best-fit nucleotide substitution model using jModelTest v.2.1.7 (Darriba *et al.* 2012) under the Bayesian information criterion (BIC). Maximum likelihood analysis was conducted in RAxML v.8.2.10 (Stamatakis 2006), and the robustness was evaluated by 1000 bootstrap pseudo replicates. Ultimately, the obtained phylogenetic tree was visualized and edited using FigTree v.1.4.4 (Rambaut 2018) and Illustrator version 22.1 (Adobe Systems Corporation, San Jose, CA, USA).

Results

Taxonomy

Cheiracanthium insigne O. Pickard-Cambridge, 1874

(Figures 1–2)

Cheiracanthium insigne O. Pickard-Cambridge 1874: 408, Pl. 52, fig. 32; Gravel 1931: 266, fig. 17L; Tikader and Biswas 1981: 70, Pl. IX, fig. 122; Chen

and Zhang 1991: 252, fig. 264; Majumder and Tikader 1991: 60, fig. 113-116; Song, Zhu and Chen 1999: 413, fig. 243K-L; Dankittipakul and Beccaloni 2012: fig. 1, 3-7; Dhali *et al.* 2017: fig. 190-195.

Eutittha gracilipes Thorell, 1895: 47.

Examined Materials. All specimens were obtained from Taiwan. **Chiayi County:** one female (TESRI-LT047), Lantan Trail, 2018-03-17, Ying-Yuan Lo leg. **Kaohsiung City:** one female (TESRI-C020126), Shoushan National Nature Park, 2017-06-10, one male (TESRI-C020159), Shoushan National Nature Park, 2017-08-12, one female (TESRI-C020171), Shoushan National Nature Park, 2017-11-04, one male (TESRI-C030145), Shoushan National Nature Park, 2017-08-04, one male (TESRI-CS031), Shoushan National Nature Park, 2018-08-03, Guo-Yuan Wu leg. **Yilan County:** one male (TESRI-Ar4714), North Guanyin Tunnel Entrance, 2020-03-02, Chi Wei leg.; one female (TESRI-Ar4722), Dongyue, 2020-03-03, Chi Wei leg. **Taitung County:** one male (TESRI-Ar2540), 2017-09-20, Fuyuan Village, Ying-Yuan Lo leg. (Figure 3).

Diagnosis. *Cheiracanthium insigne* can be distinguished from other congeneric

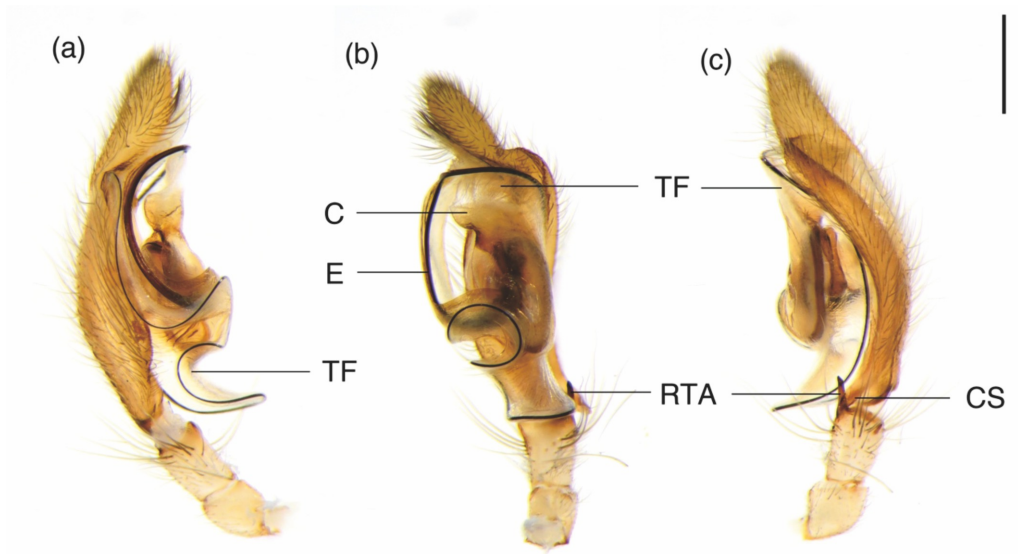


Fig. 1. *Cheiracanthium insigne*, male (TESRI-C030145). (a)–(c) are prolateral, ventral, and retrolateral views of palp organ, respectively. Scale bar: 0.5mm.

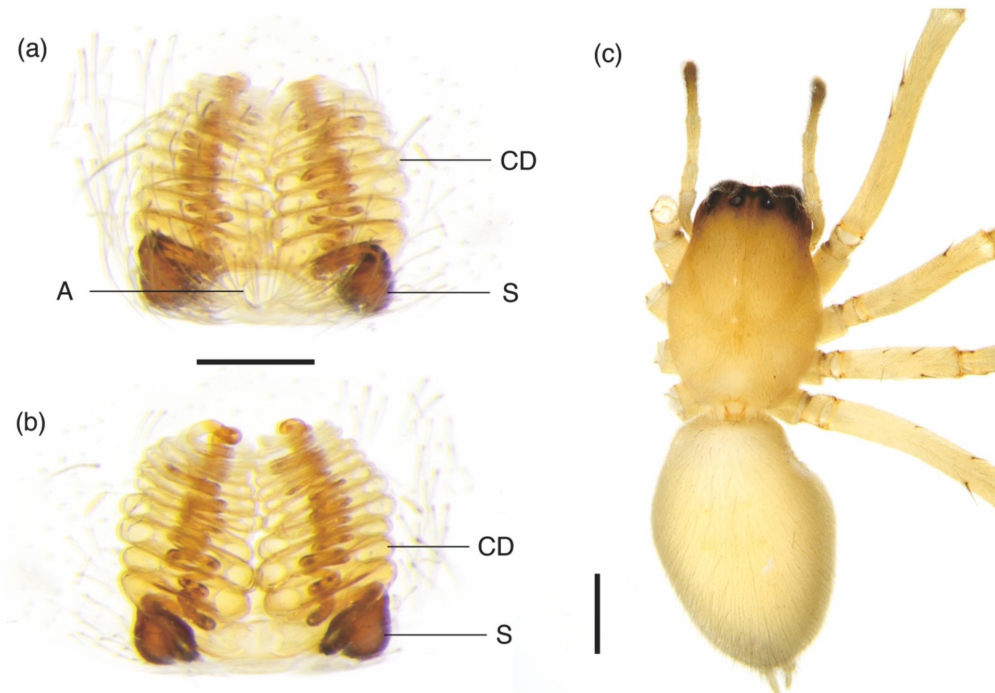


Fig. 2. *Cheiracanthium insigne*, female (TESRI-C020171). (a)–(b), ventral and dorsal view of epigynum. (c) dorsal view of appearance. Scale bars: (a)–(b) 0.2mm; (c) 1.0mm.

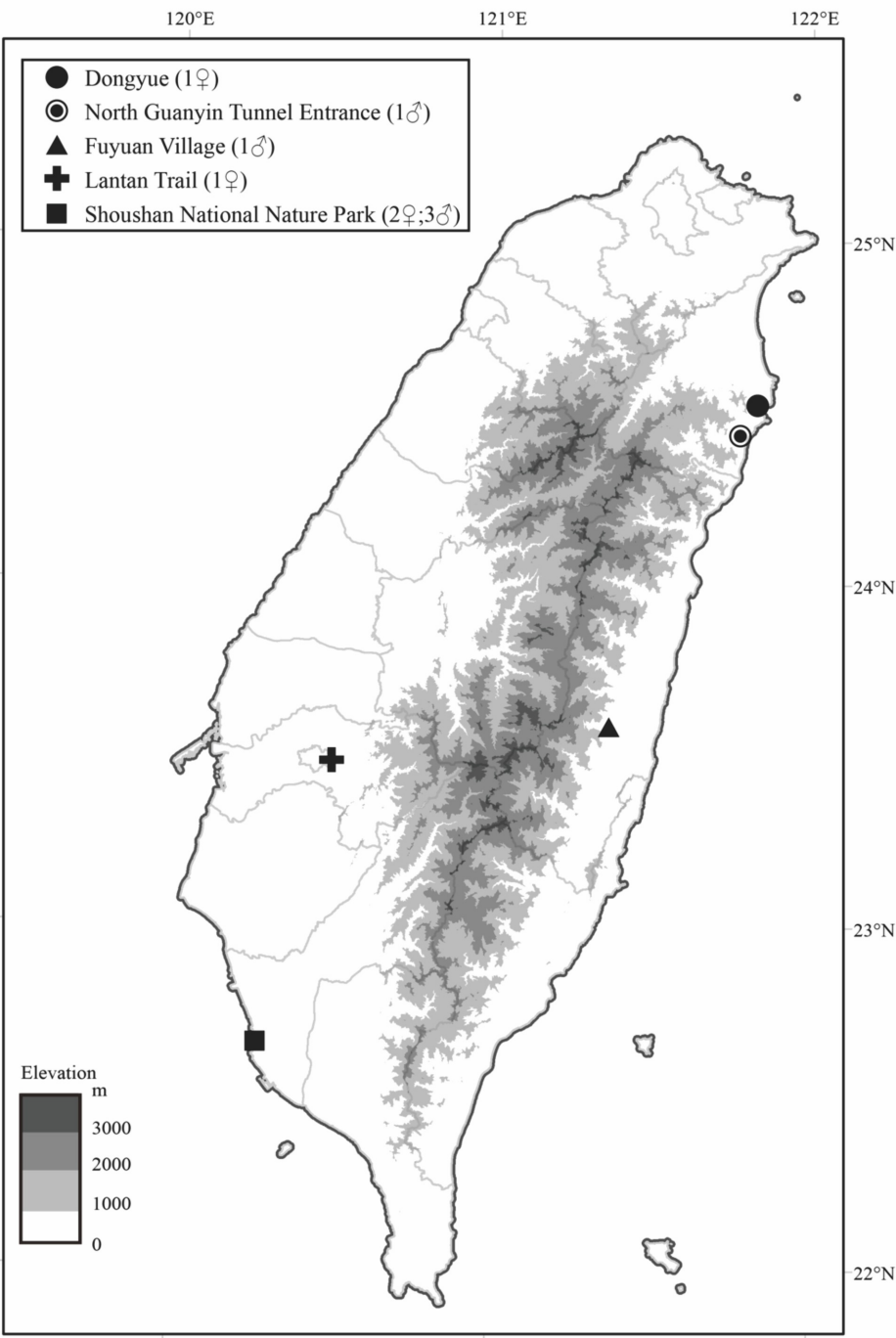


Fig. 3. Collection localities of *Cheiracanthium insigne* from Taiwan in the present study.

species by the following characteristics: (1) tegular with enormously developed and semi-transparent flange on the bulb; (2) embolus long and curved along with tegular flange; (3) basal retrolateral cymbial spur is rudimentary; (4) epigyne with a pair of elongated and entwined copulatory ducts on the anterior of spherical spermathecae.

Description. *Male* (TESRI-C030145).

Total length 5.0; carapace length 2.5, width 1.8; abdomen length 2.5, width 1.4. Carapace yellowish with indistinct cervical and radical grooves. Ocular area light brown, eight eyes are arranged in two rows with AER slightly procurved and PER straight. Eye diameters and inter-distances (mm): AME = ALE = PME = PLE = 0.16; MOA-L 0.36, MOA-AW 0.40, MOA-PW 0.52; AME-I 0.14, PME-I 0.20, AML-I 0.10, PML-I 0.12; clypeus height 0.10. Chelicera light brown, with three promarginal teeth and three retromarginal teeth; endite longer than wide, and labium equal in length and width. Sternum yellowish and posterior margin slightly convex. Pedipalps and legs yellowish; the third and fourth posterior metatarsus bear a coarser, distal curve spine on the ventral side. Measurements of pedipalps and legs (mm): Measurements of pedipalps and legs (mm): palp 4.0 (1.3, 0.4, 0.4, 1.9), leg I 15.6 (3.7, 1.1, 4.2, 4.6, 2.0),

leg II 9.6 (2.6, 0.9, 2.5, 2.7, 0.9), leg III 7.1 (1.7, 0.8, 1.6, 2.3, 0.7), leg IV 10.6 (2.6, 1.0, 2.7, 3.4, 0.9). Leg formula: I > IV > II > III. Abdomen yellowish and elongate-oval. Palp with a straight retrolateral tibia apophysis. Cymbium folded obviously in ventral and retrolateral view, and basal retrolateral cymbial spur indistinct. Tegulum with a well-developed, conspicuous, and translucent membranous flange. Tegulum apophysis absent. Embolus slender, curved, and elongated along the margin of the tegulum flange (Figure 2).

Female (TESRI-C020171). Total length 5.2; carapace length 2.7, width 1.9; abdomen length 3.5, width 2.3. Carapace yellowish with indistinct cervical and radical grooves. Ocular area dark brown, eight eyes are arranged in two rows with AER slight procure and PER. Eye diameters and inter-distances (mm): AME = ALE = PME = PLE = 0.14; MOA-L 0.34, MOA-AW 0.48, MOA-PW 0.56; AME-I 0.16, PME-I 0.28, AML-I 0.18, PML-I 0.28; clypeus height 0.06. Chelicera dark brown, with three promarginal teeth and three retromarginal teeth; endite longer than wide, and labium equal in length and width. Sternum yellowish and the posterior margin slightly convex. Pedipalps and legs yellowish. Measurements of pedipalps and legs (mm): Measurements of pedipalps and legs (mm): palp 3.2 (1.1,

0.4, 0.6, 1.1), leg I 12.6 (3.2, 1.1, 3.3, 3.5, 1.5), leg II 7.8 (2.2, 0.9, 1.9, 2.1, 0.7), leg III 6.0 (1.6, 0.8, 1.3, 1.7, 0.6), leg IV 9.2 (2.5, 0.9, 2.3, 2.7, 0.8). Leg formula: I > IV > II > III. Abdomen yellowish and elongate-oval. Epigyne with an oval-shaped atrium. Spermatheca and copulatory ducts are visible through the cuticle. A pair of copulatory ducts elongated and entwined in ten loops, and situated anteriorly to round spermatheca (Figure 3).

Distribution. China, India, Laos, Myanmar, Sri Lanka, Thailand, Taiwan (new record).

DNA Barcode

The barcode dataset in this study contains 37 sequences of five putative species in genus *Cheiracanthium*, including *C. eutittha*, *C. insigne*, *C. falcatum*, *C. insulanum* and *C. taiwanicum*, which were obtained from Taiwan; *C. triviale* and three outgroups were acquired from open data source (Appendix 1). The *COI* database contains 573 base pairs (bp) with 168 variable sites, 126 parsimony informative sites, and 28 haplotypes.

The Maximum likelihood phylogenic tree agreed with our previous assumption that our collected male and female

Table 1. The COI divergence with K2P genetic distances of *Cheiracanthium*. N means sample size. Intraspecific genetic distances are shown as: percentage of mean distance (range of distance). Within the matrix of pairwise interspecific genetic distances, lower left indicates mean distance and upper right indicates the range of distance

Species	N	Intraspecific genetic		Interspecific genetic distance (%)					
		distance (%)		<i>C. insigne</i>	<i>C. eutittha</i>	<i>C. falcatum</i>	<i>C. insulanum</i>	<i>C. taiwanicum</i>	<i>C. triviale</i>
<i>C. insigne</i>	9	1.15 (0.00–1.43)		–	13.40–15.10	11.02–11.48	10.78–13.15	7.91–9.22	0.71–4.67
<i>C. eutittha</i>	4	1.49 (0.53–2.17)		14.03	–	6.86–7.70	10.10–11.48	11.04–12.43	13.88–15.36
<i>C. falcatum</i>	2	0.18		10.40	7.22	–	9.22–11.01	9.47–10.13	11.49–12.89
<i>C. insulanum</i>	5	1.15 (0.18–2.00)		12.01	10.84	11.19	–	10.11–11.94	11.24–14.11
<i>C. taiwanicum</i>	7	0.33 (0.00–0.71)		8.52	11.71	9.83	11.18	–	8.34–9.88
<i>C. triviale</i>	7	1.95 (0.00–4.09)		3.32	14.67	12.37	13.01	9.28	–

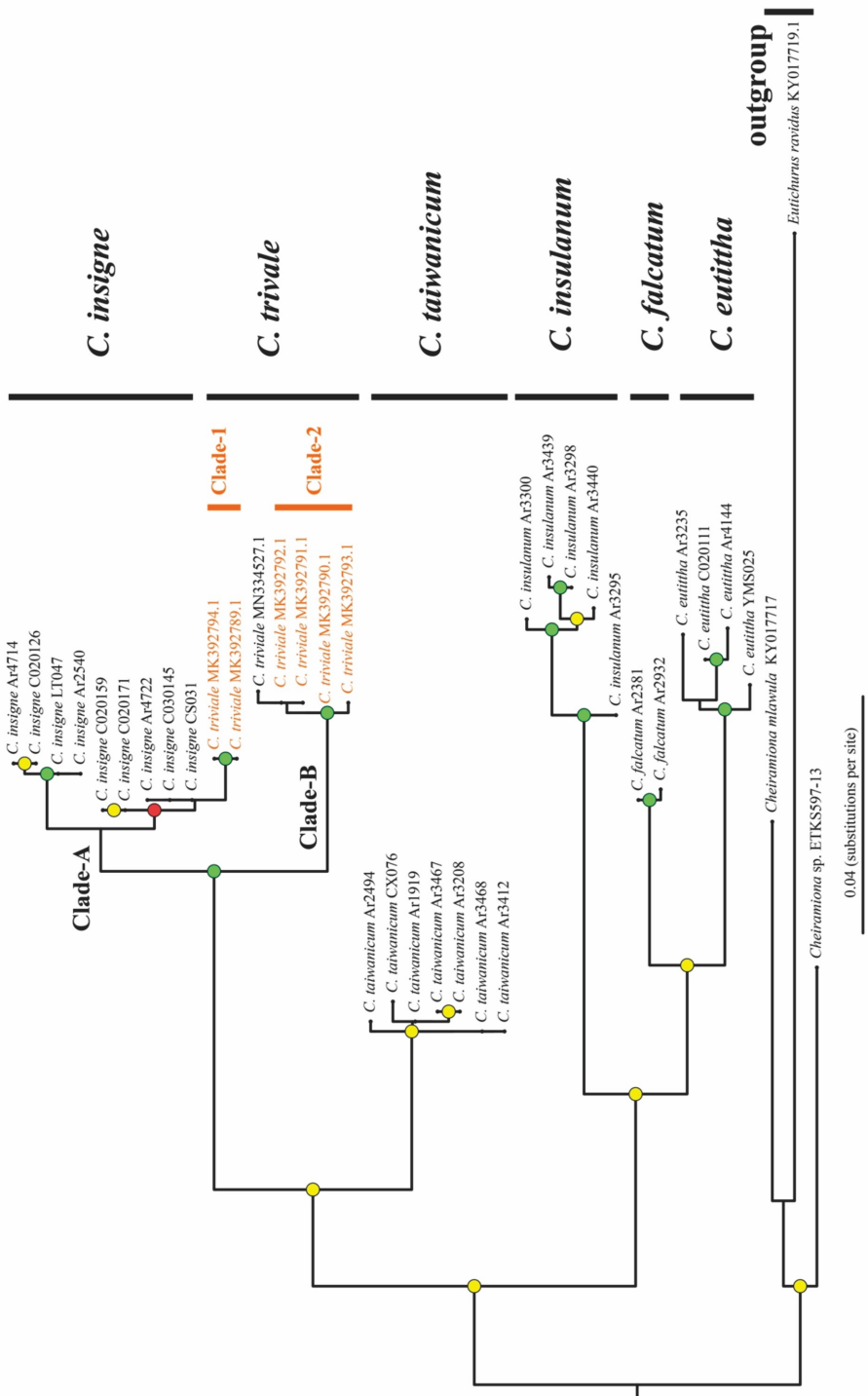


Fig. 4. Maximum likelihood (ML) phylogenetic tree of genus *Cheiracanthium* and outgroups based on the COI dataset. Colored circles at the nodes represent the bootstrap values with different levels of support: > 50% (red), >70% (yellow), and >90% (green). Organ color tips were samples collected from India that were separated into two distinct clades: clade-1 (Assam) and clade-2 (Gujarat) in Tyagi *et al.* (2019).

specimens, which we assumed as *C. insigne* from Taiwan, are conspecific. Moreover, the topology indicated that *C. insigne* and *C. triviale* belong to one clade with a high support value (bootstrap value = 100), which contains two main subclades: clade-A comprises *C. insigne* and two *C. triviale* samples, and clade-B comprises the remaining *C. triviale* samples. The mean intraspecific and interspecific *COI* genetic distances of *Cheiracanthium* in the present dataset are 0.33%–1.95% and 3.32%–14.67%, respectively (Table 1). Almost minimum interspecific distance is much greater than maximum intraspecific distance for all species. However, the mean interspecific distance between *C. insigne* and *C. triviale* is relatively lower (3.32%, ranging from 0.71%–4.67%).

Discussion

Although the male *Cheiracanthium insigne* has been reported several times and can be distinguished from other congeneric species, the identification of female remains problematic (Dankittipakul and Beccaloni 2012). According to the examined samples and barcoding information, we clarified the identification of female *Cheiracanthium insigne*. The features of female genitalia organ of *C. insigne*, with a pair of spiral and

entwisted insemination ducts on the anterior of spherical spermathecae, are incongruent with which was delineated by Gravely (1931), but fairly similar to that of *C. triviale* and *C. rupicola* (Gravely 1931; Dankittipakul and Beccaloni 2012; Liu *et al.* 2019; Tyagi *et al.* 2019). Contrary to *C. insigne*, there were only two reports which examined both sexes of *C. triviale* simultaneously (Gravely 1931; Majumder and Tikader 1991). Dankittipakul and Beccaloni (2012) examined both specimen types of female *C. triviale* and female *C. rupicola*, suggesting that *C. triviale* can be distinguished by insemination ducts with ten entwisted loops and epigynal atrium with clearly defined elongate-oval aperture, whereas insemination ducts with seven entwisted loops and poorly defined epigynal aperture in *C. rupicola*. They also proposed that the “Himalaya” form of female *C. triviale*, formerly illustrated by Gravely (1931), was *C. rupicola*. However, the female *C. insigne* was not examined in the report.

Tyagi *et al.* (2019) analyzed DNA barcoding of spiders from India and found that *C. triviale* could be separated into two distinct clades: clade-1 specimens (two females) from Assam and clade-2 specimens (four females) from Gujarat, India. In this study, we used the same sequences of *C.*

trivale and combined with the dataset of *Cheiracanthium* species from Taiwan. The ML tree shows that *C. insigne* and *C. trivale* belong to one clade with two subclades: clade-A comprises *C. insigne* and *C. trivale* samples from Assam, and clade-B comprises *C. trivale* samples from Gujarat (Figure 4). The mean genetic distance between these two subclades is 4.11%, which is much greater than the mean genetic distance within each subclade (0.91% in clade-A and 0.25% in clade-B). Our results agree with Tyagi *et al.* (2019) that *C. trivale* from two regions of India present a clear genetic differentiation, which was defined as two molecular operational taxonomic units (MOTUs) based on multiple species delimitation methods. Accordingly, we suspect that the previously collected specimens of *C. trivale* from Assam are conspecific to *C. insigne* from Taiwan; however, the original samples from Assam would be required for further confirmation of species determination.

On the other hand, both male *C. insigne* and *C. trivale* bear well-developed membranous tegular flange on the palpal organs, but male *C. insigne* can be differentiated by the former with downward elongate membranous flange and narrower anterior cymbium (Majumder and Tikader, 1991). Though male *C. insigne* is distinguishable with congeneric species, the

identification of female has been problematic for decades. This study examined both sex specimens of *C. insigne* and applied DNA barcoding information to correct sex matching for the first time, and highlighting the significance of integrated morphological and molecular information for further taxonomic research in *Cheiracanthium* species.

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